

Table S2. Details regarding 1133 transcription factor genes selected for large-scale mining and genotyping of SNP alleles and genetic association analysis using agarose gel-based EcoTILLING assay in chickpea.

SNP IDs	Kabuli/desi accession IDs	gene	Kabuli/desi chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0001	Ca_00075		<i>Ca_Kabuli_Ch01</i>	[C/T]	644318	CDS_NON_SYNONYMOUS	Protein of unknown function DUF639	CCTCACTTCATTTCAAAGGTTCT	GGATGTCCTCTCTAAGGCAGTTA	NA
SNP0002	Ca_00186		<i>Ca_Kabuli_Ch01</i>	[G/A]	1533723	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GCAAGTTCCTAGAAATTGTTCTGT	GTTCTCTCTCAAGAACATTCACTT	NA
SNP0003	Ca_00224		<i>Ca_Kabuli_Ch01</i>	[C/A]	1783923	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	GTCTTTTATTCCAAAGCTGCAAG	TATTCGTGTAACCGAACAAAGATG	NA
SNP0004	Ca_00244		<i>Ca_Kabuli_Ch01</i>	[A/G]	1962876	CDS_NON_SYNONYMOUS	Transcriptional factor B3	TCCTTCATATATAGGATGCGATT	CTAAATGGCTTCAACCTACAACCT	NA
SNP0005	Ca_00274		<i>Ca_Kabuli_Ch01</i>	[T/C]	2188472	CDS_NON_SYNONYMOUS	SNF2-related	AGAGTGAAAGGAGAGAAAAGGTGA	CTCTGTCTATGGCTTGATCTTCAG	NA
SNP0006	Ca_00347		<i>Ca_Kabuli_Ch01</i>	[G/T]	2832939	CDS_NON_SYNONYMOUS	Transcriptional factor B3	ATCTCAGGTTCAAACCTTAACCAC	AGGAAATATCAGAATGCCACAAGT	NA
SNP0007	Ca_00512		<i>Ca_Kabuli_Ch01</i>	[G/C]	4302669	CDS_NON_SYNONYMOUS	Zinc finger, CCHC-type	GTTGCATATGCTTGAAATCTCTTG	CTTTGATTGTGACAACTCACTG	NA
SNP0008	Ca_00562		<i>Ca_Kabuli_Ch01</i>	[C/T]	4780330	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	GTCCAAGGGACATTATTCAAAAAC	CAAGAGGTCTCTAGGAGGAAAA	NA
SNP0009	Ca_00613		<i>Ca_Kabuli_Ch01</i>	[G/A]	5249839	CDS_NON_SYNONYMOUS	Protein of unknown function DUF584	AAGTGCTTCACGTCATGATTGTAT	TGAGTTGGACTCTCTCAGACAAG	NA
SNP0010	Ca_00628		<i>Ca_Kabuli_Ch01</i>	[G/A]	5430809	CDS_NON_SYNONYMOUS	Protein of unknown function DUF584	ATGTTTCATTGGGTTCTCTCTTC	TCACCTGAACAAACAGAAAGACAC	NA
SNP0011	Ca_00656		<i>Ca_Kabuli_Ch01</i>	[C/A]	5666217	CDS_NON_SYNONYMOUS	DNA-binding WRKY	TGGTACTATCTCCGTGTTTCA	AGTTCGAAACAGTCAGTTTCT	NA
SNP0012	Ca_07932		<i>Ca_Kabuli_Ch01</i>	[A/G]	6679329	CDS_NON_SYNONYMOUS	WD40 repeat	TTTTAGAGACCACCTCAACAAGTG	TGGAATGACTCTGTCATAGCTGTT	NA
SNP0013	Ca_07963		<i>Ca_Kabuli_Ch01</i>	[G/T]	6952382	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1296	TGAAGTGACAGCAACATAACAAG	ATACTTACCCCTCCCTGTCACACA	NA
SNP0014	Ca_07989		<i>Ca_Kabuli_Ch01</i>	[T/A]	7325164	CDS_NON_SYNONYMOUS	WD40 repeat	GCACCGCTCAAGACAATAATAATA	AAACAACTCACACTACACCAAGAA	NA
SNP0015	Ca_08067		<i>Ca_Kabuli_Ch01</i>	[T/C]	8192580	CDS_NON_SYNONYMOUS	Zinc finger, CCHC-type	TTACATAGCTGTGCTTGGTCATT	AGGTCATTATCTCGGATTGTAA	NA
SNP0016	Ca_02909		<i>Ca_Kabuli_Ch01</i>	[T/C]	8942131	CDS_NON_SYNONYMOUS	Zinc finger, UBP-type	ATCTTTTGAAAGAGACATCCCAAC	TCGAAGAGAGGTATGCTTTATCC	NA
SNP0017	Ca_02625		<i>Ca_Kabuli_Ch01</i>	[C/A]	11285291	CDS_NON_SYNONYMOUS	Transcription factor GRAS	AGCATCCAGTTGTTATCTTCATCA	AACTCAGCTTTTACTGGTTTGG	NA
SNP0018	Ca_02472		<i>Ca_Kabuli_Ch01</i>	[G/T]	12794147	CDS_NON_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	TTCTGTGAAACAGTTAAAACTCCTC	CTTAAAGGAAAGTGATTAGGTGGT	NA
SNP0019	Ca_02459		<i>Ca_Kabuli_Ch01</i>	[G/A]	12875506	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	CGGATCAACAAACATAAACAACTC	CACAAAACCTCTCACTCCCTATT	NA
SNP0020	Ca_14071		<i>Ca_Kabuli_Ch01</i>	[G/A]	13076695	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TGACGAATCAATAGAAGAAGCTGC	TAGTCGGGAAGGCCATTACTAT	NA
SNP0021	Ca_14138		<i>Ca_Kabuli_Ch01</i>	[C/A]	13762410	CDS_NON_SYNONYMOUS	SET domain	CTTATATTTGAGACGGAGGGAGT	CAGAACTCCACACAAAATCATC	NA
SNP0022	Ca_06945		<i>Ca_Kabuli_Ch01</i>	[A/C]	16061536	CDS_NON_SYNONYMOUS	BTB/Kelch-associated	TATCAACTACCCACCAAAAGGATT	AGTTGATTTTGGGTTTGCTCTAGT	NA
SNP0023	Ca_22780		<i>Ca_Kabuli_Ch01</i>	[A/G]	17314911	CDS_NON_SYNONYMOUS	WD40 repeat	CTTCCATATCTGTTCAAGCCTTTT	CTATCTCATGAGTTGGTTGGTCTG	NA
SNP0024	Ca_22785		<i>Ca_Kabuli_Ch01</i>	[C/A]	17395543	CDS_NON_SYNONYMOUS	Domain of unknown function DUF625	CATGTTAACCAAGCCAGAGAAAAT	CCTCCAAGAATACAGGTGTGACTTT	NA
SNP0025	Ca_21411		<i>Ca_Kabuli_Ch01</i>	[C/A]	34866709	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	GAAGTAAGCTCTCCAAAATTGTCC	ACGCACCACTATCTAAACCAGATT	NA
SNP0026	Ca_13620		<i>Ca_Kabuli_Ch01</i>	[G/A]	42452801	CDS_NON_SYNONYMOUS	Transcription factor CBF/NF-Y/archaeal histone	TGAGTTGGTGGTGAGAAGAATAC	TAACAAGAGCCTCAATCACTTCTG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0027	Ca_13610		<i>Ca_Kabuli_Ch01</i>	[T/G]	42605239	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	AGATGAGAGCCATATCTGGAAAC	CAGTCTTTTCTTCCTTCCTCAA	NA
SNP0028	Ca_13608		<i>Ca_Kabuli_Ch01</i>	[T/G]	42613060	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GACCTTCCTATCTTCCTGCAATA	CAGTCTTTTCTTCCTTCCTCAA	NA
SNP0029	Ca_12938		<i>Ca_Kabuli_Ch01</i>	[T/A]	47042798	CDS_NON_SYNONYMOUS	Protein of unknown function DUF92, TMEM19	TACCTGCAACACCTTACTTTCA	CAGGTCCCTTATATTGCTGAACAT	NA
SNP0030	Ca_12602		<i>Ca_Kabuli_Ch02</i>	[G/A]	1828406	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1421	TCAACTACATCGTCGATAGAAACC	CAAGGGCTGAATGTTTAATCATC	NA
SNP0031	Ca_10563		<i>Ca_Kabuli_Ch02</i>	[G/A]	2783727	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TAAGGGAGGGTGTTTAGATGAAG	GGCCTTAAATTTCTTGATTCTCTG	NA
SNP0032	Ca_10517		<i>Ca_Kabuli_Ch02</i>	[C/T]	3366023	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	GCAAGTGGAGTTTGGTATAGTGTG	ATCATCTTTTGTGGAGTCTCTCT	NA
SNP0033	Ca_10515		<i>Ca_Kabuli_Ch02</i>	[C/T]	3410375	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	AAAGGCAAGTGGAGTTTGGTATAG	TAATGCCTCTTGAGAAAGTGGAGT	NA
SNP0034	Ca_10463		<i>Ca_Kabuli_Ch02</i>	[A/G]	3930211	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	TCTTCTTGATTGAATCTCTCGTCA	TGTTAGCTTTCGTGTTCACTTAGG	NA
SNP0035	Ca_14702		<i>Ca_Kabuli_Ch02</i>	[C/T]	5079639	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TCTTTGAACAATCAGGAAGACTG	TTAGGATCGCTCAACATATAGGG	NA
SNP0036	Ca_20380		<i>Ca_Kabuli_Ch02</i>	[A/G]	10068214	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	CTTTTGCTATACTTGCAGCAGGA	AAACTGTCTCCATATCAGACACCA	NA
SNP0037	Ca_17564		<i>Ca_Kabuli_Ch02</i>	[G/A]	10760939	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	TCAGTCATGAGTACAATGAGTTTAAGG	CATCAAATCGACACATTCACAGTA	NA
SNP0038	Ca_18061		<i>Ca_Kabuli_Ch02</i>	[A/C]	12281599	CDS_NON_SYNONYMOUS	Zinc finger, RING-CH-type	GTCAATATCTCGACAACAACAAT	TGGAAGTACGAAGTTGGTAATGAA	NA
SNP0039	Ca_18079		<i>Ca_Kabuli_Ch02</i>	[C/G]	12528825	CDS_NON_SYNONYMOUS	Zinc finger, Dof-type	ACTTTACTTACTTGCTGGCCAAAC	GCTTGCCATTGAATGTCTAAATCT	NA
SNP0040	Ca_11686		<i>Ca_Kabuli_Ch02</i>	[T/G]	13079417	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3110	CTGACCCGACTAACAAGCCTATAC	CACTTGATCGAAGTTAATCTGTCA	NA
SNP0041	Ca_14967		<i>Ca_Kabuli_Ch02</i>	[G/A]	23297412	CDS_NON_SYNONYMOUS	Domain of unknown function FMP27, domain-6, C-terminal	AAAATACGTCCAAAACAGGAGAGA	GCACCTGGTAAAGTACAAAACAACA	NA
SNP0042	Ca_21663		<i>Ca_Kabuli_Ch02</i>	[T/C]	24291665	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3133	TTGATTTCCCTTCTCCTCTAATGG	GTTCCTATCTTATGCAGGCAGTGA	NA
SNP0043	Ca_14236		<i>Ca_Kabuli_Ch02</i>	[A/G]	25022971	CDS_NON_SYNONYMOUS	Zinc finger, B-box	TGTTTCCACACTGTTGATCCTAGT	ATCAAAATGGCTACTATGCACTGA	NA
SNP0044	Ca_14280		<i>Ca_Kabuli_Ch02</i>	[C/G]	25507637	CDS_NON_SYNONYMOUS	Zinc finger, CCH-type	CATTGCTGTTTGTGATTCTGTAAAC	AGTGTAAACCTGCTTTTGGGAAG	NA
SNP0045	Ca_15694		<i>Ca_Kabuli_Ch02</i>	[T/C]	28018158	CDS_NON_SYNONYMOUS	AUX/IAA protein	AGACCAGATGAATCGATATTGACC	ATCTGGCACTTCTCTTTTCTT	NA
SNP0046	Ca_12487		<i>Ca_Kabuli_Ch02</i>	[G/A]	30702090	CDS_NON_SYNONYMOUS	High mobility group, HMG1/HMG2	CCCCCTCTTATCATTTGTTCTTTTA	GGCACTGTCAGTCTCTCTTTTTC	NA
SNP0047	Ca_16883		<i>Ca_Kabuli_Ch02</i>	[T/C]	34848480	CDS_NON_SYNONYMOUS	Bromodomain	GATATCCATTTATCCCATCTAA	ACTCTAGGACCTACTGCTTGGAGA	NA
SNP0048	Ca_09731		<i>Ca_Kabuli_Ch02</i>	[T/C]	35612895	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	GCTGACTGAGACAATGAATGAAAT	CAATTGCTTCAAGAAATGTCTCTCT	NA
SNP0049	Ca_09786		<i>Ca_Kabuli_Ch02</i>	[C/T]	36088623	CDS_NON_SYNONYMOUS	Transcription factor GRAS	CAATTCTCCACTCAAAGTCTCTCT	AAGCAACCAATCTCTATTATCC	NA
SNP0050	Ca_22148		<i>Ca_Kabuli_Ch03</i>	[C/T]	2708703	CDS_NON_SYNONYMOUS	Zinc finger, B-box	CATGATACTTTGGCCCTTAGATTTC	CAAAAACAGCAAGAACAATCTCTG	NA
SNP0051	Ca_21346		<i>Ca_Kabuli_Ch03</i>	[G/A]	3617555	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	AAGTGGCAGAAAACCTTAAACACC	GAAGTCCTGTGAGATCATCATTTG	NA
SNP0052	Ca_16540		<i>Ca_Kabuli_Ch03</i>	[T/G]	7015213	CDS_NON_SYNONYMOUS	Zinc finger, ZZ-type	TATGATGCTGTTCCAACCAATTAC	GTTTTAGCTTGAAGGGGAGTGTTA	NA
SNP0053	Ca_22696		<i>Ca_Kabuli_Ch03</i>	[A/G]	13420756	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	GC TT TCTGGGACTTGGATAATAA	CACCTTTTCTTCCCTTGTAATC	NA

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SNP0054	Ca_24617		<i>Ca_Kabuli_Ch03</i>	[A/G]	17181213	CDS_NON_SYNONYMOUS	WD40 repeat	GTACACCCAAACCAGGTCTAAGTT	TTTGTAGTGGTGGTCTGTATTTTG	NA
SNP0055	Ca_09470		<i>Ca_Kabuli_Ch03</i>	[A/G]	21020182	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	TGTTATTTTGTAGTGCTAAGGTTGC	GCTTCGTCTACCCTTTCAAAATA	NA
SNP0056	Ca_06206		<i>Ca_Kabuli_Ch03</i>	[A/G]	23028855	CDS_NON_SYNONYMOUS	Mediator complex, subunit Med12	GGAAGGAATCTCATGAGTAACTGG	GGCTATTAAGGTGGACAGTTCAGT	NA
SNP0057	Ca_06189		<i>Ca_Kabuli_Ch03</i>	[C/G]	23273069	CDS_NON_SYNONYMOUS	SNF2-related	GTTGTGGATTGTAACCAACAAGA	CACCTAAGTTCATGTTTGAGAAG	NA
SNP0058	Ca_08144		<i>Ca_Kabuli_Ch03</i>	[G/A]	27632100	CDS_NON_SYNONYMOUS	Myb, DNA-binding	GGGTACCTGGACTGACCATTTAT	ACCTTAGTATGCATTATCGCTCTG	NA
SNP0059	Ca_08113		<i>Ca_Kabuli_Ch03</i>	[T/G]	27968979	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	AAATCTCTTTGTCTTCATCAGCAG	TGAAACCTACATAGATTCATCCTCA	NA
SNP0060	Ca_07170		<i>Ca_Kabuli_Ch03</i>	[A/T]	28614919	CDS_NON_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	ACCACAAACCTCTCCAAGTAGAAC	AGAGATATCTGCTTTTGCTTTGG	NA
SNP0061	Ca_12181		<i>Ca_Kabuli_Ch03</i>	[T/C]	30837265	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	ATCTTAAGCCAACCTCATGCTAAC	TTCCATACACACGCTTAGACATTT	NA
SNP0062	Ca_00729		<i>Ca_Kabuli_Ch03</i>	[G/A]	34576769	CDS_NON_SYNONYMOUS	Transcription factor, MADS-box	CAGCAATCTCTTTGGAATTTCTTC	GGTTGTGATTCACTGTTTGTGATT	NA
SNP0063	Ca_00732		<i>Ca_Kabuli_Ch03</i>	[T/A]	34603669	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	TGAAGTCATAGAAAGCCATCAATC	GCTCAAATTCCTTATGGAATCCTC	NA
SNP0064	Ca_00756		<i>Ca_Kabuli_Ch03</i>	[G/A]	34800277	CDS_NON_SYNONYMOUS	Protein of unknown function DUF668	TAAAGAAGAATCTGATGCCACGA	CATGTCAGTTTCAAACAATTCTCC	NA
SNP0065	Ca_00917		<i>Ca_Kabuli_Ch03</i>	[C/G]	36165997	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type matrix	AATGCAGGTTACAAACACAAGGTA	CAAGTTCCTTTCATCCAGGAATAGC	NA
SNP0066	Ca_00938		<i>Ca_Kabuli_Ch03</i>	[T/G]	36282091	CDS_NON_SYNONYMOUS	Domain of unknown function DUF255	ACCCAGGTAAAGATTAACTGTCTGG	CAAGAGAGGTGTGGTTAAAGGT	NA
SNP0067	Ca_00942		<i>Ca_Kabuli_Ch03</i>	[A/G]	36330750	CDS_NON_SYNONYMOUS	Homeobox	ACAATATGGCTTACTTTGCTGACA	CACTGGACCTGGAAAATAAGAATC	NA
SNP0068	Ca_00943		<i>Ca_Kabuli_Ch03</i>	[T/C]	36345158	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	GTTAGCTCATGAAAAAGTGCATAA	CGGAGACGTAGACATATTGATTG	NA
SNP0069	Ca_01036		<i>Ca_Kabuli_Ch03</i>	[T/C]	37094437	CDS_NON_SYNONYMOUS	Transcription factor, SBP-box	CATTCATCTCTTGTGGAATCAATC	TCCTGCTTAATGGAACAGTGAGTA	NA
SNP0070	Ca_01102		<i>Ca_Kabuli_Ch03</i>	[G/A]	37635909	CDS_NON_SYNONYMOUS	Zinc finger, U1-type	TTTACTGAGCAAGGTAAGGGAGTT	TGCTTCTATATGGTTTGGCTATCA	NA
SNP0071	Ca_01189		<i>Ca_Kabuli_Ch03</i>	[T/C]	38386392	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3595	TCATTGAACTGCTACACTCATTCA	CACTAAAACCAATATCTGCCTCT	NA
SNP0072	Ca_01258		<i>Ca_Kabuli_Ch03</i>	[T/A]	38965610	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	AGGAGAAAAAGGAGAGGAATTGAT	TGCAGGGTAATAATGGGATAAAT	NA
SNP0073	Ca_01271		<i>Ca_Kabuli_Ch03</i>	[T/A]	39084916	CDS_NON_SYNONYMOUS	Domain of unknown function DUF296	TCAATGGCAGTAGAAAGCATTAAAC	CTAACAAATGGCAAGAGGTTTGAT	NA
SNP0074	Ca_07683		<i>Ca_Kabuli_Ch04</i>	[C/A]	504928	CDS_NON_SYNONYMOUS	SANT associated	GGTTAGTTGGGCTGAGATGATTAG	CATAATGTTGAAGTCAGCCAGAAG	NA
SNP0075	Ca_07798		<i>Ca_Kabuli_Ch04</i>	[A/T]	1747181	CDS_NON_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	GCCGCTCTTTCAATTTTATACTC	TACGTGTGTTAGTATTGGCTGAGA	NA
SNP0076	Ca_07804		<i>Ca_Kabuli_Ch04</i>	[C/T]	1833725	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	CTCTTGATTCTGCTTCAATCCAA	GAAAAATCACAGAACACAGATTGC	NA
SNP0077	Ca_07844		<i>Ca_Kabuli_Ch04</i>	[G/A]	2213710	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	TTGGGAAGGTACGGTTAATGTAGT	TACATAAGCTTGATACCCCTGCAA	NA
SNP0078	Ca_03781		<i>Ca_Kabuli_Ch04</i>	[G/A]	4757416	CDS_NON_SYNONYMOUS	SET domain	CAAACTTGTGAAGAGTAAGCAAA	ATGGAGAAAGACCAAAACAGAAAC	NA
SNP0079	Ca_03778		<i>Ca_Kabuli_Ch04</i>	[C/T]	4799116	CDS_NON_SYNONYMOUS	SNF2-related	AACAAAGACCTCCTGAAAATGTC	TGTGCTAAATGTATCCAGTGTTT	NA
SNP0080	Ca_03766		<i>Ca_Kabuli_Ch04</i>	[T/C]	4920706	CDS_NON_SYNONYMOUS	Zinc finger, PMZ-type	ATGAGAGTCATACATGTGGAGGAA	CTAAAGTGACCTGTTTGATTGCAG	NA

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SNP0081	Ca_03621		<i>Ca_Kabuli_Ch04</i>	[T/A]	6238367	CDS_NON_SYNONYMOUS	High mobility group, HMG1/HMG2	ACTGTGGCCCTATAGTTGATTGAG	CGTTTTCAAGATAAGCCCAATAC	NA
SNP0082	Ca_03564		<i>Ca_Kabuli_Ch04</i>	[T/C]	6765884	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	TGATGCTGTCCTTTCTTTGTAAG	ATGAACAGCAAAGACATGTCCTA	NA
SNP0083	Ca_03548		<i>Ca_Kabuli_Ch04</i>	[C/T]	6919896	CDS_NON_SYNONYMOUS	Transcription factor, SBP-box	TGAGTAGCAGTTCTTCTCTTTCA	ACTTTTAAACAGAAAGTCCACACA	NA
SNP0084	Ca_03516		<i>Ca_Kabuli_Ch04</i>	[G/A]	7185974	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	ATGATGTTGTTTCGGTGATTAGTG	AGACACCTAAAGTTGGTTGGAAAG	NA
SNP0085	Ca_03429		<i>Ca_Kabuli_Ch04</i>	[T/C]	8050770	CDS_NON_SYNONYMOUS	Tubby, C-terminal	GTGATACCTAGAGCCCAAAACATT	GGTACCATTGTGTTACCACATTTT	NA
SNP0086	Ca_08309		<i>Ca_Kabuli_Ch04</i>	[T/G]	8198702	CDS_NON_SYNONYMOUS	WD40 repeat	ATGTTTACTCGACTCCATTGCATA	ACAGTAAGAACGATAAAGCGAAGG	NA
SNP0087	Ca_08340		<i>Ca_Kabuli_Ch04</i>	[G/A]	8484976	CDS_NON_SYNONYMOUS	WD40 repeat	AAAAGAGGGAAGAAAGAACAGAT	CACCTCTTTTGGCAATTACACTG	NA
SNP0088	Ca_08371		<i>Ca_Kabuli_Ch04</i>	[A/C]	8751618	CDS_NON_SYNONYMOUS	No apical meristem (NAM) protein	ACCTGAATGCCAAACCATCTATAC	GAAGAAAGCCCTTACTAACTGCAA	NA
SNP0089	Ca_08381		<i>Ca_Kabuli_Ch04</i>	[T/C]	8848653	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TGAGACTATTAGTTGGCAAGAAGC	CCAGACAGAAATTCAAACCAAGTAA	NA
SNP0090	Ca_05487		<i>Ca_Kabuli_Ch04</i>	[C/T]	16278600	CDS_NON_SYNONYMOUS	Zinc finger, B-box	CGTTTTTCTCTGTACCTTGAAACC	AAAACCGCTAGAGCTTGTGATAAT	NA
SNP0091	Ca_05477		<i>Ca_Kabuli_Ch04</i>	[T/A]	16501291	CDS_NON_SYNONYMOUS	Domain of unknown function DUF292, eukaryotic	GTTCGTGATGCTCTCAACTTCTCC	ATTCACCTCAATAGCAACAGAAT	NA
SNP0092	Ca_05430		<i>Ca_Kabuli_Ch04</i>	[A/T]	16926614	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	CATGAGAAATTATATGTCCATGC	AACAACCTCTCAACATCTCTTTC	NA
SNP0093	Ca_18659		<i>Ca_Kabuli_Ch04</i>	[T/C]	18222762	CDS_NON_SYNONYMOUS	SET domain	TCAGTGGCATTGACAAATT	TGCCCTCTCTAGTTTATGTTTCT	NA
SNP0094	Ca_20151		<i>Ca_Kabuli_Ch04</i>	[C/T]	21830534	CDS_NON_SYNONYMOUS	Helix-turn-helix motif, lambda-like repressor	CTCTTCAGCATACCTTCAACTT	CAACTACAACCAACCTCATTTCA	NA
SNP0095	Ca_22438		<i>Ca_Kabuli_Ch04</i>	[C/A]	35574379	CDS_NON_SYNONYMOUS	Transcription factor, MADS-box	GCATGTTCAATTATCCAATGTCTC	GGCAAGAAAGTATTCGTGTTGAAT	NA
SNP0096	Ca_14853		<i>Ca_Kabuli_Ch04</i>	[A/G]	36153818	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	GAAACAAGATTTATGGGGTGCTC	CCTCTCTATTTCACCTTCAGAG	NA
SNP0097	Ca_14825		<i>Ca_Kabuli_Ch04</i>	[C/T]	36537170	CDS_NON_SYNONYMOUS	Transcriptional factor B3	AACCATCTAATCCTTTCTGTGAG	ATTTCCGACACTAACACAGATTCA	NA
SNP0098	Ca_15144		<i>Ca_Kabuli_Ch04</i>	[C/A]	37316700	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	CCCTCAAATAATGATGTGACAA	TCGACGATGTAAGAGATTTTG	NA
SNP0099	Ca_13141		<i>Ca_Kabuli_Ch04</i>	[C/T]	38038865	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3326	CAGATTACAACCACTACGCTTGAG	TTCGTACAGTGTCAACCAAACTT	NA
SNP0100	Ca_13134		<i>Ca_Kabuli_Ch04</i>	[T/A]	38195411	CDS_NON_SYNONYMOUS	Domain of unknown function DUF250	ATTACCATATGCACGCAAGTACAG	CACGTGATTTTGGTTCTTTCTG	NA
SNP0101	Ca_13128		<i>Ca_Kabuli_Ch04</i>	[C/G]	38288877	CDS_NON_SYNONYMOUS	Protein of unknown function DUF869, plant	CCCCCTAAGTTTCTCTCATAAAT	CCTCACTCAACTGAAGTTGTGACT	NA
SNP0102	Ca_13115		<i>Ca_Kabuli_Ch04</i>	[T/A]	38425720	CDS_NON_SYNONYMOUS	Zinc finger, CCCH-type	ACTACCTGACTGATTTTGTCTCC	CTAGGATTCAGGATGGTCAAGATT	NA
SNP0103	Ca_13102		<i>Ca_Kabuli_Ch04</i>	[T/A]	38659534	CDS_NON_SYNONYMOUS	Transcription factor GRAS	ATGCCAAGCTATACTCGTTAAAGG	AACATTCACCCTATCCTGACTCTC	NA
SNP0104	Ca_14868		<i>Ca_Kabuli_Ch04</i>	[G/T]	40583205	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TCACAGTGACAACATGAATACATC	TTGATGACCAAAATTGTTAGGAGTC	NA
SNP0105	Ca_10988		<i>Ca_Kabuli_Ch04</i>	[T/C]	41228918	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	AAGAATATGACACCCCTCATTTCTC	AACTCCAAAAGTGGAGACAAATTC	NA
SNP0106	Ca_10932		<i>Ca_Kabuli_Ch04</i>	[C/G]	41864846	CDS_NON_SYNONYMOUS	WD40 repeat	AACTCAACCTTACAAAACAGCTT	ATATTTATTGCCAGGACAAACGAG	NA
SNP0107	Ca_09097		<i>Ca_Kabuli_Ch04</i>	[A/T]	44239883	CDS_NON_SYNONYMOUS	BTB/POZ-like	TCTATTTTAGGCAATAGGGCGATA	TATGAGATTAGCCGTGATTCITTG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0108	Ca_09101		<i>Ca_Kabuli_Ch04</i>	[G/A]	44266819	CDS_NON_SYNONYMOUS	DNA-binding WRKY	GTTGGTAGCATTGACATTGATGAT	GATTTCAAGAGAGATTGCAAGGTT	NA
SNP0109	Ca_09120		<i>Ca_Kabuli_Ch04</i>	[T/A]	44472237	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1350	CTATGTTTGATGGTTTGAGACACC	AATATAGGTGTCAGTGTGTCGTGTCG	NA
SNP0110	Ca_09185		<i>Ca_Kabuli_Ch04</i>	[G/C]	45224997	CDS_NON_SYNONYMOUS	Protein of unknown function DUF647	CTAGTGCTGCAATGCTACTGCTAT	GTCATTAATTCACCTCATTGCTTG	NA
SNP0111	Ca_19256		<i>Ca_Kabuli_Ch04</i>	[C/T]	46612244	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	CTTCTTTTCTCACCAAGAGTGATG	ACATATGGAAGCAGAAGAACACAG	NA
SNP0112	Ca_10746		<i>Ca_Kabuli_Ch04</i>	[T/C]	48464493	CDS_NON_SYNONYMOUS	Zinc finger, CCHC-type	GGCCGTAAAGTCTAACCAATTATTT	TTCAGTTCAGGTGTGATTACATT	NA
SNP0113	Ca_18171		<i>Ca_Kabuli_Ch05</i>	[G/C]	166217	CDS_NON_SYNONYMOUS	No apical meristem (NAM) protein	AGGAGCTGATAGGATGATCAGAAC	TGAGGAATAATGAGAGTGACAAGC	NA
SNP0114	Ca_18178		<i>Ca_Kabuli_Ch05</i>	[A/C]	234410	CDS_NON_SYNONYMOUS	Protein of unknown function DUF647	TCATTTCCAGGTAGTCTCTTAACC	TCTGACATCTCTGGTTACATGGT	NA
SNP0115	Ca_26279		<i>Ca_Kabuli_Ch05</i>	[T/G]	1280977	CDS_NON_SYNONYMOUS	Transcription factor GRAS	AAATCTGATTCCGAAGAACAAGTC	CTATGGAATGGACATGGATACAA	NA
SNP0116	Ca_22620		<i>Ca_Kabuli_Ch05</i>	[T/G]	5205261	CDS_NON_SYNONYMOUS	Domain of unknown function DUF641	TATATTTGAGTCTGATGGATCATGT	CATCCATTATCAGATTCTTGACCA	NA
SNP0117	Ca_20508		<i>Ca_Kabuli_Ch05</i>	[C/T]	9961380	CDS_NON_SYNONYMOUS	DNA-binding WRKY	TACCAAACCGACAGTTGATTATTG	ACGACTCCTAACATGTCAATTGTG	NA
SNP0118	Ca_17110		<i>Ca_Kabuli_Ch05</i>	[T/C]	11864959	CDS_NON_SYNONYMOUS	Zinc finger, CCHC-type	CATTTGTAACAGTTTCCACCACTG	AATCTTTGTGCTGCTGAAGAGTT	NA
SNP0119	Ca_17657		<i>Ca_Kabuli_Ch05</i>	[A/C]	24090515	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	GGAGAAAGAAAAGAAGTTGACCA	TCCTTTGTAGCCTCAGATCATCC	NA
SNP0120	Ca_17656		<i>Ca_Kabuli_Ch05</i>	[T/C]	24097823	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3437	CAGTGGTAGTACTGTTGGAGGTA	TTCTTCITTGAAGTTCTCATCACG	NA
SNP0121	Ca_17653		<i>Ca_Kabuli_Ch05</i>	[G/C]	24153061	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3437	ACTCCTAATGGTATAGAGGCGTCA	TTCAGAAGTGACAACATCATGAGA	NA
SNP0122	Ca_09042		<i>Ca_Kabuli_Ch05</i>	[A/G]	25400604	CDS_NON_SYNONYMOUS	Zinc finger, CCCH-type	AGCATCTTCTCTATGAATGGAAC	ACGACAATGACATGTAGACACTGA	NA
SNP0123	Ca_08907		<i>Ca_Kabuli_Ch05</i>	[C/G]	27362517	CDS_NON_SYNONYMOUS	BTB/POZ-like	TAACAAACTCGTTAAACGTTGTCG	ATGCACTCTGTCTCATTTCAAAC	NA
SNP0124	Ca_13370		<i>Ca_Kabuli_Ch05</i>	[G/A]	28562734	CDS_NON_SYNONYMOUS	Domain of unknown function DUF399	GTCTACATCTGCATTTTGCTGCT	ACTAATTTTGACATGACCCCACTT	NA
SNP0125	Ca_13361		<i>Ca_Kabuli_Ch05</i>	[G/A]	28682995	CDS_NON_SYNONYMOUS	BTB/POZ-like	AGGATTCAACATAGAGAGTTTCT	TACCTGCACATAAATCTGTTTGG	NA
SNP0126	Ca_13354		<i>Ca_Kabuli_Ch05</i>	[A/T]	28757467	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	CATATCCCTCAGGAACCTGCTTTT	TTTAAGACCGGGGAGTAAGTATTG	NA
SNP0127	Ca_04684		<i>Ca_Kabuli_Ch05</i>	[A/C]	30086232	CDS_NON_SYNONYMOUS	Protein of unknown function DUF300	CTTTGTTTTGAAGGGAGGTTTAG	TCCAGGGTTTAAGGAAATAGTTGA	NA
SNP0128	Ca_04722		<i>Ca_Kabuli_Ch05</i>	[G/A]	30438913	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	CTGAACACTTGCTTGAATTCCTTG	TGATGTTCTCCCTAATAAGCAAT	NA
SNP0129	Ca_04825		<i>Ca_Kabuli_Ch05</i>	[T/C]	31194974	CDS_NON_SYNONYMOUS	High mobility group, HMG1/HMG2	ACCAAATCATGACAAGAGCTTACA	GAAGTCTAAATTAGGGTTTCGAG	NA
SNP0130	Ca_04880		<i>Ca_Kabuli_Ch05</i>	[T/C]	31758166	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	CTTTACAGCTGAGGGGTTTATGT	GGAGATTGTGCATTTAGTTGTGAC	NA
SNP0131	Ca_04898		<i>Ca_Kabuli_Ch05</i>	[T/C]	31935674	CDS_NON_SYNONYMOUS	Protein of unknown function DUF869, plant	ACAGTCGAATCTATGTTGGAATCA	TTTGAGGATCAAGTGAAGACATA	NA
SNP0132	Ca_01919		<i>Ca_Kabuli_Ch05</i>	[C/T]	33379873	CDS_NON_SYNONYMOUS	Homeobox	TGCATAAGCAGGAGAACATAATTC	GGAGGTCAGGTTATTCTCCACTA	NA
SNP0133	Ca_01800		<i>Ca_Kabuli_Ch05</i>	[A/C]	34441581	CDS_NON_SYNONYMOUS	Transcription elongation factor S-II, central domain	AAACTGTCACTGAAAGGAACATCA	TTCTTCTCCAACCAATCTTCTCT	NA
SNP0134	Ca_01790		<i>Ca_Kabuli_Ch05</i>	[G/T]	34511669	CDS_NON_SYNONYMOUS	WD40 repeat	CAAGTAACAAAGCCACGGACTAAT	GTATGGTTGATGACAACATGGAAT	NA

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SNP0135	Ca_01550		<i>Ca_Kabuli_Ch05</i>	[A/T]	36735459	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	CACTATTCTTTCTTCTCGCCAAT	ACTTGGCTAAGTTTTCCTTACCG	NA
SNP0136	Ca_01473		<i>Ca_Kabuli_Ch05</i>	[A/G]	37460980	CDS_NON_SYNONYMOUS	BEACH domain	CTCTCCCTGCTATCTTGTTTTT	ATTTGAACTGCCTGTATTAGAGC	NA
SNP0137	Ca_01417		<i>Ca_Kabuli_Ch05</i>	[C/T]	38057582	CDS_NON_SYNONYMOUS	Zinc finger, DHHC-type, palmitoyltransferase	ATGCTAACGATAGTTCCTTTTGGT	TTTCACGAGTATCCTCTCAACAA	NA
SNP0138	Ca_07428		<i>Ca_Kabuli_Ch05</i>	[C/A]	38783604	CDS_NON_SYNONYMOUS	Mediator complex subunit Med28	CTTCTCATCTGGACAGAGTTTCAA	CCAAGGGCAGCTTTACATTATTAC	NA
SNP0139	Ca_07534		<i>Ca_Kabuli_Ch05</i>	[A/G]	40078077	CDS_NON_SYNONYMOUS	Ethylene insensitive 3	GGAAACCTGAGACTCTTCTTCATC	GTATATTTCCAGTTCACCAGCTT	NA
SNP0140	Ca_07550		<i>Ca_Kabuli_Ch05</i>	[G/C]	40239397	CDS_NON_SYNONYMOUS	Protein of unknown function DUF247	CCAAGTTCTAGTGCCAAACTTTTT	TGGTGACAAGAGTTAGTCTCAAT	NA
SNP0141	Ca_07642		<i>Ca_Kabuli_Ch05</i>	[T/C]	41283253	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1296	AGGACAGTACCTTCACATCCTCAT	AGTTTGTGTACCGTTGCTTAGGT	NA
SNP0142	Ca_19218		<i>Ca_Kabuli_Ch05</i>	[C/T]	41635262	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	ACAGACAGAACTGCAAATTCTC	GTGTCAAATACGTTTCATTTGCTT	NA
SNP0143	Ca_11376		<i>Ca_Kabuli_Ch05</i>	[C/A]	42422932	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	AGAAACTTGAGGACCAAAGATGTC	CACCCTATAAGCAAGTCCTGTTCT	NA
SNP0144	Ca_11356		<i>Ca_Kabuli_Ch05</i>	[T/A]	42582262	CDS_NON_SYNONYMOUS	Transcription factor, SBP-box	TGCAGATTACTGTGATCATTGTG	CTGGAATCATCAGAAAGCATAGTG	NA
SNP0145	Ca_12641		<i>Ca_Kabuli_Ch05</i>	[C/G]	44159237	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	CTTTTGATGCGATTCTTACACATC	TAAAACTGCACCATTCTAGTTCCA	NA
SNP0146	Ca_03889		<i>Ca_Kabuli_Ch05</i>	[G/A]	44428965	CDS_NON_SYNONYMOUS	SET domain	GAACAAATGCTGTGATGATTCTC	CCTGTGAACAGTAATGATTTTGC	NA
SNP0147	Ca_03920		<i>Ca_Kabuli_Ch05</i>	[G/T]	44760347	CDS_NON_SYNONYMOUS	Transcription factor GRAS	AGTTCAGGAGCTTCACTGCTTACT	AGACTATCTTGTTCACCTCCAAGC	NA
SNP0148	Ca_03964		<i>Ca_Kabuli_Ch05</i>	[G/T]	45219258	CDS_NON_SYNONYMOUS	Protein of unknown function DUF455	GTA CTGCGTATCAATGTTGCCAT	GGCCTCAAATTTGTAATATCGAA	NA
SNP0149	Ca_03969		<i>Ca_Kabuli_Ch05</i>	[T/G]	45254112	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type matrix	TTAAGGCTCGTTGATTCTCATTC	ACAACAAGCAGCTGGTGTTCAT	NA
SNP0150	Ca_04004		<i>Ca_Kabuli_Ch05</i>	[C/A]	45559874	CDS_NON_SYNONYMOUS	WD40 repeat	ACACATGACTTTGCACCTCTTTTA	GCAGTTAGATTCCCAACTATGCTT	NA
SNP0151	Ca_04069		<i>Ca_Kabuli_Ch05</i>	[T/C]	46176366	CDS_NON_SYNONYMOUS	No apical meristem (NAM) protein	TCCTTCTATCATCATCACCCTGCTC	ATGGGTTAGGAAGTCGAATGAGTA	NA
SNP0152	Ca_04211		<i>Ca_Kabuli_Ch05</i>	[G/A]	47518533	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	TATGGACAGATTGTTCCACTCTTG	AGGGAGAGGTCITTTATGTTGATG	NA
SNP0153	Ca_04233		<i>Ca_Kabuli_Ch05</i>	[A/G]	47733645	CDS_NON_SYNONYMOUS	No apical meristem (NAM) protein	GAATGGTACTTCTCTCTCCAAGG	TACATTGGCAGCTGTTATTAATGC	NA
SNP0154	Ca_04239		<i>Ca_Kabuli_Ch05</i>	[A/G]	47774516	CDS_NON_SYNONYMOUS	Protein of unknown function DUF869, plant	CAGTCTAGAGATTTCGATGGTTTT	TCTTGAAGACCAAGTTTGTCTGT	NA
SNP0155	Ca_13257		<i>Ca_Kabuli_Ch06</i>	[C/T]	324301	CDS_NON_SYNONYMOUS	Zinc finger, FYVE-type	TCTGGTGTGTTGTAATCACTGTAA	CCGCACGATATCATTTTAACATAC	NA
SNP0156	Ca_10329		<i>Ca_Kabuli_Ch06</i>	[T/G]	2079137	CDS_NON_SYNONYMOUS	Protein of unknown function DUF760	AAGCCAGGTAGATACTTCAGGATG	AGTAGAGAAGATACGTGGCAATCC	NA
SNP0157	Ca_10431		<i>Ca_Kabuli_Ch06</i>	[A/G]	2925908	CDS_NON_SYNONYMOUS	Tify	TTCTCTCTTCTGTTACGTTTTTG	GTAAGTGAAAAATGAAAGCCACCT	NA
SNP0158	Ca_05766		<i>Ca_Kabuli_Ch06</i>	[C/A]	5341510	CDS_NON_SYNONYMOUS	ARID/BRIGHT DNA-binding domain	GCTATTGTCCAAAAAGGACCTAA	CCTGATAAAGGAGAAAGCAGAAAG	NA
SNP0159	Ca_16913		<i>Ca_Kabuli_Ch06</i>	[C/G]	6443828	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	ACATGGCCACTAGTCAATAAACA	GCTTGGTCTAAAGAAGAAGACGAC	NA
SNP0160	Ca_16923		<i>Ca_Kabuli_Ch06</i>	[C/T]	6631216	CDS_NON_SYNONYMOUS	Protein of unknown function DUF668	TCCTAATCTGATTTTGAGCTAGG	AAAGTCGAAGGCAGATTTTATACG	NA
SNP0161	Ca_16938		<i>Ca_Kabuli_Ch06</i>	[G/C]	6779147	CDS_NON_SYNONYMOUS	Protein of unknown function DUF869, plant	GGTGACAATATGAGTGGTGACTTT	TCATCTCCCATCCACCTAATTTAT	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0162	Ca_16954		<i>Ca_Kabuli_Ch06</i>	[A/C]	6913622	CDS_NON_SYNONYMOUS	SNF2-related	TAAGTGTCACTCCTAAACCACCAA	ACTCATCAAGTGTATGGAATTGGA	NA
SNP0163	Ca_09624		<i>Ca_Kabuli_Ch06</i>	[G/A]	7603195	CDS_NON_SYNONYMOUS	Domain of unknown function DUF699, exodeoxyribonuclease V alpha chain	CCATATCTGGTCTTCTGCTCTTCT	GTAGCACAATAAGTGGTGAGCTG	NA
SNP0164	Ca_08667		<i>Ca_Kabuli_Ch06</i>	[A/C]	9324122	CDS_NON_SYNONYMOUS	Homeobox	TAGATCCATTGTGCCAAAGTAAGA	GATGCTATCAATGGATTTGTTGAC	NA
SNP0165	Ca_08608		<i>Ca_Kabuli_Ch06</i>	[C/T]	9834183	CDS_NON_SYNONYMOUS	WD40 repeat	TATGGTGAACAGAGTTGAAGGA	CCAGGTCGTGCATAAAACTACAA	NA
SNP0166	Ca_08544		<i>Ca_Kabuli_Ch06</i>	[T/C]	10510996	CDS_NON_SYNONYMOUS	Protein of unknown function DUF803	ACAGCTTTCACACCCATAACCTAT	GAATAAAAGCACCTCGCAAAGTAG	NA
SNP0167	Ca_20467		<i>Ca_Kabuli_Ch06</i>	[C/A]	10991652	CDS_NON_SYNONYMOUS	Zinc finger, MYND-type	CCCTTTTGCTTAGTTTTTGTATC	ACCGTTAACCATAGCCATAATACC	NA
SNP0168	Ca_23423		<i>Ca_Kabuli_Ch06</i>	[A/G]	11394963	CDS_NON_SYNONYMOUS	Zinc finger, MYND-type	TACCTTGGTAAATGATCACCTTCA	TTTAAAGTGTCCACCACATGACT	NA
SNP0169	Ca_05025		<i>Ca_Kabuli_Ch06</i>	[A/T]	12437275	CDS_NON_SYNONYMOUS	AUX/IAA protein	ACTCACACATTTCCAATGTATCC	TACAATGTAGCAAGGAGTGAAAG	NA
SNP0170	Ca_05052		<i>Ca_Kabuli_Ch06</i>	[T/G]	12799890	CDS_NON_SYNONYMOUS	Protein of unknown function DUF2359, TMEM214	TCCTTTTCATCATCTTCTTCTTC	CATGTAATCTCCAAGTACCAATA	NA
SNP0171	Ca_05104		<i>Ca_Kabuli_Ch06</i>	[C/G]	13326969	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	AGTTTGAAATCGCTTCTTCATCTC	TAGGAGCCACTGAATTTTGCTTAT	NA
SNP0172	Ca_05200		<i>Ca_Kabuli_Ch06</i>	[C/T]	14309042	CDS_NON_SYNONYMOUS	Domain of unknown function DUF640	AGTGCAGATATTCACACTTAACAA	ACAAACCCACCTCAAAAACCTAC	NA
SNP0173	Ca_05213		<i>Ca_Kabuli_Ch06</i>	[A/G]	14416997	CDS_NON_SYNONYMOUS	Domain of unknown function DUF676, hydrolase-like	TCATATTGCTCTGCCACTTTGAT	GTGCTATACCTCGCCTATGAAGTT	NA
SNP0174	Ca_06319		<i>Ca_Kabuli_Ch06</i>	[C/G]	16932014	CDS_NON_SYNONYMOUS	WD40 repeat	CTCATTACTGTTTCATGGTTTGA	TACCATTATTATGTCCAACAAG	NA
SNP0175	Ca_06326		<i>Ca_Kabuli_Ch06</i>	[A/C]	17048493	CDS_NON_SYNONYMOUS	Zinc finger, Dof-type	TCTCCCTCTCCTCTATACCATATT	TAGTGCTAATTCAAACCTCCTTC	NA
SNP0176	Ca_06343		<i>Ca_Kabuli_Ch06</i>	[C/A]	17258827	CDS_NON_SYNONYMOUS	Homeobox	AGGTAATAAAACCTTTGGTCGTTG	GTTGAGGAATCTACAGGTAGCC	NA
SNP0177	Ca_06458		<i>Ca_Kabuli_Ch06</i>	[T/C]	18444725	CDS_NON_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	GTGGTAATTTGCAAAGACAAGGTT	ATTGTGGAATGGGTGCTTATACT	NA
SNP0178	Ca_06467		<i>Ca_Kabuli_Ch06</i>	[C/A]	18562366	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	ATAGCCTTTAAGCAACAGTCCAAC	ACTGAATCTGATCAACCAAGTCAA	NA
SNP0179	Ca_16355		<i>Ca_Kabuli_Ch06</i>	[C/A]	20766377	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	CATAGTTGAGTCAAATGGAAATGC	ACTCGGTCTTACAAAGCATAACT	NA
SNP0180	Ca_11272		<i>Ca_Kabuli_Ch06</i>	[T/G]	21675734	CDS_NON_SYNONYMOUS	Homeobox	GCTTCCTTTGTCTGTAATTTCTCT	TACACACACACACAGGGTCTAC	NA
SNP0181	Ca_11268		<i>Ca_Kabuli_Ch06</i>	[G/T]	21718674	CDS_NON_SYNONYMOUS	Myb, DNA-binding	ATTAGCTCGACAAAGTTCCTCAGT	GAGACATGAAAAGTCTCCACAA	NA
SNP0182	Ca_11216		<i>Ca_Kabuli_Ch06</i>	[T/G]	22217157	CDS_NON_SYNONYMOUS	Zinc finger, CHCC-type	GATTGGAGAAAGTCCCTCAGTTA	GCCGTGTGAGGTTTCTAAGTTAC	NA
SNP0183	Ca_11135		<i>Ca_Kabuli_Ch06</i>	[A/C]	23166355	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	AACATCGAACCGAAAGCTATTAAC	AACCTCTTATCATCATCATATT	NA
SNP0184	Ca_16676		<i>Ca_Kabuli_Ch06</i>	[C/A]	26349363	CDS_NON_SYNONYMOUS	Transcription factor GRAS	GAACCTAACAATTCTGTGCGTTTG	ACTTCTAGGACTGTTGCTTCAAT	NA
SNP0185	Ca_15224		<i>Ca_Kabuli_Ch06</i>	[T/C]	32328468	CDS_NON_SYNONYMOUS	DNA-binding WRKY	ATTAATTTGATACCGTGAGGTTGC	AAATATGCGTACTTCTCGAATCC	NA
SNP0186	Ca_23252		<i>Ca_Kabuli_Ch06</i>	[T/G]	42855091	CDS_NON_SYNONYMOUS	BTB/POZ-like	GATCTAGGCCATGATTGGATAAAC	GACTATCGGATTCGAAAAGAGAAC	NA
SNP0187	Ca_17522		<i>Ca_Kabuli_Ch06</i>	[T/C]	52227277	CDS_NON_SYNONYMOUS	Zinc finger, GATA-type	TAGTGAGATATGATTGGGCATTTG	CACCTTGAGTCTGCAGTTTATGTG	NA
SNP0188	Ca_16263		<i>Ca_Kabuli_Ch06</i>	[A/C]	54091997	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3527	AGAACCTACCAACAGGAGAAAGTG	CATCAGCGTTGGCTATACAAGTAG	NA

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SNP0189	Ca_19023		<i>Ca_Kabuli_Ch06</i>	[T/A]	55922843	CDS_NON_SYNONYMOUS	Protein of unknown function wound-induced	TCAAAATAGTCTTCTTCCAATCC	CAACTGAATTCTTAAGTCTCCAAGC	NA
SNP0190	Ca_19026		<i>Ca_Kabuli_Ch06</i>	[T/A]	55953320	CDS_NON_SYNONYMOUS	Protein of unknown function wound-induced	ATGAATGGTTTTCTGACCCCTAATC	TAGAGCATTTGAAGTCTTCTTT	NA
SNP0191	Ca_13705		<i>Ca_Kabuli_Ch06</i>	[G/A]	57382220	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	AGATTGAGAAGCTCAGTGATACCC	GCAACAATACAAAGTTCACAAAGG	NA
SNP0192	Ca_13700		<i>Ca_Kabuli_Ch06</i>	[T/G]	57436320	CDS_NON_SYNONYMOUS	Bromodomain	TGACAATCTAGTGCCATTGTAGT	GGTTTACTAATCTTGACGGTCAT	NA
SNP0193	Ca_13682		<i>Ca_Kabuli_Ch06</i>	[G/T]	57634387	CDS_NON_SYNONYMOUS	Protein of unknown function DUF936, plant	CAACTCATTAACCATCCATTGAAC	TTTTTCATTGGTCCACTAGGTCTT	NA
SNP0194	Ca_15410		<i>Ca_Kabuli_Ch06</i>	[A/T]	58650459	CDS_NON_SYNONYMOUS	WD40 repeat	AATTCCTTTACATCATCCACTTCC	ATATCAAATACTGCCTCCCAAATG	NA
SNP0195	Ca_15412		<i>Ca_Kabuli_Ch06</i>	[A/G]	58672317	CDS_NON_SYNONYMOUS	Zinc finger, B-box	AAGCGAGCTTTACGTTAGAACATT	CAAGCTTTACACCTGTGAGAAGAA	NA
SNP0196	Ca_20223		<i>Ca_Kabuli_Ch07</i>	[C/G]	218341	CDS_NON_SYNONYMOUS	Transcription factor GRAS	GAGGGACCAGAAAAGTTTGATCTTA	CGTTCTCTACAATCTGAAGTCCT	NA
SNP0197	Ca_24417		<i>Ca_Kabuli_Ch07</i>	[G/T]	610723	CDS_NON_SYNONYMOUS	Transcription factor GRAS	GGTTATACACATCCCATCTTCC	TAAACTCAATTATGCAGCTTCACC	NA
SNP0198	Ca_03291		<i>Ca_Kabuli_Ch07</i>	[T/A]	1787308	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	AAATAGAGTGCCAGAATGGATGAT	CACTTAGCCAACACATTTTCACTT	NA
SNP0199	Ca_03202		<i>Ca_Kabuli_Ch07</i>	[T/G]	2757253	CDS_NON_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	ACAACCTTTCGAAGAGTAACATTGG	CACCTACTGTGAAAACCTTGTATGC	NA
SNP0200	Ca_03139		<i>Ca_Kabuli_Ch07</i>	[G/T]	3297677	CDS_NON_SYNONYMOUS	Domain of unknown function DUF231, plant	GAATGATGTTGAAGATGTGGGTAA	TGCTTAGAGCATTACAGAATTTGC	NA
SNP0201	Ca_03128		<i>Ca_Kabuli_Ch07</i>	[A/G]	3355627	CDS_NON_SYNONYMOUS	AUX/IAA protein	AGTCATAACCCCTTGAAAGCATAG	CATCCATGCTCTCATCAAATACTC	NA
SNP0202	Ca_03113		<i>Ca_Kabuli_Ch07</i>	[G/A]	3560182	CDS_NON_SYNONYMOUS	Zinc finger, FYVE-type	CTACAGAAAGAAGTGGACGAGGTT	TTACCATGATCTGTGCTTTTACCG	NA
SNP0203	Ca_03002		<i>Ca_Kabuli_Ch07</i>	[C/T]	4497784	CDS_NON_SYNONYMOUS	Domain of unknown function DUF625	CTGGAAGAGGTAAAAATTGGAGAG	GTGGATCTTAAATTCCTCATCTAA	NA
SNP0204	Ca_06816		<i>Ca_Kabuli_Ch07</i>	[C/A]	5500318	CDS_NON_SYNONYMOUS	SNF2-related	CTTCGAATGGTACAGGTAGGCTAT	AGTTTATCTCTGACTCCCAACCAG	NA
SNP0205	Ca_06691		<i>Ca_Kabuli_Ch07</i>	[G/T]	6703849	CDS_NON_SYNONYMOUS	WD40 repeat	TCATAGATTGTTTTCGTGTGGAAC	GGTCTCAGTTAGGCCGATTATAGA	NA
SNP0206	Ca_06681		<i>Ca_Kabuli_Ch07</i>	[G/T]	6814954	CDS_NON_SYNONYMOUS	YABBY protein	CTGGATCTAGGGTTTTTCTTTTT	CTCACAGTCCCAATTATCCTTTA	NA
SNP0207	Ca_13243		<i>Ca_Kabuli_Ch07</i>	[C/T]	7756455	CDS_NON_SYNONYMOUS	SNF2-related	TGAAAACACTGACAGTTTAGCTT	TAAGTGTGAGTCTTAAACCAACAA	NA
SNP0208	Ca_15325		<i>Ca_Kabuli_Ch07</i>	[A/T]	8894362	CDS_NON_SYNONYMOUS	Domain of unknown function DUF629	GCAACCACCTTCTTCTCTCTAGG	GGCTTCCAAGAACAAATTAAGAATC	NA
SNP0209	Ca_12810		<i>Ca_Kabuli_Ch07</i>	[C/T]	10485414	CDS_NON_SYNONYMOUS	Protein of unknown function DUF702	AAAGTCTGTACAAATGTTGTCCT	AGCATTTTCTCTTGAAACAATACAGC	NA
SNP0210	Ca_12811		<i>Ca_Kabuli_Ch07</i>	[C/A]	10521449	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	GGATAGAGAAGGAACAGAAACAGG	TTCTATATTTAACCCTCCGCTTC	NA
SNP0211	Ca_09342		<i>Ca_Kabuli_Ch07</i>	[A/G]	11545846	CDS_NON_SYNONYMOUS	Lateral organ boundaries, LOB	TTTACAATAGGGAAGGACCCATTA	TTTCGACGGTTACAAGTTTACACA	NA
SNP0212	Ca_09335		<i>Ca_Kabuli_Ch07</i>	[C/A]	11638885	CDS_NON_SYNONYMOUS	BTB/POZ-like	GGCCTTGTTGGATAAATAGCTTA	AATTATCCAGGAGATTCCAAGT	NA
SNP0213	Ca_09247		<i>Ca_Kabuli_Ch07</i>	[C/A]	12730600	CDS_NON_SYNONYMOUS	Lateral organ boundaries, LOB	TTGCCAGGTGTTACAAGATAAAC	TAGTTGTGTTCCGTTGTGTGATG	NA
SNP0214	Ca_09222		<i>Ca_Kabuli_Ch07</i>	[C/A]	13059710	CDS_NON_SYNONYMOUS	BTB/POZ-like	GACAGAACAGAAAGAGATTCTGGA	AATTTCATGTCTGTGCTTCTCAG	NA
SNP0215	Ca_16064		<i>Ca_Kabuli_Ch07</i>	[T/G]	13903980	CDS_NON_SYNONYMOUS	Tubby, C-terminal	ATCCACTTTCTCAGCTCTCAAGAC	ACATTTTGCAGGTCTAAGCTTTGG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0216	Ca_23041		<i>Ca_Kabuli_Ch07</i>	[T/G]	14233343	CDS_NON_SYNONYMOUS	Protein of unknown function DUF248, methyltransferase putative	GATAATCACCCCTTCAACATCAAT	TAATATCGAAGTTTGCAACGTCAC	NA
SNP0217	Ca_23042		<i>Ca_Kabuli_Ch07</i>	[G/T]	14281993	CDS_NON_SYNONYMOUS	Protein of unknown function DUF702	TGTAGTGGTTTTTGTCAATTGTGTG	TTATTTCACTACTCACGGAACCTG	NA
SNP0218	Ca_15859		<i>Ca_Kabuli_Ch07</i>	[G/T]	17318174	CDS_NON_SYNONYMOUS	SET domain	AAAAAGAGGATCCTGATTGTCAATC	CCACAAATCCCTAACATTTTATCC	NA
SNP0219	Ca_15849		<i>Ca_Kabuli_Ch07</i>	[T/C]	17597348	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1639	ACTGAGACAAGTCATAGCACAAGC	TACTGACAGAGACACCAGACACAA	NA
SNP0220	Ca_15839		<i>Ca_Kabuli_Ch07</i>	[A/G]	17779414	CDS_NON_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	ATTGACCAAGGACCTTTTACAGAC	GTGCTAGTCAACAAACGGAATAGA	NA
SNP0221	Ca_12308		<i>Ca_Kabuli_Ch07</i>	[T/C]	18796748	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	TCTGTCAATTTGTCGTAGGACTCAC	CAAAGTAGGCATGAACCTCAAATGT	NA
SNP0222	Ca_14522		<i>Ca_Kabuli_Ch07</i>	[T/C]	21744514	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	TAATAACAGAATCTGCGTTCTTCC	TCCAAACTAGTCCAAAACCTTCTCC	NA
SNP0223	Ca_19916		<i>Ca_Kabuli_Ch07</i>	[T/A]	24021690	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	CAACTGATCTGCCTCAATCCTAT	AATGATTAGTGGTGGAGATTTTGG	NA
SNP0224	Ca_19912		<i>Ca_Kabuli_Ch07</i>	[G/A]	24181321	CDS_NON_SYNONYMOUS	Zinc finger, RING-CH-type	TGAGCTTTAGGGATGCTTTAACTT	GACACATAGGCACAGCACTACAAC	NA
SNP0225	Ca_11718		<i>Ca_Kabuli_Ch07</i>	[C/T]	30085847	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	AGTAAACGCCAGTTACGTGGTAGT	GACCGAATTTAGTAACCGATTTTG	NA
SNP0226	Ca_10028		<i>Ca_Kabuli_Ch07</i>	[A/G]	32522203	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	CAGCTTTTCCATCTTGGACTTAAT	GTGTCAGTTTGTCTTATCTTCCA	NA
SNP0227	Ca_10004		<i>Ca_Kabuli_Ch07</i>	[A/G]	32942199	CDS_NON_SYNONYMOUS	Transcription factor GRAS	ATGGTCCAGATCACAAGTCAATA	AGCGTGAAGTGAACATACAATA	NA
SNP0228	Ca_16177		<i>Ca_Kabuli_Ch07</i>	[A/C]	33573655	CDS_NON_SYNONYMOUS	CCAAT-binding factor	CGTAAGTCTCTCTATGCATTCGAC	TAAAACGGACCAAGTCTTAAACC	NA
SNP0229	Ca_17639		<i>Ca_Kabuli_Ch07</i>	[T/G]	35181619	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	AAACTTGTGTGTAGGAAAATGGAG	GGCTCAAAGTAGAAAAGTTGCATT	NA
SNP0230	Ca_17781		<i>Ca_Kabuli_Ch07</i>	[T/C]	35799073	CDS_NON_SYNONYMOUS	BTB/POZ-like	CCTGAAAATCAAGATGAAGAGGTT	GAAGAAGTGAACAAAAGAACAG	NA
SNP0231	Ca_13756		<i>Ca_Kabuli_Ch07</i>	[C/A]	36711954	CDS_NON_SYNONYMOUS	Mediator complex, subunit Med12	CAGGTATGAGAATCTTGTGTC	TATCGGAGCTATTCAACTGTAGCA	NA
SNP0232	Ca_19581		<i>Ca_Kabuli_Ch07</i>	[G/A]	39181880	CDS_NON_SYNONYMOUS	BEACH domain	GCTGGTCTGTTAGGTGTAAGTGTG	AACTCAAAAGGACGACTTTCGTAT	NA
SNP0233	Ca_17996		<i>Ca_Kabuli_Ch07</i>	[A/C]	41387475	CDS_NON_SYNONYMOUS	WD40 repeat	TCATGATACCACCTTGGCTTTTAG	CATCATACCTACACCTCCAACCT	NA
SNP0234	Ca_15697		<i>Ca_Kabuli_Ch07</i>	[C/A]	44612651	CDS_NON_SYNONYMOUS	Ethylene insensitive 3	AGCAACCTTTATGTGTTTTCTCC	AGGAGCTTCATCATAAGGAAAATG	NA
SNP0235	Ca_15708		<i>Ca_Kabuli_Ch07</i>	[A/C]	44877324	CDS_NON_SYNONYMOUS	Zinc finger, C2H2-type	GGTCTGACCTTCTTTACATGCTT	AGGCCCTGCTTCTACATATTGAC	NA
SNP0236	Ca_11909		<i>Ca_Kabuli_Ch08</i>	[T/A]	281608	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GGCTGACTTTATGAACCACTTTCT	GTACGTTACGGAAGGTAAATTCG	NA
SNP0237	Ca_11856		<i>Ca_Kabuli_Ch08</i>	[T/C]	709063	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1950	CACTTTTTCAAGGAGGATTATGT	ATTATGCATGTTTGTGTTGAGCAG	NA
SNP0238	Ca_11855		<i>Ca_Kabuli_Ch08</i>	[A/G]	714967	CDS_NON_SYNONYMOUS	Protein of unknown function DUF1950	GGGACCATCTATTTTAAACATGC	CCTTAGGCTTAGTGCCTTATTGAA	NA
SNP0239	Ca_11839		<i>Ca_Kabuli_Ch08</i>	[A/G]	822302	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	AGACAAACAGGGTTGTTGAGTACA	ATCTGTGTATCTCCAAAAGGAG	NA
SNP0240	Ca_11834		<i>Ca_Kabuli_Ch08</i>	[G/A]	855332	CDS_NON_SYNONYMOUS	Protein of unknown function DUF827, plant	TACCAAGAGTTGCAAGAGTTTACAG	CTTCTTCCTCGGTTCTTTCAATA	NA
SNP0241	Ca_11832		<i>Ca_Kabuli_Ch08</i>	[A/C]	866741	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	TAAGAAGGTGAAGTGGGAGTTAG	TGAGTGTGTTTTTGTCTTTTAGG	NA
SNP0242	Ca_15078		<i>Ca_Kabuli_Ch08</i>	[T/C]	1070728	CDS_NON_SYNONYMOUS	WD40 repeat	CATATTGCTATTGTTTGAACAGC	TAGTCTTCCAAACCGAACTTTGAT	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0243	Ca_15049		<i>Ca_Kabuli_Ch08</i>	[A/G]	1265535	CDS_NON_SYNONYMOUS	Zinc finger, CCH-type	TTCTCTAAAACACTCACACTTCG	TCTCGTGAGTTTTGGTAATGAGTC	NA
SNP0244	Ca_15035		<i>Ca_Kabuli_Ch08</i>	[G/A]	1382266	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	TTCTGATGAGGTGGTAATTGGTA	TCGACAGTTTGAAAGTTAAGACCA	NA
SNP0245	Ca_02440		<i>Ca_Kabuli_Ch08</i>	[C/T]	1675888	CDS_NON_SYNONYMOUS	Protein of unknown function DUF604	CTCTGCATGCTATCTATCTCCTCA	ATGAGCATTCACCAATGAGTACAG	NA
SNP0246	Ca_02313		<i>Ca_Kabuli_Ch08</i>	[T/C]	2664625	CDS_NON_SYNONYMOUS	Zinc finger, GATA-type	AATATCCAATGAGTGAGGGGTATT	CAAATCCTAATTGGAAGGTCCTGT	NA
SNP0247	Ca_02249		<i>Ca_Kabuli_Ch08</i>	[T/C]	3297410	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	AGATAGGTATGCATGCTAGTCCA	ATGTTTAGAAATCAAGGCCTCAC	NA
SNP0248	Ca_02240		<i>Ca_Kabuli_Ch08</i>	[T/C]	3396820	CDS_NON_SYNONYMOUS	BSD	CAGTGACAACCATACATAGCACAA	ATTTGTCTGATGCACAACAAGAAC	NA
SNP0249	Ca_02167		<i>Ca_Kabuli_Ch08</i>	[G/A]	4042424	CDS_NON_SYNONYMOUS	Protein of unknown function DUF869, plant	CCTATGTGTGCTCATGTATTTTCC	TGGAGGCTTAAATGAGAAGGATTA	NA
SNP0250	Ca_02163		<i>Ca_Kabuli_Ch08</i>	[C/T]	4073528	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	GAATCAGAGCCAATTTAAGGAAAG	GTAAGAGTGACTTGTCTCTGGT	NA
SNP0251	Ca_02124		<i>Ca_Kabuli_Ch08</i>	[A/G]	4421609	CDS_NON_SYNONYMOUS	Lateral organ boundaries, LOB	AATCCTCAAAGGTTACATACGTT	TTTCACAAGATGCTAGGACAGCTA	NA
SNP0252	Ca_02117		<i>Ca_Kabuli_Ch08</i>	[T/C]	4483130	CDS_NON_SYNONYMOUS	Zinc finger, LIM-type	GAAGAAGAAGATGGTGCATCAATA	GTTAAGATTCTGGGGGAGAGTTT	NA
SNP0253	Ca_02096		<i>Ca_Kabuli_Ch08</i>	[C/T]	4611094	CDS_NON_SYNONYMOUS	SET domain	TGAAGAAGACATGATAACGAACG	TGAAGGTATAGAGCCAATTGTCAG	NA
SNP0254	Ca_02034		<i>Ca_Kabuli_Ch08</i>	[G/T]	5197004	CDS_NON_SYNONYMOUS	Homeobox	CTGCAATTAAACACAACCATCCTC	TAGCTTGTTTGTATTGTGCATCC	NA
SNP0255	Ca_02005		<i>Ca_Kabuli_Ch08</i>	[G/A]	5399503	CDS_NON_SYNONYMOUS	Protein of unknown function DUF248, methyltransferase putative	AAATCTGCATGTAGGTGTTCTTTG	AAGATGTCCAGATATGGAAGGGTA	NA
SNP0256	Ca_01989		<i>Ca_Kabuli_Ch08</i>	[C/T]	5539044	CDS_NON_SYNONYMOUS	Protein of unknown function DUF726	TAATATCTCAACCCCTAGCCTCTG	TCTGCTTGTTTATCGGATTTAGGT	NA
SNP0257	Ca_10686		<i>Ca_Kabuli_Ch08</i>	[A/C]	7041901	CDS_NON_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	GCGGTGATTGAAAAAAAGGAG	ATTGAGGTATCAGCATGGTTTA	NA
SNP0258	Ca_11471		<i>Ca_Kabuli_Ch08</i>	[C/T]	8389117	CDS_NON_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	TATGAGTGAAGGTGAGTCCCTAT	AAACACTTATACATGCCCTCGATT	NA
SNP0259	Ca_16839		<i>Ca_Kabuli_Ch08</i>	[C/G]	11186919	CDS_NON_SYNONYMOUS	Zinc finger, RanBP2-type	CCTAGATGCAATACTCGATTGGTC	TTTCCAGAAGCAGTAACAAACAG	NA
SNP0260	Ca_16820		<i>Ca_Kabuli_Ch08</i>	[G/A]	11403754	CDS_NON_SYNONYMOUS	SANT domain, DNA binding	ACGGCGCTTTTAGTAGTTTGACT	TGTAGGGACAGGTAATGCATTTTA	NA
SNP0261	Ca_15527		<i>Ca_Kabuli_Ch08</i>	[C/G]	16145411	CDS_NON_SYNONYMOUS	Domain of unknown function DUF292, eukaryotic	CAGCTATTGCAGCCAGTATCTTTA	GCTCTTGAGGAATAAGAGAGATGC	NA
SNP0262	Ca_25873		<i>Ca_Kabuli_Scaffold_1313</i>	[G/A]	18412	CDS_NON_SYNONYMOUS	Homeobox	ATTGGAGCATCTCTTGATTTCTC	TGAAATAATCACCTGGTTACGAGA	NA
SNP0263	Ca_22581		<i>Ca_Kabuli_Scaffold_134</i>	[T/G]	218336	CDS_NON_SYNONYMOUS	SET domain	TTCGTCAAAACAGAGTCTCTTCAT	AAACCAGGATAATCTCCATACTGC	NA
SNP0264	Ca_08743		<i>Ca_Kabuli_Scaffold_1348_1</i>	[G/T]	553863	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	GCCTTTAATCGGAAGTTCGTC	ACTTCTCTTGACCATGGATAGTG	NA
SNP0265	Ca_08787		<i>Ca_Kabuli_Scaffold_1348_1</i>	[A/C]	959608	CDS_NON_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	GAGGATCATGATTTCATAGTTTG	CTCATAATCGATTCCATTCTTCTC	NA
SNP0266	Ca_21995		<i>Ca_Kabuli_Scaffold_1351</i>	[T/C]	172110	CDS_NON_SYNONYMOUS	Protein of unknown function DUF2419	ACTGCACAAGCATAATCAATCAC	AGCAGCTGATCTATTGGAAGAACA	NA
SNP0267	Ca_26665		<i>Ca_Kabuli_Scaffold_2557</i>	[C/T]	110378	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	ACCTACATCTGGTGAGTCCTAAGC	GGGCTAGTCTGTTAATCTGCATT	NA
SNP0268	Ca_24396		<i>Ca_Kabuli_Scaffold_2763</i>	[G/A]	43207	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	AGGCCGTTATCTGTTTAAATACCA	AGACCAAAATCCGTTCTCTTACAC	NA
SNP0269	Ca_27794		<i>Ca_Kabuli_Scaffold_2845</i>	[G/A]	7107	CDS_NON_SYNONYMOUS	Protein of unknown function DUF652	TTCAATTGTCCAGGTTGTAAGCTA	GGAAACATAAAGCAAGAAGCTGCA	NA

SNP IDs	Kabuli/desi accession IDs	gene	Kabuli/desi chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0270	Ca_21814		Ca_Kabuli_Scaffold_314	[C/G]	610535	CDS_NON_SYNONYMOUS	Zinc finger, CCCH-type	CTCTCTTGCTTCTGAAACAGATCA	AAGCATCACAAATGCACAGTTAC	NA
SNP0271	Ca_28178		Ca_Kabuli_Scaffold_3337	[G/A]	17956	CDS_NON_SYNONYMOUS	Domain of unknown function DUF828	CCTGGATCACTTGTCTATTGA	TCGGGTTTATGTTTAGGGTTAAG	NA
SNP0272	Ca_26273		Ca_Kabuli_Scaffold_3397	[T/C]	45363	CDS_NON_SYNONYMOUS	WD40 repeat	TTGATAGGAAGCAGGATATTGACA	ATGTCTCTGCAATGCATTAGATTTC	NA
SNP0273	Ca_22195		Ca_Kabuli_Scaffold_420	[T/G]	34145	CDS_NON_SYNONYMOUS	Zinc finger, PHD-type	TGACTATGTGGTTTCTCCTTGA	CAAGTCTATTAAACAGCCTCCACAA	NA
SNP0274	Ca_22883		Ca_Kabuli_Scaffold_421_2	[C/A]	341136	CDS_NON_SYNONYMOUS	Helix-loop-helix DNA-binding domain	CCTAGTTGGGATGTGAAGAAAAT	ACCTTGAGGTTGTTCATCTG	NA
SNP0275	Ca_24566		Ca_Kabuli_Scaffold_50	[C/T]	153631	CDS_NON_SYNONYMOUS	Protein of unknown function DUF3527	AGCCTAAATCATTCTTCTCTGTG	TAAGCATGTGCCAGAAGAACTAAC	NA
SNP0276	Ca_27547		Ca_Kabuli_Scaffold_53	[A/G]	49273	CDS_NON_SYNONYMOUS	Zinc finger, CCCH-type	CAGGAAAAGTAAATGGTCCAAAC	TTCTGAATCCTTAGGGTCTTTG	NA
SNP0277	Ca_23141		Ca_Kabuli_Scaffold_562	[C/A]	289080	CDS_NON_SYNONYMOUS	Protein of unknown function DUF642	GTGGCTCCCTAATTATCTGCTT	CATCGTATTTAACAACACCGTAA	NA
SNP0278	Ca_26833		Ca_Kabuli_Scaffold_681	[C/G]	18376	CDS_NON_SYNONYMOUS	Zinc finger, RING-type	CCTTGTGGTCACAGGTATATCAAA	AAACAAAAGGTCGAGTAAAGCAC	NA
SNP0279	Ca_23185		Ca_Kabuli_Scaffold_682	[G/C]	157238	CDS_NON_SYNONYMOUS	Transcriptional factor B3	AATCCATAATCCCAAACATATGCTG	ATTCGACTTTGCATTTATGGAGTG	NA
SNP0280	Ca_25929		Ca_Kabuli_Scaffold_753	[A/G]	8312	CDS_NON_SYNONYMOUS	Zinc finger, Dof-type	TAAAAGCCCGACAAAATACTCTC	AAGGAGATTCCTCTTTTGATGTTT	NA
SNP0281	Ca_22169		Ca_Kabuli_Scaffold_88	[C/T]	16398	CDS_NON_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	GATCTGAGTCATCTAAATCGAGCA	GTCCACAAAATAGGGAACATGTA	NA
SNP0282	Ca_28056		Ca_Kabuli_Scaffold_C111_64954	[T/A]	5778	CDS_NON_SYNONYMOUS	Protein of unknown function DUF2930	TTGGTAATGCTCTTAAAGTCACA	CGTGAAGCCTATCTAAATGTTC	NA
SNP0283	Ca_00488		Ca_Desi_Chrom1	[C/A]	5704265	CDS_NON_SYNONYMOUS	Kinase-related protein of unknown function (DUF1296)	CAATGAACCCATCTCTTGCTAGT	AGAGCCGACTAGGATTAGTAGCTG	NA
SNP0284	Ca_00882		Ca_Desi_Chrom1	[G/C]	11411433	CDS_NON_SYNONYMOUS	MYB family transcription factor	TATGGAGAAGAAGGGTTTGCTTC	CTCAAGGATGAAACGAAGAACTT	NA
SNP0285	Ca_01546		Ca_Desi_Chrom2	[A/C]	7082872	CDS_NON_SYNONYMOUS	ABSCISIC ACID-INSENSITIVE 5-like protein 2	CGATCTACAATCTTGTGAAAACG	GAGATACTACCGAAACCATCATT	NA
SNP0286	Ca_02202		Ca_Desi_Chrom3	[T/G]	697967	CDS_NON_SYNONYMOUS	Protein LHY	TTGTCCAAGACTTATGGTTAGCAG	ACAAAAGACTGATGGCACTGTAA	NA
SNP0287	Ca_02541		Ca_Desi_Chrom3	[C/T]	4356981	CDS_NON_SYNONYMOUS	WD repeat domain phosphoinositide-interacting protein 3	TGCTCATGATTCAAGAATAGGTTG	ACATGAAAATACTCAATGCACAG	NA
SNP0288	Ca_02786		Ca_Desi_Chrom3	[A/G]	8826641	CDS_NON_SYNONYMOUS	Transcription elongation factor SPT6	CATGTCACTTCATGTAGCCTATC	TTCCCTCTGATCTATCTTTCACCT	NA
SNP0289	Ca_03197		Ca_Desi_Chrom3	[G/C]	15385992	CDS_NON_SYNONYMOUS	Zinc finger CCCH domain-containing protein 5	GTTGCATATGCTTAAAATCTCTTG	CTTTTGATTGTCACAACATCACTG	NA
SNP0290	Ca_03610		Ca_Desi_Chrom3	[A/G]	19826899	CDS_NON_SYNONYMOUS	Bromodomain adjacent to zinc finger domain protein 1A	AGACAAACAGGGTTGTTGAGTACA	ATCTGTGTATCTCCAAAAAGGAG	NA
SNP0291	Ca_04110		Ca_Desi_Chrom4	[G/C]	3248872	CDS_NON_SYNONYMOUS	Transcriptional corepressor LEUNIG	ATATTATTGCCAGGACAAACGAG	AACTCAACCTTACAAAACAGCTT	NA
SNP0292	Ca_04363		Ca_Desi_Chrom4	[C/T]	7647357	CDS_NON_SYNONYMOUS	Lysine-specific demethylase 3B	CAGAAAATCTAACCACAACTGCAT	TTTGGGATGTACTTACAGGGATCT	NA
SNP0293	Ca_04406		Ca_Desi_Chrom4	[G/T]	8131383	CDS_NON_SYNONYMOUS	Transcriptional corepressor LEUNIG	CAAGTAACAAAGCCACGGACTAAT	GTATGGTTGATGACAACATGGAAT	NA
SNP0294	Ca_04679		Ca_Desi_Chrom4	[C/T]	11399103	CDS_NON_SYNONYMOUS	NAC domain-containing protein 78	CAAGGACATCCAATGATATACGTC	TGAAAATCAGAGTTACCAGCTGAC	NA
SNP0295	Ca_05622		Ca_Desi_Chrom5	[A/G]	5207791	CDS_NON_SYNONYMOUS	BEACH domain-containing protein lvsC	TTTATTCTTACGAGAGTTGTGGAA	CCATTAGAAAGCCACCTTAATTGT	NA
SNP0296	Ca_05724		Ca_Desi_Chrom5	[G/C]	6320247	CDS_NON_SYNONYMOUS	Protein ETHYLENE INSENSITIVE 3	GTATATTTCAGTTCCACGAGCT	GGAAACCTGAGACTTCTTCATC	NA

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SNP0297	Ca_05955		Ca_Desi_Ch05	[G/A]	8681026	CDS_NON_SYNONYMOUS	Two-component response regulator-like PRR95	ACTTCCCTGATCAACAAAGAGAAC	TTATCGAATCAGAGTGTGCAGGT	NA
SNP0298	Ca_06336		Ca_Desi_Ch05	[G/A]	13173580	CDS_NON_SYNONYMOUS	Protein of unknown function (DUF399 and DUF3411)	GTCTACATCTGCATTTTGCTGCT	ACTAATTTTGACATGACCCCACTT	NA
SNP0299	Ca_07258		Ca_Desi_Ch06	[A/C]	10171978	CDS_NON_SYNONYMOUS	Homeobox protein 10	GTTGAGGAACCTTACAGGTAGCC	AGGTAATAAAACCTTTGGTCGTTG	NA
SNP0300	Ca_07873		Ca_Desi_Ch07	[C/A]	7266216	CDS_NON_SYNONYMOUS	SBP (S-ribonuclease binding protein) family protein	GGATAGAGAAGGAACAGAAACAGG	TTCATATTTTAACCCATCCGCTTC	NA
SNP0301	Ca_08579		Ca_Desi_Ch08	[T/G]	8124369	CDS_NON_SYNONYMOUS	Transcription factor MYB98	TGGCATTACAGACTAGTTTCATT	GTCCATATGTCCTTCGCAAAAAT	NA
SNP0302	Ca_08625		Ca_Desi_Ch08	[C/A]	8581939	CDS_NON_SYNONYMOUS	Scarecrow-like protein 28	ATTGTTGTCACCAAGTCACAGATT	CCATCATAAAGTGTCTTGTGAAGC	NA
SNP0303	Ca_15118		Ca_Desi_Scaffold_1166	[C/G]	34273	CDS_NON_SYNONYMOUS	Dof zinc finger protein DOF5.2	ACTTTACTTACTTGCTGGCCAAAC	GCTTGCCATTGAATGCTCAAATCT	NA
SNP0304	Ca_15434		Ca_Desi_Scaffold_1290	[C/A]	33887	CDS_NON_SYNONYMOUS	Transcription initiation factor TFIID subunit 7	GCAATTTAGTGAGGATGGAAGAAG	AACCCATCAACACCTATTTTAGC	NA
SNP0305	Ca_15904		Ca_Desi_Scaffold_1484	[A/T]	25898	CDS_NON_SYNONYMOUS	BTB/POZ domain-containing protein NPY1	TCTATTTTAGGCAATAGGGCGATA	TATGAGATTAGCCGTGATTCTTG	NA
SNP0306	Ca_16252		Ca_Desi_Scaffold_1667	[T/G]	33602	CDS_NON_SYNONYMOUS	Zinc finger CCCH domain-containing protein 53	CTCAGTCACCTTCACCTTTTCTTT	ATCTTGAACAGGTCATAAATGCT	NA
SNP0307	Ca_16417		Ca_Desi_Scaffold_1774	[G/T]	44332	CDS_NON_SYNONYMOUS	Scarecrow-like protein 13	CGTCTCTCAACAATCTGAAGTCCT	GAGGGACCAGAAAGTTTGATCTTA	NA
SNP0308	Ca_08976		Ca_Desi_Scaffold_233	[C/A]	4551	CDS_NON_SYNONYMOUS	Transcription activator GLK1	GAGACATGAAAAAGTCTCCACAA	ATTAGCTCGACAAAGTCTCTCAGT	NA
SNP0309	Ca_11984		Ca_Desi_Scaffold_310	[C/G]	49502	CDS_NON_SYNONYMOUS	Zinc finger CCCH domain-containing protein 48	CTCTCTTGCTTCTGAAACAGATCA	AAGCATCACAAATTGCACAGTTAC	NA
SNP0310	Ca_18179		Ca_Desi_Scaffold_3151	[T/C]	27219	CDS_NON_SYNONYMOUS	SET domain-containing protein	TGCCATTTCGATTTGAGGTTG	TTAATGGAAAGCAGGAGAG	NA
SNP0311	Ca_10618		Ca_Desi_Scaffold_32	[G/T]	210202	CDS_NON_SYNONYMOUS	Probable WRKY transcription factor 19	GACGATGTATATCTCATGGAGGTG	AGAATACATGGCAGACTACAGTCC	NA
SNP0312	Ca_18943		Ca_Desi_Scaffold_4448	[G/A]	15163	CDS_NON_SYNONYMOUS	Protein of unknown function (DUF810)	TGGTATTGCAGTTGTAGAGACCAT	ATCCCTCTCTCTTTTCTCCTCAA	NA
SNP0313	Ca_12689		Ca_Desi_Scaffold_450	[C/G]	42711	CDS_NON_SYNONYMOUS	Transcription factor TCP7	GCACTCTCAAGTCTCAATCAGAAG	TAGAGGGGTGTGAGCTGTGAATA	NA
SNP0314	Ca_12770		Ca_Desi_Scaffold_473	[G/C]	13637	CDS_NON_SYNONYMOUS	SWI/SNF complex subunit SWI3C	TAAAACGTCACCACTTCTAGTTCCA	CTTTTGATGCGATTCTTACACATC	NA
SNP0315	Ca_19525		Ca_Desi_Scaffold_5938	[G/C]	6461	CDS_NON_SYNONYMOUS	Transcriptional corepressor LEUNIG	TACCCATTTCATTATGTTCAACAAG	CTCATTTACTGTTTCATGGTTTGA	NA
SNP0316	Ca_13464		Ca_Desi_Scaffold_624	[A/G]	69711	CDS_NON_SYNONYMOUS	WRKY transcription factor 6	AAATATGCGTACTTCTCTGAATCC	ATTAATTTGATACCGTGAGGTTGC	NA
SNP0317	Ca_13667		Ca_Desi_Scaffold_680	[G/A]	76290	CDS_NON_SYNONYMOUS	Protein of unknown function (DUF604)	ATGAGCATTACCAATGAGTACAG	CTCTGCATGCTATCTATCTCTCA	NA
SNP0318	Ca_14026		Ca_Desi_Scaffold_782	[A/C]	33500	CDS_NON_SYNONYMOUS	Unknown expressed protein	TAGCATATGAGTGAGCATTTAGGG	CAGAATGTGCAGTTTCTAAGGCTA	NA
SNP0319	Ca_00096		Ca_Kabuli_Ch01	[G/A]	777240	CDS_SYNONYMOUS	Tubby, C-terminal	CGGCTACAATAAAGCTGGTTATTC	GCAACTGTTATGACCAAAGGTGTA	NA
SNP0320	Ca_00149		Ca_Kabuli_Ch01	[T/C]	1215024	CDS_SYNONYMOUS	BTB/POZ-like	GCGAACCGAATTGTAATAAGATAG	GAGTTTTTGACAGTCCATTACACG	NA
SNP0321	Ca_00180		Ca_Kabuli_Ch01	[A/G]	1467056	CDS_SYNONYMOUS	Zinc finger, RING-type	ACTAGATACATGCGCTCAAACAA	GACCACATAAGGAATTGAACACAA	NA
SNP0322	Ca_00224		Ca_Kabuli_Ch01	[T/C]	1784006	CDS_SYNONYMOUS	Zinc finger, RING-type	GTCTTTTATTCCAAGCTGCAAG	TATTCGTGTACCGAACAAGATG	NA
SNP0323	Ca_00347		Ca_Kabuli_Ch01	[G/A]	2832969	CDS_SYNONYMOUS	Transcriptional factor B3	ATCTCAGGTTCAACCTTAACCAC	AGGAAATATCAGATGCCACAAGT	NA

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SNP0324	Ca_00431		<i>Ca_Kabuli_Ch01</i>	[A/T]	3544948	CDS_SYNONYMOUS	Zinc finger, FYVE-type	ATTATTGAAAAGATGGAGGTGTGC	GGTATTACTTATGCAACATGTCACG	NA
SNP0325	Ca_00467		<i>Ca_Kabuli_Ch01</i>	[T/C]	3853408	CDS_SYNONYMOUS	AUX/IAA protein	GTGGCAATGTAATAGCATTTTGAG	TTGCGTTTATGCTGTAAGTTTAG	NA
SNP0326	Ca_00512		<i>Ca_Kabuli_Ch01</i>	[T/C]	4302751	CDS_SYNONYMOUS	Zinc finger, CCCH-type	GTTGCATATGCTTGAATCTCTTG	CTTTTGATTGTCAACATCACTG	NA
SNP0327	Ca_00536		<i>Ca_Kabuli_Ch01</i>	[T/C]	4512566	CDS_SYNONYMOUS	Tubby, C-terminal	ATTGGGTCTACTTCAACCTACAA	CTCTGTGGAAAATTGGTATTTGG	NA
SNP0328	Ca_00562		<i>Ca_Kabuli_Ch01</i>	[C/T]	4781362	CDS_SYNONYMOUS	Zinc finger, RING-type	AACATCATGGCACTACTCACTCAT	AGCAGCACTAAGAGGGACTACATT	NA
SNP0329	Ca_00613		<i>Ca_Kabuli_Ch01</i>	[A/C]	5249846	CDS_SYNONYMOUS	Protein of unknown function DUF584	AAGTGCTTCACGTCATGATTGTAT	TGAGTTGGACTCTCTTCAGACAAG	NA
SNP0330	Ca_00628		<i>Ca_Kabuli_Ch01</i>	[A/C]	5430700	CDS_SYNONYMOUS	Protein of unknown function DUF584	GACCAACTATTTCATAGCAACGA	CAACCACCAAGTGAATATGATTA	NA
SNP0331	Ca_00656		<i>Ca_Kabuli_Ch01</i>	[A/C]	5666178	CDS_SYNONYMOUS	DNA-binding WRKY	CTAAGCGGGACAGATGTAATTTTG	GAACACATAACCATCCACTACCAC	NA
SNP0332	Ca_07916		<i>Ca_Kabuli_Ch01</i>	[C/T]	6521670	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	CTGAACAATTCAAGGTAGCCACTA	AGCGTCATAATCATTTGTATGGT	NA
SNP0333	Ca_07932		<i>Ca_Kabuli_Ch01</i>	[A/G]	6679253	CDS_SYNONYMOUS	WD40 repeat	TTTTAGAGACCACCTCAACAAGTG	TGGAATGACTCTGTCATAGCTGTT	NA
SNP0334	Ca_07994		<i>Ca_Kabuli_Ch01</i>	[G/A]	7417699	CDS_SYNONYMOUS	Homeobox	CATCATCATATTGAGAACTTTCC	ATACGATTGAGCAGCAAGAGGTAT	NA
SNP0335	Ca_07995		<i>Ca_Kabuli_Ch01</i>	[C/T]	7439421	CDS_SYNONYMOUS	CCAAT-binding transcription factor, subunit B	CAGTTCAACATGGAGAAGAAGGTA	TACACATGACCCCAAGGTATTTA	NA
SNP0336	Ca_02909		<i>Ca_Kabuli_Ch01</i>	[A/G]	8942198	CDS_SYNONYMOUS	Zinc finger, UBP-type	GAATATCTTTAGTGCTGCCAGAT	CAATGAATTGCTTGCTACTCAACT	NA
SNP0337	Ca_02837		<i>Ca_Kabuli_Ch01</i>	[T/A]	9603896	CDS_SYNONYMOUS	WD40 repeat	CATCCACTACAACAGCCTCTTCTT	ATGACCTCCTAGTCACTCCAATC	NA
SNP0338	Ca_02827		<i>Ca_Kabuli_Ch01</i>	[A/C]	9705162	CDS_SYNONYMOUS	Domain of unknown function DUF632	TGTCAGCAAAATGGAGTGATAGT	CTTGTCAGAAGAAGGGGATTAT	NA
SNP0339	Ca_02741		<i>Ca_Kabuli_Ch01</i>	[G/A]	10366383	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	TGTTGTTGTGGTTGTGACATACTC	GTTGCGATGCATTCACTTTATTAC	NA
SNP0340	Ca_02713		<i>Ca_Kabuli_Ch01</i>	[T/G]	10560690	CDS_SYNONYMOUS	CCAAT-binding transcription factor, subunit B	AATCAAGCAGTGGTCTTCATAACA	TTATCAGAGTACGTCCCATATT	NA
SNP0341	Ca_02692		<i>Ca_Kabuli_Ch01</i>	[T/G]	10710672	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	ACTTCAACTTTACGCTGCTTTCTT	TTTAACAACCTTGACCGGTGACTAC	NA
SNP0342	Ca_02626		<i>Ca_Kabuli_Ch01</i>	[T/A]	11277703	CDS_SYNONYMOUS	Transcription factor GRAS	GGTGCACTATAACTTCCATTGACA	CACCTTCTCAATCATAAGTCAA	NA
SNP0343	Ca_02625		<i>Ca_Kabuli_Ch01</i>	[G/A]	11285192	CDS_SYNONYMOUS	Transcription factor GRAS	AGCATCCAGTTGTTATCTTCATCA	AAACTCAGCTTTTACTGGTTTGG	NA
SNP0344	Ca_07131		<i>Ca_Kabuli_Ch01</i>	[T/G]	13991356	CDS_SYNONYMOUS	Homeobox	AATCTGGCAGTGAAAATCAAGAAG	TGTCATTGCTCTTGAAACAATACC	NA
SNP0345	Ca_07113		<i>Ca_Kabuli_Ch01</i>	[G/T]	14225210	CDS_SYNONYMOUS	DNA-binding WRKY	TTACAAAACCTTCACAGAGGGTGAG	ATGATATTGGTGTGGTCTTACAA	NA
SNP0346	Ca_07091		<i>Ca_Kabuli_Ch01</i>	[T/C]	14459908	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	AGCTGGTAGCTCGAATCAAATATC	GTTACCTTTGGAACCTTCACTAT	NA
SNP0347	Ca_07050		<i>Ca_Kabuli_Ch01</i>	[A/G]	14801406	CDS_SYNONYMOUS	Zinc finger, AN1-type	CCTTAACAATCGGATATCAACTAC	TCTCAATTCTCTCGTGTATCTGC	NA
SNP0348	Ca_07018		<i>Ca_Kabuli_Ch01</i>	[T/C]	15167641	CDS_SYNONYMOUS	Protein of unknown function DUF3411	CATACGGGTTATTCAACATGTCTC	CAACATCTGATCCACCACTAAAAC	NA
SNP0349	Ca_07002		<i>Ca_Kabuli_Ch01</i>	[T/C]	15319181	CDS_SYNONYMOUS	Zinc finger, PHD-type	TAGCCTCTTCAAGGATGTAGGTC	GCACTCAAGCGAAACATATGATAA	NA
SNP0350	Ca_06945		<i>Ca_Kabuli_Ch01</i>	[G/A]	16061541	CDS_SYNONYMOUS	BTB/Kelch-associated	TATCAACTACCCACCAAAAGGATT	AGTTGATTTTGGGTTTGCTCTAGT	NA

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SNP0351	Ca_06943		<i>Ca_Kabuli_Ch01</i>	[T/C]	16081438	CDS_SYNONYMOUS	Transcription factor GRAS	GCATAAGACAACGTGATTCATCACC	GACGTTAATTCTTTCTTGCTGTT	NA
SNP0352	Ca_06913		<i>Ca_Kabuli_Ch01</i>	[G/A]	16512171	CDS_SYNONYMOUS	Protein of unknown function DUF3411	AAAACTACCGCAAGGACTATCAAG	GCTTGGAAAGTCTCTCAATTGAA	NA
SNP0353	Ca_06901		<i>Ca_Kabuli_Ch01</i>	[G/A]	16636587	CDS_SYNONYMOUS	No apical meristem (NAM) protein	GATGACAAAGTAGCAACGGTATTG	GGCCTGAATTCTAGTTAACGTCAT	NA
SNP0354	Ca_06894		<i>Ca_Kabuli_Ch01</i>	[C/T]	16743569	CDS_SYNONYMOUS	Protein of unknown function DUF1218	TACCATCAACACTCCTATGCATTG	AACTGTGAGTTACATTGACCAGGA	NA
SNP0355	Ca_06867		<i>Ca_Kabuli_Ch01</i>	[T/C]	17006391	CDS_SYNONYMOUS	Protein of unknown function DUF616	TCTATAGTGTCTCGAAATGGCAA	GTTATGTTCTGTGAAGCAAGCTA	NA
SNP0356	Ca_22780		<i>Ca_Kabuli_Ch01</i>	[T/C]	17314945	CDS_SYNONYMOUS	WD40 repeat	CTTCCATATCTGTTCAAGCCTTTT	CTATCTCATGAGTTGGTTGGTCTG	NA
SNP0357	Ca_22781		<i>Ca_Kabuli_Ch01</i>	[G/A]	17328721	CDS_SYNONYMOUS	Bromodomain	TGACCAAGTAATGAGCAGAGTAA	TGCCTAGACCTTAATACTCGCCTA	NA
SNP0358	Ca_14778		<i>Ca_Kabuli_Ch01</i>	[T/G]	17576793	CDS_SYNONYMOUS	Protein of unknown function DUF789	AGGTGGATATGTCGTATCTTTC	GTCTCCTTGCTGCTATTGAGCTT	NA
SNP0359	Ca_18326		<i>Ca_Kabuli_Ch01</i>	[A/C]	24828245	CDS_SYNONYMOUS	ARID/BRIGHT DNA-binding domain	GAACCTCTACAAACCTAGGGATCA	TATTTAGGTGGTTTCGAGAGGAG	NA
SNP0360	Ca_18325		<i>Ca_Kabuli_Ch01</i>	[A/C]	24845148	CDS_SYNONYMOUS	Zinc finger, RING-type	CTAAACGACATCAAACCTGAGAGA	CCTGAGGCTTAAACCAAATAAAG	NA
SNP0361	Ca_18591		<i>Ca_Kabuli_Ch01</i>	[C/T]	26026817	CDS_SYNONYMOUS	Transcription factor, SBP-box	TGTCGTACACTAGACACACCTTCA	TACTTGCTCTGGTGGACTTGACT	NA
SNP0362	Ca_21419		<i>Ca_Kabuli_Ch01</i>	[T/G]	34727251	CDS_SYNONYMOUS	Zinc finger, CCCH-type	ATCCAATGTTTCTGTTGAAGTTCC	CAAAAAGTGGATCATATTGCTCAG	NA
SNP0363	Ca_24110		<i>Ca_Kabuli_Ch01</i>	[C/T]	35708841	CDS_SYNONYMOUS	Mediator complex, subunit Med10	AGATGAGGATACCGTAAAAATTGG	AACGTGTGCTTAAATTGTGATGAG	NA
SNP0364	Ca_23534		<i>Ca_Kabuli_Ch01</i>	[G/A]	37722095	CDS_SYNONYMOUS	Protein of unknown function DUF620	AGGTCGATGTTACATTCAACACAT	TAGAGTTCAGCACAAATGGAAGAA	NA
SNP0365	Ca_23539		<i>Ca_Kabuli_Ch01</i>	[T/G]	37862342	CDS_SYNONYMOUS	Zinc finger, PHD-type	AAAGATGAGCTTGAAGAGAAGGA	GTTGAATTGAATAAGACGGCTACC	NA
SNP0366	Ca_13548		<i>Ca_Kabuli_Ch01</i>	[C/T]	43800367	CDS_SYNONYMOUS	BTB/POZ-like	CATGACACTACTTTTGAAGGTTT	GAAACTCAITGGTGCATATTCTTG	NA
SNP0367	Ca_16982		<i>Ca_Kabuli_Ch02</i>	[T/C]	354795	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	TTCTCTCTATATATTGCGCTCCA	AGACATCACCACATTACATTTTC	NA
SNP0368	Ca_12605		<i>Ca_Kabuli_Ch02</i>	[A/G]	1797399	CDS_SYNONYMOUS	Domain of unknown function DUF3730	TTCGTCAATTTAGTCTCTGCTGTT	ATGCTCAAGTTCTGATTGAACAAG	NA
SNP0369	Ca_12602		<i>Ca_Kabuli_Ch02</i>	[T/C]	1828318	CDS_SYNONYMOUS	Protein of unknown function DUF1421	AGTCAACTGACTGACCATTCTCTG	GGTCAACACTTGAGACTACTCAGC	NA
SNP0370	Ca_10514		<i>Ca_Kabuli_Ch02</i>	[C/A]	3450904	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	AATTGAACCTGGAGAAGAGAAACG	TTAACAAGTTCGAAATCACCAGAG	NA
SNP0371	Ca_10463		<i>Ca_Kabuli_Ch02</i>	[A/G]	3930182	CDS_SYNONYMOUS	Zinc finger, PHD-type	TCTCTTGATTGAATCTCTCGTCA	TGTTAGCTTTCTGTTTCAGTTAGG	NA
SNP0372	Ca_20383		<i>Ca_Kabuli_Ch02</i>	[G/A]	10025451	CDS_SYNONYMOUS	Protein of unknown function DUF810	AAGGTGAGGTTCTATCTGTCAGT	CCCTTGTTGGTCAAGTAAGACTTT	NA
SNP0373	Ca_11686		<i>Ca_Kabuli_Ch02</i>	[T/G]	13079445	CDS_SYNONYMOUS	Protein of unknown function DUF3110	AAGCTTGACAACTCTTTTCTGT	GACATAAATCAAATGTCGAACCAG	NA
SNP0374	Ca_11681		<i>Ca_Kabuli_Ch02</i>	[T/C]	13217781	CDS_SYNONYMOUS	Zinc finger, DHHC-type, palmitoyltransferase	AGCTCAAGCTCAATTCATCAGTTA	CACAATTATGGGGTTAGAATAGGC	NA
SNP0375	Ca_18564		<i>Ca_Kabuli_Ch02</i>	[C/A]	15234951	CDS_SYNONYMOUS	Protein of unknown function DUF1675	GACTATGTCGACACCGATTATAC	GTTCAACTGGTGGCACTGATAATA	NA
SNP0376	Ca_14972		<i>Ca_Kabuli_Ch02</i>	[C/T]	23181353	CDS_SYNONYMOUS	Protein of unknown function DUF1423, plant	TCTGTTGAAGGTGAGCTATTGAG	TAGAAACTATCCCAGCCACTAAG	NA
SNP0377	Ca_14280		<i>Ca_Kabuli_Ch02</i>	[C/A]	25508579	CDS_SYNONYMOUS	Zinc finger, CCCH-type	TCTATCTTCAATCCAAGGAAGAGG	GTATTGCAGTTTCTTTGCTGATA	NA

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SNP0378	Ca_15674		<i>Ca_Kabuli_Ch02</i>	[G/T]	27724425	CDS_SYNONYMOUS	BTB/POZ-like	AGTAGTTCAGTTGATTCGTTTTG	GGAGAGAACTGGACAATGGTAAAC	NA
SNP0379	Ca_15694		<i>Ca_Kabuli_Ch02</i>	[A/G]	28017163	CDS_SYNONYMOUS	AUX/IAA protein	TGGAATCGGAAGGAATACTTTATG	TTATCGACTAATATCTGCAACCA	NA
SNP0380	Ca_16122		<i>Ca_Kabuli_Ch02</i>	[A/G]	29693107	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	TCCATGTATGAGTTGAAACTTTGG	GATAATGACAATGTAGGCCACAAA	NA
SNP0381	Ca_12474		<i>Ca_Kabuli_Ch02</i>	[G/A]	30867547	CDS_SYNONYMOUS	Zinc finger, CCCH-type	GATCTGATTGTCTCTGCCTTTAAT	CCTTAACCAATGAATTAACCCAAG	NA
SNP0382	Ca_12464		<i>Ca_Kabuli_Ch02</i>	[C/T]	31005845	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	GATGTCGTACCAAAATAGGACATGA	CACCTAGGAATGATATCACACAG	NA
SNP0383	Ca_16883		<i>Ca_Kabuli_Ch02</i>	[C/A]	34847681	CDS_SYNONYMOUS	Bromodomain	TAATCCTCTCCTATCCAAAAGGTG	ACCCAGAGAGATGGTACCAAGTAA	NA
SNP0384	Ca_09731		<i>Ca_Kabuli_Ch02</i>	[C/A]	35612587	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	AAGCAAAACAGCAGAAGCTAAAGAT	TGACAAAAATCTGATCACATAGGC	NA
SNP0385	Ca_09786		<i>Ca_Kabuli_Ch02</i>	[A/T]	36088577	CDS_SYNONYMOUS	Transcription factor GRAS	CAATTCTCCACTCAAAGTTCCTCT	AAGCAACCAAATCTCTATTTCATCC	NA
SNP0386	Ca_09827		<i>Ca_Kabuli_Ch02</i>	[A/G]	36375224	CDS_SYNONYMOUS	Domain of unknown function DUF632	TAATGGCTATGCATTCACTGACTT	TGACACCAAGTGCCTAATTTGACT	NA
SNP0387	Ca_22090		<i>Ca_Kabuli_Ch03</i>	[T/C]	4823828	CDS_SYNONYMOUS	DNA-binding WRKY	CAAAGAAGATCAATCTTGTGATGC	TCCAATTCTGTGTAACAACATCCT	NA
SNP0388	Ca_16550		<i>Ca_Kabuli_Ch03</i>	[C/T]	6840644	CDS_SYNONYMOUS	WD40 repeat	CAACCTAACAAAGTAATGGATGCAA	TTGAGAGATGGAGTTTGTTCATGT	NA
SNP0389	Ca_16540		<i>Ca_Kabuli_Ch03</i>	[G/A]	7024620	CDS_SYNONYMOUS	Zinc finger, ZZ-type	CTGATTTTCGTAAGTCCCTTTC	CTCTCTCTCTCAGATCTCTTAA	NA
SNP0390	Ca_19383		<i>Ca_Kabuli_Ch03</i>	[G/A]	11678625	CDS_SYNONYMOUS	Homeobox	GACACCTATACAACACCCACACAT	CAAGTAGAGTGCTTGTTCCAAGA	NA
SNP0391	Ca_21021		<i>Ca_Kabuli_Ch03</i>	[A/C]	12599496	CDS_SYNONYMOUS	Zinc finger, Dof-type	AGTGATGAACCAATTACCAAGTTGA	TAAGAAACACGTTTGTGCTCTTC	NA
SNP0392	Ca_22696		<i>Ca_Kabuli_Ch03</i>	[T/C]	13420776	CDS_SYNONYMOUS	Zinc finger, C2H2-type	GCCTTTCTGGGACTGGATAATAA	CACCTTTTCTTTCCTTGTACTC	NA
SNP0393	Ca_21130		<i>Ca_Kabuli_Ch03</i>	[T/C]	17936321	CDS_SYNONYMOUS	SANT domain, DNA binding	TAAGTGACATGCTGAACCTGGTCT	GAAAGGTGGAAGAATTACCTCAAG	NA
SNP0394	Ca_19620		<i>Ca_Kabuli_Ch03</i>	[T/C]	18355427	CDS_SYNONYMOUS	Protein of unknown function DUF3411	ACTATGTGTGAACCTGCATTGTCT	CAAATGTCAACTAGGCTCTCTTG	NA
SNP0395	Ca_09406		<i>Ca_Kabuli_Ch03</i>	[T/C]	20030262	CDS_SYNONYMOUS	Protein of unknown function DUF688	ACCATGTATACTTGACCACCTTT	CCAATGGGTCTTGCTAAAGAATTA	NA
SNP0396	Ca_09494		<i>Ca_Kabuli_Ch03</i>	[C/T]	21335892	CDS_SYNONYMOUS	Protein of unknown function DUF599	CAATGTGCTGCTTTGATCTTCTC	ACGGATTTTAATCCTCTATTGCAC	NA
SNP0397	Ca_20431		<i>Ca_Kabuli_Ch03</i>	[A/G]	21950186	CDS_SYNONYMOUS	Domain of unknown function DUF296	TAGTCTACACTGATGTGCATGTC	GAGCTTACACCGTCAAACCTAACA	NA
SNP0398	Ca_20412		<i>Ca_Kabuli_Ch03</i>	[T/C]	22169816	CDS_SYNONYMOUS	BEACH domain	GCGAAATCCAGTTTCTATCTCTC	AAGATGCGTTCTGACCTAGATACC	NA
SNP0399	Ca_20411		<i>Ca_Kabuli_Ch03</i>	[T/C]	22188124	CDS_SYNONYMOUS	Domain of unknown function DUF1088	GAACAAAGTCCCAAAATAAGAGGA	GGGAACCCCTATAGATGTATGCTT	NA
SNP0400	Ca_06189		<i>Ca_Kabuli_Ch03</i>	[T/A]	23273057	CDS_SYNONYMOUS	SNF2-related	GTTGTGGATTGTAACCAACAAGA	CACCTAAGTTCATGTTGCAGAAG	NA
SNP0401	Ca_06124		<i>Ca_Kabuli_Ch03</i>	[G/A]	23966110	CDS_SYNONYMOUS	DNA-binding WRKY	TGTTTGCAATTACTATGAGGTGGT	TTCTCATCCCTCTTCTAGGAGCTA	NA
SNP0402	Ca_23882		<i>Ca_Kabuli_Ch03</i>	[C/T]	25757693	CDS_SYNONYMOUS	SET domain	TCATAATTGCCACTCTGAAGTAAG	AGTTATCCAATTCAAGCATGTCTT	NA
SNP0403	Ca_08296		<i>Ca_Kabuli_Ch03</i>	[T/G]	25987920	CDS_SYNONYMOUS	Protein of unknown function DUF677	AAATGAACCTCTCTGGGTGTA	GAATACGATCTAGCAGTTCAAGCA	NA
SNP0404	Ca_08199		<i>Ca_Kabuli_Ch03</i>	[A/G]	27047840	CDS_SYNONYMOUS	BTB/POZ-like	TTTTAGCCCCAATCTAAGTGTAG	AAGGAAAATGCTAAGGGAAGAACT	NA

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SNP0405	Ca_08186		<i>Ca_Kabuli_Ch03</i>	[C/T]	27194033	CDS_SYNONYMOUS	Zinc finger, Dof-type	ATATGAAGGAAAAGGAACCGAAAG	AACATCTCCTGTGTGAATCCAATA	NA
SNP0406	Ca_07151		<i>Ca_Kabuli_Ch03</i>	[C/T]	28374024	CDS_SYNONYMOUS	Transcription elongation factor, TFIIIS/CRSP70, N-terminal, sub-type	TCGACGATATATAACTCGGGAAAT	TATGTGTACTTTCTAGTGGCTGGA	NA
SNP0407	Ca_07159		<i>Ca_Kabuli_Ch03</i>	[C/T]	28478044	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GATGTATACGGTGTTTGAGAGTGG	TTGACAGTACTCCTGCAACTCTGT	NA
SNP0408	Ca_07170		<i>Ca_Kabuli_Ch03</i>	[A/G]	28614784	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	ACCACAAACCTCTCCAAGTAGAAC	AGAGATATCTGCTTTTTCGCTTGG	NA
SNP0409	Ca_07176		<i>Ca_Kabuli_Ch03</i>	[T/A]	28706106	CDS_SYNONYMOUS	BTB/POZ-like	TACTCGGTGAGCACATATGAGAG	CACCAAGGTTAAGATAAACCAACC	NA
SNP0410	Ca_07274		<i>Ca_Kabuli_Ch03</i>	[C/A]	29690732	CDS_SYNONYMOUS	Zinc finger, AN1-type	AAGGAATGCTGTCTCAGTTCTCTTT	ATACTGCACGTGATTTGTGAATG	NA
SNP0411	Ca_07288		<i>Ca_Kabuli_Ch03</i>	[C/T]	29803866	CDS_SYNONYMOUS	Protein of unknown function DUF2048	GACCTTCTGTGTTTGTTCATCT	ATAATGTACACCCCTTCCCTCTT	NA
SNP0412	Ca_07299		<i>Ca_Kabuli_Ch03</i>	[A/G]	29898396	CDS_SYNONYMOUS	Transcription factor, SBP-box	TTCTTTACAAGTGCTCCATGATA	AGACAGAAAAGTTGGCAGAGAGAG	NA
SNP0413	Ca_07307		<i>Ca_Kabuli_Ch03</i>	[A/G]	29974532	CDS_SYNONYMOUS	Zinc finger, CCCH-type	TTGTTTGAAGCTGATCTGTTTGTG	GTTTCAAATGATAATAGGCCITGG	NA
SNP0414	Ca_12181		<i>Ca_Kabuli_Ch03</i>	[A/G]	30837147	CDS_SYNONYMOUS	Domain of unknown function DUF828	ATCTTAAGCCAACCTCATGCTAAC	TTCCATACACACGCTTAGACATTT	NA
SNP0415	Ca_12224		<i>Ca_Kabuli_Ch03</i>	[C/T]	31279502	CDS_SYNONYMOUS	Protein of unknown function DUF647	CCAATAGTGGCTATTTGACAACAC	TTATTCACTCCTTGCTGTGATA	NA
SNP0416	Ca_12234		<i>Ca_Kabuli_Ch03</i>	[T/C]	31341323	CDS_SYNONYMOUS	Domain of unknown function DUF640	CATGTTATCCCTCATTTTACCC	AAAGGATTAGTCTCTGGTTTCCT	NA
SNP0417	Ca_12236		<i>Ca_Kabuli_Ch03</i>	[A/T]	31357787	CDS_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	ACCAAAATGTAGGAGCATTAGAGG	GCCTATCAAAGAAGTGGGATCTTA	NA
SNP0418	Ca_12258		<i>Ca_Kabuli_Ch03</i>	[G/A]	31591065	CDS_SYNONYMOUS	SET domain	AAAAGTTGAACGTAGAGCAGACCT	TGACCTAACAAAGGGAGAGAAGAAA	NA
SNP0419	Ca_00791		<i>Ca_Kabuli_Ch03</i>	[G/T]	35185001	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	TATGTCGGTGATACAGTTGTGA	TGTTGTTTTTGAAAGTACCAGTGC	NA
SNP0420	Ca_00881		<i>Ca_Kabuli_Ch03</i>	[G/C]	35898320	CDS_SYNONYMOUS	WD40 repeat	AAATGTGGCTGAAGTTGAGTGATA	TTATTCATCATACTATGGCGCTGT	NA
SNP0421	Ca_00936		<i>Ca_Kabuli_Ch03</i>	[C/A]	36260865	CDS_SYNONYMOUS	BTB/POZ-like	CACCTTTACAAGAATTGTATGCTG	TTTGATTTGTGGTGTAGAATGCTC	NA
SNP0422	Ca_00939		<i>Ca_Kabuli_Ch03</i>	[A/G]	36293589	CDS_SYNONYMOUS	Zinc finger, CW-type	CTTGACACTTTCAGAAGGATTTT	ATCTCCAGAAGATTGTCTTTCAC	NA
SNP0423	Ca_00942		<i>Ca_Kabuli_Ch03</i>	[T/C]	36330815	CDS_SYNONYMOUS	Homeobox	ACAATATGGCTTACTTTGCTGACA	CACCTGGACCTGGAAAATAAGAATC	NA
SNP0424	Ca_00947		<i>Ca_Kabuli_Ch03</i>	[A/T]	36387615	CDS_SYNONYMOUS	WD40 repeat	TGCTCCTTCAACTTCTTTTAACC	TTTGTCATTTCCTCACATCATACC	NA
SNP0425	Ca_01033		<i>Ca_Kabuli_Ch03</i>	[T/G]	37067095	CDS_SYNONYMOUS	Zinc finger, RING-type	TGGTATTGTAGTTTCCAAAGACA	CCCGTCCTCTTTATTTTGATTAGA	NA
SNP0426	Ca_01036		<i>Ca_Kabuli_Ch03</i>	[A/G]	37101409	CDS_SYNONYMOUS	Transcription factor, SBP-box	ATGAAAAATCCAGACCAAGAAGTCT	CCAATTTTACTCGCACACTTCATA	NA
SNP0427	Ca_01047		<i>Ca_Kabuli_Ch03</i>	[G/T]	37160822	CDS_SYNONYMOUS	Zinc finger, Sec23/Sec24-type	CAAGAGTCAACAATTTTACCATC	CAGACATTCTGGAATCTGAACTG	NA
SNP0428	Ca_01064		<i>Ca_Kabuli_Ch03</i>	[G/A]	37303478	CDS_SYNONYMOUS	WD40 repeat	GCGTTTAGTCATTGCTCTGTTTA	TATTGAACTAGCCAACAAGTGGA	NA
SNP0429	Ca_01180		<i>Ca_Kabuli_Ch03</i>	[G/T]	38315560	CDS_SYNONYMOUS	Zinc finger, RING-type	GCTACTATTCACCTTTGGCTTTGT	CAAACATGTCTCCATATTTACGG	NA
SNP0430	Ca_01208		<i>Ca_Kabuli_Ch03</i>	[G/A]	38555941	CDS_SYNONYMOUS	WD40 repeat	CAGAACACTTCCAGTGCAATTTAC	TAGCACACTCGTTCTTGTTCTTC	NA
SNP0431	Ca_01236		<i>Ca_Kabuli_Ch03</i>	[A/G]	38771817	CDS_SYNONYMOUS	Mediator complex, subunit Med15	GGAGAAGGGGAAAAATGATATAAG	TACTTCAGTGGCAATAAGAAACCA	NA

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SNP0432	Ca_01271		<i>Ca_Kabuli_Ch03</i>	[A/C]	39084979	CDS_SYNONYMOUS	Domain of unknown function DUF296	TCAATGGCAGTAGAAAGCATTAAAC	ATCTAACAAATGGCAAGAGGTTTG	NA
SNP0433	Ca_01317		<i>Ca_Kabuli_Ch03</i>	[A/C]	39481371	CDS_SYNONYMOUS	Protein of unknown function DUF2043	CTGAACACTCAACTCAGCAATTTT	ATATGCTAATGCTACCGGTTCTGT	NA
SNP0434	Ca_01368		<i>Ca_Kabuli_Ch03</i>	[G/A]	39817122	CDS_SYNONYMOUS	Transcriptional factor B3	GTAGGTGATGAGTGAGTCAACTG	GATAGTAGAATTGATCGGGAGGAG	NA
SNP0435	Ca_27693		<i>Ca_Kabuli_Ch04</i>	[A/G]	20297	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	TTAATCCTTCACAAATGCGTAGAC	GACAGAAATACCATCTCGGAGTTT	NA
SNP0436	Ca_07691		<i>Ca_Kabuli_Ch04</i>	[C/G]	595982	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GCCAAACTATGTAACTCACACCA	AGTTCAGATCAACACAAACAGAGG	NA
SNP0437	Ca_07738		<i>Ca_Kabuli_Ch04</i>	[G/T]	1047639	CDS_SYNONYMOUS	SNF2-related	CTTGCCAAGTCCCAACTATAGAAT	TCAGAGGCATTAGACTTCAGAGTG	NA
SNP0438	Ca_07779		<i>Ca_Kabuli_Ch04</i>	[T/C]	1493927	CDS_SYNONYMOUS	DNA-binding WRKY	GGCACCTTAATTGATCTCTTCACT	AATTCTCAAGGGAACAACAAAGTC	NA
SNP0439	Ca_07797		<i>Ca_Kabuli_Ch04</i>	[C/T]	1708370	CDS_SYNONYMOUS	BEACH domain	ACCAAAGATCATTACATCCATCC	TTCAAGCATCTTCTGGTACATAGG	NA
SNP0440	Ca_07804		<i>Ca_Kabuli_Ch04</i>	[T/C]	1833570	CDS_SYNONYMOUS	Domain of unknown function DUF828	CTCTTGATTCTGTCTTCAATCAA	GAAAAATCACAGAACACAGATTGC	NA
SNP0441	Ca_12126		<i>Ca_Kabuli_Ch04</i>	[T/C]	3264351	CDS_SYNONYMOUS	Domain of unknown function DUF640	ATACGAGTCTTCAGCACAACTTT	AGGTGTTGCCCTGTAGGAAAATAG	NA
SNP0442	Ca_03781		<i>Ca_Kabuli_Ch04</i>	[T/C]	4757357	CDS_SYNONYMOUS	SET domain	CAACCTTGTGAAGAGTAAGCAA	ATGGAGAAAGACCAAAACAGAAAC	NA
SNP0443	Ca_03753		<i>Ca_Kabuli_Ch04</i>	[G/A]	5018591	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	CGGCTTCCTTCTCTCTCTTCT	ACGAGCAAAGGTAAGTCTTGATT	NA
SNP0444	Ca_03733		<i>Ca_Kabuli_Ch04</i>	[A/C]	5222669	CDS_SYNONYMOUS	Domain of unknown function DUF1981, SEC7 associated	TTCAGAGTGGGATAAAAGCGTAT	ACAGATGACTGTATGAAGCCAAAA	NA
SNP0445	Ca_03702		<i>Ca_Kabuli_Ch04</i>	[T/G]	5528421	CDS_SYNONYMOUS	Zinc finger, RING-type	GGTAATCGAGACTTTTCCAACATT	GAAGGTGGAGACCATGTAAGCTAT	NA
SNP0446	Ca_03621		<i>Ca_Kabuli_Ch04</i>	[G/A]	6238354	CDS_SYNONYMOUS	High mobility group, HMG1/HMG2	ACTGTGCCCTATAGTTGATTGAG	CGTTTTCAAGATAAGCCCAATAC	NA
SNP0447	Ca_03591		<i>Ca_Kabuli_Ch04</i>	[G/A]	6507540	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	CAATGAATGTTTCTAGGGGTTCTT	GATACTCAATTGCTTCGTCTAGCA	NA
SNP0448	Ca_03510		<i>Ca_Kabuli_Ch04</i>	[T/G]	7239917	CDS_SYNONYMOUS	WD40 repeat	CCTCTCTTCTCTCTCTCTCTCT	CCTTCCACCATAGTAGATGGTCT	NA
SNP0449	Ca_08313		<i>Ca_Kabuli_Ch04</i>	[C/A]	8236449	CDS_SYNONYMOUS	Zinc finger, RING-type	TCCTTCAGATAGCAAGACTTAGCA	AGTAACTGAAGCAATGTGGGAGTT	NA
SNP0450	Ca_08340		<i>Ca_Kabuli_Ch04</i>	[T/C]	8483482	CDS_SYNONYMOUS	WD40 repeat	AGGAGAGAGTTTTGAGGACAAATG	ATCTGGTTCTTCTCCCTCTTTT	NA
SNP0451	Ca_08341		<i>Ca_Kabuli_Ch04</i>	[C/A]	8496641	CDS_SYNONYMOUS	WD40 repeat	GCGAAGAAGCTGTATTGGAAATAG	AGGCTACTAACCAGAAGATCAAGC	NA
SNP0452	Ca_08371		<i>Ca_Kabuli_Ch04</i>	[T/C]	8751629	CDS_SYNONYMOUS	No apical meristem (NAM) protein	ACCTGAATGCCAAACCATCTATAC	GAAGAAAGCCCTTACTAACTGCAA	NA
SNP0453	Ca_08372		<i>Ca_Kabuli_Ch04</i>	[A/C]	8772215	CDS_SYNONYMOUS	No apical meristem (NAM) protein	CAAGATGGAGACTATGGTGAGCTA	TCCAGAACTTTATCTCACTTCACG	NA
SNP0454	Ca_08381		<i>Ca_Kabuli_Ch04</i>	[A/G]	8844846	CDS_SYNONYMOUS	Zinc finger, RING-type	CCTCTCATCTCTCTTCTCTTTG	CTGCGATTGTATTCTCTGACTG	NA
SNP0455	Ca_08385		<i>Ca_Kabuli_Ch04</i>	[G/T]	8873494	CDS_SYNONYMOUS	WD40 repeat	TAACAACCTCAAGATACGAAATG	TATGGATGCAGAAATCATCACTTG	NA
SNP0456	Ca_05487		<i>Ca_Kabuli_Ch04</i>	[T/A]	16278671	CDS_SYNONYMOUS	Zinc finger, B-box	TTACCGTAAGGATAAAGAACCTC	CACAAAGAAGGTGAATTGTGTGAT	NA
SNP0457	Ca_05477		<i>Ca_Kabuli_Ch04</i>	[T/C]	16501716	CDS_SYNONYMOUS	Domain of unknown function DUF292, eukaryotic	CAGGGGTAATTTTCGGTAAACATA	GGGTCACTCTTAAGGAAAAGGAGT	NA
SNP0458	Ca_05430		<i>Ca_Kabuli_Ch04</i>	[T/A]	16926527	CDS_SYNONYMOUS	Zinc finger, C2H2-type	CATGAGAAATTATATGGTCCATGC	AACAACCTCTTCAACATTCTTTC	NA

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SNP0459	Ca_05404		<i>Ca_Kabuli_Ch04</i>	[T/C]	17199316	CDS_SYNONYMOUS	Domain of unknown function DUF632	AAAAGGAGTGCTAGTCTGTCGAT	TTTCTTCTCAGTGTCTCCAAATG	NA
SNP0460	Ca_05403		<i>Ca_Kabuli_Ch04</i>	[A/G]	17202770	CDS_SYNONYMOUS	Protein of unknown function DUF3353	AGTGAAGGGTCAAAAACACCTTTA	ATGCTAACACACACCTCTCATATA	NA
SNP0461	Ca_05384		<i>Ca_Kabuli_Ch04</i>	[A/T]	17429456	CDS_SYNONYMOUS	Transcription factor jumoni/asparyl beta-hydroxylase	ATTTAAGACGCTTGGATGAAGAAC	GGACTTCAACCTTGAACCTGGTATC	NA
SNP0462	Ca_05364		<i>Ca_Kabuli_Ch04</i>	[T/C]	17652735	CDS_SYNONYMOUS	Protein of unknown function DUF829, TMEM53	CACAGGTAAAGGCTTAGCAACTTT	CCAAAGAAATGAGTTAGTGGGATT	NA
SNP0463	Ca_18633		<i>Ca_Kabuli_Ch04</i>	[G/A]	17931955	CDS_SYNONYMOUS	Protein of unknown function DUF674	CCCAAAATTAGGCCATAGATGAG	TACAACCTTGAATTGGACCATACG	NA
SNP0464	Ca_17152		<i>Ca_Kabuli_Ch04</i>	[G/A]	20436136	CDS_SYNONYMOUS	Transcription factor, TCP	AGGGAACGTCATCATTCATTCTTA	ATCGTGTCAACTTTTGTGTCTCAT	NA
SNP0465	Ca_14466		<i>Ca_Kabuli_Ch04</i>	[G/A]	22859422	CDS_SYNONYMOUS	Protein of unknown function DUF408	TCTATATTCTCATGCATGCCACT	CCATTTCTCAAAATTTAGGTCCTC	NA
SNP0466	Ca_21317		<i>Ca_Kabuli_Ch04</i>	[G/T]	27493010	CDS_SYNONYMOUS	Protein of unknown function DUF716, TMEM45	CTTTTCATCCTCTCTCTACTCCA	TTTCTATAATGCTCCTTCATGCAC	NA
SNP0467	Ca_21312		<i>Ca_Kabuli_Ch04</i>	[G/A]	27626559	CDS_SYNONYMOUS	Protein of unknown function DUF810	GTGAACTGTGTAGAGGAACCAA	CTGGTAGCATATCCAGCTATACA	NA
SNP0468	Ca_14192		<i>Ca_Kabuli_Ch04</i>	[T/G]	30301002	CDS_SYNONYMOUS	SNF2-related	AATATTCTCCTCAATGGTGCTTTC	GTTTTCCAGTCTCACCAAGAATTT	NA
SNP0469	Ca_15459		<i>Ca_Kabuli_Ch04</i>	[T/G]	32042488	CDS_SYNONYMOUS	Domain of unknown function DUF828	TTTACAAGGTAGCCACAACTTCA	GCTGCAATGTTCCACTACTTCTTA	NA
SNP0470	Ca_14853		<i>Ca_Kabuli_Ch04</i>	[T/C]	36154771	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	ATGACAGAACTGTATGCTGCTAAG	CACCTTCTGCACAAACTATACAGG	NA
SNP0471	Ca_14840		<i>Ca_Kabuli_Ch04</i>	[T/C]	36368713	CDS_SYNONYMOUS	Domain of unknown function DUF1084	ATACATGTTGCAATAGGGGTTTCT	AAATATGTCAGGAATCCACCACT	NA
SNP0472	Ca_14825		<i>Ca_Kabuli_Ch04</i>	[C/T]	36537118	CDS_SYNONYMOUS	Transcriptional factor B3	AACCATCTAATCCTTCTCTGTCGAG	ATTTCCGACACTAACACAGATTCA	NA
SNP0473	Ca_15144		<i>Ca_Kabuli_Ch04</i>	[T/A]	37316574	CDS_SYNONYMOUS	Zinc finger, RING-type	GGTTGAGTGATTTTGATTGCTTA	CGACGATGAAAGAGATTTTGATTG	NA
SNP0474	Ca_13141		<i>Ca_Kabuli_Ch04</i>	[T/C]	38039371	CDS_SYNONYMOUS	Protein of unknown function DUF3326	GGCTGATAATATAGCATGGGTTTC	CAACAACACAAACGACCACTTTC	NA
SNP0475	Ca_13128		<i>Ca_Kabuli_Ch04</i>	[G/T]	38288823	CDS_SYNONYMOUS	Protein of unknown function DUF869, plant	CCCCCTAAGTTTCTCTCATAAAT	CCTCACTCAACTGAAGTTGTGACT	NA
SNP0476	Ca_13102		<i>Ca_Kabuli_Ch04</i>	[T/C]	38659377	CDS_SYNONYMOUS	Transcription factor GRAS	ATGCCAAGCTATACTCGTTAAAGG	AACATTCACCCTATCCTGACTCTC	NA
SNP0477	Ca_14925		<i>Ca_Kabuli_Ch04</i>	[T/C]	39803305	CDS_SYNONYMOUS	SANT domain, DNA binding	TGCAAAGAGATGGTACAGATCCTA	GGACACTCTGGTCAAAGCTATTT	NA
SNP0478	Ca_14868		<i>Ca_Kabuli_Ch04</i>	[G/A]	40583219	CDS_SYNONYMOUS	Zinc finger, RING-type	TCACAGTGACAACTGCAATACATC	TTGATGACCAAAATGTTAGGAGTC	NA
SNP0479	Ca_10978		<i>Ca_Kabuli_Ch04</i>	[T/C]	41319598	CDS_SYNONYMOUS	Zinc finger, U1-type	TCATTCTGATGGGAAGGCTATAAT	GGCTAAACTTTGCATATGATTTC	NA
SNP0480	Ca_10932		<i>Ca_Kabuli_Ch04</i>	[G/A]	41864826	CDS_SYNONYMOUS	WD40 repeat	AACTCAACCTTACAAAACGAGCTT	ATATTTATTGCCAGGACAAACGAG	NA
SNP0481	Ca_09060		<i>Ca_Kabuli_Ch04</i>	[C/T]	43807399	CDS_SYNONYMOUS	WD40 repeat	TAATGATCTCCAGCTTCGCAGTA	AAATCATCAAGGCTAACACACTCA	NA
SNP0482	Ca_09097		<i>Ca_Kabuli_Ch04</i>	[A/C]	44239783	CDS_SYNONYMOUS	BTB/POZ-like	TCTATTTTAGGCAATAGGGCGATA	TATGAGATTAGCCGTGATTCTTG	NA
SNP0483	Ca_09101		<i>Ca_Kabuli_Ch04</i>	[C/T]	44266758	CDS_SYNONYMOUS	DNA-binding WRKY	CTGGTTGGATGAAGAAAACAAAC	GATTTCAAGAGAGATTGCAAGGTT	NA
SNP0484	Ca_09120		<i>Ca_Kabuli_Ch04</i>	[G/A]	44472282	CDS_SYNONYMOUS	Protein of unknown function DUF1350	CTATGTTTGATGGTTTGAGACACC	AATATAGGTGTCAGTGTCTGTCTG	NA
SNP0485	Ca_09153		<i>Ca_Kabuli_Ch04</i>	[A/G]	44906255	CDS_SYNONYMOUS	Protein of unknown function DUF803	AGATACTGCTTAATGGATGGCTTC	GGTATCAATGTGACATGGTAAGGA	NA

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SNP0486	Ca_18384		<i>Ca_Kabuli_Ch04</i>	[A/T]	45782453	CDS_SYNONYMOUS	WD40 repeat	ACTGCTCAATAGCTTTGGGTACAT	TACTACCAACCAAGGAGGTACACA	NA
SNP0487	Ca_19258		<i>Ca_Kabuli_Ch04</i>	[T/A]	46605131	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	CTTTGGAGGATGAAAGATGGTAAT	TTAAGCACGCAGTTTCTAAGTTTG	NA
SNP0488	Ca_19256		<i>Ca_Kabuli_Ch04</i>	[G/A]	46612175	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	CTTCTTTTCTCACCAAGAGTGATG	ACATATGGAAGCAGAAGAACACAG	NA
SNP0489	Ca_10847		<i>Ca_Kabuli_Ch04</i>	[A/G]	47419514	CDS_SYNONYMOUS	Protein of unknown function DUF616	TAACTGGCAAGGCCAATCTTATAG	CGTAATCTAGCAATTCGGGTTTT	NA
SNP0490	Ca_10812		<i>Ca_Kabuli_Ch04</i>	[T/C]	47819943	CDS_SYNONYMOUS	Protein of unknown function DUF248, methyltransferase putative	AAACATCCTTATCAAGGAGAGCAG	GGAAGATGGAACATTGAAGAGTT	NA
SNP0491	Ca_10755		<i>Ca_Kabuli_Ch04</i>	[C/T]	48322502	CDS_SYNONYMOUS	Basic-leucine zipper (bZIP) transcription factor	TACTATATGGATGCGACAATAGCC	ACTTTGGAGTGTTTGTGTTGTGT	NA
SNP0492	Ca_10748		<i>Ca_Kabuli_Ch04</i>	[G/C]	48382666	CDS_SYNONYMOUS	AUX/IAA protein	GGATCATCACCAACAAGTAGAACA	CGAATCTCTACCAAGAACAATGA	NA
SNP0493	Ca_10746		<i>Ca_Kabuli_Ch04</i>	[G/C]	48464434	CDS_SYNONYMOUS	Zinc finger, CCHC-type	AAATAAGACATGGTGTGGAGTCA	CAGCAGACAAATACCAATAACAG	NA
SNP0494	Ca_23018		<i>Ca_Kabuli_Ch04</i>	[T/C]	48678278	CDS_SYNONYMOUS	Transcription factor IIS, N-terminal	CCTTGAGTCAACACATCTCTATT	CGGATTCTGTAAGGAAAAATGAAC	NA
SNP0495	Ca_18171		<i>Ca_Kabuli_Ch05</i>	[T/G]	166216	CDS_SYNONYMOUS	No apical meristem (NAM) protein	AGGAGCTGATAGGATGATCAGAAC	TGAGGAATAATGAGAGTGACAAGC	NA
SNP0496	Ca_18177		<i>Ca_Kabuli_Ch05</i>	[C/G]	223384	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	CTATTTGTTGACACAACCCACAA	ACCCCTCTTCTTGTTTCATCAGATTC	NA
SNP0497	Ca_26279		<i>Ca_Kabuli_Ch05</i>	[A/C]	1281006	CDS_SYNONYMOUS	Transcription factor GRAS	AAATCTGATTCCGAAGAACAAGTC	CTATGGAATGGACATGGATACAA	NA
SNP0498	Ca_20508		<i>Ca_Kabuli_Ch05</i>	[T/C]	9961273	CDS_SYNONYMOUS	DNA-binding WRKY	GGAATCATATGCAACAGAGATGAG	GATTAATGTGTGTGAAGTCCACCT	NA
SNP0499	Ca_21977		<i>Ca_Kabuli_Ch05</i>	[A/T]	23161492	CDS_SYNONYMOUS	Zinc finger, PHD-type	GGATGATGCATAACGAATCCTTA	ATTTACCCCTAACCAACCCCTTTTA	NA
SNP0500	Ca_17665		<i>Ca_Kabuli_Ch05</i>	[G/T]	23934198	CDS_SYNONYMOUS	WD40 repeat	AAAAGTGCTGGCAGAAAACATACAT	GAGTTGGTTGCTTAAACATGACAG	NA
SNP0501	Ca_09042		<i>Ca_Kabuli_Ch05</i>	[T/G]	25399115	CDS_SYNONYMOUS	Zinc finger, CCCH-type	CAATATATAAACGCTCCCAAAGTC	AATCATGAGAATAAGCCCTTGAAC	NA
SNP0502	Ca_08907		<i>Ca_Kabuli_Ch05</i>	[C/T]	27361515	CDS_SYNONYMOUS	BTB/POZ-like	ATTTGCAACTCCAATTTCTATAGGC	AGAGTCATCACAGGTATGAAGCAG	NA
SNP0503	Ca_08872		<i>Ca_Kabuli_Ch05</i>	[C/T]	27750155	CDS_SYNONYMOUS	AUX/IAA protein	GAATATTGTGCATGTGACATTGTG	TGTATGGCACACTAGAAGGGTTTA	NA
SNP0504	Ca_13388		<i>Ca_Kabuli_Ch05</i>	[C/T]	28346497	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	TGACACATTAGTTAACGGGTGAAT	ACATAGTTTTTCTCAATGCGAGAG	NA
SNP0505	Ca_13361		<i>Ca_Kabuli_Ch05</i>	[A/C]	28682973	CDS_SYNONYMOUS	BTB/POZ-like	AGGATTCAACATAGAGGAGTTTCT	TACCTGCACATAAATCTGTTTTGG	NA
SNP0506	Ca_16670		<i>Ca_Kabuli_Ch05</i>	[T/A]	29886086	CDS_SYNONYMOUS	Bromodomain	CTAAGAGGCAAGTCTCTCTGAAA	CACACGAAATAGACTGTCAAAGG	NA
SNP0507	Ca_04764		<i>Ca_Kabuli_Ch05</i>	[G/A]	30697511	CDS_SYNONYMOUS	Zinc finger, RING-type	TCAGCCTCTACTTTTGTGTTG	AGATCAATCCATTTCAAGGCTGT	NA
SNP0508	Ca_04906		<i>Ca_Kabuli_Ch05</i>	[G/A]	32019864	CDS_SYNONYMOUS	Protein of unknown function DUF726	GTGACATCTGTTGCTTGAAATTG	CCTGTCATAGCAATCAACACCTA	NA
SNP0509	Ca_04996		<i>Ca_Kabuli_Ch05</i>	[A/T]	32978975	CDS_SYNONYMOUS	Domain of unknown function DUF676, hydrolase-like	CAGAAACAGTTGCCATAGATGAAA	ACAAAGGTTCAAGTCAATGACAC	NA
SNP0510	Ca_01919		<i>Ca_Kabuli_Ch05</i>	[A/G]	33379904	CDS_SYNONYMOUS	Homeobox	TGCATAAGCAGGAGAACATAATTC	GGAGGTCAGGTTATTCTTCCACTA	NA
SNP0511	Ca_01913		<i>Ca_Kabuli_Ch05</i>	[T/C]	33431897	CDS_SYNONYMOUS	Protein of unknown function DUF810	ATTGAAGGCATCTATCGAGGTAT	AGGTCATCTCTACGTACTGCCTTT	NA
SNP0512	Ca_01882		<i>Ca_Kabuli_Ch05</i>	[A/G]	33721544	CDS_SYNONYMOUS	Protein of unknown function DUF81	ATGAGAAGTGCCAAATCATAGTCA	CTGTGAATTTCTTATGGCAACAG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0513	Ca_01824		<i>Ca_Kabuli_Ch05</i>	[C/G]	34241269	CDS_SYNONYMOUS	WD40 repeat	TAAACTGCAGCTTCAGAGGTATG	CATAGTATATGCCATTAGATGC	NA
SNP0514	Ca_01790		<i>Ca_Kabuli_Ch05</i>	[T/C]	34511678	CDS_SYNONYMOUS	WD40 repeat	CAAGTAACAAAGCCACGGACTAAT	GTATGGTTGATGACAACATGGAAT	NA
SNP0515	Ca_01595		<i>Ca_Kabuli_Ch05</i>	[C/G]	36292611	CDS_SYNONYMOUS	WD40 repeat	AAGGGTAAAAGTGTAAGCATGG	GACCAGACAAAGTATGAGCAAATG	NA
SNP0516	Ca_01585		<i>Ca_Kabuli_Ch05</i>	[A/C]	36397489	CDS_SYNONYMOUS	Transcription initiation factor TFIID component TAF4	TGAACAACCTAGTAGCCAAATCAA	CGATGCATATACTATAACGCCAAC	NA
SNP0517	Ca_01576		<i>Ca_Kabuli_Ch05</i>	[C/T]	36441063	CDS_SYNONYMOUS	Protein of unknown function DUF620	CTTCTCAATTATCCATGCTTCTT	TGTAGCTTCTCTCTTCTCTCTCT	NA
SNP0518	Ca_01540		<i>Ca_Kabuli_Ch05</i>	[G/T]	36800497	CDS_SYNONYMOUS	Protein of unknown function DUF827, plant	GGTCCACTTCATTTTGGCTTCTAT	GCATGTTAAAGCTCTTTGGAGAT	NA
SNP0519	Ca_01510		<i>Ca_Kabuli_Ch05</i>	[G/A]	37040045	CDS_SYNONYMOUS	Protein of unknown function DUF2053, membrane	AGCTTCTCACAGTGAAGGTCTCT	TTCACTAAAAGCTTGTGCTTATG	NA
SNP0520	Ca_01503		<i>Ca_Kabuli_Ch05</i>	[C/T]	37147572	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	GAGCAAAATAGCTTAACCCAAAC	ATATTAGAGCGTAGAAGCGGTGAT	NA
SNP0521	Ca_01389		<i>Ca_Kabuli_Ch05</i>	[A/C]	38347201	CDS_SYNONYMOUS	WD40 repeat	GGTAACCTTTCGAAATTGGAAG	TCTGACGTGGGTCTGACTTAATA	NA
SNP0522	Ca_07497		<i>Ca_Kabuli_Ch05</i>	[G/A]	39713021	CDS_SYNONYMOUS	Protein of unknown function DUF3506	AAAAAGATAAGCCAACCTACCATC	ACAGGTCATGGTCTGAATGAAAA	NA
SNP0523	Ca_07571		<i>Ca_Kabuli_Ch05</i>	[A/G]	40507107	CDS_SYNONYMOUS	Zinc finger, CCHC-type	TCACATCCAATGTAAAGCATATTC	TAAATTTTGAGGGGTGTGAATAGC	NA
SNP0524	Ca_11315		<i>Ca_Kabuli_Ch05</i>	[T/G]	42928986	CDS_SYNONYMOUS	SANT domain, DNA binding	AAAGATACACTTTTGCCTGATTG	GGGAATAGGATCATTTAGTGCGTA	NA
SNP0525	Ca_12651		<i>Ca_Kabuli_Ch05</i>	[G/A]	44064495	CDS_SYNONYMOUS	Domain of unknown function DUF632	ATTATCCAGTTCACACTTCTTTGG	ATGCAAGTCTTAGTTCAGGTGGT	NA
SNP0526	Ca_03899		<i>Ca_Kabuli_Ch05</i>	[T/C]	44561095	CDS_SYNONYMOUS	Protein of unknown function DUF248, methyltransferase putative	TCACCAGGATAAGGATTAAGGAAA	GAAAGAGAAGTCGTGTGATATTGGA	NA
SNP0527	Ca_03920		<i>Ca_Kabuli_Ch05</i>	[A/G]	44760403	CDS_SYNONYMOUS	Transcription factor GRAS	AGTTCAGGAGCTTCACTGCTTACT	AGACTATCTTGTTCACCTCCAAGC	NA
SNP0528	Ca_03969		<i>Ca_Kabuli_Ch05</i>	[C/T]	45254102	CDS_SYNONYMOUS	Zinc finger, C2H2-type matrix	TTAAGGCTCGTTTGATTCTCATTC	ACAACAAGCACTGGTGTTCAT	NA
SNP0529	Ca_04012		<i>Ca_Kabuli_Ch05</i>	[T/C]	45661109	CDS_SYNONYMOUS	Protein of unknown function DUF791	GTAACAACGTTGGAGTAGCAAATG	AATCGGGCTTAACATGTCTGTAAT	NA
SNP0530	Ca_04097		<i>Ca_Kabuli_Ch05</i>	[G/T]	46403922	CDS_SYNONYMOUS	Protein of unknown function DUF3133	GGTGTTCTTGGAAATAGGAAAACG	AGACATATTGGAGGAAAATTCAGC	NA
SNP0531	Ca_04110		<i>Ca_Kabuli_Ch05</i>	[A/C]	46526963	CDS_SYNONYMOUS	Protein of unknown function DUF2044, membrane	ATGTAGAAAAGGGCTGTACTTGG	CACAATTAGAAGCTGGAACCTCA	NA
SNP0532	Ca_04172		<i>Ca_Kabuli_Ch05</i>	[C/G]	47151660	CDS_SYNONYMOUS	WD40 repeat	TCTCCGATGAAAGAGATAATGATG	GAATTGAATGCAAGTCACTGTTTC	NA
SNP0533	Ca_04239		<i>Ca_Kabuli_Ch05</i>	[C/T]	47775175	CDS_SYNONYMOUS	Protein of unknown function DUF869, plant	CTCTACTATCTCCAACCTCCGCTTC	AGCTAAAAATGCTATGGCTTCAAAC	NA
SNP0534	Ca_13320		<i>Ca_Kabuli_Ch06</i>	[C/T]	1130293	CDS_SYNONYMOUS	Domain of unknown function DUF296	CCACCAACAAAGTTTATCTCATCA	CGATTACAGTCAGAGTTAGATAG	NA
SNP0535	Ca_10329		<i>Ca_Kabuli_Ch06</i>	[T/A]	2078416	CDS_SYNONYMOUS	Protein of unknown function DUF760	CTAAAATAGGGTGACAGCGGTAGT	CCACTGATCTTGTTTGTACAGGT	NA
SNP0536	Ca_10387		<i>Ca_Kabuli_Ch06</i>	[A/G]	2548412	CDS_SYNONYMOUS	Zinc finger, RING-type	CAATAGTTGCACCATTAACCATC	TGGTTCCTAGGGAAACAGACTTAG	NA
SNP0537	Ca_10405		<i>Ca_Kabuli_Ch06</i>	[T/C]	2714894	CDS_SYNONYMOUS	Domain of unknown function DUF125, transmembrane	TAATCAAGTCGTTGCTACTGTCCT	TGGAGTCTATAATCAGTCCACAC	NA
SNP0538	Ca_10423		<i>Ca_Kabuli_Ch06</i>	[G/A]	2864713	CDS_SYNONYMOUS	SET domain	AATCAGTTAGGGGTTTCAACTA	TTGTGATCTTATGGTTCTGTGCT	NA
SNP0539	Ca_10431		<i>Ca_Kabuli_Ch06</i>	[T/C]	2926006	CDS_SYNONYMOUS	Tify	TTCTCTCTTCTGTTACGTTTTTG	GTAAGTGAAAAATGAAAGCCACCT	NA

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SNP0540	Ca_05731		<i>Ca_Kabuli_Chrom6</i>	[C/A]	5628948	CDS_SYNONYMOUS	Nin one binding (NOB1) Zn-ribbon-like	AGCTCTTAATGAAGAAAACGCACT	ACACCGAACTAGTAGCCAAATAAA	NA
SNP0541	Ca_16913		<i>Ca_Kabuli_Chrom6</i>	[A/G]	6444169	CDS_SYNONYMOUS	SANT domain, DNA binding	GCAGGTGTGTGAATAGTAGCAGAA	GGGCAGAGATGTTGAGAATTTATTA	NA
SNP0542	Ca_08667		<i>Ca_Kabuli_Chrom6</i>	[A/G]	9323775	CDS_SYNONYMOUS	Homeobox	CTAGTGACGTGTTTTCTCTCAGA	TTCTGCAGGTAAAGTCATTTGTGT	NA
SNP0543	Ca_08608		<i>Ca_Kabuli_Chrom6</i>	[A/T]	9834184	CDS_SYNONYMOUS	WD40 repeat	TATGGTGAAACAGAGTTGAAGGA	CCAGGTCTGTGCATAAACTACAA	NA
SNP0544	Ca_08563		<i>Ca_Kabuli_Chrom6</i>	[C/T]	10260274	CDS_SYNONYMOUS	Mediator complex, subunit Med10	GATCTCTCAAACAACGACACAAC	AACGTAAAAAGTTATGGCTAGGTG	NA
SNP0545	Ca_20467		<i>Ca_Kabuli_Chrom6</i>	[A/C]	10991737	CDS_SYNONYMOUS	Zinc finger, MYND-type	CCCTTTTGCTTAGTTTTGTATC	ACCGTTAACCATAGCCATAATACC	NA
SNP0546	Ca_05025		<i>Ca_Kabuli_Chrom6</i>	[A/G]	12437285	CDS_SYNONYMOUS	AUX/IAA protein	ACTCAACAACATTTCCAATGTATCC	TACAATGTAGCAAGGAGTGAAAG	NA
SNP0547	Ca_05057		<i>Ca_Kabuli_Chrom6</i>	[G/A]	12844524	CDS_SYNONYMOUS	Protein of unknown function DUF593	CAGGAACAAGTGGATGAGTATGAA	ACCTCTCTTCTAAACCAACCTTT	NA
SNP0548	Ca_05097		<i>Ca_Kabuli_Chrom6</i>	[A/G]	13243282	CDS_SYNONYMOUS	Zinc finger, CCH-type	ATCCACTGTTAATGGCTTGTTTC	TGTCAGATCTCAGACACCGTTTAT	NA
SNP0549	Ca_05213		<i>Ca_Kabuli_Chrom6</i>	[A/G]	14416981	CDS_SYNONYMOUS	Domain of unknown function DUF676, hydrolase-like	TCATATTGCCTGTCCACTTTGAT	GTGCTATACCTCGCCTATGAAGTT	NA
SNP0550	Ca_05273		<i>Ca_Kabuli_Chrom6</i>	[T/C]	14982998	CDS_SYNONYMOUS	BTB/POZ-like	AATGCAGATATAGTAGGCGCTTTT	AATGATTGTTGTCTGTCTGGACTA	NA
SNP0551	Ca_05286		<i>Ca_Kabuli_Chrom6</i>	[T/C]	15051094	CDS_SYNONYMOUS	Protein of unknown function DUF3506	TTTGATTCTCAGGAATAGTCACG	AAAAACAGATGCTACAGACAGTGC	NA
SNP0552	Ca_05300		<i>Ca_Kabuli_Chrom6</i>	[T/C]	15185723	CDS_SYNONYMOUS	Protein of unknown function DUF593	AACCTAAATCTTGAGCTAAGCAA	CTCTCTCTCTCTTAACCAATGC	NA
SNP0553	Ca_05318		<i>Ca_Kabuli_Chrom6</i>	[A/C]	15328948	CDS_SYNONYMOUS	Zinc finger, DHHC-type, palmitoyltransferase	GTTTGTGTAATGATTTAGGTTCC	TACCCGGTATCCATTATATCAGC	NA
SNP0554	Ca_06343		<i>Ca_Kabuli_Chrom6</i>	[C/T]	17262283	CDS_SYNONYMOUS	Homeobox	TTTACCTCTCGGAATCAATAAGC	GTAGCAAAAATGCAAGAGAGAGGT	NA
SNP0555	Ca_06352		<i>Ca_Kabuli_Chrom6</i>	[A/G]	17369613	CDS_SYNONYMOUS	Transcriptional factor B3	TGTAGGTCCAGTCCTTGTTACTCA	GTGTATTGTCAGGTGTTGTGGTT	NA
SNP0556	Ca_06536		<i>Ca_Kabuli_Chrom6</i>	[A/G]	19304834	CDS_SYNONYMOUS	Zinc finger, ZPR1-type	ATCTCGATACTTGCCCTCTTTTTC	GCAATATGTTTGCCAGTCCATAG	NA
SNP0557	Ca_16355		<i>Ca_Kabuli_Chrom6</i>	[T/A]	20766342	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	TACTTGGCACTTGCTATTTGAATC	GACACAATTCCTCTTTCTTGAT	NA
SNP0558	Ca_11272		<i>Ca_Kabuli_Chrom6</i>	[G/T]	21675762	CDS_SYNONYMOUS	Homeobox	CTCTCTCTCTCGTTTGTTTTGG	AGCAATCTCTGCACTTCACCTG	NA
SNP0559	Ca_11216		<i>Ca_Kabuli_Chrom6</i>	[G/A]	22217107	CDS_SYNONYMOUS	Zinc finger, CHCC-type	AAATGTGAGATTGGAGAAAGTTCC	ATAGTGAAGAATTCGCATTGAG	NA
SNP0560	Ca_11200		<i>Ca_Kabuli_Chrom6</i>	[C/T]	22370242	CDS_SYNONYMOUS	Protein of unknown function DUF1218	ACTTGGTGCTCAGTATCAGATTCA	CAAACCAATCAAACTAACACG	NA
SNP0561	Ca_16676		<i>Ca_Kabuli_Chrom6</i>	[C/T]	26349321	CDS_SYNONYMOUS	Transcription factor GRAS	GAACTTAACAATCTGTGCGTTTG	ACTTCTAGGACTGTTGCTTCAAT	NA
SNP0562	Ca_16677		<i>Ca_Kabuli_Chrom6</i>	[C/T]	26353512	CDS_SYNONYMOUS	Transcription factor GRAS	GAAATCCGTGTAAGGGAACCTCTA	AACAACAGACAAACATACGATGG	NA
SNP0563	Ca_16678		<i>Ca_Kabuli_Chrom6</i>	[C/G]	26357149	CDS_SYNONYMOUS	Transcription factor GRAS	AACTCTTCTCGAACATCAACCTC	GCCTCTATATTGCAAAACCACTT	NA
SNP0564	Ca_16690		<i>Ca_Kabuli_Chrom6</i>	[A/G]	26567360	CDS_SYNONYMOUS	Zinc finger, DoF-type	TCGTTCGTCTTCTGTCAAAGAG	GAATAAGCCCAAGTAAACCAAAAC	NA
SNP0565	Ca_14604		<i>Ca_Kabuli_Chrom6</i>	[A/G]	27537433	CDS_SYNONYMOUS	Zinc finger, RING-type	CCCTGTGTATAATTGAAACCGATA	CAATGTGACACTGTTATGGAACAA	NA
SNP0566	Ca_24048		<i>Ca_Kabuli_Chrom6</i>	[T/G]	30127756	CDS_SYNONYMOUS	Domain of unknown function DUF296	CTCATCATCCCCAATTTTCATCTAT	GTGGTCAAATTCGTCACAAATATC	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0567	Ca_16493		<i>Ca_Kabuli_Chrom6</i>	[A/T]	31024728	CDS_SYNONYMOUS	Zinc finger, Sec23/Sec24-type	GAGGATTACAAATCCATCCCATAC	CTTCAGCCACAAACTAGGACTGTA	NA
SNP0568	Ca_22063		<i>Ca_Kabuli_Chrom6</i>	[A/G]	33733259	CDS_SYNONYMOUS	Zinc finger, RING-type	TGCTTCACAGAGTTTGGATCTTC	GTTGCAACTACTACAGCTGGACAT	NA
SNP0569	Ca_15788		<i>Ca_Kabuli_Chrom6</i>	[G/A]	35129588	CDS_SYNONYMOUS	Zinc finger, PHD-type	TAGAATCTGGTTTGACTGTTCCA	GACATTCCTTTTGTGTGTGTGT	NA
SNP0570	Ca_15898		<i>Ca_Kabuli_Chrom6</i>	[C/T]	38816345	CDS_SYNONYMOUS	Transcription factor GRAS	AGCCCTAGTCCTCTATTTCATCT	AAGAAATGACCAGGTAGAGGACAC	NA
SNP0571	Ca_13854		<i>Ca_Kabuli_Chrom6</i>	[T/C]	45709318	CDS_SYNONYMOUS	DNA-binding WRKY	TTGGGTCTAAGTCAACCCATAAAC	AAGGGTCTTGTGAAGCAACTAT	NA
SNP0572	Ca_13499		<i>Ca_Kabuli_Chrom6</i>	[C/G]	49664132	CDS_SYNONYMOUS	Domain of unknown function DUF632	CCTTACAGCATCTAGTTGTCCAC	ACACATTAATGAAGCGTGTGTC	NA
SNP0573	Ca_17511		<i>Ca_Kabuli_Chrom6</i>	[A/G]	52059750	CDS_SYNONYMOUS	Auxin responsive SAUR protein	TTATGAAGGGAAGGTACCTCATGT	GGAAGTTAAATGGGATTACATGCT	NA
SNP0574	Ca_21219		<i>Ca_Kabuli_Chrom6</i>	[G/A]	55332515	CDS_SYNONYMOUS	Homeobox	ATAGGTCAGGTTTCTTGATCAGC	CTTGAAACTACCATAATGGGCAAT	NA
SNP0575	Ca_13700		<i>Ca_Kabuli_Chrom6</i>	[A/G]	57437904	CDS_SYNONYMOUS	Bromodomain	TGGCAATTCTCTAGCATAGTCAG	GTTTTGATGATATAGTGGGCTCT	NA
SNP0576	Ca_13682		<i>Ca_Kabuli_Chrom6</i>	[C/T]	57632486	CDS_SYNONYMOUS	Protein of unknown function DUF936, plant	TGATTTTATGGTGTGTCTTGAAC	GGACTTCACTCCCTTCATCTATTG	NA
SNP0577	Ca_13671		<i>Ca_Kabuli_Chrom6</i>	[T/C]	57720446	CDS_SYNONYMOUS	Transcriptional factor B3	CAGTGTATGGCGGTGAGGATTAAA	ACCGACAACATGCTAAAACTATG	NA
SNP0578	Ca_15410		<i>Ca_Kabuli_Chrom6</i>	[A/C]	58650318	CDS_SYNONYMOUS	WD40 repeat	TAGGTTGCTCCACAGACTACAAAC	AGCAATTGATGAGAAAGTCACTG	NA
SNP0579	Ca_03393		<i>Ca_Kabuli_Chrom7</i>	[A/G]	845488	CDS_SYNONYMOUS	Domain of unknown function DUF221	AGATATCCCATACAAATTGGCACT	ACACGTTGTGGTATATTGCATCTT	NA
SNP0580	Ca_03388		<i>Ca_Kabuli_Chrom7</i>	[G/A]	888900	CDS_SYNONYMOUS	DNA-binding WRKY	ATGAAGAGAACGAAATCTGAAGG	CATCTGCAAGTAAGAGCAGTGTTT	NA
SNP0581	Ca_03275		<i>Ca_Kabuli_Chrom7</i>	[G/T]	1991642	CDS_SYNONYMOUS	Zinc finger, B-box	ATAAGGAGAGATGAAGGGACAGTG	AAACACGATGACAACTACAACTCC	NA
SNP0582	Ca_03202		<i>Ca_Kabuli_Chrom7</i>	[C/T]	2757260	CDS_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	ACAACTTTGAAGAGTAACATTGG	CACCTACTGTGAAAACCTTTGATGC	NA
SNP0583	Ca_03193		<i>Ca_Kabuli_Chrom7</i>	[C/T]	2832369	CDS_SYNONYMOUS	Zinc finger, GATA-type	ACGAAAGTCCACTTCAAAATTAGG	GAGAGTGGGATACAAAGATGATA	NA
SNP0584	Ca_03139		<i>Ca_Kabuli_Chrom7</i>	[G/A]	3297560	CDS_SYNONYMOUS	Domain of unknown function DUF231, plant	AGCTCCAACCTTCCCACCTATATT	TATCAAAGTACCCTTTGGCTTCTC	NA
SNP0585	Ca_03128		<i>Ca_Kabuli_Chrom7</i>	[A/G]	3355763	CDS_SYNONYMOUS	AUX/IAA protein	AGTCATAACCCCTGAAAGCATAG	CATCCATGCTCTCATCAAATACTC	NA
SNP0586	Ca_03115		<i>Ca_Kabuli_Chrom7</i>	[T/C]	3536233	CDS_SYNONYMOUS	Zinc finger, FYVE-type	TGTCCTACCTGCTACTTCATCTTC	GCCTTCATATAGTTCTTGGTCACA	NA
SNP0587	Ca_03114		<i>Ca_Kabuli_Chrom7</i>	[A/G]	3543765	CDS_SYNONYMOUS	Zinc finger, FYVE-type	ATGTGTGAGCATGTTTGAGCTATT	TTGGTATTGTAGGGAGAAGGGTAA	NA
SNP0588	Ca_03113		<i>Ca_Kabuli_Chrom7</i>	[C/T]	3560250	CDS_SYNONYMOUS	Zinc finger, FYVE-type	CATTCTGTTTATCTTCCTCCACT	GGCTAGTGTTTCCAAAAGAAAGA	NA
SNP0589	Ca_06816		<i>Ca_Kabuli_Chrom7</i>	[A/C]	5508162	CDS_SYNONYMOUS	SNF2-related	GAAACAGTTCTACGAAGCAATGAA	GAAGGGATAGCTGAGAATTCAAAA	NA
SNP0590	Ca_06681		<i>Ca_Kabuli_Chrom7</i>	[G/T]	6815151	CDS_SYNONYMOUS	YABBY protein	ACTGCAGCAATCTATGGTCTGTTA	GCCCTTAAAACTCATCAAAGTGA	NA
SNP0591	Ca_06642		<i>Ca_Kabuli_Chrom7</i>	[A/G]	7147557	CDS_SYNONYMOUS	Protein of unknown function DUF1644	GTTGAATTCGGCATGTATTACAAG	CCCAGAGTCTAGATGGTCTCTCAA	NA
SNP0592	Ca_06627		<i>Ca_Kabuli_Chrom7</i>	[T/G]	7304614	CDS_SYNONYMOUS	Myb, DNA-binding	TGAAAGGGCAAATATGTCTAACTG	GGAGTCCAGTAGCATCATCTCATA	NA
SNP0593	Ca_13149		<i>Ca_Kabuli_Chrom7</i>	[C/T]	8535189	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	CGCTTTGTACGTATCTCTCTTTC	CATGCTAAGAACCTTTGGTCATTCA	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0594	Ca_15363		<i>Ca_Kabuli_Ch07</i>	[C/T]	8553114	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	TGAAGAACAACAACACTATCTGACATC	GACAATGGAAGAGTTGTATGGCTA	NA
SNP0595	Ca_15359		<i>Ca_Kabuli_Ch07</i>	[T/C]	8583890	CDS_SYNONYMOUS	Zinc finger, C2HC5-type	AATCGGGATATACGAGTCACATT	AACCTTGCGGTTGTGAAGTTAAT	NA
SNP0596	Ca_15325		<i>Ca_Kabuli_Ch07</i>	[T/C]	8895087	CDS_SYNONYMOUS	Domain of unknown function DUF629	ATTTTCATGCCAGTGTGATGTTAG	TTGATTTCAGGACCTTGACTGATA	NA
SNP0597	Ca_17298		<i>Ca_Kabuli_Ch07</i>	[C/G]	9555319	CDS_SYNONYMOUS	Protein of unknown function DUF1645	CACAAAAGATAAGCCACCCATATT	CCTTTTATGTCACCCAAAACCTCT	NA
SNP0598	Ca_12811		<i>Ca_Kabuli_Ch07</i>	[G/T]	10521423	CDS_SYNONYMOUS	Zinc finger, RING-type	AGGGATAGAGAAGGAACAGAAACA	TATATTTAAGCCATCCGCTTCTTC	NA
SNP0599	Ca_12840		<i>Ca_Kabuli_Ch07</i>	[G/T]	10859842	CDS_SYNONYMOUS	Zinc finger, RING-type	CAATATAGATTGGTGCAACATGA	CAACCCCTTGATGATCCTAGCTTAT	NA
SNP0600	Ca_09371		<i>Ca_Kabuli_Ch07</i>	[G/A]	11192667	CDS_SYNONYMOUS	Homeobox	TAGAAAGGCACCTCCACTATTTC	ACACAAACCTTCACCTCATCACAGT	NA
SNP0601	Ca_09222		<i>Ca_Kabuli_Ch07</i>	[G/A]	13059852	CDS_SYNONYMOUS	BTB/POZ-like	CAGAACAGAAAGAGATTCTGGAAA	AATTCATGTCTTGTGCTTCTCAG	NA
SNP0602	Ca_16024		<i>Ca_Kabuli_Ch07</i>	[C/T]	13262430	CDS_SYNONYMOUS	SET domain	ATTCCITTGCCAACAAGAACTAC	GAAGATGAGCAAGAGCATCTCAG	NA
SNP0603	Ca_16026		<i>Ca_Kabuli_Ch07</i>	[A/G]	13319871	CDS_SYNONYMOUS	Homeobox	CTGAGATATTAGGAATGGCAATCA	GAATTACTAGAGCAGCAGCAACAG	NA
SNP0604	Ca_16044		<i>Ca_Kabuli_Ch07</i>	[A/C]	13605188	CDS_SYNONYMOUS	Zinc finger, C2H2-type	TTTGCAAATGGTAGTACTTGGCTA	CCAGTCTGCAATCTCAAACATTAG	NA
SNP0605	Ca_16064		<i>Ca_Kabuli_Ch07</i>	[T/C]	13904163	CDS_SYNONYMOUS	Tubby, C-terminal	ACCCATAAGTCCAATGAGATTGT	GCACATTGTCATAGAGGAATTTGA	NA
SNP0606	Ca_23041		<i>Ca_Kabuli_Ch07</i>	[T/C]	14233368	CDS_SYNONYMOUS	Protein of unknown function DUF248, methyltransferase putative	GATAATCACCCCTTCAACATCAAT	TAATATCGAAGTTTGCAACGTCAC	NA
SNP0607	Ca_23042		<i>Ca_Kabuli_Ch07</i>	[T/C]	14282088	CDS_SYNONYMOUS	Protein of unknown function DUF702	CTCAGAGAGAGAGGTGTGACTTTG	CCATTGTTAGCAGGTATAGTTCCA	NA
SNP0608	Ca_09969		<i>Ca_Kabuli_Ch07</i>	[C/G]	14775135	CDS_SYNONYMOUS	Mediator complex, subunit Med4	CAAAGCAGTAAGTAGGTGCTGAAA	CCCTGCTAGGTAGGTCTTACAAA	NA
SNP0609	Ca_15849		<i>Ca_Kabuli_Ch07</i>	[A/G]	17597421	CDS_SYNONYMOUS	Protein of unknown function DUF1639	GCTTCTCATTTTCTGCTTGATGTA	TGCTACTCTGAATCACCTTTCCAAG	NA
SNP0610	Ca_12308		<i>Ca_Kabuli_Ch07</i>	[A/G]	18796768	CDS_SYNONYMOUS	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	TCTGTCAATTGTGCTAGGACTCAC	CAAAGTAGGCATGAACCTAAATGT	NA
SNP0611	Ca_12344		<i>Ca_Kabuli_Ch07</i>	[T/C]	19470527	CDS_SYNONYMOUS	AUX/IAA protein	ATACTTGCATGATGTCATATTCC	TCTACTTTTGGCGATGAACCTACA	NA
SNP0612	Ca_10028		<i>Ca_Kabuli_Ch07</i>	[A/G]	32522201	CDS_SYNONYMOUS	SANT domain, DNA binding	CAGCTTTTCCATCTTGACTTAAT	GTGTCAGTTTGTCTTATCTTCCA	NA
SNP0613	Ca_10015		<i>Ca_Kabuli_Ch07</i>	[T/G]	32784903	CDS_SYNONYMOUS	Transcription initiation factor TFIID	GAGGTGTTTTACCATATCATGCAA	CAACACCAATGACATAGTGAAGGT	NA
SNP0614	Ca_10004		<i>Ca_Kabuli_Ch07</i>	[T/G]	32942951	CDS_SYNONYMOUS	Transcription factor GRAS	AGTACTACCACAAGCAACATCC	GTACTGAATGGCAAGTCATGTTTC	NA
SNP0615	Ca_16177		<i>Ca_Kabuli_Ch07</i>	[C/T]	33573605	CDS_SYNONYMOUS	CCAAT-binding factor	TCTATGCATTTCGACAACTAAAAGG	TAAACGGACCAAAGTCTTAAACC	NA
SNP0616	Ca_17639		<i>Ca_Kabuli_Ch07</i>	[T/C]	35181661	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	AAACTTGCTGTAGGAAAATGGAG	GGCTCAAAGTAGAAAAGTTGCATT	NA
SNP0617	Ca_17781		<i>Ca_Kabuli_Ch07</i>	[T/A]	35799083	CDS_SYNONYMOUS	BTB/POZ-like	CCTGAAAATCAAGATGAAGAGGTT	AGAACTGCAACAAAAGAACAGGT	NA
SNP0618	Ca_13756		<i>Ca_Kabuli_Ch07</i>	[T/C]	36715249	CDS_SYNONYMOUS	Mediator complex, subunit Med12	AGACAGTTCACAGTTCTGTCTGC	TCATCCAGATCAAGCACATAACTT	NA
SNP0619	Ca_19592		<i>Ca_Kabuli_Ch07</i>	[T/C]	39399280	CDS_SYNONYMOUS	Domain of unknown function DUF296	TTTGGATGTAATGATGGGTGTAAG	CTTAGTCGTGGTCAGAAACGAGAT	NA
SNP0620	Ca_25098		<i>Ca_Kabuli_Ch07</i>	[T/C]	39768248	CDS_SYNONYMOUS	Zinc finger, CCCH-type	ATGAGATGGAGACATGGAAGAGAC	CGAAATCCAGCTTTATATTAGGG	NA

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SNP0621	Ca_17996		<i>Ca_Kabuli_Ch07</i>	[A/C]	41387509	CDS_SYNONYMOUS	WD40 repeat	TCATGATACCACCTTTGGCTTTTAG	CATCATACCCACACCTCCAACCT	NA
SNP0622	Ca_17969		<i>Ca_Kabuli_Ch07</i>	[C/T]	42166004	CDS_SYNONYMOUS	Protein of unknown function DUF810	GAGAAATCCTTTAGAGACCAGAACG	TTTAGGAATCACAGAGACAATCCA	NA
SNP0623	Ca_11909		<i>Ca_Kabuli_Ch08</i>	[A/C]	281630	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	GGCTGACTTTATGAACCACTTTCT	GTACGTTACGGAAGTAAATTGC	NA
SNP0624	Ca_11886		<i>Ca_Kabuli_Ch08</i>	[G/A]	510824	CDS_SYNONYMOUS	SNF2-related	TCTCATACTTTTGCTATGCCGATA	GTTACATTACAACCTGCCAGAAGGA	NA
SNP0625	Ca_11866		<i>Ca_Kabuli_Ch08</i>	[A/C]	649491	CDS_SYNONYMOUS	Protein of unknown function DUF1423, plant	AGAGGATTTACCATTTCATTTCAG	TCATCAATCTCTGCTTCAAGTTTC	NA
SNP0626	Ca_11856		<i>Ca_Kabuli_Ch08</i>	[A/T]	709124	CDS_SYNONYMOUS	Protein of unknown function DUF1950	CGGTGGTATAGAGTGAAATGGAAT	AAATTGAGGAGAGACCACTGAAAC	NA
SNP0627	Ca_11855		<i>Ca_Kabuli_Ch08</i>	[G/A]	714974	CDS_SYNONYMOUS	Protein of unknown function DUF1950	GGGACCATTCTTATTTTAAACATGC	CCTTAGGCTTAGTGCCTTATTGAA	NA
SNP0628	Ca_11839		<i>Ca_Kabuli_Ch08</i>	[C/T]	822976	CDS_SYNONYMOUS	Zinc finger, PHD-type	CTGTTGAAGATCAAGAAACAGGTG	TGGATTCACTCATAACCTAACCAA	NA
SNP0629	Ca_15077		<i>Ca_Kabuli_Ch08</i>	[C/T]	1077334	CDS_SYNONYMOUS	WD40 repeat	ATGGAACAACCACATACTCACAAC	TCAATGGTAATGGTGACCTTGAG	NA
SNP0630	Ca_15049		<i>Ca_Kabuli_Ch08</i>	[C/T]	1262561	CDS_SYNONYMOUS	Zinc finger, CCCH-type	AGAAACCTTCTTCACCTTCTTCT	AGGATGGCAAAAGACACATTACTT	NA
SNP0631	Ca_15035		<i>Ca_Kabuli_Ch08</i>	[A/C]	1382454	CDS_SYNONYMOUS	Zinc finger, PHD-type	TTCTGATGAGGTGGTAATTGGTA	TCGACAGTTTGAAAGTTAAGACCA	NA
SNP0632	Ca_15024		<i>Ca_Kabuli_Ch08</i>	[T/C]	1477523	CDS_SYNONYMOUS	WD40 repeat	CTATTGATATGGGTCCAAGAAAC	CTCTGAATCATTAAAGCAACCTCA	NA
SNP0633	Ca_02400		<i>Ca_Kabuli_Ch08</i>	[T/C]	2029384	CDS_SYNONYMOUS	Protein of unknown function DUF544	AAATTAGGATATCGCACAAAGAGG	CTTATTTCTCTGCCCTGCATTTT	NA
SNP0634	Ca_02336		<i>Ca_Kabuli_Ch08</i>	[A/G]	2488709	CDS_SYNONYMOUS	Domain of unknown function DUF828	AGTGTCAAAAGAAAGGACAATGTG	CCTCTTGAGCCTATGGAGTTTFTA	NA
SNP0635	Ca_02278		<i>Ca_Kabuli_Ch08</i>	[A/G]	3041947	CDS_SYNONYMOUS	Protein of unknown function DUF947	AATGGGACAAATTATGACGTAACC	CATTGGACGTAGCTTCCACTAAA	NA
SNP0636	Ca_02251		<i>Ca_Kabuli_Ch08</i>	[A/C]	3269085	CDS_SYNONYMOUS	Homeobox	TGAGCTAGATCAACCAAGTACGTC	GAAACTTAGGCTTACCAACAACAA	NA
SNP0637	Ca_02217		<i>Ca_Kabuli_Ch08</i>	[T/C]	3601517	CDS_SYNONYMOUS	Zinc finger, TAZ-type	GGAGATTGAGAGAGTAAAGGTGCT	GCCTGTTCACTAGTATGAAGTGA	NA
SNP0638	Ca_02182		<i>Ca_Kabuli_Ch08</i>	[G/C]	3911876	CDS_SYNONYMOUS	SANT domain, DNA binding	ATTAAACTGTTGCTCTGTCGTTTG	CCTCTCCACCGTCTATCATAACT	NA
SNP0639	Ca_02167		<i>Ca_Kabuli_Ch08</i>	[A/C]	4042166	CDS_SYNONYMOUS	Protein of unknown function DUF869, plant	CCTATGTGTGCTCATGTATTTTCC	TGGAGGCTTAAATGAGAAGGATTA	NA
SNP0640	Ca_02166		<i>Ca_Kabuli_Ch08</i>	[C/T]	4052702	CDS_SYNONYMOUS	SET domain	AATGTCCAAGTCCCAGTATACCTC	TCCAACGTGTTTGACACTACTGA	NA
SNP0641	Ca_02163		<i>Ca_Kabuli_Ch08</i>	[T/C]	4074135	CDS_SYNONYMOUS	Zinc finger, RING-type	GAGGAAGCAGCAGTAGTAACAACA	CCTTTCCCACTCCTAATACAAAA	NA
SNP0642	Ca_02135		<i>Ca_Kabuli_Ch08</i>	[A/G]	4322058	CDS_SYNONYMOUS	Protein of unknown function DUF3651, TMEM131	TTCTCTCTCTTCCACCATTITT	GGCAATCTTTATATGGGTGAGAC	NA
SNP0643	Ca_02124		<i>Ca_Kabuli_Ch08</i>	[T/A]	4421629	CDS_SYNONYMOUS	Lateral organ boundaries, LOB	AATCCTCAAAGTTCACATACGTT	TTTCACAAGATGCTAGGACAGCTA	NA
SNP0644	Ca_02034		<i>Ca_Kabuli_Ch08</i>	[G/A]	5197254	CDS_SYNONYMOUS	Homeobox	AGATCTCACACACACAATGGAAAT	TAGGTTCAATAACCGAGGCTTCTA	NA
SNP0645	Ca_02004		<i>Ca_Kabuli_Ch08</i>	[T/C]	5412489	CDS_SYNONYMOUS	Protein of unknown function DUF702	AGCTCATAAATCTCTCTGCACAA	ACATCTAAATCCGCTTGAGAACT	NA
SNP0646	Ca_10735		<i>Ca_Kabuli_Ch08</i>	[G/T]	6544248	CDS_SYNONYMOUS	Zinc finger, C2H2-type	CCCGGCTTATAGATATTTCTTATC	TCTATCTGGGGGATCAATATTCT	NA
SNP0647	Ca_10698		<i>Ca_Kabuli_Ch08</i>	[A/G]	6943710	CDS_SYNONYMOUS	ARID/BRIGHT DNA-binding domain	ACACTGGTCATCACAATTACCATC	TGTAGGAGGTTGTTGTGTTTCAT	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0648	Ca_10687		<i>Ca_Kabuli_Chrom8</i>	[G/A]	7037715	CDS_SYNONYMOUS	Protein of unknown function DUF647	TGGAGAACTTGACTGGTTCTATGA	AACAGGCTCTTAGAATTTGGATTG	NA
SNP0649	Ca_10614		<i>Ca_Kabuli_Chrom8</i>	[A/G]	7726879	CDS_SYNONYMOUS	Zinc finger, CCHC-type	TGAATCCGTATCAGAGTAATTGGA	GAAGCAACAGAACTGCTATACTGG	NA
SNP0650	Ca_10613		<i>Ca_Kabuli_Chrom8</i>	[T/C]	7729693	CDS_SYNONYMOUS	Zinc finger, CCHC-type	TCGTTAGAGAGTAGGAGGAAGAA	TCTAACTATTGGAACCAACTTCC	NA
SNP0651	Ca_10604		<i>Ca_Kabuli_Chrom8</i>	[T/C]	7807065	CDS_SYNONYMOUS	SET domain	CGTAACGCAAGCTTCAAATAAAC	CATTCCAAACAAAACAAGTCCTTC	NA
SNP0652	Ca_11534		<i>Ca_Kabuli_Chrom8</i>	[A/C]	9112172	CDS_SYNONYMOUS	Protein of unknown function DUF1399	ATTTAGAATGTGAGTGCAGTTGCT	TATGATCTGAGCATGGAACCTATT	NA
SNP0653	Ca_18416		<i>Ca_Kabuli_Chrom8</i>	[T/G]	10258892	CDS_SYNONYMOUS	Zinc finger, PHD-type	GTCATGGTGTAACTCTGATGCTTT	AAACAAAGCTAGAACCTGAAATGC	NA
SNP0654	Ca_16839		<i>Ca_Kabuli_Chrom8</i>	[A/C]	11186986	CDS_SYNONYMOUS	Zinc finger, RanBP2-type	CCTAGATGCATACTCGATTGGTC	TTTCCAGAAGCAGTAACAAACAG	NA
SNP0655	Ca_16820		<i>Ca_Kabuli_Chrom8</i>	[G/A]	11403805	CDS_SYNONYMOUS	SANT domain, DNA binding	ACGGCGTCTTTAGTAGTTTGACT	TGTAGGGACAGGTAATGCATTTTA	NA
SNP0656	Ca_17888		<i>Ca_Kabuli_Chrom8</i>	[A/C]	15555771	CDS_SYNONYMOUS	Protein of unknown function DUF1675	GAGCTCAATCTGTAGTAATGGAA	ACAGGACCTCAAAACAACATTCT	NA
SNP0657	Ca_15527		<i>Ca_Kabuli_Chrom8</i>	[A/G]	16145419	CDS_SYNONYMOUS	Domain of unknown function DUF292, eukaryotic	GCAGCCAGTATCTTTATTTTGGTT	CGAGGATAAAGCTCTTGAGGAATA	NA
SNP0658	Ca_21518		<i>Ca_Kabuli_Scaffold_1281</i>	[G/A]	258565	CDS_SYNONYMOUS	Transcriptional factor B3	CCTATAGCGCATATTTCCAACTCT	AATGGTTGGATATGTTGGTAGTGA	NA
SNP0659	Ca_21523		<i>Ca_Kabuli_Scaffold_1281</i>	[A/G]	316037	CDS_SYNONYMOUS	Zinc finger, RING-type	GCAAAACTCACCCACCATTATATC	CCGAAAATCCCTTCTATTAATCAC	NA
SNP0660	Ca_22581		<i>Ca_Kabuli_Scaffold_134</i>	[C/T]	218290	CDS_SYNONYMOUS	SET domain	TTCGTCAAAACAGAGTCTCTTCAT	AAACCAGGATAATCTCCATACTGC	NA
SNP0661	Ca_08786		<i>Ca_Kabuli_Scaffold_1348_1</i>	[A/G]	950995	CDS_SYNONYMOUS	Zinc finger, CCCH-type	GATTCGGTTGCAGTTTCATACTC	AGACTGCTGAATTGCACATCATT	NA
SNP0662	Ca_08787		<i>Ca_Kabuli_Scaffold_1348_1</i>	[G/A]	959780	CDS_SYNONYMOUS	Transcription factor jumonji/aspartyl beta-hydroxylase	GAGGATCATGATTGCATAGTTTG	CTCATAATCGATTCCCATTTCTTC	NA
SNP0663	Ca_21995		<i>Ca_Kabuli_Scaffold_1351</i>	[G/A]	172111	CDS_SYNONYMOUS	Protein of unknown function DUF2419	ACTGCACAAGCATAATCAATCAC	AGCAGCTGATCTATTTGAAGAACA	NA
SNP0664	Ca_21070		<i>Ca_Kabuli_Scaffold_157</i>	[T/A]	151131	CDS_SYNONYMOUS	Zinc finger, DHHC-type, palmitoyltransferase	AAAAACTTGACCTAGAAGGCTCAC	AAAATAGCAGATTGGGATTCAGAG	NA
SNP0665	Ca_26451		<i>Ca_Kabuli_Scaffold_2516</i>	[T/C]	58947	CDS_SYNONYMOUS	Domain of unknown function DUF125, transmembrane	TGCCCAAACTCTTGATTAGAGTAT	CATTAATTCAACTACGGATTCTGC	NA
SNP0666	Ca_26161		<i>Ca_Kabuli_Scaffold_2569</i>	[T/G]	58152	CDS_SYNONYMOUS	WD40 repeat	CAGTCAAACGAGCTTTGATTGTAG	TACATAAATTCAGCCCACCAATC	NA
SNP0667	Ca_26888		<i>Ca_Kabuli_Scaffold_4011</i>	[G/C]	96223	CDS_SYNONYMOUS	Protein of unknown function DUF1296	ATGTGAAACGCACATAAATGACTC	TTCTTAACTGCCTAGTGCCTACT	NA
SNP0668	Ca_22883		<i>Ca_Kabuli_Scaffold_421_2</i>	[C/A]	341095	CDS_SYNONYMOUS	Helix-loop-helix DNA-binding domain	AGTCTACTTCGCTTACCGATCAAC	GCAGTAGTAGGCTTTTCAGACACA	NA
SNP0669	Ca_22606		<i>Ca_Kabuli_Scaffold_451</i>	[A/G]	117231	CDS_SYNONYMOUS	HSA	AGCCTAAATCATCTCTCTCTGTG	TAAGCATGTGCCAGAAGAACTAAC	NA
SNP0670	Ca_24566		<i>Ca_Kabuli_Scaffold_50</i>	[T/A]	153593	CDS_SYNONYMOUS	Protein of unknown function DUF3527	TCGTGTAAACAAATGGTTTTCGTC	GTGACTTCTCGGTGTACCACTTT	NA
SNP0671	Ca_23923		<i>Ca_Kabuli_Scaffold_545</i>	[T/C]	138848	CDS_SYNONYMOUS	Zinc finger, C2H2-type	AAATCCATGCACATATACCACTG	CCGAGACTATTATCGAAGAACCAG	NA
SNP0672	Ca_28031		<i>Ca_Kabuli_Scaffold_7355</i>	[C/G]	1606	CDS_SYNONYMOUS	CCT domain	CACCGCTATTTAAAAACACCGTA	TCAGCTTTGGCTCCCTATTATC	NA
SNP0673	Ca_23375		<i>Ca_Kabuli_Scaffold_812</i>	[T/C]	332746	CDS_SYNONYMOUS	Protein of unknown function DUF642	AGGACAAGGAGTCAAAACAGGTAA	GACGGCCATACCTGAATCTATATC	NA
SNP0674	Ca_22417		<i>Ca_Kabuli_Scaffold_845</i>	[G/A]	139268	CDS_SYNONYMOUS	Zinc finger, RING-type	TATTTGTATCCTCCACATAGCA	ACCGGTTGTGAAAAAGAAATAG	NA

SNP IDs	Kabuli/desi accession IDs	gene	Kabuli/desi chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0675	Ca_27726		Ca_Kabuli_Scaffold_C11175430	[A/G]	987	CDS_SYNONYMOUS	Protein of unknown function DUF3743	AAATATGTCAGGAATTCACCACT	ATACATGTTGCAATAGGGGTTTCT	NA
SNP0676	Ca_27691		Ca_Kabuli_Scaffold_C11181782	[A/G]	6215	CDS_SYNONYMOUS	Domain of unknown function DUF1084	CCTGGATCACTTGTCTATTGA	TCGGGTTTATGTTTAGGGTTAAG	NA
SNP0677	Ca_00372		Ca_Desi_Chrom1	[T/C]	3675786	CDS_SYNONYMOUS	Auxin response factor 6	GTGGCAATGTAATAGCATTTTGAG	TTGCGTTTTAGCTGTGAAGTTTAG	NA
SNP0678	Ca_00550		Ca_Desi_Chrom1	[C/T]	6399989	CDS_SYNONYMOUS	Homeobox-leucine zipper protein ATHB-14	ATACGATTGAGCACGAAGAGGTAT	CATCATCATCATTGAGAAGCTTCC	NA
SNP0679	Ca_01851		Ca_Desi_Chrom2	[A/C]	13100484	CDS_SYNONYMOUS	Scarecrow-like protein 3	TTCTTTACTTGCTTTGCTGTGC	GAGGTTCTTGAAACTGTGGATTCT	NA
SNP0680	Ca_01922		Ca_Desi_Chrom2	[A/C]	14163542	CDS_SYNONYMOUS	Lysine-specific histone demethylase 1 homolog 3	GGAAAGAGCATAGCAACCTTATTC	GAAAATATCGGAGTGAGTGTGATG	NA
SNP0681	Ca_02202		Ca_Desi_Chrom3	[G/A]	698068	CDS_SYNONYMOUS	Protein LHY	CATCAGCTCTTCACTGCTAGAGG	ATTACACAGTGGAGCAAAGTATGG	NA
SNP0682	Ca_02392		Ca_Desi_Chrom3	[T/C]	2986233	CDS_SYNONYMOUS	WD repeat-containing protein 48	TAGCACACTCGTTTCTTGTTCTTC	GAACACTTCCAGTGCAATTACAG	NA
SNP0683	Ca_02541		Ca_Desi_Chrom3	[A/T]	4356878	CDS_SYNONYMOUS	WD repeat domain phosphoinositide-interacting protein 3	TGCTCCTTCAACTTCTTTTAACC	TTTGTCATTTCCTCACATCATACC	NA
SNP0684	Ca_02773		Ca_Desi_Chrom3	[C/T]	8499689	CDS_SYNONYMOUS	Auxin response factor 8	GAATATTGTGCATGTGACATTGTG	TGTATGGCACACTAGAAGGGTTTA	NA
SNP0685	Ca_02786		Ca_Desi_Chrom3	[G/C]	8826351	CDS_SYNONYMOUS	Transcription elongation factor SPT6	AAAACAGGTTAATAGAAGCCAGA	TATATTGTGGGTCTCATCTGTTGG	NA
SNP0686	Ca_03197		Ca_Desi_Chrom3	[T/C]	15386074	CDS_SYNONYMOUS	Zinc finger CCH domain-containing protein 5	GTTGCATATGCTTGAAATCTCTTG	CTTTGATTGTCACAACATCACTG	NA
SNP0687	Ca_03610		Ca_Desi_Chrom3	[C/T]	19827573	CDS_SYNONYMOUS	Bromodomain adjacent to zinc finger domain protein 1A	CTGTTGAAGATCAAGAAACAGGTG	TGGATTCACATACCTAACCAA	NA
SNP0688	Ca_03691		Ca_Desi_Chrom3	[C/T]	20603607	CDS_SYNONYMOUS	Transcription activator BRG1	GTTACATTCAACTGCCAGAAGGA	TCTCATACTTTGCTATGCCGATA	NA
SNP0689	Ca_03895		Ca_Desi_Chrom4	[C/T]	198665	CDS_SYNONYMOUS	Transcription factor RF2a	TACTATATGGATGCGACAATAGCC	ACTTTGGAGTGTTGTGTTGTGT	NA
SNP0690	Ca_04140		Ca_Desi_Chrom4	[G/C]	3766974	CDS_SYNONYMOUS	CCT motif family protein	CCGAGACTATTATCGAAGAACCAG	AAATTCCATGCACATATACCACTG	NA
SNP0691	Ca_04363		Ca_Desi_Chrom4	[T/C]	7647362	CDS_SYNONYMOUS	Lysine-specific demethylase 3B	GGACTTCAACCTTGAACTGGTATC	TCCGTATTTAAGACAGTTGGATGA	NA
SNP0692	Ca_04406		Ca_Desi_Chrom4	[T/C]	8131392	CDS_SYNONYMOUS	Transcriptional corepressor LEUNIG	CAAGTAACAAAGCCACGGACTAAT	GTATGGTTGATGACAACATGGAAT	NA
SNP0693	Ca_04552		Ca_Desi_Chrom4	[T/C]	9855603	CDS_SYNONYMOUS	Protein TIME FOR COFFEE	TAGCAGCATCCACTTTTCTATTG	CAGAAGTGTGCTTTGAGGAAGAA	NA
SNP0694	Ca_05622		Ca_Desi_Chrom5	[A/G]	5193039	CDS_SYNONYMOUS	BEACH domain-containing protein lvsC	TGGTAAGTTTCATCTTCTGCATA	AATGAGTCCAACATCATGTCTTAA	NA
SNP0695	Ca_05623		Ca_Desi_Chrom5	[C/G]	5232897	CDS_SYNONYMOUS	GATA transcription factor 25	GAAGATGTTTATGTTCCGGTGAT	GAAGGACAGCTGCTACAAATAGA	NA
SNP0696	Ca_05955		Ca_Desi_Chrom5	[T/C]	8680914	CDS_SYNONYMOUS	Two-component response regulator-like PRR95	ACTTCCCTGATCAACAAGAGAAC	TTATCGAATCAGAGTGTGTCAGGT	NA
SNP0697	Ca_07258		Ca_Desi_Chrom6	[C/T]	10167738	CDS_SYNONYMOUS	Homeobox protein 10	CCTTGTAACGGTTAGGAATGAAT	AAGTGCATTTAATCGCTCTCTAC	NA
SNP0698	Ca_07479		Ca_Desi_Chrom7	[T/A]	1467358	CDS_SYNONYMOUS	AP2-like ethylene-responsive transcription factor AIL1	GGATAATAGTCGAGAAAAGAAGG	GAACTTGAAACAAAGGCAATAGT	NA
SNP0699	Ca_07522		Ca_Desi_Chrom7	[A/G]	2069964	CDS_SYNONYMOUS	Transcription factor RF2a	TTAATCCTTCACAAATCGGTAGAC	GACAGAAATACCATCTCGGAGTTT	NA
SNP0700	Ca_07849		Ca_Desi_Chrom7	[G/A]	6950249	CDS_SYNONYMOUS	Homeobox-leucine zipper protein HAT22	TAGAAAGGCACCTTCCACTATTTC	ACACAAACTTCACCTCATCAGT	NA
SNP0701	Ca_07873		Ca_Desi_Chrom7	[G/T]	7266190	CDS_SYNONYMOUS	SBP (S-ribonuclease binding protein) family protein	GGATAGAGAAGGAACAGAAAACAGG	TTCTATATTTAACCCATCCGCTTC	NA

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SNP0702	Ca_08285		<i>Ca_Desi_Chro8</i>	[C/T]	4722955	CDS_SYNONYMOUS	Two-component response regulator ARR2	AGTAGCAGACATTTTCAGTGCTTTG	GCTAATGAAGGAACCTGGAGAAAC	NA
SNP0703	Ca_15142		<i>Ca_Desi_Scaffold_1174</i>	[C/T]	36613	CDS_SYNONYMOUS	NAC domain-containing protein 18	GGCTGAATTCCTAGTTAACGTCAT	GATGACAAAGTAGCAACGGTATTG	NA
SNP0704	Ca_09051		<i>Ca_Desi_Scaffold_1236</i>	[C/T]	338504	CDS_SYNONYMOUS	BEL1-like homeodomain protein 9	CTTGAAACACCATAATGGGCAAT	ATAGGTCAGGTTTTCTTGATCAGC	NA
SNP0705	Ca_15415		<i>Ca_Desi_Scaffold_1282</i>	[C/T]	75640	CDS_SYNONYMOUS	BTB/POZ domain-containing protein At3g50780	AGGTGGCATTTAAGGGTTGTATAG	GGTTGGAGATGAAGAAGAAAAA	NA
SNP0706	Ca_15434		<i>Ca_Desi_Scaffold_1290</i>	[G/A]	33898	CDS_SYNONYMOUS	Transcription initiation factor TFIIID subunit 7	GCAATTTAGTGAGGATGGAAGAAG	AACCCATCAAAACACTATTTTAGC	NA
SNP0707	Ca_15776		<i>Ca_Desi_Scaffold_1426</i>	[C/T]	64665	CDS_SYNONYMOUS	Zinc finger CCCH domain-containing protein 6	AAGACAAAGTTGCCAGGTATAAG	TTGATATGCACAGTTAGCTCCATT	NA
SNP0708	Ca_15813		<i>Ca_Desi_Scaffold_1441</i>	[T/G]	27770	CDS_SYNONYMOUS	MATH domain-containing protein At5g43560	GATCTGCTACTGCTACTGGCTTG	AAGTGTGGAAAATACTTGCTGTA	NA
SNP0709	Ca_15904		<i>Ca_Desi_Scaffold_1484</i>	[A/C]	25798	CDS_SYNONYMOUS	BTB/POZ domain-containing protein NPY1	AGTTAGATGGTTGCCTGATTCTGT	CCTACCACCTTACACTTCAAAGCA	NA
SNP0710	Ca_11082		<i>Ca_Desi_Scaffold_158</i>	[G/A]	221533	CDS_SYNONYMOUS	Protein of unknown function (DUF620)	TCGTCCATTCATTGGTTACACTAT	AGAATGAAACAGTCTCTTCGTTT	NA
SNP0711	Ca_16252		<i>Ca_Desi_Scaffold_1667</i>	[T/C]	33508	CDS_SYNONYMOUS	Zinc finger CCCH domain-containing protein 53	CTCAGTCACCTTCACCTTTTCTTT	ATCTTGAAACAGGTCCATAAATGCT	NA
SNP0712	Ca_16997		<i>Ca_Desi_Scaffold_2142</i>	[T/A]	30207	CDS_SYNONYMOUS	Zinc finger CCCH domain-containing protein 7	ACTACGTGACTGATTTTGTCTTCC	CTAGGATTCAGGATGGTCAAGATT	NA
SNP0713	Ca_11558		<i>Ca_Desi_Scaffold_252</i>	[C/T]	87593	CDS_SYNONYMOUS	B3 domain-containing transcription factor ABI3	AATGGTTGGATATGTTGGTAGTGA	CCTATAGCGCATATTTCCAACTCT	NA
SNP0714	Ca_17653		<i>Ca_Desi_Scaffold_2603</i>	[C/T]	4601	CDS_SYNONYMOUS	Transcriptional corepressor SEUSS	GCCTTCCTCTTTGAGATCAAATTC	CAGTGCCATACATCCTGAAAATAA	NA
SNP0715	Ca_11735		<i>Ca_Desi_Scaffold_271</i>	[C/T]	33434	CDS_SYNONYMOUS	Tubby-like F-box protein 8	TGTTTCTTTGAAGCAGGTGAGATA	TAGGGTATCGATAGTCCATTGTGA	NA
SNP0716	Ca_17918		<i>Ca_Desi_Scaffold_2850</i>	[C/A]	6581	CDS_SYNONYMOUS	Mediator of RNA polymerase II transcription subunit 18	TGTATAAAGTGCTTGCCCTCAGTGT	CACATAATAACCACTTCCGACTGA	NA
SNP0717	Ca_10605		<i>Ca_Desi_Scaffold_32</i>	[G/C]	80728	CDS_SYNONYMOUS	Probable WRKY transcription factor 19	ATCTCTGCTGATTTTCTCTCCAAT	CTACAAGCAGCAACAGTGAACCTT	NA
SNP0718	Ca_18458		<i>Ca_Desi_Scaffold_3563</i>	[G/C]	1235	CDS_SYNONYMOUS	C2H2-like zinc finger protein	GAAAGGTACCAACTTTCCTTTGTC	ACGCCACTGTCTCTAAAACCTTACC	NA
SNP0719	Ca_12314		<i>Ca_Desi_Scaffold_364</i>	[T/C]	38866	CDS_SYNONYMOUS	Myb-related protein 3R-1	TGCAAAGAGATGGTACAGATCCTA	GGACACTCTGGTCAAAGCTATTT	NA
SNP0720	Ca_18943		<i>Ca_Desi_Scaffold_4448</i>	[C/T]	15603	CDS_SYNONYMOUS	Protein of unknown function (DUF810)	CTGTGGTGCAAATATATCAGAGG	GCGGTTTTAATTGTATACGAGAC	NA
SNP0721	Ca_13425		<i>Ca_Desi_Scaffold_614</i>	[A/G]	105277	CDS_SYNONYMOUS	Protein of unknown function, DUF593	CACCCAATTGAGTAAGTTGTTTCA	CACTATATTCACCCACAGCATAA	NA
SNP0722	Ca_19827		<i>Ca_Desi_Scaffold_7085</i>	[A/G]	5369	CDS_SYNONYMOUS	Auxin response factor 2	TGTAGTCCAGTCCTTGTACTCA	GTGTATTGTCAGGTGTTGTTGGTT	NA
SNP0723	Ca_10810		<i>Ca_Desi_Scaffold_93</i>	[T/C]	155942	CDS_SYNONYMOUS	Protein of unknown function (DUF1644)	CCCAGAGCTAGATGGTCTCCTAA	GTTGAATTGCCGATGTATTACAAG	NA
SNP0724	Ca_14531		<i>Ca_Desi_Scaffold_940</i>	[A/C]	27874	CDS_SYNONYMOUS	Protein of unknown function (duplicated DUF1399)	ATTTAGAATGTGAGTGCAGTTGCT	TATGATCTGAGCATGGAACCTATT	NA
SNP0725	Ca_28178		<i>Ca_Kabuli_Scaffold_3337</i>	[C/T]	18022	DRR	Domain of unknown function DUF828	GACCGATTTTCTCCATTTAGTGAC	GCTGTGGAACTTGGTTATAGATT	NA
SNP0726	Ca_27768		<i>Ca_Kabuli_Scaffold_799</i>	[C/T]	3928	DRR	Domain of unknown function DUF828	GTTACCTAGTAGAACAGGGGAAAGA	TGTATTTAGTGGTTGAAACGCTCT	NA
SNP0727	Ca_28165		<i>Ca_Kabuli_Scaffold_C111</i> 81840	[A/G]	19192	DRR	Domain of unknown function DUF547	GTTACCTAGTAGAACAGGGGAAAGA	TGTATTTAGTGGTTGAAACGCTCT	NA
SNP0728	Ca_00149		<i>Ca_Desi_Chro1</i>	[T/C]	1480187	DRR	Transcription factor GTE7	AACTCCAACCTGTATTGGTTGGTC	GATGAAGATGACGATGATGAAGAC	NA

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SNP0729	Ca_00159		<i>Ca_Desi_Chrom1</i>	[C/T]	1598211	DRR	Protein FARI-RELATED SEQUENCE 11	GGATGCGTGATGATCTCATCTAA	ACTGAAGACACCATTCTCTAAAGG	NA
SNP0730	Ca_01546		<i>Ca_Desi_Chrom2</i>	[C/G]	7082948	DRR	ABSCISIC ACID-INSENSITIVE 5-like protein 2	CGATCTACAATCTTGTGAAAACG	GAGATACTCACCGAAACCATCATT	NA
SNP0731	Ca_02518		<i>Ca_Desi_Chrom3</i>	[T/G]	4174824	DRR	Unknown expressed protein	GCGTGCACAGAGTTATGTATTGAT	ATCATATTTGTTGCTTGCTGTGAG	NA
SNP0732	Ca_03068		<i>Ca_Desi_Chrom3</i>	[T/G]	13208922	DRR	far-red elongated hypocotyl 1	CCTACGATGATCTCGATACACAAG	AACGTGACACTTTATAGCCCTTTT	NA
SNP0733	Ca_04017		<i>Ca_Desi_Chrom4</i>	[T/C]	2042496	DRR	Protein of unknown function (DUF620)	AGCTAAGATTTGCTTCGGTTAGTG	GTGATTCTGGATCAAAAGTGTA	NA
SNP0734	Ca_06184		<i>Ca_Desi_Chrom5</i>	[C/T]	11335385	DRR	SMAD/FHA domain-containing protein	TGGAAACTTAGTTGCAGAAATCAG	AGGCACCTGTTATTACATTGACCA	NA
SNP0735	Ca_07787		<i>Ca_Desi_Chrom7</i>	[C/G]	6252949	DRR	zinc finger (Ran-binding) family protein	TAATTCAAATGTCTGTCCACGTC	CAACTTCTGTAGATGCAACCAT	NA
SNP0736	Ca_08198		<i>Ca_Desi_Chrom8</i>	[A/G]	3940158	DRR	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 6	ATTTCCTAGGACGTAGTGCAAAG	GCTAGGTTTTAGGGGAGAATCAT	NA
SNP0737	Ca_17150		<i>Ca_Desi_Scaffold_2238</i>	[A/G]	37374	DRR	Zinc finger with UFM1-specific peptidase domain protein	TCAACCATGCTATCTATGGCTCTA	AGGTGTGGGTTGAAGTAAAGAAG	NA
SNP0738	Ca_17182		<i>Ca_Desi_Scaffold_2259</i>	[T/A]	28398	DRR	Transcription factor MYB86	TTTAACGGTGCATCACTAAGAAAG	ATGGTATCACAACGCAATTTAGG	NA
SNP0739	Ca_08979		<i>Ca_Desi_Scaffold_233</i>	[A/C]	50084	DRR	Protein of unknown function (DUF679)	ACTTGCATCCCTAAGTTGTCTTTC	CTAACACACATCTCAATCACACA	NA
SNP0740	Ca_10605		<i>Ca_Desi_Scaffold_32</i>	[T/C]	78989	DRR	Probable WRKY transcription factor 19	TTTAACCTCTGAAGAACCATCTCC	ATTGGAGAGAAGATTAGCAGCAAG	NA
SNP0741	Ca_19685		<i>Ca_Desi_Scaffold_6521</i>	[T/C]	5184	DRR	WD40 repeat-containing protein SMU1	ATTATATCTCTGTTTATTCC	TCACATATGATAATGGTTGCACTG	NA
SNP0742	Ca_04140		<i>Ca_Desi_Chrom4</i>	[T/C]	3764973	URR	CCT motif family protein	TTCCACCTTGAACCTAGTGATGC	ATGAGTCTATGAAGCACTGACACC	NA
SNP0743	Ca_04272		<i>Ca_Desi_Chrom4</i>	[T/G]	5949743	URR	BED zinc finger; hAT family dimerisation domain	TTTGTTAGAGTGAATGTGGCTGT	GATGCATGATGTTAACACACATTT	NA
SNP0744	Ca_05237		<i>Ca_Desi_Chrom4</i>	[C/A]	22037221	URR	Protein FARI-RELATED SEQUENCE 11	TCCCGATAAATCAACTGTCTACTA	GCTTCACATTGACAATTTATGTCC	NA
SNP0745	Ca_17178		<i>Ca_Desi_Scaffold_2257</i>	[A/G]	32638	URR	Protein of unknown function, DUF617	CCACAGAAAAAGGAAGATCTCAAT	GGCATACATGGCTTTGTAGTTAGA	NA
SNP0746	Ca_12419		<i>Ca_Desi_Scaffold_385</i>	[T/C]	167051	URR	High mobility group B protein 7	CCATCAAGAACAGATATTGCAAAG	CGTGTCTAGAGAGTCAAAAACAG	NA
SNP0747	Ca_13660		<i>Ca_Desi_Scaffold_680</i>	[C/T]	16012	URR	Lysine-specific demethylase 5D	ATTCAGGTCCATGGGTTAGTAGA	TTGTTATCTTTCCAGACACTACC	NA
SNP0748	Ca_20116		<i>Ca_Desi_Scaffold_8872</i>	[C/T]	3778	URR	Zinc finger CCCH domain-containing protein	CTGAGGTAGCATCAACAAAAACAT	CTGTAAAAAGAAAGGGCAATGAAG	NA
SNP0749	Ca_10810		<i>Ca_Desi_Scaffold_93</i>	[G/C]	157340	URR	Protein of unknown function (DUF1644)	TTGCAAACCTACTACTCCAGGAATG	TCAGTCCTCAACACCCCTACTAAT	NA
SNP0750	Ca_TC07446		<i>Ca_Desi_Chrom1</i>	[C/T]	1661476	CDS_NON_SYNONYMOUS	GeBP	GCTCAATCCGTTTAAGCCAGT	CCCTAACACCAATTCTCGATG	NA
SNP0751	Ca_TC05193		<i>Ca_Desi_Chrom1</i>	[T/C]	1827593	CDS_NON_SYNONYMOUS	Jumonji	TGAGCACACAGATGACAGTGA	TACGAACACAGGCTCCAAAG	NA
SNP0752	Ca_TC04526		<i>Ca_Desi_Chrom1</i>	[G/A]	2188544	CDS_NON_SYNONYMOUS	SNF2	ACTGCTGGCAGTTCCTCTGT	CTGTTCACTGTGGCTTTGGA	NA
SNP0753	Ca_TC17243		<i>Ca_Desi_Chrom1</i>	[A/T]	2602506	CDS_NON_SYNONYMOUS	SBP	AGTGATCATTTGGTCATTAAGCA	AAAGTGGGGTGAGGAAAAG	NA
SNP0754	Ca_TC11301		<i>Ca_Desi_Chrom1</i>	[G/A]	2631901	CDS_NON_SYNONYMOUS	C3H	TCTAGGGCCACCAAGTCATC	TATCTTCGGTGTGCGGAATC	NA
SNP0755	Ca_TC17851		<i>Ca_Desi_Chrom1</i>	[G/C]	3650162	CDS_NON_SYNONYMOUS	MADS	TGTTTCCTCATCAAGCTTGC	CAAGTGAAGGTGCTTCTCCA	NA

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SNP0756	Ca_TC03663		<i>Ca_Desi_Chrom1</i>	[G/A]	3734533	CDS_NON_SYNONYMOUS	Bromodomain	AGGCTGTCCAGGTGATCTGT	GGGCAGCTTCTCTTTCCCTTT	NA
SNP0757	Ca_TC11111		<i>Ca_Desi_Chrom1</i>	[G/C]	4325063	CDS_NON_SYNONYMOUS	mTERF	TCTCCAATTTTCCCCACAAA	GCAACTGCACATCAGTGCT	NA
SNP0758	Ca_TC15990		<i>Ca_Desi_Chrom1</i>	[T/C]	4379384	CDS_NON_SYNONYMOUS	SNF2	CGTCTGGGACACCTCAAAT	CAAGTTGATTGCAGGCTCA	NA
SNP0759	Ca_TC07591		<i>Ca_Desi_Chrom1</i>	[G/T]	4866342	CDS_NON_SYNONYMOUS	BSD	GCGATCTCGAAGATTTCAGC	AGCCACATAACATGGTGCAA	NA
SNP0760	Ca_TC17358		<i>Ca_Desi_Chrom1</i>	[C/G]	5452945	CDS_NON_SYNONYMOUS	MYB-related	CCCATTAAAGAGCTCATATAGCAA	AACCTATGCTAGTTTGCTTATCCCTA	NA
SNP0761	Ca_TC08361		<i>Ca_Desi_Chrom1</i>	[T/C]	5666051	CDS_NON_SYNONYMOUS	WRKY	CTTGTTTGCGAACCTGGACAA	CGATCCAAGTTTCCACCAATT	NA
SNP0762	Ca_TC14813		<i>Ca_Desi_Chrom1</i>	[G/A]	6592726	CDS_NON_SYNONYMOUS	FHA	TCTCTCTCTGTCCGCTTCT	AGTCACCCGGAACAAATCGTC	NA
SNP0763	Ca_TC01171		<i>Ca_Desi_Chrom1</i>	[A/T]	7417345	CDS_NON_SYNONYMOUS	HB	TGCAAAACCTGTGTCATTA	GTCCAACAGGACCTCTCAA	NA
SNP0764	Ca_TC15349		<i>Ca_Desi_Chrom1</i>	[G/A]	7436472	CDS_NON_SYNONYMOUS	CCAAT	CTCAAGATTGTGGTGGGTGT	GGGGTTGTACAAAGCCAGAA	NA
SNP0765	Ca_TC11727		<i>Ca_Desi_Chrom1</i>	[G/C]	8284578	CDS_NON_SYNONYMOUS	MYB-related	TGTTGTATCTAAGCCAATTCACATCC	GCTTCAAGTACTTTATTGCATCTC	NA
SNP0766	Ca_TC04704		<i>Ca_Desi_Chrom1</i>	[G/A]	9654075	CDS_NON_SYNONYMOUS	Trihelix	GTTACCCCTCACCCCAAAGGT	CAATCTGCTGCCATTTTCA	NA
SNP0767	Ca_TC13639		<i>Ca_Desi_Chrom1</i>	[G/C]	10455472	CDS_NON_SYNONYMOUS	MYB	ACTTGCTGGATTGCAAAGGT	CCCTCAAATGCATACATGG	NA
SNP0768	Ca_TC10361		<i>Ca_Desi_Chrom1</i>	[G/A]	11285630	CDS_NON_SYNONYMOUS	GRAS	AGGCATGCTAAATTGCCAAC	CGCTGTGTCTGAAGAAAAA	NA
SNP0769	Ca_TC04427		<i>Ca_Desi_Chrom1</i>	[G/A]	12530205	CDS_NON_SYNONYMOUS	AP2-EREBP	GGGAGCTTGTGAGGATTGTA	CTCGAATTGCAACAACAAA	NA
SNP0770	Ca_TC10826		<i>Ca_Desi_Chrom1</i>	[G/C]	12928919	CDS_NON_SYNONYMOUS	G2-like	TGTGGCTGTGAGAGATCCAA	TCCCGTACTCGTGCATAA	NA
SNP0771	Ca_TC19580		<i>Ca_Desi_Chrom1</i>	[C/T]	13679988	CDS_NON_SYNONYMOUS	AP2-EREBP	GGCACACACAGAATCCAG	CTTTACCAACGCAACGCAAT	NA
SNP0772	Ca_TC14890		<i>Ca_Desi_Chrom1</i>	[T/C]	13801427	CDS_NON_SYNONYMOUS	bHLH	ACACTCTCCCTGCAAGAA	CACGACGCTTAGTGTTCAA	NA
SNP0773	Ca_TC08193		<i>Ca_Desi_Chrom1</i>	[T/C]	13994815	CDS_NON_SYNONYMOUS	HB	ATGCCTCAATGATCGGAAC	CACCAAATGCATGTCCAGAG	NA
SNP0774	Ca_TC11910		<i>Ca_Desi_Chrom1</i>	[A/C]	15378650	CDS_NON_SYNONYMOUS	bHLH	TGGACGAAATGAATGTCACC	TTTCTAGCAATCTTCACGTGGT	NA
SNP0775	Ca_TC18264		<i>Ca_Desi_Chrom1</i>	[A/C]	15606770	CDS_NON_SYNONYMOUS	WRKY	CCATCCCAATCCCTTCTTT	CAATGCAAGCTGGACAAAA	NA
SNP0776	Ca_TC14070		<i>Ca_Desi_Chrom1</i>	[G/T]	16080907	CDS_NON_SYNONYMOUS	GRAS	CAGGAGCAACACAACCTCAGG	CAACATTGCCCATCTTTCT	NA
SNP0777	Ca_TC09197		<i>Ca_Desi_Chrom1</i>	[T/C]	16680465	CDS_NON_SYNONYMOUS	NAC	TGCAGCCAATTGTCTATTCA	AGGTTACCCCGAGTACAAC	NA
SNP0778	Ca_TC08115		<i>Ca_Desi_Chrom1</i>	[T/C]	17405553	CDS_NON_SYNONYMOUS	CAMTA	AGGCTGAAGTTTTGCCTCA	GCATCAGAAGCATCCATCAA	NA
SNP0779	Ca_TC05008		<i>Ca_Desi_Chrom1</i>	[A/C]	18460430	CDS_NON_SYNONYMOUS	mTERF	CGCAAAATCATCTTCCGTA	ATGACATGCTGGTTTGTCC	NA
SNP0780	Ca_TC10403		<i>Ca_Desi_Chrom1</i>	[T/C]	20598392	CDS_NON_SYNONYMOUS	C3H	TGTGGTGAAGAATGGAACA	TACTTCCACCCATCCAGTC	NA
SNP0781	Ca_TC11725		<i>Ca_Desi_Chrom1</i>	[C/A]	21135977	CDS_NON_SYNONYMOUS	MADS	AGCTTTTGAGTACGTCCGTGA	TCCCTTTTACCACAAAAGC	NA
SNP0782	Ca_TC17860		<i>Ca_Desi_Chrom1</i>	[T/C]	23850218	CDS_NON_SYNONYMOUS	AP2-EREBP	TCCGGCACATAGAAATCACC	CCGAAAGCAAAGATCACATTC	NA

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SNP0783	Ca_TC08151		<i>Ca_Desi_Ch01</i>	[G/A]	24068638	CDS_NON_SYNONYMOUS	ARF	GCCCCGTGTAATTTGTGATT	TATTCGCGGATGGTTCACA	NA
SNP0784	Ca_TC18345		<i>Ca_Desi_Ch01</i>	[T/C]	25186105	CDS_NON_SYNONYMOUS	Tify	GTGGTTTGGCCACTACGAAT	TTGGAACATCAACGCAACAT	NA
SNP0785	Ca_TC02024		<i>Ca_Desi_Ch01</i>	[A/C]	26026317	CDS_NON_SYNONYMOUS	SBP	CCTGTACCGTCCTTTGCATT	CAGTTGCCGCAGAGACTACA	NA
SNP0786	Ca_TC03684		<i>Ca_Desi_Ch01</i>	[C/T]	33623744	CDS_NON_SYNONYMOUS	SBP	TGGAGATGCAATTGGTTCAA	TGTACACTTTGATACATCTCAGG	NA
SNP0787	Ca_TC04386		<i>Ca_Desi_Ch01</i>	[G/T]	37691837	CDS_NON_SYNONYMOUS	G2-like	CATCCAAATGGTGAGCCTCT	TCGTCTTCGTTGGACTGTTG	NA
SNP0788	Ca_TC17995		<i>Ca_Desi_Ch01</i>	[G/T]	41981594	CDS_NON_SYNONYMOUS	AP2-EREBP	CCAGCCCAATCAGACATTG	ACAAAGCGTGCTCGTTATCA	NA
SNP0789	Ca_TC15541		<i>Ca_Desi_Ch01</i>	[G/C]	43957759	CDS_NON_SYNONYMOUS	NAC	AAGCATGGTAGAGGCAAAGC	CCTTGATGTTTTCTCATCG	NA
SNP0790	Ca_TC09680		<i>Ca_Desi_Ch01</i>	[C/G]	46718906	CDS_NON_SYNONYMOUS	mTERF	GGCCTCAGAACCTCCTCTATGCTG	CAAGATTGAGGGTCGTTTTGTGG	Pr4
SNP0791	Ca_TC02465		<i>Ca_Desi_Ch01</i>	[T/C]	48002347	CDS_NON_SYNONYMOUS	PHD	CAAGCTTGAAGGAGGCAAAG	ACACCGAAGGAAAGCCTAT	NA
SNP0792	Ca_TC06936		<i>Ca_Desi_Ch01</i>	[T/C]	48218880	CDS_NON_SYNONYMOUS	Alfin-like	CAATGTTGAACAAGGTTTGATGT	CCATTTTCAAAGCTTCAACC	NA
SNP0793	Ca_TC05036		<i>Ca_Desi_Ch01</i>	[C/A]	48249846	CDS_NON_SYNONYMOUS	bZIP	GATTTGCGGTGTTTGTGTG	AAGCTTGTCCTGAGCCAATG	NA
SNP0794	Ca_TC16216		<i>Ca_Desi_Ch02</i>	[G/A]	355965	CDS_NON_SYNONYMOUS	LOB	CCCTTAAGCCGTTTATGGAA	CGCCTCATCAAAATCTCAT	NA
SNP0795	Ca_TC12565		<i>Ca_Desi_Ch02</i>	[A/T]	3202163	CDS_NON_SYNONYMOUS	HB	TCATGACTCAAGTAGATTGTCTCAAC	CATCATCACTGCCATCCCTA	NA
SNP0796	Ca_TC17714		<i>Ca_Desi_Ch02</i>	[G/A]	3353616	CDS_NON_SYNONYMOUS	MYB	TCTAGAAGCCATTTCCTAAGCA	GGACCATGGACTCCTGAAGA	NA
SNP0797	Ca_TC14300		<i>Ca_Desi_Ch02</i>	[G/A]	3410435	CDS_NON_SYNONYMOUS	zf-HD	CACAGAGGTTTGAAGCAAGAAA	CACTCCCAAACCTCTCAAGTAGCA	NA
SNP0798	Ca_TC12111		<i>Ca_Desi_Ch02</i>	[A/C]	4324332	CDS_NON_SYNONYMOUS	SAP	CATGAAACCACAATGTGCAA	TTCAATTCCACCACCAAACC	NA
SNP0799	Ca_TC01787		<i>Ca_Desi_Ch02</i>	[A/T]	5886240	CDS_NON_SYNONYMOUS	PHD	TAAACCTCGCGGAAGAGAA	AAGATTCGGGAATCCAAACC	NA
SNP0800	Ca_TC05633		<i>Ca_Desi_Ch02</i>	[T/C]	6181000	CDS_NON_SYNONYMOUS	SET	AACAACTCGCCAACATTTCC	CCCGAATCTTGTTTCACGTT	NA
SNP0801	Ca_TC23674		<i>Ca_Desi_Ch02</i>	[C/T]	6743024	CDS_NON_SYNONYMOUS	FAR1	ACGACGTTCACTTTCCATCC	GTCGGATTGTCTCCGAAAG	NA
SNP0802	Ca_TC07875		<i>Ca_Desi_Ch02</i>	[G/A]	9152974	CDS_NON_SYNONYMOUS	bHLH	CTACACCGGAACCGTGTCTC	CGGATCACTTCCACATACCA	NA
SNP0803	Ca_TC23383		<i>Ca_Desi_Ch02</i>	[T/C]	9266035	CDS_NON_SYNONYMOUS	GNAT	ATGCCTGAAACCAATCTCCA	GTGGACCCCATCGTATGTTT	NA
SNP0804	Ca_TC11796		<i>Ca_Desi_Ch02</i>	[T/C]	10330226	CDS_NON_SYNONYMOUS	bHLH	TGTGAAGATTGTCTGAAGTGGCGC	TCAGGTGGCATGGTGAGCTCT	Pr5
SNP0805	Ca_TC06938		<i>Ca_Desi_Ch02</i>	[G/A]	14248647	CDS_NON_SYNONYMOUS	GNAT	TGCTTATCGTCAAATCAATAAAAA	AATTCAATCAACTCAACTCCAC	NA
SNP0806	Ca_TC17363		<i>Ca_Desi_Ch02</i>	[G/A]	15817338	CDS_NON_SYNONYMOUS	C2C2-YABBY	CAACGAGGAGAAACTCACCA	TGCTCCAATATTCTCTCCAAT	NA
SNP0807	Ca_TC06463		<i>Ca_Desi_Ch02</i>	[G/A]	16132823	CDS_NON_SYNONYMOUS	SBP	GAGCTTGCAATTTGAACCCCTA	TCATGTTGACTCAGCTCTG	NA
SNP0808	Ca_TC06445		<i>Ca_Desi_Ch02</i>	[G/C]	16353473	CDS_NON_SYNONYMOUS	GeBP	ACCCTCTTCCAAAACCCCTTG	TTCACTCGTGGTTACATCCAA	NA
SNP0809	Ca_TC17258		<i>Ca_Desi_Ch02</i>	[T/C]	18418063	CDS_NON_SYNONYMOUS	GNAT	TGCGAGCGCATGATACATA	CCACAACACACACTTTTGAG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0810	Ca_TC05208		<i>Ca_Desi_Ch02</i>	[T/C]	18878024	CDS_NON_SYNONYMOUS	bHLH	GCTACAAAAGCCGTGTCTCC	TAAAATATGGCCAGCCCAAC	NA
SNP0811	Ca_TC10019		<i>Ca_Desi_Ch02</i>	[C/G]	21714168	CDS_NON_SYNONYMOUS	zf-HD	TTGGTGAAGTGTGAACTATGTG	TCCTCAATTAGGGTTTCTTACCA	NA
SNP0812	Ca_TC00533		<i>Ca_Desi_Ch02</i>	[T/C]	24236619	CDS_NON_SYNONYMOUS	Alfin-like	GGGGGAATATGTCAGCAAGA	GCACACCGAAGATCAGCATA	NA
SNP0813	Ca_TC14524		<i>Ca_Desi_Ch02</i>	[G/C]	25291561	CDS_NON_SYNONYMOUS	C3H	CATTGCTGAACCAATTGCAG	TCGACTGAACACAACCTGCT	NA
SNP0814	Ca_TC11707		<i>Ca_Desi_Ch02</i>	[T/C]	26158345	CDS_NON_SYNONYMOUS	FHA	CCACCACGCTCGTATCTTCT	GCAGAAGGCAACCAAGTGT	NA
SNP0815	Ca_TC11204		<i>Ca_Desi_Ch02</i>	[A/G]	27361120	CDS_NON_SYNONYMOUS	bZIP	ATGTCGAGTCCCTGAAAACG	CAACACCGCGTCACAGTTA	NA
SNP0816	Ca_TC06288		<i>Ca_Desi_Ch02</i>	[G/C]	27694185	CDS_NON_SYNONYMOUS	AP2-EREBP	ACTCTCTTTCCCGCAAATC	CAATAAATCACCGCTTCATGG	NA
SNP0817	Ca_TC12651		<i>Ca_Desi_Ch02</i>	[G/A]	30377757	CDS_NON_SYNONYMOUS	MYB	GCCTCTTAAGCTTCAAGTCATCT	AAACAACCTTTTGTGGTTTAAGG	NA
SNP0818	Ca_TC16553		<i>Ca_Desi_Ch02</i>	[G/A]	30698052	CDS_NON_SYNONYMOUS	HMG	CACCTTTCCTAATCCGAGCA	CTTACACCCAGGGGACGATA	NA
SNP0819	Ca_TC05305		<i>Ca_Desi_Ch02</i>	[C/T]	30867757	CDS_NON_SYNONYMOUS	C3H	TCACGTAGGAAGGTGTTGGA	GGCGCCATACATCTCAGAAT	NA
SNP0820	Ca_TC00798		<i>Ca_Desi_Ch02</i>	[G/A]	32769483	CDS_NON_SYNONYMOUS	FAR1	ATGCTGTGCTGGGACTCTCT	AACTTTTGTGGCTTCACG	NA
SNP0821	Ca_TC07826		<i>Ca_Desi_Ch02</i>	[G/C]	32958106	CDS_NON_SYNONYMOUS	bZIP	TCAAATTCGATACCCACAAA	GCTGAAGCCTATGCACATCA	NA
SNP0822	Ca_TC03320		<i>Ca_Desi_Ch02</i>	[A/T]	33604180	CDS_NON_SYNONYMOUS	SRS	CACCGGAGTTTGGTCTAGGT	GCAGCTGCATAAACATCGTG	NA
SNP0823	Ca_TC11772		<i>Ca_Desi_Ch02</i>	[T/C]	33661127	CDS_NON_SYNONYMOUS	HB	ACTCTTCGGGAAGCAGTAAG	GCACAACAAACAGCAATGG	NA
SNP0824	Ca_TC04916		<i>Ca_Desi_Ch02</i>	[T/C]	33727257	CDS_NON_SYNONYMOUS	SNF2	AGAACGTGGAGCAAGAGCAT	ACTCGTGCAAGTCGAGAGGT	NA
SNP0825	Ca_TC06616		<i>Ca_Desi_Ch02</i>	[T/C]	34132454	CDS_NON_SYNONYMOUS	NAC	TTGAAAAATGGATGTGAGCAA	TGGTTTGCTTTCATTTTGTG	NA
SNP0826	Ca_TC08159		<i>Ca_Desi_Ch02</i>	[G/T]	34853120	CDS_NON_SYNONYMOUS	Bromodomain	ACAGGAACCTGTTGGCTCTG	CCAACCTGGGTGAATGTGTTG	NA
SNP0827	Ca_TC06161		<i>Ca_Desi_Ch02</i>	[G/A]	35412866	CDS_NON_SYNONYMOUS	mTERF	GCACATGACATGGCTTTGTT	TTCTTTTTCAAACGGACCA	NA
SNP0828	Ca_TC12031		<i>Ca_Desi_Ch02</i>	[G/A]	35556870	CDS_NON_SYNONYMOUS	CCAAT	TCATTTCCTCCATCTTAC	AAGCAGAGAAAGGATCGTTGA	NA
SNP0829	Ca_TC06005		<i>Ca_Desi_Ch02</i>	[G/A]	36087743	CDS_NON_SYNONYMOUS	GRAS	TCGCTTGAAATGGACAGTTG	TTGAATGCTTTGCAGTTTGC	NA
SNP0830	Ca_TC11918		<i>Ca_Desi_Ch02</i>	[G/A]	36337365	CDS_NON_SYNONYMOUS	GNAT	GAGTCGACCCAATTCAACT	ACAGGACGCAAAAGCCATAC	NA
SNP0831	Ca_TC09339		<i>Ca_Desi_Ch02</i>	[G/T]	36520110	CDS_NON_SYNONYMOUS	FAR1	CGACTTTCAAGCGCTTTCTC	GGAGAGCAGCAAAGGTGAAG	NA
SNP0832	Ca_TC09302		<i>Ca_Desi_Ch03</i>	[C/T]	2706867	CDS_NON_SYNONYMOUS	C2C2-CO-like	TCCTGCAATACTCACTTCACT	GATCTTCGCCCCCTTTTGT	NA
SNP0833	Ca_TC09302		<i>Ca_Desi_Ch03</i>	[T/C]	2709320	CDS_NON_SYNONYMOUS	C2C2-CO-like	CCATTTCATCGCTCCACAAAT	TGGTCATGTTTCTCAACCTTGT	NA
SNP0834	Ca_TC14583		<i>Ca_Desi_Ch03</i>	[A/C]	3617757	CDS_NON_SYNONYMOUS	zf-HD	CCTCATGACTCATCATCCA	ACCATTTTCATCATCTCATCTCA	NA
SNP0835	Ca_TC10761		<i>Ca_Desi_Ch03</i>	[A/C]	4823888	CDS_NON_SYNONYMOUS	WRKY	CACGAAACCAACTCCATCA	CTTTGGGTCTGTGATGCTC	NA
SNP0836	Ca_TC10557		<i>Ca_Desi_Ch03</i>	[C/A]	7436178	CDS_NON_SYNONYMOUS	FHA	GCGTGTGGTGATGTCATT	TAGTGCCACAGCATCCTCAG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0837	Ca_TC01788		<i>Ca_Desi_Chr03</i>	[A/G]	10493006	CDS_NON_SYNONYMOUS	PHD	TGTGTTTTGGGTTTGGAAT	TCGTGCAGGCTTACTGATTG	NA
SNP0838	Ca_TC10092		<i>Ca_Desi_Chr03</i>	[G/T]	14026885	CDS_NON_SYNONYMOUS	ARF	ACAAAGGGGTGACAGCACAT	TGTTGAAGTTCCTGTCGAC	NA
SNP0839	Ca_TC13458		<i>Ca_Desi_Chr03</i>	[G/A]	15739519	CDS_NON_SYNONYMOUS	FHA	GCTAGGGTGCAGTGAAAAGAA	AGCAACTAGAATATCCCCTGT	NA
SNP0840	Ca_TC08082		<i>Ca_Desi_Chr03</i>	[G/A]	17174233	CDS_NON_SYNONYMOUS	LUG	GCGAATGAAACACCCCTCATT	TCAGAAGCTGCTGCGAGTAA	NA
SNP0841	Ca_TC08082		<i>Ca_Desi_Chr03</i>	[C/T]	17181273	CDS_NON_SYNONYMOUS	LUG	TCCAGCTGTTCACCTTTTCTGA	CCTCCTGTTGCCTCTGTACC	NA
SNP0842	Ca_TC10875		<i>Ca_Desi_Chr03</i>	[T/C]	17936789	CDS_NON_SYNONYMOUS	MYB	TGTGGGATATGCTGTGGAA	TTACACCTTCATAAAGATGGACGTA	NA
SNP0843	Ca_TC03750		<i>Ca_Desi_Chr03</i>	[G/A]	20174631	CDS_NON_SYNONYMOUS	S1Fa-like	CCTGGTACTTTGGCTTCAGG	AATGCCACTTCCCTTCACAG	NA
SNP0844	Ca_TC04172		<i>Ca_Desi_Chr03</i>	[T/C]	20843598	CDS_NON_SYNONYMOUS	SAP	GGCCAACTCTAATGGTGAA	CCGTCTGAAGCAACTCAA	NA
SNP0845	Ca_TC04619		<i>Ca_Desi_Chr03</i>	[G/A]	21776235	CDS_NON_SYNONYMOUS	GRAS	ACCCACAGTGACACTCACA	TTGCTTCCACAAACCTTCCT	NA
SNP0846	Ca_TC25185		<i>Ca_Desi_Chr03</i>	[G/C]	22065431	CDS_NON_SYNONYMOUS	FHA	TTCTTCACGAGTGCCTTTT	ATTCCCGGAATTCTCTCTC	NA
SNP0847	Ca_TC00438		<i>Ca_Desi_Chr03</i>	[T/C]	23278789	CDS_NON_SYNONYMOUS	SNF2	CTGCTTTGGCAATTCAGTCA	TTAAAGAAGCTGGGAAGCA	NA
SNP0848	Ca_TC24441		<i>Ca_Desi_Chr03</i>	[C/A]	23622995	CDS_NON_SYNONYMOUS	WRKY	GTTAGAGACCCGAAAATAACAAG	CGATCAATCCTATAAAGTCTCCAC	NA
SNP0849	Ca_TC08198		<i>Ca_Desi_Chr03</i>	[G/A]	23898026	CDS_NON_SYNONYMOUS	C3H	AAGGTTAGGCAGCCAGAAT	GGCTTGCCATTGAAACAGAT	NA
SNP0850	Ca_TC10203		<i>Ca_Desi_Chr03</i>	[G/A]	24542187	CDS_NON_SYNONYMOUS	mTERF	GCAAATTCACCATCGAACA	AATCCAAATTCATGCACCT	NA
SNP0851	Ca_TC10797		<i>Ca_Desi_Chr03</i>	[G/C]	25508396	CDS_NON_SYNONYMOUS	C2C2-CO-like	ATACACATTACGGGGCAATG	GTGGAGAGGAGGGGAAGAGT	NA
SNP0852	Ca_TC14790		<i>Ca_Desi_Chr03</i>	[G/A]	25757540	CDS_NON_SYNONYMOUS	SET	TCAGCAGCAAAGAGCATCAC	CGAAAGCCGAATCTGAGAAG	NA
SNP0853	Ca_TC14504		<i>Ca_Desi_Chr03</i>	[C/T]	26544003	CDS_NON_SYNONYMOUS	NAC	GAATTTTAAAGTCTTTCATCTCTCG	AGGTCTTGATTGCGACCAG	NA
SNP0854	Ca_TC06146		<i>Ca_Desi_Chr03</i>	[G/C]	26593875	CDS_NON_SYNONYMOUS	C2C2-GATA	CCCTCTCTTGTGTGTCAA	TGGAAGAGTAATTTCCCCCTA	NA
SNP0855	Ca_TC05422		<i>Ca_Desi_Chr03</i>	[G/C]	28560960	CDS_NON_SYNONYMOUS	SAP	ATTGTTTATGTGTGGCACACT	CCTTTTGTCCAATCATATAATGC	NA
SNP0856	Ca_TC05450		<i>Ca_Desi_Chr03</i>	[G/A]	28615172	CDS_NON_SYNONYMOUS	bZIP	TGGTTAGGGTTTGACGTCT	GCTTCATGCAGAACGTTGAA	NA
SNP0857	Ca_TC04863		<i>Ca_Desi_Chr03</i>	[G/C]	29843867	CDS_NON_SYNONYMOUS	bZIP	CACCTTGCTGCTTGATGTGT	TCAAAGGCTAGCATGGGATT	NA
SNP0858	Ca_TC05709		<i>Ca_Desi_Chr03</i>	[T/C]	30320095	CDS_NON_SYNONYMOUS	BSD	CTGTGGAACCATTGACGTG	CGTGTGTATGCACATGTATCTGTC	NA
SNP0859	Ca_TC07856		<i>Ca_Desi_Chr03</i>	[G/C]	30955375	CDS_NON_SYNONYMOUS	GNAT	TGCTTTGAAAGTGGGCTTCT	ATCCATCCACAAACGAAAC	NA
SNP0860	Ca_TC01852		<i>Ca_Desi_Chr03</i>	[G/T]	31359638	CDS_NON_SYNONYMOUS	Jumonji	TCCTTCCGAAGTATTTGATG	AGAAGCACTTGACCCCTAA	NA
SNP0861	Ca_TC16101		<i>Ca_Desi_Chr03</i>	[A/C]	31566643	CDS_NON_SYNONYMOUS	G2-like	GCCTCTGTCTCCATCAAAT	TGGCTTTGGAGGTATCCTG	NA
SNP0862	Ca_TC11048		<i>Ca_Desi_Chr03</i>	[T/C]	32898333	CDS_NON_SYNONYMOUS	S1Fa-like	CACAGTTTTCAGCGTCAGC	GCTTCTGTCAATAGCATACCG	NA
SNP0863	Ca_TC17632		<i>Ca_Desi_Chr03</i>	[G/T]	32900447	CDS_NON_SYNONYMOUS	S1Fa-like	CCTTTTCAAACCTCGGATTC	GAAAGGGGTCCAAGAAAATG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP0864	Ca_TC16716		<i>Ca_Desi_Chr03</i>	[T/C]	33155717	CDS_NON_SYNONYMOUS	Sigma70-like	CCCTCTACACCCCTCCCTTC	CCCTCCTTCTTTTGGGTTC	NA
SNP0865	Ca_TC01728		<i>Ca_Desi_Chr03</i>	[G/C]	34594243	CDS_NON_SYNONYMOUS	Alfin-like	CGGATCCAATAATGGCTTTC	GAGGAAAATGGATTGCTGA	NA
SNP0866	Ca_TC09243		<i>Ca_Desi_Chr03</i>	[T/C]	34848851	CDS_NON_SYNONYMOUS	C3H	CCAAAACGTGTTCCCATGCT	GCTCGGTGGAAATGTCAAAT	NA
SNP0867	Ca_TC03144		<i>Ca_Desi_Chr03</i>	[G/A]	35935079	CDS_NON_SYNONYMOUS	Jumonji	TCCAGGAAAAGAAGCCTCAA	TTTGTGTGTGTGGGTTTGG	NA
SNP0868	Ca_TC11912		<i>Ca_Desi_Chr03</i>	[G/A]	36809912	CDS_NON_SYNONYMOUS	bZIP	TCAAACCATGAATACATCAACAA	ACCCAATCTTTTCGACAAAC	NA
SNP0869	Ca_TC15928		<i>Ca_Desi_Chr03</i>	[A/T]	37102025	CDS_NON_SYNONYMOUS	SBP	ATGATGCTAGGGCTGCTGAT	TCITTCCCGGCTGCTATATG	NA
SNP0870	Ca_TC14839		<i>Ca_Desi_Chr03</i>	[T/C]	38614598	CDS_NON_SYNONYMOUS	GeBP	ATCCACCAATTGATCGCAAC	CCTAGGAAGGGTGGTTGGTT	NA
SNP0871	Ca_TC04913		<i>Ca_Desi_Chr03</i>	[T/C]	38760068	CDS_NON_SYNONYMOUS	bZIP	AGTACCCACCCACAAAAGAA	GCCATGGATTAAACACTCTCA	NA
SNP0872	Ca_TC00089		<i>Ca_Desi_Chr03</i>	[G/T]	38914646	CDS_NON_SYNONYMOUS	mTERF	ACATCGGGTACAGTTCACGA	TCTTTACCGCTGCTCCAGTT	NA
SNP0873	Ca_TC10811		<i>Ca_Desi_Chr03</i>	[G/C]	38969598	CDS_NON_SYNONYMOUS	MYB	CAGCGACTATTTGCTGGTCA	TTGCATCCTTCGGATTTTTTC	NA
SNP0874	Ca_TC08980		<i>Ca_Desi_Chr03</i>	[G/A]	39312173	CDS_NON_SYNONYMOUS	bZIP	TCAAACCAACCAGACGAATG	GAAGTTGCACACCGACGTTA	NA
SNP0875	Ca_TC17366		<i>Ca_Desi_Chr03</i>	[G/A]	39546588	CDS_NON_SYNONYMOUS	AP2-EREBP	TCCTGTGAAGGCTGTAACATATTGAG	CAACGTCCACCTCTTCTCTGCG	Pr1
SNP0876	Ca_TC02857		<i>Ca_Desi_Chr03</i>	[G/A]	39788772	CDS_NON_SYNONYMOUS	MYB-related	ATCAAATCATGGGGAGGTGA	TGATGAAAGGCCAACAACTG	NA
SNP0877	Ca_TC03090		<i>Ca_Desi_Chr03</i>	[T/C]	39816472	CDS_NON_SYNONYMOUS	ABI3VP1	GGAAGGAAAGGAAGGAAGGA	CCATGTTACCCCAATAGC	NA
SNP0878	Ca_TC03090		<i>Ca_Desi_Chr03</i>	[T/A]	39817437	CDS_NON_SYNONYMOUS	ABI3VP1	GGAAGGAAGGAAGGAAGG	GTTCACCCCAAATAGCCTCA	NA
SNP0879	Ca_TC05784		<i>Ca_Desi_Chr04</i>	[G/T]	19353	CDS_NON_SYNONYMOUS	bZIP	GAGCTGTGGATAGGGAATGC	ACCTTCCCACACTCGATCAC	NA
SNP0880	Ca_TC03717		<i>Ca_Desi_Chr04</i>	[A/C]	832308	CDS_NON_SYNONYMOUS	AP2-EREBP	TCTCAGGCTTGGTAGAGGA	GGCTCTAGCAGCTTCCTTCA	NA
SNP0881	Ca_TC01002		<i>Ca_Desi_Chr04</i>	[G/T]	1047604	CDS_NON_SYNONYMOUS	SNF2	TGGTAGGAAATGGACCAAGC	TGATGACCTATCTGCACCA	NA
SNP0882	Ca_TC14819		<i>Ca_Desi_Chr04</i>	[T/C]	1494086	CDS_NON_SYNONYMOUS	WRKY	GAGAGGCTAAATGGAAGAGATTG	CATCAAACTTTTGGTCAATTCAA	NA
SNP0883	Ca_TC09464		<i>Ca_Desi_Chr04</i>	[T/C]	1619541	CDS_NON_SYNONYMOUS	bHLH	AAGCAGAGCAACATCAACACA	TTGCCACACCACCATCTTTA	NA
SNP0884	Ca_TC01744		<i>Ca_Desi_Chr04</i>	[T/C]	2005078	CDS_NON_SYNONYMOUS	PHD	CCCTACTACTATTGAAGAACTTGAGG	TTACAACATAGTGACATACCACCAC	NA
SNP0885	Ca_TC18030		<i>Ca_Desi_Chr04</i>	[G/T]	2168233	CDS_NON_SYNONYMOUS	SAP	TCTTCCTCTGCCCACTATG	GAGCACCTTCATGCTTTTCA	NA
SNP0886	Ca_TC02133		<i>Ca_Desi_Chr04</i>	[G/A]	4276290	CDS_NON_SYNONYMOUS	Jumonji	TTGAAATCGCATTATCCAA	ATCATTTCACCTGCACCAT	NA
SNP0887	Ca_TC04020		<i>Ca_Desi_Chr04</i>	[G/A]	4745377	CDS_NON_SYNONYMOUS	G2-like	ATGCTTCGATGATGCCTTTC	TGCTATCTCTGGGGAACAG	NA
SNP0888	Ca_TC07000		<i>Ca_Desi_Chr04</i>	[T/C]	5004108	CDS_NON_SYNONYMOUS	bHLH	TGCTGGATAGTGGCTAGTGG	AGCGCACTCACCATTCTTTT	NA
SNP0889	Ca_TC05394		<i>Ca_Desi_Chr04</i>	[G/T]	5022053	CDS_NON_SYNONYMOUS	bZIP	AAATCCTTCTCTCCCATCC	GCCGACGACTCCTCTAACTC	NA
SNP0890	Ca_TC04483		<i>Ca_Desi_Chr04</i>	[G/C]	5080383	CDS_NON_SYNONYMOUS	Trihelix	CAAAACCAACCTTCTCATCA	AGGCCCACTTGAGAAGACT	NA

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SNP0891	Ca_TC01764		<i>Ca_Desi_Ch04</i>	[T/C]	5677430	CDS_NON_SYNONYMOUS	MYB-related	TTTGCGAACCATTGGATAAT	GCAATGAGGCATCAGGATCT	NA
SNP0892	Ca_TC02989		<i>Ca_Desi_Ch04</i>	[A/T]	5747340	CDS_NON_SYNONYMOUS	Jumonji	TGGTCAATTGTGACCTTCCA	CCGAACCTATTGTCGCATTT	NA
SNP0893	Ca_TC06284		<i>Ca_Desi_Ch04</i>	[G/A]	6183406	CDS_NON_SYNONYMOUS	HB	TCCTCAGTAGGTTTTCTTGA	TGCTAACATTTTGATGGCAAAT	NA
SNP0894	Ca_TC07839		<i>Ca_Desi_Ch04</i>	[T/C]	6766479	CDS_NON_SYNONYMOUS	MYB	TGGGAAGACACTCTGTGTGCT	GCCAATCCCAAGAAGAAA	NA
SNP0895	Ca_TC09768		<i>Ca_Desi_Ch04</i>	[T/C]	7394399	CDS_NON_SYNONYMOUS	AP2-EREBP	GGCGCTGGATTTCATTCTTA	TTCAAAATGTTCCAAGCCACA	NA
SNP0896	Ca_TC17077		<i>Ca_Desi_Ch04</i>	[G/C]	7974685	CDS_NON_SYNONYMOUS	C3H	GGCTACACAGGATTGGATG	GGGGGTACAGCCTTGTTTAT	NA
SNP0897	Ca_TC03473		<i>Ca_Desi_Ch04</i>	[T/C]	8390599	CDS_NON_SYNONYMOUS	BSD	CGTGGCTTAACCTTGACAT	TGTAACAAGGCAGCATCCAG	NA
SNP0898	Ca_TC13618		<i>Ca_Desi_Ch04</i>	[G/C]	8471278	CDS_NON_SYNONYMOUS	AP2-EREBP	TGCTCATATTGAGCCATTG	GAGCCAACACCTGTTAGAGGA	NA
SNP0899	Ca_TC08273		<i>Ca_Desi_Ch04</i>	[A/T]	8769821	CDS_NON_SYNONYMOUS	NAC	TTAGAAGTGTTTGGTCACATGC	GTACCTCATGGAACAAGTGG	P6
SNP0900	Ca_TC14853		<i>Ca_Desi_Ch04</i>	[G/A]	9471744	CDS_NON_SYNONYMOUS	AP2-EREBP	TGGAAGGAGGTAGTTGCACA	GACGGCACCATATCCATCTT	NA
SNP0901	Ca_TC18271		<i>Ca_Desi_Ch04</i>	[A/C]	10704805	CDS_NON_SYNONYMOUS	mTERF	ATGCTCCAGGACACTTCAGC	GGGGGCAGAAGAGTGATTTT	NA
SNP0902	Ca_TC14968		<i>Ca_Desi_Ch04</i>	[G/A]	10973664	CDS_NON_SYNONYMOUS	SAP	TTCCAGATTGTCTATGATCCTCA	CTTACTTTGTCCGCATCCA	NA
SNP0903	Ca_TC10063		<i>Ca_Desi_Ch04</i>	[G/T]	11054722	CDS_NON_SYNONYMOUS	NAC	CACAGATGAGGAGCTGGTGA	TTCTGCCTGCTCTCTTACA	NA
SNP0904	Ca_TC12822		<i>Ca_Desi_Ch04</i>	[G/A]	11600593	CDS_NON_SYNONYMOUS	Trihelix	TGGAATTGTGCACAAGGTG	TGGTACAAGCATGAGGGAAG	NA
SNP0905	Ca_TC03365		<i>Ca_Desi_Ch04</i>	[G/A]	12315577	CDS_NON_SYNONYMOUS	RWP-RK	TATTTTGGCAGATGGTGGTG	TCCAAAATGGCCTCAGCTAC	NA
SNP0906	Ca_TC03365		<i>Ca_Desi_Ch04</i>	[G/T]	12318493	CDS_NON_SYNONYMOUS	RWP-RK	GAAATGGCAGAATCTGAGGA	AAGTTCAACACCTGCAGCAA	NA
SNP0907	Ca_TC03365		<i>Ca_Desi_Ch04</i>	[G/C]	12319718	CDS_NON_SYNONYMOUS	RWP-RK	GAAACTTCATGGCCCTTGGA	GTGAGGCATCAGGTCTTGGT	NA
SNP0908	Ca_TC17891		<i>Ca_Desi_Ch04</i>	[G/A]	12964701	CDS_NON_SYNONYMOUS	MADS	AGAGGAAGCATGGGAAGAGG	CCACATTGTCATGCTGGAAG	NA
SNP0909	Ca_TC23817		<i>Ca_Desi_Ch04</i>	[G/A]	13328322	CDS_NON_SYNONYMOUS	Tify	CCTCCACAAGGGAATTGAA	TGGCTGCTCCTCACTTACA	NA
SNP0910	Ca_TC09766		<i>Ca_Desi_Ch04</i>	[T/C]	13727396	CDS_NON_SYNONYMOUS	Alfin-like	GAACGGCAACCGTATCCTTA	TGCCGAGAAACAGGGTTTAC	NA
SNP0911	Ca_TC00252		<i>Ca_Desi_Ch04</i>	[A/T]	14094264	CDS_NON_SYNONYMOUS	FHA	CAACTCCGGGATCGTAAAGA	CCAACACAGGCCCTATCACT	NA
SNP0912	Ca_TC08758		<i>Ca_Desi_Ch04</i>	[G/A]	14511914	CDS_NON_SYNONYMOUS	LIM	GAAATTGGAGCACCATCAT	AGAGGGGGAACAAGAGAAGC	NA
SNP0913	Ca_TC04213		<i>Ca_Desi_Ch04</i>	[A/T]	15539515	CDS_NON_SYNONYMOUS	C3H	TCAAACTTATGGGGAGGAA	ACGGTGTGAAGTGGAGAGG	NA
SNP0914	Ca_TC34477		<i>Ca_Desi_Ch04</i>	[G/A]	16279070	CDS_NON_SYNONYMOUS	C2C2-CO-like	GCAAAGGAAATGTGGAACGT	TCACACTCCCACTCCCTTTT	NA
SNP0915	Ca_TC16527		<i>Ca_Desi_Ch04</i>	[G/C]	16362489	CDS_NON_SYNONYMOUS	AP2-EREBP	TGTCGGAGGAATCGCTTTTA	TTTCATCATCTGCACCATGT	NA
SNP0916	Ca_TC02991		<i>Ca_Desi_Ch04</i>	[T/C]	17427472	CDS_NON_SYNONYMOUS	Jumonji	ATTACAGGCTCCCTTTTGCT	GTGCATGTCAATGGTGAAG	NA
SNP0917	Ca_TC03801		<i>Ca_Desi_Ch04</i>	[G/T]	17722046	CDS_NON_SYNONYMOUS	SNF2	ATGAAAGGGCTTCTGGGAAT	AGACATGGCCACATCGTA	NA

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SNP0918	Ca_TC17980		<i>Ca_Desi_Ch04</i>	[G/T]	17862210	CDS_NON_SYNONYMOUS	HB	CATGAACATAAGCCCAAGCA	TGCCGTGTATGTGTGAGAGAG	NA
SNP0919	Ca_TC07748		<i>Ca_Desi_Ch04</i>	[A/C]	19013085	CDS_NON_SYNONYMOUS	C3H	TGTTTCGTTGTGTGCTTGA	CAATCTCGCCTAAAAACCA	NA
SNP0920	Ca_TC07944		<i>Ca_Desi_Ch04</i>	[A/C]	19586476	CDS_NON_SYNONYMOUS	MYB-related	GGGTAACTCTAATTTCCCTCAAG	GTATCGTCTATGAGTGTATTGTGC	NA
SNP0921	Ca_TC16555		<i>Ca_Desi_Ch04</i>	[A/T]	20446814	CDS_NON_SYNONYMOUS	Sigma70-like	CGGGGTGAGAAAAATAACCA	GCCTCCAATACCTTGTCTCAG	NA
SNP0922	Ca_TC34533		<i>Ca_Desi_Ch04</i>	[A/G]	23557644	CDS_NON_SYNONYMOUS	HB	AGGGGGTTGCTTGGTTTAAT	TTTCTTCCACCATTTGGCTTC	NA
SNP0923	Ca_TC01664		<i>Ca_Desi_Ch04</i>	[C/T]	29778149	CDS_NON_SYNONYMOUS	HB	TTGTGGGCTTACGAAGAGAGA	CCCTTTTGCTTCCAATTTCA	NA
SNP0924	Ca_TC12581		<i>Ca_Desi_Ch04</i>	[G/A]	36535887	CDS_NON_SYNONYMOUS	ABI3VP1	GCCAAGATAAGCGTTTCGAC	GCCACGCCCTAGTTTTCATA	NA
SNP0925	Ca_TC02171		<i>Ca_Desi_Ch04</i>	[G/A]	36974817	CDS_NON_SYNONYMOUS	SNF2	AAAACGGTTCAGGCAATCAC	CTTCGTGACCTCTTCCATC	NA
SNP0926	Ca_TC03468		<i>Ca_Desi_Ch04</i>	[T/C]	37061273	CDS_NON_SYNONYMOUS	SET	ACATTTTCGCGACCTTGTTTC	GCTTGCCAGTCAACTCATCA	NA
SNP0927	Ca_TC00942		<i>Ca_Desi_Ch04</i>	[T/C]	37096147	CDS_NON_SYNONYMOUS	ABI3VP1	ACAATAAACGGAGGCGAAGA	TCTCCCCCTTGTGTGCTTAC	NA
SNP0928	Ca_TC00942		<i>Ca_Desi_Ch04</i>	[A/T]	37097065	CDS_NON_SYNONYMOUS	ABI3VP1	GTTGATATTGTCAAGCATATAG	TCCTTCTGAGAATCAGATTCA	NA
SNP0929	Ca_TC00942		<i>Ca_Desi_Ch04</i>	[A/T]	37097068	CDS_NON_SYNONYMOUS	ABI3VP1	TTGTCAAGCATATAGTCTATAGTC	GCTTACAAGTTACAGCCTTC	NA
SNP0930	Ca_TC11159		<i>Ca_Desi_Ch04</i>	[G/A]	37514472	CDS_NON_SYNONYMOUS	Tify	AAC TTGCTTTGAATTCCTCACTG	TGGGTTTCAATTCAAGGTGA	NA
SNP0931	Ca_TC18630		<i>Ca_Desi_Ch04</i>	[A/T]	38486601	CDS_NON_SYNONYMOUS	MADS	CAGTGTGCAAAGGAAACCAA	CCTCACAAGCTTGCAAGTTTC	NA
SNP0932	Ca_TC05974		<i>Ca_Desi_Ch04</i>	[G/C]	38659802	CDS_NON_SYNONYMOUS	GRAS	TTGAACACGAGCAGAAGTTGATTG	TAGGCAACCCCAAAACCAAGCAATTC	NA
SNP0933	Ca_TC04825		<i>Ca_Desi_Ch04</i>	[G/A]	39804794	CDS_NON_SYNONYMOUS	Trihelix	CGCCCATGGAATCTACATCT	GGAGATTTCATGCAGAAGG	NA
SNP0934	Ca_TC15768		<i>Ca_Desi_Ch04</i>	[G/A]	40230993	CDS_NON_SYNONYMOUS	Sigma70-like	TGGGTCTCTGTTCCGTTTT	TAAGGCCAAAGCGTAGGATG	NA
SNP0935	Ca_TC00983		<i>Ca_Desi_Ch04</i>	[A/T]	40578365	CDS_NON_SYNONYMOUS	Jumonji	ATCGATGAAAAGGCGAAAGA	TGGAAGAGGCAGAGCAATCT	NA
SNP0936	Ca_TC18510		<i>Ca_Desi_Ch04</i>	[T/A]	40933076	CDS_NON_SYNONYMOUS	bZIP	CAGCATCGCTATTGACTCCA	ATTCTCGGCCTTCTTCAAT	NA
SNP0937	Ca_TC04841		<i>Ca_Desi_Ch04</i>	[G/C]	41866592	CDS_NON_SYNONYMOUS	LUG	TTTCATGCAGACTCCACAGC	ATTCCTTCACTCCAGAT	NA
SNP0938	Ca_TC23107		<i>Ca_Desi_Ch04</i>	[T/C]	42354903	CDS_NON_SYNONYMOUS	bZIP	CCGAATCCATTAACAAACG	CGGTGAATTTGTTGCAGTGT	NA
SNP0939	Ca_TC01983		<i>Ca_Desi_Ch04</i>	[G/A]	43891050	CDS_NON_SYNONYMOUS	HB	CATGAGCAAGCTTCAATCA	CTCCAAAGCTTCCGACTC	NA
SNP0940	Ca_TC14573		<i>Ca_Desi_Ch04</i>	[G/C]	44393302	CDS_NON_SYNONYMOUS	C2C2-CO-like	GCAATGCAATGCAATTATCAG	CTTTTCTCATTATTCAAAACAAA	NA
SNP0941	Ca_TC14573		<i>Ca_Desi_Ch04</i>	[C/T]	44394420	CDS_NON_SYNONYMOUS	C2C2-CO-like	TTAGAAAAAGACAGAGAAAAAGAA	CTTTTCTCATTATTCAAAACAAA	NA
SNP0942	Ca_TC07900		<i>Ca_Desi_Ch04</i>	[T/C]	45416533	CDS_NON_SYNONYMOUS	HB	AGGGACCATCAGGATGTAG	CTCCACCTGTCAAGACCAT	NA
SNP0943	Ca_TC18421		<i>Ca_Desi_Ch04</i>	[T/C]	45736499	CDS_NON_SYNONYMOUS	AP2-EREBP	TTGAAGAAAAACATTGACAGAAGC	GGAGGAGGATGCCACTGGT	NA
SNP0944	Ca_TC18961		<i>Ca_Desi_Ch04</i>	[T/C]	45835578	CDS_NON_SYNONYMOUS	LIM	TTGATCAAAATGATTGTCAG	TCCACACACTTGCAACAAA	NA

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SNP0945	Ca_TC10605		<i>Ca_Desi_Ch04</i>	[G/C]	46419887	CDS_NON_SYNONYMOUS	HB	AAGGTGCATCAGTTCACACG	AAACCCCTTCATCTGCCTTC	NA
SNP0946	Ca_TC17705		<i>Ca_Desi_Ch04</i>	[T/C]	46995447	CDS_NON_SYNONYMOUS	CCAAT	ACACTGTATTAGTTTCATCCAAA	TGAAAAATCAGATTACAATTAACAAC	NA
SNP0947	Ca_TC16471		<i>Ca_Desi_Ch04</i>	[A/T]	47258388	CDS_NON_SYNONYMOUS	ABI3VP1	TTTTCGCACGTGATGATGG	CCAACCTCGAATCTTCTCTCA	NA
SNP0948	Ca_TC06172		<i>Ca_Desi_Ch04</i>	[G/A]	47445593	CDS_NON_SYNONYMOUS	LIM	CATCGACTTCAGGGGATGTT	AATCAGCACTGCATCAAAGC	NA
SNP0949	Ca_TC15885		<i>Ca_Desi_Ch04</i>	[G/A]	47884183	CDS_NON_SYNONYMOUS	HMG	CAGTGCCCTCTTAGTGCAT	TGGCGTTGAGATCAAAGATG	NA
SNP0950	Ca_TC09314		<i>Ca_Desi_Ch04</i>	[G/A]	48124866	CDS_NON_SYNONYMOUS	HB	ATTTGCCACTGGTTCCTTG	CTTGGGATTGCCACTTGTCT	NA
SNP0951	Ca_TC00756		<i>Ca_Desi_Ch04</i>	[G/T]	48276063	CDS_NON_SYNONYMOUS	SWI/SNF-SW13	AATGTTCCGTTGAGGGTCA	AGCTTTCAGCCGACGAGATA	NA
SNP0952	Ca_TC03708		<i>Ca_Desi_Ch04</i>	[C/T]	48384848	CDS_NON_SYNONYMOUS	ARF	GTATCAACTTTGCCATTTTGTG	CTTGCAAGGGAAGTCTTATAG	Pr2
SNP0953	Ca_TC15083		<i>Ca_Desi_Ch05</i>	[A/G]	166360	CDS_NON_SYNONYMOUS	NAC	GCAATAGCAGCAGCAACAAC	GAGGAATAATGAGAGTGACAAGC	NA
SNP0954	Ca_TC21593		<i>Ca_Desi_Ch05</i>	[G/A]	7382449	CDS_NON_SYNONYMOUS	bHLH	CGCAATGAACGACAGTGTTT	TGAACTCCTTGGGGACCATA	NA
SNP0955	Ca_TC19883		<i>Ca_Desi_Ch05</i>	[G/A]	7681689	CDS_NON_SYNONYMOUS	MADS	TGGGATTCCAAATTTTCCA	TTTGGTCACTTGGGCTAATG	NA
SNP0956	Ca_TC10166		<i>Ca_Desi_Ch05</i>	[G/A]	9958884	CDS_NON_SYNONYMOUS	WRKY	GGTCCAAGAGGCATGTGATT	TCCATCTTCAGGCCAACTTC	NA
SNP0957	Ca_TC24111		<i>Ca_Desi_Ch05</i>	[T/C]	10989680	CDS_NON_SYNONYMOUS	FAR1	CATGCACCCTATGAACAACG	TGAATCCCCCACAGTTGAT	NA
SNP0958	Ca_TC00525		<i>Ca_Desi_Ch05</i>	[G/A]	11384336	CDS_NON_SYNONYMOUS	C3H	TTCCATAAAAAACGCACACA	AGCCAAACATACGCTTCTGC	NA
SNP0959	Ca_TC00942		<i>Ca_Desi_Ch05</i>	[A/C]	14755276	CDS_NON_SYNONYMOUS	ABI3VP1	AGCATATAGTCTATAGTCTATA	TCACGACAAACGGCGGTCGC	NA
SNP0960	Ca_TC15918		<i>Ca_Desi_Ch05</i>	[G/A]	16677409	CDS_NON_SYNONYMOUS	C3H	ATAATGATGGGGCCAGAGATAATAG	TCATACCAAATGACTCAGAGACTGC	NA
SNP0961	Ca_TC18783		<i>Ca_Desi_Ch05</i>	[T/C]	19048521	CDS_NON_SYNONYMOUS	GNAT	GGTTCATAATTGGGCACCTC	TTTGTACATGAACCGCAAAC	NA
SNP0962	Ca_TC10952		<i>Ca_Desi_Ch05</i>	[G/T]	21801207	CDS_NON_SYNONYMOUS	FHA	TGAGCAGGATAGAGCGGATT	CATATCTCTCGGCAAGAG	NA
SNP0963	Ca_TC10952		<i>Ca_Desi_Ch05</i>	[C/G]	21801378	CDS_NON_SYNONYMOUS	FHA	CAGTCGGCAAGATTGTATTGT	CAGGACCACTCTCACAACCA	NA
SNP0964	Ca_TC16202		<i>Ca_Desi_Ch05</i>	[A/T]	24343946	CDS_NON_SYNONYMOUS	CCAAT	CCCATCAACAAAGAGAGTTGG	GGAGAGGAATCGGATTAGCC	NA
SNP0965	Ca_TC15539		<i>Ca_Desi_Ch05</i>	[T/C]	24717637	CDS_NON_SYNONYMOUS	MYB	TTTCCCTTTTGTGTGTCTCA	CAACCAATCACCACCATC	NA
SNP0966	Ca_TC16449		<i>Ca_Desi_Ch05</i>	[A/G]	26426790	CDS_NON_SYNONYMOUS	WRKY	ATCCTAAGCCAGCCCTCTA	TGATCAAACAGGGTCAGGTG	NA
SNP0967	Ca_TC01938		<i>Ca_Desi_Ch05</i>	[G/A]	27042239	CDS_NON_SYNONYMOUS	MYB-related	CGCATTCTCAAACCTCAACA	TTACCAATTGGCCCTCACTC	NA
SNP0968	Ca_TC02970		<i>Ca_Desi_Ch05</i>	[G/C]	27150196	CDS_NON_SYNONYMOUS	ABI3VP1	ACGATCTGGTGGATTGTTTC	TGTTGTGATGCGCCATTT	NA
SNP0969	Ca_TC02631		<i>Ca_Desi_Ch05</i>	[T/C]	27749046	CDS_NON_SYNONYMOUS	ARF	GTCGCTAAGCCTTTGTCTCTG	AACTCTCAATGGCGCTCTGT	NA
SNP0970	Ca_TC10514		<i>Ca_Desi_Ch05</i>	[T/C]	28253736	CDS_NON_SYNONYMOUS	LOB	TGAAATGAAAGGCATGAAAGG	CATTTTCCAAGAGTTCTAGCTG	NA
SNP0971	Ca_TC16262		<i>Ca_Desi_Ch05</i>	[G/C]	29397487	CDS_NON_SYNONYMOUS	AP2-EREBP	CTTCTGTAACCCCGCTTC	CATTGCAGTAGCCACCAAAC	NA

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SNP0972	Ca_TC06871		<i>Ca_Desi_Chr05</i>	[T/C]	29790311	CDS_NON_SYNONYMOUS	FHA	TCCATTAGATGGACCCCTTG	TCAGAAGCAAAACCCAAACC	NA
SNP0973	Ca_TC04443		<i>Ca_Desi_Chr05</i>	[C/G]	30439023	CDS_NON_SYNONYMOUS	MYB-related	TGAGAAGCTGAAAGGGAAGC	CAATGAAAAGCTACCTGCACA	NA
SNP0974	Ca_TC03920		<i>Ca_Desi_Chr05</i>	[A/T]	31244017	CDS_NON_SYNONYMOUS	Bromodomain	CGATGAACGCAAACTCAAGA	CGTTTGAAGACCCGGTTAAG	NA
SNP0975	Ca_TC18361		<i>Ca_Desi_Chr05</i>	[G/A]	33879428	CDS_NON_SYNONYMOUS	bZIP	CCCTTCTCCTTCTCTCCTCC	CACGGCATATAAAGTTGGATCA	NA
SNP0976	Ca_TC14720		<i>Ca_Desi_Chr05</i>	[G/A]	34476592	CDS_NON_SYNONYMOUS	Tify	TGACATAAGCATTTACGCCTCA	CGCCCATTAATATCAACACAAA	NA
SNP0977	Ca_TC05162		<i>Ca_Desi_Chr05</i>	[T/C]	34510155	CDS_NON_SYNONYMOUS	LUG	ACAGCAACAGCAACAACAGC	GAAATGGCAACAGGCAACTT	NA
SNP0978	Ca_TC12011		<i>Ca_Desi_Chr05</i>	[A/T]	34684944	CDS_NON_SYNONYMOUS	bZIP	TGGTACATTAACCTACCCCTTTATCTCC	AACATGGTAGCGGGAACAAC	NA
SNP0979	Ca_TC15633		<i>Ca_Desi_Chr05</i>	[G/A]	35117329	CDS_NON_SYNONYMOUS	ARR-B	ACCAGAACCGAGACAAAAC	GTGCCAAATGCCCACTATC	NA
SNP0980	Ca_TC12603		<i>Ca_Desi_Chr05</i>	[T/C]	35122407	CDS_NON_SYNONYMOUS	PHD	AAACTGGGAGCGTGAATTG	CAGCCTCAGCTTCATCAACA	NA
SNP0981	Ca_TC06000		<i>Ca_Desi_Chr05</i>	[A/T]	35389971	CDS_NON_SYNONYMOUS	C2C2-CO-like	GCCGATCCAGCAACAGAAT	CCTGTCCCACCACTAGGTA	NA
SNP0982	Ca_TC17175		<i>Ca_Desi_Chr05</i>	[A/T]	36046998	CDS_NON_SYNONYMOUS	HB	TGCTCTAGGCCTCATGAAC	GCAAAAGATTGGTGAACGA	NA
SNP0983	Ca_TC02754		<i>Ca_Desi_Chr05</i>	[T/C]	36211837	CDS_NON_SYNONYMOUS	BSD	GTCAACATGGCTTGCTCGT	GGCAAAAGAATGTTGGGAGA	NA
SNP0984	Ca_TC06070		<i>Ca_Desi_Chr05</i>	[A/T]	36283170	CDS_NON_SYNONYMOUS	LIM	GGTGAAGATATTGAGGGGCTA	TGAGACTCAAACCCCTAACA	NA
SNP0985	Ca_TC06893		<i>Ca_Desi_Chr05</i>	[T/C]	37147512	CDS_NON_SYNONYMOUS	zf-HD	CCATCCTCAAAATTTCTCATGC	GCATCCAAACCTTAAGCACA	NA
SNP0986	Ca_TC15434		<i>Ca_Desi_Chr05</i>	[A/C]	37485160	CDS_NON_SYNONYMOUS	C2C2-GATA	ACATACCTCGCTCGCCTTC	CCAGCTTCTTTAAATGGGAGA	NA
SNP0987	Ca_TC03890		<i>Ca_Desi_Chr05</i>	[G/A]	37814550	CDS_NON_SYNONYMOUS	Jumonji	AACAGTTTCTTGCCCCACAC	CCGGTCATGCTTAATGGACT	NA
SNP0988	Ca_TC11222		<i>Ca_Desi_Chr05</i>	[T/C]	37985131	CDS_NON_SYNONYMOUS	MYB-related	CGATTTTGCGAAGGATAAT	AATTTCAAGAACGCCGAAGA	NA
SNP0989	Ca_TC12007		<i>Ca_Desi_Chr05</i>	[T/C]	38149806	CDS_NON_SYNONYMOUS	bHLH	AACTGCCACCACAAGAATCG	TGAGTCCTTAGCACCACAACCTG	NA
SNP0990	Ca_TC15723		<i>Ca_Desi_Chr05</i>	[G/A]	38467232	CDS_NON_SYNONYMOUS	GNAT	CGGTACGAGCCATAGCAGA	TGTGTCTCTTGCTGGCAATC	NA
SNP0991	Ca_TC11405		<i>Ca_Desi_Chr05</i>	[T/C]	40243059	CDS_NON_SYNONYMOUS	FAR1	TTTTCCTGGCCTCTCTCAA	TGAGGATGGGATTCTGAGC	NA
SNP0992	Ca_TC06049		<i>Ca_Desi_Chr05</i>	[T/C]	40405468	CDS_NON_SYNONYMOUS	FHA	TGAGGGACCAGAAAGTTGATCTT	CAAATGGAACCTCGCAAGACCTGGCA	NA
SNP0993	Ca_TC10289		<i>Ca_Desi_Chr05</i>	[A/C]	40619677	CDS_NON_SYNONYMOUS	HB	AAATTTGTCTCTCATTTCTCA	GTGTGTGGGTGTGAAACCA	NA
SNP0994	Ca_TC11566		<i>Ca_Desi_Chr05</i>	[T/C]	41313407	CDS_NON_SYNONYMOUS	SET	AATGAATGGCCTCATTTGAA	TGTTCCACCAACACCACAAT	NA
SNP0995	Ca_TC10983		<i>Ca_Desi_Chr05</i>	[T/C]	41478089	CDS_NON_SYNONYMOUS	SWI/SNF-SW13	ATTGAAGAACACCGGCTTGT	CACAGCCTCTCATGCACATT	NA
SNP0996	Ca_TC01272		<i>Ca_Desi_Chr05</i>	[C/T]	42527654	CDS_NON_SYNONYMOUS	CAMTA	AACCTGCCCCCTCATCTTTT	ATGAACGGCTTAAGGTTGGA	NA
SNP0997	Ca_TC04623		<i>Ca_Desi_Chr05</i>	[A/C]	42984383	CDS_NON_SYNONYMOUS	ARR-B	TGCTTCACTTCCCTAGACG	AGAAGTGGAATGGGCTGTG	NA
SNP0998	Ca_TC12604		<i>Ca_Desi_Chr05</i>	[G/C]	43835527	CDS_NON_SYNONYMOUS	bZIP	TTCCCATTTCTCTTCTCTT	CACCTCTGGCCAATGAAAAT	NA

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SNP0999	Ca_TC01857		<i>Ca_Desi_Chr05</i>	[G/T]	44421018	CDS_NON_SYNONYMOUS	SET	GCAGGCTGATCAATTCCAT	TTCCCTGTTGCACAGTTTAC	NA
SNP1000	Ca_TC02822		<i>Ca_Desi_Chr05</i>	[A/T]	44560496	CDS_NON_SYNONYMOUS	HB	TCACATGGGTTCCTGGTACA	CACCAGAAGTGGTCCCAAT	NA
SNP1001	Ca_TC10914		<i>Ca_Desi_Chr05</i>	[G/C]	45076994	CDS_NON_SYNONYMOUS	Sigma70-like	GCGACGAAGATAATCCAACC	GCTGCTCGAACTCCACTAGG	NA
SNP1002	Ca_TC01071		<i>Ca_Desi_Chr05</i>	[A/C]	46175167	CDS_NON_SYNONYMOUS	NAC	TCCGATTCCGACCTACAGAC	AGCACGACTTCTCTGAGCTT	NA
SNP1003	Ca_TC11233		<i>Ca_Desi_Chr05</i>	[T/C]	46513987	CDS_NON_SYNONYMOUS	bZIP	GAGGAGACAACCGCAAGAAG	CAATGTCCAACCCCTGAAAC	NA
SNP1004	Ca_TC07991		<i>Ca_Desi_Chr05</i>	[G/A]	47223799	CDS_NON_SYNONYMOUS	C3H	GAGGAACGGAAACAGCAGAG	CCTGCTCCAAGGATATGAGC	NA
SNP1005	Ca_TC04499		<i>Ca_Desi_Chr05</i>	[A/G]	47734066	CDS_NON_SYNONYMOUS	NAC	GCAAAACACAACAACAACAAAA	TGCATTCCATCTCTTGAATTG	NA
SNP1006	Ca_TC10067		<i>Ca_Desi_Chr06</i>	[C/G]	789313	CDS_NON_SYNONYMOUS	GRAS	GACCTCCATGGCTCAATGT	GCGGAATGGACGAGTTTTTA	NA
SNP1007	Ca_TC03126		<i>Ca_Desi_Chr06</i>	[A/C]	1609229	CDS_NON_SYNONYMOUS	LIM	GTGGTGGTCATCATTTGCAG	GAACACACCTTCCCTCAGA	NA
SNP1008	Ca_TC01051		<i>Ca_Desi_Chr06</i>	[G/A]	1842423	CDS_NON_SYNONYMOUS	GeBP	AGCCACCACAAGCAACTTCT	CAATTCTGCATTGCTTGCAT	NA
SNP1009	Ca_TC04335		<i>Ca_Desi_Chr06</i>	[G/A]	2925948	CDS_NON_SYNONYMOUS	Tify	TCCATGTAACACAAAAGCCCTA	CACTCTCTTCCTTTTCTTTGG	NA
SNP1010	Ca_TC08424		<i>Ca_Desi_Chr06</i>	[G/A]	5506963	CDS_NON_SYNONYMOUS	bHLH	CAAGATTGGCCAAGGGTTAC	CTTTTGGAGGGCTTGTGTTG	NA
SNP1011	Ca_TC13769		<i>Ca_Desi_Chr06</i>	[T/C]	5688576	CDS_NON_SYNONYMOUS	LIM	TGCAAGAAAAACCTCCCAA	AACCAACAGAAATGCAAGG	NA
SNP1012	Ca_TC05745		<i>Ca_Desi_Chr06</i>	[G/A]	5789222	CDS_NON_SYNONYMOUS	SBP	CGGTGGAGGAACATTATGCGCGGA	CTGGATGCAGACCCACTAGACTAA	Pv7
SNP1013	Ca_TC26643		<i>Ca_Desi_Chr06</i>	[T/C]	6015415	CDS_NON_SYNONYMOUS	NAC	TGGGATTTACCAGGAGGTTG	TTGATGATCTGGTGCATTGTA	NA
SNP1014	Ca_TC16024		<i>Ca_Desi_Chr06</i>	[G/A]	6142063	CDS_NON_SYNONYMOUS	ARF	ACTATGGCATGCTTTGTGCTG	AGACCAGGTGGCATAACAGG	NA
SNP1015	Ca_TC09243		<i>Ca_Desi_Chr06</i>	[G/A]	6295375	CDS_NON_SYNONYMOUS	C3H	CAAAAGTGTTCCTCATGCT	TCGGTGGAAATGTCAAAT	NA
SNP1016	Ca_TC23737		<i>Ca_Desi_Chr06</i>	[T/C]	6913579	CDS_NON_SYNONYMOUS	SNF2	CGTCAACAATTGCTCATGT	AAAGGGTCCCGATATTTTG	NA
SNP1017	Ca_TC09845		<i>Ca_Desi_Chr06</i>	[A/T]	7275013	CDS_NON_SYNONYMOUS	MYB	TTAGACGAAGACGCGAAACC	CGCACGAGTTACGTGTTTAT	NA
SNP1018	Ca_TC02597		<i>Ca_Desi_Chr06</i>	[A/C]	10032665	CDS_NON_SYNONYMOUS	zf-HD	TGCCATGGCTCTCACTACAG	TGAGGTGCTGATGGGTATGA	NA
SNP1019	Ca_TC00090		<i>Ca_Desi_Chr06</i>	[C/T]	10748091	CDS_NON_SYNONYMOUS	mTERF	ACGTTTTCGCCACCTTACAC	AAACACTCGATCCTCGATGC	NA
SNP1020	Ca_TC05646		<i>Ca_Desi_Chr06</i>	[G/A]	10864322	CDS_NON_SYNONYMOUS	CAMTA	AGACCATGATTTCCTTGACG	TCGTTTGCTCTCCGTTTTCT	NA
SNP1021	Ca_TC15791		<i>Ca_Desi_Chr06</i>	[G/C]	13242976	CDS_NON_SYNONYMOUS	C3H	AACAGCCGCAACTTCAGATT	CAGAAAACCCGCTTCTGTCT	NA
SNP1022	Ca_TC16835		<i>Ca_Desi_Chr06</i>	[G/A]	13996302	CDS_NON_SYNONYMOUS	HMG	CCGAGTTGCAAGAGAAAAGAG	AAGCCCACAGGTGAAATTCT	NA
SNP1023	Ca_TC11344		<i>Ca_Desi_Chr06</i>	[G/A]	14815110	CDS_NON_SYNONYMOUS	CAMTA	ACCAAGAGCAGCAACCAAT	TTTATGCTTTTATGGGTCA	NA
SNP1024	Ca_TC10606		<i>Ca_Desi_Chr06</i>	[C/T]	15273685	CDS_NON_SYNONYMOUS	Bromodomain	CGTCTTGATCGGAACCTTTT	CAATTAGCCACTCCCACGTT	NA
SNP1025	Ca_TC02723		<i>Ca_Desi_Chr06</i>	[T/C]	15848050	CDS_NON_SYNONYMOUS	Jumonji	ATCTGCATGCTCCTCCAGT	TGTGCTGACAAATTGTGGT	NA

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SNP1026	Ca_TC16337		Ca_Desi_Ch06	[A/C]	18443828	CDS_NON_SYNONYMOUS	bZIP	GGCAAGCGAGTCTCTCCTTA	AATGCCTTCCTCTACAAGC	NA
SNP1027	Ca_TC10915		Ca_Desi_Ch06	[A/T]	18949559	CDS_NON_SYNONYMOUS	mTERF	GGGTTGCAAGGAGACAAT	TTGTATCCAAATGCCCCAAA	NA
SNP1028	Ca_TC15258		Ca_Desi_Ch06	[C/T]	20519235	CDS_NON_SYNONYMOUS	NAC	TCCCTTCTCATGTGTTGTCA	TTGTCAACAAGGCATCGAAA	NA
SNP1029	Ca_TC08439		Ca_Desi_Ch06	[A/T]	21437289	CDS_NON_SYNONYMOUS	Bromodomain	AAGCAATTGGAGGAGCAAAA	CTGCAAATTCCTGGGTGAT	NA
SNP1030	Ca_TC03453		Ca_Desi_Ch06	[G/A]	21497337	CDS_NON_SYNONYMOUS	bZIP	CTCCCTCCTACATGTATTATAA	AACCTTGAGTGGTCCCTTG	NA
SNP1031	Ca_TC00789		Ca_Desi_Ch06	[G/A]	21675697	CDS_NON_SYNONYMOUS	HB	GAGATGGAGAGGCAAGAACG	TTGACGCTAAACCTCATCC	NA
SNP1032	Ca_TC08915		Ca_Desi_Ch06	[G/C]	21716470	CDS_NON_SYNONYMOUS	G2-like	GCACATGAAGAGGTTGGAAT	TGTTGCCAGATTGGAGATG	NA
SNP1033	Ca_TC07431		Ca_Desi_Ch06	[T/C]	21777225	CDS_NON_SYNONYMOUS	AP2-EREBP	CTCTCTTCGGAACACACCA	ACATCCATTGGTGGTGCTAA	NA
SNP1034	Ca_TC00539		Ca_Desi_Ch06	[T/C]	22228859	CDS_NON_SYNONYMOUS	E2F-DP	TTTAGGAGCGAAACGAAACG	TGGGCTAGTACAACCGAGTTC	NA
SNP1035	Ca_TC02346		Ca_Desi_Ch06	[G/A]	22711105	CDS_NON_SYNONYMOUS	ARF	TGCCTTCAGTTTCATTGCAG	GTACCGTCTCCACCGTTCAT	NA
SNP1036	Ca_TC18399		Ca_Desi_Ch06	[T/C]	23284891	CDS_NON_SYNONYMOUS	NAC	AAAAACCCAGTAACACACTGCAT	AGTCCAGTTTTCAGCCAAG	NA
SNP1037	Ca_TC11438		Ca_Desi_Ch06	[A/G]	24586525	CDS_NON_SYNONYMOUS	bZIP	ATGATAGCGCAGCAGAGGTC	CGGTTTGGTAGTTTCGGTGT	NA
SNP1038	Ca_TC06796		Ca_Desi_Ch06	[A/T]	26357644	CDS_NON_SYNONYMOUS	GRAS	CAGGTCACAAGTTTCCTGTA	ACAGATTGTGCACCCGAAC	NA
SNP1039	Ca_TC02132		Ca_Desi_Ch06	[G/T]	27861705	CDS_NON_SYNONYMOUS	C3H	TCATCCCTCTCAGGATCACC	TCAGGATTCAACCTCGAAC	NA
SNP1040	Ca_TC08004		Ca_Desi_Ch06	[G/A]	28103045	CDS_NON_SYNONYMOUS	HB	CTTGATTTCGACCGTGTGATG	TGCAATCGCTTGTCTGTAAG	NA
SNP1041	Ca_TC27287		Ca_Desi_Ch06	[A/C]	30942481	CDS_NON_SYNONYMOUS	bZIP	TTGATTGGCAGTATCATCGAAC	TGTTAAGTCACATAATCCACTAGACC	NA
SNP1042	Ca_TC12166		Ca_Desi_Ch06	[T/C]	31477570	CDS_NON_SYNONYMOUS	E2F-DP	ATGCAATCCATGAACGACA	AGGACAAGCTTCGAGAGAG	NA
SNP1043	Ca_TC12166		Ca_Desi_Ch06	[G/T]	31478512	CDS_NON_SYNONYMOUS	E2F-DP	CGCTTTTGTGTTCCGACTT	AACCATCAGGAGGTTGGAT	NA
SNP1044	Ca_TC06924		Ca_Desi_Ch06	[T/C]	32082602	CDS_NON_SYNONYMOUS	C2C2-YABBY	ATGGACATGATGGCAACAGA	TTGTCTCCAATCTTGACTAAGGA	NA
SNP1045	Ca_TC17223		Ca_Desi_Ch06	[G/A]	32326867	CDS_NON_SYNONYMOUS	WRKY	TGTTTGTGTAACACCACCAA	GGATCTTGGATTGGCTGCTA	NA
SNP1046	Ca_TC02231		Ca_Desi_Ch06	[G/T]	37388155	CDS_NON_SYNONYMOUS	OPP	TTGCAAGACTACCGGAGAGG	TGATTCCGAATGCTTGGTTT	NA
SNP1047	Ca_TC15677		Ca_Desi_Ch06	[G/A]	45709378	CDS_NON_SYNONYMOUS	WRKY	ATTCTTCCGATGTTGTTGG	TTTCTTGAATCCCAGTGCT	NA
SNP1048	Ca_TC12430		Ca_Desi_Ch06	[T/A]	45713690	CDS_NON_SYNONYMOUS	GRAS	TCAACACAACGACAACCTTTG	CACGTGGTGAAGCATAATGG	NA
SNP1049	Ca_TC06153		Ca_Desi_Ch06	[T/A]	53173286	CDS_NON_SYNONYMOUS	WRKY	TTGGGGATGACCAAGTTTTC	AGTCGGCTTTATGGTGCAGT	NA
SNP1050	Ca_TC19359		Ca_Desi_Ch06	[T/C]	53654154	CDS_NON_SYNONYMOUS	bHLH	AAAGAACAAGAAATTTGTCAAGAACA	TCACCACGAAAAAGTAGGC	NA
SNP1051	Ca_TC10558		Ca_Desi_Ch06	[G/A]	54359260	CDS_NON_SYNONYMOUS	GRAS	CTGCTCCTCACAAAGCTACC	TGAGACTCCAAGCTGCTGAA	NA
SNP1052	Ca_TC04801		Ca_Desi_Ch06	[G/A]	55333022	CDS_NON_SYNONYMOUS	HB	GATGCTGGGAGAAGGAAAAA	CAGCTAAACCAATGCCATGA	NA

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SNP1053	Ca_TC11343		<i>Ca_Desi_Chrom6</i>	[C/A]	55637657	CDS_NON_SYNONYMOUS	ULT	TGAGTCAGCCCATAGGAACA	ATTCATTCAACCCCATCACC	NA
SNP1054	Ca_TC18101		<i>Ca_Desi_Chrom6</i>	[T/C]	57024461	CDS_NON_SYNONYMOUS	MADS	TCITTCACAAATTTGGTACTGACC	TGCAGCCAAAGAAAACTGA	NA
SNP1055	Ca_TC14643		<i>Ca_Desi_Chrom6</i>	[G/A]	57532005	CDS_NON_SYNONYMOUS	FAR1	CGTCATCATCTCCATTGTGG	TGAGACCGATCCATCACAAA	NA
SNP1056	Ca_TC04361		<i>Ca_Desi_Chrom6</i>	[T/C]	57720386	CDS_NON_SYNONYMOUS	ABI3VP1	GGGACATCCATCAAAATGCTT	GGAAACCGACAACATGCTAA	NA
SNP1057	Ca_TC20893		<i>Ca_Desi_Chrom6</i>	[G/A]	58112367	CDS_NON_SYNONYMOUS	MYB-related	CTTGAGGATTGCCAGAAAGC	CTGAGTCTGGGCTTGACGAT	NA
SNP1058	Ca_TC16566		<i>Ca_Desi_Chrom6</i>	[A/T]	58242882	CDS_NON_SYNONYMOUS	mTERF	AGCGAAAACACACTTCACC	GGATGATTGACCCCTCAAGA	NA
SNP1059	Ca_TC07261		<i>Ca_Desi_Chrom6</i>	[G/T]	58555767	CDS_NON_SYNONYMOUS	bZIP	CGCAGGACCCATTAGTTTCA	CCACCACCTAACAACCCCTTG	NA
SNP1060	Ca_TC10295		<i>Ca_Desi_Chrom6</i>	[C/A]	58810441	CDS_NON_SYNONYMOUS	C2C2-GATA	GACCGGTTCGTGACAAAAT	CCCCTCTTTGTTCTTCACCA	NA
SNP1061	Ca_TC17073		<i>Ca_Desi_Chrom7</i>	[T/C]	82458	CDS_NON_SYNONYMOUS	CCAAT	GGTGGACAAGGTTCTTCAGG	GGCCATGATTAAAAACATGAAA	NA
SNP1062	Ca_TC10725		<i>Ca_Desi_Chrom7</i>	[A/C]	217223	CDS_NON_SYNONYMOUS	GRAS	TCCAGATGCAAAACGTCTCAA	AACGGCGATTGCTAAATCC	NA
SNP1063	Ca_TC05104		<i>Ca_Desi_Chrom7</i>	[G/A]	888424	CDS_NON_SYNONYMOUS	WRKY	AGGGCTGAGTGATGGTGT	TGCTCAAGAAAAGCGTCTGA	NA
SNP1064	Ca_TC12210		<i>Ca_Desi_Chrom7</i>	[G/A]	1270983	CDS_NON_SYNONYMOUS	bHLH	CATGAAGTTGGCATCTTTGG	CTTCATGCACCCCTTGATGCA	NA
SNP1065	Ca_TC18204		<i>Ca_Desi_Chrom7</i>	[G/A]	1799554	CDS_NON_SYNONYMOUS	GNAT	GATGCAGATGTAGCCACGAA	CAGCCGCCAGATTTTCTAAC	NA
SNP1066	Ca_TC26550		<i>Ca_Desi_Chrom7</i>	[G/T]	2712407	CDS_NON_SYNONYMOUS	WRKY	CAACAGAAACCCACAAGCAA	CTTCTGCTGGGTTGAAAAGC	NA
SNP1067	Ca_TC10471		<i>Ca_Desi_Chrom7</i>	[G/A]	3328637	CDS_NON_SYNONYMOUS	Tify	ATAAACCGTTGATGGCGACT	CTTGCGTTGATGTAGCACCT	NA
SNP1068	Ca_TC04651		<i>Ca_Desi_Chrom7</i>	[T/C]	3353684	CDS_NON_SYNONYMOUS	ARF	TATTCGGTTCTGTCTTATGC	GGCTGATATTACATCGACATACAC	Pr3
SNP1069	Ca_TC03534		<i>Ca_Desi_Chrom7</i>	[C/T]	3794570	CDS_NON_SYNONYMOUS	SNF2	GAAATGGGACTGGGAAAAAC	GCCTTCTCATGGGGTGAGTA	NA
SNP1070	Ca_TC06361		<i>Ca_Desi_Chrom7</i>	[T/C]	4598134	CDS_NON_SYNONYMOUS	C2C2-GATA	CGCGTGTGCTTGTGTTTTAG	CCAAAATTGGACTTACAATCATCA	NA
SNP1071	Ca_TC02595		<i>Ca_Desi_Chrom7</i>	[T/C]	4624953	CDS_NON_SYNONYMOUS	ARR-B	CGAAGGCTGAGTGGAGTTTC	GCCTTGCCTTGTGCATATTT	NA
SNP1072	Ca_TC03877		<i>Ca_Desi_Chrom7</i>	[T/C]	5280205	CDS_NON_SYNONYMOUS	mTERF	TTCCCTAATCGGTCGTTTCA	TGAAGACCTGTTTCTCATTCG	NA
SNP1073	Ca_TC18473		<i>Ca_Desi_Chrom7</i>	[T/C]	6812937	CDS_NON_SYNONYMOUS	C2C2-YABBY	CACAAACCAAGTAAAGGTTTGA	GAAGGGAAAGTAGCATTGTTGC	NA
SNP1074	Ca_TC06201		<i>Ca_Desi_Chrom7</i>	[T/C]	7863835	CDS_NON_SYNONYMOUS	bHLH	GCGCATTGACATTGGTACAG	ACAAGATCCAAGGCCATCTG	NA
SNP1075	Ca_TC10269		<i>Ca_Desi_Chrom7</i>	[G/A]	8553174	CDS_NON_SYNONYMOUS	zf-HD	GGACAAGCATTCCCTGGTTA	CAGAAATTGAGCAATCTGTGTCT	NA
SNP1076	Ca_TC09491		<i>Ca_Desi_Chrom7</i>	[G/C]	10016133	CDS_NON_SYNONYMOUS	MYB-related	TCATGTCTCGGATCCTCTGA	TCGAAGAGAATTGATGACCAAA	NA
SNP1077	Ca_TC08990		<i>Ca_Desi_Chrom7</i>	[G/T]	10114849	CDS_NON_SYNONYMOUS	AP2-EREBP	TCCTCCACGTTCAAAATCAA	TTAACCACCGGTTCTCTCTC	NA
SNP1078	Ca_TC01257		<i>Ca_Desi_Chrom7</i>	[G/A]	10251662	CDS_NON_SYNONYMOUS	C2C2-GATA	CACACCATTGGCGTAATG	TTTAGCGGTATCAACCACAGG	NA
SNP1079	Ca_TC11857		<i>Ca_Desi_Chrom7</i>	[G/A]	10485720	CDS_NON_SYNONYMOUS	SRS	CCAGCTTCACGCTTCTAGG	TTTACATAGCATTTCTCTGAACA	NA

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SNP1080	Ca_TC08009		<i>Ca_Desi_Chr07</i>	[T/C]	10686471	CDS_NON_SYNONYMOUS	ARR-B	AAAAAGAAAGCGGGGAACAT	CTTTGTTTTGGCATGTGGTG	NA
SNP1081	Ca_TC15323		<i>Ca_Desi_Chr07</i>	[G/A]	11192772	CDS_NON_SYNONYMOUS	HB	TCAAACAAAACACCATCACCA	AAAGGTTGTGTGGGTGAAC	NA
SNP1082	Ca_TC16765		<i>Ca_Desi_Chr07</i>	[A/T]	11324293	CDS_NON_SYNONYMOUS	bZIP	AGGTGGTTATTCTGCGATGA	TTTTCCCTTTCTCCCTCCTC	NA
SNP1083	Ca_TC06556		<i>Ca_Desi_Chr07</i>	[A/G]	11546194	CDS_NON_SYNONYMOUS	LOB	TTGTTCCCAACCACACCTT	AAACAAATCACCACGAACC	NA
SNP1084	Ca_TC00252		<i>Ca_Desi_Chr07</i>	[A/G]	14470793	CDS_NON_SYNONYMOUS	FHA	GTTGGAAACCACAAAACATAAT	TGAAGTCGAATCGTCTGCTG	NA
SNP1085	Ca_TC08380		<i>Ca_Desi_Chr07</i>	[G/A]	17264124	CDS_NON_SYNONYMOUS	MYB-related	GATAGAGTAGTGATGAGAAGATGAAGG	GTATCATGGGTCTCTGACATATTG	NA
SNP1086	Ca_TC08333		<i>Ca_Desi_Chr07</i>	[T/C]	17317735	CDS_NON_SYNONYMOUS	SET	GGAAAGAAGATTGGCTGCTG	CTCATCGGAGGGATGTTCTC	NA
SNP1087	Ca_TC01462		<i>Ca_Desi_Chr07</i>	[G/A]	17780711	CDS_NON_SYNONYMOUS	bZIP	GTACCCCATTTTGAGGAGCA	ACTGGTTCCTGACCAATGTC	NA
SNP1088	Ca_TC00629		<i>Ca_Desi_Chr07</i>	[G/A]	18389220	CDS_NON_SYNONYMOUS	Jumonji	ATGCTGGAGAAGGCTGAAGA	TCACCGATCGATCCCTCTAC	NA
SNP1089	Ca_TC08611		<i>Ca_Desi_Chr07</i>	[C/T]	20367403	CDS_NON_SYNONYMOUS	bHLH	TATGGCATTGGATTGGAGGT	GCACACTGAACAAGCTTGAAA	NA
SNP1090	Ca_TC05041		<i>Ca_Desi_Chr07</i>	[G/A]	22826866	CDS_NON_SYNONYMOUS	bHLH	TGTTTCACAAACACACAAATCTC	TGGTCAGTTGAAGATTATACTACTA	NA
SNP1091	Ca_TC18227		<i>Ca_Desi_Chr07</i>	[C/A]	27161185	CDS_NON_SYNONYMOUS	Alfin-like	CGAAGCGTCACAGTCACAAA	GCACGTGAGCGTGAATGTT	NA
SNP1092	Ca_TC17994		<i>Ca_Desi_Chr07</i>	[C/T]	33299885	CDS_NON_SYNONYMOUS	Tify	TGATCCGAAGTGTGGACCT	TCATTTACACCCTCTAACCAA	NA
SNP1093	Ca_TC16069		<i>Ca_Desi_Chr07</i>	[G/C]	39769428	CDS_NON_SYNONYMOUS	C3H	TCAAGGTTCGTCTCTGTTC	GTAGCCAAGCTCCTCCTTT	NA
SNP1094	Ca_TC03228		<i>Ca_Desi_Chr07</i>	[T/A]	42243517	CDS_NON_SYNONYMOUS	RB	CATGCGCTGTAATACCATCG	CACTAGCACATTGCGTGTGCT	NA
SNP1095	Ca_TC03228		<i>Ca_Desi_Chr07</i>	[T/C]	42245921	CDS_NON_SYNONYMOUS	RB	TTTCTCAATTTGCGAGCAA	CATGCGTTGTGACATCCTTG	NA
SNP1096	Ca_TC03228		<i>Ca_Desi_Chr07</i>	[T/C]	42246393	CDS_NON_SYNONYMOUS	RB	CATGCGCTGTAATACCATCG	CACTAGCACATTGCGTGTGCT	NA
SNP1097	Ca_TC15016		<i>Ca_Desi_Chr07</i>	[G/T]	43044483	CDS_NON_SYNONYMOUS	CCAAT	TCCGTAACCGACGTGTAATCT	CCATGCAGGATCATTACACC	NA
SNP1098	Ca_TC11984		<i>Ca_Desi_Chr07</i>	[G/A]	47237682	CDS_NON_SYNONYMOUS	HB	TCAAATAGGCACCAACACA	AACCATGGCCATAATCCAGA	NA
SNP1099	Ca_TC02570		<i>Ca_Desi_Chr08</i>	[T/C]	156866	CDS_NON_SYNONYMOUS	SNF2	GTCAATCAGGCAGTTGACCA	CTCTCTGCTCGAAGAGGTT	NA
SNP1100	Ca_TC33713		<i>Ca_Desi_Chr08</i>	[G/A]	498219	CDS_NON_SYNONYMOUS	FHA	TTCTGAAGCGAGAAGAGGAGA	GCCCAATACCATGTTGCCTA	NA
SNP1101	Ca_TC00233		<i>Ca_Desi_Chr08</i>	[G/A]	510120	CDS_NON_SYNONYMOUS	SNF2	TGCAGGAATTGTGGTCTCTG	AAACCACTTACCGCGACATC	NA
SNP1102	Ca_TC02881		<i>Ca_Desi_Chr08</i>	[G/A]	666619	CDS_NON_SYNONYMOUS	GNAT	TGGGATCGTTGTCAAAAACA	AAGGTATAGCAAACGGGCATT	NA
SNP1103	Ca_TC12027		<i>Ca_Desi_Chr08</i>	[G/A]	891777	CDS_NON_SYNONYMOUS	GNAT	GAGCGAAGGCATTATTGAT	GTACACTCGACCGCGGTATT	NA
SNP1104	Ca_TC02610		<i>Ca_Desi_Chr08</i>	[T/C]	1261904	CDS_NON_SYNONYMOUS	C3H	AATGGTGAGGATTTGGTGGA	TAAAGGGAAGCCATGTCACC	NA
SNP1105	Ca_TC03581		<i>Ca_Desi_Chr08</i>	[C/T]	1434072	CDS_NON_SYNONYMOUS	AP2-EREBP	AAGCAAAGCTGAATTGACAGC	CCTCTGTTTACATTGCCAAA	NA
SNP1106	Ca_TC00629		<i>Ca_Desi_Chr08</i>	[T/C]	1753840	CDS_NON_SYNONYMOUS	Jumonji	TTCAATTTCAATCTCTGAACAGTG	TCACATTCTCCATCTTCAAACG	NA

SNP IDs	<i>Kabuli/desi</i> accession IDs	gene	<i>Kabuli/desi</i> chromosomes	SNPs	Physical positions (bp)	Sequence components of genome	Putative functions	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')	Primers used in Figure 2A
SNP1107	Ca_TC18250		<i>Ca_Desi_Chr08</i>	[A/T]	2011749	CDS_NON_SYNONYMOUS	HB	TGGTCTCTCAACCTCAACCTC	CCAAATATTCCATTTCACCA	NA
SNP1108	Ca_TC06727		<i>Ca_Desi_Chr08</i>	[A/C]	2580625	CDS_NON_SYNONYMOUS	AP2-EREBP	CACAAATCCGAACAAACCA	TACGAATCCGATTGGCTCT	NA
SNP1109	Ca_TC15360		<i>Ca_Desi_Chr08</i>	[G/C]	2664948	CDS_NON_SYNONYMOUS	C2C2-GATA	GTGAGTATGCTGCCGAGCTA	GGTGGAGGACAAAAGGAACA	NA
SNP1110	Ca_TC18784		<i>Ca_Desi_Chr08</i>	[A/C]	2704215	CDS_NON_SYNONYMOUS	Tify	CAACAACATGAATCATCATCACA	TTGATGGAGGAATTAGTATGAC	NA
SNP1111	Ca_TC15831		<i>Ca_Desi_Chr08</i>	[C/T]	2974401	CDS_NON_SYNONYMOUS	ARR-B	AATGCAAGGACTTGCCAAC	TCCAGTCTACATGGCATTGG	NA
SNP1112	Ca_TC12117		<i>Ca_Desi_Chr08</i>	[G/T]	3154021	CDS_NON_SYNONYMOUS	bHLH	CATCGTCCAACGAATTAGCA	CAACCCCATACCAAACAAG	NA
SNP1113	Ca_TC16659		<i>Ca_Desi_Chr08</i>	[T/C]	3396641	CDS_NON_SYNONYMOUS	BSD	ATCCACTCAACCGATTCAA	CCCAGTGGAGACTGGCTTTA	NA
SNP1114	Ca_TC16559		<i>Ca_Desi_Chr08</i>	[A/T]	3456812	CDS_NON_SYNONYMOUS	GNAT	CACCTTGGAAATTCGGTTTGT	AATCACCTTCCCTCTTGT	NA
SNP1115	Ca_TC06892		<i>Ca_Desi_Chr08</i>	[G/A]	3521637	CDS_NON_SYNONYMOUS	GRAS	CCATCACCGTTAAAATCACG	CGGCATCACTACACTGCATC	NA
SNP1116	Ca_TC15081		<i>Ca_Desi_Chr08</i>	[A/T]	3682384	CDS_NON_SYNONYMOUS	LOB	ATCTGTGCCGGTGCTTAC	CCTCCTCTTCCCAATTTCC	NA
SNP1117	Ca_TC21141		<i>Ca_Desi_Chr08</i>	[G/T]	3998501	CDS_NON_SYNONYMOUS	AP2-EREBP	ACAATGCCAAAATTTCTTCTGT	CGTGTAAAGCTACCCAGATG	NA
SNP1118	Ca_TC03617		<i>Ca_Desi_Chr08</i>	[C/T]	4056195	CDS_NON_SYNONYMOUS	SET	AGACTGCGCCCTCTATGTGT	GCAGCCAAAGTGAAAGTGCT	NA
SNP1119	Ca_TC16950		<i>Ca_Desi_Chr08</i>	[G/C]	4176714	CDS_NON_SYNONYMOUS	FHA	TTGGAGAGGATCTGTCAACCTT	TGGGAGAGTTGGAGGAATGT	NA
SNP1120	Ca_TC07096		<i>Ca_Desi_Chr08</i>	[G/A]	4421071	CDS_NON_SYNONYMOUS	LOB	AGTGCCCTTTCATCTTCTCTAC	AACATGGGTATTACGGTTACAGG	NA
SNP1121	Ca_TC07629		<i>Ca_Desi_Chr08</i>	[G/A]	4623320	CDS_NON_SYNONYMOUS	HB	CACCAGAAGTGACCCAAAT	TCTCTCCAATCCACATCC	NA
SNP1122	Ca_TC04279		<i>Ca_Desi_Chr08</i>	[A/T]	5413114	CDS_NON_SYNONYMOUS	SRS	TGTTTTGTGTGTGTATGCAA	TTTGATTGGGGTTTGATGAAT	NA
SNP1123	Ca_TC08560		<i>Ca_Desi_Chr08</i>	[G/T]	5508790	CDS_NON_SYNONYMOUS	C2C2-GATA	TCCCTCAAACAACACAACCA	AGCCTAACCTAGCGACTCA	NA
SNP1124	Ca_TC08666		<i>Ca_Desi_Chr08</i>	[T/C]	5564404	CDS_NON_SYNONYMOUS	C3H	TGCCCTTTTTCACTTGCTCT	GCAGAAGAAGGAGATGAGG	NA
SNP1125	Ca_TC19323		<i>Ca_Desi_Chr08</i>	[G/T]	6618347	CDS_NON_SYNONYMOUS	HMG	CGGCTGAACCCAAAATTAAG	CCAAAAACCCTCACTCTCG	NA
SNP1126	Ca_TC05032		<i>Ca_Desi_Chr08</i>	[G/A]	7520805	CDS_NON_SYNONYMOUS	Trihelix	CTGGAGAGGGATTCACTGTC	TCCCTGGACTTAATGCCAAA	NA
SNP1127	Ca_TC00538		<i>Ca_Desi_Chr08</i>	[A/T]	7772710	CDS_NON_SYNONYMOUS	E2F-DP	GCAATTTAGGAGCCAAAACG	TTTCCCAAGTCCAGCCTACAC	NA
SNP1128	Ca_TC02177		<i>Ca_Desi_Chr08</i>	[G/A]	8362560	CDS_NON_SYNONYMOUS	HB	TGCAACAATGCCTTTTCAA	CGGGAGAAGGTATCACTCCA	NA
SNP1129	Ca_TC05885		<i>Ca_Desi_Chr08</i>	[T/C]	11675561	CDS_NON_SYNONYMOUS	Tify	CCCTTCTTTTCGCTTCTCC	GGAGAGGAATTCCTGGAT	NA
SNP1130	Ca_TC08051		<i>Ca_Desi_Chr08</i>	[G/A]	12525828	CDS_NON_SYNONYMOUS	MYB-related	AGCGCCGAAGTCTCTATTCA	GCGCTGGTATGTGTCCTAT	NA
SNP1131	Ca_TC14771		<i>Ca_Desi_Chr08</i>	[T/C]	13906178	CDS_NON_SYNONYMOUS	C2C2-CO-like	CTGGGAAATTAATGAAGGGTTA	AAGGTATGCAGATTCAGGTG	NA
SNP1132	Ca_TC03533		<i>Ca_Desi_Chr08</i>	[A/G]	14719923	CDS_NON_SYNONYMOUS	SWI/SNF-SW13	GAACCAAAATCCCAAACGA	TCAAGTCTCAGCCAAGTGA	NA
SNP1133	Ca_TC12255		<i>Ca_Desi_Chr08</i>	[T/A]	16090020	CDS_NON_SYNONYMOUS	C3H	AATCTCCGAGAAGGTGATTGA	CGGTGACATCCAAAACCTCT	NA

Eight seed weight-associated genes with SNPs are highlighted