

Table S3. InDel markers (8628) exhibiting differentiation between high (Pusa 1103 and HPNB) and low (ILWC 46 and LPNB) pod number-containing parental accessions and homozygous bulks of a mapping population (Pusa 1103 x ILWC 46) with reference to *kabuli* (CDC Frontier) genome

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8625	C11060010	682	AATTATT/AATTATTATT	TCCGATATGCACCAATGAAA	AGGCGTCGGTTTTTCTTCT	59.9	413	INTERGENIC				
CaPOPI_8626	C11155258	5339	TTAAT/TT	CCCACATTTTCATGATTTCC	GCTTCAATGAAATCGCAATACA	60.0	456	INTERGENIC				
CaPOPI_8627	C11169592	3333	CTTTT/CTTTT	TCTTTTCCGATGTTTTACG	GGGTGCCATCAACACATACA	60.1	125	INTERGENIC				
CaPOPI_8628	C11178328	12753	CAT/CATTAT	CCATCTTTTAGGCCTCTCC	GAAGGCAACCATTCTAGGCA	60.0	925	DRR	Ca_28266	T	M-type	Disease resistance protein
CaPOPI_1	Ca1	18088	TATAA	CCGCTTGTTTTCTTTGAG	TTGATTGCTTGTGCTCCAG	60.9	543	INTERGENIC				
CaPOPI_2	Ca1	19168	GCTCTCT/GCTCT	CAGAACCGAGGAATTAAAGCG	AGGCTTGAAGCGTGGTAATG	59.8	637	INTERGENIC				
CaPOPI_3	Ca1	186383	T/TC	TTCTGCATCACCATCTGAGG	TGATGAAGATCCCCAAGAG	59.8	783	INTRON	Ca_00014			Protein of unknown function DUF707
CaPOPI_4	Ca1	236262	TAAAAAAAA/TAAAAAAAA	TGAAAGAACAATATTCCAATAACCA	GCAGCAATTGATGGTGTGAT	60.2	129	INTERGENIC				
CaPOPI_5	Ca1	831015	T/TCTCTTATAAATGA	GCCGGATTAAATATAAATCCACA	TGACCTAATAAGCCTGTTGTTT	59.2	595	DRR	Ca_00101			
CaPOPI_6	Ca1	1084300	A/AC	TCCCAAATGACTTAATCCGC	ATCGTCGGAGAAATTTGACG	59.9	608	INTRON	Ca_00134	DO	LBD	Peptidase C14, caspase catalytic
CaPOPI_7	Ca1	1084940	CTTT/CTTTT	CGTCAAATTTCTCCGACGAT	CTGCGAGTGTCTTCTGGTCA	60.1	290	INTRON	Ca_00134	DO	LBD	Peptidase C14, caspase catalytic
CaPOPI_8	Ca1	1088478	A/AC	GGCATCACATTTGTGTCGAA	TCACCCCACTATCCCGTTTA	60.5	717	DRR	Ca_00135		C2H2	Methyl-CpG DNA binding
CaPOPI_9	Ca1	1094498	AC/A	TTGAGGAATGGTGCAAGATG	TGTAATTGCTATTCATTCCTGTTGA	59.6	254	INTERGENIC				
CaPOPI_10	Ca1	1160199	GATATATATATATATATATATA/GATATATATATATATATATATATA	ATATTCGGGGAATCACCTCC	AGCCGACCTTCCCACTTAAT	60.0	578	DRR	Ca_00145			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_11	Ca1	1237664	GTC/G	CATCATCAATGAACGAG CCA	CGTAAC TTGTGTTTGC ATGAGA	60.6	626	INTERGENIC				
CaPOPI_12	Ca1	1280971	TTATATATATATATATATATA/TTATAT ATATATATATATATATATA	GGGGAAAACCTTGCTCC TAC	AGGGGGAGCAAAACAA AAT	59.9	379	INTRON	Ca_00158			Golgi apparatus membrane protein TVP15
CaPOPI_13	Ca1	1397435	CA/C	TGGAACAGCAACGTGG TAG	CAAAGG GTTGATTTC CAC	59.8	555	INTERGENIC				
CaPOPI_14	Ca1	1427442	TTATATATATATATATATA/TTATATAT ATATATATATA	TTTGC GTAATTGTTGTG TCAA	TCCACCTCACCTCACT ACC	59.2	554	DRR	Ca_00173	O		Heat shock protein Hsp70
CaPOPI_15	Ca1	1540452	CTTTTTT/CTTTTTTTTTTT	AGTCTAAAGCCCCGAT TGT	ATTTGGCGGTCTTGTG TAG	60.0	476	INTERGENIC				
CaPOPI_16	Ca1	1617458	AC/ACC	TGAAATCAAGTTGGAA GAGTCA	TAAAAGGAAATTGCGT CCG	58.9	350	INTERGENIC				
CaPOPI_17	Ca1	1723303	TTGTAT/TT	ATGTCATCTGTGACCAA GCG	TGGATGAGTGAAAATTG ATTGG	59.7	420	DRR	Ca_00216	R		NADPH-dependent FMN reductase
CaPOPI_18	Ca1	1729960	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT AA/AAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT	GGAACGACCGTTGACTG ATT	TTAACTCAGAGGAGCGC AGC	60.0	618	DRR	Ca_00217		TALE	Protein kinase, catalytic domain
CaPOPI_19	Ca1	1745242	AG/A	ATTGTGATTGCATTGCAT GG	GAGTAGGTGCCTTCCCA CAA	60.4	548	INTRON	Ca_00219		TALE	Protein kinase, catalytic domain
CaPOPI_20	Ca1	1800007	AGTT/A	TGTTGCACAAGGTCCAG AAG	TTTTGCCAAGAGATGG ATG	59.9	601	DRR	Ca_00227	P		Cation/H+ exchanger
CaPOPI_21	Ca1	1820515	AT/ATT	TGTTGACATTAAGGAAG ACCGTT	GCTGTTACTACATGCTC TTCCAA	59.9	823	INTERGENIC				
CaPOPI_22	Ca1	1835247	ATGAC/A	TCATAAGCCAGAACCCA AGC	GGTGGTGAGATTCCAA GAA	60.2	448	INTERGENIC				
CaPOPI_23	Ca1	1836845	TATTTTAATT/TATTTTAATTTTAATT	CATTTCATACCGTTTCA CG	AGCACC ACTTCTTCATTC AAAA	60.0	704	INTERGENIC				
CaPOPI_24	Ca1	1841034	TTTCTTCT/TTTCT	TCAAGGTGTTGATTTCG TAGG	TTTTGCAACCCGGTCTA TTC	60.0	595	INTERGENIC				
CaPOPI_25	Ca1	1841061	TAAAA/TAAAAAAA	TCAAGGTGTTGATTTCG TAGG	TTTTGCAACCCGGTCTA TTC	60.0	595	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_26	Ca1	1841424	A/AT	GAATAGACCGGGTTGCAAAA	CCTCTTCCGGACAACAT	59.9	302	INTERGENIC				
CaPOPI_27	Ca1	1843387	ATATT/AT	CAACCAAAAATGCGACTTGA	GCCAAGCTAAGCTGACGAGT	59.7	526	INTERGENIC				
CaPOPI_28	Ca1	1849075	AATTATTATTATTATTATTAT/AATTATTATTATTATTAT	GAATTCACGGTGTGGGACT	TGTTTGAGCCAAATGTGAA	59.8	271	CDS (large-effect mutations)	Ca_00232	K	MYB	
CaPOPI_29	Ca1	1850030	CAATTAATTA/CAATTA	GTTGTCCGTCTTCCTGTGA	GGACAACCGAAGAGGATCAA	60.0	563	INTRON	Ca_00232	K	MYB	
CaPOPI_30	Ca1	1876420	AT/ATACGTAGTTCGGTTGAGT	CGGGTCTTCAAAATGGAATG	CAAAGGAAACGTGCTTCAG	60.3	861	INTERGENIC				
CaPOPI_31	Ca1	1882571	TC/T	ATATCGTTTTTCACCCCGC	GGTGCAAATGCAAGAGTCAA	59.8	282	INTERGENIC				
CaPOPI_32	Ca1	1882903	GT/GTCAGCTTCTAT	TTGACTCTTGCATTTGCAACC	ACATATGCGATTGGGACACA	59.8	581	DRR	Ca_00237	A		SPIa/Ryanodine receptor SPRY
CaPOPI_33	Ca1	1883092	C/CT	GCACGTGGCCCACTTATACT	ACATATGCGATTGGGACACA	60.0	244	DRR	Ca_00237	A		SANT domain, DNA binding
CaPOPI_34	Ca1	1883148	G/GA	GCACGTGGCCCACTTATACT	ACATATGCGATTGGGACACA	60.0	244	DRR	Ca_00237	A		SANT domain, DNA binding
CaPOPI_35	Ca1	1888179	TAAAAAA/TAAAAAA	CCTCACCCCATTTTCGTTT	ACCATGAACCATTGCCAAGT	60.2	455	INTERGENIC				
CaPOPI_36	Ca1	1915229	CTCAT/CTCATCTGTTTCAT	TGGATACACAAAACCGAACA	CACCTTTCCATCCATCGAC	58.9	709	INTERGENIC				
CaPOPI_37	Ca1	1917237	GAAAA/GAAAA	TGGTTGATGAAAGAGAGATGGA	TGTAACAAGCAGATGGATCTTG	59.7	247	INTERGENIC				
CaPOPI_38	Ca1	1930262	ATTTTTTT/ATTTTTTTTT	GGCAACATTTTACAAAA GTTAAGG	AGTTTGATTAATGTCGGGCG	58.3	318	INTERGENIC				
CaPOPI_39	Ca1	1963997	ATATTTATTT/ATATTTATTTATTT	AGGCAACAACTTTTGCACC	TTACAATGTGCATAGCGGGA	60.2	317	DRR	Ca_00244		B3	Transcriptional factor B3
CaPOPI_40	Ca1	1966252	TTCTCT/TTCTCTCT	GGCAAGAGAGCATCAAAAGG	CAAGTGAAATTTTGATTCAAGGG	60.0	703	DRR	Ca_00245	U	bZIP	Target SNARE coiled-coil domain

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CaPOPl_41	Ca1	1968368	CAAAGAAAGAAGAAAGA/CAAAGAAAG AAAGA	TCCAATCCATTCCACCAT TT	TGCATTCCATTTAGCAG CAG	60.0	775	INTERGENIC				
CaPOPl_42	Ca1	1988980	TC/TCCC	ACCTGCCAAAAGCAGAA GAA	CAGTGAAGTTTCGGGGA GAA	60.0	776	INTRON	Ca_00248	T		Protein of unknown function DUF300
CaPOPl_43	Ca1	1990497	TAA/TA	TGGGTCAACGTTGGTGT CTA	CCACTCAAAGGCTCACACA A	60.0	769	INTERGENIC				
CaPOPl_44	Ca1	1991447	GATATATATATATATATATATATAT /GATATATATATATATATATATAT	CCAACCCTTAGGGGACA AAT	CATGTGCCAGAAAGCTC AAA	60.0	505	DRR	Ca_00249	CR	HB-other	Alcohol dehydrogenase superfamily, zinc-containing
CaPOPl_45	Ca1	2015582	TTGT/TT	CTCTAGAACCCCCA ACT CCC	CTCCAATGTTGGGAGAC TACG	59.9	499	DRR	Ca_00253	E		Amino acid transporter, transmembrane
CaPOPl_46	Ca1	2023898	TAA/TAAA	TAATGAGGGCTTGAA TT CGC	TCCGTTGTTGAGGATGA TGA	60.2	386	DRR	Ca_00255			
CaPOPl_47	Ca1	2057962	GAAAAGTTA/GA	TGTGCATGAAGCAAAA TTGA	GGCCGTGAAAGATAT TT GGA	60.2	712	DRR	Ca_00261			Protein of unknown function DUF707
CaPOPl_48	Ca1	2073961	CTTTT/CTTT	AGAGGCACGAGATTT CC AGA	AAATATCCCCGCAATAA GGG	60.0	336	CDS (FRAME SHIFT)	Ca_00263	T	M-type	Disease resistance protein
CaPOPl_49	Ca1	2085633	CTTT/CTT	TGGGTTTTGTAAATGA AAGTGA	TTGAGATTTTCCAAGCT CAAG	58.6	737	INTERGENIC				
CaPOPl_50	Ca1	2108793	GTT/GTTTT	GTTTATCTGCCGA ACC TGC	CAATGGCAGTGATCTGC TCT	59.7	678	INTRON	Ca_00267	D	NAC	WD40 repeat
CaPOPl_51	Ca1	2135161	AGTGTG/AGTGTGTG	AGAAATTTACTCCAG TC CCG	TGAACCTCGTG CATGTGA ATTCT	59.1	437	INTERGENIC				
CaPOPl_52	Ca1	2223979	TATAATAATAATAATAATAATAA TAATAA/TATAATAATAATAATAATA ATAATAATAATAATAA	AATAGGTCAGGCCAG GC TTT	TATGGATGGGAATAGGC TCG	60.1	659	INTERGENIC				
CaPOPl_53	Ca1	2239989	AATATATATATATATATATAT/AATATA TATATATATATAT	ATGGTGGCAACACA CT TGA	TGGTTTTGATTGAGCT TCC	60.0	775	DRR	Ca_00280	I		Fatty acid desaturase, type 1
CaPOPl_54	Ca1	2299530	AATATATATATATATATATATATAT A/AATATATATATATATATATATATA TATATA	CAGCAACTGCGATGAGA TGT	TCACGGCGAGTCAATAA AAA	60.0	835	DRR	Ca_00288	R		Ribonuclease Zc3h12a-like
CaPOPl_55	Ca1	2655633	AGG/AG	TCCGTGGAAATGAAC TT AGC	CATGGACTCAAAAACAG CCA	60.1	812	INTERGENIC				

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CaPOPI_56	Ca1	2663715	TGAAAAGAAA/TGAAA	GTTGCCATGCCTATAACGGT	TGAAGACCATGGACACC AAC	59.9	547	INTERGENIC				
CaPOPI_57	Ca1	2674516	CTAGATTGGAT/CTAGATTGGATTAGAT TGGAT	TGTCGGAATATGGGAAG CTC	GCCGTTGTTTCAGATC CAT	60.0	934	INTERGENIC				
CaPOPI_58	Ca1	2686910	AGTATTTGGGT/AGT	AATGTGATGCACGTTTT GGA	CAATTCACGCAACAAT CG	60.0	444	DRR	Ca_00328		MIKC	
CaPOPI_59	Ca1	2702474	CTT/CTTATT	CTGGCAGCATTGTTGT GTT	ACTTCCTCCACCACCA CTG	59.8	228	CDS (large-effect mutations)	Ca_00331			
CaPOPI_60	Ca1	2766077	CTTATGTT/CTTATGTTATGTT	AAAACAATTGATGGGC TCC	CCAATCATACGCAGGTG AAA	58.9	561	INTERGENIC				
CaPOPI_61	Ca1	2796283	T/TG	GGTGGACAGAGGCATCA ACT	AAAAGCGAGTTTCAGG GTG	60.1	530	INTERGENIC				
CaPOPI_62	Ca1	2800448	ATTTTTTTTT/ATTTTTTT	GAGAGCAAGAGCGAGC AAGT	ACCACATGAGGGGCATT TTA	60.0	439	INTERGENIC				
CaPOPI_63	Ca1	2800724	TTTT/TTTTTTATTT	GAGAGCAAGAGCGAGC AAGT	TCCATTTCTCCTTCAAG CG	60.0	754	INTRON	Ca_00344		NAC	No apical meristem (NAM) protein
CaPOPI_64	Ca1	2837552	TTCTCTCTCTCTCTCTCTCT/TTCT CTCTCTCTCTCTCTCT	CAGCACAAGCATGCCAT AGT	TGCATCTGTTCTGCTT CAC	59.9	671	INTERGENIC				
CaPOPI_65	Ca1	2851127	TAT/TATAAT	TGTCGTTTTCAATGGAC TGG	AGAGAGTATGGGGCAGT CAAA	59.5	226	INTERGENIC				
CaPOPI_66	Ca1	2862989	CAA/CA	TAATGGCCAAATTCTCTC CG	GCTTTCACCAATTCCAC GTT	60.0	691	INTRON	Ca_00348	R		Optic atrophy 3-like
CaPOPI_67	Ca1	2885377	ATTTTTTT/ATTTTTTT	GCCATTGTTAACCCGC AAT	CATTTGGAGAGGGCATA GGA	60.0	360	DRR	Ca_00351	T	M-type	Disease resistance protein
CaPOPI_68	Ca1	2901135	TTCTGAGAAAGTTATCT/TTCTGAGAAA GTTATCTGAGAAAGTTATCT	AGCTTTCACGAAAATC AGC	GCACATTTACAGTTGGG GCT	59.5	565	INTRON	Ca_00354		bHLH	Protein kinase, catalytic domain
CaPOPI_69	Ca1	2921755	A/ATATG	CAACTGGGCCAAATGCT TAT	TGATGATCACACGAGGG AGA	60.0	570	INTERGENIC				
CaPOPI_70	Ca1	2946069	TA/TAA	ATTCCATCGCCATAGCA TTC	GGGACCAACAAATTCAA ACAA	59.9	553	INTERGENIC				

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CaPOPI_71	Ca1	2965539	CAAAA/CAAA	ACATGCTGTGATTGGG TCA	AAAGCGAATTACAGAC GTGG	60.0	873	INTERGENIC				
CaPOPI_72	Ca1	2973113	TATA/TATAATA	TTTGATGTGGCGGCATA GTA	TGTTTGCCAATCACAGC TTC	60.1	281	INTRON	Ca_00361			Lipase, GDSL
CaPOPI_73	Ca1	2979509	A/ATTATTT	GGAATTCCAAACTGAT CCAA	TGCCAACAAATCCTGAA CAA	58.9	653	INTRON	Ca_00361			Lipase, GDSL
CaPOPI_74	Ca1	3003710	AATATATATATATATA/AATATATATATATATATATATATA	GAAAGGCATGCAATATG GGT	AATCTGCCGACGCAAACTAT	59.8	440	DRR	Ca_00364	A	bHLH	Helicase, C-terminal
CaPOPI_75	Ca1	3020354	AGG/AGGG	CAAGCAACATGCTGAAG GAA	ATGTCCTTAGTGTCAGG GGG	60.0	808	INTERGENIC				
CaPOPI_76	Ca1	3042228	ATTT/ATTTT	GAGCCAAGATCGATGGG AT	TTTGATGAACACAACC CCAAA	60.0	502	INTERGENIC				
CaPOPI_77	Ca1	3043596	GTATATATATATATAT/GTATATATATATATATAT	GGACCGAAATGTTGCCT AAA	GACTTGGTCAATTTGCC GAT	59.9	531	INTERGENIC				
CaPOPI_78	Ca1	3045718	TCAC/CACTACAC	CGTAATCACATACATAG GGCTCA	CATTGCACGTCATTC TTG	59.0	479	DRR	Ca_00371	I		Lipase, GDSL
CaPOPI_79	Ca1	3049357	ATT/AT	ATCCTTAAAGAGAGGGG CCA	AAACCCAGGAAAGGGTC ACT	60.0	888	INTRON	Ca_00371	I		Lipase, GDSL
CaPOPI_80	Ca1	3073093	CTTTTT/CTTTTTT	CCTCCTTACGGCGAAAC ATA	CGTTGGAATCCAATG ACT	60.1	234	INTRON	Ca_00375		bHLH	Lipase, GDSL
CaPOPI_81	Ca1	3083516	AT/ATT	TCATTTGACTGAGGCTG CAT	GGACGAGGAGTTGGATT TGA	59.4	884	INTRON	Ca_00376		bHLH	Lipase, GDSL
CaPOPI_82	Ca1	3089369	AT/ATT	AAAATCGGTCTTGGGCT CTT	CCGTGTTAGTCGTCTAT TTTTACCA	60.1	713	DRR	Ca_00378	I		Lipase, class 3
CaPOPI_83	Ca1	3094552	TAT	GGTGCTCTAGAGGCAA AGG	TTGGAACAATGACGGTG TTG	59.1	633	INTERGENIC				
CaPOPI_84	Ca1	3103121	AT/ATT	GGGTGCAATGCTGGATT ATT	GTTAAGTGAGGTCCGTC CCA	59.8	462	DRR	Ca_00380			Glyoxal oxidase, N-terminal
CaPOPI_85	Ca1	3113743	GATATATATATAT/GATATATATAT	TGATTACAATCCTTTAAG CACG	GGAATCGAACTCGAGAC TGC	57.1	564	DRR	Ca_00381			Glyoxal oxidase, N-terminal

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CaPOPI_86	Ca1	3131301	TATA/TATACTCATA	GGCCGAGCTCAGACCTTCA	ACCCATTTTCTGACAACCG	60.4	506	INTERGENIC				
CaPOPI_87	Ca1	3147144	AATATATATATATATATATA/AATATATATATATA	TCCCAATGCTGCATGTTTA	TGGGTTGAGTTGTGAGTTCG	60.1	650	INTRON	Ca_00385			LPPG:FO 2-phospho-L-lactate transferase CofD/UPF0052
CaPOPI_88	Ca1	3194081	ACGAATGGTCAG/A	GCAAGGCTTGATTCCAAA	GGTTGCACCTTCCATGA	60.2	799	DRR	Ca_00390	O	E2F/DP	14-3-3 protein
CaPOPI_89	Ca1	3783626	TATTTGCATTTG/TATTTG	TTCACAATTACCAAAAGATCG	GCGACTATCCAGGAAATCCA	57.7	433	INTERGENIC				
CaPOPI_90	Ca1	3872384	TTATATATATATATATATATA/TTATATATATATATATATATA	GGCGAGAGCAAGAAAAC	CTGACCGTTTTTCGATTTCC	60.0	393	INTERGENIC				
CaPOPI_91	Ca1	4009762	AT/ATT	CGCACACACTTTCTACGCAT	TTGATCTGGTCAAATAAGCCA	59.9	841	INTERGENIC				
CaPOPI_92	Ca1	4105789	A/AGCACT	AAAAGTTTGCTGAGGAGCCA	AAAGGGCAAGGATGTGTTTG	60.0	163	INTRON	Ca_00493	D	TCP	Cullin, N-terminal
CaPOPI_93	Ca1	4131582	AAAAATAAATAAATAAATAAATAA/AAAAATAAATAAATAAATAAATAAATAAATAAATAA	TCCGAATAAATCGCATACCC	CCAGAGAGACAGATGCA	59.8	631	INTERGENIC				
CaPOPI_94	Ca1	4157854	TA/T	GTGGACACGCGTATGATTTG	TACAGGCGATGCAATTGAG	60.0	307	INTERGENIC				
CaPOPI_95	Ca1	4211915	TTATATATATATATATATA/TTATATATATATATATATA	ATCTCTACGCGACGAAGTT	CCAAATCCGTTCCGCTAGTA	60.0	276	INTERGENIC				
CaPOPI_96	Ca1	4233360	TTTAAATTTAAATTTAAATTT/TTTAAATTTAAATTT	TAATGGGCTTCGTGGGT	GTGCAGCACATTCGAGAGAA	60.0	683	DRR	Ca_00504			Protein of unknown function DUF642
CaPOPI_97	Ca1	4444544	AATATATATATATATATATA/AATATATATATATATA	AATCGATTGGCTGAAATCCA	GACATTTAACAGCGCCCAT	60.4	663	INTERGENIC				
CaPOPI_98	Ca1	4551372	GTGAATTT/GT	AACCACGGACTAATTGCTCA	AGTGTTCAACGTGGCTGTTG	57.2	187	INTERGENIC				
CaPOPI_99	Ca1	4742142	TAAA/TAA	GACCGCGTAGATGTGGA	GGATGAGACCTCCTACTTGCC	60.1	677	INTERGENIC				
CaPOPI_100	Ca1	5106336	CT/CTCTAT	CGAGTGATTTGCTTCAT	TGTTACGCATTGTTGG	59.3	651	INTERGENIC				

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CaPOPI_101	Ca1	5376097	ATGGTGGTG/ATGGTG	AAAAGATTAGTGGCTGC CGA	TTTGTGGTGGTCAAAGT CCA	59.8	219	INTERGENIC				
CaPOPI_102	Ca1	5403862	C/CTTTATTATT	ACGGTTGACTAATTGTG CCA	TCGCATCCCTACGATAC GAT	59.1	629	DRR	Ca_00627			
CaPOPI_103	Ca1	5423307	CTTTT/CTTTT	CGGGGTAGTTTTGTAT TCCC	GGTGACGCCTTTTAATT TGC	59.6	640	INTERGENIC				
CaPOPI_104	Ca1	5425033	TTTTATTT/TTTTATTATTATTT	TCACGGTGAAAGTTCTG TGC	AAATCCCAATAAGCAAG GCA	59.9	427	INTERGENIC				
CaPOPI_105	Ca1	5484796	TAA/TAAA	CGCGCGTTGTGTTTATA AGT	TTACCAAGATTGCCCT CTG	58.9	444	INTERGENIC				
CaPOPI_106	Ca1	5500920	CTAT/CTATAAACGTCATAT	GGAAGGGAATCGATGAG AAA	TATTCATTGGTTGGGG AAA	59.1	456	INTERGENIC				
CaPOPI_107	Ca1	5611256	ATTTTTTTTT/ATTTTTTTT	TCTCAGAACCGACACTG TTCA	TGAATTCAGGTGAGCGT GAG	59.5	886	INTRON	Ca_00645		G2-like	Myb, DNA-binding
CaPOPI_108	Ca1	5803481	TTAAGATAAGAT/TTAAGAT	GCTCATGAGTCCCTAC CCA	GTCAGGGGCTCGTGAT GAT	60.1	560	INTRON	Ca_00671	O	FAR1	ATPase, AAA+ type, core
CaPOPI_109	Ca1	5804081	AT/ATT	AATAACACGGGCACAAG AGG	AGGTCCACCAGGTTTGT CAG	60.0	457	INTRON	Ca_00671	O	FAR1	ATPase, AAA+ type, core
CaPOPI_110	Ca1	5955465	AATATATATATATATATATATA/AATATATATATATATATATATATA	TGCAGTGGAAGTGTGT TGA	GAACGAGGTCGGCAAAA GTA	58.8	686	INTERGENIC				
CaPOPI_111	Ca1	6137600	T/TC	TCTCATAGAAGGCGACG GTT	CATTTCCGAGCCAGTA AAA	59.8	412	INTERGENIC				
CaPOPI_112	Ca1	6174612	TTAT/TTATAT	CCTCTCATCCACATCCA TCC	GATATCCATCGGCTTAC GACA	60.3	538	INTERGENIC				
CaPOPI_113	Ca1	6176982	A/AAT	GGTGGTAATAGTTCAGC CCG	AATCTTTGCCAATGGTTT GT	59.5	564	INTERGENIC				
CaPOPI_114	Ca1	6202713	CTTTTT/CTTTTTT	CGCTTCCTTCTTCACAC ACA	AAAAGGCAATACATCCA ATCAA	60.0	640	INTERGENIC				
CaPOPI_115	Ca1	6203281	GTTTTTTTTT/GTTTTTTTTT	CTCCTTGAGTTTTGAGA CACGA	TCGATTATGCGTAGGGA AGG	59.5	453	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_116	Ca1	6204822	AAGA/AA	TGGTTTGGTGCATCAC TTT	TCGAAATTTGTGTTCCAA AAGA	59.0	543	DRR	Ca_07880	T		DOMON domain
CaPOPI_117	Ca1	6205233	CAAAAAAAAA/CAAAAAAAAAA	GGGTATTGGATAAAAAT TTCAAAAA	TGAAATTAAGGGACGG GTTT	58.7	604	DRR	Ca_07880	T		DOMON domain
CaPOPI_118	Ca1	6206568	CTTTTT/CTTTTTTTT	TTATGCTTTCAACCA GTG	TGTCGGATAAGTGTGAT ATATTG	59.9	747	INTERGENIC				
CaPOPI_119	Ca1	6212978	AATATATATATAT/AATATATATATAT	GTGCGCAGTACAATTCT CCA	CAACCGCTCCCAAATAG AAA	59.9	573	INTERGENIC				
CaPOPI_120	Ca1	6219100	TTACGGTAT/TT	TGGGAAAAC TTGTTCCA TGAG	TTGATCTCCACATCACC AAGA	60.0	587	INTERGENIC				
CaPOPI_121	Ca1	6267078	GAAA/GA	TTTCTTGCACTGTTTGT GC	TGGGTCCCTCATTGTAC TCC	59.9	560	INTERGENIC				
CaPOPI_122	Ca1	6293780	TAAA/TAAAA	ACACACTGATCGATGAT CCC	TATCTTTTGGTGGGCC AAG	58.3	716	INTERGENIC				
CaPOPI_123	Ca1	6317430	TTAAAG/TTAAAGCCATAAATAATAAG	GCTGAGCATGTTGGAAC AAA	AAGATCCCCCATGGAAA CTC	59.8	606	INTRON	Ca_07892	B	MYB_rela ted	Zinc finger, ZZ-type
CaPOPI_124	Ca1	6338411	AAATTAA/AAA	CAACGTTGATTGGGTCA AAA	CCCTTCATACACGGACC ATC	59.4	662	INTERGENIC				
CaPOPI_125	Ca1	6453816	AT/ATT	GGTCTTGCTGACCTTGA AGC	CACGTAAAACTCTAAC GATGAA	60.0	644	DRR	Ca_07909		Trihelix	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor
CaPOPI_126	Ca1	6467793	GGAG/GGAGAG	AAAGGGCAAGATTGTG CAC	AAGGGATAATGTGTTCC CCC	59.0	197	DRR	Ca_07910	S		tRNA (guanine-N1-)-methyltransferase, eukaryotic
CaPOPI_127	Ca1	6535430	GTTATAGTTTTATAGTT/GTTATAGTT	GCGATGATCGATGACAC TCTT	CAAAGTCGAGTATCACC GCC	60.2	236	INTERGENIC				
CaPOPI_128	Ca1	6965841	CTTTTT/CTTTTTTT	GTTTTCGTTCTCTCCTC CCC	TGTCATCAGGGAACCA CAA	60.1	759	INTERGENIC				
CaPOPI_129	Ca1	6999458	TTATATATATATATATATATATAT/TTA TATATATATATATATATATATAT	AACAACGCTTTCATTG ACTTT	TTTTTCCTGAAACAGGC AGT	60.0	795	INTERGENIC				
CaPOPI_130	Ca1	7215414	AA/AACA	AACCCCAACTACAAGG TCC	CAATTTGACAAGCCCC TAA	60.1	639	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_131	Ca1	7423449	CTTTTTTTTTTT/CTTTTTTTTTTT	CCATTGGTTGCTTGGT TTT	TTTTGCTTATATGTTGG TTCTTGA	59.8	118	INTERGENIC				
CaPOPI_132	Ca1	7634571	GT/GTT	AAAGTGAATTGCTCAATT TCGTC	AATTGACACGTGAAGAT TTGTTT	59.7	777	INTERGENIC				
CaPOPI_133	Ca1	7634633	ATTTTTTTT/ATTTTTTTTTT	TCCAGCACAAATACCTTT TTACC	TGAATTCGCGTTGTTTG TGT	59.4	666	INTERGENIC				
CaPOPI_134	Ca1	7677905	CTATTATTATTATTATTATT/CTATTA TTATTATTATTATTATTATT	ATCGGAATCAAACCACT TCG	TGAGCCGGAATATTGAG ATTG	59.9	567	INTERGENIC				
CaPOPI_135	Ca1	7775058	C/CCTTAAT	AGCCCAACCCTTGACCT AAT	GCACGGAACAACATGT GAC	59.8	838	INTERGENIC				
CaPOPI_136	Ca1	7778630	CTTT/C	CCACACACATCAACCAC CAC	GGGCGATTGACTTGAGA CAT	60.8	444	INTERGENIC				
CaPOPI_137	Ca1	7790700	AAAA/AAAACGCAAA	TCCATAATGTCAAGTTT GAGCC	ACATCCACAGCACTTGC ATC	60.4	949	INTERGENIC				
CaPOPI_138	Ca1	7810637	G/GAA	AACGATTGGTTGAGACC CAG	ACCTTGTGTCTATCTGG CCG	60.0	505	DRR	Ca_08031		FAR1	Protein kinase, catalytic domain
CaPOPI_139	Ca1	7895366	GAAA/GAA	TTGCCACAAGCTAAAG GCT	TGGTCAGTTTGGCCTAT TCC	60.0	514	DRR	Ca_08038			
CaPOPI_140	Ca1	7947587	AC/ACC	TCTTCCTCCAAATTCAA TCA	TTTTTATTCTCGTGGA GTGAG	59.5	578	INTERGENIC				
CaPOPI_141	Ca1	7995324	ATAGTAGT/ATAGTAGTAGT	CGGATTGTTTTCGATAT GGG	AAGGGATTTTTATTCACA AAACAA	60.1	527	INTERGENIC				
CaPOPI_142	Ca1	8000857	ATGT/AT	CGCCATCTTCACGTCAC TTA	TCCAACCCAAATTTCAAA CA	59.9	699	INTERGENIC				
CaPOPI_143	Ca1	8006710	TG/TGG	TCTTCCCTCCTTCCTTG GAT	TAACACAAGTAGTCGCC CCC	60.0	748	INTERGENIC				
CaPOPI_144	Ca1	8035534	T/TTA	CAAATGCAATGCAATG ACC	AGGCATCTTTTCAGGTT CCC	59.9	782	INTRON	Ca_08051	M	FAR1	NAD-dependent epimerase/dehydratase
CaPOPI_145	Ca1	8125888	G/GACATATTAAAA	TGTTGGGTTACGAGGGA GTC	TTGCGGGTTTTTAACCT GAG	60.0	526	INTERGENIC				

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									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_146		Ca1	8127338	CTT/CTTT	CCCTCCTTCCAGAAAC CTT	AATCCTGCAGTGAAACC ACC	59.5	708	INTERGENIC				
CaPOPI_147		Ca1	8403563	TTAATAATAATAATAATAATAATAAT AATAATAATAATAATAATAATA/TTA ATAATAATAATAATAATAATAATAAT ATAATAATAATA	CCCCTAAAAATTAGTCG AACTCC	GAGTCTTTGTCCCCAGC AAG	59.4	474	INTRON	Ca_08076			
CaPOPI_148		Ca1	8415420	AG/A	ATGGGTGAAACGACAA CTC	TTTTCTTTTGCATCATC TTTG	60.1	910	INTERGENIC				
CaPOPI_149		Ca1	8830262	TTATATATATATATATATATATATA/TT ATATATATATATATATATATATA	GCTACCTTAGCCTCTCC ATGC	GGAATGCCATAGAAACA CCAA	60.4	811	INTERGENIC				
CaPOPI_150		Ca1	8909387	T/TCC	AGGCCAAAAGGTTTTTGG GTT	GTGAGGCGTGAAGTGG TTTT	59.9	806	DRR	Ca_02914			
CaPOPI_151		Ca1	9233850	GTTTTTTTTTTTT/GTTTTTTTTTT	TGAGTTCTTTGAATTTG CGTG	GTTGCGTCTAGCAACTT TCTG	60.3	637	INTERGENIC				
CaPOPI_152		Ca1	9871519	ATT/A	CTTAGTCCACGTGCAAA CGA	AAAGTGCGGGCCAATAT CTA	59.9	600	INTERGENIC				
CaPOPI_153		Ca1	10040103	ATTT/ATT	ATGCATCGAAAACCAAC ACA	TGCAATCCGGGCTTACT ATC	60.0	378	INTRON	Ca_02784	LK		
CaPOPI_154		Ca1	10057638	CATATATATATATATAT/CATATATAT ATATAT	TGATGGGAGCAATGAAT GAA	TCAAATCCGACTTGAG GGA	60.0	542	INTERGENIC				
CaPOPI_155		Ca1	10064752	TTATATATATATATATA/TTATATATAT ATATATATATATATA	ATGCAAAATCTCCCCCT CTT	TCATTGATTTTAATTGG ACGA	59.9	750	INTERGENIC				
CaPOPI_156		Ca1	10323177	G/GAGCT	TTGAGTGCTTCACCATTT GC	GTTGTATTGGCTCTCCT CGC	59.8	463	INTRON	Ca_02746	B	C2H2	WD40 repeat
CaPOPI_157		Ca1	10414677	CAGGAATNNNNNNNNNAGGAAT/CAG GAAT	TTCTAAACGAGGCTTTT CAGTTG	GCATGTTGCTGATGATG GTC	59.9	489	DRR	Ca_02735	R	ERF	3-hydroxyisobutyrate dehydrogenase- related, conserved site
CaPOPI_158		Ca1	10458891	TACACACA/TACACA	CCAATTTAGTAGGCC AAA	AGCATTGAAACCAACC AGC	59.9	583	DRR	Ca_02729		HSF	Survival protein SurE- like phosphatase/nucleotid ase
CaPOPI_159		Ca1	10471260	TTATATATATATATATATA/TTATATAT ATATATATATATA	TTCTCCATTCGCACTCA CAC	TCAAATTTGGAGGCTGG AAC	59.8	312	INTERGENIC				
CaPOPI_160		Ca1	10513925	CTTATTTATTTATTTATTTATTTAT TTATTTATTTAT/CTTATTTATTTATTTA TTTATTTATTTATTTATTT	CCAGATTTCTTTTCCC CTC	GGGTAGGCCACAGACT GTCTTA	59.9	634	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_161	Ca1	10944660	TAAAAAAAAA/TAAAAAAAAA	GCGACCTCGTGAATGAAA	GGCATAATTGTTCCACAAA	61.1	534	INTERGENIC				
CaPOPI_162	Ca1	11102279	ATTTTTTTTT/ATTTTTTTTT	TGCCGCGAATTTAGATCTT	TCGGTGTGGTGTCGTTATC	59.8	255	DRR	Ca_02649	C		Mitochondrial carrier protein
CaPOPI_163	Ca1	11145101	TTATATATATATATATATATAT/TTATATATATATATATATATAT	TTTGAGTCCAAATTGAAAGCT	CGGATCAAAATTCGCACAAAT	58.8	837	INTERGENIC				
CaPOPI_164	Ca1	11148737	CAATAATAAAT/CAATAAAT	CGTGAATTGGTAATGTGGCA	GGCTAACTTGAAGTCGTGGC	59.4	693	INTERGENIC				
CaPOPI_165	Ca1	11170203	CATA/CATATATA	ATGAGGGTATCCGAGCCATA	CCACAAGAGTTTTGCCATTG	59.4	378	DRR	Ca_02641			Protein of unknown function DUF3527
CaPOPI_166	Ca1	11190216	ATTACT/ATTACTTACT	TATGGCTAGCTGGTGAAAGCA	TAGAATCCCACGCAGCTCTT	59.6	304	INTRON	Ca_02639			
CaPOPI_167	Ca1	11324975	GAAGA/GAAGAAAGA	CTGCATCGGGGATACTTACC	TTTTGACCGAGCCAGATACC	60.5	317	INTRON	Ca_02622			
CaPOPI_168	Ca1	11456505	TTATATATATATATATATA/TTATATATATATATATATATA	AACCGAGTGCCCTTTAAACA	TTGTTTTGCATTTTGGGACA	59.6	273	INTERGENIC				
CaPOPI_169	Ca1	11868314	TTATATATATATATAT/TTATATATATATATATATATAT	GCAAGTATGCAACAACCTTCC	TTGCATATATTGCACACCGC	59.6	346	INTERGENIC				
CaPOPI_170	Ca1	11977187	CAAAAA/CAAAAAA	GCAATTGGATGACATTGCATA	ACAGACAGGGCACAGGATCT	59.4	479	INTERGENIC				
CaPOPI_171	Ca1	12195477	CTTTTTTTTT/CTTTTTTTTT	TTGTTTGTTCCTTGTGGCA	AGAAAAATGCGATGGTCTTT	60.1	250	INTERGENIC				
CaPOPI_172	Ca1	12420239	CAAAAAA/CAAAAAA	AAATGCAATCTTGGTTTCA	TTTTGGTAATGTGCCCATGATA	58.1	595	INTERGENIC				
CaPOPI_173	Ca1	12550318	ATTTTTTTTT/ATTTTTTTTT	CGTCTTTATTTATGCGAGCG	TAATGCCGATGGTGTCAAA	59.9	252	INTERGENIC				
CaPOPI_174	Ca1	12580190	TAAAAAAAAA/TAAAAAAAAA	TAATCACTCACCATCGCCA	TTCATGTTGGTGTGGCACT	60.1	476	INTERGENIC				
CaPOPI_175	Ca1	12727627	TTATATATATATATATATAT/TTATATATATATATAT	CCTTACGGACAACCAAGCAT	GCAAAAGAATTGCAACAAAGA	60.0	419	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_176	Ca1	12947634	ATAAATTTAA/ATAAATTTAAATTTAAATTTAA	AACCTTGTGGTCGTTTTGGC	TGCTTATTGGTGCTGCTTTG	60.0	647	INTERGENIC				
CaPOPI_177	Ca1	12956423	CAAAAAA/CAAAAA	TTGTCGGATACCTGCTCAGT	TTGCAAAATTCGGACAAACAA	58.3	455	INTERGENIC				
CaPOPI_178	Ca1	12988934	C/CGGG	ATCGGCATCCTTCCTTCTTT	GACGCTAAGCCCCCTTCTCT	60.0	354	INTERGENIC				
CaPOPI_179	Ca1	13005887	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TCGTCATCTAGCACCAGCAC	TCCCTCGTAAAGACCCATCT	60.0	347	INTERGENIC				
CaPOPI_180	Ca1	13007507	TTAT/TTATATAT	CACGGGTCCAGATGGTTAGT	CCAAGCATCTTGGTGCAATA	59.8	322	INTERGENIC				
CaPOPI_181	Ca1	13117590	TAATAAAATAAAAATAAA/TAATAAAATAAAAA	TGTTGTTTACGGAATTTGGTTTT	TTTCGTTGTATATTAAGCACGG	59.7	547	INTERGENIC				
CaPOPI_182	Ca1	13134589	TAAAAAA/TAAAAAA	CGATGGATGACTTCCCGTAT	TTTACGTTGACGCACGAGAC	59.8	587	INTERGENIC				
CaPOPI_183	Ca1	13674092	ATTTT/ATTT	AACGGTTCGATTCGGTTTTT	TGAAATTTTCGCATTACACA	59.9	382	INTERGENIC				
CaPOPI_184	Ca1	13676261	ACT/ACTCT	CCGCTACAAGGCGATAGAAG	GGGTGCATCATAGGTGGCT	60.0	856	DRR	Ca_14132			
CaPOPI_185	Ca1	13680810	ATTTTT/ATTTT	TGGTTGAAGTGTGAACAGGC	CCAATTTCCCTACCCCAAT	59.7	559	INTERGENIC				
CaPOPI_186	Ca1	13686356	T/TCTC	TTGTACGGGTGGTGCAAAA	GAGGGTGACTCTGCTGGAAC	59.9	655	INTRON	Ca_14134		MYB_related	Glycoside hydrolase, family 16
CaPOPI_187	Ca1	13690477	CAA/CAATCGGTTTTATAA	CCGGTTATTTAACCATAACCAA	TGCAAGGAACAAATGGCATA	57.9	200	INTERGENIC				
CaPOPI_188	Ca1	13692764	CTTTT/CTTTTT	CGCCAGTGGTTATGCTCTTA	AAGGAACCACACTTGAAACCG	58.9	875	INTERGENIC				
CaPOPI_189	Ca1	13694461	GTA/GTAATA	CCACTTCGCCACGTTTTTAT	CGGTTTATCGTCAAAGCGAT	60.0	379	INTERGENIC				
CaPOPI_190	Ca1	13696144	TAAAA/TAAAA	TTTGC GTTACGAATTTGATGA	AGAA GTTGAAC TACGATCACA	59.2	757	INTERGENIC				

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CaPOPI_191	Ca1	14385063	CAA/CAA	AATCGTCTCCGTACACACA	GCGAATTGCAGACTGAAACA	60.2	662	DRR	Ca_07096		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_192	Ca1	14682464	CTTTT/CTTT	TCCATTGTTGAGCGAAAACA	TGGATGAAGGATCAACCACA	60.2	659	INTERGENIC				
CaPOPI_193	Ca1	14777698	TAAAAAAAA/TAAAAAAAA	CAATGACCTTGGTCCTCTG	TTAACTGCAGCCATGCACTCT	60.5	799	DRR	Ca_07052	R		Phosphatidylethanolamine-binding, conserved site
CaPOPI_194	Ca1	14893455	GTTTTTTTT/GTTTTTTTT	AGGGACAAGGTTGGGTTT	TTAAACTTTGCACGGAGGG	59.7	291	INTERGENIC				
CaPOPI_195	Ca1	14995847	ACATGCATGCA/ACATGCA	CAGCGCTTTCCCAATAAG	CCAAAAGGGTGGAGATTGA	59.8	359	INTERGENIC				
CaPOPI_196	Ca1	15326926	CATATATATATAT/CATATATATAT	GTTAAGCATCCCAAGTTGGA	AGCCAAGAGTTTGTGGAGTTG	59.9	626	INTERGENIC				
CaPOPI_197	Ca1	15811388	TAAAAAAAA/TAAAAAAAA	GCGAGATTTTCGACTTCG	TGCGGCAACGTAATTGTAA	60.1	590	INTERGENIC				
CaPOPI_198	Ca1	15835234	TTTATTATTATTATTATTATTATTATTATT/TTTATTATTATTATTATTATTATTATTATT	TCGTTTGCCGTTAACTAGGG	TTGGCCTAACCTGAAAGCAT	60.1	768	INTERGENIC				
CaPOPI_199	Ca1	15849587	AATATATATATATATATATATATATATATATATATAAATATATATATATATATATATATATATATATATATA	CCCCATTTTGTCTCTGCA	ATTCTTGAGGAGCGGGTAT	59.9	872	INTERGENIC				
CaPOPI_200	Ca1	16078538	CTTTTTTTTT/CTTTTTTTTT	TGCATGTTGTTGGTAGAGTCAA	GCACAAGGTATGCCAAATGA	59.2	632	INTERGENIC				
CaPOPI_201	Ca1	16096244	TG/TGG	ATGTAAGATTGGAAGCGGCA	CAATTGTTCCCCACTTGCTT	60.6	298	INTERGENIC				
CaPOPI_202	Ca1	16116426	GA/GAA	AATGCAACGGTTGGTTGAT	GCACAAATGAAAAGCAGAACA	60.2	826	DRR	Ca_06940	R		General substrate transporter
CaPOPI_203	Ca1	16155793	ATT/AT	GGCAACTCCATTGAATTCGT	AATCCCCACCCTAAATGACC	59.9	333	INTERGENIC				
CaPOPI_204	Ca1	16159274	AAAAA/AAAAACAAAA	ATGGTTTTAAGCATTCCCA	TTAAGTTGCGAGGTTGCTCA	59.3	457	INTERGENIC				
CaPOPI_205	Ca1	16160389	TT/TTCT	CATGTGGATTGTCTTTGCG	GCACAAGATCCTCAAACTGG	60.1	238	INTERGENIC				

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CaPOPI_206	Ca1	16162054	CTT/CTTT	TCCTCATGGCTTTTCATTCC	TCAATCTTCATAGGCTGAACGA	60.0	796	INTRON	Ca_06938	R		General substrate transporter
CaPOPI_207	Ca1	16167140	TAAAA/TAAAAA	TTTTTAGCATGGCACGT TTT	CGGGTTGGATTAGATTTCAAG	58.4	378	INTERGENIC				
CaPOPI_208	Ca1	16187503	AGTTTATGACG/AG	GTGTCACCATTGGCAATACG	TTCTTCGACCTCACAATCC	59.8	382	CDS (large-effect mutations)	Ca_06937			GH3 auxin-responsive promoter
CaPOPI_209	Ca1	16203089	TC/T	CTTGTGTGGGAAGGTC ACT	TGTGTGACCCCTGCTGATA	60.0	685	INTERGENIC				
CaPOPI_210	Ca1	16583164	AATATATATATATATATATA/AAATATATATATATATATA	TTTGGCACTTTCTCATTC CC	GCCATGTATGGTCCAAGGTC	60.1	793	INTERGENIC				
CaPOPI_211	Ca1	16629521	TTTAATTAATTAATTAATT/TTTAATTAATTAATTAATTAATTAATT	AACGTTTGAGGATTCGGTTG	GAAACTCCAGCTCCAAACG	60.0	370	INTERGENIC				
CaPOPI_212	Ca1	16707141	TTATATATATATATATATATATATA/TTATATATATATATATATATATATAT	CTTTACAACCGCCACAAC ACC	CGAACAAAGTGCTTGTGGAA	60.4	755	INTERGENIC				
CaPOPI_213	Ca1	17185713	TTTGATATTTGATTAT/TTTGATATTTGATTATTGATATTTGATTAT	GCGTTAAAGTTGGAACCCA	TGACGTGACATCGAGAGTCTG	60.0	594	INTERGENIC				
CaPOPI_214	Ca1	18181716	AATATATATATATATATATATATA/ATATATATATATATATATATATATATA TA	CGAATACTCATGGTTTTTGATCTG	ACCCAACGTAGCACGTTACC	59.9	626	INTERGENIC				
CaPOPI_215	Ca1	18300800	ATTT/ATT	AGCAAGAAAATTGAAGGCCA	GGAAGCTTTAAAGGGAGCAAA	59.8	161	INTERGENIC				
CaPOPI_216	Ca1	18301437	AATT/A	TGATAAGCTAACAGGCCAAAAA	ACATGGGCTAGCAAGAAACC	58.9	417	INTERGENIC				
CaPOPI_217	Ca1	18317638	T/TG	TCATTTTCAACCTTAGCAACA	TGGAAGGTATACGCGGGAG	59.6	690	INTERGENIC				
CaPOPI_218	Ca1	18325523	AGG/AG	CGGATCATTACACACTTGCG	GCCAAAGCCATGTTTTCAAT	60.1	324	INTERGENIC				
CaPOPI_219	Ca1	18328170	GTTTTT/GTTTTTTT	TTAAAACCAAAAATGGGCG	GAGGCAAAGCTTCCAAATCA	59.7	475	INTERGENIC				
CaPOPI_220	Ca1	18364053	GAAA/GAAAA	CCCGTAGCAAGACTTGAAGC	TTGGAGAAACTTTTCCGCTG	60.0	627	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_221	Ca1	18441371	CACAAGAGAC/CAC	CCCTCTGTATGCCAGTCGAT	TGGCATTGATGATGGCTTTA	60.1	771	INTERGENIC				
CaPOPI_222	Ca1	18472041	CAAAAAAAAA/CAAAAAAAAAA	CCTACATTCGCACGAGTTCA	TTTTTCTCCAGTTTGGTCCT	59.9	404	INTERGENIC				
CaPOPI_223	Ca1	18688865	TTGT/TT	TAGCAGCTGGAGGAACATGA	GCACCCAGTGTAAAGACC	59.5	301	INTERGENIC				
CaPOPI_224	Ca1	18868658	CGG/CGGGAATGG	AATCGATTGATTCAGCC	CGTTTTTCAAAGCGAGGGTA	60.0	707	INTERGENIC				
CaPOPI_225	Ca1	18899804	CTATATATATATATATATAT/CTATATATATATATATATATAT	GCTTCAATGTGCACGATACG	TTCTTTGTTGGTAGGGCACC	60.3	237	INTERGENIC				
CaPOPI_226	Ca1	18928985	CTTATTTATTTATTTATTTAT/CTTATTTATTTATTTATTTATTTAT	TTTACCCTATCCACACCCC	TCCAATGATTCCTGTTTTGC	60.8	613	INTERGENIC				
CaPOPI_227	Ca1	19150973	CTT/CT	AACTAGCCCGTCTTTGGGTT	GAAACAAAAGCTTTACGGTCA	60.0	488	INTERGENIC				
CaPOPI_228	Ca1	19498678	TTTTGATCCTTTGAT/TTTTGAT	GCCCGAGTTAACAACAACG	ATCGATTTCTCAGCAC	60.5	374	INTERGENIC				
CaPOPI_229	Ca1	19903627	TA/TAATTGGCAGCA	TGGGCTGAAAAGCAACTTCT	ACCAGTGCTGTTCCCAATC	60.0	233	INTRON	Ca_08847	K		RNA polymerase I associated factor, A49 like
CaPOPI_230	Ca1	19909063	TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATAT	CCATAATTTTTGGATCCTCCT	TTTGCTTATGAGAAAAAGGAGATGT	57.1	235	INTERGENIC				
CaPOPI_231	Ca1	20097334	CNNNNNNNNNNNNN/CNNN	TTTCGTTTGCGATAGTGTCC	TCATTTCAAGATCCTGGTTCC	60.1	250	INTERGENIC				
CaPOPI_232	Ca1	21746056	AC/ACACATATCAGCTTTC	CTATTGCCCCCTCCTCTAC	TACCGATACCTCCAAGTGCC	59.9	585	INTRON	Ca_22116	S		Uncharacterised protein family FPL
CaPOPI_233	Ca1	21772275	CATATATATATATAT/CATATATATATATATATAT	CTTTGTCTCCCCATCCTCA	AAAAGTGAGACGAAAAAGTTGTCC	60.0	342	DRR	Ca_22115		MYB	
CaPOPI_234	Ca1	22131328	AATATATAT/AATATATATAT	GTGTGGACATGCCTAAACG	GTTGCAATTGAGGTGCTGAA	59.1	403	INTERGENIC				
CaPOPI_235	Ca1	22131513	GAAAA/GAAAA	GTGTGGACATGCCTAAACG	GTTGCAATTGAGGTGCTGAA	59.1	403	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_236	Ca1	22132039	G/GC	GGATGGTAGTTCAGCACCTCA	GAGCATTAGTGCTTGGCACA	60.1	774	INTERGENIC				
CaPOPI_237	Ca1	22384776	G/GAACAAGTGTGT	CTTCAGATCCTTGAGCTGCC	TGAATCTTTGTGTCCCAACC	60.1	539	INTERGENIC				
CaPOPI_238	Ca1	22745256	AATATATATATATATATATATATA/A AAATATATATATATATATATATATA TA	CTCCAGAAATTTTGCCCTCCA	GTTAGGCCGAGGCTCTCTTT	60.2	480	INTRON	Ca_20613	BD	bHLH	Nucleosome assembly protein (NAP)
CaPOPI_239	Ca1	22886112	GAA/GAAA	TGATTTGGGGTTTTGGGTAA	GGGTGAGTCTTTGAGGTGTG	60.0	531	INTERGENIC				
CaPOPI_240	Ca1	22896758	CTTTTTTTTTTTTT/CTTTTTTTTTT	GCACCGTTTACACGCTTTT	GATGAAACCGAGGACCA GAA	60.2	400	INTERGENIC				
CaPOPI_241	Ca1	23192284	TTAATAATAATAATAATAATAATAAT AATAATAATAATAATAATAATAATAA /TTAATAATAATAATAATAATAATAA TAATAATAATAATAATAATAATAATA TAATAATAATAATAATAATAATAATA	TTCGAAACTTTTGGCCACTT	TTGGATTTTGCCACATTTT	59.7	527	INTERGENIC				
CaPOPI_242	Ca1	23386171	GTTATTATTATTATTATTATTATTAT TATTATTATTATTAT/GTTATTATTATTAT TATTATTATTATTATTATTATTAT	ACAAGAATGGCAAATGGAGC	TTTGCCCCACTAACTCTTGG	60.1	537	INTERGENIC				
CaPOPI_243	Ca1	23496241	CT/CTTT	AGGGTGGATCAGTTCCGATTG	TTATATTAATTGGGTGCGCT	59.9	376	DRR	Ca_19314			
CaPOPI_244	Ca1	23516838	CAAAAA/CAAAA	GGAATCCAAACCAAAACCT	TTGGTGTGGTTTTTGTGGAA	60.0	634	INTERGENIC				
CaPOPI_245	Ca1	23571644	AA/AAGTCTCCGATCTTTTGA	TGTGTTGGCTTAAACATTTGAT	GGGCAATGTTGGTGGTACTC	58.6	810	INTERGENIC				
CaPOPI_246	Ca1	23784964	ATTTTTTT/ATTTTTT	GTCAACCAATTGACCCCAAC	TGCCAAGAAAAACCCATGAA	60.1	663	INTERGENIC				
CaPOPI_247	Ca1	23838777	ATGTGTGTGTGT/ATGTGTGT	AATGCCCAACCATAATTTCA	TGTACGAGAAGTCTGTGTC	60.0	593	INTERGENIC				
CaPOPI_248	Ca1	23966814	GA/GAA	AACTGTGGAGGAATCCATGTC	GCTTCAAGTCTTGCTACGGG	59.9	490	INTERGENIC				
CaPOPI_249	Ca1	24030518	CG/CGTGTTG	CCAATTCAAAGCTCCC AAA	CAGATCCTCCTTTCCCAACA	60.0	424	DRR	Ca_19291	OK		E3 ubiquitin ligase, domain of unknown function DUF908
CaPOPI_250	Ca1	24098971	GATATATATATATATATATATATAT ATA/GATATATATATATATATATATAT ATATA	AGGCATGGTGTGGAGTCAT	TGCATTTTCCACGTTCAAG	60.4	526	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPl_251	Ca1	24154735	ATTTTT/ATTTTTT	GGGTGCCATCATAGCA AGT	CAGATACTGCAGCCTCC ACA	60.0	516	INTERGENIC				
CaPOPl_252	Ca1	24242300	TAAAAAAAAA/TAAAAAAAAA	ACCAACTCATCCCTTC CCT	ATGATTGCAGCATTTCA CGA	59.8	638	INTERGENIC				
CaPOPl_253	Ca1	24611579	AATATATATATATATA/AATATATAT ATATA	TGCCCACTTGATAACAAC AAAA	CATCGCCTTTGACGAAT ACA	59.1	330	INTERGENIC				
CaPOPl_254	Ca1	25058286	AATATATATATATATATATATATAT/ AATATATATATATATATATATATAT ATATAT	CATCCTGCAACACATGC TCT	TCATGCAAATTCAAAAGA AATGA	59.9	794	DRR	Ca_18316			Pectinesterase, catalytic
CaPOPl_255	Ca1	25382145	AC/A	GAATCACTAGGCTTGCC AGG	GGGGTGAGAGAACGTTT GAA	59.8	714	INTERGENIC				
CaPOPl_256	Ca1	25458751	AATATATATATATATATATATATAT ATATA/AATATATATATATATATATATA TATATATATATATATA	GACGTCGCTTCCGAAGT TAG	TCACTCAGGTTGCCAAA ACTT	60.0	538	INTERGENIC				
CaPOPl_257	Ca1	25507843	CAATAATAATAATAATAATAATAATA ATAATAATA/CAATAATAATAATAATAAT AATAATAATAATAATA	TCTCTGGCAACC GTTCT TCT	GAATGAAGTCCAAGGGT CCA	60.0	341	INTERGENIC				
CaPOPl_258	Ca1	25526955	A/ACG	TTCGTAATGGACGGGAT GAT	GGGTTTTGCATGTTGAG CTT	60.2	510	INTERGENIC				
CaPOPl_259	Ca1	25688981	TAAAAAA/TAAAAAA	AATGTCCCCAACAGAGT TGC	TCGTATCGAACTTGCCC ATT	60.0	542	INTERGENIC				
CaPOPl_260	Ca1	26142349	TTAC/T	CTTCGCACAACCATTGA CAC	TTCTGCTGTTGCTGAT TTG	60.2	206	CDS (large-effect mutations)	Ca_18596	R	ZF-HD	Pentatricopeptide repeat
CaPOPl_261	Ca1	26208589	CATATATATATATATATATATATAT ATATA/CATATATATATATATATATAT A	CAGCCACCCCAAACTTT TTA	TCACCACCAGAGACAAA CCA	60.0	419	INTERGENIC				
CaPOPl_262	Ca1	26263650	ATATTATTATTATTATTATTATTA/AT ATTATTATTATTATTATTATA	TCACCCAACAAGATCGT GAA	CCAAGCCCAATATCCAA CAT	60.1	780	INTERGENIC				
CaPOPl_263	Ca1	26358637	TTTTAGT/TTTTAGTTTTAGT	TGTGTTCATCCTTTCCAC CA	GGGTTCAACTTCAAAAG CCA	59.9	754	INTRON	Ca_18604	U	LSD	Snf7
CaPOPl_264	Ca1	26589205	ATTTTTTTTT/ATTTTTTTTT	TTCTTAACATTCTCCGCT GG	TGATGTTGCATCAACCA TTTT	60.2	168	INTERGENIC				
CaPOPl_265	Ca1	26592081	C/CTGACAGTGA	ACACACAAATTTTGACC GCA	GCAATTTTCTCCAATTGC GT	60.0	801	INTERGENIC				

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CaPOPI_266	Ca1	26683611	TG/T	CAATTGTGTAAACGTGCGG	TTGCATTTGGTTTGACTCCA	60.0	538	INTERGENIC				
CaPOPI_267	Ca1	26774824	TCTTTCCNNNNNNNNCTTTCC/TCTTCC	TTGACCCCTTCTTAGCACCT	ACAATGAGTCGTGCGACAAA	59.9	212	INTERGENIC				
CaPOPI_268	Ca1	26866750	ATTTTTTTTT/ATTTTTTTTTT	TCTCAGTGGAAACGAAACC	TCTCCACCATCTTCCTCTTCA	60.1	679	INTERGENIC				
CaPOPI_269	Ca1	26876468	C/CG	TTGTGCATCCGTCTATCCAC	TCGGTGGAAATTGTAATGAGAG	59.5	937	INTERGENIC				
CaPOPI_270	Ca1	26958726	GTTT/GTTTT	TGAGCGTGAAAAATTGTGGT	CCGACCAATAGACTTTTGTTGA	59.2	204	INTERGENIC				
CaPOPI_271	Ca1	27282873	GTATA/GTATATA	AAAATCCAACATCTCCCACC	CCCTGAGACTCACGAAGAGG	60.0	561	INTERGENIC				
CaPOPI_272	Ca1	28322869	GAAAAAAAA/GAAAAAAAA	GAGAACACAACCTTGACCCAAA	GTTACCAGCCCATCAATGCT	59.1	376	INTERGENIC				
CaPOPI_273	Ca1	28449282	ACGAATATTTTCCGAATATTTCCGAATATT/ACGAATATTTCCGAATATT	TGGATTGGTTGAAGGAGGTC	CTCTGTCACTGGCGTCAATCAT	59.9	695	DRR	Ca_18508			
CaPOPI_274	Ca1	28550132	ATTTTTTTTT/ATTTTTT	TGGAAGCACGCTTAAGGACT	TTTCCAATCGATTTGCTTC	60.0	664	INTERGENIC				
CaPOPI_275	Ca1	28550236	T/TG	CTGACACAGGGGAGAAAAA	TTTCCAATCGATTTGCTTC	60.1	159	INTERGENIC				
CaPOPI_276	Ca1	28713213	TTA/TTAGAAAGAGTGTA	TTCATTTCTCTGATTCCCACG	TCCGCATTATAACCTCTGCC	60.0	425	INTERGENIC				
CaPOPI_277	Ca1	28906702	TAAAAAA/TAAAAAA	TATGGAGAGCAGCGACTCAA	TGTTGGGTTGCACAACATTC	59.7	184	INTERGENIC				
CaPOPI_278	Ca1	28910299	CATT/CATTAAATT	GAAATGATCGGTGGAGGAA	CTTGCGTGTGACAGGATAT	59.9	620	DRR	Ca_18486	R		Sugar/inositol transporter
CaPOPI_279	Ca1	28910424	TA/T	GAGTCATTGGTGCTTG GTT	CTTGCGTGTGACAGGATAT	60.0	385	DRR	Ca_18486	R		Sugar/inositol transporter
CaPOPI_280	Ca1	28910492	GATTAA/GATTAAATTAA	GAGTCATTGGTGCTTG GTT	CTTGCGTGTGACAGGATAT	60.0	385	DRR	Ca_18486	R		Sugar/inositol transporter

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CaPOPI_281	Ca1	28930954	A/ATT	TGAAAAGTTTCTTTGTCCCTTTG	TGGTGTGCCTTCAAATCA	59.7	349	INTERGENIC				
CaPOPI_282	Ca1	28935215	ATTTTTTT/ATTTTTTTTT	TTTGTGGCAGTTTGTG	CAGTCAACATTGATGTGACGTTAT	57.3	490	INTERGENIC				
CaPOPI_283	Ca1	28936099	ATTTTTTT/ATTTTTTTTT	GAAATTTGACCAGAGCTGCC	TCGGTCACCGTTTTAGTTT	59.8	465	INTERGENIC				
CaPOPI_284	Ca1	28936233	AT/ATGTAATT	GAAATTTGACCAGAGCTGCC	GGACCAATTACTCTGGTGGAA	59.8	650	INTERGENIC				
CaPOPI_285	Ca1	28939471	AAAATAAAACAAA/AAAA	CCATGTGTGAACCTAATTGTT	GTTTTGGCGTTGGTTTCACT	58.7	226	INTERGENIC				
CaPOPI_286	Ca1	28941503	CAA/CAAAA	TGGGGTTTAGGGTGTCACAT	CTTTGTAAAGGCAGCTCCG	60.1	207	INTERGENIC				
CaPOPI_287	Ca1	28943560	GG/GGTG	ACTTGGGACAAATCACATGG	TGATCACCAGCTTTCCATG	58.3	252	INTERGENIC				
CaPOPI_288	Ca1	28944496	TTATATATAT/TTATATAT	TTGGCACCAGACTTCATATTG	AAATGTACTTTGCGGCACAT	58.6	775	INTERGENIC				
CaPOPI_289	Ca1	28944803	AACTA/AA	TTTCAATTGCATTAATCCGTTT	CAATAAAAATTGCGGTCGCA	59.0	963	INTERGENIC				
CaPOPI_290	Ca1	29124803	ATTT/ATTTT	AGTGGCATTGGGCAAAATAC	ACCAAATATACGCGTCTGCC	59.8	350	INTERGENIC				
CaPOPI_291	Ca1	29636835	AA/AAGA	TCACAAATCTCAACCCTCCC	ATCAGTTGGAGCCTGGTTGT	59.9	497	INTRON	Ca_24382	AR		K Homology, type 1
CaPOPI_292	Ca1	29637072	GAAAAAAAA/GAAAAAAAAA	ACAACCAAGGCTCCAATGAT	ATGCTGCCAGCCTACAAAT	59.6	503	INTRON	Ca_24382	AR		K Homology, type 1
CaPOPI_293	Ca1	29709028	ACC/AC	AAGATTTGTTGAGGCGTGG	GACGAGAATGGAGATGGGAA	60.1	580	INTERGENIC				
CaPOPI_294	Ca1	29738380	GTATATATATATATATATAT/ATATATATATATATAT	TATTTGGATTTTGCTCGG	AAACCGGTAAATCTCCGCT	59.9	699	INTERGENIC				
CaPOPI_295	Ca1	29791416	GAAAA/GAAAAA	TCCGATAAAATCTCCGTTCCG	AAAAACACGTTCCCTCTTCTT	60.0	323	INTERGENIC				

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CaPOPI_296	Ca1	29842423	AC/A	TCATCAAAGGCATGCAA ATC	GACCAAAACACAACGCA ATG	59.6	359	INTERGENIC				
CaPOPI_297	Ca1	29846530	CTTTT/CTTTT	TGGATTGGGGATCATT ATT	TCAACATTTGGAAGCAC AAGA	60.0	897	DRR	Ca_24388			
CaPOPI_298	Ca1	29846735	A/AATATATATATAT	AGAACGGTTTTCTGTCC GTG	TCAACATTTGGAAGCAC AAGA	60.1	689	DRR	Ca_24388			
CaPOPI_299	Ca1	29846941	TAAAAAAAA/TAAAAAAAA	TGTTGCCAACTGAAAT CGT	ATACAGACACCGAATGG GGA	59.2	828	DRR	Ca_24388			
CaPOPI_300	Ca1	29848026	ATGT/AT	TCTTTTCATCAGGCCA ATC	GGAAAGTGAGGGAACCA ATG	60.0	228	INTRON	Ca_24388			
CaPOPI_301	Ca1	29853119	TAA/TA	TCCACGAGATTTCTTT GG	TGTCATCTCTCTGCT GGC	60.0	357	INTERGENIC				
CaPOPI_302	Ca1	29853730	GTGGAAGTCT/GTGAAGTCTGGAAGT CT	TTGCATTCTAGTTCA GCC	TATCGCTCGACCTCTGC TTT	60.2	602	INTERGENIC				
CaPOPI_303	Ca1	29856647	CITT/CTTTT	GCATTCCTGCTCAAGA CTC	AGACAAGGGAGAGTCCC ACA	60.0	812	INTERGENIC				
CaPOPI_304	Ca1	30432201	CTTTTTT/CTTTTTT	CCACAATATCAAGGGC CAC	AGAGAAAACAAAGGCG CAA	60.2	471	INTERGENIC				
CaPOPI_305	Ca1	30475519	ATTT/ATTTT	AGGATGCATGGGATGAA AAG	AAACTTCTACTCGGGCC CAT	59.9	766	INTERGENIC				
CaPOPI_306	Ca1	30627831	AATATATATATATATAT/AATATATATA TATATATATATATATAT	CTTGGGAAGTGGAGAGC AAG	CCAACGTCACTTCCAAG GTT	60.0	797	INTERGENIC				
CaPOPI_307	Ca1	30682856	CATATATATATATATATAT/CATAT ATATATATATATAT	GTTGGTCCCTAGCAC GTA	TCCGCCTAGGAGATAGC AGA	60.0	672	INTERGENIC				
CaPOPI_308	Ca1	30740126	CTGT/CT	TGGGAGCACAACTACA CAA	ACATTTGCCACCGTTAG AGG	60.3	901	DRR	Ca_22454	OE	WRKY	Peptidase S10, serine carboxypeptidase
CaPOPI_309	Ca1	30745547	C/CT	TTTTTGGGTTTCTTTTC CC	TGCAATATGTATCGTGG ATGG	60.1	817	INTERGENIC				
CaPOPI_310	Ca1	30770184	TAAA/TAAAA	AGTGGCTTGAGGAGTT GGT	CGTTCGGCTTTCTTCTT CTG	61.1	535	INTERGENIC				

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CaPOPI_311	Ca1	30790839	TGTAAC/T	TTTTTGATGGTTCAACGA GAA	GGTTGAATAATTGAAAA GAGGTGG	58.3	250	INTERGENIC				
CaPOPI_312	Ca1	30874605	A/AT	TGTGATGCAGTTGCTCC ATT	CAAGCGTCATGCCAAAC TTA	60.3	624	INTERGENIC				
CaPOPI_313	Ca1	30993040	AAAAATTAAAATTAAAATTAA/AAAAATT AAAAATTAAAATTAAAATTAA	TCCTCCGATCGAGTAG TGG	AAACATGAAATGGACAA TACAAAAA	60.2	398	INTERGENIC				
CaPOPI_314	Ca1	31090559	CAA/CA	CGCTCGCTCATTGAATA ACA	CTCCACGACCATCCTGA AAT	60.0	417	INTRON	Ca_25826	S		Cysteamine dioxigenase
CaPOPI_315	Ca1	31141128	C/CA	ATTATTGAGTTGGCCC CTC	TCCACTTTTGTGCTTTA GGC	60.2	376	INTERGENIC				
CaPOPI_316	Ca1	31162887	T/TG	CCGGGGATTGCCATATA ACT	CTAATAGGCTGCATCGG AGG	60.9	342	INTERGENIC				
CaPOPI_317	Ca1	31163466	TGG/TAGAGG	ACTTTTCGGGAGAAGCA CAT	CGTTCGTCTTTCTCTT GC	59.9	360	INTERGENIC				
CaPOPI_318	Ca1	31238518	ATT/AT	CATCGTAAGCATGTGGT TGG	TAATGGCCCCATAGCAG AAG	60.0	861	DRR	Ca_21848	R	FAR1	Strictosidine synthase, conserved region
CaPOPI_319	Ca1	31428294	ATATTTTATTTTATTTTATTTTAT/A TATTTTATTTTATTTTAT	TCAACAGTTGATGGGT GAA	TGAGATGGAGGTGATGG TGA	59.9	370	INTERGENIC				
CaPOPI_320	Ca1	31592114	CT/CTTT	TCAGCTGCAGTTCCAAC ATC	GCACAAGTCCTTGAGGA AGC	60.0	375	INTRON	Ca_21868	F		Orotidine 5'-phosphate decarboxylase domain
CaPOPI_321	Ca1	31600651	AC/A	GGATGGAAGAGAAATTG GGA	AGGATCATGTTGTGGT TGC	58.9	899	INTERGENIC				
CaPOPI_322	Ca1	31716302	A/AC	TCGGTATTTGCCATGAG ACA	AAACAACCTTCATGCCTT GG	60.1	482	INTERGENIC				
CaPOPI_323	Ca1	31768486	TTATA/TTTTTATATA	ACACATTATATTAATGC GCGA	TGCCAAACGATAGGTTG TTG	57.4	646	INTERGENIC				
CaPOPI_324	Ca1	31783488	AATATATATATATATATATAT/AATA TATATATATATATATAT	TGGATTGGGCTGGAATT AAA	TATAACCGACGAGGGAC GAG	60.3	466	INTERGENIC				
CaPOPI_325	Ca1	31803627	TAAA/TAAAA	CTTACGGTGAAGGAGAA CGG	ATCATTCTTTTATGCGTT TGACT	59.7	793	INTERGENIC				

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CaPOPI_326	Ca1	31995451	T/TCAC	TGCTTTGAAGACCATGTGGA	AAAAGGATTCATGCGTGTCC	60.2	354	INTERGENIC				
CaPOPI_327	Ca1	32030892	AATATATATATATATATATATATATATATATATATATAT/AATATATATATATATATATATATATATATATATATATAT	CATGGATGGGTTTTGTACCC	TTGGAAGGAGCCCTTACCTT	59.9	771	INTERGENIC				
CaPOPI_328	Ca1	32037255	CA/CAA	GGGAAAACTTTTGTGTGGGA	TTGGCAAATCGATTAGACTGG	59.8	802	INTERGENIC				
CaPOPI_329	Ca1	32037334	CTTTTT/CTTTT	TCCAGTCATGTGGCTTCCTCA	CTGAGCTTGTGACCAAACTCG	60.4	559	INTERGENIC				
CaPOPI_330	Ca1	32037356	CTTTTT/CTTTT	TCCAGTCATGTGGCTTCCTCA	CTGAGCTTGTGACCAAACTCG	60.4	559	INTERGENIC				
CaPOPI_331	Ca1	32080106	T/TC	TTCCCCATGTCGATCTAAGC	AACCCTGAACAGATTGTCTGG	60.0	612	INTRON	Ca_26405			Uncharacterised protein family Ycf68
CaPOPI_332	Ca1	32080183	C/CGGCGATTACT	TTCCCCATGTCGATCTAAGC	AACCCTGAACAGATTGTCTGG	60.0	612	INTRON	Ca_26405			Uncharacterised protein family Ycf68
CaPOPI_333	Ca1	32151710	TAAAAAAAAA/TAAAAAAAAAAAAA A	TGAAGGTGTGAGCAGATTCG	TCGGGTGGAGAATTCCTATG	60.0	593	INTERGENIC				
CaPOPI_334	Ca1	32153452	TTTATTTTAT/TTTATTTTATATTATTTTA T	GTTTTGGCGTTGGTTTCACT	TGGGTTTGACCCTATGTGTG	60.0	353	INTERGENIC				
CaPOPI_335	Ca1	32153737	TTATATATATAT/TTATATATATATATA T	CACACATAGGGTCAAACTCCA	ATACATGGATTGGTTGGGGA	59.3	585	INTERGENIC				
CaPOPI_336	Ca1	32222272	ATTTT/ATTTT	ACAACCTCTCATGCTCGCAA	GGTGGCATACTCAACGAGT	59.6	620	INTRON	Ca_26127		Trihelix	
CaPOPI_337	Ca1	32267954	T/TG	AAGCTATGTCAAGGAATGTGATTT	CCGTGTTTTTGAAAATTGACAC	58.3	378	INTERGENIC				
CaPOPI_338	Ca1	32454365	A/AG	AGGAAACACATGAAGGCACC	TCTTCGTTGCTACTCCATGC	60.0	572	INTERGENIC				
CaPOPI_339	Ca1	32911601	AAATAATAATAATA/AAATAATAATAAT AATAA	CAAAATGGAGCAAGAAA CAGG	CAAGTTCAACGAGCGCCTAT	59.7	892	INTERGENIC				
CaPOPI_340	Ca1	33105635	TC/T	TGCCAAGAACGATAAAAGCA	TTCTGCATTTTCCTTGAGCA	59.4	101	DRR	Ca_19438			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_341	Ca1	33336930	GAAAAA/GAAAA	CAATGGCAACAAGGTCAATG	TCACATCTGTTGGTAACGGG	60.0	856	INTRON	Ca_19441		MIKC	Transcription factor, K-box
CaPOPI_342	Ca1	33746473	GTATATATATATATATAT/GTATATATAT	CCAATCGATTTCCTCCAAA	TTTCATCAAAAACCCCCTTG	59.9	779	INTERGENIC				
CaPOPI_343	Ca1	33765021	AAATAAAATTAATAAATAATAAAAT/AAATAAAAT	GCGACCGAATATGGAACAGT	TAGGCTAGGTCGTCGGTTG	60.0	301	INTERGENIC				
CaPOPI_344	Ca1	33777775	ATTT/ATT	CATGCTCAATACACGGATGG	AACGTTCTTGAGTGGCTTGG	59.9	870	INTERGENIC				
CaPOPI_345	Ca1	34057382	C/CA	GGGGATTAAAGTCTTGGACA	AAAGAAAGGCACTAAGGCC	59.9	156	INTERGENIC				
CaPOPI_346	Ca1	34147315	C/CTG	TCAAATCGATTGGGACATCA	TACTCGCCAAACTCTCACA	59.9	900	INTERGENIC				
CaPOPI_347	Ca1	34286273	ATATTTTTATTTTTATTTTT/ATATTTTTATTTTT	TATGCATCGGACAAGAGTC	TTGGAAAAGCCACCTACAC	59.8	448	INTERGENIC				
CaPOPI_348	Ca1	34332252	GA/G	AATTGGAAGCAGGGGTTT	GGATTGTACCCTTGGGGTTT	59.8	849	INTERGENIC				
CaPOPI_349	Ca1	34371294	AAAGAAG/AAAGAAGAAG	AAACGGGTGCAAGAAGATTG	TCTTTACGACCTTTGTGGC	60.1	233	INTERGENIC				
CaPOPI_350	Ca1	34386272	GTTT/GTTTT	AATCTGGAGGCGGTAAAGTT	ATATCGGTCAAACGCACACA	60.0	413	INTERGENIC				
CaPOPI_351	Ca1	34647577	CCA/CCATTAACA	GGGAGCAAGAAGTTGGTTGA	TAGTCCAACAATGGCCAACA	60.2	132	INTERGENIC				
CaPOPI_352	Ca1	34666828	TAAAAAAAA/TAAAAAAAA	TGTTTCAGGATGTCGACCAA	GTTACCGCAGAGGGACGTAA	60.1	640	INTERGENIC				
CaPOPI_353	Ca1	34667053	ATTTTTTTTT/ATTTTTTTTT	AGACTGCTCGGTCCAAAGAA	GTTACCGCAGAGGGACGTAA	60.0	264	INTERGENIC				
CaPOPI_354	Ca1	34812970	ATTTTTTTTT/ATTTTTTTTT	CACAACAATGTGGGTTGAGG	ACCAAGAACAAAATGGTGCC	59.8	428	INTERGENIC				
CaPOPI_355	Ca1	34971020	CAAAAAA/CAAAAA	AAATACCCCTTTTCCACG	TGAAAACGCTCAATGCCATA	60.0	689	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_356	Ca1	34978712	GT/GTT	ATGGCATGGTGGATTTT GTT	CTAGAAAGTTGCAGCCC AGG	60.1	525	INTRON	Ca_21407			
CaPOPI_357	Ca1	35096364	AT/A	TTGATGTGGTCGGAGAT TGA	ACAATTTTCAGCAACCC GAG	60.0	588	INTERGENIC				
CaPOPI_358	Ca1	35153435	GTTTTTTTTTTTT/GTTTTTT	TTTGTTTCCGATTGCT AGG	GGTTGTATGGCTCCCAA GAA	60.1	409	INTERGENIC				
CaPOPI_359	Ca1	35165919	GTTTTTT/GTTTTTTTTTTTT	TCATCGCAGGTGTACCA TGT	CACCTAAGGGAATCGGT CAA	60.0	377	INTERGENIC				
CaPOPI_360	Ca1	35261821	ATT/AT	TGGATTGTCATGGTCTG GAA	AATGGTCTTGAATTTTGC CG	59.9	640	INTERGENIC				
CaPOPI_361	Ca1	35266220	ATAT/ATATTAT	CGCGGTAGAGTTATTGG AAAA	TGGGGATACGTAGGAGC AAG	59.3	682	INTERGENIC				
CaPOPI_362	Ca1	35281570	TC/T	ATGACACGTCATTCGTT TCG	GGTTCGAGACATCCATA ATTCA	59.6	733	INTRON	Ca_26099	QI	bHLH	Cytochrome P450
CaPOPI_363	Ca1	35281940	TA/TAA	AAACGTGATCTATACAG TTTCCAAAA	TTACATCTGGAACAA CGC	59.4	529	INTRON	Ca_26099	QI	bHLH	Cytochrome P450
CaPOPI_364	Ca1	35283797	TGGGGG/TGGGG	GGGTGTGTTTGATAGGA GGG	CTCCCTTCCATCTCCT CTT	59.3	139	INTERGENIC				
CaPOPI_365	Ca1	35284017	ATTT/ATT	GAGATGGAAGGGGAGG AAAG	GCACAAAGAAAAATAC AAGTCCA	60.0	273	INTERGENIC				
CaPOPI_366	Ca1	35284253	TT/TTGT	GAGATGGAAGGGGAGG AAAG	TCTGATCAAATATGTGG CAGAAA	60.0	657	INTERGENIC				
CaPOPI_367	Ca1	35321165	GTTT/GTTTT	CATCATTCGTTTCAAAAT TGTTG	ACGAAGGTTTGAGACAT CCA	59.4	586	INTRON	Ca_26101	QI	bHLH	Cytochrome P450
CaPOPI_368	Ca1	35540299	AA/AATA	GGGGTGCTCAACTTGT TGT	GGCCAAGGTAAGGGTG AGAT	60.0	254	INTERGENIC				
CaPOPI_369	Ca1	35679606	CAAAAAAAAA/CAAAAAAAAA	GTGCACAACCTTGTTG GTC	TAGCCAACATGCCATAC GTC	60.1	604	INTERGENIC				
CaPOPI_370	Ca1	35899211	TTTTAGACAC/TTTTAGACATTTAGACAC	CACCTCCCTGAGTTG TTA	GCAAGCTCCAAATGGAT TACA	60.1	404	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_371	Ca1	35977319	TA/TAA	AACTCGTTGGAAC TTCC CTCT	GCAAGCAGCCTTGTTGA CTA	59.2	540	INTERGENIC				
CaPOPI_372	Ca1	36044248	CGG/CG	CGATTTCCCTGCATGTT TTT	GCCTGTGATAGGCGGTA CAT	59.9	540	INTERGENIC				
CaPOPI_373	Ca1	36063199	TCC/TTTTTCCCC	CGTTCGTGGTCCCTTAA CTT	TTGCGTTACGGATTGTA TGA	59.1	227	INTERGENIC				
CaPOPI_374	Ca1	36166710	CATTATTATTATTATTATTATTATT/ CATTATTATTATTATTATTATTATA	TCGTTGCCTATGGTAC TCC	CCAACGATTCATACAGG GCT	60.0	574	INTERGENIC				
CaPOPI_375	Ca1	36726460	GAAA/GAAAA	ACAGGAACGACCAGAG AAA	ATAGTTTTGGGCGGGC TAC	59.8	502	INTERGENIC				
CaPOPI_376	Ca1	36727739	TCC/TC	AGGCTGCATTTTAGTCC ACG	ACGACCACTGCAAACAC AAA	60.3	218	INTERGENIC				
CaPOPI_377	Ca1	37075088	TTAAA/T	GCCCTCAGATGAGAGTC AGG	ATTCTGCAGCACGGATC TCT	59.9	830	INTERGENIC				
CaPOPI_378	Ca1	37078511	TTAT/TTTATAT	CCATTCCAAAAGGAGT TGG	TGAAATGTTGGAGTGA TGTA	59.4	938	INTERGENIC				
CaPOPI_379	Ca1	37078904	TTAAATAAATAAATA/TTAAATAAATAAA TAAATAAATA	TGTGACACCCTAAACCC TAAGAA	TTGATTGCTTGC GTGTT CTC	59.9	499	INTERGENIC				
CaPOPI_380	Ca1	37122051	CAAAAAAAAA/CAAAAAAAAA	CGTATCTCGTATCACCG ACG	AGTTGCGCTCCTCCTAA TCA	59.2	873	INTERGENIC				
CaPOPI_381	Ca1	37122104	CAAAAAAAAA/CAAAAAAAAAAAAAA	CGTATCTCGTATCACCG ACG	AGTTGCGCTCCTCCTAA TCA	59.2	873	INTERGENIC				
CaPOPI_382	Ca1	37122520	AGG/AG	TGCAATCATTTGGTGCTT AGG	AAAAAGCGCCGTAAAT GAG	59.7	710	INTERGENIC				
CaPOPI_383	Ca1	37122699	GTTT/GTT	GGAGGAGCGCAACTTAA TCA	AAAAAGCGCCGTAAAT GAG	60.4	372	INTERGENIC				
CaPOPI_384	Ca1	37122810	TACAAC/TACAACAAC	GGAGGAGCGCAACTTAA TCA	AAAAAGCGCCGTAAAT GAG	60.4	372	INTERGENIC				
CaPOPI_385	Ca1	37125192	GATGGAGATGGTTTGCAATGGAGATG/ GATGGAGATG	AGCGGTTTAGGGTTTAG GGA	CCAAATGTGCATACGAA CCA	60.0	113	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_386	Ca1	37128515	ATTTTTTT/ATTTT	CAATTCCACAGGTACGCTT	TTGGTCTCATCAATGATTGTA AAAA	60.0	568	INTERGENIC				
CaPOPI_387	Ca1	37391477	TTATATATATATATATATATAT/TTATATATATATATATAT	CTGTCAATTGAGATGCGACG	GCGATTACGGTACCACGAGT	60.4	600	INTERGENIC				
CaPOPI_388	Ca1	37410363	GAAAAAA/GAAAAAAA	TGAATGAGGAGCACGCTTGTG	CTGTTGTTGCCAACGGTTT	60.0	445	INTERGENIC				
CaPOPI_389	Ca1	37412282	CCATG/CCATGCATG	CGTGGATGATGCTTTTCTCA	TGCTTCTCATCTGCTTGTG	59.8	580	DRR	Ca_21842	R	GRAS	Pentatricopeptide repeat
CaPOPI_390	Ca1	37420598	ATTTT/ATTT	GGGAAAAGGAAACCCAAA	TGAGTGAGGGAGACAAAGGG	60.1	950	INTERGENIC				
CaPOPI_391	Ca1	37421082	CCTCACTCACTCACTCACTCAC/CCTCACTCACTCACTCAC	ACTTGACGGGGACTCCACTA	ACATGTTCTTGCTGTCTGTG	59.6	637	INTERGENIC				
CaPOPI_392	Ca1	37424329	CATATATATATATATATATAT/CATATATATATATATAT	AAAAAGTATTGAACAAACACGCT	TGAAATCCAAATTAAATGCTGAA	57.2	549	INTERGENIC				
CaPOPI_393	Ca1	37424983	AC/A	GCAATTTAATTTGGATTT CATGG	TCACATCCATCCACGGTACA	59.6	761	INTERGENIC				
CaPOPI_394	Ca1	37425153	G/GAT	GCAATTTAATTTGGATTT CATGG	TCACATCCATCCACGGTACA	59.6	761	INTERGENIC				
CaPOPI_395	Ca1	37425620	ACG/A	TGTACCGTGGATGGATGTGA	TATGCATCCTCACGGTTTG	60.8	675	INTERGENIC				
CaPOPI_396	Ca1	37426537	ATT/AT	CTTCAAAACCGTGAGGATGC	TCTGAGCTTCTGATGCTTGC	60.6	916	INTERGENIC				
CaPOPI_397	Ca1	37433380	CAA/CAACGTAAA	AATAAATTAGTGCAGCA AACC AA	GGCAAAGAGAGGAAAGTGGA	58.0	756	INTERGENIC				
CaPOPI_398	Ca1	37433540	TATAATAGATAATAGATAATA/TATAATAGATAATA	TGAAAAACATCTCTCTAA TAGGCG	ACCACTGCACCAAGGGTAAG	59.0	532	INTERGENIC				
CaPOPI_399	Ca1	37489959	AT/ATT	ATTGTCCAGTTTCCTCACCG	CGATTGTAATCGATTGGG	60.0	594	INTERGENIC				
CaPOPI_400	Ca1	37490066	AT/AATGTATT	ATTGTCCAGTTTCCTCACCG	TGAACTCTGAGCGTGTGACC	60.0	775	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_401	Ca1	37516914	TAAAAA/TAAAAA	AGGGAGGACGAAAATGACCT	ACCAATCTCGTGCATCC AAT	59.9	567	INTERGENIC				
CaPOPI_402	Ca1	37712787	A/ACATGTG	GGTGTGGAGGTGTAATGGG	CATGTCCCGTATTTCGCT TTT	60.1	639	INTERGENIC				
CaPOPI_403	Ca1	37724930	CCACACAC/CCACACAC	ACCCTGTTGCTGCCAAATAC	GCTCCAATCCCCTCAGATCA	60.0	664	INTRON	Ca_23534			Protein of unknown function DUF620
CaPOPI_404	Ca1	37758491	TA/TAA	TGACGAGGTTCGTGATGATG	AGCGAATGATTCAACCAACC	60.7	489	INTERGENIC				
CaPOPI_405	Ca1	37771437	CTTTT/CTTTT	CTGTGGCCCGACAAAGTATT	TCGTATATGCAGCAAGTGGC	60.0	627	INTERGENIC				
CaPOPI_406	Ca1	37809250	ACTTTTCCTTTCT/ACTTTTCCT	TGCCTTTGGGGATTTTATCA	TTTTGCATTAAAAATGGATGAA	60.3	579	INTERGENIC				
CaPOPI_407	Ca1	37849378	G/GA	CCTAAGGGCCGTAGTAACCTG	AGGATCCACCAAGCAAAATCA	60.0	154	INTRON	Ca_23538	T	E2F/DP	Zinc finger, RING-type
CaPOPI_408	Ca1	37913733	TAAA/TAA	ACGTTGCGCACCTATCTCAT	CCTTATGCGGTAATCCCTGA	59.6	563	INTERGENIC				
CaPOPI_409	Ca1	37917967	ATATGACAGTTA/ATA	TCCACAAGTTATTCGACGAAAC	TTCCATTGATCTACGTTATGTTTG	59.1	558	INTERGENIC				
CaPOPI_410	Ca1	37927331	TAAA/TAAATTGTATCAAA	ATTTTGATCGCGGAAGTTTG	TCAATCAACCAGATTTTGCATT	60.1	553	INTERGENIC				
CaPOPI_411	Ca1	37927862	G/GTA	TGCAAAATCTGGTTGATGAG	TCCCAGATCAAAATTGGGTT	58.8	745	INTERGENIC				
CaPOPI_412	Ca1	37928853	CT/CTGAAT	CCGTGCAACAATGTCAATTTC	GACCACCATATTAACCGTCACA	60.0	571	INTERGENIC				
CaPOPI_413	Ca1	37929646	TAAAAAAAA/TAAAAAAAAA	TGTGACGGTTAATATGGTGGTC	TTGACTTGTTTTGCGGATTG	59.6	817	INTERGENIC				
CaPOPI_414	Ca1	37993665	CAAAAA/CAAAAA	GTGAGCCCTTTACCAATCCA	CAATCCCACAGGTACGCTT	59.9	654	INTERGENIC				
CaPOPI_415	Ca1	38024874	TATGAATGAAT/TATGAATGAATGAAT	GCAAGCTCAGTTCAGTTCC	TGCATCAATTATGGCTCCAA	60.0	655	INTRON	Ca_27443	S		Zinc finger, GRF-type

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_416	Ca1	38030335	TTAAAAATAAAATAAAATAAA/TTAAAT AAAAATAAAATAAAATAAAATAAA	AGCTCGAAACATGGTAT CCAA	CTAGCCATCCTCAGCGA GAG	59.6	662	INTERGENIC				
CaPOPI_417	Ca1	38060326	CGG/CG	GGTTTGCCGTTCTTCT CCA	CTTGTTGCGACGATGAA AAA	60.1	310	INTERGENIC				
CaPOPI_418	Ca1	38070666	T/TA	AACCATTGGGGGAGAAT AGAA	TTGTTAGAACCATTGGG GGA	59.7	362	INTERGENIC				
CaPOPI_419	Ca1	38070895	ATGTGTGT/ATGTGT	CTCCCCCAATGGTTCTA ACA	CACTGGAATCCGTTTCT TTTG	59.8	587	INTERGENIC				
CaPOPI_420	Ca1	38071534	TACACACAC/TACACAC	CTCCTCCTCATTACCC AAC	ACACACCCACTCTCCTT TGC	59.5	189	INTERGENIC				
CaPOPI_421	Ca1	38110776	AT/ATTTT	GGGAGCATCCATAACAT TGC	GCCATTTCAAACACATC ACG	60.3	188	INTERGENIC				
CaPOPI_422	Ca1	38131605	C/CT	CGTAACTCGTGTGGGT GAA	GAAGCAAGAGGCAACTC CAC	59.6	379	INTERGENIC				
CaPOPI_423	Ca1	38193154	TAAAAAAAAA/TAAAAAAAAA	CGAACAACTCACCGGA TCT	CCAATGGAGTCCCAAAA AGA	60.1	724	INTERGENIC				
CaPOPI_424	Ca1	38273940	CAAAAAAAAA/CAAAAAAAAA	TATTTGGGGACCAAAAC TGC	CATGTTTGAATGCGAG TTG	59.8	637	INTERGENIC				
CaPOPI_425	Ca1	38284193	TC/T	GCCAACACATGGTGAAA GTG	AACAAAGTTTGCAATTG GGC	60.0	939	INTERGENIC				
CaPOPI_426	Ca1	38476810	TTAT/TTATAT	TTGCAAGTACGTTCTCC AAAA	GTGTTACAGCCCTTCA TCC	58.5	280	INTERGENIC				
CaPOPI_427	Ca1	38479463	AATATATATATATATATATATATAT A/AAAAAAAAATATATATATATATATA TATATATATA	AGCGTGAATGTGACGTC TTG	TTAAAGAGATTCGCAGC GGT	59.9	100	INTERGENIC				
CaPOPI_428	Ca1	38487463	ATTTTTTTTT/ATTTTTTTTT	TGCTACCTGCAACCACT GAG	GTCAACTTTAAGGGGGC GTC	60.0	872	DRR	Ca_13962			Proteasome assembly chaperone 3
CaPOPI_429	Ca1	38495552	AATTATTATTATTATTATTATTATTA TTATTATTATTGTTATTATTATTATT A/AATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT GTTTTT/GTTTT	AACACCTTCCTGATCCT CCC	TGGCGAACTTTTAAGAA TGGA	60.3	659	INTERGENIC				
CaPOPI_430	Ca1	38577185	GTTTTT/GTTTT	CCATTTTCTGTCCCTTT CA	GCATTGGCTAAGCATGG ATT	59.9	760	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	Tfs	NCBI-nr database
CaPOPl_431	Ca1	38597715	ATAATTTTAATTTTAATTT/ATAATTTTAA TTT	CATTTCCTCCCTGTT GTT	TGTAGTGCTGCACCA AGG	60.0	551	DRR	Ca_13956			Vacuolar protein sorting-associated protein 62
CaPOPl_432	Ca1	38766832	ACT/ACTCT	GAGCTTCTCAAGTCGG TGG	GTTTGAATACCCTGAG CCA	60.0	222	INTERGENIC				
CaPOPl_433	Ca1	38790509	AC/A	AGAGCTCTGAAGTCAAG CGG	GAAATCCTTGTTGCC TT GGA	59.9	163	DRR	Ca_13953			Vacuolar protein sorting-associated protein 62
CaPOPl_434	Ca1	38886459	AAAATAAA/AAAA	GCATGTTGTATGCTT TC CA	ATTTATCCATCCATGT CC	60.1	863	INTERGENIC				
CaPOPl_435	Ca1	39028142	AATATATATATAT/AATATATATAT	TCATGGAAGGAGCAAT CACA	TAAGGTTTAGGATGCCC CA	60.2	764	INTRON	Ca_13946			
CaPOPl_436	Ca1	39038586	GTATATATATATATATATATATATAT ATATATATA/GTATATATATATATATAT ATATATATATATATATATATA	CGATTTTGAATTGGGT CTCA	TTAAATAGGCTTCCAG GCCA	59.9	708	INTRON	Ca_13946			
CaPOPl_437	Ca1	39144961	CACGTAC/CAC	CATCCTTTCAGGATTG GTT	TTGTGCTTGGCAAATG CAG	59.9	494	INTRON	Ca_13942		ARF	Plant lipid transfer protein/Par allergen
CaPOPl_438	Ca1	39147028	AT/ATT	AAAAATGATCAGGAAAA TCATGT	ACAACCTCTCATGCTG CAA	58.7	339	DRR	Ca_13942		ARF	Plant lipid transfer protein/Par allergen
CaPOPl_439	Ca1	39261977	A/AT	GGTTTGCTGTGAGCCT TAG	AAACACAAGTCCAATCA AAAGG	60.0	421	INTERGENIC				
CaPOPl_440	Ca1	39384808	T/TA	GGGCCAAGAACAACAA AAA	TTCCACCAATCAATTAG GCA	60.0	105	INTERGENIC				
CaPOPl_441	Ca1	39444170	TAAAA/TAA	AATGATGGAAAAGCCGA ATG	GGAGGGACCTGAAGTCA CAA	59.9	838	INTRON	Ca_13931	Z	NAC	IQ motif, EF-hand binding site
CaPOPl_442	Ca1	39598601	TC/TCCC	TTTTCGTTATTTAAGCT AC AACGG	GCGAAGATGGTGCCAAT AAT	57.7	930	INTERGENIC				
CaPOPl_443	Ca1	39609113	AATAT/AAT	ATGGCCTTTCATTTTCAA CG	TTGTCTCAAGCGTTCAA TTTT	59.9	725	INTERGENIC				
CaPOPl_444	Ca1	39675431	CATATATATATATAT/CATATATATAT ATATATATATATATAT	CACCAAAGACAGGACCA CCT	CCTAGGGTTTTTGTTG GGT	60.0	784	DRR	Ca_13920			Acid phosphatase/vanadiu m-dependent haloperoxidase-
CaPOPl_445	Ca1	39871055	TAA/TAAAA	CATTGGCCACCTTTAGG AAA	TGCATTGCTTCAGTCAT GGT	59.9	329	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_446	Ca1	39976327	CA/CATA	TTTAAGAGAAGCGTTTG AGCG	CTTTGACTACGTTTCCC CGA	59.8	211	INTERGENIC				
CaPOPI_447	Ca1	40225071	ATTATTT/ATTATTTATTTATTT	GTTGGAAGTGTCCATTG GCT	AAGTCCGTTTCAGGGTT GTG	60.0	355	INTERGENIC				
CaPOPI_448	Ca1	40380273	CTATA/CTATATATA	CCTGGTCCCACTTTTAC GAA	GAAAAAGCGCTGTAAT GGC	60.0	487	INTRON	Ca_13892		Trihelix	
CaPOPI_449	Ca1	40391433	ACCCCC/ACCCCCC	TCCTGAAGGGGATTCAT CAG	GTTAGCGGATCGCGAAT ACT	60.0	610	INTERGENIC				
CaPOPI_450	Ca1	40424994	C/CCAAAATATTATAA	TGCAAAACTTTGTTCATC GAG	GCATCATTCTCCTTCGA GACA	59.0	748	INTERGENIC				
CaPOPI_451	Ca1	40426155	ATTTTTTTT/ATTTTTTTTTT	CTTTACTGCGTTGGACC ACA	ATAAATTGGATTTCACCC GC	59.8	544	INTERGENIC				
CaPOPI_452	Ca1	40534315	GAAA/GAAAA	CAATTTTGACCATGGAA CCC	TGAATTGACCTCGCAGA TTG	60.0	730	INTERGENIC				
CaPOPI_453	Ca1	40535465	TTAATAATAATAATAATA/TTAATAA TAATAATAATAATAA	CATGCGTTCCTTGTTGTT AGA	ATCACAGTTTGCCAAG TCC	59.7	599	INTERGENIC				
CaPOPI_454	Ca1	40535882	AATATATATATATATATATAT/AAATATA TATATATATATATATATAT	GATGATGATGATGTCGT GCC	ATCACAGTTTGCCAAG TCC	59.9	311	INTERGENIC				
CaPOPI_455	Ca1	40795125	AATATATATATATATATATAT/AAATA TATATATATATATATAT	TGAAATCAATTGAGGAC ATTCTG	ACGTAGCGAGCCTCGAA TTA	59.9	547	INTERGENIC				
CaPOPI_456	Ca1	40861492	GTTTTTTTT/GTTTTTTTTTTTTT	ATTTCTAAACCCGCAAA CCC	TCCACCCACGATACTGA TGA	60.2	941	INTERGENIC				
CaPOPI_457	Ca1	40889769	TTATATA/TTA	GCATCTCTTGATGCCCT TTT	AACATACGCCATACCCA AGC	59.3	289	INTERGENIC				
CaPOPI_458	Ca1	41058981	CTTTTTTTTT/CTTTTTTTTTT	GCATGGGAAATGGATTC TCT	TGGCTCATAACAGTTT TCTGG	58.9	679	INTERGENIC				
CaPOPI_459	Ca1	41503912	TCC/TC	TCGATTATGCGTAGGGA AGG	CTTGGTGGTTTGAAAC TCAAT	60.1	540	INTERGENIC				
CaPOPI_460	Ca1	41695402	CTA/CTATA	TACTCCATGCCAAACCA GCA	CCAACCTGAAATACAAA AGCCA	60.3	486	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_461	Ca1	41704419	CATAAAT/CATAAT	GGGGAATTTTCATTT GTGG	TGTTTTGGTTTCAAGGG ACA	60.4	311	INTERGENIC				
CaPOPI_462	Ca1	41704503	CTTTTTT/CTTTTTT	GGGGAATTTTCATTT GTGG	TGTTTTGGTTTCAAGGG ACA	60.4	311	INTERGENIC				
CaPOPI_463	Ca1	41705653	ATTTTTTT/ATTTTTTT	CATCACCGTAACATGAC TTACCA	TCCCAATAATTTTCCTT TTCG	59.8	723	INTERGENIC				
CaPOPI_464	Ca1	41718814	T/TG	GGGTGCAATGTCGATTC TGT	TCATCTCTCAGCCCCAC TCT	59.9	156	INTERGENIC				
CaPOPI_465	Ca1	42432936	AATATATATATATATATATAT/AATATA TATATATATATAT	CAAATTCCTCTTGCTCCA CC	TGAAAGCTGATGAAAT GGTC	59.7	695	INTERGENIC				
CaPOPI_466	Ca1	43119967	AATATATATATATATATATA/AATATAT ATATATATATA	TTTCCGGGAATAAATCC CTC	GAAGGAGAGTTGCGTT GAC	60.1	361	INTERGENIC				
CaPOPI_467	Ca1	43335241	AATATATATATATATATATATATATAT ATATATATAT/AATATATATATATATAT ATATATATATAT	CGTGTATATATGCGCAC CCA	CACAAACGAAAAAGTCG GAT	60.4	788	INTERGENIC				
CaPOPI_468	Ca1	43469250	A/ATATATTATT	GAGGGTTTGACGCTCTT GTC	AACGCATCGGTAAACAC TCC	60.0	547	INTERGENIC				
CaPOPI_469	Ca1	43638401	A/ATATGTC	CGCTTCATGTGTGTTGC TTT	ACCCCTCCTAAGTGGGT TGA	59.9	857	INTERGENIC				
CaPOPI_470	Ca1	43867975	AATATATATATATATATATATATA/A ATATATATATATATATATATATATATA TATATA	TTGCTGGCATAAGTGAA TCG	CCGTGAATTTTCATGGA ATAAA	59.8	711	INTERGENIC				
CaPOPI_471	Ca1	44172001	GTTTTT/GTTTTTT	ACCTATGCCCACTGATG AGG	GCAATTGCCAATGACGA CTA	60.0	750	INTERGENIC				
CaPOPI_472	Ca1	44247311	GTTTTTTTTT/GTTTTTTTTT	TTCTCCAGACTCTAGCC CGA	AGCTTCTCAGTAGGGG CTC	60.1	592	INTERGENIC				
CaPOPI_473	Ca1	44351850	TTATATATATATATA/TTATATATATAT ATATATA	TGAAATTCGGAAGAACC AGG	CGCATTCCCTTCACCTC TAA	60.0	111	INTERGENIC				
CaPOPI_474	Ca1	44467119	GTT/GTTT	ATGCAGCTCAAAAACAG CCT	GGTTCACCCAAAGATGG CTA	60.0	537	INTERGENIC				
CaPOPI_475	Ca1	44650256	T/TC	TCGTTTGCGTCATTGGA TTA	AGGGAGGACGAAAATGA CCT	60.1	444	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_491	Ca1	45749239	GAAAAAAAAA/GAAAAAAAAA	TTGTGCGCTTGACTGATGTT	GTTTGGCGTTGGTTTCACT	60.5	857	INTERGENIC				
CaPOPI_492	Ca1	45941271	AATATATATATATA/AATATATATATATA	GAAAGGAGATCACGAGCAGC	GTTGAATGGAACAGGCGAGT	60.1	723	INTERGENIC				
CaPOPI_493	Ca1	45941295	GATATATATATATATATATATAT/GATATATATATATATATATATATAT	GAAAGGAGATCACGAGCAGC	CAAGTCGTGGGGAGCATAT	60.1	846	INTERGENIC				
CaPOPI_494	Ca1	46023584	CACTAGTTACTAGTTACTAGTTACTAGTTACT/CACTAGTTACTAGTTACTAGTTACT	TTTTCCACCAACAAACCTCA	AGTTGTGGAATCTGCCTGCT	59.0	330	INTERGENIC				
CaPOPI_495	Ca1	46088799	CTATATATATATATATATATATATATATAT/CTATATATATATATATATATATATATATAT	TAAGTCCGTAAGTGGTGCCC	GGGCTTTCCAAAGTGTTATCC	60.0	586	INTERGENIC				
CaPOPI_496	Ca1	46186559	AGTGATTGGTTTGTGTTGTGATTGGTTTGTTG/AGTGATTGGTTTGTGTTGTGATTGGTTTGTGTTGTGATTGGTTTGTGTTG	AAAGCACACGATTTTCAACC	TTGGGCATCTAGCACTTCCT	60.0	775	INTERGENIC				
CaPOPI_497	Ca1	46278771	ATGGCCTGGCCTGGCCTGGCCTG/ATGGCCTGGCCTG	ACCTTCAGTCAGGGGCCAT	AAGTCTGGTCTGGCCTGAAA	60.0	538	INTERGENIC				
CaPOPI_498	Ca1	46286614	CTTTT/CTTT	CCAAGTTATGCTTGATCGCA	CGAGAACCATCCTGCATTTT	59.8	820	INTERGENIC				
CaPOPI_499	Ca1	46286661	GTAGGGATA/GTA	CCAAGTTATGCTTGATCGCA	CGAGAACCATCCTGCATTTT	59.8	820	INTERGENIC				
CaPOPI_500	Ca1	46352138	CACAAC/CACAACAAC	AGCGATGCATGTCTCAAGTG	TGCCCTTCTTCTTTTCTAGTG	60.0	396	INTERGENIC				
CaPOPI_501	Ca1	46491737	CAAG/CAAGAAG	GATGCATCTCACCAAGGTT	CGGTGCAAACTCTACGTCA	59.9	420	INTERGENIC				
CaPOPI_502	Ca1	46523548	CAAAAAAAAAAAAAA/CAAAAAAAAAAAA	GTGGACAAACCTGCATTCCT	ACCATGCACAGTTGCTGAGA	60.0	675	INTERGENIC				
CaPOPI_503	Ca1	46524349	TAAAAAAAAA/TAAAAAAAAA	TGAAGCATGCACAAATCTC	TTGATGTAGCAACGGCTGAG	59.8	843	INTERGENIC				
CaPOPI_504	Ca1	46525859	GAAAAA/GAAAAA	CCCACCTGGATACAAGGCTA	AGTAGAGGGAGTTCGGGTGC	59.9	711	INTERGENIC				
CaPOPI_505	Ca1	46526676	TAAAA/TAAA	TTAAATTCGAGGCGGAAA	ACATGGTTGTGGTGGTGATG	59.7	698	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_506	Ca1	46528558	CT/CTT	TTAAATTCCTCCTCG GCT	AACTCTGGGAACCCCTC TGT	60.0	398	INTERGENIC				
CaPOPI_507	Ca1	46530950	CAAATTGAAATTGAAATT/CAAATTGAAATT	ATTTGAGAATGTTCCGG CAA	GTCTGCGGATAATTTGC CTT	60.4	665	DRR	Ca_21551	M		Pectinacetylsterase
CaPOPI_508	Ca1	46531041	T/TG	GCGAAAATAATGTGTAT GCAGA	GTCTGCGGATAATTTGC CTT	60.1	139	DRR	Ca_21551	M		Pectinacetylsterase
CaPOPI_509	Ca1	46539360	CAAA/CAAAA	TCCCAACAGCCTGATA ACC	CTGATGACAAAAGGGGG AGA	59.9	744	INTERGENIC				
CaPOPI_510	Ca1	46598729	GATATATATATAT/GATATATATATATAT	TGATTTGTTAGCTTGTG GCAA	TGGAAGCATGATCCTCA ACA	59.4	477	INTERGENIC				
CaPOPI_511	Ca1	46831943	CTTTT/CTTT	GTGGTTGGTTTGCAAGA GGT	AACTGGGTGAGAGCCTG AGA	60.0	725	INTRON	Ca_25116	U		
CaPOPI_512	Ca1	46856347	GCT/GCTGAAC	ATGCAATCCGATAAGCA ACC	ACGATTTTAGAAGAGGC GCA	59.9	980	INTERGENIC				
CaPOPI_513	Ca1	46916401	GATATATATATATATATATA/GATATATATATATATATATATATA	CAGCAAGCACCAACCCAC TTA	TTGCCAGTTATTTTGTCA AGG	59.9	363	DRR	Ca_12949			
CaPOPI_514	Ca1	47016631	ACTCTCTCTCTCT/ACTCTCTCTCTCTCTCT	ATTGCCTCTCAGTCGCG TTA	AAAATTGCACATCGTGA GGG	60.9	531	INTERGENIC				
CaPOPI_515	Ca1	47116478	AATATATATATATATATATATAT/AATATATATATATATATATAT	ACACGCTTCCCTGTTGA CAT	TAGGCCTGAACGGGAT GAC	60.6	772	INTRON	Ca_12935		ERF	Protein kinase, catalytic domain
CaPOPI_516	Ca1	47455552	TTAATAATAATAATAATA/TTAATAATAATAATAA	TTGGGGTCAGTCAAACA CAA	CGGTGAAATAGGTATGC CAAA	60.0	600	INTERGENIC				
CaPOPI_517	Ca1	47630703	TAAAAAGAAAAAGAAAAAGAAA/TAAAAAGAAAAAGAAAAAGAAAAAGAAA	CGTGTCGGCAAAGTAA AAT	GTGATGCACGCAGTAAT TGG	60.0	517	INTERGENIC				
CaPOPI_518	Ca1	47630977	AC/ACC	GGCCTTCCATCGTGAAT AAA	TTTCGAATCCAGAACT GCC	59.9	916	INTERGENIC				
CaPOPI_519	Ca1	47676057	ATTTTTTTTTT/ATTTTTTTTTTTTT	AATCCCTCCCTGCCTAA AAA	ATGTGGTGGTCCAATCA ACA	59.9	619	INTRON	Ca_12903			
CaPOPI_520	Ca1	47875198	AT/ATT	GA AAAACAAGACCCGCG ATA	TTCTATTGCTCACCCC TTG	60.1	466	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_521	Ca1	47916750	ATT/ATTTCAAGT	GTTGGTGATGCCACTGA ATG	GAGAGAAAGGCAAGGT GGG	60.0	979	DRR	Ca_12885	O	M-type	ATPase, AAA+ type, core
CaPOPI_522	Ca1	47945221	TCAAGCCA/TCA	AGGACAGTGCCAAAAGA TGG	GTCATGTATGCATTGGG CAG	60.1	226	DRR	Ca_12882	R		Tetratricopeptide TPR- 1
CaPOPI_523	Ca1	48064288	TTATATATATATATATATATATAA/TT ATATATATATATATATATA	TGGGTGGATAGTAGAGA GGC	TCTGAATAGGTTTGGTC GGC	60.0	404	INTERGENIC				
CaPOPI_524	Ca1	48091761	TAAAAAAAA/TAAAAAAA	TCTGGAGATGGGACCCTC TTG	CCAAATCGGAGGAAGTT GTT	60.2	700	INTERGENIC				
CaPOPI_525	Ca1	48114146	TTATATATATATATATATATATAT/TTA TATATATATATATATATAT	TGATTGTTGTTGGGCCA CTA	TTTGTCTCCATTTTGCT TTTG	60.0	807	INTERGENIC				
CaPOPI_526	Ca1	48172069	AAATAAATAATAATAATAATAATAATA ATAATAATAATA/AAATAATAATAATAAT AATAATAATAATAATAATAATAATAA TAATAATA	TAAATGGCAGGTAAAGG CGA	AGACTTTGCTGCCACCT CAT	60.6	315	DRR	Ca_12862	R	WRKY	Leucine-rich repeat
CaPOPI_527	Ca1	48236817	TAA/TA	TGGGTGTTGCCCATATA TCA	TTTGgatccatttcattt gatt	59.6	626	INTERGENIC				
CaPOPI_528	Ca2	42172	TTATATATATATATATATATATA/TTAT ATATATATATATATA	TGGCAGTCTGTTTCACG TTT	CAAGGGACCAGATTCTG CAT	59.3	553	INTERGENIC				
CaPOPI_529	Ca2	55390	GACACACACACACACA/GACACACA CACACACACACA	GCACCGGGAGATACGTA AGA	TCACGGCTTCACAAAC AAG	60.1	798	INTERGENIC				
CaPOPI_530	Ca2	228183	GTTTTTTTTT/GTTTTTTTTT	TTCGAAACGTGGATGA ATG	GCAACCATCTGACCAAG TGA	59.5	418	INTERGENIC				
CaPOPI_531	Ca2	285679	AAATAAATAATAATAATAATAATAATA ATAATAATAACTAATAATAATAATAAT AATAA/AATAATAATAATAATAATAATA ATAATAATAATAATAATAACTAATAAT	AAACGACTCACACCCGA AAC	GCCATTGATTcattttctt cg	60.0	614	INTERGENIC				
CaPOPI_532	Ca2	422540	G/GTCCTTCCT	AGAGTTGGAGGGTGCA GCTA	CTTCgaatccaaccttg gtg	60.0	829	INTERGENIC				
CaPOPI_533	Ca2	469349	TA/TAA	CCCAGACAACCTTGCA GAT	ATGAAGTGCAAACCATG CTG	60.1	674	DRR	Ca_16986			
CaPOPI_534	Ca2	753916	CTTTTTTTTT/CTTTTTTTTT	TTGCCCATTAACCTTACC CG	ACTTGtgcatttgcatta gttc	59.8	555	DRR	Ca_17000		ARF	
CaPOPI_535	Ca2	833993	TAATAAAATAAAATAAAATAAAATA/TAA TAAATAAAATA	TTGCATCATGGTTATGC GAC	CATAGCCTCGTAcAtGC AACA	60.5	490	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_536	Ca2	904938	GGTGT/GGTGTGT	TGAGCAGGTTGTTC	CAGGGTCTGTGGCATTCT	59.8	575	INTERGENIC				
CaPOPI_537	Ca2	1233900	C/CG	CGTTTTTGAAGCCATTGT	CTGCCATAAAGGCTGCGAT	60.0	830	INTERGENIC				
CaPOPI_538	Ca2	1558409	TCGGAAGNNNNNNNNCGGAAG/TCGGAAG	TCGAAATTTTAGGCCACGAC	TGAGGTTGTGCTTTGACCA	60.1	631	INTERGENIC				
CaPOPI_539	Ca2	1640062	ATTTTTTTTT/ATTTTTT	AGATCATGTGCAAAAAGGGG	AGTAACCGTGAGGGAACGTG	59.9	509	INTERGENIC				
CaPOPI_540	Ca2	1728113	AATTATTATTATTATTATTATTATTATTATTATT/AAATTATTATTATTATTATTATTATTATTATTATT	GAAGACACACATATTTGGCA	GTTTGTGTGTTGCAGTGG	57.7	491	INTERGENIC				
CaPOPI_541	Ca2	1835747	TTATATATATATATATATATATATAT/TTATATATATATATATATATATAT	CACAATGCACCATGTGACAA	TGGAAGTGAAGCCATATCCC	60.0	831	INTRON	Ca_12601			Raffinose synthase
CaPOPI_542	Ca2	1879905	CAAAAAA/CAAAAAAA	AACATCTCTAGCGTGTGCCA	CACACCCACTCCCTTGTCTT	59.5	711	DRR	Ca_12598	YU		Bacterial Ig-like, group 2
CaPOPI_543	Ca2	1919646	TC/TCTCC	TTGAAGCGATGTGGTTGAAG	CCAAACAACATATGCCCGTT	59.8	339	INTERGENIC				
CaPOPI_544	Ca2	2169056	C/CG	AACCTCTCCAAGAGGATCGG	GGAGAGTGAAACGGATGGAA	60.6	648	INTERGENIC				
CaPOPI_545	Ca2	2169072	TTCTCTCT/TTCTCTCTCTC	AACCTCTCCAAGAGGATCGG	GGAGAGTGAAACGGATGGAA	60.6	648	INTERGENIC				
CaPOPI_546	Ca2	2235889	TTATTA/TTATTACTATTA	TCTTGCACAACTATTTCTGG	AAAAAGCAAAGAAATTGTGAGAA	59.8	330	INTERGENIC				
CaPOPI_547	Ca2	2373367	AATATATATATATATATATATA/AAATATATATATATATATATATATA	AAAATTGTCAGGTTCCGCGC	GGTGGTGATTTGGTGCTCTT	60.0	896	DRR	Ca_12541	R	DBB	RAG1-activating protein-1-related
CaPOPI_548	Ca2	2546989	AT/ATCATAGTTT	CCCCTCGATCAAAAGAAA	TTGAATTGCTTTCCAGTGTCC	60.0	705	INTRON	Ca_10592	R		Haem peroxidase, animal
CaPOPI_549	Ca2	2624920	CGGCTGGCT/CGGCT	GGCCAAGTTGCTGAAGGATA	CGCTAAGAGGCCGTTATCAA	60.2	610	INTRON	Ca_10586			Ribonuclease H domain
CaPOPI_550	Ca2	2692293	ATTTTTTT/ATTTTTTT	AAAGGTGATGAAGCAGATTTTGA	TGGTGTCTCTCTCTCTCTAATCG	60.1	478	INTERGENIC				

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CaPOPI_551	Ca2	2749945	CTTT/CTT	ATATGGATTATGCCCCAAA	TTGCATTTTTTCAGAGGAGG	60.0	580	INTRON	Ca_10569	GMO	E2F/DP	Nucleotidyl transferase
CaPOPI_552	Ca2	2977761	A/ACTT	CAACTTGCCAAACAGCTTCA	TGGTGCAAGGATAGTAGCAGCA	60.0	620	INTERGENIC				
CaPOPI_553	Ca2	2978014	CTAT/CTATAT	TTGCTGTAATTGTTGCACATGA	CCTCCCCAACTTGTAATTCTG	60.2	542	INTERGENIC				
CaPOPI_554	Ca2	2984359	CTTTTTTTTTTT/CTTTTTTTTTT	GCTCACAACAGCAAAAACCA	TCTCTTTCTTAGACCGGAGCA	59.9	443	INTERGENIC				
CaPOPI_555	Ca2	2984403	GAT/GATATAT	GCTCACAACAGCAAAAACCA	TCTCTTTCTTAGACCGGAGCA	59.9	443	INTERGENIC				
CaPOPI_556	Ca2	2985774	ATGT/AT	GTGAAGCTGTATGGCCCAAT	AGATCTGGGTCGGGAAAAGT	60.0	540	INTERGENIC				
CaPOPI_557	Ca2	2987500	TAAAAAAAA/TAAAAAAAAA	GCCAAATGATTCGGTTGCTA	GCCGACCATGGAGTAATGT	61.0	700	INTERGENIC				
CaPOPI_558	Ca2	2996172	ATTT/ATT	TTCTAAGGACCAACGCAACA	GTATGATCGATTATGCGCGA	59.3	434	INTERGENIC				
CaPOPI_559	Ca2	3000644	ATTTTT/ATTTT	TGATTCAATTGTGAAGTTTAATGTG	GGAGAAACATCACGTTGACC	59.4	949	INTERGENIC				
CaPOPI_560	Ca2	3001687	CAAA/CAAAAA	TTCCAATTTTCGGCAACTTC	GCTGATGAAGGAGAGGAACG	60.1	915	INTERGENIC				
CaPOPI_561	Ca2	3009059	ACCCCC/ACCCC	ATTCGCTTGCCTCTTTGTGA	CCCGAAACTTTCTGTGCATT	59.8	658	INTRON	Ca_10544	G		Glycosyl transferase, family 14
CaPOPI_562	Ca2	3011716	G/GA	TGATTTGGGGTGTTCAGAAA	TCCGCACACCAACATTAAA	58.9	657	INTERGENIC				
CaPOPI_563	Ca2	3016524	GAAAAAAAA/GAAAAAAAAA	TGGGAGAGATAAACGCTGCTGC	TCCTTACAACTCAAAAGTGC	60.4	353	INTERGENIC				
CaPOPI_564	Ca2	3022835	TTAA/TTAATAA	CCCGACTCGAAAGTTCTCA	AAAATTGACACGGCTTCGTC	60.4	544	INTERGENIC				
CaPOPI_565	Ca2	3024878	ATTTTTTT/ATTTTTTTTTT	CTGGTTTTCAAACGCGCTACT	CGGGGTCGGTATTATTTTGA	60.8	799	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_566	Ca2	3029449	TTTAATAATTATT/TTTAATAATTATTAAATATTATT	ACCGCTCTATTAAGGGC GAG	TCCATCGCAATTGAATAA TGA	60.7	765	INTERGENIC				
CaPOPI_567	Ca2	3030942	CAAGA/C	TTTTCATTTTCTCCCTTCCT	TCCATCGCAATTGAATAA TGA	59.1	592	INTERGENIC				
CaPOPI_568	Ca2	3031259	ATTTT/ATTTT	TCAATTGCGATGGATAG AGAAA	AATTGGTGTACCGATTG CGT	59.7	647	INTERGENIC				
CaPOPI_569	Ca2	3033081	TA/TAA	AACGCAACAAGCTCCAA AAG	CGTTAGGCCTTATCCTA GCC	60.4	902	INTERGENIC				
CaPOPI_570	Ca2	3038248	GAAAAAA/GAAAAAA	ACTTGCACTTGGAGTG CCT	CCCTTGTGCCTTATGGT TTG	59.9	784	INTERGENIC				
CaPOPI_571	Ca2	3042033	TTTTGTTTGCTT/TTT	TGCCAAATCATGCGTTT TTA	CTCTGATGCGAAGGTTG ACA	60.1	100	INTRON	Ca_10543			Conserved hypothetical protein CHP00275, flavoprotein HI0933-
CaPOPI_572	Ca2	3047152	CTTT/CTTTT	TGAAATTTACGGGCCT TCA	GTGGAAAACTGGACCC TCA	60.4	643	INTRON	Ca_10543			Conserved hypothetical protein CHP00275, flavoprotein HI0933-
CaPOPI_573	Ca2	3047767	TGG/TGGG	TGAGGGTCCAGTTTTTC CAC	AACCAAGTTGGCCCAA AA	59.9	266	DRR	Ca_10543			Conserved hypothetical protein CHP00275, flavoprotein HI0933-
CaPOPI_574	Ca2	3090922	TA/T	GAGACTTTTGGGCATGG AAA	TGGTCAGTCAAATTCTC CGA	60.1	368	INTRON	Ca_10541	T	HD-ZIP	Protein kinase, catalytic domain
CaPOPI_575	Ca2	3096490	ATTTT/ATTTT	TGGTTTTCTTAAACATG CAA	CTTTATCTTCATTTGCGC GG	58.2	134	DRR	Ca_10541	T	HD-ZIP	Protein kinase, catalytic domain
CaPOPI_576	Ca2	3098929	TTTTCTT/TTT	CAAATGCTTCACGAAAG GGT	AGCCACAAAACCACAAC ACA	60.1	361	INTERGENIC				
CaPOPI_577	Ca2	3099476	ATTT/ATTTT	GTTGTGGTTTTGTGGCT GTG	CCAATGCTTGACCCATC TTT	60.0	649	INTERGENIC				
CaPOPI_578	Ca2	3104148	TAAAAAA/TAAAAAA	GGAAACGCCGAGACATA CAT	GCACAACCTTTTGGCG TAT	60.0	360	DRR	Ca_10539	P	WOX	Porin, eukaryotic type
CaPOPI_579	Ca2	3113326	AACCTATACTT/AACCTATACTTATACTT	ATTTGTTCTGGCCACCT TTT	AGCTTGATGCTGCAATT CCT	60.7	535	INTRON	Ca_10538			Auxin efflux carrier
CaPOPI_580	Ca2	3118907	TAAAA/TAAAA	TGCACCAGAATGCCTTG TTA	TGGCCTTCACATTTCAAA CA	60.3	752	INTRON	Ca_10537		AP2	Pectate lyase/Amb allergen

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_581	Ca2	3126083	CTATATATAT/CTATATATATAT	AACGATTCCATGACTAATTGAA	TTGAACGGTTTAAATGTGGCT	57.7	518	INTERGENIC				
CaPOPI_582	Ca2	3154111	A/AT	TTCGTCTGTCATCCAAAT	TTTGACGGTGAAAAAGTGATATG	58.0	975	INTERGENIC				
CaPOPI_583	Ca2	3156648	GTCT/GTCTCT	GGTCAGAACAAAGGGTTGGA	GTTTGTTCCTTCTAGGCC	59.9	488	INTERGENIC				
CaPOPI_584	Ca2	3158875	GTATTATTATTATTAT/GTATTATTATTATTATTAT	CGCAAAAGTTGCATGAAGAA	TCTAAGAAATTTGCCCAATG	60.0	295	INTERGENIC				
CaPOPI_585	Ca2	3159298	ATTTTTTT/ATTTTTTTTT	CGCAAAAGTTGCATGAAGAA	TGCAGGACGGTCTAACAATG	60.0	600	INTERGENIC				
CaPOPI_586	Ca2	3162145	CAAAAA/CAAAAA	CTCTTGCTTCTCTCTCCC	GGCCTTCTGTGAGAAGCATTT	60.5	788	INTRON	Ca_10531	S		Cysteamine dioxygenase
CaPOPI_587	Ca2	3166543	T/TA	CATGTTTTAGCCCAACAAA	TTCCGCACATCAACACAAAT	59.6	849	INTERGENIC				
CaPOPI_588	Ca2	3169671	ATTTTTTT/ATTTTTTT	TTGTCGGTTTAACTTGTGTGC	TTTTCCAAGGGATTTCACCTCT	60.1	892	INTERGENIC				
CaPOPI_589	Ca2	3184404	AAAA/AAAATAAA	TGCATATCCTTGTTCCCA	CTTCCATGGGCTGTGAGAAAT	59.9	486	INTRON	Ca_10528	T	HD-ZIP	Protein kinase, catalytic domain
CaPOPI_590	Ca2	3185239	AAGA/AA	GATGTTGGAGGGCACCTAGA	GTGAAGGAGGGTTTGGAACA	60.1	661	INTRON	Ca_10528	T	HD-ZIP	Protein kinase, catalytic domain
CaPOPI_591	Ca2	3199849	TT/TATTATTAGT	GAGCATGTGTTGGTGAA TGG	TCACCGAGGTTAGATCTCG	60.0	309	INTERGENIC				
CaPOPI_592	Ca2	3200285	TCA/T	CGAGATCTAACCTCCGGTGA	TTGATGCATGCTGCTACAAAT	60.2	811	DRR	Ca_10527	K	HD-ZIP	Helix-turn-helix motif, lambda-like repressor
CaPOPI_593	Ca2	3200442	CAT/CATAT	GGAGTTGAATTAGCCTCTTTATCC	TTGATGCATGCTGCTACAAAT	58.8	503	DRR	Ca_10527	K	HD-ZIP	Helix-turn-helix motif, lambda-like repressor
CaPOPI_594	Ca2	3200504	AA/AAAAAGATA	CATTTCCCGATTTTAGATTATGC	AATTGAAGGAAACATTTGCCA	58.9	511	DRR	Ca_10527	K	HD-ZIP	Helix-turn-helix motif, lambda-like repressor
CaPOPI_595	Ca2	3200632	CAATT/CAATTAATT	AAGGAGTATCAACCAAAACAGAGG	AATTGAAGGAAACATTTGCCA	59.9	423	DRR	Ca_10527	K	HD-ZIP	Helix-turn-helix motif, lambda-like repressor

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_596	Ca2	3203039	AT/A	TGGATTCTTGACACTGC CAC	ATGCTCTTCCCTGTCTC CAA	59.7	348	INTRON	Ca_10527	K	HD-ZIP	Helix-turn-helix motif, lambda-like repressor
CaPOPI_597	Ca2	3205849	TC/T	ATTGTGGAGACATAACC GCC	ACATCGAGACGTACGGG AAA	59.8	284	INTERGENIC				
CaPOPI_598	Ca2	3630204	CATATATATATATATATATATAT/C ATATATATATATATATATATATAT	TGAAACAAGCATATGCG TCAA	TTTGCTTCAATAATTGC ACA	60.3	158	INTRON	Ca_10502	P	ERF	SPX, N-terminal
CaPOPI_599	Ca2	3723233	TATTATCAATTATCAATTA/TATTATCAA TTA	ATTTCTGTTGCGTTTTGG ACT	TGGTCAATTTTGTTC CA	59.6	234	INTERGENIC				
CaPOPI_600	Ca2	3723695	TAAAAA/TAAAAAA	TGGCAACAATAATTGA CCA	TTCTCAAATTGCAACAC CA	59.9	752	INTERGENIC				
CaPOPI_601	Ca2	3733191	TTAGAGACTAA/T	ACCTGCAACATGTGCGA TAA	TGCATGAGATTGGAAT GGA	60.1	349	DRR	Ca_10489	G	C3H	Alkaline phosphatase D-related
CaPOPI_602	Ca2	3741294	CT/CTTT	GGTGGAGAGGGATGAT GAGA	GCAGAGCACCAACACA AGA	60.0	605	DRR	Ca_10487			Plastocyanin-like
CaPOPI_603	Ca2	3743015	A/AATACAAATGGTG	CACCACTGGATTTAGCC GTT	TCCTTTTCGCTGATGAA ACA	60.0	722	INTRON	Ca_10487			Plastocyanin-like
CaPOPI_604	Ca2	3743829	CTTTTT/CTTTTT	TTGGCCAATACTCCAAC CAT	CAGCAAGTCCCACGAAA GAT	60.2	311	INTRON	Ca_10487			Plastocyanin-like
CaPOPI_605	Ca2	3745143	TAAAA/TAAA	GAAGCACTGGACCTCCC ATA	TGACTTGGAATAGATTG GACCAT	60.1	630	INTERGENIC				
CaPOPI_606	Ca2	3746503	TTA/TTAAACATA	TCCACATTGCACCAACA CTT	TTGCTCCTCTGGTCCTC ACT	60.0	925	INTERGENIC				
CaPOPI_607	Ca2	3754940	GA/GATA	TCCTTCAACTGTGGAAC CAA	GCTTCTTGTTGGGCTT AGG	59.1	751	DRR	Ca_10486	DL		Hus1-like protein
CaPOPI_608	Ca2	3761698	TAA/TAAA	ACCTCCATTGCTGTTTT TG	CTCGAACATGCATAGA ATGA	60.0	262	INTERGENIC				
CaPOPI_609	Ca2	3766913	ATTTTT/ATTTTTT	AGAACCATGTGCTTCAT CCC	CAACACAATTGAATGGC AGG	59.9	478	INTERGENIC				
CaPOPI_610	Ca2	3771310	TTATATATATATATATA/TTATATATAT A	GCTCGACGGAATAGCAT TTT	TGGCCAAGCATGATCTA ACA	59.3	612	DRR	Ca_10483	E		Chorismate mutase, AroQ class, eukaryotic type

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_626	Ca2	4527479	GAAGACAAAAAACATAAGACAAAAA AAACAT/GAAGACAAAAAACATAAGA CAAAAAAACATAAGACAAAAAACAT	GCAATTTCACTCTTCT GCC	TGACGAAGCCCAATA ACA	59.8	523	INTERGENIC				
CaPOPI_627	Ca2	4700407	ATTATTTATTTATTTATTTATT/ATT ATTATTTATTTATTTATT	TCTCACGGTTGTGAGGA CTG	CCTACCTCTGGAGTGTC CGT	59.9	926	INTERGENIC				
CaPOPI_628	Ca2	4812881	ATTTTTTT/ATTTTTTTTT	AACCGTTCCGTTCCAA GTG	TCCCCAACAGAAATTT GAG	60.0	731	DRR	Ca_21090		MYB	Transferase
CaPOPI_629	Ca2	4892794	CATATATATATATATATATATATAT ATATAT/CATATATATATATATATAT ATATATATATATATATATATAT	GCGGACATAAGGAAGAT GTGA	AGGTCTGCGAAGATGGA AAA	60.1	606	INTERGENIC				
CaPOPI_630	Ca2	4894086	TA/TAGACAACCTCA	TTGAACACAACGAGC CAC	TTTTGTCAATTTCTTGC TCCA	59.9	493	INTERGENIC				
CaPOPI_631	Ca2	4895677	AA/AATATGA	CCAGGATAAACAGCCC AGA	TGGATGCTTTCCCAACT TTC	60.1	467	INTERGENIC				
CaPOPI_632	Ca2	5096452	AATATATATATATATATATATAT/AATA TATATATATATATATATATAT	GTTTTGTGGTGAGTT GGA	TTTGAAAGAGTCCGAAT TCAAATA	59.6	570	INTERGENIC				
CaPOPI_633	Ca2	5135372	AATATATATATATATATATATATAT ATATATATATATATAT/AATATATATAT ATATATATATATATATATATATATA T	TGATTTATTTCCACGCT ACG	TGTTTCTCCCCAGTTTT GG	60.0	952	INTERGENIC				
CaPOPI_634	Ca2	5163788	CAAAAAAAAA/CAAAAAAAAA	TGCGAGAAAGTGAATTC CAG	GGAATGATGATGGGGTT TTG	59.0	658	DRR	Ca_14696			
CaPOPI_635	Ca2	5286155	AATATATATATATATATATATATAT ATA/AATATATATATATATATATATATA TATATATA	TTTCATGCCTCCCATTTCT TC	CGCTCTGTCAACATGTC AGC	60.0	752	INTRON	Ca_14679	T		Protein phosphatase 2A, regulatory B subunit, B56
CaPOPI_636	Ca2	5566169	GAAAAAAAAA/GAAAAAAAAA	TGGGAGTATCCTTCACT GCC	TTTCGATTTTCTTCCCT TT	60.1	836	INTERGENIC				
CaPOPI_637	Ca2	5626731	ATTTTTTTTT/ATTTTTTTTT	GAACCAATATAGCCGC AAA	TTTGCTGCAACAACCTC AAG	59.9	782	INTRON	Ca_14650	I	C3H	Alpha/beta hydrolase fold-1
CaPOPI_638	Ca2	5674299	TCTTTACTTTACTT/TCTTTACTTTACTT TACTT	ATTAGTCCACTGTGCTG GGG	GCTTCCAAATTGCTTGT CC	60.0	815	INTRON	Ca_14646	O	FAR1	ATPase, AAA+ type, core
CaPOPI_639	Ca2	6317566	GTATATATATATATATATATATATA TAT/GTATATATATATATATATATATA TATAT	CACCAATGATGACGAC GAC	ATTCACGTCGTTCTGT TCC	60.0	324	INTERGENIC				
CaPOPI_640	Ca2	6505178	TA/TAA	CGTAATAACGCGAGGA AAA	TGAGCAGGGGAAGAG TAGA	60.1	548	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_641	Ca2	6522206	AT/ATT	GGAAGTGAAGGTCACG GTGT	TGAGCACGAATAATTGC AGC	60.0	593	DRR	Ca_20947			
CaPOPI_642	Ca2	6640316	TAAAAA/TAAAAAA	ATGGCCACGAATCTGAA GAG	ACGGTTGTTTGGCATT GAT	60.2	890	INTERGENIC				
CaPOPI_643	Ca2	6640452	GAAAA/GAAAAA	AAAAAGGTCCTAGGTTG GGA	ACGGTTGTTTGGCATT GAT	59.8	473	INTERGENIC				
CaPOPI_644	Ca2	6641737	CATATAT/CATATATATAT	GTATTCAGGGCGGAAGG AAT	AATGCAAACGACAAAGG AGG	60.3	500	INTERGENIC				
CaPOPI_645	Ca2	6641916	TG/T	GTTCTATGGGACAGGG TCA	TATCACTACCAGAGCG GGG	59.8	476	INTERGENIC				
CaPOPI_646	Ca2	6642515	TTATATATATATATATA/TTATATATATAT ATATATA	CCCCGCTCTGGTAGTTG ATA	ACCCACTTTGAGAAACG TGC	60.1	479	INTERGENIC				
CaPOPI_647	Ca2	6643765	AT/ATT	ATGGAACAAGCAGCGAA GTT	GTTGATACGAGGGGTT GAA	59.9	537	INTERGENIC				
CaPOPI_648	Ca2	6643843	CTTTTTTTTT/CTTTTTTTT	ATGGAACAAGCAGCGAA GTT	GTTGATACGAGGGGTT GAA	59.9	537	INTERGENIC				
CaPOPI_649	Ca2	6648530	TAAAAA/TAAAAAA	TTATCGATCGTCGGTGT CAA	TTCCATATGCACCTCCC ATT	60.1	612	INTERGENIC				
CaPOPI_650	Ca2	6648980	ATTTTTTTTT/ATTTTTTTTTT	AGCCTAATGGGAGGTGC ATA	TATGAGGGGTTGAATT GGA	59.6	563	INTERGENIC				
CaPOPI_651	Ca2	6815005	ATTATTTATTTATTTATTTA/ATTAT TTATTTATTTATTTA	GAAATTTTAGCGCAAC AGC	TCCAATCCCATTGTCCA CTT	59.9	703	INTERGENIC				
CaPOPI_652	Ca2	6831436	AC/A	CCTGTGACATGTTGCCT TTG	AAATGGGCTGAGTTTGA ACA	60.2	360	INTERGENIC				
CaPOPI_653	Ca2	6867609	CAAAAAAAAA/CAAAAAAAAAA	TAACCACATTGCAAGCC AAA	CAATCAAAATGCAACAG ACACA	60.1	451	INTERGENIC				
CaPOPI_654	Ca2	7144237	A/AG	GGACCGGAATCATAATG CAA	TTTTTCCGTAAAAGTCCC CC	60.7	743	INTERGENIC				
CaPOPI_655	Ca2	7171869	TTAT/TT	CGGCCATTAAATTTCTG ACA	TTGCATTATGTTTCTGG CAAA	58.6	320	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_656	Ca2	7171912	TATTTAATTTAATTTAATT/TATTTAATTTAATT	CGGCCATTAAATTTCTGACA	TCATTTCATAACGAGTGACCA	58.6	584	INTERGENIC				
CaPOPI_657	Ca2	7172121	CTATATATATATAT/CTATATATATAT	TTTGCCAGAACATAATGCAA	TCATTTCATAACGAGTGACCA	59.2	285	INTERGENIC				
CaPOPI_658	Ca2	7172172	ATTTTTTTTT/ATTTTTTTTT	TTTGCCAGAACATAATGCAA	TTTTGGAAAAATGAAGGACCA	59.2	774	INTERGENIC				
CaPOPI_659	Ca2	7173102	GAAAAA/GAAAAA	CTCAATCCAAACACAGCTT	AATGACCACCTCTTGTTGCC	58.8	787	INTERGENIC				
CaPOPI_660	Ca2	7276294	CAAAA/CAAAA	TCCACCACAATCGTTAAGCA	AGCGGAGATTTTACCGGATT	60.1	676	INTERGENIC				
CaPOPI_661	Ca2	7302005	TTATATATATATATATATA/TTATATATATATATATATATA	TGTAGCAAAACGTGCAGACC	GGATATTTTGCTCTCTCGCAA	59.9	159	INTERGENIC				
CaPOPI_662	Ca2	7535934	TAAAAAAAAA/TAAAAAAAAA	AACCGGACATTTTGTGGAG	TGCACAAATGGTGGAAGAA	59.8	626	INTERGENIC				
CaPOPI_663	Ca2	7540916	TATAGTAATAAATAGTAATAAT/TATAGTAATAAAT	AATATTGGAACCTCCCAACC	TTAATCGTCCAACCTCCCAACC	60.0	890	INTERGENIC				
CaPOPI_664	Ca2	7555681	GTTTTTTTTT/GTTTTTTTTT	AATTTTGC GTTCATCGGAGA	AATCACACGACACCGGAGA	60.6	178	INTERGENIC				
CaPOPI_665	Ca2	7617731	CTAAAAATAAATAAA/CTAAAAATAAATAAATAAATAAATAA	CCAAGATCTCGTAGTGCAACA	TGGGTTTAGTCCGTTTTTCCTC	58.9	468	INTERGENIC				
CaPOPI_666	Ca2	7657147	CTTTTT/CTTTTT	TTATGTGGGGGATTTGGATG	TTCCAGTCCTTTTCATTCC	60.4	705	INTERGENIC				
CaPOPI_667	Ca2	7675590	TAAAAA/TAAAAA	ACTCCGATTGGAGAAAGG	AAATGAGTTTACATTCA CGGTACA	60.4	882	INTERGENIC				
CaPOPI_668	Ca2	7681881	TAAAA/TAAAA	GAAAAAGAGCCACGGTGTA	GCGAGAAAAAGATTGTGAGAA	60.1	383	INTRON	Ca_18121	R	ERF	Multi antimicrobial extrusion protein
CaPOPI_669	Ca2	7682063	CTTTTT/CTTTTT	GAAAAAGAGCCACGGTGTA	TTCCAGCTCCAAGCTCATT	60.1	643	INTRON	Ca_18121	R	ERF	Multi antimicrobial extrusion protein
CaPOPI_670	Ca2	7695766	TG/T	GGCGGGACAATTATTTGAA	CCATATAGGAAGTACGAGTACGTGA	59.8	401	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_671	Ca2	7699107	TAAAAAAAA/TAAAAAAAA	CCAAAAATTGTGGAGATTGG	GCTGATGATGCCTCCATTTT	59.3	846	INTERGENIC				
CaPOPI_672	Ca2	7699126	TAAAAAAAA/TAAAAAAAA	CCAAAAATTGTGGAGATTGG	GCTGATGATGCCTCCATTTT	59.3	846	INTERGENIC				
CaPOPI_673	Ca2	7703919	AAATAAAATAATAAAATA/AAATAAAATA	TCTCTTTATTGGGGCATTGG	AGATGTAAGGGGTGTGAAAA	59.9	910	DRR	Ca_18123	R	ERF	Multi antimicrobial extrusion protein
CaPOPI_674	Ca2	7706488	AAAATAATTAAATAATTAAAT/AAAATAATTAAATAATTAAATAATTAAAT	GCCTATTTTGTCTTTCCTGC	TCATCCACTTTCTTGCCTGT	59.0	689	INTERGENIC				
CaPOPI_675	Ca2	7709881	TAAAAAAAA/TAAAAAAAA	TGACACATGCAAAACACCT	AGAAGCACGAAGATATGCACCT	60.0	619	INTERGENIC				
CaPOPI_676	Ca2	7716515	TA/TACCTGA	ATGGGCTTTAAATGTGGCAG	ACCCCGTTTGGCTTCTATTT	60.0	105	DRR	Ca_18124			
CaPOPI_677	Ca2	7718496	C/CT	CCTGCCACCACTCTTAGCTT	TGGGATGCTACCTCCTATGG	59.5	511	INTERGENIC				
CaPOPI_678	Ca2	7718955	TGAAA/T	GAGCTTCATTGAAATCGGGA	TCATATAGGAGGTCGCACCC	60.2	821	INTERGENIC				
CaPOPI_679	Ca2	7720508	TAAA/TAA	TAATCCGCCTAAATGGATGC	CTCCCATAGGATGAAGGGT	59.9	530	INTERGENIC				
CaPOPI_680	Ca2	7720908	AAT/A	TTCACCCCCTTCATCCTATGG	TCCAAATGTTTGTGATTGTGC	59.7	490	INTERGENIC				
CaPOPI_681	Ca2	7724864	TA/TAAAGAGATTGAGA	ACCAGAGACACTGCAGCAAA	AACAAGATTCTCGAATGCTCC	59.6	464	INTERGENIC				
CaPOPI_682	Ca2	7725038	ATTTT/ATTT	ACCAGAGACACTGCAGCAAA	AGCCATTTGAGACTGTGCAA	59.6	789	INTERGENIC				
CaPOPI_683	Ca2	7731377	GAAAA/GAA	GTGGTTGTGATGTTGAACGC	CTCCCGCTAACTCCTCTTCC	60.0	697	INTERGENIC				
CaPOPI_684	Ca2	7743405	CG/C	ATCCATCATGTTTCATGCCT	ATCTCCACCCGTTCTCTGTGA	60.2	579	INTERGENIC				
CaPOPI_685	Ca2	7743661	AATC/AATCGATC	TCAAGAGAACGGGTGGAGAT	GATTCAAAATGTGAGCGCAA	59.7	530	INTERGENIC				

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CaPOPI_686	Ca2	7747929	TAAAAAAAA/TAAAAAA	TGGTGAAATGCTGCAGAAA	CTCAACTTGTCGATGCC TCA	60.4	147	INTERGENIC				
CaPOPI_687	Ca2	7753358	C/CAAT	CGGAGGTTTGGTGTAAC TGA	AGCTTGCCATTGCAGCT ACT	60.0	447	INTRON	Ca_18125		MYB_related	NPH3
CaPOPI_688	Ca2	7771490	ATTTTTTTTT/ATTTTTTTTT	ACCATTATTATTTCGT GTTAATGA	GGTACCATGGATGATAT TTAGCC	57.3	188	INTERGENIC				
CaPOPI_689	Ca2	7772671	AAAAAATAAAAA/AAAAA	CAATTGGTGGCCGTTAT TTT	TGCCCTAAGGGAATAA GCTA	59.7	750	INTERGENIC				
CaPOPI_690	Ca2	7773617	TTAAATAAAAT/TTAAATAAAATAATAA AAT	GCTGAGCCCAACAAGC TAA	CCACTGTGGAAGGTAA ATGC	60.5	845	INTERGENIC				
CaPOPI_691	Ca2	7778320	ATT/ATTT	AGACCTCTTACTGTGCG CGT	TGCACTTTGTCCCTC AAT	60.1	321	INTERGENIC				
CaPOPI_692	Ca2	7780730	ATTTTTTTTT/ATTTTTTTTT	TTGTCTCCATCCTCAGC CTT	TGTTGTTTGAGTTGGGA CACA	59.8	995	INTERGENIC				
CaPOPI_693	Ca2	7782164	AG/A	TCATTTCAATCCCCCATC AT	TTTGATGCTATGCGAAG GAG	60.0	388	INTERGENIC				
CaPOPI_694	Ca2	7786133	AC/A	GCTCCTTTGGTGATCG CTC	CATTCCATTCCATGTTG CAC	59.8	369	INTERGENIC				
CaPOPI_695	Ca2	7788989	TC/T	GCTCTTTTACGTTTGCC AGC	TGTTTTAGATTGTCTTCT ATTTACGG	60.0	566	INTERGENIC				
CaPOPI_696	Ca2	7790064	CA/CATGTTA	AGAGTTGGCCAATTGGT TTG	GAATGTCAAGCATTGTG AAGGA	60.0	467	INTERGENIC				
CaPOPI_697	Ca2	7815016	TAATAACAAATAACAAA/TAATAACAAAT AACAAATAACAAA	TTTTACCAACACCGTC AAA	AAATAATCGTGGCCTTG CAC	60.0	901	INTERGENIC				
CaPOPI_698	Ca2	7824116	T/TG	TGTCTCGTGATCTGGT TTG	TGACTTTGTGTCGGAAT TTG	59.7	258	INTERGENIC				
CaPOPI_699	Ca2	7881274	GTAT/GTATCGTTAT	GCCACTCCAACACCAAT TTC	TGGAGACCACATGGAGA TGA	60.4	423	INTERGENIC				
CaPOPI_700	Ca2	7881305	TTAT/TT	GCCACTCCAACACCAAT TTC	TGGAGACCACATGGAGA TGA	60.4	423	DRR	Ca_18136			

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CaPOPI_701	Ca2	7881740	ATATTCC/ATATTCTATTCC	TCATCTCCATGTGGTCTCCA	TGCAATGACCACCCACTTA	60.0	642	DRR	Ca_18136			
CaPOPI_702	Ca2	7887346	AATAT/AATATAT	GTGCAGAGGAGCAAAAGGAC	TGGAATTTGAGACATGTCAACC	60.0	889	DRR	Ca_18137	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_703	Ca2	7887518	ATTTTTTT/ATTTTTTTT	AAGCAAATACATCTCGAAGTTCT	TCCCAAGAAAAGCTTCAACC	57.8	550	DRR	Ca_18137	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_704	Ca2	7887647	CAACATA/C	AAGCAAATACATCTCGAAGTTCT	TCCCAAGAAAAGCTTCAACC	57.8	550	DRR	Ca_18137	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_705	Ca2	7916006	A/AC	CTCATTTGCATCCGATTGGT	TATCGAAAGTTTCCGCGTTT	60.9	525	INTERGENIC				
CaPOPI_706	Ca2	7922625	TAA/TA	GAAGCATCACTAGGTGGGGA	CAACCAAAACCATTTCAAACACT	60.1	369	DRR	Ca_18141		bHLH	Protein kinase, catalytic domain
CaPOPI_707	Ca2	7933926	ATT/AT	TTCCTTAAGCGTGCTTTCA	CCAAATAACCCACAATCGG	59.6	539	INTERGENIC				
CaPOPI_708	Ca2	7940136	ATTTTTTT/ATTTTTTTT	TCTTGACCGTTAGATTGAACCA	CAAAATGGACAAAATTGGAGC	59.6	714	INTERGENIC				
CaPOPI_709	Ca2	8166930	AAATAATAATAATAATAATAAT/ AAATAATAATAATAATAATAATA ATAAT	CCTAGGGATGCGACCATCTA	TCCTCCTCTTTTGGCACATT	60.1	385	INTERGENIC				
CaPOPI_710	Ca2	8332435	GTTATTATTATTATTATTATTATTAT TATTATTATTATT/GTTATTATTATTATTA TTATTATTATTATTATTATTATTATT	CTACGGAGGATGGAAC TGGA	TTTGGTGATCTGGGGAGAAG	60.1	734	INTRON	Ca_21468	TU		Phosphatidylinositol 3-/4-kinase, catalytic
CaPOPI_711	Ca2	8343398	AATATATATATATAT/AATATATATATATA TAT	CCAGTGT TTGACCTCCAAGC	TTTGCAACAACGCGAAATAG	60.7	743	INTERGENIC				
CaPOPI_712	Ca2	8420270	AACA/AACACA	CCAAGTTTGAAATGCCGATT	GCTGCATGATCTTATGCTCG	59.9	451	INTERGENIC				
CaPOPI_713	Ca2	8478800	AATTT/ATT	CCC GTATGAATGAACGGAAC	CTACCCCCACATTTCAATCG	60.2	519	INTERGENIC				
CaPOPI_714	Ca2	8478910	ACT/A	CCCGTATGAATGAACGGAAC	CTACCCCCACATTTCAATCG	60.2	519	INTERGENIC				
CaPOPI_715	Ca2	8708914	ATTTTTTTT/ATTTTTTTT	GCCACACCCGAAGAAAT AAA	TTCATTTTGCTCCATCAC TTTC	59.9	714	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_716	Ca2	8777880	ATTTTTTTTT/ATTTTTTTTT	CATGTCCTCAGGTGGTGTG	TTTGTCTGGGATGAAC TGA	60.0	807	INTERGENIC				
CaPOPI_717	Ca2	8820736	ATTTTTTTTT/ATTTTTTTTT	TTACCATGATGTCGGTGTG	GTGAGCAAATGTTTCGG GAT	60.2	690	INTERGENIC				
CaPOPI_718	Ca2	9277232	AGG/AG	ATCGTGCAATCAACCTGTCA	GTTCATGCAAATTGGG TCC	60.1	439	DRR	Ca_20035			Domain of unknown function DUF231, plant
CaPOPI_719	Ca2	9287043	ATTTTTTTTT/ATTTTTTTTT	CTCTTTCTCCTCCGAAACA	AAGGGTTTTGTTGAAAG GGG	59.4	706	INTERGENIC				
CaPOPI_720	Ca2	9408358	CTT/CTTCTATTATT	CATCAAAAACAGCAGCGAAA	TCGTGCTTCTTTCCATC CA	60.0	934	INTERGENIC				
CaPOPI_721	Ca2	9485330	TTTTTATTTTATTTATTTT/TTTTATTT TATTTT	TTATGCGCCACATCACATTT	CGCCGAAAAGGTTACAC AAT	60.0	604	INTRON	Ca_20024	T	M-type	NB-ARC
CaPOPI_722	Ca2	9494071	T/TA	GAACTGCAACAACAACGACAA	GGTCTCGAAATCCCTGATGA	59.8	609	INTERGENIC				
CaPOPI_723	Ca2	9500229	CGTATGCTAGACCTGG/CGTATGCTAG ACCTGGGTATGCTAGACCTGG	AGAGGTTGGGGGAGAA GAAA	GCAACAACAGCAGAGAC AATG	60.0	213	INTERGENIC				
CaPOPI_724	Ca2	9650270	CATATATATATATATA/CATATATATA TATATA	GAAGGGGTATGAACGAAGCA	TGAGTAGGGATGGAGGACCA	60.1	590	INTERGENIC				
CaPOPI_725	Ca2	9884034	AATATATATAT/AATATATAT	TAA GTTGTGTGGCATC GGA	CCGACCTAATCACTCAT AAATATCG	60.1	322	INTERGENIC				
CaPOPI_726	Ca2	10013835	ATTTTTTTTT/ATTTTTTTTT	TACTCACCCAAATCCGCTTC	TAGACCCTCATCCTCAT CCG	60.1	393	INTERGENIC				
CaPOPI_727	Ca2	10032701	AATATATATATATATA/AATATATATATA	TTCTTCAGAGAAAAGAG TGGTTTTT	CCGTGTTTACGCTCTGT TGA	59.1	392	INTERGENIC				
CaPOPI_728	Ca2	10187103	AATATATATATATATATATATA/AATAT ATATATATATATATATATATA	AAGGCGAGAACAAGCCATT	CCTGAATATGCGGCGTT ATC	59.8	314	INTERGENIC				
CaPOPI_729	Ca2	10498057	CTTTTTTTTT/CTTTTTTTTTTT	TGACCAATCGGAAAGAAAAA	AGGGAATGAGAGCAATG ACG	59.6	454	INTERGENIC				
CaPOPI_730	Ca2	10779124	TTA/TTACATA	CAC TTTCTTATGCACCGCA	GCAGCGAGTAGGAGAAA TGC	59.9	663	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_746	Ca2	12933106	A/AT	AGGTTGAAAGAACCCCTACT	ATCGGTTGGTTGGTGAAATG	60.1	834	INTERGENIC				
CaPOPI_747	Ca2	12933573	CACCAACCAACC/CACCAACC	TCATTGACAAGGAAAGACATGA	CGAATTGGTTTTGGGATTG	59.6	413	INTERGENIC				
CaPOPI_748	Ca2	12934202	AAA/AAACAA	AGAAAGCAAGCAAATCCAA	TTCCAACACCTCACGATCA	59.8	488	INTERGENIC				
CaPOPI_749	Ca2	12937651	ATTTT/ATTTTT	GATTGCTTCTCTATGCCG	GTTTTGGCGTTGGTTTCACT	59.8	353	INTERGENIC				
CaPOPI_750	Ca2	12939688	AATATATA/AATATA	TTTTGGTGTTGAGGGTGCA	TTAATCAAAGCGGCAAGAA	60.0	564	INTERGENIC				
CaPOPI_751	Ca2	12941200	CAAAA/CAAA	TGTGCTTCTCTGATTTGG	GGCCAAAGACGGATATGTA	60.2	888	INTERGENIC				
CaPOPI_752	Ca2	12941800	T/TA	CATATCCGTCTTTGGCCATT	CCTTGAACAATTTGGGCAGT	59.8	643	INTERGENIC				
CaPOPI_753	Ca2	12947970	G/GT	TGCTTTTATGAGCATTACGGG	CGACTTCAAATCCCTTCGAG	60.1	777	INTERGENIC				
CaPOPI_754	Ca2	12952557	ACATATCATATCA/ACATATCA	AAAGCATTTTATCCCGACCA	TTTTTCATCTCACTCTCTCCCA	59.4	787	INTERGENIC				
CaPOPI_755	Ca2	12952944	TGTCATGATTAT/TGTCATGATTATAGTCATGATTAT	TGGGAGAGAGTGAGATGAAAA	ACGGATGTCTAATCCGTGTTGG	58.9	308	INTERGENIC				
CaPOPI_756	Ca2	13247575	ATTTTTTTT/ATTTTTTTT	TGAAAAGCTAAATGCATGGAA	TCATGACCATGGACCACTA	58.4	937	INTERGENIC				
CaPOPI_757	Ca2	13957739	TGG/TG	ATTATCCCCACCCACCTAC	TTTCAAAAACGGTGGTGTA	59.8	755	INTERGENIC				
CaPOPI_758	Ca2	13959549	ATTTTTTTTTT/ATTTTTTTTTT	TGAAATTTGTGATTTAGTTGCTTAAAA	CATAGATTCCCCACCCAATG	59.6	752	INTERGENIC				
CaPOPI_759	Ca2	13983591	ATTTTTTTTTT/ATTTTTTTTTT	ACACGAGGCGGAGAAATAAA	TGCAATTGTGTCATTGT	59.7	893	INTERGENIC				
CaPOPI_760	Ca2	14086143	C/CT	GCTTCTGATGGTGCACTTGA	TGGCCTAAAGCAAGCTCTA	60.0	371	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_761	Ca2	14192522	GAAAAAAAAA/GAAAAAAAAA	TACAAATTGGATGCGGT TGA	CCCTCTGCAATGTCGGT AAT	59.9	755	INTERGENIC				
CaPOPI_762	Ca2	15479768	ATTTTTTTTT/ATTTTTTTTT	GGGGTTCTTCAAAATG GGT	CAAACCTGGGGATGAAA ACG	60.0	461	INTERGENIC				
CaPOPI_763	Ca2	15557649	AATATATATATATATATATATATA/ATATATATATATATATATATATATA	GAAAGCAATTGGGCTAC TGG	CCAAAAACGTCTTTTCAA TGG	59.7	251	INTERGENIC				
CaPOPI_764	Ca2	15589036	ATTT/ATTTT	ATACGCCTCAACAAAT GGC	CTGCTTTGCTTGATTCC GTT	60.0	376	INTERGENIC				
CaPOPI_765	Ca2	15691178	TTATATATATATATATATATAT/TTATATATATATATATATATATATAT	GACTGTCCAATTTGTG GGG	TTTTTGGCATCAAGTTGT CTTTT	60.2	581	DRR	Ca_18540			Alpha-1,4-glucan-protein synthase, UDP forming
CaPOPI_766	Ca2	17046294	AATAAATT/AAAAATTATAAATT	CTATTCATCCACGAAT GCC	TCCATGGAGGATATTTA TGTCG	60.3	523	DRR	Ca_24768		G2-like	Zinc finger, TTF-type
CaPOPI_767	Ca2	17061321	TAATATATA/TAATATATAAATATATA	TTTGGCTCGGAAGCTT TTA	AGGAAGAGTGGAGTTGC GAA	60.0	498	INTERGENIC				
CaPOPI_768	Ca2	17061679	T/TCCA	TTTCGCACTCCACTCTT CCT	CGGTAAAAATCTCTGCT CGC	60.0	190	INTERGENIC				
CaPOPI_769	Ca2	17551687	G/GC	ATGTGGTTGATAAGGCC TCG	AGCAATGCAATGCTCT GAA	60.0	398	CDS (FRAME SHIFT)	Ca_16000	OE		Peptidase S10, serine carboxypeptidase
CaPOPI_770	Ca2	18225059	GTTTTTTTT/GTTTTTTTTT	TTGTTTTGATGGATGATT TGGA	AAGCAACATTTGGAAT GGC	60.2	460	INTERGENIC				
CaPOPI_771	Ca2	18391802	AATATATATATATATATA/AATATATATATATATATA	CAAAGCGGGTAGCAAGG ATA	GCCGCTCCTCTTCAAGT AAA	60.2	524	INTERGENIC				
CaPOPI_772	Ca2	18584340	GAAAAAAAAA/GAAAAAAAAA	ATGTACCTCCGCCTCAT TTG	TCTCTGGCAACCGTTCT TCT	60.0	257	INTERGENIC				
CaPOPI_773	Ca2	18610007	TAA/TAACAA	TTGATCCCTTATTTCTG CG	TTATTTACCGTCGTGT CCA	60.0	492	INTERGENIC				
CaPOPI_774	Ca2	18764616	GAATAATAATAATAATAATA/GAATAATAATAATAATAATA	ATTTGCCTCCCTCAACC TTT	TGCTTCATGGGTGCAT TGT	59.9	841	INTERGENIC				
CaPOPI_775	Ca2	18833380	TAAAAAAAAA/TAAAAAAAAA	TCGAAAAATCCCTTGAA AAAGA	GGACCTATCAAGTGAGC TTGTG	60.0	551	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_776	Ca2	19008979	TAAAAA/TAAAAAAA	GGCTATATCTCCCATGCAA	GCAAGAAACGAGGAAAGAAGG	59.9	663	INTRON	Ca_15954		bHLH	Terpene synthase-like
CaPOPI_777	Ca2	19207562	TAAAAAA/TAAAAAAA	ACAAACCAAAACCCAAACAA	TTTCACCGACCCAAACAAT	60.1	663	INTERGENIC				
CaPOPI_778	Ca2	19219016	ATTTT/ATTT	CCCGTGAGATCCTCCTACA	TGAATCTACGGCTTTCTGGG	60.1	498	INTERGENIC				
CaPOPI_779	Ca2	19705772	GAAAA/GAAAAA	TATTTTGGATTTTGGCTCGG	AGGAAGAGTGGAGTTGCGAA	59.9	475	INTERGENIC				
CaPOPI_780	Ca2	19791685	C/CG	TAGGCCATTTTCGTCTCAC	AATCCAATGACACAACGCA	60.1	392	INTERGENIC				
CaPOPI_781	Ca2	20280019	TAAAAAAAAA/TAAAAAAAAA	GCAAGGTTTGACAGTGAGCA	CATCGACAACCAATCCACAG	60.0	554	INTERGENIC				
CaPOPI_782	Ca2	20353586	T/TG	TCTCCCTCCTCTCCATTT	CATTAAGAGGTTCCCCCTCC	60.0	844	INTERGENIC				
CaPOPI_783	Ca2	20451589	CAAAA/CA	ACCAAATTGACTCGGTGCTC	TGTGGGATGACCCCTTTTGT	60.1	460	INTERGENIC				
CaPOPI_784	Ca2	20647114	AATATATATATATATATAT/AATATATATATATATATATAT	ATCACTCGCACAAACCA	TTGGAAGGAGCCCTTACCTT	60.2	920	INTERGENIC				
CaPOPI_785	Ca2	20970910	ATTCCCT/A	AACAAAGGAACAAATGGCG	AGGGACAAAGGGCAAGAAAT	60.0	853	INTERGENIC				
CaPOPI_786	Ca2	21088001	TA/TAAAAGCATCA	AGAACGATGACACGTTGGT	CTTCTGTCCAAAAGCAGCC	60.4	812	INTERGENIC				
CaPOPI_787	Ca2	21312312	GTTTTT/GTTTTTTTT	TATCAGAGTTCTCCCAACCG	AGAAACCACAACGCAACACA	60.1	356	INTERGENIC				
CaPOPI_788	Ca2	21314611	AG/AGG	CAAACCTTTCAAGGTGCAT	GCACTGCCCAAGAATTTA	60.0	443	INTERGENIC				
CaPOPI_789	Ca2	21596317	TTTATTATTATTATTATTATTATTAT/TATT/TTTATTATTATTATTATTATTATTATTATT	AATCCCTCCCTTCGTCACTT	TCCCTTTCTACAAGCGTTCA	59.9	210	INTERGENIC				
CaPOPI_790	Ca2	21672716	ATT/AT	TGATGCCGTGCCATAAATAG	TAACCTTGCCTTTGGGTGAG	59.5	595	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_806	Ca2	23932608	TAAATTAAATGAATAAAATTAAT/TAAATTAAT	AAGGCATCCAATCAAAGCAC	CTCAAGATTTTAGCGCCGTC	60.1	460	INTERGENIC				
CaPOPI_807	Ca2	23989802	AAAAACAAAACAAA/AAAAACAAAACA AAACAAA	AATTCGTTGAGCCGGTC TAGT	AGCACGGGGAGTATGAGAAA	60.1	421	INTERGENIC				
CaPOPI_808	Ca2	23990182	AAAAACAAAACAAA/AAAAACAAAACA AAACAAA	TCTCACTCCCCGTGCTTT	ATCCCCACACCAGATGCAC	59.7	565	INTERGENIC				
CaPOPI_809	Ca2	24102909	GT/GTT	TGGGGGATCCAAGTTAA AAA	GAAACTCTCCGGCATT CAA	59.2	428	CDS (FRAME SHIFT)	Ca_21670	S		Transmembrane receptor, eukaryota
CaPOPI_810	Ca2	24252139	TAA/TAAGAAA	GATCCTCAAATCGACCT CCA	TGTCACCATTGGTCTCC AAA	60.0	465	INTERGENIC				
CaPOPI_811	Ca2	24563119	TCCCC/TCCC	CCATCTACTGCCCTTGG AAA	GATCCAGGCAAGGTCAA TGT	60.1	260	INTERGENIC				
CaPOPI_812	Ca2	24943252	CTTT/CTT	AACCCCTCCAAAGAACG ACT	AGGGCCCCACTAATCC TTA	60.0	680	INTERGENIC				
CaPOPI_813	Ca2	24948166	CTTTT/CTTTT	GGTGAGACTTTCGAGGG CTA	GGCATTGAACGTTTTC CAA	59.4	295	INTERGENIC				
CaPOPI_814	Ca2	25171520	TCACAA/TCAA	GGAATGAGCTGAATGG GAA	CCAGAGGGGATGTTGAG AAA	60.0	551	INTRON	Ca_14250	T	M-type	Disease resistance protein
CaPOPI_815	Ca2	25241576	GATATATATATATA/GATATATATATA TATATATA	TATTTGGATTTTGGCTC GG	AAATGGAGGAAGGAGG GAGA	59.9	433	INTERGENIC				
CaPOPI_816	Ca2	25352886	ATTTTTTTTT/ATTTTTTTTTT	AAAGACACATGACAT AACTCCTC	ATGGGGGATGGACCTAG AAC	57.9	685	DRR	Ca_14268			Histone acetylation protein 2
CaPOPI_817	Ca2	25427657	TTATATATATATATATATATATATATA TAT/TTATATATATATATATATATATAT ATAT	TGTTGTTGAAGATGAAA TATTGGC	TTTGGCGTAGTGAAGTT GACA	60.2	723	INTERGENIC				
CaPOPI_818	Ca2	25535050	CTTTTTTTT/CTCTTTTTTTTTTTTTT	CCAGATTTGAACTGGGG AAA	AATCAAGTGGGTTCGAG TGG	59.9	551	DRR	Ca_14283	R	MYB	Integrase, catalytic core
CaPOPI_819	Ca2	25619256	CTTTTTT/CTTTTTTT	TTGAGAGACCAAGTGT CCAAA	AAGTGACTATTCCTCG GTCCCT	59.8	829	INTERGENIC				
CaPOPI_820	Ca2	25767704	GAAGTTAAGTT/GAAGTT	ATGAATTTTGGCATCCAA CC	CGTGGACAAAGATCGTG ATG	59.6	654	INTRON	Ca_14294	G	NAC	Glycoside hydrolase, family 1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_821	Ca2	26504489	CAA/CAAAA	CCGACGTCCAGTCAGAA TTT	CTCAATTGGACACCGTT CCT	60.1	772	INTERGENIC				
CaPOPI_822	Ca2	27153936	TTATATATATATATATATATAT/TTATA TATATATATATATATAT	TCCAAACTAGGTGGCAA CAA	TTGCCCACTCATTTCTT TC	59.2	478	INTERGENIC				
CaPOPI_823	Ca2	27401550	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	GCCGTTGGGTTTGAGTT AGA	CCAAATCACCTCCAGTC ACC	60.1	678	INTERGENIC				
CaPOPI_824	Ca2	27436271	CAAA/CAA	TCCTACGTATCTTTTGAT GCGA	CGTGCCCAATCTCTCAA TCT	59.7	382	INTERGENIC				
CaPOPI_825	Ca2	27560889	TTCCCTCCTATCCCTC/TTCCCTC	GGTGCATTGGGAACCT TTA	CTGCAGCATCCCTACAC TCA	59.8	767	INTERGENIC				
CaPOPI_826	Ca2	27614728	AAATAATAATAATAATAATAATAATA ATAATAATAATAATGCTAATAATAATA AATAATTGTAATAATAATAATAATAAA CAATAATAATAATAATAA/AAATAATAAT	CGCGCGAGCCATAATCT AGT	CGACGCCAATCTGCTTA TTT	62.6	625	INTERGENIC				
CaPOPI_827	Ca2	27692325	TG/T	AGACAAAACGTTCAAGT TGTCG	TCTTTAATTGCATGCGC AAA	59.3	762	DRR	Ca_15671		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_828	Ca2	27804750	TCC/TC	CAGGAAACTCTGCCITT TCG	TAGCAGCTGTATGGTGC AGG	60.0	137	INTERGENIC				
CaPOPI_829	Ca2	28157957	TTATATATATATATATATATAT/TTATA TATATATATATATATATATATATAT	GCATGGACATTCAAAA TGAGA	CCATGTCTAAGTGGCAG GGT	59.9	583	DRR	Ca_14385	O	MYB_related	SANT domain, DNA binding
CaPOPI_830	Ca2	28235432	AATATATATATATATATATA/AATATAT ATATATATATATATATA	TCCAAATAGCGACTTCC CAC	GCTGCATGTTCTTATGC TCG	60.1	849	INTERGENIC				
CaPOPI_831	Ca2	28465231	CAAAA/CAAAA	TCATCGCAGGTGTACCA TGT	GGTATCAGAGCCCACCA TGT	60.0	908	INTERGENIC				
CaPOPI_832	Ca2	28465336	AAT/A	AAGAGAGGTCACTTTGG CGA	GCAATTCACAGGTAT GCT	60.0	886	INTERGENIC				
CaPOPI_833	Ca2	28465620	A/AT	AGCTCCATTGCAAAAAC ACC	GCAATTCACAGGTAT GCT	60.1	553	INTERGENIC				
CaPOPI_834	Ca2	28569036	TGG/TGGG	TCTCCAATGATTGGAA GGC	GACTGGACGTAACCCAC GTT	60.0	913	INTERGENIC				
CaPOPI_835	Ca2	28569281	T/TC	CATCTGTAATGATGCGC CAC	GACTGGACGTAACCCAC GTT	60.1	503	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_836	Ca2	28617666	TTTTATTATTTATTTATT/TTTTATTATT TTATTTATTTATTTATT	ATCGACTCCCGAACTCAAAA	CCACGGTTCCTAGAGCCATTA	59.7	621	INTERGENIC				
CaPOPI_837	Ca2	29220253	GATATATATATATATATATATA/GATA TATATATATATATATATATATATATAT A	AGGCATGGTGTTGGAGTCAT	CTAGTTCGTAACCCGTGCGT	60.4	253	INTERGENIC				
CaPOPI_838	Ca2	29220546	GATAATAATAATAATAATAATAATAA TAAT/GATAATAATAATAATAATAAT AATAAT	CACGTGTCAAACCTTGCCAAAT	GTAACCGTTGGAGCACCACT	59.6	534	INTERGENIC				
CaPOPI_839	Ca2	29238503	A/AGTT	TGTGGAACACCAACGAA TGT	ACCTCCCCTAATGTCAATG	59.9	746	DRR	Ca_14317			
CaPOPI_840	Ca2	29238544	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAA/AAATAA TAATAATAATAATAATAATAATAATA ATAATAA	TGTGGAACACCAACGAA TGT	ACCTCCCCTAATGTCAATG	59.9	746	DRR	Ca_14317			
CaPOPI_841	Ca2	29239999	AAT/A	GGCTGCTGATCCTGTTCTTC	CTGACGGACGGACTCATTTT	60.0	482	INTERGENIC				
CaPOPI_842	Ca2	29240150	TC/TCACC	CTTAGAGCATCTCCAACGGC	GAAGCATCGTTCCTCCGTA	60.0	134	INTERGENIC				
CaPOPI_843	Ca2	29240273	ATTTTTTTT/ATTTTTTT	CTTAGAGCATCTCCAACGGC	CAACGGTGAACCTCAATATGGG	60.0	671	INTERGENIC				
CaPOPI_844	Ca2	29240382	TCCC/TCC	CTTAGAGCATCTCCAACGGC	CCTTGCACTATCATTTTCGGA	60.0	803	INTERGENIC				
CaPOPI_845	Ca2	29252004	GTT/GT	TCAAAGGTGCACTCTTGCTATT	TGGCTTCGGAAAGACTAAA	59.0	502	INTERGENIC				
CaPOPI_846	Ca2	29253047	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTA TT/TTTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT	GACACCCAAATATAGTGTCAACGA	CCCGGGTATAGGGTCTCACT	60.2	583	INTERGENIC				
CaPOPI_847	Ca2	29339791	CAAA/CAAAA	CCACAGCCCTACCTGAACAT	CCCCAAGGTATGCAGTGGATT	60.0	502	DRR	Ca_25183	TZ		Zinc finger, LIM-type
CaPOPI_848	Ca2	29444244	ATTTT/ATTTT	AAATCCGACTGTCTAACCCG	TTTTCTCTCCAATTTAGTCCAA	59.1	826	INTERGENIC				
CaPOPI_849	Ca2	29445927	AACCCGAACCC/AACCCGAACCCACCC GAACCC	TGTCTAACCCGTCTAACCCG	CCCTACCTAGGGGTGGAACAT	60.0	138	INTERGENIC				
CaPOPI_850	Ca2	29534597	ATTTTTTTT/ATTTTTTT	AGAGTCGCTCCCAAGCAATTA	GGAGTGGTTGACGTTGGATT	60.0	472	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_851	Ca2	29608982	TAAAAAA/TAAAAA	TTTGCCACAACAAACGTG	TGAAATTTCCCTACGATGCC	60.6	504	INTERGENIC				
CaPOPI_852	Ca2	29829940	TT/TTTCGAAAAAAT	CTTTTCGTCGGAGTTGTCC	TCGTCTCTGTTTTCTCGT	59.7	476	INTERGENIC				
CaPOPI_853	Ca2	29962779	G/GC	AGCCAACGGACCACTAACAC	TTGCCATTCTTCTCGTCT	60.0	237	INTERGENIC				
CaPOPI_854	Ca2	30095996	TAAAAAA/TAAAAA	CATTCGCTACATTTTGGT	GGAGAGAGGCCAATTTTCA	59.8	226	INTERGENIC				
CaPOPI_855	Ca2	30096276	TA/TAAA	CATTCGCTACATTTTGGT	GAAGCTGCTTGTGTGCCATA	59.8	876	INTERGENIC				
CaPOPI_856	Ca2	30125989	TAAAAA/TAAAAA	TTCCACTTATGGTGAATAATGATTTT	TTGTGAGCATGAGAAGTTGTTG	59.3	641	INTERGENIC				
CaPOPI_857	Ca2	30146454	CAAAAA/CAAAAAA	GCCCCAACCAATTTTGA	AAGACCCAGAACTTCCCGT	59.9	452	INTERGENIC				
CaPOPI_858	Ca2	30174020	CTT/CTTT	TTATCCCGCATATTGGA	AGTCCTTGGGACCGAAAGT	59.3	227	INTERGENIC				
CaPOPI_859	Ca2	30243585	CTT/CT	TTCTACTCCACATTTTAACGA	GCCTGTATCCAGCCATTGT	59.9	467	INTERGENIC				
CaPOPI_860	Ca2	30341034	TAA/TAAA	TGTCTTATCCTGAACCAAACTCG	ATTTGGTCAACCACCAAAA	59.8	537	INTERGENIC				
CaPOPI_861	Ca2	30342844	ATTTT/ATTT	TGCCTAATTTGACTTCC	TCTCTAATCTGCTACGCATCCA	59.0	439	INTERGENIC				
CaPOPI_862	Ca2	30342955	TAAA/TAAA	TGCCTAATTTGACTTCC	TCTCTAATCTGCTACGCATCCA	59.0	439	INTERGENIC				
CaPOPI_863	Ca2	30343145	TAAA/TAA	TGGATGCGTAGCAGATTAGAGA	CGTCACTTGGTCACTTGTG	60.0	581	INTERGENIC				
CaPOPI_864	Ca2	30343408	TTAATAAA/T	TGGATGCGTAGCAGATTAGAGA	CGTCACTTGGTCACTTGTG	60.0	581	INTERGENIC				
CaPOPI_865	Ca2	30343585	CACCAAGTGACCAAGTGAC/CACCAAGTGAC	CAATCAATAATTTGACGTCGG	CATTTACGGGGCTCTTAAA	59.4	658	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_866	Ca2	30345200	TG/T	TAAGTTGGGCGAAATCA TCC	TGGGGTGGGTGTTTGA AAA	59.9	524	INTERGENIC				
CaPOPI_867	Ca2	30361475	TATC/TATCGATC	TCCGCTAATAGTGGCAG ATAAA	ACCAATTTGTGAAAGCT GGC	58.9	617	INTERGENIC				
CaPOPI_868	Ca2	30369374	TAAAA/TAAAA	TGTACTTCCTCCGATTC CAAA	TGAATGACGACGACGGT AAA	59.6	632	DRR	Ca_12515	Q		Multicopper oxidase, type 1
CaPOPI_869	Ca2	30373739	TAAAAAAAA/TAAAAAAAA	CGGGAATGAAAAGTGGA AGA	CCAGGGGCAAAACAAG TAA	60.0	518	DRR	Ca_12514	S		Fcf2 pre-rRNA processing
CaPOPI_870	Ca2	30375213	TAAAAAA/TAAAAAA	AATTGAATCAACCCCTT CC	GGTTTGAAGCTAATGTC GTGC	60.0	737	DRR	Ca_12514	S		Fcf2 pre-rRNA processing
CaPOPI_871	Ca2	30375265	CT/C	AACCCCTTCCTTTTGT GTC	TTGATTTTGGGGTGCG TAA	60.2	963	DRR	Ca_12514	S		Fcf2 pre-rRNA processing
CaPOPI_872	Ca2	30391104	AT/ATT	TTGCATTCTCAAGGCTC AGA	TTTTGGGAGTGCTTGGT TTC	59.7	461	INTRON	Ca_12512	R		Leucine-rich repeat, cysteine-containing subtype
CaPOPI_873	Ca2	30395203	CATATATATA/CATATATATATA	CCCAACAACAACAAAG CCT	AAACCAGCATGACAAA GCA	60.0	289	INTERGENIC				
CaPOPI_874	Ca2	30433778	TA/TAA	CGGTTGGCCCTTAAGTC TAA	TCCTCAAACCCAAAATG GTC	60.0	674	INTERGENIC				
CaPOPI_875	Ca2	30447611	A/AT	CTTTTGCTTCTCGGCC TTG	CGTGCTCATCTCCATTG TTG	60.0	891	INTERGENIC				
CaPOPI_876	Ca2	30447804	TTG/TTGTG	AACAAAAGGGGTTGGAA AGC	ATCTCCTCAGCATTGTC GCT	60.3	809	INTERGENIC				
CaPOPI_877	Ca2	30449164	TAAAAAA/TAAAAAA	TGTTGCAAGAGAAAGA ACTTCA	TGACGGTGGCAATCGAT ATT	59.2	557	DRR	Ca_12507			
CaPOPI_878	Ca2	30456719	TAAAAAA/TAAAAAA	TTCTGATTCGATCTC ACC	CATACCTGGGGATGCA AAG	60.0	601	DRR	Ca_12504		WOX	Homeobox
CaPOPI_879	Ca2	30457303	A/AT	TGCATCCCCAAGGTATG ACT	CCACCATTAGATTTCGG GTT	60.3	649	DRR	Ca_12504		WOX	Homeobox
CaPOPI_880	Ca2	30461396	CTTTTTT/CTTTTTTTT	AAAAAGAAGTGGTTGTC CGC	AAACGATGCTTATCCG TGAA	59.2	929	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_881	Ca2	30480817	TAAA/TAAAA	CTGCGTCCCATTTCAG AAT	ATGTGTCTTTGGGAGCC AAC	60.1	880	INTRON	Ca_12502	G		Major intrinsic protein
CaPOPI_882	Ca2	30481523	TTTAAAAAAT/TTTAAAAAATATGTTAAA AAAT	GTTGGCTCCCAAAGACA CAT	TCGATTTTCATTAAAGTG TTGGA	60.0	631	INTERGENIC				
CaPOPI_883	Ca2	30489361	TTAT/TT	TGCAAGTTTGATGGAG TGC	TAGAACCCCAATTTTGTG C	59.8	363	INTERGENIC				
CaPOPI_884	Ca2	30490798	AA/AACA	AGCCCAATGTGTAAGCC AAC	AAGCTTTTGCAAATGGG AGA	60.0	410	INTERGENIC				
CaPOPI_885	Ca2	30514265	AAGA/AA	CACCAAAATCACCCACAA TCA	ATGGGCTGGTATATCAT GGG	60.2	972	INTERGENIC				
CaPOPI_886	Ca2	30527508	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TTGAGATGCGTTGCAAT AGG	CGTGCCACTTTCTTCCT TTC	59.8	681	INTERGENIC				
CaPOPI_887	Ca2	30553379	GAAAA/GAAAAA	TTTTTATGAGGCGTGGA AGG	CCATGAACACGCCAAAC ATA	60.1	874	INTERGENIC				
CaPOPI_888	Ca2	30555764	AAG/AAGACACGTGTAG	AAACATAACCTTTTGCC CG	TCACTCCAAGCTTCCCA AAT	59.0	257	INTERGENIC				
CaPOPI_889	Ca2	30558600	CTAT/CTATATAT	GATGCATACAAAAGTCA CCCC	GGATTGATGAAGTGGTT GGG	59.3	254	INTERGENIC				
CaPOPI_890	Ca2	30568142	AT/ATGT	CTTGTTTGTGCGAGTCG CTA	GGTCATACCAAGGCCAA GAA	60.2	453	INTRON	Ca_12495	E		Amino acid transporter, transmembrane
CaPOPI_891	Ca2	30573602	CGGG/CGGGG	TGGCTCATGACCCCTTT ATC	GGCCCCCTTTTCATTTTCA TT	59.9	709	DRR	Ca_12495	E		Amino acid transporter, transmembrane
CaPOPI_892	Ca2	30574328	TAAAAA/TAAAAAA	CCATTGAGGAGTGGAGA ACTTT	CTTGTGTGTTCCCAATG CAA	59.6	783	INTERGENIC				
CaPOPI_893	Ca2	30575054	AT/A	TGCAGCAACAATTATCC AGC	GACACACACCTCGTTTG CAT	59.8	858	INTERGENIC				
CaPOPI_894	Ca2	30622722	A/ACCGTAATCC	CTTGTCGAGAATCACGG AGC	CACGTTGACCCCTTTTG TCA	60.8	380	INTRON	Ca_12490	R		Yippee-like protein
CaPOPI_895	Ca2	30623473	TAAA/TAAAAA	TGACAAAAGGGTCAAC GTG	CCGCAATCAATTTAGCG AAT	59.6	686	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_896	Ca2	30623593	TTATGTTTTAT/TTATGTTTTATATGTTT TAT	AGTAGAGCCCGACAAGA TGC	CCGCAATCAATTAGCG AAT	59.5	483	INTERGENIC				
CaPOPI_897	Ca2	30624454	C/CT	TCATGAATGCAACGTGG TTT	TTTTGCTGTTTGTTTAC GTCAT	60.0	646	INTERGENIC				
CaPOPI_898	Ca2	30642500	GAAAAAAAA/GAAAAAAAAAAAA	TGCAGTTGCCGACAATT TTAT	TCCTCGGTAAACCAACA AGC	60.5	128	INTERGENIC				
CaPOPI_899	Ca2	30645883	TAAAAAAAA/TAAAAAAAAAAAA	TGCTGGGTTGATGGATG TAA	TGCATGCATGGATCCCT AA	59.9	816	INTERGENIC				
CaPOPI_900	Ca2	30647034	CAT/CATAT	TTGACGTACCCAACCAT TGA	CCCTCACTTAAGCCCA AAA	59.8	443	INTERGENIC				
CaPOPI_901	Ca2	30665443	ATTTTTTTTT/ATTTTTTTTT	TCATGGTGGACCGTAAT CTG	CTACTGCCTTGGAATCC TTTT	59.4	403	INTRON	Ca_12489	QI	bHLH	Cytochrome P450
CaPOPI_902	Ca2	30665911	ATTTTTTTTT/ATTTTTTTTTTT	AAAAGGAATCCAAGGCA GTAG	TCCATTACCATCATACG CCA	57.5	788	INTRON	Ca_12489	QI	bHLH	Cytochrome P450
CaPOPI_903	Ca2	30672058	ATTTT/ATT	GGGCTGATCCAACACGT TAT	CCATGGGAAACGTTGGT AAC	59.8	396	DRR	Ca_12489	QI	bHLH	Cytochrome P450
CaPOPI_904	Ca2	30672151	TGGGG/TGGG	GGGCTGATCCAACACGT TAT	CCATGGGAAACGTTGGT AAC	59.8	396	DRR	Ca_12489	QI	bHLH	Cytochrome P450
CaPOPI_905	Ca2	30675995	A/AC	TTAAGTGGGTTGCGCTT TTT	AAGAACTGGACGTTGG TGG	59.8	536	INTERGENIC				
CaPOPI_906	Ca2	30676386	GAAAAAAAA/GAAAAAAAAAAAA	ATCCACCAACGTCCAAG TTC	CCTTGGTATGACCCTAA TTCCT	59.8	532	INTERGENIC				
CaPOPI_907	Ca2	30676782	ACTAGC/ACTAGCTAGC	GCTCCAGCAAAAATAGA AATGG	TCATCAATCAAATACTT ACGCAGA	60.1	504	INTERGENIC				
CaPOPI_908	Ca2	30690091	CT/CTTT	GCGGTGTTTGTGGGT AGT	GGAGCACACAGATGCGA ATA	59.9	335	INTERGENIC				
CaPOPI_909	Ca2	30690274	A/AT	TTAGGGGAACGTGAAT TGG	CGGTCACTGCACACA CAA	59.8	444	INTERGENIC				
CaPOPI_910	Ca2	30690585	AAATAATAATAATAA/AAATAATAAT AATAATAATAATAA	TATTCGATCTGTGTGC TCC	CGTGGTTGAGTAGATGT GCC	59.8	670	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_911	Ca2	30695617	CTTTTTTTTT/CTTTTTTTTT	CCCATGCATATCACGTTTG	ACGCAGGGCCATGATACTAC	59.8	361	DRR	Ca_12487	KLB	YABBY	High mobility group, HMG1/HMG2
CaPOPI_912	Ca2	30701503	T/TAATC	TTATCTGCCCTGGATTCTGC	TTGGAAGAGGCCAAATATGC	60.2	753	INTRON	Ca_12487	KLB	YABBY	High mobility group, HMG1/HMG2
CaPOPI_913	Ca2	30702625	GAAAAA/GAAAAA	CTTCGCCCATCAATGACAC	AATCTCTTCAATCCCCGTT	60.1	566	INTRON	Ca_12487	KLB	YABBY	High mobility group, HMG1/HMG2
CaPOPI_914	Ca2	30702934	ATTTTTTTTT/ATTTTTTTTT	AACGGGGGATTGAAGAGATT	GCAAATTCTGCGGGTGTAT	59.8	508	INTERGENIC				
CaPOPI_915	Ca2	30703181	TAAAAAA/TAAAAA	AACGGGGGATTGAAGAGATT	CGCATACATACGGTGATGTC	59.8	882	INTERGENIC				
CaPOPI_916	Ca2	30704814	CAA/CAA	AAATTCAAGTCAACGCACAT	CCCACTTTGATAACAAATCC	59.2	445	INTERGENIC				
CaPOPI_917	Ca2	30720315	TATTA/T	TTGTGGCCGTTAATTTGTGA	GTTGATGTTATCAAATAACAATTCA	60.0	344	INTERGENIC				
CaPOPI_918	Ca2	30720521	CAAAAAA/CAAAAAA	TTGTGGCCGTTAATTTGTGA	CGAGTTTCTTTTCCGTCA	60.0	787	INTERGENIC				
CaPOPI_919	Ca2	30720601	TAAAAA/TAAAAA	TTGTGGCCGTTAATTTGTGA	TTGTTGTGGATGCGGTTAAA	60.0	917	INTERGENIC				
CaPOPI_920	Ca2	30732861	A/AG	TCACAGAAGGGTTTTGTGTC	AAAATTGTGAACGGAGACCG	59.9	394	INTRON	Ca_12484	T	RAV	C2 calcium-dependent membrane targeting
CaPOPI_921	Ca2	30737308	TAAAAAAA/TAAAAAAA	TTTTGCCATGGTCTTGGATT	TCAAGAAAATTGCCAACCT	60.3	618	DRR	Ca_12484	T	RAV	C2 calcium-dependent membrane targeting
CaPOPI_922	Ca2	30737463	TAAAAA/TAAAAA	TTTTGCCATGGTCTTGGATT	TGGGCCCTCATGATATTGAT	60.3	720	DRR	Ca_12484	T	RAV	C2 calcium-dependent membrane targeting
CaPOPI_923	Ca2	30773455	GAAAAAAA/GAAAAAAA	TGACTCCATCCACTTATCCCA	CCCATGAGTTTATGTTGGGG	60.3	158	INTERGENIC				
CaPOPI_924	Ca2	30788694	TTTTATTATTATT/TTTTATTATTATT	TCTATCTCACCACTCAAGC	TGCATGTCAAGTTGGATTCAT	59.3	774	INTERGENIC				
CaPOPI_925	Ca2	30790808	GAAAAAAA/GAAAAAAA	CACTCAGGGGATGAATGTACG	CGAAGTTTGACATGAGCTG	60.4	480	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_926	Ca2	30794649	TAAAAAAAA/TAAAAAAAA	TGATTCTCGACTGAAA CATGAG	TTGCATTTCACTGGAGA CGTT	59.4	641	INTERGENIC				
CaPOPI_927	Ca2	30796973	CAAA/CAAAA	CGTGTCCCTGATATTT GCC	GGGACAGTTTTGTTGT GGC	60.3	108	INTERGENIC				
CaPOPI_928	Ca2	30799752	T/TGAC	CCATGAAGTTGAAGGCA AGA	TCTCTGGTGGGAAGTT CAG	58.8	556	DRR	Ca_12478	R	MYB	Protein kinase, catalytic domain
CaPOPI_929	Ca2	30846096	GAAAA/GAAAAA	CCTTTGCGAACTTGAAG ACC	TCCTCCCTCTTGCAAGT TTA	59.9	815	INTERGENIC				
CaPOPI_930	Ca2	30848508	TTGATAAT/TTGATAAATGATAAT	TTGAAGGACCAAAATCA TGAAC	CATACAACGCAAGCTAG GCA	58.9	533	INTERGENIC				
CaPOPI_931	Ca2	30860320	TAA/TAAA	TGAACAAAAAGGTTGGG TGA	TGCTCAACTTTGACCCA TTG	59.0	487	INTERGENIC				
CaPOPI_932	Ca2	30860644	CAAA/CA	TGGGTCAAAGTTGAGCA TGA	CACCTTTGAAAGAGCT GGA	60.2	557	INTERGENIC				
CaPOPI_933	Ca2	30872234	CAT/CATAT	CAAAAGCACACAAGCC AGA	AATTTAAAGAAAGGCCG GGA	60.0	268	INTRON	Ca_12473	U		Synaptobrevin
CaPOPI_934	Ca2	30883523	TGCG/TG	CACATCAACAGGGCAAA ATG	GTGTGTGCAATCTCTGG CAT	60.0	682	INTRON	Ca_12473	U		Synaptobrevin
CaPOPI_935	Ca2	30887613	AT/A	TCAAGGAGGATTACAT GGG	AAAGGGAAAGTTGCATC ACG	59.7	826	INTERGENIC				
CaPOPI_936	Ca2	30890128	AAAATAAATAAATAAA/AAAATAAA TAAATAAA	GATGATGTAATGGGAG CCAA	CATTTGTTGAATGTTGC CCA	59.8	697	INTERGENIC				
CaPOPI_937	Ca2	30890896	ATTTTT/ATTTTTTT	CTCTTTTCGAGTCTCAC CGC	ATGCCATGACGTGAACA AAA	60.1	566	INTERGENIC				
CaPOPI_938	Ca2	30892153	A/ATGTAC	AGGATGGGTTTCTGTGT TGC	CTAAGGGGCAAAAGCGT ACA	60.0	617	INTRON	Ca_12472			
CaPOPI_939	Ca2	30901717	TG/T	TCATTGGTGTTCACGG GAT	TAGCCTTTGCAATATG GGG	60.1	886	DRR	Ca_12470	DO		
CaPOPI_940	Ca2	30945167	GT/GTCT	GACCATGGAATCGGACA AGT	CTTCTGCATCCCCTTG TGT	59.8	684	INTRON	Ca_12469	U	bHLH	Clathrin, heavy chain/VPS, 7-fold repeat

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CaPOPI_941	Ca2	30963140	GT/G	TAAGCCCATTGAACTGCTCC	CACAATTGCCTACACCATCG	60.2	780	INTERGENIC				
CaPOPI_942	Ca2	30997225	A/AT	TCACCCCTCGTATCCACAACA	ATGTGGCCATTGACAAGTGA	60.0	245	DRR	Ca_12465		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_943	Ca2	31013894	TAAAAAAAA/TAAAAAAAAA	GTGGTAGAGGGAAGGCAACA	TCATGGATTGTGGTGTGCT	60.1	615	INTERGENIC				
CaPOPI_944	Ca2	31017880	A/ATTG	TCCTTGATGCTAAGGTTGCC	GACCCATCTCCAATAGCCCT	60.2	584	DRR	Ca_12462	R	G2-like	Bacterial surface antigen (D15)
CaPOPI_945	Ca2	31041300	GGAA/GGAAGAAGAA	TACATCGGCGTTCCTTAAC	GGCTAAATTACATCTGTGGTCCTT	60.0	553	INTERGENIC				
CaPOPI_946	Ca2	31051512	GTATATATATATAT/ATATATATATATATATATATAT	CCAAACGGCCACTAATGTCT	CTGCATTTCATCCCAAGT	60.0	614	INTRON	Ca_12459	D		Rad21/Rec8-like protein, C-terminal, eukaryotic
CaPOPI_947	Ca2	31085057	T/TTAAA	CACCAACATAACAATGTCGAA	ACCACAAATGGAGAAGGTGC	58.5	942	DRR	Ca_12455			
CaPOPI_948	Ca2	31105983	TAAAAA/TAAAAA	TGTGGATTATCACCCTCCAA	TTTTTCCCGCTTAAATGTAGC	58.8	557	INTERGENIC				
CaPOPI_949	Ca2	31108593	ATTTTT/ATTTTT	TCCAACCAAGTGCAATCCA	TGCTAGATTGGCCAGGTAA	59.9	792	INTERGENIC				
CaPOPI_950	Ca2	31118846	ATATTATTATTATTAT/ATATTATTATTATTAT	AACGCCAAGTCAAGACGAGT	AAGTATGTTGCATTGCGATTTTT	59.9	352	INTERGENIC				
CaPOPI_951	Ca2	31125141	TTCT/TT	TCTCTTCGGTCTGCCATTTT	CCACATTGGGTATTTTTGGG	59.8	581	INTERGENIC				
CaPOPI_952	Ca2	31131673	GAATAATAA/GAATAATAATAA	TTTGGACAGCAAGAAGATGG	CATGCAAGAAATGCAAGGAA	58.8	473	INTERGENIC				
CaPOPI_953	Ca2	31133111	CAA/CAAA	GGTGATCAAAACATCGTCG	TTAGGTGGAGAGGGTGAGGA	60.0	807	INTERGENIC				
CaPOPI_954	Ca2	31138425	AA/AATA	TGATGAGACGTTGGTCAACA	TTTCCTCCTTGTTCACTCC	60.1	464	INTRON	Ca_12449			Domain of unknown function DUF231, plant
CaPOPI_955	Ca2	31146520	CA/CACTAATTTTAGA	CTAGAAAGTCGGCGCTATCG	TTGGCCTGAAGAATGACCTC	59.9	557	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_956	Ca2	31151939	A/AT	AGCCAAAGTGAGAAAGG CAA	AAGGATCCAAGCCCACT TCT	60.0	740	INTERGENIC				
CaPOPI_957	Ca2	31158685	GAAAA/GAAA	GGGAACCTGGATTACCA CCT	TCCATTCAATGCTCACC GTA	60.1	179	INTRON	Ca_12447	L	ERF	SNF2-related
CaPOPI_958	Ca2	31160632	ATTTTTTTTTT/ATTTTT	AGTTTGAGAGGAAACA CGCA	TTTTGAACGTCACTTTAT GATCG	59.9	426	INTERGENIC				
CaPOPI_959	Ca2	31172482	TATTTAAT/TAT	CCTTGAATAAAATATGG GGCA	TCAATAACTTTTAACAGT CCGACAA	60.0	526	INTERGENIC				
CaPOPI_960	Ca2	31172925	AATATATATATA/AATATATATATATA	TTGTCGGACTGTTAAAG GTTATTGA	TAGTGC GCGACATTTTA TGC	59.2	265	INTERGENIC				
CaPOPI_961	Ca2	31177108	ATT/ATTT	TCCAATTTGATATCGGT CTCCTG	AAACATAAAACAACGTG AGACAAA	60.3	970	INTERGENIC				
CaPOPI_962	Ca2	31178815	CTTTTTTTTT/CTTTTTTT	TGTAACAAAAAGGGAGG AAAAA	ACGCAGATGCCAAAGTT GTA	57.9	691	INTERGENIC				
CaPOPI_963	Ca2	31180716	TAA/TAAA	GGCCAATTGCTAAGTGG ATG	GCTTTGATTCTTGCAAT GTCC	60.5	364	INTERGENIC				
CaPOPI_964	Ca2	31189040	GATCA/GATCATCA	CAATAGGGTTTGCATCC CAC	TTTCATGGTTGAGAGCCA CTG	60.2	532	INTRON	Ca_12445	Q		Multicopper oxidase, type 1
CaPOPI_965	Ca2	31232642	GTTAATTAATTA/GTTAATTA	TGTCATCAAGATGCGTC AAAG	CCATTGTGATGTTGGTG GAA	59.9	830	INTERGENIC				
CaPOPI_966	Ca2	31233960	AG/A	GGGTGGAATCATGGTG AAC	TTGGTTGGAAGGAATGG AAG	60.0	436	INTRON	Ca_12440			
CaPOPI_967	Ca2	31240228	TCAA/T	CTGCCCCCACTATTTCT CAA	GAAACACTTGGCATGTT AAGGA	60.1	479	INTERGENIC				
CaPOPI_968	Ca2	31244339	AGG/AG	CAAGACTCAGGTGGGT TGT	AAATCCATTGGGAAATG CAG	60.0	547	INTRON	Ca_12439		C3H	Biotin/lipoyl attachment
CaPOPI_969	Ca2	31286944	A/ATAATG	TGGTATATTTGCACGGA CCA	AAATGCGAGTCTAAGAG GATGC	59.8	330	INTERGENIC				
CaPOPI_970	Ca2	31294019	AG/AGAGG	AGACCGTCGGTTTCAAT GAC	AAAAATCTTTAACAAGCG GGT	60.0	494	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_971	Ca2	31299649	TAAAAAAAAA/TAAAAAAAAA	GCTGCAATGGAAATGCA TAA	GCGAATTTACAATCCC ACT	59.7	972	INTERGENIC				
CaPOPI_972	Ca2	31300005	A/AG	CATTCCAATGTGCAACC TCT	GCGAATTTACAATCCC ACT	58.6	535	INTERGENIC				
CaPOPI_973	Ca2	31317559	GTT/GTTT	ATGGCAAATTATGGCC AAG	GAGTGGGTGGTTGTTT GGT	60.0	831	DRR	Ca_12431	U		NSF attachment protein
CaPOPI_974	Ca2	31352669	CTTTT/CTTT	CCCTTGCTGTGGATGGT AGT	TCCAAAATCTGCAAGAG GCT	60.0	569	INTERGENIC				
CaPOPI_975	Ca2	31355084	AT/ATT	GCATGGAAAATGAAGG CAT	GAATGCATTGCTCATTT GGA	59.9	674	INTERGENIC				
CaPOPI_976	Ca2	31365474	CT/C	TTTACGGCAGAATTGGA CCA	TGGCTTTTCCCTACTTC CA	59.2	361	INTERGENIC				
CaPOPI_977	Ca2	31367430	TA/TAGGCAA	ATTGTAATGCGGTTCCG AAG	CTCCACACGTGCCATCA TAC	60.0	485	INTERGENIC				
CaPOPI_978	Ca2	31367840	CTATA/CTA	GTATGATGGCACGTGTG GAG	CCTTCCCTTTCCTTGA AAA	60.0	399	INTERGENIC				
CaPOPI_979	Ca2	31386815	TAAA/TAA	CAGTCGAATCCGCCATA TCT	TTGGGAATCGCATTTTT CTC	60.1	587	INTRON	Ca_12422		MYB_rela ted	Plant peroxidase
CaPOPI_980	Ca2	31388110	TAAAA/TAAA	TCAGGGGACAATAACTT GGC	TCCATTACCCACTAGA CCCA	59.9	919	DRR	Ca_12422		MYB_rela ted	Plant peroxidase
CaPOPI_981	Ca2	31388227	TAAAA/TAAAAA	CATCAGTCCCCTCACTG GAT	TCCATTACCCACTAGA CCCA	59.9	707	DRR	Ca_12422		MYB_rela ted	Plant peroxidase
CaPOPI_982	Ca2	31388368	TTT/TTTTCTT	CATCAGTCCCCTCACTG GAT	CGAAACAGTTCCCGAAA GAA	59.9	866	DRR	Ca_12422		MYB_rela ted	Plant peroxidase
CaPOPI_983	Ca2	31407170	GAAAAAA/GAAAAAA	TGGAACCCAGCCGTATA AAG	TCCTTGCTCAAGGTCAT TCA	60.0	223	INTRON	Ca_12421		ERF	Protein kinase, catalytic domain
CaPOPI_984	Ca2	31419525	T/TGG	GGCTTTCCATTTTGGGT TTT	ATTCCAATGTGGAAGGA CAA	60.2	258	INTERGENIC				
CaPOPI_985	Ca2	31439958	GAAAAAA/GAAAAAA	CAAATGTCAAGGTGAAA ATCCA	TGCTCCTTATGCCAACT CCT	59.8	492	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_986	Ca2	31450111	TCC/TC	TTCCCAATCGATCTACGAG	ATTGTGGAGAATCTGCA GGG	60.0	313	INTERGENIC				
CaPOPI_987	Ca2	31456735	ATTTTT/ATTTTTT	AGCGCGCAATATGTCTA CCT	CCACTCTAGCTCGGTCC TTG	59.9	300	DRR	Ca_12418		Trihelix	
CaPOPI_988	Ca2	31534378	CG/CGG	AGGAAAGCAACGTGAAC AGC	CCAAGACAGGCAAAGAA AGC	60.4	519	INTERGENIC				
CaPOPI_989	Ca2	31534854	TT/TTCT	GCTTTCCTTGCCTGCTT GG	ACTTTGTCCACTGCCAA ACC	60.0	331	INTERGENIC				
CaPOPI_990	Ca2	31550288	CTTTTT/CTTTTTT	ACAAATATCCCATCCCA CGA	TGCACGTAAAATTGCCT AAAA	60.0	721	INTERGENIC				
CaPOPI_991	Ca2	31562756	ACC/ACCC	CACCTTAGGAATCCCCA CCA	AGCTTGAAACCCTTGAC CCT	59.8	476	INTERGENIC				
CaPOPI_992	Ca2	31657254	CTTTTTTT/CTTTTTTTT	GAACGTGGAAAACCTCC ATCA	GTTGGGAGGGTTCACCT CTG	60.0	570	INTERGENIC				
CaPOPI_993	Ca2	31670858	CGTCGCTGTCGCTGTCGCTGTCGCTG/CGTCGCTGTCGCTG	ACCGCCACCATTGTAGT CTC	CCGAGCCATCAAAAGAT GAT	60.0	434	CDS (large-effect mutations)	Ca_17848			
CaPOPI_994	Ca2	31678680	TC/T	GGAGCGCTTTAAACACA AGC	TGGAAACCAAGGTCCAA GTC	60.0	517	INTERGENIC				
CaPOPI_995	Ca2	31694754	A/AAT	GCTTTTCATAAGAAGCG TTGTAA	AATTGAGCTTGTGTATG TGGA	57.9	305	INTERGENIC				
CaPOPI_996	Ca2	31697056	TTTT/TTTTTATTT	GTGTGCAGGTAAGGCTG ACA	ATTTGGCATTGGGTTGG ATA	59.9	759	INTERGENIC				
CaPOPI_997	Ca2	31713656	TAAG/TAAGAAG	TCGGTTTCTCCTTCACC ATC	TTGTCAAACACGCAATC CAT	60.1	595	INTERGENIC				
CaPOPI_998	Ca2	31746177	AATAT/AATATAT	CGAGTTGTAAAAATTTGG CTTCC	GGGGATGTGTATTAAG GGGG	60.0	914	INTERGENIC				
CaPOPI_999	Ca2	31794099	TAA/TAAA	TGTGTACGTGTGCATGG AAG	ATCCTTGGCCTTTTGGC TAT	59.2	247	INTRON	Ca_17840			Glycine rich protein
CaPOPI_1000	Ca2	31794610	GAAAAA/GAAAAAA	ATAGCCAAAAGGCCAAG GAT	CTGGTCTGTCACTTTCA GCG	59.9	804	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1001	Ca2	31799253	TAAAAA/TAAAAA	AAATGTCAACGTGGCGTACA	GCACGAGGATTGCTATGTGA	60.0	832	INTERGENIC				
CaPOPI_1002	Ca2	31814386	CAAAAAA/CAAAAAA	GGAGGCAACAACAAGGAGAG	CCATCTTTCAAGCCAAC TCC	59.8	685	INTRON	Ca_17839			IQ motif, EF-hand binding site
CaPOPI_1003	Ca2	31828278	ATTGTT/ATTGTTGTT	AAAAATCGCCATTGTTTTGG	AAAAATAGGGAATCCGGTGC	59.8	510	INTRON	Ca_17836		MYB_related	
CaPOPI_1004	Ca2	31828392	CTTTTTT/CTTTTTT	AAAAATCGCCATTGTTTTGG	AAAAATAGGGAATCCGGTGC	59.8	510	INTRON	Ca_17836		MYB_related	
CaPOPI_1005	Ca2	31838256	GTGCGGTG/GTGCGGTGGAATATGCGGTG	ACTTGACGATGGTTTTGGC	CTAACCGCGAAACCAAA CAT	60.0	393	DRR	Ca_17834			
CaPOPI_1006	Ca2	31853745	ATTT/ATTATATTTT	CAACCGTAGCCACCTAAA	AATGCGCAAAGAAAGTT TGG	60.0	610	INTERGENIC				
CaPOPI_1007	Ca2	31853792	AA/AAGA	CAACCGTAGCCACCTAAA	AATGCGCAAAGAAAGTT TGG	60.0	610	INTERGENIC				
CaPOPI_1008	Ca2	31861522	ATTTT/ATTT	TTGCAAAATGCTTGAGAGAAAA	ATGGCCTATGCCAATGA AAC	60.0	459	INTERGENIC				
CaPOPI_1009	Ca2	31882952	CTTTATTTATTTAT/CTTTATTTATTTATTAT	TTTCTGGTGGGATCAGCTCT	GACATCCTGCGCCAGTT ATT	59.8	591	INTRON	Ca_17830	D	LBD	RZZ complex, subunit Zw10
CaPOPI_1010	Ca2	31883010	AAGAG/AAG	TTTCTGGTGGGATCAGCTCT	GACATCCTGCGCCAGTT ATT	59.8	591	INTRON	Ca_17830	D	LBD	RZZ complex, subunit Zw10
CaPOPI_1011	Ca2	31892832	TC/T	CATTTGGTGGTCAAAAGAAA	TTCTACCCAAGAAAACATGCG	60.0	473	INTERGENIC				
CaPOPI_1012	Ca2	31905190	ATTTT/ATTTT	AATAAGGTGTTTGGGGGAG	GGTATTCGTTGCGTCATGTG	60.0	450	INTRON	Ca_17827		C3H	
CaPOPI_1013	Ca2	31905735	CTACTACT/CTACTATACTATACTATACT	TTCCAACGGTGAAAACAACA	CGATATAGGGTTGGTTTGCG	60.0	207	DRR	Ca_17826	O		Zinc finger, RING-type
CaPOPI_1014	Ca2	31912393	TTATCTA/TTATCTATCTA	TGAGAAATCTCCATCCCGAG	CGCATCCTTGACAACCTGTA	60.0	650	INTRON	Ca_17826	O		Zinc finger, RING-type
CaPOPI_1015	Ca2	31920016	AATTATAATCAATTAT/AATTATAATCAATTATTATAATCAATTAT	TTCAGAAGAAGGAAACAGCACA	GATCCACAAAATTGGTTT TTCA	60.0	877	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1016	Ca2	31921460	TA/TAA	GGAAAGTCAAACCTTA AATGGGA	TCTGTATCGCATGGTTG CTT	59.9	533	INTERGENIC				
CaPOPI_1017	Ca2	31925279	GTTTTTTTTT/GTTTTTTTTT	GACCAGCCTCCCTAACCTTC	TGTTGCCGATAGACCATGAA	60.1	538	INTERGENIC				
CaPOPI_1018	Ca2	31939044	ATTTTTTTT/ATTTTTTTT	ATCACATTGCAAAGCAACGA	TGTATTCACGGTTTGGGTTTT	60.3	586	DRR	Ca_17823	R	C3H	Zinc finger, CCCH-type
CaPOPI_1019	Ca2	31945989	ATTTTTTTTT/ATTTTTTTTT	CACATGGAAGGCTAAAGGAA	CCACAAGTGTGGATGACAGG	57.8	838	INTERGENIC				
CaPOPI_1020	Ca2	32088009	TTAATAATAATAATAATAATAATA/T TAATAATAATAATAATAATAATAATA	TCAGCAAGCAAGCATTA TGG	ATGGGGAACGTTGACAG AAG	60.0	605	INTERGENIC				
CaPOPI_1021	Ca2	32127033	TGC/TGCGC	TGCAAGTTGTGATGGGT TGT	TGCTGTTCTGCACGGA GTC	60.0	650	INTRON	Ca_17812	O		Ubiquitin
CaPOPI_1022	Ca2	32146442	AT/ATT	ATTCCCACGCCACTTAG ATG	CACTGTCACAGAGATAA GATGCAA	60.0	807	INTRON	Ca_17808		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_1023	Ca2	32161753	TCCCC/TCCC	AGGCCATTAAGCATGAC ACC	TTCTTGGAACCCCTGCAT ACC	60.0	867	INTERGENIC				
CaPOPI_1024	Ca2	32163428	CATA/CATATATATATA	TCAAAGAGACATGATTT GTCCA	GGTCAATCAGCTGTGAG CAA	59.6	415	INTERGENIC				
CaPOPI_1025	Ca2	32173774	TC/T	ATGTTTTGATTGGGGCT TTG	TAAATCAGCCCTTTTGG TGG	59.8	631	DRR	Ca_17806		WRKY	Glycoside hydrolase, family 9
CaPOPI_1026	Ca2	32209131	T/TG	GCAAAGATAGACACCAC CCC	AACCATTCCCATGGAAC AAA	59.4	577	INTERGENIC				
CaPOPI_1027	Ca2	32209334	CTATATATA/CTATA	TCCATGGGAATGTTTT GAT	TTGAAGAGGAAGTTTTG GCA	60.0	342	INTERGENIC				
CaPOPI_1028	Ca2	32209671	TC/TCC	TCCATGGGAATGTTTT GAT	TTTTAGTGTGCACCAAT GTCAA	60.0	899	INTERGENIC				
CaPOPI_1029	Ca2	32210099	CA/CAAATA	TCAGCTTCAATTATCTCC AACAA	TCGGCGACAAAAATCAC ATA	58.9	644	INTERGENIC				
CaPOPI_1030	Ca2	32210241	TA/T	TGACATTGGTGACACT AAAAA	CCACGTCATCTTCCTTT GGT	59.1	505	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1031	Ca2	32211970	A/AG	ATGGAATTCTGAATGGTGGG	AAAACCACAAAATGGGGTCA	59.6	763	INTERGENIC				
CaPOPI_1032	Ca2	32213171	GTGAT/GTGATGAT	CAACATGACAAGGACTTTCCAA	TTACCGGTATCGCAAGGAAC	60.0	529	INTERGENIC				
CaPOPI_1033	Ca2	32213424	CAAA/CAAAA	AGGGATAGATAACGGCACA	AAGGCCCTGCTAGAATGATG	59.6	504	INTERGENIC				
CaPOPI_1034	Ca2	32243132	TCAA/TCAACAA	TCTGAGGGGATTCGTTATGC	TCCATAACTCTTGCCAAACC	60.0	524	CDS (large-effect mutations)	Ca_10292		bHLH	Protein kinase, catalytic domain
CaPOPI_1035	Ca2	32282292	CATTAGTGATT/CATTAGTGATTGATT	ACCCTCCAGGGTGCTAAGAT	GCCCAACATTTTCTGGTTGCT	60.0	726	INTRON	Ca_10287	S		
CaPOPI_1036	Ca2	32293632	AAGAAATTCAGAAATTC/AAGAAATTCAGAAATTCAGAAATTC	AAACCCTACGAAGTTTGCA	TTGTCACCCGTCCAAATACA	59.6	237	INTERGENIC				
CaPOPI_1037	Ca2	32332565	AAAAATAAATAAATA/AAAAATAAATAAATAAATAAATA	CGCCAAAGTCATTGATTGAA	CATCTTGTACAGCCATAGCCA	59.7	338	INTERGENIC				
CaPOPI_1038	Ca2	32340350	TGG/TG	TCCATTCAATGCTTTCAAATTC	TTGTGGTCATTTAAGGTGGTTG	59.1	530	INTERGENIC				
CaPOPI_1039	Ca2	32341023	GAAT/GAATGTTAAAT	CAACCACCTTAATGACCACAA	AAAAACAATGTCATGCAGAGG	59.8	682	INTERGENIC				
CaPOPI_1040	Ca2	32353326	G/GA	GAACGACAACAATTCGCCT	CAATGGATTCTTTGGCCTT	60.1	513	DRR	Ca_10283			
CaPOPI_1041	Ca2	32353407	TGAAC/T	GAACGACAACAATTCGCCT	CAATGGATTCTTTGGCCTT	60.1	513	DRR	Ca_10283			
CaPOPI_1042	Ca2	32357617	CTTT/CTTTT	TCCCAACTCTTCGAATCGT	TTGGATGATAGACATTGAAATTTTG	59.7	367	INTERGENIC				
CaPOPI_1043	Ca2	32358261	CAAAAAA/CAAAAAA	TCAAAATTTCAATGTCTATCATCCA	GCGAGGATGAGAAGTTGTTGT	59.7	658	INTERGENIC				
CaPOPI_1044	Ca2	32362657	TAAAAAA/TAAAAAA	GCAAAAGCACAACTCAATCA	AATGACCACAATTTGCATGTA	59.7	260	INTERGENIC				
CaPOPI_1045	Ca2	32369826	CT/CTCGT	TGGTTTCAAGGTCTTCCACA	GAAAAGTTAAATCCAAATAACATTC	59.1	794	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1046	Ca2	32379585	AATTAAATTTT/AATTAAATTTTGATTAAATTT	TGTGCGAGTTTATTGCGTA	CATTGGTTCAAATGTCATGG	60.3	624	INTERGENIC				
CaPOPI_1047	Ca2	32380306	GTTTGAATTTAATTA/GTTTGAATTTAAT	AACTAACTTTTCGCAGC	GGCAACTTGGCCAACAC	59.9	587	INTERGENIC				
CaPOPI_1048	Ca2	32393042	ATTTTTTTT/ATTTTTTTTT	TGCCCATCCTTATGCTCTTC	ATCACGTGCAACCACAA	60.2	626	INTERGENIC				
CaPOPI_1049	Ca2	32393117	T/TC	TGCCCATCCTTATGCTCTTC	ATCACGTGCAACCACAA	60.2	626	INTERGENIC				
CaPOPI_1050	Ca2	32393187	AATAT/A	TGCCCATCCTTATGCTCTTC	ATCACGTGCAACCACAA	60.2	626	INTERGENIC				
CaPOPI_1051	Ca2	32393441	TGG/TGTGGG	TGCGACTTTTTCGTGTGA	GGGCTTGTGACGCAT	59.5	588	INTERGENIC				
CaPOPI_1052	Ca2	32393633	TAACATAATAA/TA	GACTTGTGGTTGCACGT	GGGCTTGTGACGCAT	59.6	445	INTERGENIC				
CaPOPI_1053	Ca2	32399194	T/TATTAATGTCTAA	TCTTGCACGGGTGAGAA	CCTATTGAAGAGTGCC	59.4	587	INTERGENIC				
CaPOPI_1054	Ca2	32399302	ATTTTTTTTT/ATTTTTTTTTT	AATTTGGGGCACTCTTCAAA	GCCTCTTCAAAGTCGTTCA	59.5	219	INTERGENIC				
CaPOPI_1055	Ca2	32417284	ATTTTTTTTT/ATTTTTTTTTT	AAATTTGCGTGGAAGGTTG	CTCTGGTGGCATGTATCAA	60.0	207	INTRON	Ca_10278		bHLH	Protein kinase, catalytic domain
CaPOPI_1056	Ca2	32423881	CAAAA/CAAAAA	TGAGGCATGATAATTGAGCG	TGTTGTTCATCAATCACGCAG	59.8	536	DRR	Ca_10277			Protein of unknown function DUF247, plant
CaPOPI_1057	Ca2	32476919	ATGT/AT	CATGGATGGTGCTTCAATG	CAACTGCAATGTTCCATATTG	59.9	885	DRR	Ca_10273	R	C3H	Leucine-rich repeat
CaPOPI_1058	Ca2	32480670	T/TA	TCCACATGCTTCCAATCAAA	ACCACTCCAACCAAGTCGTTT	60.0	584	INTERGENIC				
CaPOPI_1059	Ca2	32480992	GTTT/GTT	CATGCTTCCAATCAAACACG	CAACGCCTCAAGTAGGGTA	60.1	740	INTERGENIC				
CaPOPI_1060	Ca2	32481790	ATATAT/A	GGGTGGAATGCAGAAGAAA	AAGCTTTCGGTGATTGCTGT	60.1	535	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_1061	Ca2	32642955	ATTTTTTTTT/ATTTTTTTTT	CAAAGTTGAGGAAAGGC CAG	GGAATCACCCATCCACA TTC	59.8	869	DRR	Ca_10258			
CaPOPI_1062	Ca2	32713700	TTTTTTTT/TTTTTTTTTT	AACGCATCGGTAACAC TCC	GAGGTACTACAGCTTGC CCC	60.0	234	INTERGENIC				
CaPOPI_1063	Ca2	32713895	CAAAAAA/CAAAACAAAAAA	AACGCATCGGTAACAC TCC	TGTTTTGCAGCAAGATG TCC	60.0	695	INTERGENIC				
CaPOPI_1064	Ca2	33257195	ATTTTTTTTT/ATTTTTTTTT	ATCGCATTTTGCCTTTGT TT	GCTGTCGTTTGACGAT AAA	59.6	801	INTERGENIC				
CaPOPI_1065	Ca2	33306373	TTATATATATATATATA/TTATATAT ATATA	GAATCCGTTTCCGAGTT TGA	TCAATGGAATCAAAGTT GAAGG	60.1	644	INTERGENIC				
CaPOPI_1066	Ca2	33345639	GTT/GT	CTCCATTTTGGGCAGGT TTA	GGATGATCTGTTTTTCG CGT	59.9	573	INTRON	Ca_10191	T	FAR1	Protein kinase, catalytic domain
CaPOPI_1067	Ca2	33346809	C/CA	ATGCACATGAACCGATT GAA	AAACAAGGTTGAATCAC GCC	59.9	718	INTRON	Ca_10191	T	FAR1	Protein kinase, catalytic domain
CaPOPI_1068	Ca2	33398441	TACACAC/TACAC	AGAGCCTACAGCAAGCC AAA	AAATGCAGGGTCACAAC ACA	60.2	205	DRR	Ca_10186	T	M-type	Disease resistance protein
CaPOPI_1069	Ca2	33405227	AATATATATATA/AATATATATA	AAAGAGACATGACTTTG TCCATCA	TTTCGCTACCCATCATAC CC	60.0	586	INTERGENIC				
CaPOPI_1070	Ca2	33639777	TAAAAAAA/TAAAAAAA	CGACGGAATAGTTTGCT CTCT	CGGAAAACCGTAGCTTA ATACG	58.6	892	INTERGENIC				
CaPOPI_1071	Ca2	33715359	ANNNNNNNNN/ANNNNNNNN	CAAAAGGCGTGCATGAA TTA	CTTGCCCTATTTTCTCG CG	59.7	271	DRR	Ca_10165	K	G2-like	SNF2-related
CaPOPI_1072	Ca2	33959397	ATATTTATTTATTT/ATATTTATTT	GGCTAATTTTCGTTATAT GGATGC	ACTAGTGATGGCCGAAA TGG	60.1	764	INTERGENIC				
CaPOPI_1073	Ca2	33984310	CTATATATATATATATATATATA/C CATATATATATATATATATATATAT A	TGGCTATGATACAATT GGC	CCCTTTGCAAGAGACTC CAA	59.5	869	INTERGENIC				
CaPOPI_1074	Ca2	34028835	AC/A	AAAGGGGTTTGGCTAT GCT	CATGATCATAATTGCATG GAAAA	60.0	229	INTERGENIC				
CaPOPI_1075	Ca2	34353805	GTTTTTTTT/GTTTTTTTTT	AGTTGAAGGAGTGCATG AGGA	TAGGAGGCATATGTGAG GGG	59.9	633	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1076	Ca2	34355206	CTTGGGCT/CTTGGGCTTTGTGGGCT	TCTTTGATGCAATGCCA GAG	ATCATTGAGGTGCCAT CAT	59.9	975	INTERGENIC				
CaPOPI_1077	Ca2	34355457	TAAAAA/TAAAAAA	ATTCTTGGGCTGTGTTT TGG	GGGTGATGAGGACTGG TTGT	60.0	725	INTERGENIC				
CaPOPI_1078	Ca2	34515091	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTAT/ TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTAT	TGCCAATGTAATGATTA GGA	AGCGTAAGTTTCGAGGA CCA	59.0	766	INTERGENIC				
CaPOPI_1079	Ca2	34654101	GTATATATATATATATATATATATAT/ GTATATATATATATATATATATATAT	AGGACGAGACAAAATGA GCC	TGGAACCAAGGTCCAA GTC	59.3	219	INTERGENIC				
CaPOPI_1080	Ca2	34683764	TC/TCC	GTTTTTCGCAACCACT TTC	CGCTTTTTGCACTAACC TCC	59.6	682	INTERGENIC				
CaPOPI_1081	Ca2	34684386	CAACGTTAAC/CAAC	ACAATACTGCGGCCTGT TTC	GATTCCGATCGTTTTTCA CG	60.1	830	INTERGENIC				
CaPOPI_1082	Ca2	34684923	ATTTTTTT/ATTTTTTTT	TCGTGAAAAACGATCGG AAT	TGCTTGATTTTAATGGAT GCC	60.4	550	INTERGENIC				
CaPOPI_1083	Ca2	34685252	CATAAATAAATAAATAA/CATAAATAAA	TCGTGAAAAACGATCGG AAT	TGGAGAGAAACAAAATG GGG	60.4	816	INTERGENIC				
CaPOPI_1084	Ca2	34685921	TAAAAAA/TAAAAA	CCAAACTGGGGAGAA CAA	TACGATAGGGGATCTC ACG	59.9	503	INTERGENIC				
CaPOPI_1085	Ca2	34983521	AATATATATATATATATATATATATAT ATATATATATA/AATATATATATATATATA TATATATATATATATATATATATA	CAAATGCATGCTCCCT AAT	CTAAAGCCCAAGCTG CAC	59.9	450	INTERGENIC				
CaPOPI_1086	Ca2	35258590	A/ATT	AAAAAGTTTTAACACGG AGGTTTTT	TGTTGTTGGATTGGACA TGG	59.8	487	INTERGENIC				
CaPOPI_1087	Ca2	35288109	ATTTTTT/ATTTTTTT	TGCTTTATAGTGCTATTA TGTGCCA	CGTCATTAAGGGGAA CCAA	60.1	757	INTERGENIC				
CaPOPI_1088	Ca2	35288455	TT/TTAT	TTCGATGGTATGCAGTA ATTGG	TTCCCATGAAAGAGAGG TGG	59.9	433	INTERGENIC				
CaPOPI_1089	Ca2	35289402	ACCCCC/ACCCC	ACCCACCTCTTTTCTTG GG	TGGTCCTCGAAATTGT AATGA	60.3	609	INTERGENIC				
CaPOPI_1090	Ca2	35298866	AA/AACA	TGGGGGCTTAGAGCTTT GTA	CGATGTTGTGATCTGA TATCGT	59.8	527	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1091	Ca2	35303488	ATTTTT/ATTTTTTT	TTCCGAATAAGGATTTCTGG	ATGGTTTGGGAAAAGAACCC	58.2	137	INTERGENIC				
CaPOPI_1092	Ca2	35304698	C/CG	GCTTGGAAACAGCCTCAGAC	CAGGGTGGTACTGCAATGTG	60.0	536	INTERGENIC				
CaPOPI_1093	Ca2	35329169	AATATATATATATATATATAT/AA TATATATATATATATATATAT	CAATTTTGAAGACGATTTTGA	TGTCCCGAAAAAGTTCA TCC	59.1	330	INTERGENIC				
CaPOPI_1094	Ca2	35944964	CAAAA/CA	TCCAACCATACCTGAAAGGC	CTCGTGCGAACTTGTGTGTT	59.9	313	CDS (large-effect mutations)	Ca_09769			Ferredoxin-dependent bilin reductase
CaPOPI_1095	Ca2	36146623	GAAAAA/GAAAAA	AAACAGCAACAAAAATCCAA	TTTGAAATCAAGAGGTGGG	59.5	201	INTERGENIC				
CaPOPI_1096	Ca2	36146917	TCCCCC/TCCCCC	AGGGAAACCCACCTCTTGAT	AAATCCAAAGTGCTTGCGTT	59.8	623	INTERGENIC				
CaPOPI_1097	Ca2	36224008	CTTTTTTTTT/CTTTTTTTTTT	TTTTCACCACGACACACAAA	TGCACGTTTATAAGGAATCGG	58.6	354	INTERGENIC				
CaPOPI_1098	Ca3	62942	AATATATATATATATATATA/AATAT ATATATATATATATATATATA	TTCTCTCGAGGATAGTCGGA	AGTTAAACGAGGGGTTTGCC	57.6	936	INTERGENIC				
CaPOPI_1099	Ca3	135372	CA/C	GTTGTAATGGGGCTTAGGCA	TTGGTCGTTTGAGCCTTTCT	60.0	478	INTERGENIC				
CaPOPI_1100	Ca3	213670	AATATATATATATATATAT/AATATATA TATATATATATATAT	TTCTTTTCCAATTTGCAAGG	TCACGTAGAATGCTATCACTTTGA	60.0	544	DRR	Ca_22935	M	MYB_related	Glycosyl transferase, family 48
CaPOPI_1101	Ca3	451560	ATAACGTGATCTTA/ATA	AGCAGAAAGGAGAATGGGT	ACGGTGAAGCTCCGAAATA	60.1	734	INTERGENIC				
CaPOPI_1102	Ca3	454494	AGGG/AGG	GGATTGGAGTGTTCAAGCAT	TTGTCATTAGTTTCAATCTCACCAA	59.9	460	INTERGENIC				
CaPOPI_1103	Ca3	454633	GATATATATATATAT/GATATATATATAT	GGATTGGAGTGTTCAAGCAT	TTGTCATTAGTTTCAATCTCACCAA	59.9	460	INTERGENIC				
CaPOPI_1104	Ca3	474304	GTTTTT/GTTTTTTT	ACGTTGCGAGCAGAGATTTT	TTGGCTTCTGAATTTGTTCC	60.0	655	INTERGENIC				
CaPOPI_1105	Ca3	571479	GTT/GTTGATT	GTGAGTGGTGAGGGCCTAAT	TTGCATACCTCGTATCATCCC	59.0	407	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1106	Ca3	613347	ATTTTTTTTT/ATTTTTTTTT	TGGAGCTTTGTTTGGACCT	AGTAAGTGTGTCGTTGGC	59.7	409	INTERGENIC				
CaPOPI_1107	Ca3	726429	ATTTTTTT/ATTTTTTTTT	TCCTGTATCTTACCAAAACAGGC	GTTTGTGTGTCGGCTTACGGT	59.6	715	INTERGENIC				
CaPOPI_1108	Ca3	781722	CAA/CAAAA	AAACGCGCCACTAATGACT	AGCAAGAGTGCAAAGTCGGT	59.8	546	DRR	Ca_22643	V	B3	Protease inhibitor I4, serpin
CaPOPI_1109	Ca3	794982	GTTTTTTTTTT/GTTTTTTTTTT	TAGAGGGAGGAGGTGCAAGA	GGTGATATAGACGGGGCAGA	59.9	686	INTERGENIC				
CaPOPI_1110	Ca3	939073	GTT/GTTTT	ATTGTTCTGCTCTGGGTTG	GGGACCACAGCACCTATGTT	60.1	296	INTERGENIC				
CaPOPI_1111	Ca3	943806	ATCT/ATCTCT	GTAATTCATCCCATGTCCC	AGCCTGGTAAGCCTTTTGT	60.0	515	INTERGENIC				
CaPOPI_1112	Ca3	1149110	TAAAAAAAAAAAA/TAAAAAAAAAAAA	TGTGCAATCGTTTTAACCCA	TGAGGGGTAATTTGAACCGA	60.0	272	INTERGENIC				
CaPOPI_1113	Ca3	1149320	ATTTTTTTTT/ATTTTTTTTT	TGTGCAATCGTTTTAACCCA	CCCTTACCACAAAATCAACTCA	60.0	719	INTERGENIC				
CaPOPI_1114	Ca3	1288242	GTTTTTTTTTT/GTTTTTTTTTT	TGGTGAGATCAACGATACGC	TGTAACAAATCTCCGAGGA	59.7	371	INTRON	Ca_19421	R		
CaPOPI_1115	Ca3	1371048	CAAAAAAAAA/CAAAAAAAAA	CGGATCTCAGTTCGTGGGTA	CAGAGAGAGCGAGAGGGAGA	61.1	567	INTERGENIC				
CaPOPI_1116	Ca3	1403982	GAA/GAAGAAA	TCCCCCGTAATAGGTGCATA	TCITTTGTTTCTGCGAACCT	60.2	521	INTERGENIC				
CaPOPI_1117	Ca3	1533357	TCAAAA/TCAAACTCCAAA	ACCCAAAAGCTAACTTGCCA	GCATCAACAAAGCAGCAGAA	59.7	533	INTERGENIC				
CaPOPI_1118	Ca3	1534003	AAACTGCAACTAACT/AAACTGCAACTAACTGCAACTAACT	TTCTGCTGCTTTGTTGATGC	GTGGATGGGTGTTTTCCATC	60.1	774	INTERGENIC				
CaPOPI_1119	Ca3	1573297	TAAAAAAAAAAAA/TAAAAAAAAAAAA	ATAAGACCAAAGAAGCGGCA	GCATGCAATTGTTTGACAC	59.8	607	INTERGENIC				
CaPOPI_1120	Ca3	2065051	AATTATTATTATTATTATTATTATTATTAA/ATTATTATTATTATTATTATTATTATTAA	CGACCATGTAGTGAGGCAAAA	AATAATTGCCCTACACAACAA	59.7	685	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1121	Ca3	2176981	GATTATTATTATTATTATTATTATTATTATTATTATTATTATGATTATTATTATTATTA/GATTATTATTATTATTATTATTATTATTATTATTATTATTATGATTATTATTATTATTA	ACGGATTGTGTTTTGCTTCT	CCTCTTCTTCGGTGATCTTTTG	57.3	906	INTERGENIC				
CaPOPI_1122	Ca3	2273008	CAAAAAAAAA/CAAAAAAAAA	TAAAGGATCGGACCCACTTG	GC GGATCCAAGAGTTCAATC	59.9	822	INTERGENIC				
CaPOPI_1123	Ca3	2327052	CAAAAAAAAA/CAAAAAAAAAA	GATACGGAACCATCGCACTT	TTGGTTTCGTTCTCCATTCA	60.0	343	DRR	Ca_19393	K	MYB	SANT domain, DNA binding
CaPOPI_1124	Ca3	2414966	A/AC	TTAATGAGGGGCTGAATTGG	AAGCGTACCTGTGGGAATTG	59.9	259	INTERGENIC				
CaPOPI_1125	Ca3	2855993	TAA/TAA	CTTGTTGGAATTGCATGTG	CGTTTTGGAAGGTAGGGTGT	60.0	514	INTERGENIC				
CaPOPI_1126	Ca3	2930472	ATCTC/ATCTCTC	AGGCGATGGAGGATAAAACC	CGGAAACGAGTGAAACC AAT	60.3	502	INTRON	Ca_22158	D		Tetratricopeptide repeat-containing
CaPOPI_1127	Ca3	2962592	TTTATTATTATTATTATTATTATTATTAT/TTTATTATTATTATTATTATTATTATT	AGAGGCAACAAGAACC GAA	AACTCGGTGCCAACAGTCTT	59.9	596	INTERGENIC				
CaPOPI_1128	Ca3	3022233	A/ATTTTCC	AGTTTTGGTAATTGTTGTGTTTATTT	CTCTAAGCCCCACAGATCG	57.8	328	INTERGENIC				
CaPOPI_1129	Ca3	3054800	TAAAAAAAA/TAAAAAAAA	TCTACGTATCTCTCGGTGCG	TGCTTCTTCGTTGTTGCCA	59.1	639	INTERGENIC				
CaPOPI_1130	Ca3	3185857	TAAAAAAAA/TAAAAAAAA	CGCCTCTCTTTTCTATGCG	TGTTGCTGTTGTTGCCTCTC	60.1	468	INTERGENIC				
CaPOPI_1131	Ca3	3235341	AGCTTCAGTCGCT/AGCT	TGGAGTGAGCTGTGGTTGAG	TGGTCACCACTTGGGTGTTG	60.0	840	INTERGENIC				
CaPOPI_1132	Ca3	3235471	TAA/TAA	ATAGGCCAAGCAACCAAGA	GACGATGGTGAAGATGACGA	59.7	663	INTERGENIC				
CaPOPI_1133	Ca3	3235549	GCACACA/GCACACACA	ATAGGCCAAGCAACCAAGA	GACGATGGTGAAGATGACGA	59.7	663	INTERGENIC				
CaPOPI_1134	Ca3	3272993	TTATATATATATATATATATATATATATATA/TTATATATATATATATATATATATATATA	TTGTAGTATCCCGACAA TGTA AAA	TGATTCAACAATGATCCCA	57.7	687	INTERGENIC				
CaPOPI_1135	Ca3	3411224	CATATATATATATATATAT/CATATATATATATATATATATATATATATAT	TGAATTTTTAAATGATTTCTGCAA	ATAGTCGGCAAAACCTCCT	59.1	785	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1136	Ca3	3424341	CAAAAAAAAA/AAAAAAAAAA	TTGCTCATGCGGTCTATCAA	CGTTGACAAAGGGATCGAGT	60.4	600	INTERGENIC				
CaPOPI_1137	Ca3	3632559	ATTTTTTTTTTTTT/ATTTTTTTTTTTTT	TTTGAGTCTAACCCGAACTAA	GTGGGGTAGGCAGAGACAAA	59.6	765	INTERGENIC				
CaPOPI_1138	Ca3	3818047	GT/GGAT	ATGCTCTGCACTTGCACTA	TTCATCGCCTCAAAGTTGTTG	59.9	707	INTERGENIC				
CaPOPI_1139	Ca3	3847338	CATATATATATAT/CATATATATATATAT	AGGAAGAGTGGAGTTGCGAA	ATTTTGGTTCGGAGGCTTTT	60.0	496	INTERGENIC				
CaPOPI_1140	Ca3	3881329	AAAAATATATAAAATATATAAAATA/AAATATATAAAATATATAAAATA	AGGTAGGCAAGTCTGAGGCA	CAACGCATGACCAAGACAG	60.0	773	INTERGENIC				
CaPOPI_1141	Ca3	3962696	AAAAATATTT/AAAAATATTTAATATAAAATATTT	AGTTCATGGGCTTTTCCTT	AGACTGTGGCACACAATGGA	59.9	552	INTERGENIC				
CaPOPI_1142	Ca3	4042829	GATATATATATATATATATATATAT/GATATATATATATATATATATATAT	ACACGAAGAGCAGGATCGTT	AAACAAAAATAAAACTCGGAGACA	59.9	743	DRR	Ca_21325	QR		
CaPOPI_1143	Ca3	4073796	CT/CTT	CTCAACATCCACCATGC AAT	TGCAAAATTCATCAAATGCATAA	59.4	746	INTERGENIC				
CaPOPI_1144	Ca3	4076583	ATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT/ATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	ATAGTCCTCACCCACGCATC	AAGCGTACCTGTGGGAATTG	60.0	607	INTERGENIC				
CaPOPI_1145	Ca3	4622794	ATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT/ATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	TTGTCAAGTTAGGGCACAATTTT	TCTTGAAGTGTGTGGCCATT	59.9	627	INTERGENIC				
CaPOPI_1146	Ca3	4689138	TAAAAAA/TAAAAAA	CAGCTTGCATTTGCTTTTGA	TTGCTCCTACGTATCTCCCG	60.1	888	INTERGENIC				
CaPOPI_1147	Ca3	4965548	ATTTT/ATTTT	CGGGGAATGTGATTGATAGG	GTTGGAGAGATCGGTGGAAA	60.1	948	INTERGENIC				
CaPOPI_1148	Ca3	4965627	T/TGAG	TGCAAACTCGGAGCAGAGAA	GTTGGAGAGATCGGTGGAAA	59.7	510	INTERGENIC				
CaPOPI_1149	Ca3	4966098	CTTTTTTT/CTTTTTTT	TTTCCACCGATCTCTCC AAC	AAACCCGCTCCTTTCAA AAT	60.1	514	INTERGENIC				
CaPOPI_1150	Ca3	4975195	AATATATATATATATA/AATATATATATA	CAAAGTTCAATACGCCAGCA	AGGTTTTGGCGTAACTCCCT	59.9	455	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1151	Ca3	5182639	ATTTTTTTTT/ATTTTTTTTT	TCTCTTTCTAAAAGTAGG CAACCA	TTGAGGTGCCAAAGCT ACT	58.7	492	INTERGENIC				
CaPOPI_1152	Ca3	5239462	AATATATATATATATATATATAT/AA TATATATATATATATATATATATAT	TGAGATCAGTTTTGTG GAGGA	CAGTCACCACCCTTGCT TTT	59.7	482	INTERGENIC				
CaPOPI_1153	Ca3	5270478	TATCAATC/TATC	ACGAAACGAAAGCGAGA AAA	CGACCTCGAAATAATCG GAA	60.0	521	INTERGENIC				
CaPOPI_1154	Ca3	5286221	ATTT/ATT	CACCCCTCCCAAACAT CT	TTGTGAGTGCATTTGAT TTTGTT	59.8	876	INTERGENIC				
CaPOPI_1155	Ca3	5288032	AATATATATATATATATATAT/ATA TATATATATATATATAT	AGAAGGTCGCATCTCCA AGA	TGGCACTTGATTCAC TGC	60.0	456	INTERGENIC				
CaPOPI_1156	Ca3	5347423	CAATAATAATAATAATAATAATA ATAATA/CAATAATAATAATAATA TAATAATA	TTGCTCCTACGTATCTC CCG	TTGTGACAATTTGATGG TTCTAAA	60.2	563	INTERGENIC				
CaPOPI_1157	Ca3	5502243	TG/T	TGCGTTTTTCTGCATTC TG	ATTCTGCGCGACTATCA ACC	60.0	661	INTERGENIC				
CaPOPI_1158	Ca3	5507746	AATATATATATATATATATATATAT ATAT/AAATATATATATATATATAT ATATATATATATATAT	TATTTTGGATTTTGGGCT CG	GGAGGGATAAGGTTTCT CGC	59.9	427	INTERGENIC				
CaPOPI_1159	Ca3	5520403	GTATATATATATATATATATATA/G TATATATATATATATATATATA	CAAATGACGACGACGAT GAC	GAATGATGACAATGCGG TTG	60.1	503	INTERGENIC				
CaPOPI_1160	Ca3	5689325	ATTT/ATT	TTGGTCAATGTGGCTTC TCA	TGAACCTGAGCGTGTG ACC	60.2	439	INTERGENIC				
CaPOPI_1161	Ca3	6243942	CTTATT/CTT	TGATGGACTTCGTGCTC TTG	CCTCAGGATAAAACAGC CCA	60.0	298	INTERGENIC				
CaPOPI_1162	Ca3	6289426	CATATATATATAT/CATATATATATAT AT	CGGTTCCAGAACTGCATT GAA	CCTTACAAGGCCACCA ATA	59.8	457	INTERGENIC				
CaPOPI_1163	Ca3	6386934	TGG/TGGG	TGTACGAGAAGGTCGTG TGC	GCCCAACAGCAAGCTAT TTC	59.9	574	INTRON	Ca_24834		Trihelix	
CaPOPI_1164	Ca3	6587330	T/TA	TTGAAGGGTTCATGAA TGA	GGAGGTCGAAAATGACC AAA	60.0	741	INTERGENIC				
CaPOPI_1165	Ca3	6664320	TAAAAA/TAAAAAA	TGAAATTATGGGTGGGC ATT	GCTGAAAAAGTGCCGAA GAA	60.0	569	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1166	Ca3	6672422	TTTTATTATTATTATTATTATTATTAT /TTTTATTATTATTATTATTATTATTAT TTTAT	GCGCCGCAATAGAATAG AAG	CAACAAAGGGAGGCAAA TGT	60.0	672	INTRON	Ca_25772	A		
CaPOPI_1167	Ca3	6772905	GTTT/GTT	TCCCTTTGTCTTTTCGCA CT	CACTGCCGTTCTTCACT TCA	59.9	383	DRR	Ca_16559	R	NAC	Pentatricopeptide repeat
CaPOPI_1168	Ca3	6774064	T/TTAA	TTTGCTGGACTTTGAAG CCT	CCCGGTCTAGAGAGAA AGA	60.0	640	DRR	Ca_16559	R	NAC	Pentatricopeptide repeat
CaPOPI_1169	Ca3	6788233	AATTTATTAT/AAT	TTTTTCACTATTGTGTGA AATCAGT	TTTCCTACCATATTCCTG CT	57.0	826	DRR	Ca_16556	R	NAC	Pentatricopeptide repeat
CaPOPI_1170	Ca3	6821985	TTATATATATATATATATATATA/TT ATATATATATATATATATATATATA TATA	GCGTGATCCCAAGCTAC AAT	CATCTTTTAAGGTGCGG GTG	60.1	139	INTERGENIC				
CaPOPI_1171	Ca3	6838667	AGCA/AGCAGGATCCAATGCAATGGCA	GGAACCCCAACATCATC ATC	GCAGCCAATTTGTTGC ATA	60.0	547	CDS (large-effect mutations)	Ca_16550	R	bHLH	WD40 repeat
CaPOPI_1172	Ca3	7076805	CG/CCCGAATGTG	TCTTCGATTCCATTCCAA CC	TTGGGGGAGACGATATT CTG	59.9	701	INTERGENIC				
CaPOPI_1173	Ca3	7367436	CGAAGAAGA/CGAAGA	TGATTGTTTGTCTGGTG GGA	CACTCTCTCCTTGGCC TTG	59.9	331	INTERGENIC				
CaPOPI_1174	Ca3	7467677	AACATTAGA/AACATTAGACATTAGA	CCACACCCCTCACACTT TCT	AGCAAAGGGGATGAAAA GGT	60.0	461	INTERGENIC				
CaPOPI_1175	Ca3	7580880	TAAAAAAAA/TAAAAAAAAA	GTGGTTCCGGAAAAGAT GAA	CCCCATCCATTTCCCTAT CT	59.9	373	INTERGENIC				
CaPOPI_1176	Ca3	7792015	TAT/TATTATTCTTTCCCTAAT	TAGGTAAAGGTGGTTTG CCG	TGAGGGATAGATGCAGG TCA	60.0	611	INTERGENIC				
CaPOPI_1177	Ca3	7880432	TCTAG/T	AGGAAGAGTGGAGTTGC GAA	TATTTTGGATTTTGCTC GG	60.0	503	INTERGENIC				
CaPOPI_1178	Ca3	7922530	TTATATATATATATATAT/TTATATATA TATATATAT	AGGAAGAGTGGAGTTGC GAA	TATTTTGGATTTTGCTC GG	60.0	504	INTERGENIC				
CaPOPI_1179	Ca3	7959750	TTAATTTGATTATGTTAAGTAATTTGAT TATGTTAA/TTAATTTGATTATGTTAAGT AATTTGATTATGTTAAGTAATTTGATTA TGTTAA	TTGGCATAGGTCATGGA AGTT	TTTGCCAATGTTGCTAG CTG	59.4	848	INTERGENIC				
CaPOPI_1180	Ca3	8059631	GTTT/GTT	TGTGCGACCATCTACTG CTC	GCAATCTCTCAACTCG GTC	60.0	813	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1181	Ca3	8245494	TCT/TCTTCTGCT	TGCGCCTCTTCTAAAAA CGT	TATCGCAATCAGAGGAA CCC	60.0	670	INTERGENIC				
CaPOPI_1182	Ca3	8393314	GTATATATATATATATAT/GTATATAT ATATATATATATATAT	GTTGGTCCCTAGCAC GTA	TATTTGGATTTCGGCTC GG	60.0	602	INTERGENIC				
CaPOPI_1183	Ca3	8523296	ATTTTTTTTT/ATTTTTTTT	CACATGACAAAATTGGT GGAA	CGTTAAGGCACATCTCA CTCC	59.3	508	INTERGENIC				
CaPOPI_1184	Ca3	8754025	GTATATATATATATATATATATATA T/GTATATATATATATATATATATA TATAT	AAATCCTTGGCCTTTC GAT	GATGAGGTATGTGCGTG TGG	59.9	863	INTRON	Ca_23720		B3	Protein of unknown function DUF674
CaPOPI_1185	Ca3	8942193	AT/ATT	TGGGGAAAAACCCTTAC CTT	CACATGATTTCAATTGG CTTTG	59.7	326	INTERGENIC				
CaPOPI_1186	Ca3	9186815	CTATATATATATATATATATATA/CTA TATATATATATATATATATATA	TCCACAACACGATAAC ATTGA	TGTAACAAGCATTTGTC GGG	58.9	693	INTERGENIC				
CaPOPI_1187	Ca3	9189477	AATATATATATATATATATATATAT ATATAT/AATATATATATATATATAT ATATATATATATATAT	AAAGGTTTGGTTGGAGA TACG	TTGGCTGCAAAATATCC CTC	58.1	856	INTERGENIC				
CaPOPI_1188	Ca3	9577976	AGG/AGGG	TTGCGTTCAAAGACTCG ATG	TGAATTGCAGAATCCCA TGA	60.0	575	INTRON	Ca_20977			
CaPOPI_1189	Ca3	10159468	T/TA	TGGGGCAACAAAGCTA TTC	CTAAGGGCGCTACAACA AGC	60.1	107	INTERGENIC				
CaPOPI_1190	Ca3	10312456	TAAAA/TAAAAA	TGACACGCAATATAGAA CCG	CATCTTGGTGTGTGAAA GCG	57.3	598	INTERGENIC				
CaPOPI_1191	Ca3	10350276	CAAGAAG/CAAGAAGAAG	ATTGCCAAATCGGTTCA GTC	GCCAAACCCTTACGAGA TCA	59.9	459	DRR	Ca_18818			
CaPOPI_1192	Ca3	10398321	G/GATTGATCTTTCCC	CGGATTGCCAAGTACAA GGT	CAAACCAACACGACAC AAC	60.0	770	DRR	Ca_18819	J		Ribosomal protein L10/acidic P0
CaPOPI_1193	Ca3	10684192	CTATTATTATTATTATTATTATTATT ATTATTA/CTATTATTATTATTATTAT TATTATTATTA	TTTCATCCAATGCTTCAG GA	TTGTGGTTGCATCCCTA ACA	59.2	822	DRR	Ca_18828	O		Glutaredoxin
CaPOPI_1194	Ca3	10846962	AATATATATATATATATATATATAT A/AATATATATATATATATATATATA TATATATA	CCAAATGACGACTTCCC ACT	CAAGACGTCGTC AAAAT CCC	60.0	683	INTERGENIC				
CaPOPI_1195	Ca3	10860554	TG/T	GCACACTGGTGTTGGAT TTG	TCAATGGTAACTTCCCC AGC	60.0	851	INTRON	Ca_19358	G		Acetylhexosaminidase , subunit a/b

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1196	Ca3	10923237	T/TC	GCTGATTGAAATCGAGC ACA	TTAAACAAGCACCAAG GGC	60.0	347	INTERGENIC				
CaPOPI_1197	Ca3	11044475	CAAAAAAAAA/CAAAAAAAAA	GCATCCATCCAACGAC TTT	CATTACATCTTATTTGAG GGAGAGC	59.9	286	INTERGENIC				
CaPOPI_1198	Ca3	11182328	GAAAAAAAAA/GAAAAAAAAA	AGGTGCCCTTCTTTTG GTT	GCATCGTCGACCTTGAG AAT	60.0	527	INTERGENIC				
CaPOPI_1199	Ca3	11273271	ATTTTTTTTT/ATTTTTTTTT	GCGCGCGGATAAAATAA ATA	TCATGACGCAGCACTTT TTC	60.0	738	INTERGENIC				
CaPOPI_1200	Ca3	11497481	ATTATTTATTTATTTATTTATTTAT GTATTTATGTATTTATGTATTTATTTAT CATTTATTTATTTATTTATTTATTTAT TTATTTATTTATTTATTTATGTATTTATG	GGGTTTGCACTTGAAGG TGT	CCTCCGAGCCAAATAC AAA	60.0	617	INTERGENIC				
CaPOPI_1201	Ca3	11587128	CAAAA/CAAAA	TTTGGGCTTACTTTCCAT GC	GGTGTCATTTCTTTGC GGT	60.1	543	DRR	Ca_19379			Transposase, MuDR, plant
CaPOPI_1202	Ca3	11765428	ATTT/ATTTT	GATCAGATCTGGCAGCA ACA	TGGCATACATCTAGGG GAG	60.0	574	DRR	Ca_19390			
CaPOPI_1203	Ca3	11877050	TAAAAAAAA/TAAAAAAAA	TTCAAACCTTCAATTT GCTC	GCGATTTTGGTGAAATC CAT	58.4	594	INTERGENIC				
CaPOPI_1204	Ca3	11919605	GAA/GA	CGGAAATTGAAATCGGA AAA	ATCGCGAAAGTAGTCTC CCA	59.9	633	INTERGENIC				
CaPOPI_1205	Ca3	12140676	A/AT	TTCTATTGCTCACCC TTG	GAAAAACAAGACCCGCG ATA	60.1	525	INTERGENIC				
CaPOPI_1206	Ca3	12697436	GTTTTATTTTTATTTTTATTTTTATTT TATTT/GTTTTATTTTTATTTTTATTT TATTTTTATTTTTATTTT	AGCTTGCCAACCTCTGG GTA	TGCAAAACGTGTCATCC ATT	59.9	670	INTERGENIC				
CaPOPI_1207	Ca3	12715466	T/TACACATTAAG	TATTTCCCGATTAATGCA GCC	GTCCCGAATGCAATGTC TCT	59.9	667	INTERGENIC				
CaPOPI_1208	Ca3	12747032	TGGG/TGG	CCTACGGACGGGAATGT AGA	CGTTTTTCTAAGCGAGG GTG	59.9	398	INTERGENIC				
CaPOPI_1209	Ca3	12911294	C/CCT	TATCGAGTGTTCCGGT TCC	CAGGTTACAGTGAGCAA GAA	59.9	337	INTERGENIC				
CaPOPI_1210	Ca3	12969818	TAAAAAA/TAAAAAA	TTACACCAATCCCCCA AGA	CATGCAAGGTTGGGCTA GAT	60.2	400	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1211	Ca3	13097036	A/AT	CCTTCTTTACGGGACCC AAT	TCATCAGTATCGTGGT GGA	60.2	364	INTERGENIC				
CaPOPI_1212	Ca3	13236644	AATATATATATATATATATAT/AATATA TATATATATATATATAT	AAGACCTGTGGGATCAT TGC	TTTTGTGATAGGTTCTT GATGC	59.9	928	INTERGENIC				
CaPOPI_1213	Ca3	13313491	CATTATTATTATTATTATTATTATTA TTATTAAATATTATTAT/CATTATTATT ATTATTATTATTATTATTAATATTAT TATTAT	AACCCACCTCTTGATTTC A	CGACAATTTTGTGGTG ACG	59.4	637	INTERGENIC				
CaPOPI_1214	Ca3	13796912	CAAAAAAAAA/CAAAAAAAAA	TATCATGCATTTGCGGT TGT	CCTGAGAGAGAAAGGG GCTT	60.0	650	INTERGENIC				
CaPOPI_1215	Ca3	13827207	TTATATATATATATATAT/TTATATATA TATATATATATAT	CTACTCCGACACTGAA GCC	TTTTCCAGGAAGGAATC GTG	59.9	527	DRR	Ca_25325			
CaPOPI_1216	Ca3	13836046	TAAAAAAAA/TAAAAAAAA	TGAGCTGATGGTGAAGT GATTT	TGGTTGAGCTTCAGACA TGC	59.7	530	INTERGENIC				
CaPOPI_1217	Ca3	14653349	A/AG	AGGAGCTTCTGCCATTG AAA	TAAAGGAGCAAAGGCC AGA	60.0	408	INTRON	Ca_22505	O		Zinc finger, RING-type
CaPOPI_1218	Ca3	14801451	GATATATATATATATATATAT/GATAT ATATATATATATATATAT	ATGAGCCACAAGCTCCA AGT	TGCCATTTGGTGAACGA TTA	59.9	357	INTERGENIC				
CaPOPI_1219	Ca3	14843003	AATATATATATATATATATATATAT A/AATATATATATATATATATATATA TATA	GAGAAAGAAGATATCGG ATTCTCAA	AAAAATCAACGCAGTGG GAG	59.3	356	INTERGENIC				
CaPOPI_1220	Ca3	14874833	GCC/GCCC	AGGTCATTTTCGTCCTC CT	CAACACACCTGTTGGA TGC	59.9	679	INTERGENIC				
CaPOPI_1221	Ca3	14880871	TG/TGTCG	TTTCGGTCATTTTCGTC CTC	ACACACCTATCGGATGC ACA	60.1	616	INTERGENIC				
CaPOPI_1222	Ca3	14902851	GAA/GAAA	CGGTGGGAGAACTCT GATA	TTCACATGACATCATCC CGT	60.1	474	INTERGENIC				
CaPOPI_1223	Ca3	14919264	GTTT/GTTTT	CGATTGTGTTTGTACAA GGG	GAAGCAAATCGATTGGG AAA	60.0	303	INTERGENIC				
CaPOPI_1224	Ca3	15039270	TC/T	CAACACGATCATGACAA GCA	GCATTTTGCAATTTGTCAA CG	59.2	677	INTERGENIC				
CaPOPI_1225	Ca3	15047295	TA/T	TACTTTGTGCCATGCTC TGC	ACACAAGCCAACACATC CAA	60.0	117	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1226	Ca3	15072147	AATATATATATATATATATATATA/AATATATATATATATATATATATA	GAGTGGTGTGGAGTCA TGTTT	AGACATGTGTTCCCTT CCG	59.0	424	DRR	Ca_17011			
CaPOPI_1227	Ca3	15232531	TAAAAA/TAAAA	CTTTTACAGCGCTTTTGG GG	TTCGTAATGGACGGGAT GAT	59.9	245	INTERGENIC				
CaPOPI_1228	Ca3	15318264	TAAAAAAA/TAAAAAA	CGAAGGAGCTTTTCTTG TGG	CGCATTTTGCAATTGTCA AC	60.0	651	INTERGENIC				
CaPOPI_1229	Ca3	15388201	CATATATATAT/CATATATAT	AAACACATGCGCTTTCA TTG	AATCGATTGGCTGAAAT CCA	59.7	479	INTERGENIC				
CaPOPI_1230	Ca3	15463471	CATATATATATATATATATA/CATATATATATATATA	TTTGTGGATTGCATTG ATGA	TGAATTCAACCGTAAACG GAA	59.9	783	INTERGENIC				
CaPOPI_1231	Ca3	15503247	C/CTAAAAATTAGGGAA	ATTGGGAAGTGGGGAAA CTC	CGGGGTACATTGATAGC GTT	60.2	800	INTERGENIC				
CaPOPI_1232	Ca3	15524418	GTTTTT/GTTTTTTT	GACGTGTGTGTGGAAG AGC	CGGCCAAAGTAATGGAT TGT	59.3	720	INTERGENIC				
CaPOPI_1233	Ca3	15660475	TA/TAA	AAGTGAGCTAACGGGG GTTT	TGGACAGAGCAAGTGAG GTG	60.0	140	INTERGENIC				
CaPOPI_1234	Ca3	16133157	GTTTTATTTTATTTTATTT/GTTTTATTTT ATTTTATTTTATTT	CGTCTCTTGAAGCGATG AAA	CATTGTTGGTCACTAGC AAATCA	59.1	698	INTERGENIC				
CaPOPI_1235	Ca3	16133384	CAATAATAATAATAATAATAATAATA ATAATAATA/CAATAATAATAATAATAAT AATAATAATAATAATAATAATA	CGTCTCTTGAAGCGATG AAA	ATAAGCCGTCATCTGC CAC	59.1	807	INTERGENIC				
CaPOPI_1236	Ca3	16133499	TA/TACACAAAGAA	TTTGCCCCATTATAACA AAA	ATAAGCCGTCATCTGC CAC	57.2	625	INTERGENIC				
CaPOPI_1237	Ca3	16137267	CATATATATATATATATA/CATATATATATATATATATA	TGGCACATCTAAAAATA GGAGGA	AGAAAGTCGCATCCCAG AGA	60.0	544	INTERGENIC				
CaPOPI_1238	Ca3	16138352	TTATATATATATATATATATATATA/TTATATATATATATATATATATATA TATATATA	GCCACAATCTGTCCCA ATA	TAGTGAAGGCATTGGCA GAA	60.7	855	INTERGENIC				
CaPOPI_1239	Ca3	16166714	TTTTG/TTTTGCTTTG	TCAACCATCTGGGTTGG AAT	CCCCTAGCAAAGGAAAC AAA	60.2	674	INTERGENIC				
CaPOPI_1240	Ca3	16168531	AG/A	TGGAGGAGGATTCCAT CTG	TGCTTTCTTGCCCTGTTT TT	60.0	547	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1241	Ca3	16171083	T/TG	TACAGCGCTTCATTCCA CAG	CGTGCATGAGCAAAAGA AAA	60.0	468	INTERGENIC				
CaPOPI_1242	Ca3	16182804	ATTTTTTT/ATTTTTTTTTT	CCGGCATCACCTATCAG AGT	TCCGACCTCCTTGAGA AGA	60.1	583	INTERGENIC				
CaPOPI_1243	Ca3	16190775	CA/C	TCGCGGTTCTTGATGAT GTA	AGCTCGACTTATCCTTC GCA	60.2	423	INTERGENIC				
CaPOPI_1244	Ca3	16195131	AT/ATT	TGATAAAAGACTAACGA TGCAAAACA	TAAACCATCAATCTGCC ACG	60.1	655	INTERGENIC				
CaPOPI_1245	Ca3	16195368	CATATAT/CATATATAT	ACGTGGCAGATTGATGG TTT	TTTGATGTTGCGGTAGA GGA	60.4	350	INTERGENIC				
CaPOPI_1246	Ca3	16195709	AC/A	ACGTGGCAGATTGATGG TTT	GAACGTACGGAAGAGAA GCG	60.4	754	INTERGENIC				
CaPOPI_1247	Ca3	16197261	TCTTAA/T	CTGCATCGAATTAATGC AACA	AAGGGGGATCATGGA ACT	59.7	316	DRR	Ca_18251			
CaPOPI_1248	Ca3	16212378	A/AACATTC	ATGCACITTTGCCACTGT TGT	GAGGGGATGATGCTTCA AAA	59.2	879	INTERGENIC				
CaPOPI_1249	Ca3	16347875	CAAAAA/CAAAAAA	GCGTTTTATGTTGCTG GGT	TATGGAAGGTGAGACAG GGG	60.0	690	INTERGENIC				
CaPOPI_1250	Ca3	16423935	AATATATATATATATATATAT/AATATA TATATATATATATATAT	TCCAGAAAAAATCTTC TTCACG	CAAGGATGGGTTGATCG TCT	58.9	702	INTERGENIC				
CaPOPI_1251	Ca3	16518599	A/AACC	CTTTGGAGCAAGCTGGG TAG	TTTTGCGATGTTTGATC GTT	60.0	544	INTERGENIC				
CaPOPI_1252	Ca3	16544552	GTTATTATTATTATTATTATTATTAT TATTATTATTATTA/GTTATTATTATTATT ATTATTATTATTATTATTA	TGCTCGACATGTTTCTC CTT	CCACACAACTGACAAC TCCA	58.4	605	INTERGENIC				
CaPOPI_1253	Ca3	16778238	GAAAAAA/GAAAAAA	TCCTATGGTGGCTCATC TCC	TTTTGCCTCAACAATCTC CC	60.0	359	INTERGENIC				
CaPOPI_1254	Ca3	16820332	AATATATATATATATA/AATATATATAT ATATATATA	AGAGGACATCGTTAGC TGC	AAGAAAGAAGGGTCCC AAA	59.5	633	INTERGENIC				
CaPOPI_1255	Ca3	16885390	CTATATATATATATATATA/CTATATA TATATATATATA	CATTTTCATCAAAGGTC GCA	CAAATTTGCCACTGTCTT GC	59.7	244	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1256		Ca3	16954725	CATATATATATATATATATATATA/CA TATATATATATATATATATATATA	TAAATGACCAAGCCGGA AAA	CGTTTGATCGATTGCAG TTC	60.4	573	INTERGENIC				
CaPOPI_1257		Ca3	17033772	AAATAATAATAATAATAATAATAATA ATAATAATAATAAT/AAATAATAATAATA ATAATAATAATAATAATAATAATAAT AATAATAAT	ATGCGATCATGTGGATG AGA	TACCCCTGTTGGTCCT GAG	60.0	840	INTERGENIC				
CaPOPI_1258		Ca3	17039245	CAAAAAA/CAAAAAAA	TTCTAACTTTGCTGTCCC ATTTT	GGGGTAAAACCAGGAG GAAG	59.2	750	INTERGENIC				
CaPOPI_1259		Ca3	17122676	ATTTTTTTTT/ATTTTTTTTTT	AATGCACCACTTTATGC ACG	CCAGTTTTCATTCAGGC ACA	59.6	358	INTERGENIC				
CaPOPI_1260		Ca3	17201946	TTATATATATATATATATATATATA TATATATAT/TTATATATATATATATAT ATATATATATAT	AAAATCAACATGGTGG GGA	AAGGCATGATGTTGGAG TCA	60.0	398	DRR	Ca_24619	S		Domain of unknown function DUF862, eukaryotic
CaPOPI_1261		Ca3	17217773	TCC/TC	ACAAATCGGACACCGTTT CAT	TCATGTGGCAACACTGT TCA	60.2	253	INTERGENIC				
CaPOPI_1262		Ca3	17491839	AATATATATATATATA/AATATATATAT A	TGAATTCATGGCTAAAA GCCT	GCAAAGATGATAATTCG GCAA	60.1	654	INTERGENIC				
CaPOPI_1263		Ca3	17579559	TAAAA/TAAATAAAAA	TGCATTTTCCACCAACATC GT	AATCACCGAGCTGAAAT CAAA	60.0	912	INTERGENIC				
CaPOPI_1264		Ca3	17819480	AATATATATATATATATATATATAT ATATA/AATATATATATATATATATATA TATA	AACGATCTGATTGTAAT GTGTTTCTT	GTCGTGAACGGTGCTAC ATC	59.4	884	INTERGENIC				
CaPOPI_1265		Ca3	17940721	GAAAAAAAAA/GAAAAAAAAA	GGCTAAATTACATTTGT GGTCCC	GGCTAAATTATATTCGT GGTCCC	60.8	382	INTERGENIC				
CaPOPI_1266		Ca3	18015978	TTATATATATATATATATATATATA TAT/TTATATATATATATATATATAT ATAT	TCAGCAATAGAAGCCAA ATGC	CGAACTTTGCCGTACGT CTT	60.4	470	INTERGENIC				
CaPOPI_1267		Ca3	18241779	CTATATATATATATA/CTATATATATA TATA	CTCTACCACGCGATTAC GGT	GGAAGTGATGGGTGAAA TGG	60.2	390	INTERGENIC				
CaPOPI_1268		Ca3	18268210	GAAAAAAAAA/GAAAAAAAAA	AACGAAGAAGTTGAGGT GGC	CCGAATTGCTCTTCATT GGT	59.3	940	DRR	Ca_19613	O		PI31 proteasome regulator
CaPOPI_1269		Ca3	18345308	TAAAAAA/TAAAAAA	GGTTCCCTCCTAAGTT AAGGGT	GCGGTGCAATCAGTAAA CCT	60.1	271	DRR	Ca_19619	O		Glutathione S- transferase, N- terminal
CaPOPI_1270		Ca3	18647131	ATTTTTTTTT/ATTTTTTTTTT	AATTGATTTAAGCCCAA AATAGA	AGAAGTGGCAAGATGGA TGG	57.5	576	DRR	Ca_19638	Q		Multicopper oxidase, type 1

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CaPOPI_1286	Ca3	19402891	AGA/AGATGA	ACCCAATCCAAGTTTGT CCA	GAAGGCGACTCTAAAGA CTG	60.2	632	INTERGENIC				
CaPOPI_1287	Ca3	19560633	TAAAAAAAA/TAAAAAATA	TCAGTGCGATGGAGAAA TCA	TGACATTTTAACCTTGA GTTGC	60.4	453	INTERGENIC				
CaPOPI_1288	Ca3	19639547	CT/CTTATAT	TGCAATCAAGAGAGGAC ACAA	CGAGAAATAGCTCACGA GGC	59.4	521	INTERGENIC				
CaPOPI_1289	Ca3	19969942	GATCAACGCATC/GATCAACGCATCAAC GCATC	CATAAGGATCGGGGAACA AA	AGGATCATCCATCGTCT TCG	59.8	541	INTERGENIC				
CaPOPI_1290	Ca3	20005707	AATATATATATATATATA/AATATATATAT ATATA	CCACAACAGAACGATGT TGG	TTCCCCAAACTATTATG CATGG	60.0	312	INTERGENIC				
CaPOPI_1291	Ca3	20011560	GTTGACACTT/GTTGACACTTGACACTT	GCAATTGCAAGAGCGTG ATA	TTTGGCATGCAATCAAA CAT	60.0	277	DRR	Ca_09404			
CaPOPI_1292	Ca3	20445164	TTATATATATATATATATATATAT/TTA TATATATATATATATATATAT	AGTGCCACATGTAACAC CCC	GTTTTGGCGTTGGTTTC ACT	60.7	815	INTERGENIC				
CaPOPI_1293	Ca3	20526351	TTATATATATATATATATATATATATA TAT/TTATATATATATATATATATAT	TGCATGTTCTTAGCGTC GTC	AATTCACAAGACGCCAT TCC	60.0	504	INTERGENIC				
CaPOPI_1294	Ca3	20617847	AATATATATATATATATATATATA/AATAT ATATATATATATATATATATA	AATCGATTGGCTGAAAT CCA	TCGAGTTTGAGCATGTG AGG	60.4	809	INTERGENIC				
CaPOPI_1295	Ca3	20750487	CTTTATTTATTTTATTTTATTTTATTT ATTATTTATTTTATTTTATTT/CTTTA TTTTATTTTATTTTATTTTATTTTATTT ATTTTATTTATTTTATTTTATTTT	TGTTATGTTGGGTTTGG GCT	TGCAGATGGGTTGAGTG TGT	60.2	875	INTERGENIC				
CaPOPI_1296	Ca3	20988635	AATATATATATATATATATATATATATAT ATATATATATATAT/AATATATATATAT ATATATATATATATATATATATATATA TATAT	CAAGCTGAAGGACTTCCC ACA	ATTATGTGGCGAGTGAC GGT	59.0	477	INTERGENIC				
CaPOPI_1297	Ca3	21097843	ATTTTTTTTT/ATTTTTTTTTT	GGCATTTTGATTTGATTC GC	CAAAATTTGTGTTTCAAA AACCAT	60.4	653	INTERGENIC				
CaPOPI_1298	Ca3	21311568	GAAAAAAAA/GAAAAAAAAA	CACGTCACATCGAATT TTT	CATGTCATTTCAACCCA CGA	59.6	542	INTERGENIC				
CaPOPI_1299	Ca3	21319728	AACCTACTTA/AACCTTA	TGCTGTTCTAGTGTTCT AATTGCTC	GCCTGCCAGACGTTTTA CAT	59.2	562	INTERGENIC				
CaPOPI_1300	Ca3	21424576	CTTTTT/CTTTTT	ACGTAGTTGGGTCTTGG CAC	CAAAATCTGTCCCCTCT GGT	60.0	385	INTERGENIC				

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CaPOPI_1301	Ca3	21599415	CAAAAAA/CAAAAAAA	G CAGCAGTGTGTTGCAG AAG	TCTCTTGATCGCCTAAC AC G	59.8	941	INTERGENIC				
CaPOPI_1302	Ca3	21635589	GCATCATCA/GCATCA	AAGCATGCCAAACCAA AAC	TGAACATCAAAGATCTG CGG	60.0	521	INTRON	Ca_09516			
CaPOPI_1303	Ca3	21897869	ATATTATTATTATTATTATTATTA/T ATTATTATTATTATTATTATA	GAGTTGAGTGTTGCCAG GGT	AGCTACCAAGCTGATGG TGAA	60.2	296	INTERGENIC				
CaPOPI_1304	Ca3	21989858	TTATATATATATATATATATATATATA TATAT/TTATATATATATATATATATAT ATAT	TGAAGCAAACCAATAA ATCCA	GACCGGTGGTAGACCTT TGA	59.5	592	INTERGENIC				
CaPOPI_1305	Ca3	22042563	CTTTTT/CITTTTTT	AGGAAAAGTGCCATGTGA AAAA	TCGTAGGTCAAGTTCAG ACCG	59.6	764	INTERGENIC				
CaPOPI_1306	Ca3	22377503	TGTT/TGTTAGTT	TTCATTAACGCTTATTC CTC A	TGCAACTCTAACAGCGA CA A	58.8	694	INTERGENIC				
CaPOPI_1307	Ca3	22661182	AATTATTATTATTATTATTATTATTATTA TTATTATTATTATTAT/AATTATTATTATT ATTATTATTATTATTATTATTATTAT	AGAGAAGGTGAGGGGG GTTT	AGCCTGATAGGTGGTGG AAA	60.0	763	INTRON	Ca_06245	R		SPX, N-terminal
CaPOPI_1308	Ca3	22934054	G/GCCGATACAATTTGT	CCACATTATGCCTTCGG TTT	GGTTTTCGCGATATTTT CCA	59.8	210	INTERGENIC				
CaPOPI_1309	Ca3	22936637	TTAATAATAATAATAATAATAATAAAT AATAAAAAATAAATAATAATAATAA TAATATTAATATTATAATAATAATAATA ATAATAATAATAATAATAATAATAAAT	ACCACAAATTCGAGGA CGA	TGAAAGATGTGGGTAGC AATAA	60.5	778	INTERGENIC				
CaPOPI_1310	Ca3	23016776	TCCTACCT/TCCT	GCACACCTATGTGGTCT TGC	CCATTTTGTCSAGGTTT GGTT	59.2	615	DRR	Ca_06208	QR	B3	Oxoglutarate/iron-dependent oxygenase
CaPOPI_1311	Ca3	23102761	CTATATATAT/CTATATATATAT	CACCTGTGCACATTCAC AGACA	CCTTGAAGGTTAACAATT TC GT	59.6	543	INTERGENIC				
CaPOPI_1312	Ca3	23112762	TT/TTTCCTTGATACTTCGT	TGATGCCAATTTGGTTC TGA	TTC GAATCCGTCACAAA TGA	60.0	628	INTERGENIC				
CaPOPI_1313	Ca3	23201611	TAGGTCGATCAG/TAG	AAAAAGGAGAGTTCTCC GGC	ATCGAGCGAACACATTG TCA	59.8	677	INTERGENIC				
CaPOPI_1314	Ca3	23308159	CTTTTTTTTT/CTTTTTTTTTTT	TTGCCTTCATGCTTTCTC AA	CATGTTCCGATATGCCA CTG	59.5	461	INTERGENIC				
CaPOPI_1315	Ca3	23424382	TATTAaaaaat/tattataaaaattaaaa at	cattgtctggactacat t g t g t g a	gaagggatcaatttcta ccca	60.0	674	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1316	Ca3	23530917	AATATATATATATATATATATAT/AATATATATATATATATATATAT	ACCCATTAGCGTAGGAGTGC	AACGTAAATGCACTTGACCG	59.2	786	INTERGENIC				
CaPOPI_1317	Ca3	23541848	TTATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATATATATATATAT	ATAAGTTGGCGTTGCCTCTG	CGTCATATGGCGAAATAGATTG	60.3	518	INTERGENIC				
CaPOPI_1318	Ca3	23551096	AACAATTTACAATTTACGATTTACAATT/AACAATTTACAATTTACAATTTACGATTTACAATT	TCCCATTTTGATTCCCTTCA	TCCCTAAATCGCTGAATCTGA	60.2	363	INTERGENIC				
CaPOPI_1319	Ca3	23830553	ACTCTCTCTCTCTCTCTCTCTCTCTCT/ACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	TCACGAAATGGTCCCCTTA	GGGACCAAAACTGGAGAGAA	60.3	878	INTERGENIC				
CaPOPI_1320	Ca3	24033300	TTAATAATAATAATAATAATAATAA/TAAATAATAATAATAATAATAA	TCCAAGAAAAGTGTGGAATG	CCTTCCTACGCCTCAAACTCA	59.1	376	INTERGENIC				
CaPOPI_1321	Ca3	24117383	TTACATACATACATAC/TTACATACATAC	GAAGAGGTGCTTGGTGAGAGA	TACACCAGAATTTGCTCCC	60.4	342	DRR	Ca_06107	O		Calreticulin/calnexin
CaPOPI_1322	Ca3	24193117	ATTT/ATT	TAAGTTTCAGTTATGGCCG	CGCCACTATGTCGGCTATTT	60.0	695	INTRON	Ca_06100	J		Aminoacyl-tRNA synthetase, class II (D/K/N)
CaPOPI_1323	Ca3	24272959	GAATAATAA/GAATAATAATAA	GCATGTCCGTTACCTCCACT	GCGATTTATTATTAGAGATTATTAGCG	60.0	646	INTERGENIC				
CaPOPI_1324	Ca3	24701158	ATTTTTTTTT/ATTTTTTTTT	TTTGGCACATCTATTCAACTGC	CGCATTCTTGGGATGCTTAT	60.1	136	INTERGENIC				
CaPOPI_1325	Ca3	24984768	CTTTTTTTTT/CTTTTTTTTT	TATATGGGCTGCTCTCCCTG	TTTTGCTTTTGAAGCCAAACC	60.2	663	INTRON	Ca_06031		SAP	
CaPOPI_1326	Ca3	25585812	TAAAAAAAA/TAAAAAAAA	TGTTTCGTTTTTGTCCCCCT	TCCATTGCAATCGTACTTAATGA	58.7	735	DRR	Ca_05976		B3	Transcriptional factor B3
CaPOPI_1327	Ca3	25758872	TAAAAAAAA/TAAAAAAAA	GGATCCGGTGCTACTCCATA	ATTTGAGGTTGTGATTATGCAA	59.9	713	INTERGENIC				
CaPOPI_1328	Ca3	25888060	AT/ATT	TGTGGAAGACATCCTTACTGC	ACCTGACCTATTTCCACCCC	59.2	551	INTERGENIC				
CaPOPI_1329	Ca3	25888907	GTTTTTTT/GTTTTTTT	CAGGTCATGCCAGACTTTGA	TCTGACCCGACCTGGTCTAC	59.8	578	INTERGENIC				
CaPOPI_1330	Ca3	25889145	ATTTTTTT/ATTTTTTTT	GTAGACCAGGTCGGGTCTAGA	TGATATGTCACATTGTGCGAC	60.1	403	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1331	Ca3	25891751	TAAA/TAAAA	CGGTTCTTAATTGAAAA GGC	CAACGCTTTGTTCTCTC AACA	58.7	341	INTERGENIC				
CaPOPI_1332	Ca3	26020458	CATATATATATATATATATAT/CATATAT ATATATATATATATATAT	CCCACTAAAGGCCCAT TCA	TTCAAATTCACGCCCCT AAC	59.8	789	INTERGENIC				
CaPOPI_1333	Ca3	26071275	ATTTTT/ATTTTTTT	TGTGTTTGTGGTTTCA TCTTG	TGTCAACGTGATTGGAG CAT	59.9	563	INTRON	Ca_08292		MYB_rela ted	SAM dependent carboxyl methyltransferase
CaPOPI_1334	Ca3	26071877	TAAA/TAAAA	TGCTCCAATCACGTGGA CAT	AGACGCTGCAACATCAA AGC	60.1	397	INTRON	Ca_08292		MYB_rela ted	SAM dependent carboxyl methyltransferase
CaPOPI_1335	Ca3	26114065	AG/A	TTTATCTGGGGACTTC GTG	AGGAAAAACACGGGCA AGA	59.9	364	INTRON	Ca_08292		MYB_rela ted	SAM dependent carboxyl methyltransferase
CaPOPI_1336	Ca3	26114282	ATTATAGTTTTATT/AT	TTTATCTGGGGACTTC GTG	ATACACCGATGGAGGGC TTT	59.9	838	INTRON	Ca_08292		MYB_rela ted	SAM dependent carboxyl methyltransferase
CaPOPI_1337	Ca3	26115029	AACG/A	TGGCATGGTACTCAACC AGA	TTACATGAATGATTGTT GGGT	60.1	545	INTRON	Ca_08292		MYB_rela ted	SAM dependent carboxyl methyltransferase
CaPOPI_1338	Ca3	26245714	C/CA	CGCCTGTACCGTTGAT ACT	ACCCATTCCAGTGTTT TCA	60.0	678	INTRON	Ca_08279	QI	B3	Cytochrome P450
CaPOPI_1339	Ca3	26349764	GTTAACA/G	TCTGCATTGTCCAAAC CAA	TTATCCATGATTGGGA GGG	60.1	737	INTERGENIC				
CaPOPI_1340	Ca3	26777304	GTATATATATATATATAT/GTATATATAT ATATATATAT	CACTCATCACACGGGA CAC	CAATGAATCGATGAAAT GAATTG	60.0	754	DRR	Ca_08228	P		Cation/H+ exchanger
CaPOPI_1341	Ca3	26872317	CAGAGAGAGAGAGAGAGAGAGAGAG/ CAGAGAGAGAGAGAGAGAGAGAGAGA G	CAATGTGCTCGATTTC CCA	TTACATTCTTGCTCGT CA	59.8	389	INTERGENIC				
CaPOPI_1342	Ca3	26961684	ATTTTTTTTTTTT/ATTTTTTTTTTTT	CACGGTTGTGATGACTC GAC	GTCGCGTCAACGTTTGT TTA	60.2	538	INTERGENIC				
CaPOPI_1343	Ca3	26998517	AATATATATATATATATATATATATAT AT/AATATATATATATATATATATATAT ATATATATATATAT	TGGGATGTTTCAAATTC TGC	AAAATGGCATTGGTGTG GTT	59.9	576	INTERGENIC				
CaPOPI_1344	Ca3	27382854	GTTTTTTTTTTTT/GTTTTTTTTTTTT	GCGGTAAAGAAGGCAA GTG	TGTGGGTACCTTAAACC CTAAAAA	59.9	591	INTERGENIC				
CaPOPI_1345	Ca3	27648871	AATATATATATATATATATATATAT/AATA TATATATATATATATATATAT	AATCCCATGGCACTGAG AAC	AGCGTGATCACATTCAC AGC	59.9	670	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1346	Ca3	27854154	TGG/TG	TCGATAATGAGTGATTA GGTGGG	ACCTCACCCCTCGAATGT CAC	60.2	459	INTERGENIC				
CaPOPI_1347	Ca3	27854804	T/TA	GGATTGAGAGGGGAGA AAGG	TTTGAAAGCAAGAGCGT CAA	60.0	516	INTERGENIC				
CaPOPI_1348	Ca3	27856755	TAAAAAAAA/TAAAAAAAA	CGAAGATGAAGAGGCTT GAAA	CAACAACCTTCTGATGCT CGC	59.6	593	INTERGENIC				
CaPOPI_1349	Ca3	27866552	TTAATAATAATAATAATAATAATAAT AATAATAATAAATAGTAATAATAATAA TA/TTAATAATAATAATAATAATAAT AATAATAATAGTAATAATAATAATA	TCAGAATTTTGGTGAGT TGGC	GGGATTCGCTGGTTATC TCA	60.1	552	INTERGENIC				
CaPOPI_1350	Ca3	28113252	ATTTTTTT/ATTTTTTT	TCCTTCTCCTCTTCCTC CA	TGTTTGTGCAATTGAATT ATAGTTATG	58.9	849	INTERGENIC				
CaPOPI_1351	Ca3	28188438	CAAAA/CAAAA	ACCCATAACGCACTCGT TTC	TCCTCCATTTTTCGTTTT CG	60.0	434	INTERGENIC				
CaPOPI_1352	Ca3	28191077	CTTTTTTTTT/CTTTTTTTTT	TAAGATGCGTGGGTTTA GGG	GCTTGTGTTTAAAGCGC TCC	60.0	659	INTERGENIC				
CaPOPI_1353	Ca3	28293830	TAAAAAAAA/TAAAAAAAA	GATTACTGCTAGGCCCC AAAT	ATCCCACTTGCAACACT TCC	59.5	147	INTERGENIC				
CaPOPI_1354	Ca3	28294648	AATATATATATATATATAT/AATATATA TATATATATATATATAT	TACCAGTACCAGGAGG AGG	TGGTGGGTAATCCGATG AAT	60.1	670	INTERGENIC				
CaPOPI_1355	Ca3	28428889	TTATATATATATATATATA/TTATATAT ATATATATATATATA	AGGCAACTCGATTCAAG CAT	AAACAACAAGCCCAAC AAC	59.8	923	INTERGENIC				
CaPOPI_1356	Ca3	28514570	ATATTATTATTATTATTATTATTATT ATT/ATATTATTATTATTATTATTATT ATT	CAAAGAAAATGGTGGGG ATG	AAATTGGACTATGCCAC CGA	60.2	841	INTERGENIC				
CaPOPI_1357	Ca3	28797139	CAA/CAATTCGATAA	CAAGGAGCTGTTTGCT TCA	GTAAATGGCACGCGGT AGT	59.2	609	INTERGENIC				
CaPOPI_1358	Ca3	28797825	A/AG	CATAGTCTGCGAAACCA GCA	GGTGAATTGATCGGAG AGA	60.0	454	INTERGENIC				
CaPOPI_1359	Ca3	28799476	G/GTC	TCTTGGACCTCACTGGG TTT	TGTCCTTGATCTTGTTTC CG	59.5	836	INTERGENIC				
CaPOPI_1360	Ca3	28799571	AG/A	TCTTGGACCTCACTGGG TTT	TGTCCTTGATCTTGTTTC CG	59.5	836	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1361	Ca3	28859122	CAAAAAAAAA/CAAAAAAAAAA	TTTCCC GACTTGTCCT TTA	ATGACATTTCGCCAAC ACA	59.5	432	INTERGENIC				
CaPOPI_1362	Ca3	28966806	TTATATATATATATATATATAT/TTATA TATATATATATATATATATAT	TGCATATTTAGAATTTAC GAACGAGA	ATTCAAGAAAGTTCGCC GTG	59.6	850	INTERGENIC				
CaPOPI_1363	Ca3	28984656	GTCTCTCT/GTCTCT	GAGAACGCAAGCTAACG GAC	GGATCAGAGAAAACGTG GGA	60.0	326	INTERGENIC				
CaPOPI_1364	Ca3	28994933	AC/A	CAAATTAAGCAGAGCCC GTC	TTTTGGACAATGTCAAC CCA	59.8	165	INTRON	Ca_07207	KTDL		GCN5-related N-acetyltransferase (GNAT) domain
CaPOPI_1365	Ca3	28995118	CAA/CAAA	CAAATTAAGCAGAGCCC GTC	CGGAATTTGAACAAAAC GCT	59.8	769	INTRON	Ca_07207	KTDL		GCN5-related N-acetyltransferase (GNAT) domain
CaPOPI_1366	Ca3	28999636	CT/CTT	TCTGAATTTCTGTACCG CCC	GGGATAGGGCATGTGT GAGT	60.1	536	INTRON	Ca_07207	KTDL		GCN5-related N-acetyltransferase (GNAT) domain
CaPOPI_1367	Ca3	29053872	TTATATATATATATATATA/TTATATAT ATATATATATATA	TCCTCCGCTCTTTCATT GG	GGTTGGGGGAGTGTTA GCTT	60.0	456	INTERGENIC				
CaPOPI_1368	Ca3	29228366	TTATATATATATATATATAT/TTATATA TATATATATATAT	TCGGAGGCAGAGACAAG TTT	TTAATTGGGGGAAATCC ACA	60.0	364	INTERGENIC				
CaPOPI_1369	Ca3	29334875	TTATATATATATATATATAT/TTATATA TATATATATATATATAT	GGGTGGCTCATGAAGCT TAG	TCTCAACCGTTTTGGTG ACA	59.8	576	INTERGENIC				
CaPOPI_1370	Ca3	29446926	GCA/GCACA	CAGCAGGGGCATACGTT AAT	GATTCCCCCTCCCTGATT CTC	60.0	306	INTERGENIC				
CaPOPI_1371	Ca3	29506460	CGTT/C	TGCCCTGT CATCAATG TTA	TCAATCCCATCAATCAT CA	59.9	598	DRR	Ca_07256	T	FAR1	Protein kinase, catalytic domain
CaPOPI_1372	Ca3	29563741	TATTCAAATAAATT/TATTCAAATAAATT CAAATAAATT	GCACATGCGGTCCTTTA ACT	TTCCCTCTCTCCCTCT CTC	60.1	648	INTERGENIC				
CaPOPI_1373	Ca3	29572508	TTTA/TTTAGCCTAAAAAGTATTA	GGACCAATT CGGAAAAA GAA	TTGGCACCCCAAATTTTA AG	59.0	359	DRR	Ca_07262	R	bHLH	Pentatricopeptide repeat
CaPOPI_1374	Ca3	29748543	CATTATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT ATTATTATTAT/CATTATTATTATTATTATT TATTATTATTATTATTATTATTATTATTA	TGCACCAAGTCACTAAC AAAAA	GGTGGCCCTCAACTTTC TTT	58.4	404	INTERGENIC				
CaPOPI_1375	Ca3	29752847	TAAAAAAAAA/TAAAAAAAAA	AATCGAGATGCCTTAGT GCG	CCTATTCCCACCCCTT TTA	60.4	868	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1376	Ca3	29771272	CTTTTTTTTT/CTTTTTTTTT	GGATTGCATTATTGCCAAGTT	GCGAGACATTTTGGGTGAAT	59.0	264	INTERGENIC				
CaPOPI_1377	Ca3	29772076	ATTTTTTTTT/ATTTTTTTTT	CCAGCTCCACAACCATTCTT	GCAAAATGTTCTGGTCGCATA	60.1	391	INTERGENIC				
CaPOPI_1378	Ca3	29779379	TTATATATATATATATAT/TTATATATATATATATATAT	GAGGAAAGCTTGTGCTTGG	CCGAATATAAATCATTGTGAAA	60.0	323	DRR	Ca_07285			
CaPOPI_1379	Ca3	29970428	CATATAATATAATATAAT/CATATAATATAATAT	GCAATAACATCGAGGTCAGG	AACGACTCAGATGAAATGCAA	60.8	454	INTERGENIC				
CaPOPI_1380	Ca3	30071057	TAAAAAAAA/TAAAAAAAA	TAAAAGCCAATGGAATGGG	ATCGCTCTCTCTCTCAACACA	59.9	247	INTERGENIC				
CaPOPI_1381	Ca3	30100381	ATATTATTATTATTATTATT/ATATTATTATTATTATT	TTGCACATTTACTCAACGC	ATTCCAGAAATGCGACCTTG	59.7	319	INTERGENIC				
CaPOPI_1382	Ca3	30339041	AAA/AAATAA	CCTCCTCCAACCATGAAATG	CCTGTGTGGTCAGAAAGGGT	60.3	496	INTERGENIC				
CaPOPI_1383	Ca3	30450479	ATCTTCTTCTTCTTCTTCT/ATCTTCTTCTTCTTCT	TCATGGGCCACAGCATATAA	GTCGTGCCAGCACAGAAGTA	59.9	366	INTERGENIC				
CaPOPI_1384	Ca3	30602335	TTGA/TA	GCCCTCAGATGAGAGTCAGG	AAATTAACCCCTCATCCCG	59.9	842	INTERGENIC				
CaPOPI_1385	Ca3	30930504	GTTTTATTTTATTTTA/GTTTTATTTT	GCATGGACCGTTTAAATTTG	TTTAGGTGAAAAATTCATTAGAAAA	58.0	818	INTERGENIC				
CaPOPI_1386	Ca3	31101603	ATTTTTTTTT/ATTTTTTTTT	ATGGTCCCAATGAAATCAA	TGTGTTGTCTCTGGCCTTTG	60.0	843	INTRON	Ca_12207			Zeta toxin, P-loop nucleoside triphosphate hydrolase
CaPOPI_1387	Ca3	31290021	T/TTGA	GGTTCAAACGTGTTCCCTTG	ACGCTCTCAAATCGACCATC	60.4	929	DRR	Ca_12225	P	ERF	General substrate transporter
CaPOPI_1388	Ca3	31293455	TG/TGG	TGGGATGTTTGAGAAAAGCA	ATCCCATCCCACCAACAATA	59.2	522	INTERGENIC				
CaPOPI_1389	Ca3	31295937	AAAAA/AAAAACA	GGACCATGGACTCCAGAGA	TCGTCCTCATCAGTTGAT	60.0	688	INTRON	Ca_12226	K	MYB	SANT domain, DNA binding
CaPOPI_1390	Ca3	31296813	CGTGTG/CGTGT	TCGGTTTTAAGGGAAGCAAA	TGCTGCAATAGCTGACCATC	59.7	806	INTRON	Ca_12226	K	MYB	SANT domain, DNA binding

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CaPOPI_1391	Ca3	31298126	GTTATTATTATTAT/GTTATTATTATTAT	GGACTTTTGGCACGATGTTT	TTTGCAACTTTTGACGGACA	60.0	716	DRR	Ca_12226	K	MYB	SANT domain, DNA binding
CaPOPI_1392	Ca3	31298291	CT/CTTTT	TGAGAGGTCGATTTTGGAGG	TTTGCAACTTTTGACGGACA	60.2	506	DRR	Ca_12226	K	MYB	SANT domain, DNA binding
CaPOPI_1393	Ca3	31319681	GAAAA/GAAAAA	CGTGGCTCCTCAAAGTCTC	ATGCACAAGGCTTCCATACC	60.0	599	DRR	Ca_12232	U	bHLH	VHS
CaPOPI_1394	Ca3	31326387	GTTTT/GTTT	CGGGTACAGCCGGTAA GTAA	GGGTGCCTTTAAAGTGTGGA	60.0	639	INTERGENIC				
CaPOPI_1395	Ca3	31328317	ATTTTT/ATTTTTTT	TCCAAC TAACCGCAATTCAA	TCATGGCAAATTTAGGATGTTG	59.2	447	INTERGENIC				
CaPOPI_1396	Ca3	31336604	T/TC	AGCAGGCCTGGACTTTACT	GGAATGCCAACGAATGAAA	60.3	555	INTERGENIC				
CaPOPI_1397	Ca3	31339236	T/TC	CCAACCCATGTACCGACATT	AGAGACCGTTTCATGAGATTG	60.5	525	INTERGENIC				
CaPOPI_1398	Ca3	31343075	CAATAAAAAATAAAAAATAAAAT/CAATAA AAATAAAAAAT	TGGCAAGTTTTCACCTTCATT	GATCACGGGAGGATCGACTA	59.6	792	DRR	Ca_12234			Domain of unknown function DUF640
CaPOPI_1399	Ca3	31353219	CAAAAA/CAAAAAA	TCCCTAAAAGTTTCTTCA TCCAA	GAATGACATATTGTGGCAGCA	59.2	225	INTERGENIC				
CaPOPI_1400	Ca3	31364505	CTTTTTTT/CTTTTTTTTT	ACCAATGTCTCGCAAGCTCT	GGTAAACATTTGCATCGTTGG	60.0	458	INTERGENIC				
CaPOPI_1401	Ca3	31366021	A/ATT	CCCTCTTGTGCCTGTCTTTC	CAACGGGAATCTTCCGTTCTA	59.8	469	INTERGENIC				
CaPOPI_1402	Ca3	31371532	TATCAT/TATCATCAT	GGATCAGCCCAATTGGTAAA	TAGACCATAAGCCCCTGACG	59.8	322	INTERGENIC				
CaPOPI_1403	Ca3	31381715	GATATA/GATA	TAAACCTTGGCTGGGTCAAC	TTGTTTATTTTGTTCTGTCGTGTT	60.0	403	INTERGENIC				
CaPOPI_1404	Ca3	31381813	AT/A	TAAACCTTGGCTGGGTCAAC	TTGCTACCATTGTAAGCTTGTTT	60.0	611	INTERGENIC				
CaPOPI_1405	Ca3	31391982	ATTTT/ATTT	CGTGCCCAATTATCAA CAA	TCTTGCTCATGGTGCTTCTG	60.4	793	INTERGENIC				

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CaPOPI_1406	Ca3	31402077	TAAAA/TAAAAA	TGTACACGTCGGTGAACAACT	TGTGGCGACAACCTAACTTTGA	59.1	634	INTERGENIC				
CaPOPI_1407	Ca3	31413249	AA/AATA	TGTTGCACGTTGGACAA GTT	GACTGCTACCAACCCAGCAT	60.2	374	DRR	Ca_12238	A		H/ACA ribonucleoprotein complex, subunit Nop10
CaPOPI_1408	Ca3	31426177	C/CCCAACAAGTGT	TGAGTCCTCATCGGTCAA	TCATCAATGACTAAATT TGT TTTGTA	60.2	573	DRR	Ca_12239	R	YABBY	Protein kinase, catalytic domain
CaPOPI_1409	Ca3	31441706	AT/ATGAAATT	ACAATTTTGGAAACCCCTAA	TTTGCAAGTGCAACTTC TGC	57.5	669	DRR	Ca_12242			PAK-box/P21-Rho-binding
CaPOPI_1410	Ca3	31446074	CTTTT/CTTTT	CATCCCAATTGCAATTG GTT	TGGAGGCTATTGGTACAGGG	60.6	531	DRR	Ca_12243	G		Glycolipid transfer protein domain
CaPOPI_1411	Ca3	31471455	CTTATTTATTTATTT/CTTATTTATTTATTTATTT	AAAACCCAAAAGCTGAATCG	CCCAAAGTTGGCATGAAGTT	59.2	624	INTERGENIC				
CaPOPI_1412	Ca3	31476304	ATTTT/ATTTT	TGGTTCAGATTGTTTG GTGA	CAACAGTGAGTGAAACAACCA	59.0	568	INTERGENIC				
CaPOPI_1413	Ca3	31478334	TCC/TCCC	TGGTGTGTGTTAGCCATAAAGG	GGGGCCTCTTCTTTGT TTC	59.9	614	INTRON	Ca_12246			Glucose-methanol-choline oxidoreductase, N-terminal
CaPOPI_1414	Ca3	31495232	CTTT/CTT	CCAAAATGGTGAGAGACTTCG	TTCGGTGCTTTGTCTCTTCC	59.7	809	INTERGENIC				
CaPOPI_1415	Ca3	31498407	ATTT/ATTTT	CTAGCTCGGGTTTTCTGACG	TTGGCCACAGTTTAACCAACA	60.0	531	DRR	Ca_12248	T		RHO protein GDP dissociation inhibitor
CaPOPI_1416	Ca3	31519164	C/CT	TACACGTGGCCTCAAACAAA	TCAAGCATGGTTCCAATCAG	60.1	364	INTERGENIC				
CaPOPI_1417	Ca3	31530560	TTGGGT/TTGGGTGGGT	AACTCCTTCTGCACATTGGG	TGGGAAATAGATCGGTC TCG	60.1	449	INTRON	Ca_12252	E	TALE	Oligopeptide transporter
CaPOPI_1418	Ca3	31540731	CTATATATATATATATATATA/CTATATATATATATATATATA	CTGTCCATTGTCCAACACG	CACATGGGTGACATCTGAGG	60.0	566	INTRON	Ca_12253	LK		BRCT
CaPOPI_1419	Ca3	31560705	A/AAG	TGTTCACTGCCAAACTCTGC	GCAGTGCACAACTGATG GTT	60.0	585	INTERGENIC				
CaPOPI_1420	Ca3	31563003	CATA/CATATA	GAATGGTGTTCTTTGTCCC	AATTTCACCCAAAGACACGG	59.2	274	INTERGENIC				

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CaPOPI_1421	Ca3	31566099	CG/C	AAGGGCATGGGAAAA TAG	TTTTCATGCATTTGAGAC GC	60.1	338	DRR	Ca_12255		G2-like	Myb, DNA-binding
CaPOPI_1422	Ca3	31595214	CATTATAAACAT/C	TTGATGTTATTTATTGGT GCAAAA	AGTAACGACAACCTCCG TGG	58.5	623	INTERGENIC				
CaPOPI_1423	Ca3	31602428	GAGTGCTAGTGCTA/GAGTGCTAGTGC TAGTGCTA	GCACGAGCACAACCTCA AAA	AAAGAACCATCATCGCA GGT	60.0	618	INTERGENIC				
CaPOPI_1424	Ca3	31602911	ATGTT/ATGTTGTT	ACCGAATATTCATGCT CCA	CCAAGTGATGTGTCATG GCT	60.3	565	INTERGENIC				
CaPOPI_1425	Ca3	31607270	ATTTTTTT/ATTTTTTT	TACCCTAACGGTGCTCC ATC	AAGATCATCCCCAAAA CCC	60.0	567	INTRON	Ca_12260			Gnk2-homologous domain
CaPOPI_1426	Ca3	31609545	T/TTA	GACAAAGCCAGAACCTT TGC	ACCCAAGCAGGCATACA AAC	59.9	538	DRR	Ca_12260			Gnk2-homologous domain
CaPOPI_1427	Ca3	31611126	GAAAAGTAAAAGTAAAA/GAAAAGTAAA A	TTTGGATTAGCCATAACA TCCA	CTTCCACCTTCGTGGAA AGA	59.3	617	INTERGENIC				
CaPOPI_1428	Ca3	31629115	ATTTTTT/ATTTTT	GTTTGTTTCGAGGTG GTT	ATTTTGGAGGGATTGG AGG	60.0	498	INTRON	Ca_12262	T		RNA recognition motif domain
CaPOPI_1429	Ca3	31755384	CTATATATATATATATATATAT/CTAT ATATATATATATATATATATAT	GCAGCTAAGAAGATTG GCCT	TTTGCGATATGAACCAA ATCA	60.0	467	INTERGENIC				
CaPOPI_1430	Ca3	31810634	AAC/AACCTTTGAC	TGTGTGATTGCACAGGA ACA	TTAGCGTGGGCAATAG TCA	59.7	253	INTERGENIC				
CaPOPI_1431	Ca3	31852962	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT/T TTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT	TTTAGGGAATGGGTCA TGG	TCAATCTGTCTCGTTTG ATTGA	59.6	576	DRR	Ca_12289	G	STAT	Ribokinase
CaPOPI_1432	Ca3	31908295	TAAAAAAAAAAAA/TAAAAAAAAAAAA	GAGGTGAAAATGGTGTA GATTAGAG	TCGTTCAACACCAAATG GAA	57.5	863	INTERGENIC				
CaPOPI_1433	Ca3	31912229	GAAAA/GAAA	CTCGGATACTGCCGATT GAT	TGCTGTTCTCTGTGAT TGC	60.1	958	INTRON	Ca_12292			Protein of unknown function DUF3741
CaPOPI_1434	Ca3	32399895	CATATATATATATATATATATATATAT ATATATAT/CATATATATATATATATAT ATATATATATATATATATAT	TTTCTTTCCGAAAATGGA GA	TGTGAATCCCGCTTTAA CAA	57.4	523	INTERGENIC				
CaPOPI_1435	Ca3	32563568	TTATATATATATATATAT/TTATATATA TATATATATATATAT	CGAAAGAAAAAGAAAAC ATCGC	GAAGGTGGCTCGGCATA TAA	60.2	574	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1451	Ca3	34161169	GAAAA/GAAAAA	GAAGCAAATCGATTGGGAAA	CTGGGGTTCCACTGTGACTT	60.0	239	INTERGENIC				
CaPOPI_1452	Ca3	34365238	T/TC	TGACCCAAAATGTGACTTGC	ATGCCAAGAATCCAACCTCGT	59.5	865	INTERGENIC				
CaPOPI_1453	Ca3	34456382	AGG/AG	TCCCTGTTTGGTTGTTGAT	GTAGTGTGGTTTGTGGGG	60.2	418	INTERGENIC				
CaPOPI_1454	Ca3	34474422	TAAAAAAAA/TAAAAAA	AAAAATCAATTTATGCCGTTGT	TTATGCCGGATTGACACTCTT	57.7	478	INTERGENIC				
CaPOPI_1455	Ca3	34520648	GAA/GAAA	AAAGACGAAAGGGAACACCA	GAAATTGGAACAAAGTCCGA	59.6	411	INTERGENIC				
CaPOPI_1456	Ca3	34521509	CTTTTT/CTTTTTT	ACCCATCTTGCGTTTTTCAG	TTAAATGGCGGCAAATTGAT	60.1	310	INTERGENIC				
CaPOPI_1457	Ca3	34565949	AA/AAGA	TGCTTTAGTTTGGCTTTGGC	TGATAGGATTTGTTGGAATCG	60.4	876	DRR	Ca_00727	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_1458	Ca3	34568477	CCTCCGA/CCTCCGACTCCGA	GTTTGTGCCAGTCCAAAGT	ACAAACACAACGCCAAACAA	60.0	549	INTERGENIC				
CaPOPI_1459	Ca3	34582473	TG/T	GGGGTGTGAAGAATCGAGA	GGGAAATAGCGGTTTGTCA	60.1	614	INTERGENIC				
CaPOPI_1460	Ca3	34605719	CTTTTAATTTTTAATTTTTAAT/CTTTTAAATTTTTAAT	ATGTCCTTGGTTGGCAGAG	GGGTTTGAGGAGAGGAGAA	60.1	404	INTERGENIC				
CaPOPI_1461	Ca3	34608178	ATTG/A	TGGAGAAACAAATACGGGA	TTGGGTAGACATTTTCCCTTG	58.1	575	INTERGENIC				
CaPOPI_1462	Ca3	34619372	CAAA/CAA	CGGCTCAGTGATCCTCTTTC	CAAAGGGAAAAGATAACCAACA	60.0	334	INTERGENIC				
CaPOPI_1463	Ca3	34623936	ATTTTT/ATTTT	CAGATAATTTGGGCAAGAGAA	GGAGCCAAGCTCCAGTTATT	57.0	716	INTERGENIC				
CaPOPI_1464	Ca3	34626639	C/CAAATGATT	TTTGCAAACCAATTCTTCAAA	GATGGGTCTATTGGTGGA	59.6	938	DRR	Ca_00734	FH		Permease, cytosine/purines, uracil, thiamine, allantoin
CaPOPI_1465	Ca3	34660669	GAA/GAAA	TCTTGCACCAGCAATTTGAG	TAAACCAATGGATAGCCGA	60.0	824	INTRON	Ca_00740	AJ	NAC	RNA recognition motif domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1466	Ca3	34665269	TGGGGG/TGGGG	CAAGAAGGTGGGAGGAT TCA	TTGGTACAAGCCCAGAC AAA	60.0	593	INTERGENIC				
CaPOPI_1467	Ca3	34674867	TAAAAA/TAAAAAA	GGAGGAACCTCAAAACCA CAA	GTTCGACTGGTG CAGA TCA	59.9	659	INTERGENIC				
CaPOPI_1468	Ca3	34681160	ATAAAATTAAT/ATAAAATTAATTA AAAT	AGGGGCCATGCTAATCT TCT	TTTGAAGGGAGAAATCC ATCA	60.1	552	DRR	Ca_00743	V	GRAS	Lipase, GDxG, active site
CaPOPI_1469	Ca3	34681675	GTTTTTTT/GTTTTTT	TGATGGATTTCTCCCTT CAAA	TTGGTTGTGGACCTGTG GTA	59.5	475	DRR	Ca_00743	V	GRAS	Lipase, GDxG, active site
CaPOPI_1470	Ca3	34685742	TAAAAAA/TAAAAAA	TTATGTCTCGTTTGGTG GACA	TTAGTGACATGCGTGGC TTC	59.0	586	INTERGENIC				
CaPOPI_1471	Ca3	34717035	CAAAATTAAT/CAAAATTAATTA AATT	AAAACATGTAGATCCATT TGAGTGA	AACTTTTGGCTTTCCG GTT	59.0	640	INTERGENIC				
CaPOPI_1472	Ca3	34721625	ACTATCATTCTATCA/ACTATCA	CAATCCGTTTAGAAGCT CCG	TGTTGCACGTAGCCTAA GAAA	59.6	625	DRR	Ca_00746	GMW	ERF	Exostosin-like
CaPOPI_1473	Ca3	34731798	TAAAAAAA/TAAAAAAA	TTTTCTGCCAAATCATC CC	AAGAAAGAGTACCGTCG CCA	59.9	671	DRR	Ca_00748			Protein of unknown function DUF81
CaPOPI_1474	Ca3	34732162	TAAA/TAAAA	TGGCGACGGTACTCTTT CTT	CACACTTTTAGGCCACC CAT	59.9	389	DRR	Ca_00748			Protein of unknown function DUF81
CaPOPI_1475	Ca3	34737485	CTTTTTTT/CTTTTTT	TGCTCTTCGGTTCGTTT CTT	ACCCAAGGATACAATGC CAA	60.0	650	DRR	Ca_00749	J		Ribosomal protein L24e
CaPOPI_1476	Ca3	34739285	TT/TTGGT	AGGTAGAGCCAGTGAG GTGG	TCCTTGGATGTGGTGGA ACA	59.3	841	DRR	Ca_00749	J		Ribosomal protein L24e
CaPOPI_1477	Ca3	34739482	ATTTT/ATTT	AGGCAATCAAAGTTAA AGGTG	TCCTTGGATGTGGTGGA ACA	57.5	508	INTERGENIC				
CaPOPI_1478	Ca3	34746354	GAT/GATCAT	TGGTGATACTAAGAG ACACGTCAA	GGGGAGGAGGAAGAAG CTC	59.2	810	INTERGENIC				
CaPOPI_1479	Ca3	34749435	TC/T	TGGGGGAGAGCGTCAT AAT	TGTCCTCGACATTTCTCT CCA	59.4	834	INTERGENIC				
CaPOPI_1480	Ca3	34749745	A/ACCTTAT	CGTCAATATTGTTGCA GGC	TATGGGTGGTTCATT CAC	59.2	332	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1481	Ca3	34753443	TAA/TAACAA	TCCAAAACCAACAAC CAA	CTAAATGTCCCCGTC TCA	59.8	689	INTERGENIC				
CaPOPI_1482	Ca3	34755544	T/TA	TTTTTCCATTTACCGGT CG	TTTTCAAGTGGCATCAA CCA	59.8	587	DRR	Ca_00751		HD-ZIP	F-box domain, cyclin-like
CaPOPI_1483	Ca3	34762413	T/TA	GGTGCTCAAAATGGTCG AGT	GCTCCTGGTTTTGTCTT TGC	60.1	360	INTERGENIC				
CaPOPI_1484	Ca3	34790577	CATATTAATATTAAT/CATATTAATATTA ATATTAAT	CCTCACAGCTGCCCTA TTA	AAAACACACAGGGCATG ATAA	60.2	692	INTERGENIC				
CaPOPI_1485	Ca3	34797791	GAAAA/GAAAAA	TTGTCAAACATTGCAACA AGAA	CACACTGAAGGTCTCCG GTT	59.3	902	INTERGENIC				
CaPOPI_1486	Ca3	34797856	GTTTTTTTT/GTTTTTTT	TTGTCAAACATTGCAACA AGAA	CACACTGAAGGTCTCCG GTT	59.3	902	INTERGENIC				
CaPOPI_1487	Ca3	34818875	AAATAATAATAAT/AAATAATAATAATAA TAAT	TTGTTGTCGCCATCATT GTT	ACTCCCGCAGTCCCTAT TCT	60.0	455	INTRON	Ca_00758			Glycosyl transferase, family 2
CaPOPI_1488	Ca3	34836958	TTTTTTTAAATTTTTTA/TTTTTTTA	GTGGTAATCCAACCGTC GAG	GAACCGATCCAACATGC TTT	60.4	443	INTRON	Ca_00761	G		Enolase
CaPOPI_1489	Ca3	34840506	GTTTTTTTTT/GTTTTTTTTT	GTTGGTGATGAAGTGG CTT	ATCCGGTCCCCATAACT TTC	60.0	457	INTRON	Ca_00761	G		Enolase
CaPOPI_1490	Ca3	34845314	GCAAA/G	ATGGGTACACACGAAAA GCA	ACACCCCGTACTTCAA ACA	59.1	563	INTERGENIC				
CaPOPI_1491	Ca3	34851854	TATAA/TATAATAA	ACAAACCCCTTCACTTGG CAC	ACCGCAAACCTCTATGTT GGG	60.0	648	INTRON	Ca_00763		C2H2	Zinc finger, C2H2-type
CaPOPI_1492	Ca3	34852048	CTACTTTA/CTACTTTACTTTA	ACAAACCCCTTCACTTGG CAC	ACCGCAAACCTCTATGTT GGG	60.0	648	INTRON	Ca_00763		C2H2	Zinc finger, C2H2-type
CaPOPI_1493	Ca3	34866347	CTATT/CTATTATT	TACCATGATGATGAAGC GGA	TCAACCGAATCAACAAC CAA	60.0	308	DRR	Ca_00764	A	C2H2	RNA polymerase II, large subunit, CTD
CaPOPI_1494	Ca3	34872921	ATTTTTT/ATTTTTTT	CACAAATGCGATTAAGG GCT	CATGTTGAATGGAAGCA CACA	60.1	685	INTERGENIC				
CaPOPI_1495	Ca3	34873766	CAAAAAA/CAAAAAA	AACACATTTTTGCAAGTG CG	GGCTTCTGAAAAACACA GCC	59.8	728	INTERGENIC				

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CaPOPI_1496	Ca3	34887394	GT/GTT	TCTTCCACACAAAACCTCC	ACGTGCATCACAAAACAAA	59.9	571	INTRON	Ca_00767	G	ERF	Fructose-bisphosphate aldolase, class-I
CaPOPI_1497	Ca3	34897346	TAAAAAA/TAAAAAAA	AGAACAAATTTGGCGCAAC	AGTTTTGTCGGTCCATGAGC	60.1	537	INTERGENIC				
CaPOPI_1498	Ca3	34906102	CTTTTTT/CTTTTTTTTT	TGGATGGTGATTATCCGACTC	TCCAAGTCTTTCAATACA AACACA	59.8	605	INTERGENIC				
CaPOPI_1499	Ca3	34910960	GTTTTT/GTTTTTTT	TCAAGGTCAAGTGTCGCAAA	CTTTGGTCGACGATGAGGAT	60.3	819	INTERGENIC				
CaPOPI_1500	Ca3	34913784	GTATATATATA/GTATATATATATA TA	ACCCGTTTCTTTGTTGTTGG	CTATCCAAGAAGCATCCCA	59.9	427	DRR	Ca_00768		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_1501	Ca3	34913867	AA/AACACTTGA	TGGGGATGCTTCTTGGA TAG	AAAATTTCGAGGCCCAT ACC	60.0	154	DRR	Ca_00768		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_1502	Ca3	34914599	T/TCGGG	TGGGAAGATGGAGGAAGAAA	GCCGGTTTCACACTTTTGAT	59.6	387	INTERGENIC				
CaPOPI_1503	Ca3	34916105	GTTTT/GTTTTTT	TCGACCATCGTCATACTCCA	TCTCCCTTCATATGACCCTT	60.1	671	INTERGENIC				
CaPOPI_1504	Ca3	34932929	TAAAAAA/TAAAAAAA	ACTTGCTTGCACCTCGTTT	TTGAAAGATGACTCTTCA CCGA	59.9	631	INTERGENIC				
CaPOPI_1505	Ca3	34943202	ATTT/ATTTT	TGCATTTTGTGATTGTGTGTG	GCTGGCTCTTGGGTATGAG	60.5	454	INTERGENIC				
CaPOPI_1506	Ca3	34943765	ATTTTTTTTT/ATTTTTTTT	GTGTTTGCTTGCTTTGACCA	CGGAACTACTCCATCGTGAA	59.9	384	DRR	Ca_00771		S1Fa-like	Golgin, RAB6-interacting
CaPOPI_1507	Ca3	34953897	TAAAAA/TAAAAAAA	CCCGTGATTCTCTACACA	GAACTCGCTTGAGGACGAAG	58.6	395	INTERGENIC				
CaPOPI_1508	Ca3	34954280	TC/T	CTTCGTCTCAAGCGAGTTC	TGCATGCAGGAGAAGTATTTATT	60.1	681	INTERGENIC				
CaPOPI_1509	Ca3	34958868	ACCCG/ACCC	GCAACACCATGATAACGTGC	GATGAGATGTTGCGCCTGTT	60.0	220	INTERGENIC				
CaPOPI_1510	Ca3	34964095	GCC/GCCCC	GGTGACCATGAAGCTCGTTT	GCAATCAACAAACAAGTGTGC	60.1	488	INTERGENIC				

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CaPOPI_1511	Ca3	34967661	GTATTTTATTTGATATATTT/GTATTTT	TGGTGGTTTGGACTTG ATG	ATCTGTAATTGGCAGGC AGG	59.4	773	INTERGENIC				
CaPOPI_1512	Ca3	34970200	CTTTTTTT/CTTTTTTT	AACACCAACAGATCCC CAG	CAAGCTAAAATGGCTTC CCA	59.8	234	INTRON	Ca_00772		GRF	WRC
CaPOPI_1513	Ca3	34972470	TA/T	ATGAAGCTTTGGATTGT GGG	TCCACAGCGTACCAACA AAA	59.9	491	INTRON	Ca_00772		GRF	WRC
CaPOPI_1514	Ca3	35019374	A/AG	CCCCTGAAAATCGTATC ACAA	GCTGAGTTTAATGACCC GGA	59.8	765	DRR	Ca_00776	Q	E2F/DP	ABC transporter-like
CaPOPI_1515	Ca3	35030161	GC/GCTACTAAAGTTC	GATGTCCAATCCGACG ACT	GAAACCGGATTTTCCCA CTT	60.1	370	INTERGENIC				
CaPOPI_1516	Ca3	35031349	CAA/C	ACTCATCTGTTCCACA GCC	ATTCATGATGGTCCCTC AGC	60.1	584	INTERGENIC				
CaPOPI_1517	Ca3	35033028	GATATA/GATA	TTCAAAGTAGTCACACC AACGG	TTTCATGTTGTTCCCCCA AT	60.1	477	DRR	Ca_00777	R		
CaPOPI_1518	Ca3	35035644	TA/TAA	GCTGAAGTCCGGATTAC CAA	TCATGCTGCTTCAAAGG TTG	60.1	701	INTRON	Ca_00777	R		
CaPOPI_1519	Ca3	35040031	GA/GAA	CATTCCAACCACTTC CCT	GAACAACCAACATCTTT GGG	59.8	521	INTRON	Ca_00777	R		
CaPOPI_1520	Ca3	35040555	ATT/AAAAAAAAGTT	AGCAAGGCCATCTTTCT TCA	TCAAGCTCTGCATATGG GTG	60.0	259	INTRON	Ca_00777	R		
CaPOPI_1521	Ca3	35061749	A/AAGTGT	TCAATACCCAGCACCA AAT	TTCTGCCTTCCATTCAAA CC	60.2	710	CDS (FRAME SHIFT)	Ca_00778	Q	E2F/DP	ABC transporter-like
CaPOPI_1522	Ca3	35077901	ATTTT/ATTTT	GTCCATCACGACTTGGA CCT	TGCAGTCCAGCATTGGT AAC	60.0	281	INTERGENIC				
CaPOPI_1523	Ca3	35086678	ATTTT/ATTTT	TCTGCTTCATGTGGCAA AAG	CATGTTGGAGACTGCGA TTG	60.0	487	INTRON	Ca_00781		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_1524	Ca3	35086999	TGTTGCAGTTGCAGTTG/TGTTGCAGTTGCAGTTGCAGTTG	TGTTGTGGTGGTGTGT TCC	TCACTCATTTGCGTTCT TG	60.3	458	CDS (large-effect mutations)	Ca_00781		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_1525	Ca3	35100602	TAAAAAA/TAAAAAA	TTATAAAGTTTGGGGCA CCG	CAACAGCGGTACAATCA TCG	59.8	701	INTERGENIC				

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CaPOPI_1526	Ca3	35101262	TTAAAAAGTAAAA/TAAAAAGTAAAAAGTAAAA	CGATGATTGTACCGCTGTTG	CGAAGGAAGTGTATCCGAA	60.1	885	INTERGENIC				
CaPOPI_1527	Ca3	35106644	AATATATATATATA/AATATATATATA	TGTCAAATGGGAAAGGGAAG	TTTGCTGCAATACATTTTCAGG	59.9	608	INTRON	Ca_00783	S		Protein of unknown function DUF914, eukaryotic
CaPOPI_1528	Ca3	35117240	CTTT/CTT	GGTGCACCATAACAACAACAA	CATGGCATCGTAACAACGAC	59.7	580	DRR	Ca_00785	G	C3H	Metallo-dependent phosphatase
CaPOPI_1529	Ca3	35119008	G/GCACTTTTA	AGTTGGACCCACTTTGTGG	AAAATGGATGGGTCTGTGTC	59.9	545	INTRON	Ca_00785	G	C3H	Metallo-dependent phosphatase
CaPOPI_1530	Ca3	35136413	CTAT/CTATATAT	ATACCACTAGCACGCACACG	TTTATGCATATCACATCAACAAAAA	59.8	660	INTERGENIC				
CaPOPI_1531	Ca3	35138675	TAA/TAAA	AGGGCCAGATTCTCTTG GTT	GTCAGATGAATCCCGCATC	60.1	563	INTRON	Ca_00787	G	C3H	
CaPOPI_1532	Ca3	35143342	ATTT/ATTTT	CACATGCACTTTGGAGTTGG	TCTTCGTCTCCCTCCATTTC	60.2	428	DRR	Ca_00788	G	C3H	Metallo-dependent phosphatase
CaPOPI_1533	Ca3	35147082	T/TAAAGA	GTCGGAGCCAAAAATGA AAA	TGTGTTTCTTTCCAGCAGAGAC	60.1	317	INTERGENIC				
CaPOPI_1534	Ca3	35166785	TAGAAAG/TAG	TGGCATGTGTTTGTCA TTT	AATGTGACCAACTTCCTCGG	59.8	859	INTERGENIC				
CaPOPI_1535	Ca3	35187164	GTCT/GTCTCT	GGGCACTAAAACAAAAGGCA	TCAAATCCTGTGGTTGTGGA	60.1	588	DRR	Ca_00791		bZIP	Basic-leucine zipper (bZIP) transcription factor
CaPOPI_1536	Ca3	35204680	AT/ATCT	TGGCCAAATCACAAACCTATT	AATACCAATTTGGCGAGTGC	59.3	560	INTERGENIC				
CaPOPI_1537	Ca3	35213093	CTTTT/CTTT	GCCATCACATTCATGACAAAA	TGATATTGCAAGAAACCCCA	59.4	758	INTERGENIC				
CaPOPI_1538	Ca3	35215168	TTTTTCCTTTTCATTTTCCTTT/TTTTCC TTTTCATTTTCCTTTTCATTTTCCTTT	GCGAAGAAAAAGAGGTG GTG	GTAATCGACAGCCTGCAACA	60.0	316	INTRON	Ca_00796	C		Ubiquinol-cytochrome C reductase, UQCRX/QCR9-like
CaPOPI_1539	Ca3	35230228	CAA/CAAA	ACTCGCCTAAATTCTGCACG	GAAACTCCACGCTGAAAGC	60.4	502	INTERGENIC				
CaPOPI_1540	Ca3	35241980	CTT/CTTAGTT	GGGACGCTCATACAATG GTT	CGCACAGTGAAGTGCAAGT	59.8	331	INTRON	Ca_00801			SOUL haem-binding protein

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CaPOPI_1541	Ca3	35247904	CATATATAT/CATATAT	CACTATCTTTGGGCGGT TGT	TTCTCTGACCGTGAAAG TGG	60.0	382	INTERGENIC				
CaPOPI_1542	Ca3	35248340	AATTATATT/AATT	ACCACTTTCACGGTCAG AGA	TACAATTTGCACTCCAC CCA	58.3	870	INTERGENIC				
CaPOPI_1543	Ca3	35260978	TACT/TACTGTAAGTCACT	ATGGGAACCAATTGTT GGA	GCCTTGTGTTGGGCTA TGT	60.0	537	DRR	Ca_00803	O		Glutaredoxin
CaPOPI_1544	Ca3	35261808	CGTCATAATGTCATAATGT/CGTCATAA TGT	ACATAGCCCAACACAA GGC	GAACAGTTTCACCCCCA AAA	60.0	584	DRR	Ca_00803	O		Glutaredoxin
CaPOPI_1545	Ca3	35265195	TC/TCC	TTGGAGTCAGAAAT CCCA	GCAACGAGGATTGACCG TAT	59.4	820	INTERGENIC				
CaPOPI_1546	Ca3	35284220	ACT/A	TCACGTTCAACGATTGG CTA	CCTCGCTGATGCTTGT GTA	60.3	151	INTERGENIC				
CaPOPI_1547	Ca3	35291358	GAAAA/GAAAA	ATGCATGCAGATCAGAC GAC	TGCACAAATGGGTTCTG TGT	59.8	283	INTRON	Ca_00808	U		Signal recognition particle, SRP54 subunit, GTPase
CaPOPI_1548	Ca3	35299387	TAAA/TAAA	CCTCTGGCATCGAAAGA AAG	ATTGAAGGCCCTCTACA GCA	59.9	639	INTRON	Ca_00809	T		PAK-box/P21-Rho-binding
CaPOPI_1549	Ca3	35300047	CAAAAA/CAAAAA	AAAAGGAATGTTGGCC TGA	GGCTGGCCTTCTGATGT TAG	59.5	773	INTRON	Ca_00809	T		PAK-box/P21-Rho-binding
CaPOPI_1550	Ca3	35303259	AAAG/A	ACTAACCATTCGCTGCC ATC	CACCACCCTCATTGT TTG	60.1	821	INTERGENIC				
CaPOPI_1551	Ca3	35303338	TAAAAAAAA/TAAAAAAAA	AGTAAGGAATTGGGGA GCC	CACCACCCTCATTGT TTG	59.4	683	INTERGENIC				
CaPOPI_1552	Ca3	35307396	TAAA/TAA	CAATCATGCGATTGCA TTC	ATTTGGTTTTGCGATGA AGC	60.0	636	INTRON	Ca_00810	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_1553	Ca3	35307977	AT/ATT	GCTTCATCGCAAAACCA AAT	TATAATCGCAAAATGC CGC	60.1	212	INTRON	Ca_00810	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_1554	Ca3	35317314	TATATAATATAATAT/TATATAATAT	TGACGTTGTTGAGATG AAAA	TGTCGGTCCACTCTCTA CCC	59.2	590	INTRON	Ca_00811			Condensation domain
CaPOPI_1555	Ca3	35329937	TA/TAA	ATAATATGCGCCTGCTT GCT	TCCAAATCGGCTCGTAA AAC	59.9	473	INTRON	Ca_00812	Z	MYB_related	Kinesin, motor domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1556	Ca3	35336928	GT/GTT	TCTAAACTCTCGCCCTTG	ACCGAACCTTTTGGGTTGTA	59.4	607	INTRON	Ca_00813	G		Glycoside hydrolase, family 32
CaPOPI_1557	Ca3	35361414	AAATAATAATAATAAA/AAATAATAATAATAA	GGAAGAAGAAGCTACGCCAA	AGAACCAAACCAACCACTCG	59.6	696	INTERGENIC				
CaPOPI_1558	Ca3	35362095	ATATTATT/ATATTATTATT	CGAGTGGTTGGTTTGGTTCT	TGCTTAATTTTCAACAAAGTTGC	60.0	789	INTERGENIC				
CaPOPI_1559	Ca3	35365941	ATTTTTTTTT/ATTTTTTTTTTT	ACAACGGGGTGTCACTAC	TTGGTGGGTATCTTGTGAAGC	59.7	681	DRR	Ca_00817			Protein of unknown function DUF584
CaPOPI_1560	Ca3	35368592	TA/T	TCAACTCACCACCAATCAA	GCCGATTCTGAATATGTGTAAGG	59.9	617	INTERGENIC				
CaPOPI_1561	Ca3	35370619	GAAAAAAAA/GAAAAAAAA	AAAATGTTTTACAGTCCGTTTG	CCAAATCTTTGGCACTCGAT	58.1	388	INTERGENIC				
CaPOPI_1562	Ca3	35390580	CG/C	TAGATCGGACGGTCGAATC	CACGCACCTAGAACTTGACAG	60.0	704	INTRON	Ca_00819	O		Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
CaPOPI_1563	Ca3	35393263	CTTTTT/CTTTTTT	AAGGAGATGCATGCCCTATG	CACCATCCCATATTGGACC	60.1	715	INTRON	Ca_00820			Protein of unknown function DUF1022
CaPOPI_1564	Ca3	35395949	AG/A	AAGTGACCACTCCAAACT	TGAAGACATGCAAATGTTACCA	59.6	575	DRR	Ca_00820			Protein of unknown function DUF1022
CaPOPI_1565	Ca3	35396014	CAAAAA/CAAAA	AAGTGACCACTCCAAACT	ATCTGTGTCGACCGAAAAGG	59.6	721	DRR	Ca_00820			Protein of unknown function DUF1022
CaPOPI_1566	Ca3	35397271	TGTC/T	GATTCTCTTCACCGCTGCTC	ACAAACCGTTATTTCCGCA	60.1	663	INTRON	Ca_00821	KA		Dcp1-like decapping
CaPOPI_1567	Ca3	35403982	ATCT/AT	TTCGCCTGCTCTTTTTGT	TTGGTCAAATCATTCAATCAGA	60.1	730	INTERGENIC				
CaPOPI_1568	Ca3	35436004	ATTTTTTTTT/ATTTTTTTTT	GAAATAACGTTCCGCGTGTT	CATCATTGCCAAGTGCAAGT	60.0	454	INTERGENIC				
CaPOPI_1569	Ca3	35440193	T/TCA	AACTGTGCAGCATATCCATAAA	CAAGGGCGGGTCTAGTATGT	57.4	410	INTERGENIC				
CaPOPI_1570	Ca3	35468557	TG/T	CGAACCATGCTTTGGAGATT	GCAGATGGTCCTTTTTCAGC	60.1	472	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1571	Ca3	35488328	GAAA/GAA	CTCGCTGGAATTTGCTA ACC	AGGACGTTGCTGCAAGA TTT	59.8	502	INTRON	Ca_00832	S		TLDC
CaPOPI_1572	Ca3	35505847	TAAAA/TAAA	CCGTCTCCAATATAAC CCA	TGTTTGGAGGGAAAAACA AGG	59.6	334	INTERGENIC				
CaPOPI_1573	Ca3	35528890	ATTAT/ATTATTTTAT	AACGTCGACCAGCCTAC ACT	ATCCACACAAAACCTCGG CAT	59.8	422	INTERGENIC				
CaPOPI_1574	Ca3	35532624	TG/T	CACATAATGTTGGCGTG GTC	ACCGTATGTGGACTCTC GCT	59.8	797	INTERGENIC				
CaPOPI_1575	Ca3	35558006	TAA/TA	ATCCCGCGTAATTCCTC TCT	ATCCCTAACATTTCCG ACC	60.1	403	INTERGENIC				
CaPOPI_1576	Ca3	35562721	A/AT	TGATCTATTTGGTGGAT ATGAGG	TGCAATAGGTAAAGCCA CCT	58.0	795	INTERGENIC				
CaPOPI_1577	Ca3	35568618	AACGTACGT/AACGT	TGTGGCATGCAATGCT TAT	TCCTGTGTTGTTGTGTC CGT	60.1	572	DRR	Ca_00841			NIF system FeS cluster assembly, NifU, C-terminal
CaPOPI_1578	Ca3	35574829	AG/A	TTCAAGATTGAAAATGCT TTGTG	AATCGCATCGGCTAAAC AAT	59.3	412	INTERGENIC				
CaPOPI_1579	Ca3	35591231	TAAAA/T	CACACCTTTGAAGATGG GTCT	TGTCTCCGGATAGATGA CATTG	59.1	287	DRR	Ca_00843		bZIP	Late embryogenesis abundant protein, group 2
CaPOPI_1580	Ca3	35596803	ATTTTTTT/ATTTTTTTTT	GTC AACGCAAGCGAAAA CTA	CGAAAAATCATCCGAG AAA	59.1	524	DRR	Ca_00844		bZIP	Late embryogenesis abundant protein, group 2
CaPOPI_1581	Ca3	35600454	TAA/TAAA	AATTTACAGTCCCGTC ACA	CAATGCGACTGGGTTTA CCT	59.0	334	DRR	Ca_00845			Late embryogenesis abundant protein, group 2
CaPOPI_1582	Ca3	35602083	CATGTTTTAT/CAT	GGGTGCGTTAGTGCAAT TTT	GCCATGCTTTAACGAAG AGG	60.0	940	INTERGENIC				
CaPOPI_1583	Ca3	35614019	ATTTTTTTTT/ATTTTTTTTTT	TGATCAAGATTGAATTT TTGTTTTTC	ATCCCCGTGTGTTGTG TTT	59.8	256	INTERGENIC				
CaPOPI_1584	Ca3	35618022	GTTTTTTTT/GTTTTTTTT	TGCGTACCTTAATCAGG AACAA	TTTACGCGGCGTATTT TAC	59.6	882	INTERGENIC				
CaPOPI_1585	Ca3	35618119	T/TC	TGTGAAACGAACAAAGC TTAAA	TTTACGCGGCGTATTT TAC	57.7	555	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1586	Ca3	35626631	ATTTTT/ATTTTTTT	TTGAATCTGAATCACCGCTTT	CCAAAAGGAGTATGGATCAGTAA	59.7	459	DRR	Ca_00850			
CaPOPI_1587	Ca3	35635776	CTTTT/CTTT	GTAATTTTGGCGCTGGTGT	GCGAATGCATAGAGCCTACC	60.0	635	INTERGENIC				
CaPOPI_1588	Ca3	35644626	TTCTC/TTCTCTCTC	CTCCCAAGAGTGAGAGCACT	CAGTTGGAGGTACCACCGTT	60.0	269	INTRON	Ca_00852	S		
CaPOPI_1589	Ca3	35652779	GTT/GTTTT	AAGTGTGTTGGTGGTGGTGGT	CCACTGTCCAGTCTCTGCA	60.2	499	INTRON	Ca_00853			
CaPOPI_1590	Ca3	35678085	TTCT/TT	TTGAGCACGACAGAATCACT	ACAATGGCCCAACTCTGTTC	59.8	441	DRR	Ca_00855			Glycosyl transferase, group 1
CaPOPI_1591	Ca3	35679181	ATTTTTTT/ATTTTTTT	TTCATTCTTTGGCTTGGGAC	CGTCATGGTCGTGGCTTTAT	60.1	959	DRR	Ca_00856	R	SBP	Malate transporter, aluminium tolerance
CaPOPI_1592	Ca3	35697688	TAAAAAA/TAAAAAA	TTTCATATCCACCCGTAACA	TGAATTTGCCTAATTTGGTCC	58.8	628	INTERGENIC				
CaPOPI_1593	Ca3	35699071	CTGTAATGTAAT/CTGTAAT	ACGAATCTCTCAACCACTCGG	TGAGGCTCTCTTTGTGACTTTG	60.1	711	INTERGENIC				
CaPOPI_1594	Ca3	35699306	TAAAAA/TAAAAA	GCTTCCTGGTAGGACAAACAA	TGAGGCTCTCTTTGTGACTTTG	59.2	455	INTERGENIC				
CaPOPI_1595	Ca3	35703336	CAAAAA/CAAAAA	CGGATATGCGGACAAAAACT	TTAGCTTTGGGGTTTGTGG	60.0	600	INTERGENIC				
CaPOPI_1596	Ca3	35703988	CA/CATAATAA	CCATCAAACCCCAAGCTAA	CACGTGTTCTTTTCAACCTCTCG	59.9	942	INTERGENIC				
CaPOPI_1597	Ca3	35706702	AAAATTAAATT/AAAATT	TCGGCCACTATTTCTTCCAC	CGTTGTGCCATAATTGGGAT	60.1	985	INTERGENIC				
CaPOPI_1598	Ca3	35725827	TAAAAA/TAAAAA	AAATCATAAGAACAAGGAGGATCG	GCACCCCTCCTTAGAGTCC	59.9	549	INTERGENIC				
CaPOPI_1599	Ca3	35725900	CTAAA/CTAAAGTAAA	TGTGTGTGTCTACCAAAATACTCG	TTTCCACACTCTAATCGGGG	59.1	743	INTERGENIC				
CaPOPI_1600	Ca3	35726533	TTATATA/TTATATATATA	CCCCGATTAGAGTGTGGAAA	GCACCTTCACATGGTGTGGT	59.9	410	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1601	Ca3	35730551	CATT/CATTAAATT	TTAAAAGCCATGGGCA TAA	TGGTGGTGCTGGACAAT TAG	60.3	125	INTERGENIC				
CaPOPI_1602	Ca3	35733605	CTTT/CTT	TCTCCCTTTCTTTCAAT TT	AAAAACGTTAATTGAGA CAGCAA	57.7	360	INTERGENIC				
CaPOPI_1603	Ca3	35767362	AAAAA/AAAAATAAAA	GGGTGCTTCCTCAATCT TCA	GACTTTGAAGTCGGCA AAA	60.2	798	INTERGENIC				
CaPOPI_1604	Ca3	35768780	T/TC	CCTTATCCCCGAAATTT GAA	GCGGATAGCAAATCGTT CAT	58.9	271	INTERGENIC				
CaPOPI_1605	Ca3	35768860	TAAAAA/TAAAAAAA	CCTTATCCCCGAAATTT GAA	GCGGATAGCAAATCGTT CAT	58.9	271	INTERGENIC				
CaPOPI_1606	Ca3	35770921	GTAAT/GT	GCAATGGTGCAGTAAAG AGA	AATTGAGGTCCCGTCAG TTG	60.0	448	DRR	Ca_00863	U	bZIP	Target SNARE coiled-coil domain
CaPOPI_1607	Ca3	35776584	TTATATAT/TTATATATAT	GGTGGTTTTGCACTTTT GCT	TCACATACTCGCCAGAC TGC	60.2	712	DRR	Ca_00865	R	G2-like	RNA recognition motif domain
CaPOPI_1608	Ca3	35779416	CTTTTTTTTTTT/CTTTTTTTTTTT	GCAAACTCTGTGCTCCT GTC	TTCCATTTCACTCACCAC CA	60.0	548	DRR	Ca_00866	K	NF-YA	CCAAT-binding transcription factor, subunit B
CaPOPI_1609	Ca3	35783476	ACTATTC/AC	TGGAAGTCAACTCAAT GCG	CTTACATCGAGCCGACA CAA	59.8	745	INTRON	Ca_00866	K	NF-YA	CCAAT-binding transcription factor, subunit B
CaPOPI_1610	Ca3	35783609	ATGT/ATGTGT	TGGAAGTCAACTCAAT GCG	CTTACATCGAGCCGACA CAA	59.8	745	INTRON	Ca_00866	K	NF-YA	CCAAT-binding transcription factor, subunit B
CaPOPI_1611	Ca3	35784715	TAAAAA/TAAAAA	GGTGCTGCTCCTGAATT AGC	GGCTCCAATCTAATGGG GTT	60.0	798	INTERGENIC				
CaPOPI_1612	Ca3	35788163	GATAAATTTTTATAAA/GATAAATATTT TATAAATATTTATAAA	CCTTCACCTTAGGCCAT TGA	CACCTTGATTTACCACA CTCG	60.1	645	INTERGENIC				
CaPOPI_1613	Ca3	35796430	CTTTT/CTTT	GCAATCTTGAGCTGGAG ACC	GGCACAAGTCAAATGGT CAA	60.0	909	INTERGENIC				
CaPOPI_1614	Ca3	35799677	ATTTTT/ATTTT	TAAGTCAATTTGATTGC GGA	TGCTTTTGCAAGTGTTTT TGA	60.2	610	INTERGENIC				
CaPOPI_1615	Ca3	35801766	TAA/TA	TTACCATGATTGAGGCA CCA	CCTTGTTTGGTTTTGGTT GG	59.9	395	INTERGENIC				

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CaPOPI_1616	Ca3	35809791	CTTTT/CTTTT	CCGGAAGGAAAATCCA AAT	TGCGGTTGTTTGTGT GTT	60.1	297	INTRON	Ca_00868			
CaPOPI_1617	Ca3	35811115	TTTTTTTTTTTTTTTTTTTT A/TTTTTTTTTTTTTTTTTTA	TTTTGGGTTTCTCACTG CC	TGGTAGTAAATCACTCG CAGTTG	60.1	455	INTERGENIC				
CaPOPI_1618	Ca3	35811467	CTATAT/CTAT	TGAACAATAAAATCAA CTGCG	TCTGAATTTCTCCGTG GAT	59.2	450	INTERGENIC				
CaPOPI_1619	Ca3	35833491	TTA/T	TGTGAGAAAGCATCAA ACCT	CAAACTACGGTCGGTG CCT	57.5	238	DRR	Ca_00871			Dihydroneopterin aldolase
CaPOPI_1620	Ca3	35852219	AAGGAATTGACTAG/AAG	CCGGCCTGTCAGACCTA ATA	TGGCCAACAAGACAATT TCA	60.1	639	INTERGENIC				
CaPOPI_1621	Ca3	35856021	ATTTTTTTTTTT/ATTTTTTTTTTTTT	CTTTGACCGAAGCATT GGC	ACCCCAAAAAGGAGTG TTC	59.8	435	INTERGENIC				
CaPOPI_1622	Ca3	35859927	TGGG/TGGGG	GAAATCAATTGAAAGAA AGCCA	TGTCAACAATGTTATCTT CACAAAA	59.6	808	INTERGENIC				
CaPOPI_1623	Ca3	35859979	ATCTTCTT/ATCTT	AAACGTCATAATTGCTTA TGGG	TGGCTTTTGTGTTGAAGA TTTTG	58.1	205	INTERGENIC				
CaPOPI_1624	Ca3	35862589	ACCC/ACC	TTCAACTGTTCTACGGC AACA	TGGGGTTTCCAAAAGTT CAG	59.4	654	INTERGENIC				
CaPOPI_1625	Ca3	35873093	TC/T	TTCAATGGGAATGGGAA TGT	GTCTCCGACACCGACAC TTT	60.0	663	INTERGENIC				
CaPOPI_1626	Ca3	35887062	CT/CTAATAATT	GCAACATGAAAGCACGT TTG	CGTTGGAACCTGGAACC ATT	60.3	507	INTERGENIC				
CaPOPI_1627	Ca3	35894033	AACCTTTTACC/AACC	CACACAAATTGGTTGGT GCT	TCAAAAGTTTGACTCCTA AACGG	59.5	508	INTERGENIC				
CaPOPI_1628	Ca3	35894525	GTATATATATATATA/GTATATATATATA TATATATATA	TGAAACCTTTTACCAGA CTCCAA	GTTAATCAAAGGCCGA CAA	60.0	952	INTERGENIC				
CaPOPI_1629	Ca3	35895341	CAAAAA/CAAAAAAA	TTTCCTTAGGACGCGAA GAA	CGGAAGTTCCAATGGAG AAA	60.0	553	INTERGENIC				
CaPOPI_1630	Ca3	35911655	AG/A	GCATGCGACTCATTTAC CAA	TCGAATTATTTTGAGTT GGTTTG	59.7	599	INTERGENIC				

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CaPOPI_1631	Ca3	35917238	AC/A	ATCTTAGCCCACTCAATCCG	GTGTCGTAAGCCTCCTCGAA	59.2	522	INTERGENIC				
CaPOPI_1632	Ca3	35928795	ATTTTTTT/ATTTTTTT	GATGGGCATCATTAGTGTTTGA	TTCAGTTGCACCTCAACGTC	59.8	336	DRR	Ca_00885			
CaPOPI_1633	Ca3	35947883	CTTT/CT	TCTGTCTAGCCGTAGTCCTG	TTGAAATTTTGACCGCATCA	59.5	434	DRR	Ca_00889	J		Ribosomal protein L35A
CaPOPI_1634	Ca3	35960562	AGTTTGATT/AGTTTGATTGTTTGATT	TCCGACTTGGTAAACAGCA	TTTGACGAAATAAATTTGAAAAA	59.3	398	DRR	Ca_00891	V	GRAS	Alpha/beta hydrolase fold-3
CaPOPI_1635	Ca3	35960868	TAA/TAAA	GGATGCTACATTTCTTGTGG	TGAAGGAGGGAGAAACATGG	59.4	835	DRR	Ca_00891	V	GRAS	Alpha/beta hydrolase fold-3
CaPOPI_1636	Ca3	35973469	AC/A	TGCCAGTGATCATCGAAAAA	AGGGGCAAAGGTAACAAAGC	60.2	374	INTRON	Ca_00892	C		FAD-linked oxidase, C terminal
CaPOPI_1637	Ca3	35973692	CG/C	TGCCAGTGATCATCGAAAAA	TTCTGTGAAGGATGCAGCAG	60.2	778	INTRON	Ca_00892	C		FAD-linked oxidase, C terminal
CaPOPI_1638	Ca3	35974404	GAA/GGAAA	TAGCAACATCTGCTGCATCC	ATCACACGGGAAATCTGAGC	60.0	721	INTRON	Ca_00892	C		FAD-linked oxidase, C terminal
CaPOPI_1639	Ca3	35982476	TGG/TG	TCGAAAAGAACTTTATCCGCA	TGAATTGCTGTAGCCTGTGG	59.8	408	DRR	Ca_00893			Zinc finger, RING-type
CaPOPI_1640	Ca3	35990406	ACTG/A	TGAATTTACACCCTGCCCTC	GCTCGAGATGAAGGGACTTG	59.9	331	INTERGENIC				
CaPOPI_1641	Ca3	35994489	CT/CTAAATATT	TGAATGATGTTTCATTCCATCA	GAATTCGGAACAAAACGTTCA	58.8	311	INTERGENIC				
CaPOPI_1642	Ca3	36019541	AT/ATGT	ACCTTTGGATTTCATGGTTGG	CCGATAGCCATTGGACACT	59.6	614	INTERGENIC				
CaPOPI_1643	Ca3	36020478	ATT/ATTT	AGGTGAAGGTTGCGTTAGTGA	TCAAATTGTGTGGGAGAAACA	59.8	536	INTERGENIC				
CaPOPI_1644	Ca3	36021252	GAT/G	GTTTGCGGATTTGGTTGAGT	TATTTTAGGACCGCCTGACG	60.0	442	DRR	Ca_00901	O	CAMTA	MATH
CaPOPI_1645	Ca3	36032758	ATTTTTTT/ATTTTTTTT	GGTCATTTTGTTTCAGCGTT	TCGATTGGATAGTGCCATCA	60.0	705	DRR	Ca_00902	S	bZIP	Ubiquitin-associated/translation elongation factor EF1B, N-terminal

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CaPOPI_1646	Ca3	36040732	ATTTT/ATTT	CCACCAGTGCAGAAGTGA AGA	TCCGAACTGGAGAGTGT GAA	60.0	461	INTRON	Ca_00902	S	bZIP	Ubiquitin-associated/translation elongation factor EF1B, N-terminal
CaPOPI_1647	Ca3	36041204	ATT/AT	TTCACACTCTCCAGTTCC GGA	AAGTCGACGTTTGTGAAG GAGTTC	59.4	699	INTERGENIC				
CaPOPI_1648	Ca3	36043188	AC/ATC	TGGAATGAATTAAACCAT CACG	GCCACAAATCATGCTG AAA	59.7	245	INTERGENIC				
CaPOPI_1649	Ca3	36045650	ATT/ATTT	TGTGATTGAAAAGATGT GTCAAAA	GGGTACGGAGTGGAG GTAT	59.5	622	INTERGENIC				
CaPOPI_1650	Ca3	36076083	ATAAAA/ATAAAATTAAAA	TGTCAAAATTTGATTG CCA	CCTTGTTGAAACAAATG CAAGA	59.9	539	INTERGENIC				
CaPOPI_1651	Ca3	36086627	AC/ACC	ATTCCAACGGAAAACAT CCA	CTCCAAACAAAGCCTA CGA	60.2	605	INTRON	Ca_00907	I		Phosphatidic acid phosphatase type 2/haloperoxidase
CaPOPI_1652	Ca3	36089072	GAAAAAAAAA/GAAAAAAAAA	CACCTACTAAAAAGCGT GCTGA	TCCAAACAAACAAAG CCC	59.6	146	INTERGENIC				
CaPOPI_1653	Ca3	36107876	ATTTT/ATTT	CAATCCCTTTAACITCGC CA	GGTGGGTGACAATGATT TCC	60.1	658	INTERGENIC				
CaPOPI_1654	Ca3	36109027	CTTTTT/CTTTTTT	TCCATGCCATCAAAATC AAA	TTTCGTGAAGGCATACT CCA	59.9	316	DRR	Ca_00909	J		Ribosomal protein L21e
CaPOPI_1655	Ca3	36109369	CTTG/CTTGTTG	TGGAGTATGCCTTCACG AAA	TGCCGTGGTTAAGGGAA TAG	59.3	652	DRR	Ca_00909	J		Ribosomal protein L21e
CaPOPI_1656	Ca3	36120455	TGGG/TGG	AAAGCACCTGCAAGAAG GAA	GGCTTGGTCTCTTCCAA TCA	60.0	479	INTRON	Ca_00911	D		
CaPOPI_1657	Ca3	36120818	TA/TAA	TGATTGGAAGAGACCAA GCC	CAATGGTGCAACAACT TGG	60.2	680	INTRON	Ca_00911	D		
CaPOPI_1658	Ca3	36129655	GATATA/GATA	TTGCTCGTTTGATTGGT GTG	TTTTTGTGATTTACGTA AGGGTA	60.7	589	DRR	Ca_00912	YU		NPL4
CaPOPI_1659	Ca3	36129790	T/TC	TTGCTCGTTTGATTGGT GTG	TTTTTGTGATTTACGTA AGGGTA	60.7	589	DRR	Ca_00912	YU		NPL4
CaPOPI_1660	Ca3	36135574	ATT/AT	CAATTAATTGGTTTGGAT TTGA	TTTAGCACCGTTCTGGT GTG	58.0	873	DRR	Ca_00913		M-type	Plant peroxidase

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database	
CaPOPI_1661	Ca3	36136545	CA/CATACATACATA	GCTTTGACACGTTTGCTTCA	ATTGTGGGAAGTGCTTACGG	60.0	368	INTRON	Ca_00913			M-type	Plant peroxidase
CaPOPI_1662	Ca3	36138195	TAAAAAAAA/TAAAAAAAAA	AGCTAATGAGCGGAAGCAAA	AATCTCCAAATTGGTGGTGG	60.1	558	INTERGENIC					
CaPOPI_1663	Ca3	36148820	TAAAA/TAAA	TTGCTTATGTCTCACGGCTG	CACCTTTGGAAGCAAACAGAG	60.0	901	INTERGENIC					
CaPOPI_1664	Ca3	36168799	CTCATAAGTCA/CTCA	GCCTGCGAAAGACAAAGTTC	ATTTGCAAGAGCTGCTGTTT	60.0	610	INTRON	Ca_00918	KTDL			BRCT
CaPOPI_1665	Ca3	36178743	TAA/TAAA	TGGATAAGACCGGAGAAATGC	TCCTTATAAAATTATCATGCACTCAA	60.0	690	DRR	Ca_00921	Q	B3		Pyridine nucleotide-disulphide oxidoreductase, class-II
CaPOPI_1666	Ca3	36195467	TTTTATTATTATTATTATTATTATTATTATT/TTTTATTATTATTATTATTATTATT	TATTGCCGACGTGAGTCTGA	TTCCCTTCTTTTCGTCTGC	60.4	283	DRR	Ca_00923			bHLH	KIP1-like
CaPOPI_1667	Ca3	36203025	CACTTAC/CAC	ATCGAAGCCGGTTAGTTT	TACATCTTAATTGGGCCGGA	60.0	168	INTERGENIC					
CaPOPI_1668	Ca3	36204918	ATTT/ATTTATTAAGTTT	GTCGTTGGAGTCTTTGCAT	TTCAACAAATGTTGACCGAA	60.3	452	DRR	Ca_00925				rRNA processing
CaPOPI_1669	Ca3	36207784	GA/GAA	TGGGTTCAATAGCCACATCA	GTTCAAACCTCGTTGCCATCC	59.9	237	INTRON	Ca_00925				rRNA processing
CaPOPI_1670	Ca3	36208259	CTT/CTTACATATAATTTTT	GAGGCAACGAAGTTTGAAACC	GGTTTCGTCGTCGTTTGAAGT	59.7	675	INTRON	Ca_00925				rRNA processing
CaPOPI_1671	Ca3	36218063	CAAAAAAAAA/CAAAAAAAAAA	TTGATGTCTCCCACAAGCTG	TAATCAGATGATCGCGCAAG	59.8	480	INTRON	Ca_00927			CO-like	Zinc finger, B-box
CaPOPI_1672	Ca3	36219342	GTTT/GTT	CATGTGGCGAAGAGAGTGAA	GTATTTCTTTGGGCGTGAA	60.0	531	INTERGENIC					
CaPOPI_1673	Ca3	36219993	TCA/T	TTACGCCCCAAAGGAATAC	ACCGGTGATGACTCCAGTTT	59.9	757	DRR	Ca_00928				Ubiquitin
CaPOPI_1674	Ca3	36226234	AATAGAT/AATAGATAGAT	TGGAGCCCATCGAAATAAAG	CCACATGGTGAAGAGCAGAA	60.0	729	INTERGENIC					
CaPOPI_1675	Ca3	36226833	CGAGGAGG/CGAGG	CACGAAATCCGAAATGGAAC	TTGTTTGCTCTGATTTTGAGA	60.3	537	INTERGENIC					

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1676	Ca3	36230990	T/TA	TCCAGTCCTTTCCTTTGGA	TGAGTTAAAGGACCACATGCC	59.6	353	DRR	Ca_00929	J		Ribosomal protein S19/S15
CaPOPI_1677	Ca3	36241653	CC/CCAC	TTCGCAGAAAACTATGCC	TCCGTATTCGAATTGAGACAA	60.2	808	INTERGENIC				
CaPOPI_1678	Ca3	36250776	AAATAATAATAATAATAA/AAATAATAATAATAA	GCAAAGCCAAACCGCTATAA	AACGCTAACGTTGGTTCAC	60.2	935	DRR	Ca_00933	O		Glutaredoxin
CaPOPI_1679	Ca3	36274277	T/TA	TGGGTTTTTCATTGGTTGGT	AAGCCGACTTCAAGAAGGAC	60.1	419	DRR	Ca_00937	J	Dof	Peptide chain release factor class I/class II
CaPOPI_1680	Ca3	36283526	ATTTTTTTTT/ATTTTTTTTTTT	GCGGTCGTGTGACAGGTACT	TCTTATGCCGTTTTCTTCG	61.2	654	DRR	Ca_00938	R		Domain of unknown function DUF255
CaPOPI_1681	Ca3	36286597	ATTTTTTT/ATTTTTTTT	TCATTTTGGCAACTTACCACC	TGCCTGAATTTATTGGGAATG	59.9	754	INTERGENIC				
CaPOPI_1682	Ca3	36295270	TTGTTTTCATGTTT/TTGTTT	TGTAGAGAACGGAAATGGG	TAAGGTGGCGAGGATTGAAC	59.9	593	INTRON	Ca_00939			Zinc finger, CW-type
CaPOPI_1683	Ca3	36308195	T/TC	TTTGCCACTTGATACAGCAGA	TTGAACCTAAACGATGACACCTT	59.5	309	INTERGENIC				
CaPOPI_1684	Ca3	36312854	AAA/AAATTAAGTAA	CTATGCACGAGTTTGGGGTT	CAATCAAGAAGCGCATTGAA	60.0	586	DRR	Ca_00941	D	TCP	Cullin, N-terminal
CaPOPI_1685	Ca3	36320561	CTTTTTTT/CTTTTTTTTTTT	GTCTCAAGCAATCCTCAGCC	CAACGAGAGAGTGGATGGT	60.0	442	INTRON	Ca_00941	D	TCP	Cullin, N-terminal
CaPOPI_1686	Ca3	36328591	GAAA/GAA	CACGATGAAATCACTATGAAAAGC	CGTCCAGACCTCCATTGTT	60.0	440	INTERGENIC				
CaPOPI_1687	Ca3	36352882	AT/ATT	TCACCTCGAGCAAACAAGTG	AAGCACCATTTGTAGTTTTCATGT	60.0	380	INTERGENIC				
CaPOPI_1688	Ca3	36356666	CAAAAAAAAA/CAAAAAAAAAA	ATTTAAAGTCACGCGGAGC	TCCAGGTATGCGGTAGTTCC	59.4	373	DRR	Ca_00944			
CaPOPI_1689	Ca3	36371742	ATTTTTTT/ATTTTTTT	GGGTTTTCTAGTCCCCAAG	TGTTTTTCATTATGTGCCCG	59.8	483	INTERGENIC				
CaPOPI_1690	Ca3	36381407	ATTTTTT/ATTTTTTT	TTTTGAGAGCGCATTTGTG	CCATGCTTCCACGTCTAAT	60.0	352	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1691	Ca3	36396966	AAAATT/AAAATTTCAAATT	CTCACATCTGATCGAAG GCA	ACTGTAACTTTGTGCTC CCG	59.9	332	INTRON	Ca_00950	P		Heavy metal transport/detoxification protein
CaPOPI_1692	Ca3	36397163	TTATATATAT/TTATATATATATAT	CTCACATCTGATCGAAG GCA	TGCAGCAGCAGAACCATTAC	59.9	708	INTRON	Ca_00950	P		Heavy metal transport/detoxification protein
CaPOPI_1693	Ca3	36399143	ATTTTT/ATTTTTTT	ATAATTGGGCCACACATCGT	TGCAATGTGGAATCAGAGAA	60.1	208	DRR	Ca_00950	P		Heavy metal transport/detoxification protein
CaPOPI_1694	Ca3	36399524	T/TG	ATAATTGGGCCACACATCGT	AACAAGCAAGCGCAACACTA	60.1	712	DRR	Ca_00950	P		Heavy metal transport/detoxification protein
CaPOPI_1695	Ca3	36410249	GAAAAAAAA/GAAAAAAAAAAAA	CGGAAATGTCATGTGTGTC	ATGTTTGTCCTTGCTCCC	59.8	458	DRR	Ca_00953		HSF	Rapid Alkalinization Factor
CaPOPI_1696	Ca3	36410296	GTTTTTT/GTTTTTTTT	ATGGTTGTTTCATCGTCCCAT	ATGTTTGTCCTTGCTCCC	60.1	126	DRR	Ca_00953		HSF	Rapid Alkalinization Factor
CaPOPI_1697	Ca3	36418781	GAAAA/GAAA	TCCTCCTTACCACATCGGTC	ACGTAGAAACAATGGCCGTC	59.9	929	INTRON	Ca_00954	G		Glycosyltransferase, ALG3
CaPOPI_1698	Ca3	36420292	GGAGC/G	TGTTTTTCGCTCATCCATTG	TGGTAGAAATCACGATGCCA	59.7	710	INTERGENIC				
CaPOPI_1699	Ca3	36420971	AATATATATATAT/AATATATATAT	TGGCATCGTGATTCTACCA	GGCCATGGTGATTGTAAAGG	60.1	746	INTERGENIC				
CaPOPI_1700	Ca3	36443050	ATG/A	TTGCAATTGAAGTTCCCA	GGCAAGCTCATTCTGCTTC	60.1	427	INTRON	Ca_00959	R		WD40 repeat
CaPOPI_1701	Ca3	36443105	GCATCAT/GCAT	TTGCAATTGAAGTTCCCA	GGCAAGCTCATTCTGCTTC	60.1	427	INTRON	Ca_00959	R		WD40 repeat
CaPOPI_1702	Ca3	36454087	CGAT/CGATCATATTGGAT	TGATTCGGTTTGTGCTGTGT	CGTGACAGCCCATAGTTGAA	60.2	931	INTERGENIC				
CaPOPI_1703	Ca3	36455748	AC/AGTTTACTCTTAATACATC	TCAAATTACAACAAGGGCGA	CGTAAGGGAGCAAAGTGTC	59.2	792	INTERGENIC				
CaPOPI_1704	Ca3	36458050	AG/A	TGGGTCCCAAAAGTGGTATC	CAATTTGGCCACTTGAA TGA	59.6	772	INTERGENIC				
CaPOPI_1705	Ca3	36458326	ATTTTT/ATTTTTTT	TTTGCAAGTGGCGGTAGTT	TGTTTTGCAAGGTGAAT TGG	60.7	525	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1706	Ca3	36490446	T/TCAC	CAGGGTCACCTGCTCAA AAT	TCCAAGATCAGTTGACT GCG	60.1	333	DRR	Ca_00965			Pectinesterase inhibitor
CaPOPI_1707	Ca3	36525538	AAT/AAAATCTTTAT	TCCAAGGACTAAAACGT CCAA	TCCAAGAGACTCATCC CAAA	59.6	519	DRR	Ca_00969			Late embryogenesis abundant protein, group 3
CaPOPI_1708	Ca3	36529799	AAAGA/AA	CCCTATCCAACATTCA GGG	ACCAAATGGTGGAAC TGC	60.0	722	DRR	Ca_00971	U		Exocyst complex subunit Sec15-like
CaPOPI_1709	Ca3	36530182	T/TC	GATTTAGCAGGAGTGCC GAG	TCGGATCGACTCTTTGG AAC	60.0	686	DRR	Ca_00971	U		Exocyst complex subunit Sec15-like
CaPOPI_1710	Ca3	36596139	GAAAAAA/GAAAAAA	AAAGTTTTGGCAAGTC GGA	AGAGCAAGGAAACCGAA TCA	59.7	596	INTERGENIC				
CaPOPI_1711	Ca3	36597966	TAAAAAAA/TAAAAAA	TAACCAACAACCGCATG AAA	TCAATTCTTAAAGAGG TGGA	60.0	242	INTERGENIC				
CaPOPI_1712	Ca3	36608541	T/TA	TGGCTCAAAGATAGGAT GGG	CCCTTCTCCATCAATCT CA	60.0	315	DRR	Ca_00981			
CaPOPI_1713	Ca3	36609637	CATATAT/CATAT	ATTGAAATGCGGGTTCT CAG	TTGATCACACGAGGAG CTG	60.1	519	DRR	Ca_00981			
CaPOPI_1714	Ca3	36614124	TGTA/T	TTGCATTTCAAAAGTTTC GC	TGTGGCTCAACGAGAGA TTT	58.9	277	INTERGENIC				
CaPOPI_1715	Ca3	36624385	CAAAAAAAAA/CAAAAAAAAA	TGATTTCACTGCACCA CAT	TGCAACACAACTCCTTT GC	60.0	517	INTERGENIC				
CaPOPI_1716	Ca3	36624455	ATTTTTTT/ATTTTTTTT	TGATTTCACTGCACCA CAT	TGCAACACAACTCCTTT GC	60.0	517	INTERGENIC				
CaPOPI_1717	Ca3	36624904	GTTT/GTTTCTTTTTT	TGCAAAGGAGTTTGTGT TGC	AACATAAAGAACAGAG CGGAGA	59.9	211	INTERGENIC				
CaPOPI_1718	Ca3	36625899	TTATTTATTTA/T	ATTCTACTGACTGTGCG CCT	CAACAGGAAGGGGATTA GAAAA	59.7	356	INTERGENIC				
CaPOPI_1719	Ca3	36636712	CTTTTT/CTTTTT	CGGATAACACTTGTGT TGAGTTT	GTCTTTCTTGATCCCG ACG	59.5	776	INTERGENIC				
CaPOPI_1720	Ca3	36638153	TG/T	TCGTCAACTCGCAACTC ATC	AAAAAGCCAAACAATTCT AGAAACA	60.0	487	INTERGENIC				

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CaPOPI_1721	Ca3	36638232	AATTTT/A	TCGTCAACTCGCAACTC ATC	AAAAAGCCAAACAATTCT AGAAACA	60.0	487	INTERGENIC				
CaPOPI_1722	Ca3	36652791	TGGG/TG	TCACAAAGAAAGCCAGC TCA	TCCAGAGCTTTTCATGG CTT	59.7	451	DRR	Ca_00986		bZIP	Cellulose synthase
CaPOPI_1723	Ca3	36682594	GTTTTTTTTT/GTTTTTTTTT	TTCATCGATGTTCCGAC AAA	CCAACTCGGTTCATTTA CTCG	60.0	536	INTERGENIC				
CaPOPI_1724	Ca3	36688981	TTCTTTATCTTTATCTTTATC/TTCTTTA TCTTTATCTTTATCTTTATC	AGGGGAGACAACCATAG GCT	GTGATGTGATTGGCTGG TTG	60.0	862	DRR	Ca_00990	O	C3H	Zinc finger, CCCH-type
CaPOPI_1725	Ca3	36697642	ATT/AT	CGACGCATATTTCAAT GACTT	TCTTTGGCAACAGGTT GGT	59.1	634	INTERGENIC				
CaPOPI_1726	Ca3	36697708	AC/A	CGACGCATATTTCAAT GACTT	AGTTGCATGCTTCTTTT GGC	59.1	645	INTERGENIC				
CaPOPI_1727	Ca3	36707043	CT/C	CTCCTCCCAGTGGTAAC AAA	CAGTGAAAAATTGAATC CCCA	57.6	595	INTERGENIC				
CaPOPI_1728	Ca3	36707318	TA/TAAA	CAAAAACAGTTTGGGGA TTCA	CATTTGACCTTACGTCC ATCC	59.8	502	INTERGENIC				
CaPOPI_1729	Ca3	36707636	TTTTATTTATT/TTTTATTTATTATTTAT T	CAAAAACAGTTTGGGGA TTCA	GATGATGGAAGGGGATG AGA	59.8	868	INTERGENIC				
CaPOPI_1730	Ca3	36716843	GC/G	TTTTATTTGAGGGGTGA CCG	GATGGATTGGTCGTGAG GTT	59.8	554	DRR	Ca_00995	O	MYB	Heat shock protein DnaJ, N-terminal
CaPOPI_1731	Ca3	36735770	AATAAATAAATAAATAAATAAATA/A AATAAATAAATAAATA	TACGTGGCCTATTAGGT GGC	GCATATGGTGATTGCTG ACTCT	60.0	648	INTERGENIC				
CaPOPI_1732	Ca3	36735874	TAAAAAA/TAAAAAA	TACGTGGCCTATTAGGT GGC	CGGCGGAGTCAGGTAAT AAA	60.0	834	INTERGENIC				
CaPOPI_1733	Ca3	36735945	AT/ATT	TACGTGGCCTATTAGGT GGC	ATGGGTAACCGGGTGTA TCA	60.0	874	INTERGENIC				
CaPOPI_1734	Ca3	36751775	C/CCTATTACAAGGAAA	TAACATCCATGGCCTCA CAA	CGGTTTGCTTTTGATA ATGG	59.9	835	INTRON	Ca_00998		C2H2	Glycoside hydrolase, family 3, N-terminal
CaPOPI_1735	Ca3	36752520	AAGTAGTAGTAGTAGTA/AAGTAGTAGT AGTAGTAGTA	ACGAATCAACTTGGCCT ACG	AGGGCAATGTACAATGG AGG	60.1	602	INTRON	Ca_00998		C2H2	Glycoside hydrolase, family 3, N-terminal

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1736	Ca3	36756795	TAAAAA/TAAAAAA	AAGTGCTTGTGCTGGA GTG	TCGTCGCATCTACAAAC AAAA	59.1	529	INTERGENIC				
CaPOPI_1737	Ca3	36932559	GAAAAAAAAA/GAAAAAAAAA	GTTACGATTTTCATTGG CGA	CTTTGGTATGTTGGGCC TGT	58.6	917	DRR	Ca_01018		WRKY	DNA-binding WRKY
CaPOPI_1738	Ca3	37017817	AATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATA	CAGAAGGCCAGGAGAA GAAA	TGTGCGTGAAGTTTCAT GGT	59.5	707	INTERGENIC				
CaPOPI_1739	Ca3	37030222	AATATATATATATATATATATATATA/AATATATATATATATATATATATATATA TA	GAAAAGCCCATTTTGTG TCG	AAAGGTTTGAAAATGGA TGGTC	59.7	593	DRR	Ca_01031	G	C3H	Protein kinase, catalytic domain
CaPOPI_1740	Ca3	37150967	ATTTTTTT/ATTTTTTTT	TTTTGCTTGCCTGAAAT TG	CCAAATGATAATCCATG GGC	59.9	604	INTERGENIC				
CaPOPI_1741	Ca3	37191129	TAAAAAAAAA/TAAAAAAAAA	TGGTTTCATTCATCTTT GCAG	GCCCAATCAACCCATT TTA	60.1	445	INTERGENIC				
CaPOPI_1742	Ca3	37428682	T/TGGA	TTGAGGATCAGCTACAC CCC	TGGAACAATTTGGTGG TGA	60.1	546	INTERGENIC				
CaPOPI_1743	Ca3	37594905	TTATATATATATATATATATATA/TTATATATATATATATATATATA	GTCCGCCCTAAAAGGT AGC	TCAAAACACCACATCAAA ACG	60.1	188	INTERGENIC				
CaPOPI_1744	Ca3	37989883	GTATATATATATATATATA/GTATATATATATATATATATATATA	TGTCACGGGTGGACAAA TTA	TAGGCGATTGTAGGGCT TTG	59.8	749	INTERGENIC				
CaPOPI_1745	Ca3	38129457	CATATATATATATA/CATATATATATA TATATA	CAAAAGCCGACCAAAA TTA	GGGCATGGGCAATAATC TAA	59.9	398	INTERGENIC				
CaPOPI_1746	Ca3	38139076	A/AC	TTGCATTAACTTGAAGC TTTTT	TCAGGCCAACCCAGTAC ATT	58.0	416	INTERGENIC				
CaPOPI_1747	Ca3	38141259	TTA/T	GGAAAGTCATGATGTCC TTTTT	GTCATTGTAAATGGCG GCT	57.2	436	INTERGENIC				
CaPOPI_1748	Ca3	38141514	ATTTTTT/ATTTTTTT	CCGCCATTACAAATGA CACT	TCGTCAAATTATTTAGC GCAT	59.9	536	INTERGENIC				
CaPOPI_1749	Ca3	38149993	ATTA/ATTAACCTTA	AGTTATTACATGCGGCA GGG	GCCAAACAGTGTGTAA TTCG	60.0	752	DRR	Ca_01158	C		Cystathionine beta-synthase, core
CaPOPI_1750	Ca3	38154708	CGGAGGA/CGGAGGAGGA	AGAGCGGAAAAGTTATC GCA	TTCATGTTGCCCTTTTG ACA	60.0	477	DRR	Ca_01160	L	MYB_related	DNA-directed DNA polymerase, family B, exonuclease domain

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CaPOPI_1751	Ca3	38164329	TG/TGAGAGAGAG	TATTCCTCCCAATTCCTAGC CC	CAAGATGCTGGCACAGAAA	60.1	740	INTRON	Ca_01160	L	MYB_related	DNA-directed DNA polymerase, family B, exonuclease domain
CaPOPI_1752	Ca3	38170265	TAA/TA	CCCAGATCTGCCTAATG GAA	GATGGGTTTGGAACATC CAG	60.0	594	INTRON	Ca_01160	L	MYB_related	DNA-directed DNA polymerase, family B, exonuclease domain
CaPOPI_1753	Ca3	38174447	A/AT	TTCACATCCCACTCATC GG	CTGGCACTGGCATTCTC AAT	60.5	628	DRR	Ca_01161		NF-YA	Lipoxygenase
CaPOPI_1754	Ca3	38205894	TAAAAAAAA/TAAAAAAAA	ACAACACTCGGCCTATC ACC	CTCCCCCTTCTCCAGGATAG	60.0	768	DRR	Ca_01163	E		Creatinase
CaPOPI_1755	Ca3	38206711	GAAAAAAAAA/GAAAAAAAAA	CTATCTGGAGAAGGGG GAG	GCTATTGCATTGGAGTT GCTC	60.0	706	DRR	Ca_01163	E		Creatinase
CaPOPI_1756	Ca3	38206767	AAGAG/AAG	CTATCTGGAGAAGGGG GAG	GCTATTGCATTGGAGTT GCTC	60.0	706	DRR	Ca_01163	E		Creatinase
CaPOPI_1757	Ca3	38215897	CTT/CTTCTTTCATT	TGTTGCCTGGAAATGAG TTG	TGCTGCATTGAAATCGA GTC	59.7	688	DRR	Ca_01165	R		
CaPOPI_1758	Ca3	38219148	A/AC	CTACCGGCTACTTCTT GCG	TATGCATGGTGAAAAAG CGA	60.0	463	DRR	Ca_01166	Z	B3	Kinesin, motor domain
CaPOPI_1759	Ca3	38221107	TCTCCT/TCTC	CCACTGGTGATTGAGG GGT	GAGAACTCATGTGCCGG AAT	60.0	566	CDS (large-effect mutations)	Ca_01166	Z	B3	Kinesin, motor domain
CaPOPI_1760	Ca3	38228425	A/AGTGTGAATAC	ATGATCCACTGAGATTC CGC	CCAGAGTGTGACGCTTT TGA	60.0	472	DRR	Ca_01168	R	bHLH	Pentatricopeptide repeat
CaPOPI_1761	Ca3	38240356	TCCCC/TCCC	GTGGTGAGTTCAAGTCC GGT	ACCGTTAGAGGAGAGGAGCC	60.0	475	INTERGENIC				
CaPOPI_1762	Ca3	38241149	A/AAT	GGCTCCTCTCTCTAAC GGT	GACAAGTGCAACAATTT TCATCA	59.8	527	INTERGENIC				
CaPOPI_1763	Ca3	38241297	TTTATT/TTT	TTGATGAAAATTGTTGCA CTTG	TTGCTAACACAAAAGTAT TTGAATGTC	58.7	189	INTERGENIC				
CaPOPI_1764	Ca3	38690322	AATATATATATATATATATA/AATATATATATATATATATATATATA	GAAGCAGGGAGAGGAGAAAC	TGTCATAGGAGATTATGCCAA	60.2	910	DRR	Ca_01224	K	Trihelix	SANT domain, DNA binding
CaPOPI_1765	Ca3	38764047	TAAAAATAAAA/TAAAAATAAAAAATAAA A	TGGGCTCCGAGAGTCTT ATG	CGTGGATTAAATCGCTAC CGT	60.4	253	DRR	Ca_01234		bZIP	Basic-leucine zipper (bZIP) transcription factor

[illegible]

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CaPOPI_1781	Ca4	1677374	TAAAAAA/TAAAAA	TCCAAACTAGTCCGACG TGA	AGCTGCTGGAGGAGTTG GTA	59.3	450	INTRON	Ca_07795			
CaPOPI_1782	Ca4	1771183	TATATATA/TATATATAACATATATA	GATCAATATCTCCATGC GGG	GTTGGGCACCGTCATAA AGT	60.3	423	INTERGENIC				
CaPOPI_1783	Ca4	1775612	TT/TTTCAATTTTGTCT	GAGAAATGGAGAGGGAA GGG	TCGTCTGACACCACCAA CAT	60.0	718	DRR	Ca_07800	K	HSF	Heat shock factor (HSF)-type, DNA-binding
CaPOPI_1784	Ca4	1782351	TAA/TA	TGGTTTGGATTGGAGC TGT	TAGATCCGGAATGAAGA CCG	60.5	361	INTRON	Ca_07801	T		Protein kinase, catalytic domain
CaPOPI_1785	Ca4	1791916	AGTTAGTTTGTTA/AGTTAGTTTGTTAG TTTGTTA	CGATATTGTCAAATGCG GTG	CAATGATCACACCAAGG TCG	60.0	741	INTRON	Ca_07801	T		Protein kinase, catalytic domain
CaPOPI_1786	Ca4	1831456	TTA/TTATA	TCCAATAAGGTTGCCTA AGGA	GAGATTAAGCCGGAAGA CCC	58.7	256	DRR	Ca_07804			Domain of unknown function DUF828
CaPOPI_1787	Ca4	1848187	TATAATAATAA/TATAATAATAATAA	AGAAGCAAAAGAGCCCT TCC	ATAGGAATATAGGCGCG GGT	60.0	323	INTERGENIC				
CaPOPI_1788	Ca4	1855105	TTTAT/TTTATTAT	CACGACCCTTTTCGATTG TTT	AAACCAGCTGCCAATTC TGT	60.0	430	INTERGENIC				
CaPOPI_1789	Ca4	1943645	CATATATATATATATATATATAT/CAT ATATATATATATATATATAT	GCACATGGTGTGAAACT GCT	TTGGGGAGATGGAAGAA AAA	59.8	662	INTERGENIC				
CaPOPI_1790	Ca4	2022623	AAATAATAATAATAATAATAATAATA ATAATAA/AAATAATAATAATAATAA TAATAATAATAA	AACGTGTTTGAGTGCGA AAA	TCGAGATGCGATTATGT GGA	59.4	819	INTERGENIC				
CaPOPI_1791	Ca4	2032207	TC/T	TGCTGAGTTCGAGGAAA GGT	CACATCTCTTGTTCGCT CCA	60.0	517	CDS (FRAME SHIFT)	Ca_07822	D		RNA-processing protein, HAT helix
CaPOPI_1792	Ca4	2032547	CTGTGTGTGT/CTGTGTGT	TGCTGAGTTCGAGGAAA GGT	CACATCTCTTGTTCGCT CCA	60.0	517	INTRON	Ca_07822	D		RNA-processing protein, HAT helix
CaPOPI_1793	Ca4	2034424	CTTTT/CTTTTT	ACCAGATACCGACCAA AAG	TTCTGCATACTTGCTCC ACG	60.0	352	INTRON	Ca_07822	D		RNA-processing protein, HAT helix
CaPOPI_1794	Ca4	2035282	GTTTTT/GTTTTTTT	CGCGCCAGAAGTATGTG ATA	TGGGCAGCTTAGACTGG ACT	59.9	275	INTRON	Ca_07822	D		RNA-processing protein, HAT helix
CaPOPI_1795	Ca4	2035697	ATTT/AT	AGTCCAGTCTAAGCTGC CCA	TGGAATCATGCCATGCT AGA	60.0	436	DRR	Ca_07823	R	MYB	Reverse transcriptase, RNA-dependent DNA polymerase

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1796	Ca4	2035798	A/AGTGT	AGTCCAGTCTAAGCTGC CCA	TGGAATCATGCCATGCT AGA	60.0	436	DRR	Ca_07823	R	MYB	Reverse transcriptase, RNA-dependent DNA polymerase
CaPOPI_1797	Ca4	2139392	TCCCCC/TCCCCCC	TATCTGGAACGACGACA TGC	TCGTTCGCCATTAAAGA GGT	59.7	558	INTERGENIC				
CaPOPI_1798	Ca4	2445623	AATATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATA	GGAGGTCACAACCACTC CAA	CGGACTTTCGACTTTCT TGC	61.0	654	INTERGENIC				
CaPOPI_1799	Ca4	2589224	CAGTTGCAAGTTGCAAG/CAGTTGCAA GTTGCAAGTTGCAAG	AAGATCGATCAGTTCCA CCG	ATTGGGAACCAACTGAC GAG	60.1	396	INTERGENIC				
CaPOPI_1800	Ca4	2688293	AT/A	AGCATGCTTCCACAAAG GAT	TTGGAGGTTGTGTTGTT GGA	59.7	532	DRR	Ca_12072			Domain of unknown function DUF296
CaPOPI_1801	Ca4	2729716	A/AGACATCAT	AGGGCTTGTAATGCCCT TTT	TTGGCTTCACAAGATAC CCC	60.0	654	INTRON	Ca_12075	Z		Actin-like
CaPOPI_1802	Ca4	2755654	CAAAAA/CAAAAAA	AATTCGTTGCACAATTTG GTT	GCATGCTAAATGCCATC GTA	59.4	801	INTERGENIC				
CaPOPI_1803	Ca4	2819881	TAAAAA/TAAAAAA	TTGTTACCTCAATCGTG GGG	TTGCCCTTACAAC TAC CAC	60.7	674	INTERGENIC				
CaPOPI_1804	Ca4	2891639	A/AG	TGTTGTGGTGCCACCTT TTA	TAATACACACGGCCAAG CAA	60.0	823	INTERGENIC				
CaPOPI_1805	Ca4	2894996	GAAAAAAAA/GAAAAAAAAA	AAAAGAAACGGAGGAAG TGTC A	TAAATACGGTGATCGGC CTC	60.1	127	DRR	Ca_12086	P	ERF	General substrate transporter
CaPOPI_1806	Ca4	2897791	ATATTTATTTATTTATTTATTTT/ATA TTTATTTATTTATTTATTTATTT	AAAAAGACATGCTTTCAA ITTGG	AAGCCTTGTTGGAGCAGT TGT	59.5	948	INTERGENIC				
CaPOPI_1807	Ca4	2929266	CATATATATATATATA/CATATATATA TATATATATATA	AAATGGCAATGAAATCC CTG	TCACTCTATCAAAATGTT C AAGCAA	59.8	628	INTERGENIC				
CaPOPI_1808	Ca4	3017713	ATTATTTTAAATTTATTTTAAATTTATTT TAAATTTATTTTAAATTTATTTTAAAT/A TTATTTTAAATTTATTTTAAATTTATTTT AAATTTATTTTAAATTTATTTTAAATTTA	GACAAATAGTGGGGCA ACC	TTGTATTGTTGGTGAGG CCA	59.3	902	INTERGENIC				
CaPOPI_1809	Ca4	3069954	TTTTATTATTATTATTATTAT/TTTTATT TATTTATTATTATTATTAT	AAACCAAACTGGCGAA AAA	TGAGAAAACATATTGGG AAGGC	59.6	686	DRR	Ca_12105			
CaPOPI_1810	Ca4	3081231	TAAAAAAAAA/TAAAAAAAAA	TCGCCCTTAATTGTTT GTC	TGCTAGGTGGCCCTGT GAT	59.9	571	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1811	Ca4	3832898	ATTT/ATTTTTT	CGGAGGGTACGAACCTGTAA	ACTGTTGTGGAAATCTGGGC	60.0	484	INTERGENIC				
CaPOPI_1812	Ca4	3966806	GAAAAAAAAA/GAAAAAAAAA	CCGTCGCTAACACACTCAA	TGCACCAACAATCCTTGCTA	59.9	814	INTERGENIC				
CaPOPI_1813	Ca4	3989437	AATATATATATATATATATAT/AATA TATATATATATATATATATATAT	TCCC GTTCCAAA CTTT CA	TGATAGCACAAAATCGTGGA	60.5	594	DRR	Ca_03854	G		Major intrinsic protein
CaPOPI_1814	Ca4	4030815	CAAAAA/CAAAA	TGGATCCACTAATAACATGGGA	CCTTTAAGGGGATTGAAGGA	59.2	516	DRR	Ca_03849		Dof	Zinc finger, Dof-type
CaPOPI_1815	Ca4	4031880	GTTTTTTT/GTTTTTTTTT	GGGTTTGTTTTATTGATTTTGA	GATCTGGAAAGGAGAAGGGC	57.2	238	INTERGENIC				
CaPOPI_1816	Ca4	4039327	TACTC/T	TTTTGGTTTGGTAATTGTGGG	TGATGGAGAAATCCTCACCC	59.6	456	INTERGENIC				
CaPOPI_1817	Ca4	4044991	A/AATTGGATC	GGGTGCATTGTGTGGAACCTT	TTGGTACGTGTAGAACA TCGTG	59.8	676	INTERGENIC				
CaPOPI_1818	Ca4	4045724	ATTTTTTTTT/ATTTTTTT	TGTTGGGTTTGTTTCTCCT	GCTTGATAATTTAAGGCCACCA	59.4	515	INTERGENIC				
CaPOPI_1819	Ca4	4086337	TAAAAAAAA/TAAAAAAAAA	GGGGCGTGTCAAAGTTAAA	ACCATCCGTATAAAGCACGC	60.0	453	INTERGENIC				
CaPOPI_1820	Ca4	4104993	TTATAT/TTAT	GAAGTGGGAATGGGCTGTTA	AAGTTAGGGGGACACAA CCC	59.9	677	DRR	Ca_03843	T	BBR-BPC	Protein kinase, catalytic domain
CaPOPI_1821	Ca4	4116752	TA/TACA	ACATGTTGGAAATCCGG GTA	TCGGCTACTCAAACAAAGGTG	60.1	516	INTERGENIC				
CaPOPI_1822	Ca4	4121415	ATT/AT	CTCATATGAACGGCCCCA TCT	TGTTTGTACGGACTCGA CCA	59.9	403	INTERGENIC				
CaPOPI_1823	Ca4	4196538	ATTTT/ATTT	ATTGGCCGGAATTTGTA CTG	TAACCCAAGGCCATATC CTG	59.8	841	DRR	Ca_03838	R		Alpha/beta hydrolase fold-1
CaPOPI_1824	Ca4	4302695	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATAATATTATTAT TATTATT/ATATTATTATTATTATTATT TTATTATTATTATTATTATTATTATT	GCATCTCCAAATGCGCA TCT	TGAGTCCAAAACAAATG GTGTC	60.2	730	INTERGENIC				
CaPOPI_1825	Ca4	4471743	TAAGAAAAATACAAG/TAAGAAAAATAC AAGAAAAATACAAG	ACATTTGATCACGGTCC TCC	AGGCATTGATTCTTCGT TCG	59.8	615	INTRON	Ca_03810	GOT		Tetratricopeptide TPR 1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1826	Ca4	4478589	TAAGTTAAAAGTTAAAAGTTAAAAGTTAAA AAA/TAAGTTAAAAGTTAAAAGTTAAAA	TGTAGACGCGCAGAGAG AGA	AATCATTTGCCTGGTGC TTT	60.0	593	INTERGENIC				
CaPOPI_1827	Ca4	4480054	TT/TTATTTGAAT	TCCTCCATTTTCCACG CTA	TTTCATCCTCCATGTGA CCA	60.6	409	INTERGENIC				
CaPOPI_1828	Ca4	4480380	TC/TCC	TGGTCACATGGAGGATG AAA	TTTAATACCTCGTATTTC CTATCAAGA	59.9	609	DRR	Ca_03809		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_1829	Ca4	4481135	TAA/TAAA	TGAAATCAAATTTTCTCA AGGC	AAACGACATTACGTTATT TCTTCATT	58.4	120	DRR	Ca_03809		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_1830	Ca4	4481516	T/TTC	TGAAATCAAATTTTCTCA AGGC	GTTCCGCCTCTTCTACC TCC	58.4	760	DRR	Ca_03809		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_1831	Ca4	4481679	TAAAAAAAA/TAAAAAAAAA	TTTTGCTTTTGATTACTT TCTTTTT	GTTCCGCCTCTTCTACC TCC	57.2	314	DRR	Ca_03809		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_1832	Ca4	4487412	AT/ATTAATAAAGT	TCAGACTCTCCGAACG ATT	CGTACGACGTCTTTCGT CAA	59.8	281	DRR	Ca_03808			DNA-binding SAP
CaPOPI_1833	Ca4	4488536	TAAA/T	ACAGCACATTCTGGTG GTG	TCTGCTAACAGGGGAT TGG	59.6	450	DRR	Ca_03808			DNA-binding SAP
CaPOPI_1834	Ca4	4502063	C/CG	GCTGGATCCGTCGTTAC AAT	CCATCTGAGAAAGCTAG CCG	60.0	441	DRR	Ca_03807		FAR1	Lipase, GDSL
CaPOPI_1835	Ca4	4503851	TAAAAAAAA/TAAAAAAAAA	TTCTCCCTCCGTCTCAC ATC	TGGAGGCAATGATTTTG TCA	60.2	421	INTRON	Ca_03807		FAR1	Lipase, GDSL
CaPOPI_1836	Ca4	4508477	T/TA	GTCTCTGGTTTACCGT GCC	ATGAGTGGTTTGCCACA TGA	59.6	452	INTERGENIC				
CaPOPI_1837	Ca4	4511887	ATTTT/ATTTTTT	CGTTGTTGGTGAACTG CAT	CCGGCGAGAATTTTCA ATA	59.6	700	INTERGENIC				
CaPOPI_1838	Ca4	4517245	AAGA/AA	AAAATGCGTTTCACTCG GAC	CCGTTTTTCGTACAATT CA	60.1	550	INTERGENIC				
CaPOPI_1839	Ca4	4527520	TTATATATATATATATATATATATATATATATATATAT TATATAT/TTATATATATATATATATATATATATATATATATATAT	AAGGTATGCTGTTTCAA GGGAA	AATGTGCATCTGCCACC ATA	60.0	892	INTERGENIC				
CaPOPI_1840	Ca4	4537624	TAATAAAATAAAATAAAAT/TAATAAAAT AAAATAAAATAAAAT	TGCATCGCCCATATCAA TAA	TATTGGACCGACCCTGA AAA	59.9	511	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1841	Ca4	4539713	TTA/TTATA	TCGACCCAACCTATTTCCAC	GGTTAACCGTCGTAACA CACTTT	59.8	340	INTERGENIC				
CaPOPI_1842	Ca4	4568058	ATTTGATTTT/ATTTGATTTTGTATTT	GTGGGGCATTACGATAC CAC	GGGGAAGCCATATCACATCA	60.1	636	DRR	Ca_03802	UZ		Vps52/Sac2
CaPOPI_1843	Ca4	4574989	AA/AAAGTA	TGCCACTAAATAGGGTT GGC	CGTTCTGAAAACGCGCT TAG	60.0	460	DRR	Ca_03801			Domain of unknown function DUF296
CaPOPI_1844	Ca4	4576739	GAAAAA/GAAAAAA	TCCATATGATTTGAACCTC GATTTTT	GGTTGGTTTAAACCGTTG GAA	60.1	729	INTERGENIC				
CaPOPI_1845	Ca4	4589864	CTTT/CTT	TTTCGCTCAATGTGAAAA GC	AACGGAGGCAGTAATTG TCG	59.0	322	INTERGENIC				
CaPOPI_1846	Ca4	4784534	ATTTTTTTTT/ATTTTTTTT	CCCTTCGGAAGACCACA TAA	TTCAATTCTTTACCCCGT TCA	59.9	657	DRR	Ca_03778	K	G2-like	SNF2-related
CaPOPI_1847	Ca4	4826016	AT/A	GGATTGATTGCAGTTCC AAAA	GGCAAAATGCCTTTAGACCA	59.9	445	DRR	Ca_03777	O	FAR1	Peptidase M41
CaPOPI_1848	Ca4	4840884	AC/A	TTGGGCCTTTGTGGAGT AAG	TACCAAGTGGTGATGG TGG	60.1	496	DRR	Ca_03775			Transposase, PttA/En/Spm, plant
CaPOPI_1849	Ca4	4842046	AAATAATAATAATAAT/AAATAATAA TAAT	TGAGAAGAAGGGGCTTA GCA	CGAGGAGGTTATTGGCG TAA	60.1	754	INTERGENIC				
CaPOPI_1850	Ca4	4875484	GC/G	AGCCTATGGCTTGGCCT ATT	GCCTAAGCTTGACTTGT GGC	60.1	687	INTERGENIC				
CaPOPI_1851	Ca4	4891737	AATTATTATTATTATTATT/AATTATTATT ATTATTATTATT	TGCCTTGATCGTTCCA TCA	TTCTGCTTTTTCTTTCC GA	60.1	540	INTRON	Ca_03769	Z	NAC	IQ motif, EF-hand binding site
CaPOPI_1852	Ca4	4897344	ATTT/ATTTT	CTCTGCAGCCTTGATTG GTT	ATGGAGTATGGGGCTGT GAC	60.4	278	INTRON	Ca_03768	K		SSXT
CaPOPI_1853	Ca4	4978107	AAATAAATAA/AAA	GTCTAATCCCCCATTTT GGC	TCTTGTGGTCGTTGCTT GAG	60.5	557	INTRON	Ca_03758	R		Barwin
CaPOPI_1854	Ca4	5081255	GATTATTATTATTATTATTATTATTATTA T/GATTATTATTATTATTATTATTATTATT ATTAT	CACCAGCAATAGCTTGC TCA	GAAAAACAGGGCTAGCA ACG	60.2	711	CDS (large-effect mutations)	Ca_03748	K	Trihelix	MYB-like
CaPOPI_1855	Ca4	5300098	TAAAAAAAAA/TAAAAAAAAA	GGCTGGAGAAAAAATAT GCG	AAAAGGAGTTTGAAGG GGA	59.8	598	INTERGENIC				

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CaPOPI_1856	Ca4	5525661	GAAAAAAAAA/GAAAAAAAAA	TATTTAGCCAAAAGGCG AGC	TCCATGTGAATATGATG AACCA	59.3	320	INTERGENIC				
CaPOPI_1857	Ca4	5570234	CTTTTTTTTT/CTTTTTTTTT	TGATGCATAAGTACAGG TGGG	AAGTTTTGGCTTTAAAT AGTGCA	58.5	581	INTERGENIC				
CaPOPI_1858	Ca4	5655244	TATA/TATAAATA	TGAACCCCAACCAAT AAA	GCACCGCTCAAAATGAA ATA	60.0	928	DRR	Ca_03683	R		F-box domain, cyclin-like
CaPOPI_1859	Ca4	5707384	AATATATATATATATAT/AATATATATATATATATAT	AAGCTAAGCACCGGTAA CGA	TTACAGTCTTGAAATTTT CCG	59.9	711	DRR	Ca_03679	DKL	MYB_related	Transcription regulator cyclin
CaPOPI_1860	Ca4	5961971	T/TGTG	CCTCTAATATCGTCGT CCAA	ATAATCGGTGCGGATTT CCT	59.3	668	INTERGENIC				
CaPOPI_1861	Ca4	6145049	ATTTTTTTTT/ATTTTTTTTT	ATCCCTCAGAATCGGC TAT	TTGCTCTATGCATTTGTT CCTG	59.9	565	INTERGENIC				
CaPOPI_1862	Ca4	6186297	GTTTTTTTT/GTTTTTTTT	TGTGTTTTCTCAATTGA CGATG	GCCATTGAACCAATTA AGAG	60.0	751	INTERGENIC				
CaPOPI_1863	Ca4	6271908	GTATATATATATATAT/ATATATATATATATATATAT	AAAAATTACGGGATGCA TAAAA	TCCCAAACAATGACAA AAA	58.9	775	INTERGENIC				
CaPOPI_1864	Ca4	6389441	TT/TTCCTTATGTGGAAAT	GCCCCACCTTCAGTGT AAA	ATGCTGGCAAATGATGT CAC	60.0	728	DRR	Ca_03602		ERF	X8
CaPOPI_1865	Ca4	6581955	TAAAAAAAA/TAAAAA	GCACGTGTGTAATGGTG CTC	TCTTGCTCAACGAAAT CCC	60.2	612	INTERGENIC				
CaPOPI_1866	Ca4	6875620	TGG/TG	GACAGTTTTGTGCAATC CGA	AACCTATACCCGCACAA TGC	59.7	859	INTERGENIC				
CaPOPI_1867	Ca4	6907181	TTATATATATATATAT/TTATATATATATATAT	TTTGAAATGGCGACTTC CTT	CCAAATGGCAACTTCCA ACT	59.7	569	INTERGENIC				
CaPOPI_1868	Ca4	7089091	GA/GAACAAAAGAGATTCACA	CTTTGCATACCCCTCTC GAC	TTGGGAGATTGGTTTC AAG	59.7	644	INTERGENIC				
CaPOPI_1869	Ca4	7127718	GAAAAAAAAA/GAAAAAAAAA	AATTTGGACAATACCCG GAA	AGGGAAGGGGAAGAAG ATCA	60.3	580	INTERGENIC				
CaPOPI_1870	Ca4	7388463	CAAAAAAAAA/CAAAAAAAAA	TTTCTCTAATCCCGAC TCA	TGTTGTTGTCAAACACC TCAAA	58.8	565	INTERGENIC				

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CaPOPI_1871	Ca4	7415395	TAA/TA	TTTCTGTCCTCACCTCACC	TGTAGTTTGGACGGTAGGC	60.1	535	INTRON	Ca_03496	F	YABBY	CTP synthase, N-terminal
CaPOPI_1872	Ca4	7620418	GATATATATATAT/GATATATATATATAT	CGATTTTGTGAAGTGTGTC	TTCATCGCCGACAAAGTAA	59.3	837	INTERGENIC				
CaPOPI_1873	Ca4	7710147	AATATTATTATATATTA/AATATTATTATATATTATATATTA	TCGTACCCCTCTCGTCATC	ACAGAATGCCTCATTGGTGG	60.1	927	DRR	Ca_03470	R	Nin-like	Pentatricopeptide repeat
CaPOPI_1874	Ca4	8039801	ATAAAATTAATAAACTAAATTAATAAACTAAAA/ATAAAATTAATAAACTAAATTAATAAACTAAAACTAAAA	TTCGAAATTTGGATTGCCA	TTTGTGCGAGATAGGTACGAAA	60.0	267	INTERGENIC				
CaPOPI_1875	Ca4	8115754	CATATATATATATATATATATATA/CAATATATATATATATATATATA	GCTGCTAGGGATGCTGTTC	GAATATTGGCCAAAGGCTTCA	60.0	208	INTRON	Ca_03421		M-type	Plant peroxidase
CaPOPI_1876	Ca4	8169426	GTCGATC/GTC	GACATCCGAAATGGGCTAAA	ATTTCCAAGTCCACGGTTTG	59.9	907	INTERGENIC				
CaPOPI_1877	Ca4	8169626	TAAATAAAAA/TAAATAAAAAATAAAAA	TATGGCACCTCCAGTTGAAA	TGTTAAATCCTCCAGACGGC	59.1	858	INTERGENIC				
CaPOPI_1878	Ca4	8186328	CTATATATATATATA/CTATATATATATA	TGCTTTTCATTTCAGAAATCC	TTTCACCTCCTGGTAGACGG	60.2	626	DRR	Ca_08308	T		Signal transduction histidine kinase, phosphotransfer (Hpt) domain
CaPOPI_1879	Ca4	8187730	TCC/TC	CTAAGCCGAGCAGAAGCAAT	TCCCTTTAATGCAAAGGTGG	59.8	499	INTRON	Ca_08308	T		Signal transduction histidine kinase, phosphotransfer (Hpt) domain
CaPOPI_1880	Ca4	8193266	TAAAAAAAA/TAAAAAAAAA	GCATCTCTCCAAGATGTCTGC	TGGGAATTGGGAGCTATCAG	60.0	620	DRR	Ca_08309	R		WD40 repeat
CaPOPI_1881	Ca4	8206232	GTATA/GTATACTATA	CAAGGGGTTGAAGTTGCAATT	TTGAAGCCACCTCTGATCT	60.0	763	INTERGENIC				
CaPOPI_1882	Ca4	8209835	CTTTTTTT/CTTTTTTT	AGACCAAGAGAGAGAGAGCCC	GGGTTTGGTTTGTGCGTAGT	60.0	306	INTERGENIC				
CaPOPI_1883	Ca4	8216534	GTT/GTTT	CGAATCCGCTTCGTGTTAAT	CGACCCGCTTAATATGTGGT	60.1	507	INTERGENIC				
CaPOPI_1884	Ca4	8216710	T/TG	CGAATCCGCTTCGTGTTAAT	CGACCCGCTTAATATGTGGT	60.1	507	INTERGENIC				
CaPOPI_1885	Ca4	8222692	A/AC	TTCTGTCTTTGTTGTTCGGG	TGCTAAGGATTATGCAGGGG	59.9	483	INTRON	Ca_08312			Endonuclease/exonuclease/phosphatase

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CaPOPI_1886	Ca4	8223032	GAAAAAAAA/GAAAAAAAA	CAACCTTTGGTGTGGC TTT	ACGCGATAATCCAATCG AAC	60.0	252	INTRON	Ca_08312			Endonuclease/exonuclease/phosphatase
CaPOPI_1887	Ca4	8226617	TG/T	TATATGTGTTGCTGTGG GGG	GTACACCAAGGCGATTG GAT	59.3	969	INTERGENIC				
CaPOPI_1888	Ca4	8281328	CA/CCTAA	TTGGTGTCAATCGCCTT TTT	CAATCGCAAGGATAATG GCT	60.5	711	INTERGENIC				
CaPOPI_1889	Ca4	8293335	AT/AATT	CAATGGTTTTGCTTTTG GCT	TTCTCGAATGCGAAGAG TCA	60.1	492	INTERGENIC				
CaPOPI_1890	Ca4	8295749	ATTTTATT/ATTTTATTATTTTATT	TCAACCTCATTCAACC ACA	CCTGCGACAATCTGAAG GAT	59.9	840	INTERGENIC				
CaPOPI_1891	Ca4	8305998	GAAA/GAA	CATCATGCAGTCGCCTC TAA	ACCACATCTGCCATCAA TCA	60.0	510	INTRON	Ca_08319	S		Oxoglutarate/iron-dependent oxygenase
CaPOPI_1892	Ca4	8308551	TAA/TAAA	TAAAGGTGAGGGCATG TCA	TATGCAAAACCAATTGA CCA	60.1	321	INTERGENIC				
CaPOPI_1893	Ca4	8309234	TCAACACAA/TCAACACAACACAA	GAATTTAAGAGGAAGGC GATGA	TTCAACCTAATTCGTAG GCG	59.7	450	INTERGENIC				
CaPOPI_1894	Ca4	8310925	CAAAAA/CAAAAAA	CATGTGTGGGACTCTTT GGA	CTCAACACGGTTCTGCT CTG	59.5	764	INTERGENIC				
CaPOPI_1895	Ca4	8315933	CTT/CTTATT	GGACCCGTGATGCTGTT TAT	TCTCGGTTGATGTCATT ATGCT	59.8	586	INTERGENIC				
CaPOPI_1896	Ca4	8316304	GTTTTTTT/GTTTTTTT	GCATAATGACATCAACC GAGAG	AAAAGAAATGGTTGTTTC TCGTTC	59.6	235	INTERGENIC				
CaPOPI_1897	Ca4	8316722	ACTCT/ACT	GAACGAGAAACAACCAT TTCTTTT	CACGAGTGACACGCCAT TTA	59.9	583	INTERGENIC				
CaPOPI_1898	Ca4	8325707	TAT	ACGGGGCTGTTACTTTA CCC	TTCTCAATGGGTGCGTA CAA	60.2	739	INTERGENIC				
CaPOPI_1899	Ca4	8333443	GCTTCTTC/GCTTC	TCAAAGGTGATCATGGA TGG	ACCCTTGCCAAAACACT ACG	59.3	593	INTERGENIC				
CaPOPI_1900	Ca4	8342865	T/TTAAG	GAGCTTCAACCACAAGC ACA	GCTTTTTGAGCAACTCG TCC	60.0	691	CDS (FRAME SHIFT)	Ca_08321			E3 Ubiquitin ligase

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1901	Ca4	8372871	T/TG	TCTTTTCTGCCCACTA GC	CAGCTGAGTTGTGAGGT CCA	59.5	150	INTERGENIC				
CaPOPI_1902	Ca4	8373181	TACA/TACACA	GGCAAAATGGACCTCAC AAC	GGAGAGTCGGTCTTTGT GGA	60.4	706	INTERGENIC				
CaPOPI_1903	Ca4	8373461	AAC/AACCAC	TGAGCATAAAGTGGCAT TGG	GTCGGTCTTTGTGGAGA GGA	59.7	398	INTERGENIC				
CaPOPI_1904	Ca4	8377254	ATTTTTTTTTT/ATTTTTTTTTTTT	CCACATATATCTGCCCC ACC	TGACTGTGTGCACTGAA ACAA	60.0	563	DRR	Ca_08327	KL		BSD
CaPOPI_1905	Ca4	8377411	AT/ATATATATATT	TAGTGTACGTGTTGGG GCA	GGGTGAGACTGAAGCTG GTC	60.0	949	DRR	Ca_08327	KL		BSD
CaPOPI_1906	Ca4	8377585	ATTT/ATT	TTCGTCCATTGAATCCT GA	CCTGCAAGCACTTACGA CAA	59.0	891	DRR	Ca_08327	KL		BSD
CaPOPI_1907	Ca4	8381452	TAAAAAA/TAAAAAAA	CAATCCGTTAAGGACCT GGA	GATGATTCCTTGCTGG AAA	59.9	388	INTRON	Ca_08327	KL		BSD
CaPOPI_1908	Ca4	8384923	AGGGGGG/AGGGGG	GCCGCAATAGTGTGTTT GGT	GCGTATCGGTTGGAATT GTT	60.0	807	INTRON	Ca_08327	KL		BSD
CaPOPI_1909	Ca4	8396183	T/TG	TTTACAACACATTGCGC ACC	CGTTTATTGACGGAAGG CAT	60.6	681	DRR	Ca_08329	O	B3	Chaperonin Cpn60
CaPOPI_1910	Ca4	8400811	GAATTACTAAT/GAATTACTAATTACTAA T	CTTAAGCATCAAAGCCC GAG	CCTCAATTGCCACCAAA ACT	60.0	469	INTRON	Ca_08329	O	B3	Chaperonin Cpn60
CaPOPI_1911	Ca4	8413764	T/A/T	AATGGTGAACAAGGAGC AGG	TCAAATATTAACCTCAAG CGCA	60.1	714	INTERGENIC				
CaPOPI_1912	Ca4	8422191	GAAA/GAA	AAGACGGATGCATTTTG CTC	GACACATGCCCAACTGA ATG	60.2	841	INTERGENIC				
CaPOPI_1913	Ca4	8441953	GTTTGT/GTTTGTATTTTGT	AGCAGGAGAGCTGAGAT TGG	TACTGTGTATCGGGGCA ACA	59.7	731	INTRON	Ca_08335	R		Polycomb protein, VEFS-Box
CaPOPI_1914	Ca4	8467235	CCATCATCATC/CCATCATCATC	GGCAAGCATTCAATTC CAT	GGTTGGGATGTTATGTT CGG	59.9	449	INTERGENIC				
CaPOPI_1915	Ca4	8475153	ATTT/ATT	TGGACCGTACATTTTCG TGA	GTGGTAGCAGAAGGAG CAGG	60.0	829	INTRON	Ca_08339	G		Phosphofructokinase domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1916	Ca4	8478290	A/AT	TTTAGCTTGCCAAAACA GCA	CCTTTCTTCGTACGTCT CGC	59.6	607	INTRON	Ca_08339	G		Phosphofructokinase domain
CaPOPI_1917	Ca4	8489479	CACATACA/CACA	CCCAAATCACACACATG AGC	AGAGTTGTTTCATCTCC AAACG	60.0	415	INTERGENIC				
CaPOPI_1918	Ca4	8497257	TAAACTGAAGAACT/TAAACTGAAGAA ACTGAAGAACT	AGCGTGAGAGGAACCTG TGT	GA CTGGCAACAGCAATT TGA	59.9	564	INTRON	Ca_08341		CPP	WD40 repeat
CaPOPI_1919	Ca4	8509176	CTTTT/CTT	GCCTTCTGGACAAAACG AAG	TCTGCAGGTGAAGCAAC ATC	59.9	578	INTRON	Ca_08343	YU		
CaPOPI_1920	Ca4	8514326	CTTTT/CTTTT	TGTCGTGCGGTAAGTTT GAC	GAAGCAAAGCTAGGGT GTG	59.8	449	DRR	Ca_08343	YU		
CaPOPI_1921	Ca4	8521020	CATA/CATATATA	AATTCAACCAATAAATT CCCA	CACGCAAAATGAAAGGT TGA	57.4	308	INTERGENIC				
CaPOPI_1922	Ca4	8522151	TG/T	TGTGATTGTTAGGATGA TGACG	CCAAAAC TGGGAGAAA CAA	58.5	288	INTERGENIC				
CaPOPI_1923	Ca4	8522296	GT/GTT	GCAGTTTTGGTCCCCCT ATT	GCAGTTTTGGTCCCCCT ATT	60.2	328	INTERGENIC				
CaPOPI_1924	Ca4	8612629	T/TTA	TTTCTTTCTGCTGTCGG CTT	CATGCCATCCACTATGT TGC	60.1	393	INTERGENIC				
CaPOPI_1925	Ca4	8613689	TTTTCT/TT	TGCATTTGGTTGAAAT GAAA	TGGTGGGCCTACGAGTA AAG	59.0	374	INTERGENIC				
CaPOPI_1926	Ca4	8621480	GAAAAAAAA/GAAAAAAAAA	GTGCATGACCCCTTCTT GTT	TGTCAGGCAACAGAAA CCA	60.0	889	INTERGENIC				
CaPOPI_1927	Ca4	8689007	A/AT	AGGACCCACAACATCCA CAT	ACCAATCCATGCACGCT ACT	60.1	505	INTERGENIC				
CaPOPI_1928	Ca4	8698891	AAGAGTAGTAGAGTAGT/AAGAGTAGT	AAGCTGGCCACTGTAG CAT	TCACAACTCTGACAACC CAA	59.9	246	INTRON	Ca_08365	G		Glycoside hydrolase, family 13, N-terminal
CaPOPI_1929	Ca4	8704241	G/GC	TTTGTACCCAACAGGGC ATT	ATGCATGCGTTGACAAT GTT	60.2	569	DRR	Ca_08366	J	NAC	Ribosomal protein L6
CaPOPI_1930	Ca4	8705159	GTT/GTTT	TCAATGGTGAGCAAA TCA	GGTTCCCTTCCCAATT TAG	60.0	399	DRR	Ca_08366	J	NAC	Ribosomal protein L6

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1931	Ca4	8709656	CAAAAAAAAA/CAAAAAAAAA	AATTTGTGGGTGGGCAT AAA	TGCATTGAGAGAATCAC CAACT	60.1	701	INTERGENIC				
CaPOPI_1932	Ca4	8709676	TG/T	AATTTGTGGGTGGGCAT AAA	TGCATTGAGAGAATCAC CAACT	60.1	701	INTERGENIC				
CaPOPI_1933	Ca4	8720139	AAAGT/AAAGTTTAAGT	GGCTGATGGAGAATTCC AAA	ACCAAAGACCAGATTGG CAC	60.0	860	INTRON	Ca_08368	Q		Multicopper oxidase, type 1
CaPOPI_1934	Ca4	8730605	CGTG/CTG	TTCACACCAACCCCTC AAA	ATTTTGAAGAACAATC CGC	60.0	517	INTERGENIC				
CaPOPI_1935	Ca4	8730686	TAA/TA	TTCACACCAACCCCTC AAA	ATTTTGAAGAACAATC CGC	60.0	517	INTERGENIC				
CaPOPI_1936	Ca4	8733054	TGGG/TGG	AAAAATCACCCAAAATTA ACATCT	CACTTTCCTTGCTCCCT CTG	57.2	867	INTERGENIC				
CaPOPI_1937	Ca4	8748201	AG/A	CATTTCAATCATTACCC CC	TCACAACATGAGAATGG GACA	60.0	218	INTERGENIC				
CaPOPI_1938	Ca4	8753314	TGCTGGAACGCTGGAAC/TGCTGGAAC	TTCTTTCCAGTCATTTG GG	CCAAATGGAGCTTCCAC TA	60.0	841	INTRON	Ca_08371		NAC	No apical meristem (NAM) protein
CaPOPI_1939	Ca4	8758495	A/AG	TCACCATTGCTGAGTTG GAA	TGCTCATGTCTTCTAAA GATCCA	60.1	762	INTERGENIC				
CaPOPI_1940	Ca4	8836055	TATTTTAAATTTT/TATTTTAAATTTTAA TTTT	TGACCTGTAGGGCCGTA ATC	TCACCAAATCGAAGCTC AAA	60.0	508	INTERGENIC				
CaPOPI_1941	Ca4	8836902	T/TG	AGCTTCGATTGGGTGAG GTG	TTGAGTTTCAATATGGT GATGTGA	60.3	854	INTERGENIC				
CaPOPI_1942	Ca4	8858467	TTACTAA/TTACTAATATTATAATACT AA	TTGGTTTCCAAGTTCCC ATC	TTCAACTTCGAGCAAAA GGG	59.8	602	INTRON	Ca_08382		MIKC	
CaPOPI_1943	Ca4	8861999	CAAAAAAAAA/CAAAAAAAAAAAAA	CGAGGGAGCATTATGCA ACT	TCCTTCGCCTCTCAAGA AAA	60.2	432	DRR	Ca_08383	C		Globin, subset
CaPOPI_1944	Ca4	8867611	AT/A	AGCTCCCATACAGGAC CTT	GTAGCCACCATTTTCCT CCA	60.0	374	INTERGENIC				
CaPOPI_1945	Ca4	8890826	CAGGTAG/CAG	TTTGAGGAGTGTGTGGT GGA	ACCCAACTCGCACTTTG AAT	60.1	360	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1946	Ca4	8896251	CAAAA/CAAAA	GTCGCTAAACTGCAAA GGC	TTTGTCCGGATGAGTTA TCAAA	60.0	477	INTERGENIC				
CaPOPI_1947	Ca4	8903771	GAATTAAT/GAAT	GGATCTCATTGGTTCTA TGGG	CGAGTGTGGTGGGTTTT CTT	58.3	490	INTERGENIC				
CaPOPI_1948	Ca4	8903859	CATAT/CAT	GGATCTCATTGGTTCTA TGGG	CGAGTGTGGTGGGTTTT CTT	58.3	490	INTERGENIC				
CaPOPI_1949	Ca4	9030140	ATTTTTTTTTT/ATTTTTTTTTT	TGGTGTGGAGTCATGC TTT	AAATTTGCAATGACGGC TTC	59.1	656	INTERGENIC				
CaPOPI_1950	Ca4	9066423	ACC/AC	GCAACCCGTAGGTGTAG GAA	TGTGCGTTGGTAGTCAA TGTG	60.0	546	INTERGENIC				
CaPOPI_1951	Ca4	9079145	ATTTTTTTTTT/ATTTTTTTTTT	AGTTGGAAGTCGCCAA GAA	ATGGTGCAGTTCTTGCC ATA	59.9	629	INTERGENIC				
CaPOPI_1952	Ca4	9371255	GAAAAAAAA/GAAAAAAAA	GGAGCATATGCCTCGTT GTT	TGGAAATCAACTTTTGT GACA	60.1	549	INTERGENIC				
CaPOPI_1953	Ca4	9388140	C/CTTCAT	TCGTGTTGCGCCTAACA AT	AGTTTTTAATCCGTGCG TCG	60.3	976	INTERGENIC				
CaPOPI_1954	Ca4	9460620	ATTTTTTTTT/ATTTTTTTTT	TTGGTGAATAAATGCC AAA	TTGCGTGTTTTAAGAATT CGG	58.9	283	INTERGENIC				
CaPOPI_1955	Ca4	9569592	CTT/C	CAAATGTCGAATTAAAGT ATTGCG	TTGTCCTTCTCCATTGT CC	59.9	355	INTERGENIC				
CaPOPI_1956	Ca4	9630289	ATTAGTTAGTT/ATTAGTTAGTTAGTT	CCTCTTCCAAACAAATCT TCG	CCAGCTCATCAAAGCCA TTT	58.8	550	INTERGENIC				
CaPOPI_1957	Ca4	9632653	TG/T	TGGATTGTCGTGATCTC AAA	CACACCCGTACTCAGCA TTG	57.6	630	INTERGENIC				
CaPOPI_1958	Ca4	9653112	TAAAAAAAA/TAAAAAAAA	GGGTGTGACGATGACAG CAA	AAATCGTCGCAATCAG TCC	59.6	208	INTERGENIC				
CaPOPI_1959	Ca4	9658674	TAAAAAA/TAAAA	TGCAATTGATACCGAG CCT	TCCCTTCTTTGAGGGA TTT	60.6	914	INTERGENIC				
CaPOPI_1960	Ca4	9732872	A/AC	CGGTGGTTGATAAAGTC GTG	GAATTCAAATGGGGAAA TGC	59.0	416	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_1961	Ca4	9764739	GTTTTTTT/GTTTTTTT	TCAGGCGGGTTTATAGACA	CTCTGCTCACAACCCAA CAA	58.2	701	INTERGENIC				
CaPOPI_1962	Ca4	9847676	TAAAA/TAAA	GAGTTGCAGGGGATGTAGGA	CACAAAGAAAGGCCTGG AAG	60.1	240	INTRON	Ca_08462	Z		VHS
CaPOPI_1963	Ca4	9857350	TGTGCGAGTGCGAGTGCGAGT/TGTGCGAGTGCGAGT	TGAGACGTTTTTCACAC CCA	CTGCAACAATGAATCTT GAAGT	60.1	469	INTERGENIC				
CaPOPI_1964	Ca4	9923455	AATATATATATATATATATA/AATATATATATATATATA	TGTGAACGTCGTCGTAT GGT	CCGATAACAAAAGCTCT CGC	60.0	892	INTERGENIC				
CaPOPI_1965	Ca4	10033685	TTATATATATATATATATAT/TTATATATATATATATATATAT	CTAGTTCGTAACCCGTG CGT	AGGCATGGTGTGGAGT CAT	60.2	248	INTERGENIC				
CaPOPI_1966	Ca4	10057169	AAAATTCAAATTCAAATTCAAATTCAAA/AAAATTCAAATTCAAATTCAAA	AACGTGCATCGACACTT TGA	AACGGAAGAATACGCC TTTA	60.3	542	INTERGENIC				
CaPOPI_1967	Ca4	10173137	ATTTTTTT/ATTTTTTTT	CCCGTTATTTTGACGA AACA	TGTGTTGAGTGGTGGCA TTT	59.9	791	INTERGENIC				
CaPOPI_1968	Ca4	10233239	GACAATTATTTGGTACAATTAT/GACAA TTATTTGGTACAATTATTTGGTACAATT AT	TGTCGGTTGTTGCTTGA AGA	ATACAATCATTTCCTCCG CA	60.4	403	INTERGENIC				
CaPOPI_1969	Ca4	10460957	CATATATATATATATATATATAT/CAT ATATATATATATATATATATATATATAT	TTAATTCCAATGGCGGG TAG	TCACATTCAGCTTTTGGT CG	59.8	428	INTERGENIC				
CaPOPI_1970	Ca4	10624424	TTAATAATAATAATAATA/TTAATAA TAATAATAATA	GGATGTCCCAAAGGGTT TTT	GGATGATTCTGGAGCGA GAC	60.0	303	INTERGENIC				
CaPOPI_1971	Ca4	10657750	T/TCTAACACTCTTTCC	ATACAAAAACATTTGGG CCG	TTACATGAAGTGGCGA GAC	59.7	417	DRR	Ca_04301			Tetratricopeptide TPR-1
CaPOPI_1972	Ca4	10939792	G/GAGTGTGGTC	GCAGCAAAAGGGATAA CCA	AAGAAACCTCGTGTGCC ATC	60.1	231	DRR	Ca_04328	GMW	NAC	Exostosin-like
CaPOPI_1973	Ca4	11209323	TAAAAAA/TAAAAAA	TTAGTGTTGAATTGACG GCG	CAATGCCTAGAATCAGC GGT	59.7	960	INTERGENIC				
CaPOPI_1974	Ca4	11220000	AAATAATAATAA/AAATAATAATAATAA	ATTTCTTCGTGTACCGC ACC	CTGATAGACCGACACAC ACACA	60.0	465	INTERGENIC				
CaPOPI_1975	Ca4	11285447	C/CAA	TCCACATGCACCTGTGA ACT	AGTAGTGCCTCAAACCA CGG	60.2	382	DRR	Ca_04361	GE	GATA	Domain of unknown function DUF250

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CaPOPI_1976	Ca4	11340703	CG/C	TCATCACGTCGAATTC AA	CTCCTTGCCCAATTGT GT	59.9	333	INTERGENIC				
CaPOPI_1977	Ca4	11435815	AAC/A	CGGAGGTTTCAGTTCAG CTC	GTGAATTGGTCGAGCGG TAT	60.0	906	DRR	Ca_04378	S		
CaPOPI_1978	Ca4	11506583	CTTA/CTTAATTA	CTCGACATCATGGTTCA TGG	CGGATCTATGCATGGGA TAA	59.9	507	INTERGENIC				
CaPOPI_1979	Ca4	11551467	TTTTTTTTAATTTTTTA/TTTTTTTTA	ATCCAAAAGCCCCAAT AAC	TCACTGTTGCATCTCCA AGC	60.0	844	INTERGENIC				
CaPOPI_1980	Ca4	11567821	CA/CACGAATA	TTTCTTTTGCCTCATT CAA	TTCCACCTGATCATCATT TCA	59.7	463	INTERGENIC				
CaPOPI_1981	Ca4	11866901	TATAATAATAATAATA/TATAATAATA	GAATAGACCAGGCCAGA CCA	CTATTAGGCTGACAAG GCG	60.1	493	INTERGENIC				
CaPOPI_1982	Ca4	12027795	AAAAAGAAATAAAAAAGAAATAAA/AAAA AAGAAATAAA	GATGTCGTCATGGCTGT TTG	TCATTGCGTTCTTTAGT GCG	60.1	510	INTERGENIC				
CaPOPI_1983	Ca4	12313260	G/GA	ATATTTTCGATGTGCAG GGC	TGAAGGAGGCTTCTAGG ACG	59.9	545	DRR	Ca_04455	J		Ribosomal protein L36e
CaPOPI_1984	Ca4	12334767	C/CTATT	GTCCTCCAAGTACCCCA AAA	AGGTTAGGTCGTCGCTC AAG	59.9	377	INTERGENIC				
CaPOPI_1985	Ca4	12490666	TGTAGTAGTAGTAGTAGTAGTAGT A/TGTAGTAGTAGTAGTAGTAGTAGT TAGTAGTAGTAGTAGTAGTA	GGAATATGGCAGCAGAC GAT	GCCTGCATATGGCTAAG AGC	60.1	734	DRR	Ca_04472	R	NAC	Pentatricopeptide repeat
CaPOPI_1986	Ca4	12504806	CAAA/CAAAAA	TGGCACCAAGATACCA TCA	TGCAACCGCAATATTTA CCA	59.9	328	INTRON	Ca_04474		MIKC	
CaPOPI_1987	Ca4	12505639	GTCTTAA/GTCTTAAATATCTTAA	GCAAGGACAAGGATGT AGG	TCAACCGCAATTGAGAT TTTC	59.6	677	INTERGENIC				
CaPOPI_1988	Ca4	12506017	ATTTTTTT/ATTTTTTTT	TCAATTGCGGTTGAATT ATCA	AAGCTGCTCTCAACACC CAT	59.0	485	INTERGENIC				
CaPOPI_1989	Ca4	12518595	ATTTTTTT/ATTTTTTTT	GGAGCCTTACACATGTG GCT	TCATTTGTGAGATTGTCA CGTT	60.1	364	INTERGENIC				
CaPOPI_1990	Ca4	12528293	AT/ATT	TTCTTCGACCAACAAA ACC	CATGGGACCCTAGCGTT AAA	59.9	573	DRR	Ca_04475	C	bZIP	Cytochrome b561, eukaryote

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CaPOPI_1991	Ca4	12529895	TAA/TAAA	AACGTGTTCAAACCTCGG AGC	ACAACACCTTATTCTGC GCC	60.3	630	INTERGENIC				
CaPOPI_1992	Ca4	12529954	CTTTT/CTTTTT	AACGTGTTCAAACCTCGG AGC	AGCTTAGCTGGGTGGGT TTT	60.3	707	INTERGENIC				
CaPOPI_1993	Ca4	12529978	T/TC	AACGTGTTCAAACCTCGG AGC	AGCTTAGCTGGGTGGGT TTT	60.3	707	INTERGENIC				
CaPOPI_1994	Ca4	12532996	C/CA	ATGAATTTGATGAGCAG GGC	GTTCCAGTTGCCCTGTG TTT	60.0	349	DRR	Ca_04477	K	MYB	SANT domain, DNA binding
CaPOPI_1995	Ca4	12542560	TAAAAAAA/TAAAAAAA	TGCCAAATTGTGTTGT CGT	TATGACGGGAATGCATT TGA	60.0	631	INTERGENIC				
CaPOPI_1996	Ca4	12566654	AG/A	TCAGTCTTCCATATTCT CTCCG	AAAACCCAGGAGGTCAG CTT	59.7	619	INTERGENIC				
CaPOPI_1997	Ca4	12567928	AATATATATAT/AATATATAT	ATTCGGCAATTCTACCC CTT	GAGGTAGAGCTCGACGA TGG	59.8	446	INTERGENIC				
CaPOPI_1998	Ca4	12571013	GTATATA/GTATA	GGCTCACATCAGGAATG GAT	GGCTCTTGGTCATTGGA TGT	59.9	968	DRR	Ca_04479	E		Homoserine kinase
CaPOPI_1999	Ca4	12572622	TAAAAAAA/TAAAAAAA	TGGAAGAGCATGCAAAA CAA	TGAGATCTTGAGGCATG GTG	60.4	644	INTERGENIC				
CaPOPI_2000	Ca4	12578358	TAT/TATACCAGCAT	AGGCTTCTTAGGCATTG GGT	ATTCTTGTAATCCCGCG TTG	60.1	346	INTRON	Ca_04480	L		DNA mismatch repair protein MutS, C-terminal domain
CaPOPI_2001	Ca4	12581069	TAA/TA	TTTTAGTTGCCGCCTTT TG	CTTCAGGAGGGTGATAC CGA	60.2	468	INTRON	Ca_04480	L		DNA mismatch repair protein MutS, C-terminal domain
CaPOPI_2002	Ca4	12589173	ATTTTTTTTT/ATTTTTTTTT	CTTTCGAGATCTGATGC GTG	ACAACGTCTTCCATTAC GCC	59.5	753	INTERGENIC				
CaPOPI_2003	Ca4	12589473	G/GA	TGTGGCATTTTGGTAAT GCT	ACAACGTCTTCCATTAC GCC	59.0	200	INTERGENIC				
CaPOPI_2004	Ca4	12592291	ATA/ATACAAATACTTGATGTA	TGACTGCCGCTTTGTCA TTA	TTTCGATTCAAACCAAA CC	60.4	588	DRR	Ca_04481	R		
CaPOPI_2005	Ca4	12593132	AT/ATGTTGT	TCACTGTAAGTCCATGC CTCC	GCCCTTGTCAAAACAAG TTGA	60.1	454	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2006	Ca4	12593182	TAAAA/TAAA	TCACGTGAAGTCCATGCCTCC	GCCCTTGTCAAAACAAGTTGA	60.1	454	INTERGENIC				
CaPOPI_2007	Ca4	12597000	AT/ATCTAATGGT	CACATGGTTCAGGTTCTT	CTTATGGCGTGGCCTTAAC	59.8	820	DRR	Ca_04482	R		Cytochrome b5
CaPOPI_2008	Ca4	12604165	CTTTTTTTTTTT/CTTTTTTTTTTT	CGATTTCACTTCCCCAATT	AGCAGCAGAAAGCATGGACT	59.0	209	INTERGENIC				
CaPOPI_2009	Ca4	12644877	CATATATATATATATAT/CATATATATATATATATATAT	TCACCTGTTAGTATGACACAACA	TTTGAGGCCATTAGTTTGGG	57.3	877	INTERGENIC				
CaPOPI_2010	Ca4	12676299	CATATGTGATATGTGATA/CATATGTGATATGTGATGTGATA	GATCTCGGGTTAGATGGTCG	TCCACTCTCGCTCTCAATCC	59.5	740	INTERGENIC				
CaPOPI_2011	Ca4	12715012	TA/TATAGAAAGA	AGAAGCGATGCAGACAACCTT	AGGGGCGAATATCGCTAACT	59.1	373	INTERGENIC				
CaPOPI_2012	Ca4	12724267	GAAAAAAAAA/GAAAAAAAAA	CCAAGTGCAATGACGAGCTA	CAAGGATATGGATCCAAATGTGA	60.0	610	INTERGENIC				
CaPOPI_2013	Ca4	12866217	GGG/GGGAGCTTTATTTTTTGG	TAGACTCCACTAAGCCCCTCA	CCTTCCAACGCAACATTCT	59.7	294	DRR	Ca_04506	T	FAR1	Protein kinase, catalytic domain
CaPOPI_2014	Ca4	12885868	ATTTTTTTTT/ATTTTTTTTT	AGGTCATTGGTGTGCAAGGT	TGAAGCTGACTGCACTTTGG	60.4	666	DRR	Ca_04508	R		Glucose-methanolcholine oxidoreductase, N-terminal
CaPOPI_2015	Ca4	13028368	CTTGTTG/CTTGTTGTTG	TGCACGCTCCACATTATTTC	CTTTTCTGGGGCAAATTGAA	59.7	367	INTRON	Ca_04525	T	bHLH	Protein kinase, catalytic domain
CaPOPI_2016	Ca4	13068436	AATATATATATATATATATAT/AAATATATATATATATATATATATATATAT	GCTCAATTTTCTTAGGCGG	TGTCGCAACAATTTGTCCTT	59.0	432	INTERGENIC				
CaPOPI_2017	Ca4	13133292	ATTTT/ATATATTTTT	CAGCCGCCTCAACTATTAC	CCATCCATGCAATTGAACAC	59.7	408	INTERGENIC				
CaPOPI_2018	Ca4	13325790	ATTTTT/ATTT	TTGATCATCCTATTTCAAAAGTTCA	ATTTTCGACTCCACACACGG	59.1	640	INTERGENIC				
CaPOPI_2019	Ca4	13433311	TA/T	CGAGCAAACACAATGAATGG	TTGGTTGGTTCATTGGTTGA	60.1	569	INTERGENIC				
CaPOPI_2020	Ca4	13509527	ATTTT/ATTTTATTAATAAATTTATTTTT	CCTCTTCACGGTGCTCAATT	CCTCGTTTTAAGCCCAATCA	60.3	158	INTERGENIC				

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CaPOPI_2021	Ca4	13604124	GA/G	TTCAGACCCAGTTTCA TCA	GACATGTATCGTGTGCG GTC	59.1	631	INTERGENIC				
CaPOPI_2022	Ca4	13617448	TG/TGG	GGGCCTTTTCTTCAGCT TTT	TGCATGTTATCCGCAAT CTC	59.8	713	DRR	Ca_04579			Protein of unknown function DUF1677, plant
CaPOPI_2023	Ca4	13643715	GTT/GTTT	ATAGTTGTTGAAGGGG ACG	GGGTGAAGAATGTATGC CAAA	60.0	798	INTERGENIC				
CaPOPI_2024	Ca4	13657824	ATATT/AT	TGCATGCATGAATAGTG TTTGA	TCTCCCAATGTGATTGC TCA	60.1	395	INTERGENIC				
CaPOPI_2025	Ca4	13666161	ACTG/ACTGCTG	CCCATTTACCTCTTTG GAA	TTCCCGCACAAAATAGA TCC	59.9	840	CDS (large-effect mutations)	Ca_04586	Q	B3	Cytochrome P450
CaPOPI_2026	Ca4	13691259	GTT/GT	CCATTTATTTCCGGCATT TC	AGCCGACCAAACTAT TGG	59.3	271	INTERGENIC				
CaPOPI_2027	Ca4	13692964	TGTATCAGTAT/TGTAT	TGTATCAAGTTCGTCCA CCG	TTGATTACGCCTGTTT CC	59.6	247	DRR	Ca_04590			XS domain
CaPOPI_2028	Ca4	13730284	TTATATATATATATATATATATAT/TTATATATATATATATATATATATAT	AACACATAACCACTTCG CCC	TGCAGCGAAATTATTCG AGA	59.9	458	INTERGENIC				
CaPOPI_2029	Ca4	13743876	GAA/GAAGCATATGCAA	CTGGTTTCATGCCCTAC AAT	TCAAAGCACTAGCCACA TGC	59.8	740	DRR	Ca_04598	R	MYB_related	Pentatricopeptide repeat
CaPOPI_2030	Ca4	13757687	ACTTGC/AC	TAACTGTTGCCATGGT TCA	AAGATGGGGAGAGGGA AAGA	60.0	649	INTRON	Ca_04600		NF-YB	Aminotransferase, class IV
CaPOPI_2031	Ca4	13776936	GTATATATATATA/GTATATATATA	TGTGTCTGCCCATGAGT GTT	ATATGCGGTTTCATCCTT GC	60.2	301	INTERGENIC				
CaPOPI_2032	Ca4	13896280	CGAAGAAGAAGAAGAA/CGAAGAAGAA GAA	TACACTGGCCCATCATC TTG	GCCTCGTTGGAATGATT TGT	59.5	482	INTERGENIC				
CaPOPI_2033	Ca4	13908536	TC/T	CTCCTCCGATGTCTGGA AAA	CGCGGTTGCTTCAATTC TAT	60.2	232	INTERGENIC				
CaPOPI_2034	Ca4	13909254	CA/CAA	CATCACGATTGACGAG TTGA	AAAAACATGACTCCAAA CACCA	59.7	636	INTERGENIC				
CaPOPI_2035	Ca4	14011652	TAA/TAACAA	GCACCGACTTGCTGATG TAA	GCCTCATGCTCCAATTT TGT	59.9	755	INTERGENIC				

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CaPOPI_2036	Ca4	14196867	CTATATATATATATAT/CTATATATATATATAT	CACTCGTGTTTCCAAG GTT	TTGCAAGTGCATCCAA TTC	60.0	584	INTERGENIC				
CaPOPI_2037	Ca4	14397300	GATATATATATATATATATGTATATATATATATA/GATATATATATATATATATATATATATGTATATATATATATA	TAAATGCATGCTCCCC TAT	AACACATCCGGGATCCA TTA	60.4	273	INTERGENIC				
CaPOPI_2038	Ca4	14405755	ATCTCTCTCT/ATCTCTCT	ATGTGCATGCCAAGTTG TGT	ACCTATAAGCCCTTGC GCT	60.0	963	DRR	Ca_05663	E	MYB	Amino acid transporter, transmembrane
CaPOPI_2039	Ca4	14406037	GTCTTT/GT	TTGGTTCACATTGTAC CCC	TTGTTGCTGGAGTTGGA TCA	60.5	639	DRR	Ca_05663	E	MYB	Amino acid transporter, transmembrane
CaPOPI_2040	Ca4	14406133	CAAA/CAAAA	TTGGTTCACATTGTAC CCC	CCATTGGTTGGGATATG GAG	60.5	892	DRR	Ca_05663	E	MYB	Amino acid transporter, transmembrane
CaPOPI_2041	Ca4	14416755	TTATATATATATA/TTATATATATATATA	TCATTTCAAACCTTAA CTCCA	TTGCGGTCAATTGTATG AAGAC	59.9	392	INTERGENIC				
CaPOPI_2042	Ca4	14677950	CAAAAAA/CAAAAAA	TGTTGGGCAAAATAAT TGA	CAAACCTTACCACCGTC TTG	59.5	424	INTERGENIC				
CaPOPI_2043	Ca4	14967549	GTAATAATAATAATAATAATAATAAT AA/GTAATAATAATAATAATAATAAT AATAATAATAA	CAAAGTGCTTTTGTACC CCC	CCGTTTGTTTTGGGACA TCT	59.5	899	INTERGENIC				
CaPOPI_2044	Ca4	15012755	AATATATATATATA/AATATATATATATATATATA	TACTCCCAATGGCGAC TTC	GACATTTCGAACTTGAAT TTCT	60.1	322	INTERGENIC				
CaPOPI_2045	Ca4	15045995	CTATATATATATATATATATATATATA TATATA/CTATATATATATATATATATATA TATATATATATATA	GAAAATTATATCTTTCC CAAATGC	GGAGGAGAGAGACGAA GGCT	58.5	402	INTERGENIC				
CaPOPI_2046	Ca4	15048181	TATAA	CAAAAGCTGTAACACCC CGT	AATCGATTGATTCAGCC CAG	60.0	528	INTERGENIC				
CaPOPI_2047	Ca4	15216075	TAAAAAAAAA/TAAAAAAAAA	TGAACCAAAATCATCG CAA	AGGCTCTTGTTAAGCGA CCA	60.1	402	INTERGENIC				
CaPOPI_2048	Ca4	15221737	ATTTTT/ATTTTTT	AGGGTGCGATCAGGTAA ATG	AACAAGTGGTGCGATTG TGA	60.0	430	INTERGENIC				
CaPOPI_2049	Ca4	15252487	GTA/GTACATATA	TTTTTGAGTGAAACCA GTTTG	CCAACCATGTTGGTGTG CTA	59.2	533	INTERGENIC				
CaPOPI_2050	Ca4	15272177	AG/A	GTTTCGGCTAATGGGT GAA	TTGCTTGAATTTGGGT TTTG	59.9	878	DRR	Ca_05572	A		Zinc finger, RING-CH-type

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CaPOPI_2051	Ca4	15473254	TTATATATATATATATAT/TTATATATATATATAT	TTGGACCGAAGAAATTG TCA	CTCCGTTAATCCTCATG CGT	59.1	702	INTERGENIC				
CaPOPI_2052	Ca4	15481101	AATA/AA	TAGTAGGGCTCTTGCTC CCA	CCAATTGTACCGGGATC TTC	60.0	933	INTERGENIC				
CaPOPI_2053	Ca4	15643039	T/TTACTGTAGGGA	TGCACCGACAAACTGAA GTC	ACGCGTGAGTTTGCTCA CTA	59.9	592	INTERGENIC				
CaPOPI_2054	Ca4	15891944	CTTT/CTTTT	CGACGTCAACACAAATT GC	AGATGCGCGGTGATTAG AGT	58.7	802	INTERGENIC				
CaPOPI_2055	Ca4	15892004	AC/ACCGACTC	CGACGTCAACACAAATT GC	AGATGCGCGGTGATTAG AGT	58.7	802	INTERGENIC				
CaPOPI_2056	Ca4	15898293	T/TA	CCTTCAAAATTTGTGAGT CCG	ATGGGAATTGGTGAATG GAA	59.6	941	INTERGENIC				
CaPOPI_2057	Ca4	15926036	AAAGA/AAAGAAGA	GTTTCCCTTACGCCAGA TGA	GCATTGCTGTATTGGTG CAT	60.1	532	DRR	Ca_05513	R		Beta-lactamase-like
CaPOPI_2058	Ca4	15926090	ACT/ACTCT	AGCAGCACCCACCAAT ATC	TGCTGGTGTCTAGTTG GCA	60.0	674	DRR	Ca_05513	R		Beta-lactamase-like
CaPOPI_2059	Ca4	15939075	AT/ATT	GTGCACCGTAACGAAG TTT	TTCGTTGAGGTTTGGA TTC	60.0	452	INTERGENIC				
CaPOPI_2060	Ca4	15945430	AAAA/AAAAATCAAA	AGTCCAGCCTCTGCACA AAT	GGAGCAAGATGGAACAA TCAA	59.9	212	DRR	Ca_05512	O	C2H2	Heat shock protein DnaJ, N-terminal
CaPOPI_2061	Ca4	15950510	GTTATTTTATT/GTTATTTTATTATTAT TTTTATT	AAAAGGGATTGTCTTCC CAGA	CAAAGGTAGCCCTGCTT CAG	59.9	601	INTERGENIC				
CaPOPI_2062	Ca4	15962571	ACTT/ACTTCTCTT	CAGGAAATTGTGCATCA TGG	TGGTGCATGACTGAATG GTT	59.9	723	INTERGENIC				
CaPOPI_2063	Ca4	15969051	CAA/CA	TAAGCGTTAACTTGCA CCC	TGGTTGTGGCGATTACA AGA	60.1	494	DRR	Ca_05510	J	NF-YA	CysteinyI-tRNA synthetase, class Ia
CaPOPI_2064	Ca4	15983115	AATT/AATTATT	TGATGTTGATGATATGA CGTGG	ATTGTTCTGCAATGAG GGG	59.3	729	INTERGENIC				
CaPOPI_2065	Ca4	16000633	TACA/TA	CGATGTATTTTTGTAG TCAAGC	TATTTCCGCACACCAAT GA	58.8	392	INTERGENIC				

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CaPOPI_2066	Ca4	16027847	A/AG	AATTTTGGCTTTTTCGCTG	ATCATATCCATCAAACGGC	60.1	536	INTERGENIC				
CaPOPI_2067	Ca4	16028817	CGTGTGT/CGTGTGTGT	TGATTTTACACAAGGGTAATTTTG	CGCCGCATACTGTAATGTA	57.3	951	INTERGENIC				
CaPOPI_2068	Ca4	16048595	TG/T	GACCATTTTTGGTGATTGGG	AGGTACCACCAACCAAGTGC	60.0	258	INTRON	Ca_05504	J	bHLH	GlutamyI/glutaminyI-tRNA synthetase, class Ic
CaPOPI_2069	Ca4	16066680	CAAAA/CAAA	TCTCGATTGAAGTGCATGGG	CATTAGAGTTCACTTGGCGG	59.8	514	INTERGENIC				
CaPOPI_2070	Ca4	16066890	ATTTT/ATTTT	AGAACCGATTTTGGTGATGC	GGGACCAGTGATTTAATTAGCC	59.9	705	INTERGENIC				
CaPOPI_2071	Ca4	16080327	CTTTTTTTTTTT/CTTTTTTTTTTT	TTCCTCACGTGATCCCTTTC	ACAATTGCTCCAACGGTCAT	60.1	567	INTERGENIC				
CaPOPI_2072	Ca4	16095440	TA/TAA	AGCCCAAGAAAGAAAACGCT	AAGGCAAAAGTCGTCCAATC	60.4	726	INTERGENIC				
CaPOPI_2073	Ca4	16095927	GATAATATAATATAATATA/GATAATATAATATAATATAATATA	TACAGAATCGCTCCCTCAC	TACATGGTTCGGTTGGGTTT	60.2	665	INTERGENIC				
CaPOPI_2074	Ca4	16120236	AATATATATATATATATA/AATATATATATATATATA	TCGAAAGCATTCTTCTCAAA	TGGTTTGACCTATTTATGGTTGG	59.9	550	INTERGENIC				
CaPOPI_2075	Ca4	16138106	TTTATTATTATTATTATTATTATTAT/TTTATTATTATTATTATTATTATTATTATT	CAATGACATTACTTGGGCCTT	GGGAGAAGAAAAGAATGGAA	59.0	391	INTERGENIC				
CaPOPI_2076	Ca4	16186698	T/TC	TTGTTTACAAGAGATGTTTGTCAATT	AAACCACGACTCCAAGCAAT	59.5	372	DRR	Ca_05493	Z		Domain of unknown function DUF292, eukaryotic
CaPOPI_2077	Ca4	16329274	A/AAGCATAC	TTGGACGATAGTACCGTATTCAA	CGAAGCAAAATAGCAAGACTGC	58.6	815	INTERGENIC				
CaPOPI_2078	Ca4	16787893	CTTTTTTT/CTTTTTTT	CCCTTTAAATGAGAGATTGAAG	ATCGTCACGTGCAACAATC	57.7	628	INTERGENIC				
CaPOPI_2079	Ca4	16827901	AATATTGATTATA/AATATTGATTATATTGATTATA	ACGCCAACATTTGTGAGTGA	TCGGATTCACTTAGTTGCACA	60.2	853	INTERGENIC				
CaPOPI_2080	Ca4	16846897	C/CTT	ACATGTGCCTTGGGACTAGC	GCGAAAAGTCGAAGATCTG	60.1	571	INTRON	Ca_05437			Amino acid-binding ACT

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CaPOPI_2081	Ca4	16925907	TAAAAAAAAA/TAAAAAAAAA	TGCAAAACGTCGCTGTCTAC	TGGTCACTGGTCACTCTTGG	60.1	566	DRR	Ca_05430	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2082	Ca4	16933042	TAAAAAAAAA/TAAAAAAAAA	CCAAATAAACTACTTTGTGAGACGA	CACACTCTGCCTCCACTGAA	60.0	388	INTERGENIC				
CaPOPI_2083	Ca4	16943222	TATGAATGAAT/TATGAATGAATGAAT	CTCAAGCTCAGTCCCAGTCC	TGCGTTTTGTTGGTGTAGC	60.0	668	INTERGENIC				
CaPOPI_2084	Ca4	16984107	ATTTTTTT/ATTTTTTT	TAACAAGGGTGCCATGTGTG	ATTGATTTGGCAATGGTGGT	60.4	822	INTRON	Ca_05426	U		Zinc finger, Sec23/Sec24-type
CaPOPI_2085	Ca4	17017613	ATTTT/ATTTT	GGAAGTTGACTTGTGCGGAT	TTGTTCTGAAAGAAACGGG	60.1	527	INTERGENIC				
CaPOPI_2086	Ca4	17029753	ATTTTTTTTT/ATTTTTTTTT	ACCATTTCCTCCTGTGTTGC	CAAAAATTTGAGGGTTCAAACA	60.0	728	INTERGENIC				
CaPOPI_2087	Ca4	17047766	ATTTTTTTTT/ATTTTTTTTT	GAACCCAGTGACAACCTCT	AAGCGACCAGTTGAAGGAAA	60.2	662	DRR	Ca_05418	DA		mRNA splicing factor SYF2
CaPOPI_2088	Ca4	17047788	ATTTTTTTTT/ATTTTTTTTT	GAACCCAGTGACAACCTCT	AAGCGACCAGTTGAAGGAAA	60.2	662	DRR	Ca_05418	DA		mRNA splicing factor SYF2
CaPOPI_2089	Ca4	17063810	TAAAAAAAAA/TAAAAAAAAA	CAAAAGAAAAGCTTTATACGGTGA	TTTCGGTTTATGTAGCAGCCC	59.0	558	INTERGENIC				
CaPOPI_2090	Ca4	17071722	ATTTTTTTTT/ATTTTTTTTT	GGGCTGCTACATAAACCGAA	TCCGACATGCCATTTGTTA	60.1	189	INTERGENIC				
CaPOPI_2091	Ca4	17081756	TTATA/TTATATA	TACCGGAAGATTTCGGAAATG	CTGCAGGTAAGCATCCC AAT	59.9	694	INTRON	Ca_05415			
CaPOPI_2092	Ca4	17081772	TAATA/T	TACCGGAAGATTTCGGAAATG	CTGCAGGTAAGCATCCC AAT	59.9	694	INTRON	Ca_05415			
CaPOPI_2093	Ca4	17082915	CTTTT/CTTTTTT	TCAGCTCACTCTCGCTTTGA	TGATGGAAGAATAAGGGGTCC	60.0	503	DRR	Ca_05415			
CaPOPI_2094	Ca4	17090015	ATATTTATTTATTTATTTATTT/ATATTTATTTATTT	CCAACATTAAACGGCCCTA	GCATTTTCACAATGTGGTGC	59.8	698	INTERGENIC				
CaPOPI_2095	Ca4	17101140	TAACAAC/TAACAACAAC	TGGTTTGATTATTGTGTGTC	CATTGGTTTTAACAAGTTGTTGTTGT	58.4	472	DRR	Ca_05414			Plastocyanin-like

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CaPOPl_2096	Ca4	17101199	A/AC	TGGTTTGATTATTGTG GTGC	GTTCTTGA AATTCAC GAATA	58.4	812	DRR	Ca_05414			Plastocyanin-like
CaPOPl_2097	Ca4	17101268	TAAAAAA/TAAAAAAA	TGGTTTGATTATTGTG GTGC	TCGAGAGTTGGGTCATG GTC	58.4	881	DRR	Ca_05414			Plastocyanin-like
CaPOPl_2098	Ca4	17101583	AG/A	TGATGTTAACTGACAAT GCTGTTT	GTCGAGAGTTGGGTCAT GGT	60.0	322	DRR	Ca_05414			Plastocyanin-like
CaPOPl_2099	Ca4	17141313	T/TC	TTTCAATCGTATCAAGTT TTTGC	AAACTGAAAGCCTAAT TCCAA	58.4	682	DRR	Ca_05410	CR	Nin-like	Monoxygenase, FAD binding
CaPOPl_2100	Ca4	17157766	TTAAT/TTAATAAT	AGAACC TTGCTATGCGT CGT	CATGGTGTGGACAAGAT TGG	59.9	501	DRR	Ca_05407			Translation initiation factor 3
CaPOPl_2101	Ca4	17167273	T/TC	TTCCA CTCTCCACCATT CC	CACCAACAAGGATCGGA TTT	59.9	429	INTERGENIC				
CaPOPl_2102	Ca4	17193639	ATTTT/ATTT	AAGCAGCAAGGATCAC CAAAT	CCCCATTAGTATTGCCG CTA	59.7	532	DRR	Ca_05405	T		Protein phosphatase 2C, manganese/magnesium aspartate binding
CaPOPl_2103	Ca4	17196085	TTCTCTCTCTCTCTCTCTCTCTCTCT /TTCTCTCTCTCTCTCTCTCTCTCTCT	CCTCAACCATGGCCTGT ACT	AGTTGCATTGGAGACAA GGG	60.0	118	INTERGENIC				
CaPOPl_2104	Ca4	17203357	TAAGA/TAAGAAGA	TGTGCTCCATGTCTCTT TGC	CTCTTGGCTGGTAGCTT TGG	60.0	611	INTRON	Ca_05403			Protein of unknown function DUF3353
CaPOPl_2105	Ca4	17206399	ATTTTT/ATTTTT	AACCGTTTGATGCGAAA AAT	ATCTATTGCCATCTGCC AGG	59.5	925	INTERGENIC				
CaPOPl_2106	Ca4	17206661	T/TA	AATCAATCAACCAAGAA CGGA	ATCTATTGCCATCTGCC AGG	59.4	598	INTERGENIC				
CaPOPl_2107	Ca4	17206969	TAAAAAAAA/TAAAAAAA	CCTGGCAGATGGCAATA GAT	GAAAATGGATCCGACGA AGA	60.1	593	INTERGENIC				
CaPOPl_2108	Ca4	17209722	CT/CTT	CCATTTCAGAAAAGGCCA AGA	AAGCCTCGGGTAAAATT GGT	60.2	442	INTRON	Ca_05402	C		ATPase, alpha/beta subunit, nucleotide-binding domain
CaPOPl_2109	Ca4	17210535	CTT/CT	TTCAGGGAGTTCCATCA ACC	TAGCCTTCTGAATCCC CCT	59.9	448	INTRON	Ca_05402	C		ATPase, alpha/beta subunit, nucleotide-binding domain
CaPOPl_2110	Ca4	17247653	GAAAAAAAA/GAAAAAAAAA	TTTATGTTTGCCAACTC CC	TTTTTAGGGACGCAATT CAAA	59.8	539	INTERGENIC				

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CaPOPI_2111	Ca4	17247848	TAAAAAAAA/TAAAAAAAAA	TTTATGTTTGCCAACTC CC	TTTTTAGGACGCAATT CAAA	59.8	539	INTERGENIC				
CaPOPI_2112	Ca4	17250847	ATTTT/ATTT	GCCGAAAAACCAAGTG TGT	CGTTGGATTCTTTCTC CTC	60.0	514	INTERGENIC				
CaPOPI_2113	Ca4	17253834	AAATAA/AAA	TGCAATATCATTTTCATG TTCTTG	TGATGAAGTGAGTCGCT TGG	59.0	843	INTERGENIC				
CaPOPI_2114	Ca4	17253939	T/TA	TCAACATCTAGTTAGAG GTGCAAAA	TGATGAAGTGAGTCGCT TGG	59.4	780	INTERGENIC				
CaPOPI_2115	Ca4	17254750	GTAATAA/GTAA	CAAATATTGTCCAGCC AAA	TCCTTAATCTTGACCAGC CCG	59.6	898	INTERGENIC				
CaPOPI_2116	Ca4	17257056	ATTTT/ATTT	CCAACAAGCATTACATT GCG	ACGTTGACATTCCAGCA TGA	60.1	423	INTERGENIC				
CaPOPI_2117	Ca4	17257974	AATA/AATATA	ACATGGCAGTTGGATT CAT	TCATGGGTACCCACCT TAG	60.2	605	INTERGENIC				
CaPOPI_2118	Ca4	17284874	GATA/GA	TTGAATATGAGCCTCCA AGAGA	CTTGTTGAGGCTTTGGG TGT	58.9	794	DRR	Ca_05393	R		Ankyrin repeat-containing domain
CaPOPI_2119	Ca4	17285160	ACT/A	CATTTCCTTTGAGTCATG AGAGG	CTTGTTGAGGCTTTGGG TGT	60.1	310	DRR	Ca_05393	R		Ankyrin repeat-containing domain
CaPOPI_2120	Ca4	17286686	CATTGGATTGGATTG/CATTGGATTG	TGCATTTTCATGCCTTTG CTA	TGATTAGCCCGTATTTT GGG	60.4	648	INTRON	Ca_05393	R		Ankyrin repeat-containing domain
CaPOPI_2121	Ca4	17290871	GTTTAATT/GTTTAATTTTAATT	CCAAGTATGGCAGGTGG AAT	TCATGAGCTAGAATGGT TGTA AAAA	59.8	615	INTERGENIC				
CaPOPI_2122	Ca4	17297028	TA/TAA	TTTGCCTCAGCTGTGTT GAC	TCATCAGCTGGACAAC TCG	60.0	607	INTRON	Ca_05392	R		Ankyrin repeat-containing domain
CaPOPI_2123	Ca4	17313521	TAAA/TAA	GCTAGACAGGTTTGCCT TCG	AAGGCTCCTGCAAGCAT TTA	60.0	966	INTERGENIC				
CaPOPI_2124	Ca4	17314621	ATTTTTT/ATTTTT	ACGCGATTGAGAACAAA AGG	CTTCCCCACTCACAGTC CAT	60.2	604	DRR	Ca_05390	M		Mechanosensitive ion channel MscS
CaPOPI_2125	Ca4	17315192	TAAA/TAAA	ATGGACTGTGAGTGGG GAAG	TTGGTCCAACAGCTTGA TGA	60.0	716	DRR	Ca_05390	M		Mechanosensitive ion channel MscS

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2126	Ca4	17318086	A/AG	CTCAAAAGTGGGATAGG GCA	ACAGCGTGAAACAAGAT CCC	60.1	429	INTRON	Ca_05390	M		Mechanosensitive ion channel MscS
CaPOPI_2127	Ca4	17329245	TCACA/TCA	GGCATGATAAAGAGGGA GGA	TAACTCTCACGTGCAA TCG	59.1	386	INTERGENIC				
CaPOPI_2128	Ca4	17354782	TAAAAAAAA/TAAAAAAA	TATTGATTCGGTCAATTA TGACA	TGGATTAGGCCTTGAAG CAT	57.1	728	INTERGENIC				
CaPOPI_2129	Ca4	17360464	TTATATATATATATAT/TTATATATATA TATATATATATATATAT	GTGTGCGATTGAGTTGA ACG	CTTGCTGGGCTTTTCAA GAC	60.3	579	INTRON	Ca_05388	T	NAC	Protein kinase, catalytic domain
CaPOPI_2130	Ca4	17365284	TA/TAA	CCCCGCTTACACATTC TTA	TATTGGTGTAAACCGAAC GCA	60.0	557	INTRON	Ca_05388	T	NAC	Protein kinase, catalytic domain
CaPOPI_2131	Ca4	17367667	AC/ACC	TAAATGTGATTTGCGAG CGA	ATGCATGGAGGTGATGA TGA	60.4	284	INTERGENIC				
CaPOPI_2132	Ca4	17376716	ATTTTTTTTT/ATTTTTTTTTTT	CCCCCATCTTCAAATGT GTT	AGATGTAGCAACGCAAA CCA	59.6	698	DRR	Ca_05387	R		F-box domain, cyclin-like
CaPOPI_2133	Ca4	17388357	TAAAAAAAAAAAAA/TAAAAAAA	AAATCGCCATTTGGAAC TTG	CACGATCATGTGTTCCA CAA	59.9	308	INTERGENIC				
CaPOPI_2134	Ca4	17420097	TA/TAA	TCGTTCAACCATTCAT CAT	TCCGAATGAGTGACCAA AATC	59.9	612	INTERGENIC				
CaPOPI_2135	Ca4	17421248	G/GTTTAA	CCCGTGAGTTGTTGGA GTT	TCGATAATTTGAAACCG CCT	60.0	569	INTERGENIC				
CaPOPI_2136	Ca4	17423293	TTATATA/TTA	GTGTGGGTTGGCTTTCA TCT	GAAACGCTATGATGCCG TAAA	60.0	492	INTERGENIC				
CaPOPI_2137	Ca4	17431572	GC/G	TCTGTCAATTCCTGCCATT TTT	TCGCAATGTAGCTCCCT CTT	59.6	858	INTRON	Ca_05384	K		Transcription factor jumonji/aspartyl beta-hydroxylase
CaPOPI_2138	Ca4	17436350	CTTTT/CTTT	AAGATCCTGCCCTCAA GAT	TGCTCCAAGTGTGGT GAC	60.0	459	INTRON	Ca_05384	K		Transcription factor jumonji/aspartyl beta-hydroxylase
CaPOPI_2139	Ca4	17448021	TATTTTCATTTTC/TATTTTCATTTTCATT TTC	GAGTTGAGGAAACAATT ATGTCAAA	TTCTTTTCTGCGATTTC TCG	58.7	654	INTERGENIC				
CaPOPI_2140	Ca4	17470871	GTGGCTA/GTGGCTAATGGCTA	GTCCCAACCAAGAAAGC AAA	CACTTGAAGAGGCTCCA TCC	60.1	343	DRR	Ca_05380	AB		SKI-interacting protein SKIP, SNW domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2141	Ca4	17475440	GT/GTTGTTATT	CGGGCAGTAGCATTAGA TGG	GGATGAATGGGAGGTG GTTA	60.6	210	INTERGENIC				
CaPOPI_2142	Ca4	17484481	ATTTTTTTTT/ATTTTTTTTTT	TCGCCTGATGCTTGAC TTG	AGGAGGCTTTTCCACAG GTT	60.0	361	INTRON	Ca_05379	O		Oligosaccharyl transferase, STT3 subunit
CaPOPI_2143	Ca4	17532742	TAAAA/TAAAAA	CCCATCTTGTTTGGTTC ACA	CTGAAAGGGCATAAAGG CAA	59.4	954	INTERGENIC				
CaPOPI_2144	Ca4	17533392	CTT/CTTT	CTTTTGTGGTGCCAT TTT	GGCATTGTGCTGAGTGA TTTT	60.1	679	INTERGENIC				
CaPOPI_2145	Ca4	17533529	GT/G	CTTTTGTGGTGCCAT TTT	TGCAAGAAGAAGGAAGC CAT	60.1	713	INTERGENIC				
CaPOPI_2146	Ca4	17534928	TAAAAAAAA/TAAAAAAAAA	TTTTTGTGTGTGCGG TTT	TGTGTCAAAGATGGTAT TTCAATG	60.1	410	INTERGENIC				
CaPOPI_2147	Ca4	17535175	ACT/ACTCT	TTTTTGTGTGTGCGG TTT	GGCTGGAAGTGAGCTAG TGG	60.1	811	INTERGENIC				
CaPOPI_2148	Ca4	17545627	TAAAAAAAA/TAAAAA	AGTTTAGGGGCAAGCAC TGA	TGCATCGGAGATCACAT CTT	59.9	363	INTERGENIC				
CaPOPI_2149	Ca4	17552174	GTT/GTTT	AAGTGAGGCCACTGGAA AGA	ATGTGTTGGAACCTTTC CGC	59.8	204	INTERGENIC				
CaPOPI_2150	Ca4	17600797	TC/T	AAGGGTGATGGACGAAA AAC	TTAAATGGTCGCATAGA GCAA	58.9	682	INTERGENIC				
CaPOPI_2151	Ca4	17600811	TAAAAA/TAAAAA	AAGGGTGATGGACGAAA AAC	TCCAACAACATCAAATTC ATCC	58.9	951	INTERGENIC				
CaPOPI_2152	Ca4	17601510	TC/T	GGATGAATTTGATGTTG TTGGA	CCGTGTCTATCCCCATT TTG	59.7	515	INTERGENIC				
CaPOPI_2153	Ca4	17617805	GAAAAA/GAAAAA	CATCTAGTGTGGGGAA TGTGA	ACGTTTCGCCCTACATC ATT	59.9	838	INTERGENIC				
CaPOPI_2154	Ca4	17629803	ATTTTTTT/ATTTTTTTTTT	CTTTTCCGCGAACACAT TTT	GTACATACATGGACGCG ACG	60.1	587	INTERGENIC				
CaPOPI_2155	Ca4	17636026	C/CCAAGATATA	GGCCTCATCTCTAGCCA ATG	CCAAGGAAGTTTCACCA GGA	59.8	297	INTRON	Ca_05367	Z	WRKY	IQ motif, EF-hand binding site

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2156	Ca4	17637226	CTATT/C	ACACAAGTTAGGTGGGG CAG	CTGCATCTGTAGTGAGG CCA	60.0	346	INTRON	Ca_05367	Z	WRKY	IQ motif, EF-hand binding site
CaPOPI_2157	Ca4	17637458	GAC/G	ACACAAGTTAGGTGGGG CAG	GCATGGCTTGATGTGAG AGA	60.0	475	INTRON	Ca_05367	Z	WRKY	IQ motif, EF-hand binding site
CaPOPI_2158	Ca4	17640423	CTTTTTTT/CTTTTTT	CAAGAAGAAGTGGTGGG GAA	GAACCCCTTCCATCGAG TCA	60.1	524	DRR	Ca_05367	Z	WRKY	IQ motif, EF-hand binding site
CaPOPI_2159	Ca4	17649020	TTTTAAA/TTTTAAATTTAAA	CCAAAGAGCTGAAATGC ACA	GGAAGCCGAAAACTAA GGC	60.0	399	DRR	Ca_05365	H		Molybdopterine cofactor biosynthesis C (MoaC) domain
CaPOPI_2160	Ca4	17656569	GATA/GATATA	AATTTGGGGCGTTACAA ACA	GTGCAAGATCCGCTACC AGT	60.2	427	INTERGENIC				
CaPOPI_2161	Ca4	17697196	TAAAAAAAA/TAAAAAAAAA	GGAAATTTGGAAAGTTG GCA	ATAAGGTTCCCTTGCA ATC	59.9	564	INTERGENIC				
CaPOPI_2162	Ca4	17715218	GAAAAAAAA/GAAAAAAAA	CTGTTCTCACATCAGC CAT	GGAGTCACCTCCAAAT TGA	59.7	143	INTERGENIC				
CaPOPI_2163	Ca4	17715291	CTT/CT	TCAATTTGGAGGGTGAC TCC	TACCAGCTTTGGTTTCT GCC	59.9	250	INTERGENIC				
CaPOPI_2164	Ca4	17715629	AT/ATATATT	TCAATTTGGAGGGTGAC TCC	GCGCTGATGCAATACAT ACAC	59.9	532	INTERGENIC				
CaPOPI_2165	Ca4	17717044	TGG/TG	TCTGTCAAAGTCGGTGC AAG	ATAATGGCGCCACAGAA AAG	60.0	821	INTERGENIC				
CaPOPI_2166	Ca4	17720367	CTGATCTTGATC/CTGATCTTGATCTTG ATC	ACCCTCAGCATGGTCAA AAG	TAGTGGTGGCTCCCCTA ATG	60.1	480	DRR	Ca_05352	KL	bHLH	SNF2-related
CaPOPI_2167	Ca4	17735379	ATATT/AT	TTTTTAAAGGGCCGAT TG	TGATTGTACGTCATCA AAATTC	59.9	554	INTERGENIC				
CaPOPI_2168	Ca4	17735574	T/TA	TCACGATCGAAAACTT ATTTG	AAACATGACAAAAGTTG ATGTTGAA	59.1	916	INTERGENIC				
CaPOPI_2169	Ca4	17740594	GTTTTTTTT/GTTTTTTTT	ATATGGCAAGGAACAAC GGA	TACCTTGGAATTGGCTG GTC	60.3	664	INTERGENIC				
CaPOPI_2170	Ca4	17757375	T/TC	TAAACCAACCCACACC ATT	ACAATGCCTTTTGCCA CTC	59.9	252	DRR	Ca_05349	O		Peptidase S9, prolyl oligopeptidase, catalytic domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2171	Ca4	17758892	GTTTTTTTT/GTTTTTTT	TTTGATGCAACAAGTTCCTG	CGATGAAGGAGTTCTCAGCC	58.8	499	DRR	Ca_05349	O		Peptidase S9, prolyl oligopeptidase, catalytic domain
CaPOPI_2172	Ca4	17766593	TAAAA/TAAA	ATTGCATTGTGCTCCACTTG	AGGGGTTGGTATAGTAGAAGGAA	59.7	512	DRR	Ca_05348			
CaPOPI_2173	Ca4	17769321	GAACAAACAAACAAACAA/GAACAAACAAACAA	GAGCCCATTCCAAAGATGA	TTCAGCCTCGACCAGTTT	60.0	814	INTRON	Ca_05348			
CaPOPI_2174	Ca4	17772365	AACCTT/AACCTACTT	TCTCATCCCGATTCCAAAG	CGTAAGTTTCCCGTTCCAAA	60.0	387	INTRON	Ca_05347	R		D111/G-patch
CaPOPI_2175	Ca4	17775890	TAAA/TA	TGCATTAGCAAAAAGTACCA	GGCACTGCCGTCAAAAGTAT	59.4	525	DRR	Ca_05347	R		D111/G-patch
CaPOPI_2176	Ca4	17777647	CATCTGAATCTGAA/CATCTGAA	CCTTAGGGGAGATTGCAATTC	TGCAGATAAATGGCCAAACA	59.9	852	INTERGENIC				
CaPOPI_2177	Ca4	17821019	AAGA/AA	GGAAGTGCATGATTGTTCCCA	AGATGTGGGCATGTGTTTCA	59.8	805	INTERGENIC				
CaPOPI_2178	Ca4	17827610	A/AT	TCAACTTCGGTGCTTGACAG	TTGGGGTACACGAACAAATGA	60.0	141	INTERGENIC				
CaPOPI_2179	Ca4	17830486	ATTTTTTTTT/ATTTTTTTTTT	TGGCTTGCAATCTCAATCAG	TTTGGATGCATAGGCCATTT	59.9	296	INTERGENIC				
CaPOPI_2180	Ca4	17847500	CTCCTTTTCATC/CTCCTTTTCATCCTTTTCATC	TGAACGATGGTGGAAGACA	GCAGAGCTCTTTGGCAGAGT	60.1	391	INTRON	Ca_18621	J		Methionyl-tRNA synthetase
CaPOPI_2181	Ca4	17862487	CTTT/CTT	TTTTCTTCGGATGGAATGC	ACAAAAATGGCAATGCACAA	60.0	571	INTRON	Ca_18623		WOX	Homeobox
CaPOPI_2182	Ca4	17862773	AGT/AGTGT	TTTTCTTCGGATGGAATGC	ACAAAAATGGCAATGCACAA	60.0	571	INTRON	Ca_18623		WOX	Homeobox
CaPOPI_2183	Ca4	17863620	CTTATTGGAATTATTGGAATTATT/CTTATTGGAATTATT	TTTGATTGTGGCTTTTGCAG	ACGAGCTAAAGGATGGGTTG	59.8	540	DRR	Ca_18623		WOX	Homeobox
CaPOPI_2184	Ca4	17942733	CTATATATATATAT/CTATATATATATATATAT	CATCGTCAGCACATCACAAA	CTTAGGAGGTCTTGCCCCTC	59.2	447	INTERGENIC				
CaPOPI_2185	Ca4	18033913	CT/CTT	CTGAGTGACCTCCCTTCCAA	TCATTCCAGAAGGAGATGGG	60.2	433	INTRON	Ca_18645			

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2186	Ca4	18121565	TAAGAAG/TAAG	GCTGCACCATGAGATCT TGA	ATGGTGCTGGAAGTTGC TTT	60.0	440	INTRON	Ca_18652			Chalcone isomerase, subgroup
CaPOPI_2187	Ca4	18196212	ATTT/ATTTAATCTTTTT	GTGGTCCAGATTCTCCC AAA	TGTCGCTTCAGCAAAA GAA	59.9	549	INTERGENIC				
CaPOPI_2188	Ca4	18407838	AATATATATATATATATATATA/AAT ATATATATATATATATATATA	TAATAGGAACCCACACC CCA	ATGCTCCGGTGAACAAT CTC	60.0	360	INTERGENIC				
CaPOPI_2189	Ca4	18446227	GTTTTTT/GTTTTTTT	TCTCACGGTTGTGAGGA CTG	GGTGGAGGTGAAGTAA ACAA	59.9	304	INTERGENIC				
CaPOPI_2190	Ca4	18515805	TATAAATAAATAAATAAATAAAT/T ATAAATAAATAAATAAATAAATAA T	TTTTTGAGATTGTACG GGA	TCAGCGTTTGTGTG ACTT	58.1	738	INTERGENIC				
CaPOPI_2191	Ca4	18649901	AATATATATATATATATATATATAT ATAT/AATATATATATATATATATAT ATAT	CTCTTTGGTTCTACGGC TGC	TATGGCTTACGAGGGAC TGG	60.0	911	INTERGENIC				
CaPOPI_2192	Ca4	18781017	TAAAAAAAAA/TAAAAAAAAA	GAGAAACAACGCAGGGA AAC	ATTATTGCCGCCAATTCA AA	59.7	350	INTERGENIC				
CaPOPI_2193	Ca4	18821207	CATTATTATTATTATTATTATTAT/C ATTATTATTATTATTATTATTATTAT T	AAAGTCGCATTCTGGGG ATA	ATGTGCCAACTTCGACA ATG	59.5	722	INTERGENIC				
CaPOPI_2194	Ca4	18860078	TTATATATATATATATATATATAT/TTA TATATATATATATATATATATATATAT AT	GAGAAACTCCGCTCTTG TGG	GAACTCCCCGCCAACA CTA	60.0	700	INTERGENIC				
CaPOPI_2195	Ca4	18993059	GTTTTTTT/GTTTTTTT	CGTTAAGAATGCGTTGC AGA	TCGCAACTTTTGTGGT TTTT	60.0	302	INTERGENIC				
CaPOPI_2196	Ca4	19045820	A/AT	GGGCTTGCTTGGTTTGA ATA	TCAACTGCACGTGTTAA ATGC	60.1	825	INTERGENIC				
CaPOPI_2197	Ca4	19046060	CAAAAAA/CAAAAAA	TGAAATGAGATTAGAA CCACCA	TCTTCACCTGCATCGAA ATG	59.9	677	INTERGENIC				
CaPOPI_2198	Ca4	19198535	CTTTTTTTTT/CTTTTTTTTTTTT	AGAGGCGGGTGAGAAAT TGT	CGTGCTATTCGGCAATC ATA	61.0	707	INTRON	Ca_14019	O		Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
CaPOPI_2199	Ca4	19294536	TTATATATATATATATATATATAT/T TATATATATATATATATATATATATAT ATAT	GCATACTCTGTCCTTTC GTCC	GGCTGCCATCACTTCAT CTC	58.8	586	INTERGENIC				
CaPOPI_2200	Ca4	19643688	CTTTTT/CTTTTTT	GGTGCAGTTGTTTGATG CAC	ATGCGATTTACATGGTT GGC	60.2	255	INTERGENIC				

[illegible]

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CaPOPI_2216	Ca4	21514634	ATGT/ATGTGT	TTGGAATCATGAGTTGA TCTCG	AGAAGAACCACGACAAA GGC	60.1	656	INTERGENIC				
CaPOPI_2217	Ca4	21529168	CAAAA/CAA	TGGGGGATTGTATTCCA AAA	TATGGAATGGACCTCCT GCT	60.0	499	INTERGENIC				
CaPOPI_2218	Ca4	21529316	T/TA	TGGGGGATTGTATTCCA AAA	TGAAATCGTCACCGTCT CAA	60.0	886	INTERGENIC				
CaPOPI_2219	Ca4	21657934	TTATATATATATATATATA/TTATATAT ATATATATATATATATA	AAATGTGAAAGCCACAA CCC	CCATGTAGCATGGCAAC AAC	59.8	570	INTERGENIC				
CaPOPI_2220	Ca4	21804779	CTGT/CTGTTATGT	CCGCATCATAAACAGCC TTT	CTAAAGCTGGTGCTTTT GGC	60.1	159	INTERGENIC				
CaPOPI_2221	Ca4	21910161	ATTTTTTTTTTT/ATTTTTTTTTTT	TGCCCGTAGTTGTACCA TGA	CGATGCAAACGTGGATT ATG	60.0	383	INTERGENIC				
CaPOPI_2222	Ca4	22097668	ATTTTTTTTTTT/ATTTTTTTTTTT	TGAAGCACCTTTGTATGA GGA	GACGTGATAACATGAAG GATGC	59.4	850	INTERGENIC				
CaPOPI_2223	Ca4	22134995	CATAT/CAT	GCACCTATGGTGGCAAA AAC	TTTGATGCCACACATTGA AGA	60.4	506	DRR	Ca_20134	J		Brix domain
CaPOPI_2224	Ca4	22309344	ATTTTTTTTT/ATTTTTTTTTTT	TGCTTTGTTCAATTGCTT GC	AGTGCCAAGTAAGGTTG CTGA	60.0	566	INTERGENIC				
CaPOPI_2225	Ca4	22324512	TAAAAAAAAA/TAAAAAAAAA	CGCTGATTCATCCTTTTC GT	TTGAACTCCTTTCTGGG TGG	60.2	937	INTERGENIC				
CaPOPI_2226	Ca4	22381273	AATATATATATATATATA/AATATATATAT ATATATATA	CAGTGGCGAAATCTGCA TTA	TGGACGTAGGTTGTTGT GGA	59.8	702	INTERGENIC				
CaPOPI_2227	Ca4	22441886	CTA/CTATA	TCCAATGGTGGAATA AACG	TCAATCACAAATTTCAAG GAGG	59.7	848	INTERGENIC				
CaPOPI_2228	Ca4	22499567	A/ACACGACGCTAAAATACCC	ATGCAATGCGTATATGC CAA	TACATGGTGACCGCGAT AGA	59.9	352	INTERGENIC				
CaPOPI_2229	Ca4	22508434	CATATATATATATATATATATAT/C ATATATATATATATATATATATATA TATATATATAT	TGGAAGGAAAACAATCG AGG	GCATTGCAATAATCCAT CCA	60.0	647	INTERGENIC				
CaPOPI_2230	Ca4	22546535	AATATATATATATA/AATATATATATAT A	CATTTTGTTTCAAAGC CGT	CCAGGGGATGAGATCAT AGG	60.0	714	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2231	Ca4	22601747	TAAAAAAAA/TAAAAAAAAA	GTCGCTCTTCCATTCA TTT	GATTTCCCTTGTCAACA ATCA	60.1	229	INTERGENIC				
CaPOPI_2232	Ca4	22656873	TA/TAGAAAAGCAGA	GACACTCAAGGCTGAAG TAGAAAA	ACCTGACAACCCCAAT TGA	59.1	246	INTERGENIC				
CaPOPI_2233	Ca4	22664879	AA/AAGA	TCGCGTTCGATTGTTC ATA	GGTCATTCTTATTGATTG ACCCA	60.2	570	INTERGENIC				
CaPOPI_2234	Ca4	22674188	CAAAAAAAAA/CAAAAAAAAA	AATGCATGTTGCACCAC AGT	GCTGAAAAGGAAGGGAA AGG	60.0	292	INTERGENIC				
CaPOPI_2235	Ca4	22675724	TTT/TTTCTT	CACAGAAAAGTGAACG CGA	ATGGCAATTAGGGTGTG CTC	60.0	325	INTERGENIC				
CaPOPI_2236	Ca4	22703169	ATTTTT/ATTTTTTT	GTGCAAAACAGGAGCAA CAA	GCCTCCAATCCATGTCT GAT	59.9	322	INTERGENIC				
CaPOPI_2237	Ca4	22719677	TATAAA/TAA	TTTTGGCACGTCTTCTC AACT	CATCGACGATTGTACCA AAAA	59.9	548	INTERGENIC				
CaPOPI_2238	Ca4	22723833	TGGGGG/TGGGGGG	TCTAACCCGCAACAT CAA	AGGCCACGAAAGTGAAG AGA	60.1	527	DRR	Ca_14476			Protein of unknown function DUF593
CaPOPI_2239	Ca4	22727877	TAAA/TAA	TTGGTTCCTTTATTAAC AATTTTTG	GGGACAAACGTTTTTGC TATG	59.3	809	INTERGENIC				
CaPOPI_2240	Ca4	22735575	AAAA/AAAATAAA	TTGAAGTTGTCGATCCC CTC	CATATTCAACGCAACAA CGC	60.1	553	DRR	Ca_14475	T	FAR1	Protein kinase, catalytic domain
CaPOPI_2241	Ca4	22746108	ACC/ACCC	GGAAGAAGCATGTGGGT TGT	TTGGCCTTGAGACCAGC TAT	60.0	721	INTERGENIC				
CaPOPI_2242	Ca4	22755158	ATTTTT/ATTTTTTT	CTATGTGCGTCGTCAGG AAA	CCAAAAACGGTTTCACC AGT	59.9	595	INTERGENIC				
CaPOPI_2243	Ca4	22765623	CTT/CTTT	TGGGGACCTTCCCAATA TAC	TATGGCCGATGCTACAA CAA	58.6	219	INTERGENIC				
CaPOPI_2244	Ca4	22766072	AATATA/AATATATATA	TAATTACTTCCGCGGA TGC	GGGTAGCCTTTGCTTG GAG	60.1	424	INTERGENIC				
CaPOPI_2245	Ca4	22766863	T/TGG	GCATAATCAAAGCATT GGC	ATCGATTCTCAGTTGGA CCG	58.3	756	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2246	Ca4	22767329	AACAC/AAC	CCAAGTGAATCGATGGT	TCTCCTTTCAAATTCCTCAA	59.9	274	INTERGENIC				
CaPOPI_2247	Ca4	22792612	ATTT/ATT	CCTTGAGTGAGTTTGACAGGAA	AAACCATAAGCCCCAAACC	59.4	577	DRR	Ca_14472			
CaPOPI_2248	Ca4	22793993	ATTT/ATT	CGAGTGGCAGAACTTCAAAA	GAATTATGCCGCAAGTACGA	59.0	318	DRR	Ca_14472			
CaPOPI_2249	Ca4	22799910	AAAA/AAAAAATTAAA	TCGGTGATTTGTGTGTGA	GTGCAATCATGCAATCAAGG	59.5	672	INTERGENIC				
CaPOPI_2250	Ca4	22824416	CCGT/CCGTACGT	TCTATTCCCGGTGTGAGC	TGCACTCTAATGGGATTATTTGA	60.1	147	INTERGENIC				
CaPOPI_2251	Ca4	22825034	TAAAAA/TTAAAAAA	TCCTCTAAACATTTGTGTTGCA	TCACTCTTACTATGGAAGCCAA	58.7	609	INTERGENIC				
CaPOPI_2252	Ca4	22837601	CAAAA/CAAAA	TTGAAATGGCAAGAGGGTC	ATGCATGGGTGAAATACCC	60.1	556	DRR	Ca_14468			
CaPOPI_2253	Ca4	22837725	AAATAATA/AAATAA	TTGAAATGGCAAGAGGGTC	ATGCATGGGTGAAATACCC	60.1	556	DRR	Ca_14468			
CaPOPI_2254	Ca4	22848996	TAAAAAA/TAAAAAAA	TTCATTATCTGTTCCCTCCCA	ACGACTGGCTAAGGTGCTGT	59.4	546	INTERGENIC				
CaPOPI_2255	Ca4	22864646	TAGAGAGA/TAGAGA	TGAGACTGCAATTGGCTTG	ACGACGATGTTCAATTCACA	60.0	914	DRR	Ca_14466	S		Protein of unknown function DUF408
CaPOPI_2256	Ca4	22867454	GAAAAAAAA/GAAAAAAAA	GATCTTCATCCCCTGCAGAC	CACCACCACCACAAAACACT	59.6	292	INTERGENIC				
CaPOPI_2257	Ca4	22884702	CAAAA/CAAA	TTTGGTACCCAATTTTCCCA	GGTGAAAGCGTTTGATGAT	60.0	564	INTERGENIC				
CaPOPI_2258	Ca4	22889620	TATAAAATAAAATAAA/TATAAAATAAAATAAAATAAA	GGGTCAGGATACTTACAACCCA	TCCACCCCAATTTTATCA	60.1	717	INTERGENIC				
CaPOPI_2259	Ca4	22896917	GTTTTTTTTT/GTTTTTTTTT	CGATGCGCATGATAGAAAGA	AACGGAAACCCACTTAAGG	59.9	590	INTERGENIC				
CaPOPI_2260	Ca4	22897920	ATTTTTTTTT/ATTTTTTTTT	GGTTGGCTTGTGATCTCAT	TGCTTGTGGTCTGAAACCTG	59.9	463	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2261	Ca4	22898673	CAAAA/CAA	AACCCCACTTAAAGGCAAC	AGGGTGAAGAAGCTCACACAA	60.2	684	INTERGENIC				
CaPOPI_2262	Ca4	22901962	CAAAA/CAAA	AGGGACTCAGTTTTCTGCGA	CAGACAAGCCTCTCGATTCC	60.0	593	INTERGENIC				
CaPOPI_2263	Ca4	22914105	GTTTTTTTT/GTTTTTTTTTTT	AAAACCCCTTTTGCTTCCGTT	TCCTACCAAAAACCTCATTCACAA	60.0	458	INTERGENIC				
CaPOPI_2264	Ca4	22914458	CTTT/CT	ATTGCGCTTGCATCATCTTT	CCAAAGTTTCAACTTCGAGACA	60.8	671	INTERGENIC				
CaPOPI_2265	Ca4	22921547	TAA/TAAAAATAAATAAAAAA	TCGTCCGAACACAATCAT	TGATCTCGTGCTTCTACGTGTT	60.0	311	INTERGENIC				
CaPOPI_2266	Ca4	22933272	CAAATAAAAAATAAAAAAT/CAAATAAA AAT	CTATAGTGACCGCACTCGC	TTCCAAAATTCAGGAATCGC	60.8	774	INTRON	Ca_14461			Heat shock protein DnaJ, N-terminal
CaPOPI_2267	Ca4	22933918	CTGAACAATT/CTGAACAATTGCGGTGA ACAATT	AGAAACCCAAAAGGGGAGAGA	TTTGAACCCAAGCTTCAACC	59.9	750	INTRON	Ca_14461			Heat shock protein DnaJ, N-terminal
CaPOPI_2268	Ca4	22973209	TAAAAA/TAAAAA	ATTTTATTGGCATCGGCATT	TGCGAATGTGCTTTCTGTCT	59.3	672	DRR	Ca_14460			
CaPOPI_2269	Ca4	22974338	A/AAT	ATTTTGGGCGAAATCCTTTT	GAACCACTCATCCTCCC AAA	59.8	442	DRR	Ca_14460			
CaPOPI_2270	Ca4	22981343	ATTTTTTT/ATTTTTTT	TCCGCCGTTCTAAATTC TTG	CAAGCCCTCTCCCTCTC TTC	60.2	874	INTERGENIC				
CaPOPI_2271	Ca4	22984796	GTTTA/GTTTAACTTTA	CAAATTCCTTTAGTGC CACA	TGCTTATGTGTTCCATT GCTC	60.0	802	INTERGENIC				
CaPOPI_2272	Ca4	23002548	ATTATTTATTTATTTTATT/ATTATTT ATTTATTTTATTTTATT	TCGATCGCTGATGTCAA ACT	TGGGCTTGACCTATGTG TGT	59.4	147	INTERGENIC				
CaPOPI_2273	Ca4	23002623	TTTACTATTACTATT/TTTACTATTACTA TTACTATT	TTTATGGCGGCTGGTT TAC	ACGATGCATTGATTGA TGTT	60.0	546	INTERGENIC				
CaPOPI_2274	Ca4	23018840	AA/AATTA	CAAAATAAATCAAATGAT TGAAGTGA	GGCCTGACGACACAGCT AAT	58.6	651	INTERGENIC				
CaPOPI_2275	Ca4	23020256	TTAT/TT	TCATGACCAAGAAACAA CGG	TCACATATCAAATGTTGG CACA	59.5	354	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2276	Ca4	23027444	T/TC	CCATTGGGAATTAGGCA TTG	AAGTTGTGGATCGATT CGT	60.1	868	INTERGENIC				
CaPOPI_2277	Ca4	23055622	TAAGAA/TAAGAAAGAA	TGAATTAAGGATTGCAT GAACA	CCGTTGAATGGAAAATC ACC	59.5	530	DRR	Ca_14459			
CaPOPI_2278	Ca4	23056577	TAAAAAAAAA/TAAAAAAAAA	ATGAATAGCATGCCAG ACA	TCATGTGGGCTCATTG GTA	60.1	771	INTERGENIC				
CaPOPI_2279	Ca4	23060568	ATTTTTTTTT/ATTTTTTTTT	ATGGGCATTATGCAGTC ACA	TTTGCCAATTTATCATGT TTGC	60.0	766	INTERGENIC				
CaPOPI_2280	Ca4	23067690	GTTTTTTTTT/GTTTTTTTTT	CGGAAATAACTGACCGC AAT	GGAATCGAAAGTCGTGG AAA	60.0	373	INTERGENIC				
CaPOPI_2281	Ca4	23077402	TAAAAAAAAA/TAAAAAAAAA	ACCAAAGAATCCATCGG TTG	TGAATTCATGTGTATTGT CGGA	59.8	842	INTERGENIC				
CaPOPI_2282	Ca4	23077586	ATTTTT/ATTTTT	AAGAAAAGGTTGCGTT TGA	TGAATTCATGTGTATTGT CGGA	59.7	644	INTERGENIC				
CaPOPI_2283	Ca4	23078030	GAAAAA/GAAAAA	TTTGAAGAACCAGAGTT TGAAGAA	TTCAATGCCCATATCGT GA	59.5	656	INTERGENIC				
CaPOPI_2284	Ca4	23079340	CAAA/CAAAA	AATTGCAAGTGACTGG ACC	CCGAGCCAAATCCAAA ATA	60.0	787	INTERGENIC				
CaPOPI_2285	Ca4	23134474	ATTGTTGTTGT/ATTGTTGT	ATGCTGCGAAATTGTTG AAA	AAAAGCGTTGTAAATTG GATTGA	59.3	342	INTERGENIC				
CaPOPI_2286	Ca4	23135482	GAAAAA/GAAAAA	ATTGAGCAATGAGAGGT CCG	GATGATGCATGCCATTT GAG	60.2	752	INTERGENIC				
CaPOPI_2287	Ca4	23217567	AATATATATATATATAT/AATATATATATATATATAT	CTCTAGGGAAGCGACCT CCT	CCAACAACCATTGTGGG AGT	60.0	633	INTERGENIC				
CaPOPI_2288	Ca4	23525491	GTTTTTTTTT/GTTTTTTTTT	TGAGATTATATGCACGC GGA	TGAATCGCGAAAGTAGT CCC	60.2	574	INTERGENIC				
CaPOPI_2289	Ca4	23756363	TTATATATATATATATAT/TTATATATATATATATATAT	TTGGAACGTAATTTGAT GCG	CCCGTTGCTTCTGTATG CTT	59.6	872	INTERGENIC				
CaPOPI_2290	Ca4	23960230	AAATAATAATAATAATAATAAT/AAATAATAATAATAATAATAAT	GTCTGTGATTTGGTGCA ACG	AGGCCAATGAGGCAAGA GTA	60.2	617	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2291	Ca4	24100684	AATATATATATATATATATATATA/AATATATATATATATATATATATATA	AATGGTCCAAGGAAAA GGG	ATCCCCAATTGGAACCT ACC	60.2	753	INTERGENIC				
CaPOPI_2292	Ca4	24115337	ATATAT/ATATATATCTATAT	CACACGTGCATGGATAG AGG	TTCACCGTGGATGAATT TGA	60.1	341	INTERGENIC				
CaPOPI_2293	Ca4	24140540	AT/ATATT	TTATTTACCGTCGTGT CCA	TTGTGTGTTGGCCGATT TTA	60.0	234	INTERGENIC				
CaPOPI_2294	Ca4	24273906	TTATATATATATATATATATATATA/TTATATATATATATATATATATATA	GGGGGAGTTGTTATTCG GTT	GAAAAGTGTGTCTGTGT GTGC	60.1	646	INTERGENIC				
CaPOPI_2295	Ca4	24359275	TAAAAAAAA/AAAAAAAAAA	GGGAGGTGGGAGTAA ATGT	TGTGGCTTCCAATGTA CGA	60.1	571	INTERGENIC				
CaPOPI_2296	Ca4	24368839	TAAAAAAAA/AAAAAA	TTTTTCCGACTTGGTCC TTT	GGACTTTGGTTCTCTTG GCA	58.7	381	INTERGENIC				
CaPOPI_2297	Ca4	24427573	GTT/GTTT	CTGGAAATCCTCCTCC TCC	TTCGTCTCAACAATCTCC CC	60.0	346	INTERGENIC				
CaPOPI_2298	Ca4	24442934	GCA/GCATTCA	TCGCCTTCAAGAAAAC CAC	GGCATGAAATCCATCAC CTT	60.2	568	DRR	Ca_20866	R	NAC	Pentatricopeptide repeat
CaPOPI_2299	Ca4	24455402	TTATATATATATAT/TTATATATATATATAT	AGCACCAAAGCCACCAT TAC	AGCCTCTTTTGGGACC ACT	60.0	236	INTERGENIC				
CaPOPI_2300	Ca4	24478956	CAA/CAAA	CGGTTCTACACAAGTTG CGA	TCGATTATGCGTAGGGA AGG	59.9	746	INTERGENIC				
CaPOPI_2301	Ca4	24479035	ATTTTTTT/ATTTTTTTTTT	CGGTTCTACACAAGTTG CGA	TCGATTATGCGTAGGGA AGG	59.9	746	INTERGENIC				
CaPOPI_2302	Ca4	24510502	CTGGAACATTGGAACATTG/CTGGAACATTG	CTGCAAAAGCCCTCACA AAT	TCCTCTTGACACCACA AGA	60.2	969	INTERGENIC				
CaPOPI_2303	Ca4	24553735	GATTAT/GAT	TGGTGCGATTGTGGA ATA	GAGTAGATGTCCAACA GCG	59.9	361	INTERGENIC				
CaPOPI_2304	Ca4	24828297	ATTTTTTTTT/ATTTTTTTTTT	TGGAATTTCAGACTGCC TTG	GGGCACGAAGAAGCACT ATC	58.8	716	INTERGENIC				
CaPOPI_2305	Ca4	24897433	GAAAAAAAA/GAAAAAAAAA	TGCACAAACCTTTCAAT GCT	TTTTTGAATTTGAACGA AACA	59.3	775	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2306	Ca4	24905867	ATTTTTTTTTTTT/ATTTTTTTTTTT	GCAATTTTGCAACATGGA	CCTTCAGCCTTTTGTGG	59.7	140	INTERGENIC				
CaPOPI_2307	Ca4	24940280	GAAAAAAAAA/GAAAAAAAAA	TTGTTGTCGCAATGGAA TGT	TGCTTGGTCACTTTGGC ATA	60.0	315	INTERGENIC				
CaPOPI_2308	Ca4	25070539	TTTTATTATTTATTTATTTATTT/T TTTATTTATTTATTTATTT	TTTGCAAAACCAATGAATACTT	GTTTGAGCCCATTCACGAT	57.8	596	INTERGENIC				
CaPOPI_2309	Ca4	25071336	CA/C	TGAGACTGCTTGGCTACCCT	ATCTGAATCATCCAAGCCA	60.0	488	INTERGENIC				
CaPOPI_2310	Ca4	25097629	CAAAAA/CAAAAA	TCAATGATGGTGACTTGGGA	TACCCATTGTGCTTGGGTC	59.9	820	INTERGENIC				
CaPOPI_2311	Ca4	25177814	CAGAGAGA/CAGAGA	TCCTTGATCGGTAAAGTCGG	TAAAGGACCAAGTCGGGAAA	60.1	373	INTERGENIC				
CaPOPI_2312	Ca4	25186812	TAAAAAAAA/TAAAAAAAA	CCACAGGGTTAAGTTTC CGA	GCCAACTCTCCTCCCTACC	60.0	657	INTRON	Ca_16562			Coenzyme F420 hydrogenase/dehydrogenase beta subunit, N-terminal
CaPOPI_2313	Ca4	25205443	TAGATTGGCACAAGATTGG/TAGATTTGG	GATGGAGGATCAGCCACATT	ATGGTGGAATGCCTCAAAAG	59.9	648	INTERGENIC				
CaPOPI_2314	Ca4	25213751	GAG/GAGATCATAG	TCATTCAACGTCATCGTATCAA	TGTGTTGTATCAATATCGAAGGC	59.0	562	INTERGENIC				
CaPOPI_2315	Ca4	25228841	AATATATATATAT/AATATATATATATAT	ATGATTACCTCGGCATGGAG	AGCACGAGATCAAAGCAAA	59.9	349	INTRON	Ca_16565			
CaPOPI_2316	Ca4	25290328	GTTTTTTT/GTTTTTTT	TCACACCGTGAGATTTTCCA	GAGGCTCCAGATCGAAGTTG	60.1	629	INTERGENIC				
CaPOPI_2317	Ca4	25292705	GTTAATTAA/GTTAA	GGCAGAAATTTGAACGTGGT	GGACAAAAGAAGAGCAAAAGG	60.0	227	INTERGENIC				
CaPOPI_2318	Ca4	25352495	GGTT/G	GGAAATGGTCTTTGAAAGCC	AGCCTTACGCATGTATTGCC	59.9	719	INTERGENIC				
CaPOPI_2319	Ca4	25352610	T/TA	GGAAATGGTCTTTGAAAGCC	AGCCTTACGCATGTATTGCC	59.9	719	INTERGENIC				
CaPOPI_2320	Ca4	25353133	GAAAAAAAA/GAAAAAAAA	CGTCGCACTAAGACGATGAA	GGGTAAGGGTACGTTGAGTCC	60.0	415	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2321	Ca4	25358106	TTAAATAAAATAAATAAATAA/TTAAATAAATAAATAA	GGGACTACTTTCGCGAT TCA	ATTACACGCTTGACAGAC GAA	60.2	842	INTERGENIC				
CaPOPI_2322	Ca4	25365917	ATTTT/ATT	AATTTTGTGGCCCTCC AAT	TGCTATGGCACAAAGTCT CCA	60.5	547	INTERGENIC				
CaPOPI_2323	Ca4	25367189	A/AT	TTTATTGTAGGTGGAGG CGG	GGCCAAATTGATGCAAA GTT	60.0	271	INTERGENIC				
CaPOPI_2324	Ca4	25457334	ATTTTTTT/ATTTTTTTT	CATTTTACTCATCGATCT TTGTGG	TGGACAAAATCATGTCT CTTTGA	59.9	336	DRR	Ca_16577			
CaPOPI_2325	Ca4	25466972	TAAAAAA/TAAAAAAA	TATAGGGAGCGGAACAC ACC	TCTAACTCCAGTAACG CCG	60.0	840	INTERGENIC				
CaPOPI_2326	Ca4	25468253	ATTTTTTT/ATTTTTTTT	CAAAATACAAATGTGAT GGAAAA	TTTTTGTTCCTTATTGT TTGACA	58.0	648	INTERGENIC				
CaPOPI_2327	Ca4	25470351	CTTTTTTTT/CTTTTTTTT	TGCAATTATCCAAAGAT GTATGAAA	TCCTTTTGTCCGTCGTC TCT	59.8	479	INTERGENIC				
CaPOPI_2328	Ca4	25478172	TAAAA/TAAAA	TGTGATGCAGTTGCTCC ATT	GACCTTGCTCTCTTGAT GGG	60.3	703	INTERGENIC				
CaPOPI_2329	Ca4	25501013	TAAAAAAA/TAAAAAAA	GGGCATTGGTAACCTCA AAA	CCAATTGTGCTCTCCTC TCC	59.8	909	INTERGENIC				
CaPOPI_2330	Ca4	25512047	CTTTATT/CTTTATTTATT	GCCACTGAATTGTCGGA GAT	ACCCCAATGAATGAAA ACA	60.1	324	INTRON	Ca_16579	S		TMS membrane protein/tumour differentially expressed protein
CaPOPI_2331	Ca4	25523236	TAAAA/TAAA	TGTGGTGGTGATCCTTG AAA	GATTCTCGCATCTGCTA GGC	59.9	786	INTERGENIC				
CaPOPI_2332	Ca4	25527454	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TCATGTGTAATTTTATC TCAAGGAA	GGCTTGATTGATTCACA TCCT	58.3	743	DRR	Ca_16580			Plant disease resistance response protein
CaPOPI_2333	Ca4	25579370	TAAAAAAAAA/TAAAAAAA	AAATCGGCTCCTTTTAAA ACAATA	TCCTCTCGACGTTTTTG GC	59.5	699	INTERGENIC				
CaPOPI_2334	Ca4	25596032	TTAT/TTATAT	AGTGATGTGGCAACAA TGA	TGCATTTTACAGCGCTTT TG	60.0	515	INTERGENIC				
CaPOPI_2335	Ca4	25623331	CATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTA AT/CATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTA	CACCGGAACCAAGCTTT TTA	GAGGAGGTTTGTGGAT GGA	60.1	376	INTERGENIC				

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CaPOPI_2336	Ca4	25651231	CTTTTTTTTT/CTTTTTTTTTTT	CGTTTGCTGTGAAATG GGA	CAAGCGGTAAAGCACTAG GGA	59.5	825	INTRON	Ca_16590	G		Glycosyl transferase, family 14
CaPOPI_2337	Ca4	25758636	CTTTT/CTTTTTT	TGCACTTCAGTTAAATG GGC	AGAACTTGCGTGGTGAT TCC	60.1	530	INTERGENIC				
CaPOPI_2338	Ca4	25768326	TAAAAA/TAAAAAA	ATGTTTCGTGCAATGGT CAA	CACATGGCTGAACGAGA AGA	60.0	382	INTERGENIC				
CaPOPI_2339	Ca4	25776089	G/GAC	TGGAATGAGAGGGGAA GATG	TCCGAGACAGGTATTTT GGC	60.0	366	INTERGENIC				
CaPOPI_2340	Ca4	25783388	CTTTT/CTTTTT	GCGTGATGCATGATCTA GGA	TCTTTTGATTCCGAGTT GGG	59.8	658	INTERGENIC				
CaPOPI_2341	Ca4	25790471	CAAACGAAACGAAACGAAAC/CAAACG AAAC	CCTCAAATTCGAATTGTG CC	TCATCCTCACCCCCAGT TAG	60.3	646	INTERGENIC				
CaPOPI_2342	Ca4	25812288	CT/C	ATGGTTGTTGCAAGTTT CCC	CCTTGAAGACATATGGT GGCA	59.8	522	INTRON	Ca_16599	R		Aminoglycoside phosphotransferase
CaPOPI_2343	Ca4	25822023	ATTTTTTTTT/ATTTTTTTTT	ACGCAAGAGCAACATCT ACG	TGAAGTCTCGGGTTCAA ACA	59.1	617	INTERGENIC				
CaPOPI_2344	Ca4	25822369	CAAAAAA/CAAAAAA	TGTTTGAACCCGAGACT TCAC	CGTGGCATTGAAAAAG CAT	60.1	611	INTERGENIC				
CaPOPI_2345	Ca4	25844453	AATTATTATTATTATTATTATTATTA ATGTTATTATTATTATTATTATTATT/ AATTATTATTATTATTATTATTATTA TTATTAATGTTATTATTATTATTATT	CAC TTGGG TCACTGCTG AAG	GATGCTGCATGTGTTGA TCC	59.5	662	DRR	Ca_16601	R		Ankyrin repeat
CaPOPI_2346	Ca4	25847698	T/TG	CATGCTACCAAAGCGAT TGA	ATCGATTTCGCGAGTCT TGT	59.8	370	INTERGENIC				
CaPOPI_2347	Ca4	25884525	TA/T	AGCAACCAAATCGAAAC ACC	GGGAAATTTTGGAACCA ATG	60.0	307	INTERGENIC				
CaPOPI_2348	Ca4	25916811	CTTTTTTTTT/CTTTTTTTTTTT	ATGGTAACAGATATCGC CGC	ATTGTAGCATTGCCCAA AGG	60.0	627	DRR	Ca_16606	I		Thiolase
CaPOPI_2349	Ca4	25924178	ATTTTT/ATTTTTT	TGATGATGCATTGATG TGT TTG	CTTGTAAGTTGTAGGCG GGC	59.3	778	INTERGENIC				
CaPOPI_2350	Ca4	25937535	GC/GCTTTTGCTC	TCGACGTTGTCCATT TG	ACACGAGCGTTTGAGCT TTT	60.0	621	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_2351	Ca4	25954241	A/ATTC	TTGCAAGAATCCATCCA TCA	TTGAGCATTTCAGCAGA AGC	60.0	493	INTERGENIC				
CaPOPI_2352	Ca4	25956176	ATTTTTTTTTTTT/ATTTTTTTTTT	ATATTGGGACCGTTAA GGG	TTTGGGTGTGTGACTG CAT	59.9	784	INTERGENIC				
CaPOPI_2353	Ca4	25962811	GTATATATAT/GTATATATATAT	TGGTTGGAAGCTCCAGA AGT	GAAAAGGTGAGGAATCG CTG	59.8	275	DRR	Ca_16607		B3	
CaPOPI_2354	Ca4	25962938	CTT/CT	TGGTTGGAAGCTCCAGA AGT	GTGGAAGTTGTGTGGC CCT	59.8	577	DRR	Ca_16607		B3	
CaPOPI_2355	Ca4	25963240	GAAAAAAA/GAAAAAAA	AATCCAAGCACCAAAAG CAC	GTGGAAGTTGTGTGGC CCT	60.1	353	DRR	Ca_16607		B3	
CaPOPI_2356	Ca4	25963279	TTTTATTT/TTTT	AATCCAAGCACCAAAAG CAC	GTGGAAGTTGTGTGGC CCT	60.1	353	DRR	Ca_16607		B3	
CaPOPI_2357	Ca4	25965378	ACCCCC/ACCCCC	GGTGTGCAAGAGGACTG GAT	GGTCCAAGATATGCC AAA	60.1	481	INTERGENIC				
CaPOPI_2358	Ca4	25966069	ATTT/ATTTT	GGCATGGACAACCTCAC CTT	CGAAATCCTCAAAATCG GAA	60.0	484	INTERGENIC				
CaPOPI_2359	Ca4	25967972	ATTTTTTT/ATTTTTTTTT	TTGTACCCTTGTCACAA CAA	TGGTTGGATACTTGCA TGG	60.0	180	INTERGENIC				
CaPOPI_2360	Ca4	25968820	GTTT/GTTTT	TTCTTCTGCCCAAAATG CT	CCTCAAGCAGACCTTTG GAG	59.8	412	INTERGENIC				
CaPOPI_2361	Ca4	25969511	ACC/AC	TCCCTTGCCTCTAGCCA GTA	GCAGATGTTCTCAACAG CCA	60.0	350	INTERGENIC				
CaPOPI_2362	Ca4	25970159	AC/A	TGGTTGGGTCTTGTTT GTT	CACCTGCTATGGATGCA ATG	60.2	709	INTERGENIC				
CaPOPI_2363	Ca4	25975114	TGGGG/TGGGGG	ACACATGTTGGCCAATG AGA	GAGTCCGATTCCATGA GGA	60.0	621	CDS (FRAME SHIFT)	Ca_16608			
CaPOPI_2364	Ca4	25978445	CT/CTTT	TGCCTCAAAGGCTTCAT CTT	AGCACTCATCCTCGGT AGA	60.0	435	INTERGENIC				
CaPOPI_2365	Ca4	25979689	TG/TGG	GTCCTCGTCAGGAGTT GAG	CCACTGTTGCTGCGAGA TAA	59.8	707	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2366	Ca4	25983794	A/AC	TGACAACCCAGATTGTGA	TGGGTCCATGTTCCAATTTT	59.9	671	INTERGENIC				
CaPOPI_2367	Ca4	25984075	TA/TAA	CGATTTTAAACAGCGTGGT	TGGGTCCATGTTCCAATTTT	60.0	276	INTERGENIC				
CaPOPI_2368	Ca4	25984442	TGAGAG/TGAGAGAG	AGATCCTGTTGACACGGCTT	CGGTTGTTGTTGTGATTGCT	59.7	524	INTERGENIC				
CaPOPI_2369	Ca4	25987244	AATATATATAT/AATATATATATATATATAT	TCTACTCTCGTCGCAGCTCA	TGCTTAGGCATTACCCAG	60.0	250	INTERGENIC				
CaPOPI_2370	Ca4	25987622	TCC/TC	TTCAACTGGGGTAAATGCCCT	TGTTCTAGTCCAGATCAAAACGA	59.4	323	INTERGENIC				
CaPOPI_2371	Ca4	25988978	AAAGAAGAAGAAG/AAAGAAGAAG	AAGCTGGATGTGGACTTTGCT	AGTTCCAATTGGCCTCCCTT	60.3	404	INTERGENIC				
CaPOPI_2372	Ca4	25989281	TCCCC/TCCC	AAGCTGGATGTGGACTTTGCT	AGTTCCAATTGGCCTCCCTT	60.3	404	INTERGENIC				
CaPOPI_2373	Ca4	25989322	GTTTTT/GTTTTTT	GTACGCGATCTAGTCCCAA	CCGGGGAGAAAGTTCTAGTG	60.1	168	INTERGENIC				
CaPOPI_2374	Ca4	25994447	G/GT	ATCCACAACCGAGTTAGCGT	TACCCACACCCCTCAATCTT	59.6	389	INTERGENIC				
CaPOPI_2375	Ca4	25994721	AC/A	TTAAGATTGAGGGGTGTGGG	CACCACTTCATTGCGGACTT	59.8	516	INTERGENIC				
CaPOPI_2376	Ca4	25995802	ATTTT/ATTT	CCCTAAATCAAAGCAGCGTC	TGCACTGTTGTTGTTGCTGA	59.8	470	INTERGENIC				
CaPOPI_2377	Ca4	25996238	GAAAAAAAAA/GAAAAAAAAA	CCCTAAATCAAAGCAGCGTC	AACGTTGAGGAACAAACACG	59.8	949	INTERGENIC				
CaPOPI_2378	Ca4	25998410	TTA/TTATGTA	TATTGTTGCCCTGCATGTGT	TGGAGGCCAATTGTGTTCTC	60.0	531	DRR	Ca_16609		B3	
CaPOPI_2379	Ca4	26011159	AT/AACAGAACTCCT	GAAACCCACAACAATAATGG	AGCATCATGGATTCTCCG	60.1	438	DRR	Ca_16611	C		Aldo/keto reductase
CaPOPI_2380	Ca4	26015617	AATAAATATA/AATA	TGCGAGGGCTAGCTTAAAAA	TGAGACAAAAGTTTGC GTG	60.1	635	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2381	Ca4	26058753	TAAA/TAAAA	AGGAACCAATCCTACCA GCC	TCTGGTCATGCATCCTT TGA	60.3	433	INTERGENIC				
CaPOPI_2382	Ca4	26110333	TCCC/TCCCC	CCAACAATCTCCCCCTT TTT	GCATCTGGTTGCAGTTC TCA	60.2	583	INTERGENIC				
CaPOPI_2383	Ca4	26118906	CTTTTTTTTT/CTTTTTTTTT	CTGGATTCCAACAATCT CCC	TTCTTTGCTTTGCGCTT TT	59.3	851	INTERGENIC				
CaPOPI_2384	Ca4	26176935	GAAAAAAA/GAAAAAAA	CACAATCAATCAGCCCC TTA	TGTCATTTTTGGCGTAG TGC	59.5	500	INTERGENIC				
CaPOPI_2385	Ca4	26203930	TTATATATATATATAT/TTATATATATA TATATATATATATAT	TTGGAAATAAGGACAAA ACACC	TCCAAATTTGCTGGAAT CCT	58.0	626	INTERGENIC				
CaPOPI_2386	Ca4	26236726	TAAAAAAAAA/TAAAAAAAAA	GTTACGATTGTGTTCCG CCT	TAATCTCACTGCGCACC TTG	60.0	368	INTERGENIC				
CaPOPI_2387	Ca4	26251759	CTTTTTTTTT/CTTTTTTTTT	TAAACGCAATCGGAAG ACC	GAGAACTTTCCGCTGC TTG	60.1	545	INTERGENIC				
CaPOPI_2388	Ca4	26251857	ATTTTTTTTT/ATTTTTTTTT	AGCTTCATGTAACACC CCG	GCCCTCAGATGAGAGTC AGG	60.0	453	INTERGENIC				
CaPOPI_2389	Ca4	26276734	ATAATTAA/ATAA	GGTGCTACAGTGTCGAA GCA	TGCATTTTACAGCGCTTT TG	60.1	725	INTERGENIC				
CaPOPI_2390	Ca4	26308021	CTTTTT/CTTTTT	ATAAACATCATCGGGC GAC	TTCAGTGGCATTGAGAC ATTG	59.8	405	DRR	Ca_25307	S		
CaPOPI_2391	Ca4	26326139	GAAAAAAA/GAAAAAAA	CTCCAACAGCATCAATT CCA	GATCCTGGGATTGTGAG CAT	59.6	724	DRR	Ca_25306	R		Alcohol dehydrogenase superfamily, zinc-containing
CaPOPI_2392	Ca4	26363618	T/TTTAC	GCCAAATTTCTTCGTT GA	ATTCCCCAAGAACATCA CCA	60.1	613	INTERGENIC				
CaPOPI_2393	Ca4	26389354	TTATATATATATAT/TTATATATATATATA T	AGGAAGAGTGGAGTTGC GAA	TCATATTCGGTAGCCGT TCC	60.0	759	INTERGENIC				
CaPOPI_2394	Ca4	26495554	GAAAGTTGTT/GAAAGTTGTTCAAAGT TGTT	AACGATTATCCTGTGTC CCC	CCCGAATACAAACCCAA GTC	60.0	844	INTERGENIC				
CaPOPI_2395	Ca4	26529457	ATCTCTCTCTCTCT/ATCTCTCTCTCT CTCTC	ATAGCAGCAATTTCCAT CCG	GTCCACGAAGTAAGTC CCA	60.1	286	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2396	Ca4	26620467	A/AGTAATT	CCGAAACCGAACACAGATT	TGGGAACAAAACACAGCAAG	60.0	819	INTERGENIC				
CaPOPI_2397	Ca4	26624241	C/CG	CCAAAAGTCCAACGATTGCT	TGTGCATGGTGCTTTTTGAT	60.1	447	INTERGENIC				
CaPOPI_2398	Ca4	26648267	ATTTTTTTTT/ATTTTTTTTT	TCGAACAGAAACCTGAGCCT	GATTCGGGAGTTGGTTGATG	60.0	440	INTRON	Ca_24999	L		Excinuclease ABC, C subunit, N-terminal
CaPOPI_2399	Ca4	26664091	TAAAAAAAA/TAAAAAAAAA	TGATACAATTGATTCGGCCA	TTTTTGTACGCGAGCTCTA	59.9	371	INTERGENIC				
CaPOPI_2400	Ca4	26672920	CTTTT/CTTT	ACGGATGTCGTAGGGTCTA	AAGACCCGAATCAGCATTTG	60.5	438	INTERGENIC				
CaPOPI_2401	Ca4	26748572	GAAAAAAAA/GAAAAAAAAA	GGGTGTGAGTTGAAATGACG	TTTGTGCAACAACACCATTT	59.0	858	INTERGENIC				
CaPOPI_2402	Ca4	26752184	ATTTTTTTTTT/ATTTTTTTTTT	TTGGGATCATAGAATCAATTTGGT	TGATCACGGTCACTCCAAAG	59.6	475	INTERGENIC				
CaPOPI_2403	Ca4	26753050	GAA/GAAA	AACACTCGCAAAATCTTCGG	ATTGTTTGAGTTGCCGCTCT	60.2	623	INTERGENIC				
CaPOPI_2404	Ca4	26763494	TAAAAAA/TAAAAAA	AAAAATACCGCGTCATTTCAAT	TCGCTCAAAACACAACGAG	59.8	572	INTERGENIC				
CaPOPI_2405	Ca4	26765991	GAAAAAAAA/GAAAAAAAAA	AGTTTTGGCCCTTTTGATT	AAAAACTCGCACACAACGTGTTA	59.8	508	DRR	Ca_20437	K	MYB	SANT domain, DNA binding
CaPOPI_2406	Ca4	26787145	CTTTTTTTTTT/CTTTTTTTTTT	GCGACTATGTCCGTCAACTG	TCGAAGCATGAAAGAAAAGGA	59.3	803	INTERGENIC				
CaPOPI_2407	Ca4	26847079	AAAAATAAAATAAAATAAAATA/AAAAATAAAATA	GGAGAACGTTAAGGCAGCAG	GTGGTGTAGGTTTCGATCCG	60.0	689	INTERGENIC				
CaPOPI_2408	Ca4	26847495	A/AC	AGCTTCAAGTCGGATCGAAA	AAAATCTTGTGGGAATAATTCAA	60.0	216	INTERGENIC				
CaPOPI_2409	Ca4	26876873	ATTTTTTTTTT/ATTTTTTTTTT	CCACCGTTGTGCCTCTTATT	GCCAGAGAATGATCGAGAGG	60.0	439	INTERGENIC				
CaPOPI_2410	Ca4	26898145	CTTTTTTTTTT/CTTTTTTTTTT	CGAAACTCAAAACAACGGG	CGGCCCAATTCAAATAAAA	60.5	588	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2411	Ca4	26903304	T/TG	ACTCGATTGGTCCATGCTTC	ATGTTTTGGACGCACACAGA	60.1	532	INTERGENIC				
CaPOPI_2412	Ca4	26905366	TAAAAAAAAA/TAAAAAAAAA	TGAAAGCCCAAACTAATCAAGA	ATTGCTCGGTCGGTTTAGTC	60.1	471	DRR	Ca_20443	R	G2-like	RNA recognition motif domain
CaPOPI_2413	Ca4	26991333	ATTTTTTTTT/ATTTTTTTTT	ACAAGGAAGCGCACCTGTAA	GTGCGACGAGCAAGAATGTA	60.0	762	INTERGENIC				
CaPOPI_2414	Ca4	27017251	GTTTTTTTTT/GTTTTTTTTT	CCTTGCATCTCAGGGACAT	TGAGACCGGGTTTGAGTACC	60.1	453	INTERGENIC				
CaPOPI_2415	Ca4	27074666	GAAAAAAAAA/GAAAAAAAAA	ATTGGCATCAGAGCCAGTCT	TTTTCCAAGAGAGCGCATTT	59.8	566	INTERGENIC				
CaPOPI_2416	Ca4	27079794	AAA/ACAA	AAACACTACCCGGCATCAAG	CAATTTCTGCACTCTCGCA	60.0	516	INTERGENIC				
CaPOPI_2417	Ca4	27087434	TA/TAAAA	TTATTGCGATGCCGACTATG	AATGATGTGGCTGGGTTAGC	59.7	656	INTERGENIC				
CaPOPI_2418	Ca4	27149358	ATTTTTTTT/ATTTTTTT	CGATGATGCTACCAGAGGGT	CGGGGATTCCCATATCACTA	60.1	611	INTERGENIC				
CaPOPI_2419	Ca4	27168549	CAAAAA/CAAAAA	AGGGCCAAGGGACAATAAGT	TGTTTTGTCAATGTCCCTA	59.8	523	INTERGENIC				
CaPOPI_2420	Ca4	27184150	AAATAATAATAATA/AAATAATAATAATAATA	TTTCTTGTCCTTGGTGTG	TAGAAACCGGTTGCCAAGAA	59.7	744	INTERGENIC				
CaPOPI_2421	Ca4	27217904	CAAAAAAAAA/CAAAAAAAAAA	TGTAGTGGCATGTTTGGCAT	TTTGAGGACTTTTGGGTTG	60.0	662	INTERGENIC				
CaPOPI_2422	Ca4	27241081	CTTTTTTTTT/CTTTTTTTTTTT	AAGGACCAAGTCGGGAATAA	AGGTTTTGATGTGTTGACGG	60.8	705	INTRON	Ca_20460			Protein of unknown function DUF3527
CaPOPI_2423	Ca4	27258927	ATTTTTTTTT/ATTTTTTTTT	AGCGCGGAGAGATAGTTGAA	TGGGTGACTTCATTTGACA	60.1	393	INTERGENIC				
CaPOPI_2424	Ca4	27267123	TAAAA/TAAAA	CCCTCAACTCAACTGAGATCC	TGCATTGGTTGAATTTGGA	58.7	568	DRR	Ca_20461	R		Sugar/inositol transporter
CaPOPI_2425	Ca4	27283830	GTTT/GTTTT	TATTGGTCGTCAGCAGCAG	TTTCCCAATCGATTGCTTC	60.0	681	DRR	Ca_20463			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2426	Ca4	27285679	G/GAA	TATTTTCGAGGCGTGCAAC	CCAGCCTACCCCTTTTATCTG	60.0	549	INTERGENIC				
CaPOPI_2427	Ca4	27357133	GAAAA/GAAA	TTGATTGGTGACATCAT	TAAACTTGTCCTCAACCCC	59.8	561	INTERGENIC				
CaPOPI_2428	Ca4	27367807	CTTTT/CTTT	GCATCCTTGCTCACAAC TCA	TAAAGGCCCAAAGAAGC AAA	60.0	415	INTERGENIC				
CaPOPI_2429	Ca4	27376069	TAA/TAAA	ATCCTCTCCATTCTTG CCT	TTGCTTTCACAGTCCAAT GC	60.0	304	INTRON	Ca_21323			
CaPOPI_2430	Ca4	27379933	CAAAAAA/CAAAAAAA	ATGGTACAAAGTGCAAGGC	GAGAAAAGCAGGTGAA TGC	60.0	748	DRR	Ca_21323			
CaPOPI_2431	Ca4	27380010	ATTT/ATT	ATGGTACAAAGTGCAAGGC	GTGGACTGCAGTGGTCTTT	60.0	909	DRR	Ca_21323			
CaPOPI_2432	Ca4	27405693	TAAAA/TAAAAA	GAGTTGGTATTTCAATTTGTCGG	GTGGTTAAGATGGACCA CCG	59.8	531	INTERGENIC				
CaPOPI_2433	Ca4	27483001	ATTTTTT/ATTTTTTT	GAAATCCAAGCCATTCTCCA	TGGTTGCGGAAATAAACACA	60.0	485	INTRON	Ca_21318			
CaPOPI_2434	Ca4	27491121	ATTTTTTT/ATTTTTTT	ATGCAGCACCTAGTTTTGCG	CATGTTGTCGCTCTCATGT	60.3	531	INTERGENIC				
CaPOPI_2435	Ca4	27491848	ATTTTTTT/ATTTTTTT	TACGCGCTTCTTTCAATCA	CGTCCCCCTCCTCAAACATA	59.6	503	INTERGENIC				
CaPOPI_2436	Ca4	27496407	CTG/CTGTG	TCGGAAACGAATTGGGAATA	GGAGTTTGAGAAAGGGGTCC	60.3	750	INTERGENIC				
CaPOPI_2437	Ca4	27503266	AG/AGG	GGGGTTCTCCTTGAACCACT	CCTGCCATTTCTTCCAAAA	60.3	343	INTERGENIC				
CaPOPI_2438	Ca4	27512574	CAAAAAAA/CAAAAAAA	GTTGGCTGGGTGAAATCTA	ATACGCGCTCCCTTAAC TTG	59.9	806	INTERGENIC				
CaPOPI_2439	Ca4	27548804	TAAAA/TAAA	TTCCCCATTCTTAACACCA	TTCGCAACTCCACTCTT CCT	60.2	672	INTERGENIC				
CaPOPI_2440	Ca4	27574473	ATTTTTTTTTT/ATTTTTTTTT	CACCCTTACCTTGACCCCTT	GCTCGTATGCGTCAATTCAA	60.2	571	INTRON	Ca_21314			Peptidase C48, SUMO/Sentrin/Ubl1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2441	Ca4	27580274	GAAAAAAAA/GAAAAAAAAA	TGGGGTCCATGTACCAC TTT	AAGAAATGTCCTCAGG TGC	60.1	305	INTRON	Ca_21314			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_2442	Ca4	27594072	CTTTTTT/CTTTTTTTT	ATCAGAGGTTGCGCAAA AAT	TTTCCTTCCAAATTTACG CC	59.7	668	INTRON	Ca_21314			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_2443	Ca4	27604352	AAATGTTGATAAT/AAAT	ATTAGGAGTCTTGCTGC CCA	CCCTCCGAACCTCTCAA CAG	59.8	320	INTRON	Ca_21314			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_2444	Ca4	27637430	TG/TGG	TTTGGAGTGGTGGTTCT CAA	CCAATGATTTTCATGCCA CA	59.1	482	DRR	Ca_21310			
CaPOPI_2445	Ca4	27649411	TTTTATTT/TTTT	AAAATAAGGCATGGTGT TGG A	TAGTTTGTAAACCGTGC GTC	59.3	256	INTERGENIC				
CaPOPI_2446	Ca4	27656062	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA AA	GCGAGCATGAGAAGTTG TTG	TTTAAATAGACTCCCGA TGTC A	59.6	101	INTERGENIC				
CaPOPI_2447	Ca4	27859134	ATTTTTTTTT/ATTTTTTTTTT	ACCTCTCTTTTAGGTGT GCC	GGGAGATTTGGGGTTT GAT	60.4	569	INTERGENIC				
CaPOPI_2448	Ca4	27865338	AAATAATAATAATAATAATAATAATA ATAATAATAATAA/AAATAATAATAATAA TAATAATAATAATAATAA	TCCTAAACAAATGCAC CCA	TTAGGCTTGATATGCCG ACC	59.0	557	INTERGENIC				
CaPOPI_2449	Ca4	27920147	GTATATATATATAT/GTATATATATAT ATATATAT	GCCCATCAAAACCCACA TAC	CACAATCCTTTTCAACC GCT	60.1	466	INTERGENIC				
CaPOPI_2450	Ca4	27928820	CACAAC/CACAACAAC	AGCGATGCATGTCTCAA GTG	AGCGCTTTGTGACCTCC TTA	60.0	754	INTERGENIC				
CaPOPI_2451	Ca4	27929931	GTTTT/GTTTTT	CCTTCTCATTGCGAACC CTA	TGGTTGCACCACATTTG ACT	60.2	427	INTERGENIC				
CaPOPI_2452	Ca4	27943723	ATTTTT/ATTTTT	CGATTGAATTAAGCCCA GGA	TCTCCATTTTCGTCCGTA GG	60.0	403	INTERGENIC				
CaPOPI_2453	Ca4	27951126	CTT/CTTTCATT	TGTGTAACCTCCCCAT GAT	AAAGGGCACCAAACT CCA	60.1	858	INTERGENIC				
CaPOPI_2454	Ca4	28042488	T/TG	GTCCTTTTCCTTGGCC TTC	CCTGAGGATAGCCTCGT GAA	60.1	159	INTERGENIC				
CaPOPI_2455	Ca4	28093890	GAA/G	GAGAGTGCTCCTTTGGG AAA	GGGAAAAATTGCTTGGT GAA	59.4	300	DRR	Ca_23175			Crotonase, core

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2456	Ca4	28108572	TAAAAAAAA/TAAAAAAAA	GCAATGTTGGCGAAGT ACA	AGTGTGTGCTTGTGGGA TCA	59.7	301	INTERGENIC				
CaPOPI_2457	Ca4	28109349	ATTTTT/ATTTTTTT	CGGGGGTAGGGTTTAG AGA	GCTGCTTGGTTGTGCTA TGA	60.3	491	INTERGENIC				
CaPOPI_2458	Ca4	28120543	TAAAAA/TAAAAAA	CCAACCTCCCTCCCTT TTA	CAATACGAGCACCTGGC TCT	60.3	994	INTERGENIC				
CaPOPI_2459	Ca4	28120712	ATTTTTTTTT/ATTTTTTTT	CATCAGTCAAACGCACA AAAA	CAATACGAGCACCTGGC TCT	59.8	433	INTERGENIC				
CaPOPI_2460	Ca4	28122657	GAAAAAAAAAAAA/GAAAAAAAAAAAA	CCCCGAGTTTGAGAAAT TGA	CCTCCGTCCTCTTTCT TTC	60.0	393	INTERGENIC				
CaPOPI_2461	Ca4	28147858	AT/ATTTAATAATTT	GGGAAAAGCCCCAACT AAG	TCCAACGTCGATTATGA CCA	59.9	424	INTERGENIC				
CaPOPI_2462	Ca4	28159857	TAAAAAAAA/TAAAAAAAAAAAA	TTTGGGGGTACAAGGGA AAT	TGCAACCTCATACTGGG AAA	60.4	645	INTERGENIC				
CaPOPI_2463	Ca4	28160415	GAAAAA/GAAAAAA	CAAAATGCCCTTTGGCA CTA	TGACACGTTGTTGTTTT GACA	61.0	457	INTERGENIC				
CaPOPI_2464	Ca4	28179566	AGGGG/AGGGGG	TGGGTAAAGTTCTGCCC ACT	TAGCATGCTCGAAAACG AAA	59.6	129	INTERGENIC				
CaPOPI_2465	Ca4	28180097	ATTTTTTTTT/ATTTTTTT	TCGAGCATGCTATAGTC CGA	ACCAATGTCCAACGGGA ATA	59.5	869	INTERGENIC				
CaPOPI_2466	Ca4	28184807	ATTT/ATTTT	GACCTTTGTTGACCTTG CGT	TGTTGAGTTGGAGATGA AGCA	60.2	595	INTERGENIC				
CaPOPI_2467	Ca4	28209971	T/TA	ATTGATGGAGCGAATCG AAC	AATTCTCTTTTGGTGG GCT	60.0	891	INTERGENIC				
CaPOPI_2468	Ca4	28254483	CAACAA/CAACAAGACAAACAA	GGGGAACCTCTCCAAGTC ACA	CGTGGAACCAACCTTG TCT	60.1	703	INTERGENIC				
CaPOPI_2469	Ca4	28274340	CAAAAAAAAA/CAAAAAAAAAA	CCAGAAGCAGAAAAACC AGG	TTTGAAACTGTCGCGAC TCA	59.8	631	INTERGENIC				
CaPOPI_2470	Ca4	28306771	CAAAAAAAAA/CAAAAAAAAAA	TGATGGTCCATGAAGTC ACAT	CGAGCCAAATCCAAAA CAT	58.8	430	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2471	Ca4	28321521	CCGTACAGGCGTACA/CCGTACA	TCGAGTTGTGAAATTGAGCG	GCTGAAGAACCCGAGAAAGA	60.0	202	INTERGENIC				
CaPOPI_2472	Ca4	28331028	CAAAAAAAAA/CAAAAAAAAA	CTTGAAGGGACGGCTAGATG	TTGCCATAATGTTGAGAAGGG	59.8	458	INTERGENIC				
CaPOPI_2473	Ca4	28336605	CAAAAAAAAAAAAA/CAAAAAAAAAAAAAA	CAAAGCAGGGAGTTTCCATC	TGGTTTAAGTCTCGGCTGT	59.7	723	INTERGENIC				
CaPOPI_2474	Ca4	28338433	GTTT/GTT	TGACTCGGGCTGCAGATTAT	GCTTTGAGCCCCATGAATA	60.8	739	INTERGENIC				
CaPOPI_2475	Ca4	28342637	GCCC/GCCCC	TCACAAATCCTGGTGTTGA	GGAAGAAAGCAATGGTGGA	59.9	359	INTERGENIC				
CaPOPI_2476	Ca4	28346696	A/AT	ACCACAGGTGAAAGAAACCG	TTTTCAACTCTATCCGTAGCCC	60.0	340	INTERGENIC				
CaPOPI_2477	Ca4	28372820	ATTTT/ATTTT	TAAGGGAAGGGGCTCTAGGA	CCCCTAAATTTAAAGGCCC	60.2	389	INTERGENIC				
CaPOPI_2478	Ca4	28380287	ATTTT/ATTTT	ACTTTTCTATTTTTAAGTCATCAAT	CTTCAAAGTTGCCGGTGATT	57.3	919	INTERGENIC				
CaPOPI_2479	Ca4	28390462	TAA/TAAA	GTCATCAAAAGCCGACGAAT	GGCCACAATTTTGAAGAGA	60.1	786	INTERGENIC				
CaPOPI_2480	Ca4	28401988	TAATTAA/TAATTAATTAATAAAATTA	ACTTGGATGAAGGGAAAGGG	GCATTTGCAAAAATTTGAA	60.3	561	INTERGENIC				
CaPOPI_2481	Ca4	28414876	CAAT/CAATAAT	GCCCCATGTTTGCTTAAT	GGATTGAGCATCCGTCAAGT	59.8	741	INTERGENIC				
CaPOPI_2482	Ca4	28420944	TAAAGTTAGAAGAA/TAA	GTGTGGGCGGAAAAATCTAA	CACAGTGAAAACCGATGGA	59.9	693	INTERGENIC				
CaPOPI_2483	Ca4	28423269	T/TA	TAGGTTTCCCATGTGGTGT	AGCACTTGCCCTTAGGAGT	60.1	697	INTERGENIC				
CaPOPI_2484	Ca4	28447880	ATTTTTTT/ATTTTTTTT	TCTTCTGTGTAGCGGATTG	GCTCAACCTTGAGACCAAGC	60.0	252	INTERGENIC				
CaPOPI_2485	Ca4	28457671	TCTCTA/TCTCTATTTAACTCTA	TACAAAGCACCTGACCTCC	CCCAAATCAAAGCAAGCAAT	60.1	765	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2486	Ca4	28501292	AAATATTTTATTATT/AAATATTTTATTAT TAATATTTTATTATT	GCACGCACACACATAT CCC	TTTGCAGGCACAAAAGA CAG	59.9	747	INTERGENIC				
CaPOPI_2487	Ca4	28505491	TAAAAAAAA/TAAAAAAAAA	GGATTTACGGTGGTCT TTT	TCACACACCTCAAAACC CCT	58.9	433	INTERGENIC				
CaPOPI_2488	Ca4	28534748	ATTTTTTTTTT/ATTTTTTTTTT	TGGTCAACATGCCAAAG AAA	TTGTTTTCTCTCCAAACA AATG	60.1	958	INTERGENIC				
CaPOPI_2489	Ca4	28535714	TTT/TTTATT	GCCAGCTCCAATTACAA TGC	CATGTCTTTTGAATTTTG ATCAGC	60.6	816	INTERGENIC				
CaPOPI_2490	Ca4	28581947	TAAAAAAAAA/TAAAAAAAAA	CATTTCCCCACACCAATT TC	AAGGATGATGATTGTGC ATGT	60.0	379	INTERGENIC				
CaPOPI_2491	Ca4	28581991	CAAAAAAAAA/CAAAAAAAAA	CATTTCCCCACACCAATT TC	AAGGATGATGATTGTGC ATGT	60.0	379	INTERGENIC				
CaPOPI_2492	Ca4	28623056	A/AGAATTTGG	ATATGGTTGCGCACAAA TGA	TGTCCGAAACATTAAAC CCA	60.0	704	INTERGENIC				
CaPOPI_2493	Ca4	28714992	GATAT/GAT	AGAGCCAACGCTCATAG GAA	TTAAATCCCTCCTCG GCT	60.0	531	INTERGENIC				
CaPOPI_2494	Ca4	28783547	CTTTTTTTTT/CTTTTTTTTTT	TGGAAGCTTGCTCCTT CAT	CAAGTGATTTGCCTAT TCTGG	60.0	124	INTERGENIC				
CaPOPI_2495	Ca4	28791900	TCACA/T	TGCCCTCATGGTTATC CTA	CACAGAGTTCGACACCG CTA	60.3	580	INTERGENIC				
CaPOPI_2496	Ca4	28793395	TAA/TAAAAACAA	CCAAAATTACACCAACG GTTT	TTGTTGCGATGCTCATT CTC	59.2	275	INTERGENIC				
CaPOPI_2497	Ca4	28806476	T/TA	TGTTTGTTTTGCAAGCA GG	GCAAGAAGCCATCCACA AGT	59.9	351	INTERGENIC				
CaPOPI_2498	Ca4	28849010	GAAAAAAAA/GAAAAAAAA	AGAGGAAATGATGCCAC AATG	AAACACTTGCCTAACCT GGC	59.9	794	INTERGENIC				
CaPOPI_2499	Ca4	28850439	ATTATTTTATTTT/ATTATTTTATTTT ATTTT	GTCAGAGGCAGTGAGC CTTC	TTTtagCTTTCCAACGC CTG	60.1	500	INTERGENIC				
CaPOPI_2500	Ca4	28856354	ATTTTTTT/ATTTTTTTTT	GCGCGAATATCTCAACC AAT	TCCACCAACAACAAGAT CCA	60.1	212	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2501	Ca4	28887918	TAAAAAAAA/TAAAAAAAAA	TGCCCTATTTGTGTCCAGG	TGCGTTTGGCTGATGTTAAG	60.9	573	INTERGENIC				
CaPOPI_2502	Ca4	28910424	ATTTCTTTTCTTTTCTT/ATTTCTTTTCTT	CTGTTTCCTCCAACTGGG	TGTAGAGGAATGTCTCGCCC	59.6	393	INTERGENIC				
CaPOPI_2503	Ca4	28910579	A/AC	CTGTTTCCTCCAACTGGG	TGTAGAGGAATGTCTCGCCC	59.6	393	INTERGENIC				
CaPOPI_2504	Ca4	28913641	AAATAATAATAATAATAAT/AAATAATAATAATAAT	TACGTCGCTCCATGCAAATA	CAACGTCCTCCCATTTGTTT	60.2	822	INTERGENIC				
CaPOPI_2505	Ca4	28914437	GA/GAAA	AAACAAATGGGAGGACGTTG	TGTTCCAGATATTTTGCCGA	59.8	508	INTERGENIC				
CaPOPI_2506	Ca4	28925061	CAAAAA/CAAAAAA	GGGGTGGTTTTAGCTTGGT	TAGCCAGTTTGGAAGGAAA	60.2	773	INTERGENIC				
CaPOPI_2507	Ca4	28925610	TAA/TA	TTTCCTCCAACTGGGCTA	AATGCGGTCTTCCCCTAAGT	59.7	622	INTERGENIC				
CaPOPI_2508	Ca4	28988768	TAAAAAAAA/TAAAAAAAAA	AAAAGTCGACAGTTTGTTC	ACTGGGTGTCAATTGCTC	58.8	681	INTERGENIC				
CaPOPI_2509	Ca4	28990312	CAAAAA/CAAA	GTTTCGCAATCTGGGTTGT	AACACGTGTAGCAAAGCACG	60.0	770	INTERGENIC				
CaPOPI_2510	Ca4	29037043	GAAAA/GAAAAA	CCATTGAGCTACACTGTGCG	TTGGACAACGCTTCAAACTG	60.5	434	INTERGENIC				
CaPOPI_2511	Ca4	29049755	TTA/TTAAAGCGAGAAATA	GGTTTTATAGGGCATGCTGG	TCCCAAGAAATCAATGCTCC	59.4	749	INTERGENIC				
CaPOPI_2512	Ca4	29064946	TA/T	GTTTCCGAAGGTTTTGAT	TCATCTTGGATCACACTCAACC	60.2	424	INTERGENIC				
CaPOPI_2513	Ca4	29065135	TAAAAAAAA/TAAAAAAAAA	GTTTCCCGAAGGTTTTGAT	TCATCTTGGATCACACTCAACC	60.2	424	INTERGENIC				
CaPOPI_2514	Ca4	29085024	CT/CTT	AAGGAGAAAAGTGGGGGAGA	ACGTATCCCCAGGTGCAATA	60.0	602	INTERGENIC				
CaPOPI_2515	Ca4	29110502	ATTTT/ATTTT	TGCAACATGGATGGGAATA	CACGGTTTCTAACACCAATTGA	59.7	617	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2516	Ca4	29156658	CATGCAAATGCAAA/CATGCAAA	AGTTGGTTTGGTGGTGA AGG	GCATGGTAAAGGCTGTT GGT	59.9	841	DRR	Ca_23711			Domain of unknown function DUF296
CaPOPI_2517	Ca4	29159894	CAT/CATAT	TGATTTTCAAAGAGAAAC CCG	TTCTGCGATGTCATTT GTT	59.2	450	INTERGENIC				
CaPOPI_2518	Ca4	29190573	GA/G	GCCAGTCTTCTCAAACA GCC	TTTGACCAAGTGGAAAA GAAGA	60.0	648	INTERGENIC				
CaPOPI_2519	Ca4	29191237	CTTTTTTT/CTTTTTTTT	CCAAGTGGTTCCAACA ATCT	GGAGAAAAGTTAGGGG GTGC	58.9	119	INTERGENIC				
CaPOPI_2520	Ca4	29202977	AATGATAG/A	TCACCCGATGTCACCT ATT	ACATGCCATTGAATTAC GCA	60.2	449	INTERGENIC				
CaPOPI_2521	Ca4	29205093	C/CCAAG	ACATATGGCTTCGCATG ACA	TTAGGAGTGGCTTTGGA TGG	60.1	492	INTERGENIC				
CaPOPI_2522	Ca4	29238761	A/AATT	CCATGAGATCCACATAA TCCG	TTGCAAGAATCCATCCA TCA	60.2	513	INTERGENIC				
CaPOPI_2523	Ca4	29244811	CAAAA/CAA	CCGAGATGGTTTGGAG AAA	GCTTCATAGCTTGCAAA GGG	60.0	488	INTERGENIC				
CaPOPI_2524	Ca4	29245084	ATA/ATACTTA	GCCCTTTGCAAGCTATG AAG	TGGTGCAATTTGGTTGG TAA	60.0	418	INTERGENIC				
CaPOPI_2525	Ca4	29270177	CTTTTTTT/CTTTTTTT	TTTCCCGACTTGGTCCT TTA	TCGACTCCCACCTAAT GAC	59.5	696	INTERGENIC				
CaPOPI_2526	Ca4	29274800	GTTTTTTTTT/GTTTTTTTTTT	TTGGCGTGATAATTACA TGAGG	GCCTACCGAAATGAAT GAA	59.9	864	INTERGENIC				
CaPOPI_2527	Ca4	29278808	GTTTTTTTTT/GTTTTTTTTTT	CCACCGGATTTATGAAG GAA	GGGCATGAAATATGAGA CTGC	59.8	415	INTERGENIC				
CaPOPI_2528	Ca4	29292913	ATTTTTTTT/ATTTTTTTTT	ACACGCTAGCCATTAGA GCC	TCCTTTCTTTCCAAGAG GTTCA	59.5	306	INTERGENIC				
CaPOPI_2529	Ca4	29310722	ATTTTTTTTT/ATTTTTTTTT	GTGGTGTCATCTCGGT CTT	TAAGCCAGCAACTCCAG GAT	60.0	658	INTERGENIC				
CaPOPI_2530	Ca4	29321184	ATTTTTTT/ATTTTTTTTT	AACACATCAGCAAATGG CAA	TGGGTTCCGGTACAAGC TAC	60.1	682	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2531	Ca4	29330235	ATTTT/ATTT	TTTGTTCAGATTGCGCTTG	GAGGGGATCCATTTTCCCTA	60.0	762	INTERGENIC				
CaPOPI_2532	Ca4	29348534	AGGGGGG/AGGGGGGG	GTTGTGCGGAAGCCATTAT	GAGGACTGGACGTACCCCTG	60.0	248	INTERGENIC				
CaPOPI_2533	Ca4	29356210	ATTTTTT/ATTTTT	GCGGGTTTCCTTTTATAGGC	TTTTCCAGCATGTGTGCATC	59.9	311	INTERGENIC				
CaPOPI_2534	Ca4	29356293	CTTTTTTTT/CTTTTTTTT	GCGGGTTTCCTTTTATAGGC	TTTTCCAGCATGTGTGCATC	59.9	311	INTERGENIC				
CaPOPI_2535	Ca4	29363363	TAA/TA	CTCGCGGTATCTTCATGACT	AAAAACAGACAGGTACGAGTG	57.9	313	INTERGENIC				
CaPOPI_2536	Ca4	29368326	TC/T	TCGATTGTTTAGAGGCTATACGTG	TCGCTTGTGAGAGAGGACAA	59.7	511	DRR	Ca_14154			
CaPOPI_2537	Ca4	29388732	ATTTT/ATTT	GGCATCCCAGATCTGAATAAA	AAGTCGGTACAGCACCAATCC	60.0	931	INTERGENIC				
CaPOPI_2538	Ca4	29418053	GAATAAATAAATAAA/GAATAAATAAATAAATAA	TTGCTCCTACGTATCTCCG	AACTTCACCGTACACCACC	60.2	836	INTERGENIC				
CaPOPI_2539	Ca4	29418531	TT/TTAT	GGTGGTGTACGGTGGAAGTT	GTCAAGGCAGACCAGAAAGC	59.7	383	INTERGENIC				
CaPOPI_2540	Ca4	29419703	A/AC	TGATTTTACATCTGCACCATGA	GGCATAAGCTTGCAATGTGA	59.0	262	INTERGENIC				
CaPOPI_2541	Ca4	29421150	TAAAAAAAAAAAAAAAAA/TAAAAAAAAA	TCGCCGTTGCTTTTCTACTT	AGAGAGCCAAACGGCAGATA	60.0	728	INTERGENIC				
CaPOPI_2542	Ca4	29426569	ATTTTTTTTT/ATTTTTTTTTT	ATCCAGCGAATTTTACCAGA	TTTTGACACACACACACCCA	59.5	781	INTERGENIC				
CaPOPI_2543	Ca4	29498412	ATTTTTTTTT/ATTTTTTTTT	TTGGATTGATTTTGGATTGTC	AACTTGATTGAATATTGCCATTG	60.0	779	INTERGENIC				
CaPOPI_2544	Ca4	29503488	ATTTTTTTTT/ATTTTTTTTTTTT	TGTATGCCCTCCTCTTTGTCA	GGGGTACTCAACCCACAATAA	59.6	735	DRR	Ca_14160			
CaPOPI_2545	Ca4	29515377	TAAAAAAAAA/TAAAAAAAAA	CGATGAGAGATGGTTAGGGTG	GGGAAGAAGCTTGATTCACCT	59.6	436	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2546	Ca4	29544316	GATAT/GAT	CCATCAAACCACAACAAACA	CCCAATTTCTTCGGTTT	57.8	706	INTERGENIC				
CaPOPI_2547	Ca4	29545135	AATTATTTATTATTTAT/AATTATTTATTTATTATTTAT	CATACGTGATACGCTGGGTG	GTGAGGGAGGACCAAAACAA	60.0	659	INTERGENIC				
CaPOPI_2548	Ca4	29547360	CTTTTTTT/CTTTTTTT	TCCACACATCCAAACAAA	TTGGTCCCTATAAGTTGGCG	59.8	613	INTERGENIC				
CaPOPI_2549	Ca4	29564628	GTTTT/GTTTTT	GAACGGTCCATGCAAAAGTT	AGTTTCCCGATCCTTAGTC	60.0	535	INTERGENIC				
CaPOPI_2550	Ca4	29566926	GTTTTTTTTTT/GTTTTTTTTT	CTCTTTGCCCTGCGATTAG	TGAAACCAGATTTTGATCCG	60.0	701	INTERGENIC				
CaPOPI_2551	Ca4	29582409	TAAAA/TAAA	AGCTGTATTGGCCTCCTT	GCCGAATAAAACCTCAACAA	60.1	212	INTERGENIC				
CaPOPI_2552	Ca4	29619182	AG/A	TTGTCGTGGTGATTAATGAAAA	GCCGACACCTTCAATCAAT	59.4	751	INTERGENIC				
CaPOPI_2553	Ca4	29622506	ATTTTTTT/ATTTTTTTTT	CCCCACGATCCTGAATAAA	AACGATGATCGCAACAACAA	59.8	281	INTERGENIC				
CaPOPI_2554	Ca4	29626397	CTTTTTTTTTTT/CTTTTTTTTT	ACCCCATTTATCCTCATCA	CTTAGTGAGTGGAGAGCGCC	60.1	398	INTERGENIC				
CaPOPI_2555	Ca4	29626809	CTTTTTTT/CTTTTTTT	CTAGGAGAAGGGGATTGG	TGTGTTGAATTCTTGATTGGG	59.9	239	INTERGENIC				
CaPOPI_2556	Ca4	29640045	TAAAGA/TAAAGAAAGA	GCCTGTCTGCATTGTTCTT	CGGACAGCAACAATTCTCTT	60.3	753	INTERGENIC				
CaPOPI_2557	Ca4	29658881	TGAGGAG/TGAG	CTTTTGAGGCATTCCACAT	ATTTTGTTGGGTGCTCTTG	59.9	176	INTERGENIC				
CaPOPI_2558	Ca4	29681493	G/GT	ATCCCCACACGATGAATAA	CCAAAGAGCTGAGCGAAAT	60.0	404	INTRON	Ca_14166	Z	MYB_related	Kinesin, motor domain
CaPOPI_2559	Ca4	29684929	ATTTTTTTTT/ATTTTTTTTT	GCCCTGGCCTAAGAATAACC	CAAGCCAACAGAACCTGGAT	59.9	562	INTRON	Ca_14166	Z	MYB_related	Kinesin, motor domain
CaPOPI_2560	Ca4	29699958	TTG/TTGGATG	TGGCCTTATTGCTTTTTGG	CCAACATCATGCTCTCCAAC	60.1	446	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2561	Ca4	29701374	G/GTTTAAATTC	AGATCTTCCCTCATG GCT	CCTTGACAAGAAGCAAC ACG	60.0	474	INTERGENIC				
CaPOPI_2562	Ca4	29702135	CTTTTTT/CTTTTTTTT	AATTAGGTGTGAGGGC AAA	TTTCATTTTAAAACCC CTCA	59.4	421	INTERGENIC				
CaPOPI_2563	Ca4	29717512	GAAATAATA/GAAATAATAATA	GTTGGCATTTCTCCACT CGT	GTGCCCAACAACAAGG ACT	60.1	458	INTERGENIC				
CaPOPI_2564	Ca4	29719863	ATTTTTT/ATTTTTTTT	GAGTTGCGCCCAACTT TTA	AGGAACAGCAAGAACGG TGT	60.2	883	INTRON	Ca_14167			Domain of unknown function DUF231, plant
CaPOPI_2565	Ca4	29776445	TAAAAAAAA/TAAAAAAAAA	TATTTGGGCTGGTGT TGT	TGGGCCACCCTATACCA ATA	60.2	729	INTRON	Ca_14170	K	HD-ZIP	Homeobox
CaPOPI_2566	Ca4	29793706	TAAAAAAAA/TAAAAAAAAA	AGATGTTGCTTCCCA GAA	CAAAAGAACCTTAGCTT CCCC	59.7	718	INTERGENIC				
CaPOPI_2567	Ca4	29821605	CTTTTTT/CTTTTTT	GACTCATCCAAGGTTGC CAT	TTTGATGGCTCAGAAAG CCT	59.9	524	INTERGENIC				
CaPOPI_2568	Ca4	29866382	CAAA/CAA	TGGGAGGAAGTTGACT CAG	CTTCGCACCTCTATCTT GCC	60.2	465	INTERGENIC				
CaPOPI_2569	Ca4	29900525	TTATA/TTA	AACAAAGAAGACACGG GGT	CTTCTCGCATAATC GAC	58.6	574	INTERGENIC				
CaPOPI_2570	Ca4	29925448	G/GC	ATCGGACAGAGTTGACC CTC	GTTTCCAAATCGTGGC CTA	59.1	686	INTERGENIC				
CaPOPI_2571	Ca4	29932586	TAAAAAAAA/TAAAAAAAAA	TCTACGGCGTCTAGTGG ACA	AGCCCCGAAAGGATCTAA AGG	59.5	487	INTERGENIC				
CaPOPI_2572	Ca4	29933754	ATTTTTT/ATTTTTTTT	AGCCACACGATGTTGAT TGA	TGATTAGGAATCACCC GTT	60.1	845	INTERGENIC				
CaPOPI_2573	Ca4	29941572	TAAAAAA/TAAAAA	CCGTGTAGGTATGATCT TTTGG	CCTTCTGTAAATCGG CAA	58.5	324	INTERGENIC				
CaPOPI_2574	Ca4	29987923	GATGGTAT/GATGGTATGGTAT	GAGCAGAGCTGCCTAAT GCT	GGCGTTGTTGTAGAGTG CAA	59.9	419	INTERGENIC				
CaPOPI_2575	Ca4	30045432	CATATAT/CATATATAT	GCGTGCATAAGTGGTTG ATG	ACTCACGGTGATGAGTG TGG	60.1	345	DRR	Ca_14181		S1Fa-like	Protein kinase, catalytic domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2576	Ca4	30046973	GAAAAAAAAA/GAAAAAAAAA	TGAATGAAATTTCTGGCAGG	CGTTTTGTTTGTGGCACATT	58.7	280	INTERGENIC				
CaPOPI_2577	Ca4	30075059	CTAA/CTAATTGTTTTATAA	TCGAAACCAACCACCTTTTC	GCAATTCGACAATGCACAAAC	59.9	547	INTERGENIC				
CaPOPI_2578	Ca4	30077264	ATTTTT/ATTTTTTT	GCATATTGGGAGCGCTTTA	TGGATGATTGTGACAAAATTGC	60.2	508	INTERGENIC				
CaPOPI_2579	Ca4	30082739	AAAAACAAACAG/AAAAACAAACAGTGGAAACAAACAG	TGCGTTGTATCATGTCTGTT	TCTGTTTGTTCCTCCGTTT	60.0	389	INTERGENIC				
CaPOPI_2580	Ca4	30086302	TTTTCATG/TTTTCATGCAAACTTTCATG	TTGATGTGGACTTCTTTCGCG	TTTTCGCGTAAACCTTTG	59.8	238	INTERGENIC				
CaPOPI_2581	Ca4	30086898	ACTTCT/ACT	ACGCCGAAAAACACTTTCAC	TCCATTCGACTGTCCTTCAA	60.2	630	INTERGENIC				
CaPOPI_2582	Ca4	30097465	GAAA/GAA	GCAAAACGGGACTAGACATA	CCAGGGGTGCCTTAGATTT	60.1	307	INTERGENIC				
CaPOPI_2583	Ca4	30118694	CATAGATA/CATAGATAGATA	CTCCTTCATTCTCCTCCCTCC	AAGGTGGGTAAAGAACCGC	60.0	778	INTERGENIC				
CaPOPI_2584	Ca4	30120661	TAAAA/TAAA	TTTGACATCCATCTTAGTCAGC	CCCTGGGTGCGTTAGTTAT	60.1	379	INTERGENIC				
CaPOPI_2585	Ca4	30122560	GAA/GAAAA	ATGTCAATGGGCCACTTAGC	GTGGGGCCATTGATGAGTAA	60.0	962	INTERGENIC				
CaPOPI_2586	Ca4	30134439	CAAAAA/CAAAA	TCCTTTTGCATTACTATCCAAGC	GGGGTTCCATGTAAAAATT	59.7	419	INTERGENIC				
CaPOPI_2587	Ca4	30141789	TTAT/TT	GAACAATGACCAAGTGAATTTTGA	TATGGGATGCGTTGAGATGA	60.3	428	INTERGENIC				
CaPOPI_2588	Ca4	30148542	ATTTTTTT/ATTTTTTTTT	GTTGTGTCTGTGAGTGTCTCC	TTAGTCCCTTACGTCGTGGG	59.5	302	INTRON	Ca_14185			Plastid lipid-associated protein/fibrillin conserved domain
CaPOPI_2589	Ca4	30178438	AAATTTCAATATTTAATTTCAATAT/AAATTTCAATATTTAATTTCAATATTTAATTTCAATAT	CAAGCAATTATGGTGCACTG	AGTGAGGCAAATGGAAATGG	59.2	669	INTERGENIC				
CaPOPI_2590	Ca4	30184517	TA/T	CGAGGGGCGTAAAAATCATA	GCGAGATTTGTTCCGTGT	59.9	579	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2591	Ca4	30185691	TAAAAAAAA/TAAAAAAAAA	CATCGCTAACTCAGTGC CAA	AATGCGTTACGGGTGAA ATG	60.0	876	INTERGENIC				
CaPOPI_2592	Ca4	30210048	ATATCACTTT/AT	GGTTTGCTTATGGGGCA GTA	CACCCCGAATGAACTTT AGAA	60.0	631	INTERGENIC				
CaPOPI_2593	Ca4	30211443	T/TA	ACATCAAAACAAACAGCG CAC	CCGCTAAATTGCCAA TAA	59.8	714	INTERGENIC				
CaPOPI_2594	Ca4	30226816	CAAAAA/CAAAA	GCTTATGCAATGCACGA AAA	CATGGGTGAAATGGAG ACA	59.8	528	INTERGENIC				
CaPOPI_2595	Ca4	30330570	CTATATATATATATATATA/CTATATA TATATATATATATATA	TTCGATGGCTAGATTAC ATACTGC	CCCCTCAACTCAAGAA TATG	59.7	561	INTERGENIC				
CaPOPI_2596	Ca4	30351459	CTTTTTT/CTTTTTTT	TCTTTGAAACACATCACT TTCG	AAAATTGATCGGTGGT GGA	57.9	314	INTERGENIC				
CaPOPI_2597	Ca4	30390669	T/TA	CTACTGAAGCCCAACGA AGG	CTTCAGATTCTGTGCC ATT	59.9	864	INTERGENIC				
CaPOPI_2598	Ca4	30404870	AATAACAT/AAT	TTAACTGTTGGTGCAGC GTC	CGTCACATTTAACACGC CAT	59.9	798	INTERGENIC				
CaPOPI_2599	Ca4	30415073	GCATCATCATCATCA/GCATCATCATCA TCATCA	TTGAACATATAGGGAGG CGG	CCATCCTTTTCAATGCG AGT	59.9	423	CDS (large-effect mutations)	Ca_14197			
CaPOPI_2600	Ca4	30423088	TAAAAAAAA/TAAAAAAAAA	AGGGGCAAAAATACTGC TTG	CTTGATCGGCTCATGTG TTG	59.2	938	INTERGENIC				
CaPOPI_2601	Ca4	30429374	TATTCATT/TATT	TGATGCCATATCCTTA GCC	ATTTGGTTTGGCATTGTT GC	60.0	811	INTERGENIC				
CaPOPI_2602	Ca4	30468296	AAT/AATAT	ATTGTGCATATCCCTC CCA	CCTTAATCCACCAAAAG CCA	60.2	747	DRR	Ca_14199		G2-like	Myb, DNA-binding
CaPOPI_2603	Ca4	30468822	AAA/AAAGAA	TGGCTTTTGGTGGATTA AGG	GGTCTCACGACCAAGTC ACA	59.9	438	DRR	Ca_14199		G2-like	Myb, DNA-binding
CaPOPI_2604	Ca4	30477859	CTTTT/CTTTTTT	AAAATCAATCGGGACA TCA	GAATCAACAAAGCCCC AAA	60.1	648	INTERGENIC				
CaPOPI_2605	Ca4	30501632	AGT/A	TGGGGATTATCCCTTC AAA	GCAAGTGTCAACTCACT CAATCA	59.2	595	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2606	Ca4	30535832	TATAAATAAATAAATAA/TATAAATAA TAAATAAATAAATAAATAA	CCATTGAGAATTAGAAA TCACCA	CCAAATTTCCCAAGGGT TCT	59.4	582	INTERGENIC				
CaPOPI_2607	Ca4	30536932	GTTTTTTTT/GTTTTTTTTTTTTT	ATCATTGAACGACCGGA AAC	CGGATACAATGGCAATC AAA	59.8	431	INTRON	Ca_14204		NAC	No apical meristem (NAM) protein
CaPOPI_2608	Ca4	30537523	CA/CATA	TTTGATTGCCATTGTATC CG	CAAAATGGAAATGCAAG AACAA	59.4	803	INTRON	Ca_14204		NAC	No apical meristem (NAM) protein
CaPOPI_2609	Ca4	30538166	AAAGAAG/AAAGAAGAAG	TTGTTCTTGCAATTCAT TTTG	CGCCATCTTCTCTTCTT TG	60.0	380	CDS (large-effect mutations)	Ca_14204		NAC	No apical meristem (NAM) protein
CaPOPI_2610	Ca4	30542137	TAAAAA/TAAAAAA	TAAGGCATGATAAGGCC GAC	GTCATGTCACCCGTGAT GAG	60.1	299	DRR	Ca_14205			
CaPOPI_2611	Ca4	30552355	TG/T	TGTCGCATGCAACCTCT TAG	ACCTGTGTGTTCCCTTC CAC	60.0	528	INTERGENIC				
CaPOPI_2612	Ca4	30558963	GC/G	CCCCTTTGGCATCTAT CAA	TCATCTCATTTTGCTTCC CT	59.9	510	INTERGENIC				
CaPOPI_2613	Ca4	30561689	TAAAAA/TAAAA	GGAGGCACCATACTTTT CCA	AGAATGGCCACTTCAAG TCAA	59.9	198	INTERGENIC				
CaPOPI_2614	Ca4	30566057	CGGG/CGG	TTTTTGCAATTGGGCATA CA	ACTGGGTTTGGGTACC CTC	59.9	515	INTERGENIC				
CaPOPI_2615	Ca4	30570798	TAAAAAAA/TAAAAAAA	TGCTTCTCAATGACTAAC ACCAA	TGTTGGTGTGACTTTTC CTTCT	59.8	881	INTERGENIC				
CaPOPI_2616	Ca4	30573766	T/TC	CATTATGATCACAGACG ATGGTG	TCCTCTTCGATCAAGCA TCC	60.3	259	DRR	Ca_14206	A		D111/G-patch
CaPOPI_2617	Ca4	30582286	GAAAAAAAAA/GAAAAAAAAA	TTCCCTCCCTTCCTTTGA GT	TTTTCTGCAAGTTTGTC GTTG	60.0	615	INTERGENIC				
CaPOPI_2618	Ca4	30585901	CTTTTCTAATTTTCTA/CTTTTCTA	AAAGTCAAGTCATCCCA AACA	GAAACAGAAAACGGGAA CCA	59.4	381	INTERGENIC				
CaPOPI_2619	Ca4	30619694	CAAAAA/CAAAA	ACTCACTCTGCCCTGT GTT	CCAACCTGGTTCCAACA AAAA	59.8	566	INTERGENIC				
CaPOPI_2620	Ca4	30653740	AC/ACC	TGCCATTGATGCTAAA CAA	GAATGATGTCGCGGTAG GAT	60.1	513	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2621	Ca4	30685617	TTA/TTATCAATA	GGGAAGAATGGATTGGGAT	GGATGTTTCATTCCACCAAAG	60.0	192	INTERGENIC				
CaPOPI_2622	Ca4	30697175	CTTTT/CTTT	AGATTCCATGGCACACACAA	CCCCAAGATTAAACAAAGGCA	60.0	647	INTERGENIC				
CaPOPI_2623	Ca4	30741967	TCAATATTGAACA/T	ATCCGGTTCCTTTTGGTTC	TAAGGACCGGTGATCTGACA	60.2	656	INTERGENIC				
CaPOPI_2624	Ca4	30755137	ATTTTTTT/ATTTTTT	CAGTAGGAAGTCACATCCCAGA	GCAACTGAGCTGAGAGCGTA	60.5	860	INTERGENIC				
CaPOPI_2625	Ca4	30760524	ATT/ATTT	TTTGGAAGCGGTCTCAGTCT	AAACGAATACTGCAACGCAA	60.0	217	DRR	Ca_14211		ERF	C2 calcium-dependent membrane targeting
CaPOPI_2626	Ca4	30790861	TAAAAAAAA/TAAAAAAAAA	GAATTTTGGCCATCACCACT	TGTCTGCACACCCATTTTA	59.8	530	INTERGENIC				
CaPOPI_2627	Ca4	30844654	CTTTTTTTTT/CTTTTTTTTT	CACCTGCTTTTGACCACTCT	GGCAATTGCTTTACGCTAGG	60.1	959	INTERGENIC				
CaPOPI_2628	Ca4	30866796	A/AC	AAGTTGCCTCTGCCTTTGAA	ATGTTTGCAACCCGTTTCTC	60.0	255	INTERGENIC				
CaPOPI_2629	Ca4	30873864	ACC/ACCC	CAAAGAGAGAACTTGCACCG	GGAAAGCGAGAAGTTGAACG	60.0	566	INTERGENIC				
CaPOPI_2630	Ca4	30880709	ATT/ATTTT	TGCAGAGTAAACCAGCAACG	TTGCAAGTTGTGACTGAGGC	60.1	557	INTERGENIC				
CaPOPI_2631	Ca4	30880741	CAA/CAAA	TGCAGAGTAAACCAGCAACG	TTGCAAGTTGTGACTGAGGC	60.1	557	INTERGENIC				
CaPOPI_2632	Ca4	30887008	TCTCCTC/TCTC	CCTGACCCTACAAGCCAATC	GTAGTCTCGCAAGGACTCCG	59.6	218	INTERGENIC				
CaPOPI_2633	Ca4	30928717	TAAAAAAAA/TAAAAAAAAA	CAATGTCCATGTGACCAAAA	TCTGTGCACCATCTCAGTC	60.4	949	INTERGENIC				
CaPOPI_2634	Ca4	30968151	CTTTTTTT/CTTTTTTT	CACATCCCTTGCCATTTCTT	CCCGCATTTGTAACCATCTT	59.9	827	INTERGENIC				
CaPOPI_2635	Ca4	31063154	AATATATATATATATATATAT/AATATATATATATATATATATAT	GAGGGGATGAATCATTAACG	GTAAGACCCCGCATTGTGTT	59.8	499	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2636	Ca4	31079661	TGG/TG	GCTCGTGTCTTGCAGAAA	CCAATTACCACAGATTCGGG	60.0	337	INTERGENIC				
CaPOPI_2637	Ca4	31106521	CCTT/CCTTCTT	ATAAGAGTGTGGCGGTTGG	TGGTTGAAATGGACGACAAA	60.0	584	INTERGENIC				
CaPOPI_2638	Ca4	31108602	GGAAGAAGAA/GGAAGAAGAAGAA	GGATCAGGCCCTATTGTGA	AGTTGGCTTTGCTTGATGCT	59.9	476	INTERGENIC				
CaPOPI_2639	Ca4	31110947	TAAAAA/TAAAAA	GCTAAAGCAATCACCAGGC	CGGTTTGGTGACATAGCTGA	59.9	412	INTERGENIC				
CaPOPI_2640	Ca4	31137565	GAAAAA/GAAAAA	TTTCCGAATCGGGAGTAGA	GTTCTGCCATCCAACCTTA	60.4	113	DRR	Ca_14223		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_2641	Ca4	31140324	TAAAA/TAAAAA	ACTTCCATTGCTTCAGCAT	AAATGATTCTGGTGGGACA	59.8	536	INTRON	Ca_14223		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_2642	Ca4	31172943	TA/T	TCGCCTAAGGTAAGGGCTTT	TTACACCAATTCCTCCCAAGA	60.2	421	INTERGENIC				
CaPOPI_2643	Ca4	31182932	T/TC	CGCATATTAGCATGGAGGGT	TCGCTCGAACCAGAGTTCTT	59.9	317	INTERGENIC				
CaPOPI_2644	Ca4	31192815	TGG/TG	TTGAAGGAGAAGCCAGAGTCA	TGAGGCATGCAGAAACGTAG	60.1	238	INTERGENIC				
CaPOPI_2645	Ca4	31194912	CTTTTTTTTT/CTTTTTTTTT	TTCCATGTTGTGTTGAAGCA	GCACATTGCAAGGGTATGTA	60.1	822	DRR	Ca_14224		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_2646	Ca4	31195163	GAAAAA/GAAAAA	TTTCCCGACTTGGTCCTTTA	TGCATGCAGATCTTGCTCTC	59.5	643	DRR	Ca_14224		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_2647	Ca4	31200114	TA/TAGACCA	TTGTCTTAGGCAGCACTGGA	TGGTGAACGAAAGTGACGTG	59.6	903	INTERGENIC				
CaPOPI_2648	Ca4	31230420	TTCTCTCTCT/TTCTCTCTCT	CTTCCATCTCACTCCCTCG	TAGCCGACAGGGTCTCAGTT	59.8	435	INTERGENIC				
CaPOPI_2649	Ca4	31235705	ATTTTTTTTT/ATTTTTTTTT	CAATTGCGGTTTCCACTTTT	TTCATGCATTTTCAATGGGA	60.0	434	INTERGENIC				
CaPOPI_2650	Ca4	31236090	ATATTATTATTATT/ATATTATTATTT	CAATTGCGGTTTCCACTTTT	TTTTTACCGTGGGTGAATCC	60.0	956	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2651	Ca4	31258911	GTT/GT	CAGGTCGTGCCAATTCTTT	GGCTAGGATTGCAACAGGT	60.1	264	INTERGENIC				
CaPOPI_2652	Ca4	31259145	GATATATATATATATATATATAT/GATATATCTATATATATATATATATATATAT	CAGGTCGTGCCAATTCTTT	TTCATTGACGAATGTACATCA	60.1	404	INTERGENIC				
CaPOPI_2653	Ca4	31274972	TAAAAAAAAA/TAAAAAAAAA	CTATGGCACACACCAGCAAC	GATCAAGTAGGGCGGATCA	60.2	699	INTERGENIC				
CaPOPI_2654	Ca4	31275360	ATTTTTTTTT/ATTTTTTTTT	TTCAATTAGGGTTGGGTCG	ACAGTTTGTCGTTGTTGGT	59.8	631	INTERGENIC				
CaPOPI_2655	Ca4	31279281	ACCC/ACC	GCCACCTGTCCAACCTCTA	ATACCCAAGAGGGTATGGC	60.1	454	INTERGENIC				
CaPOPI_2656	Ca4	31284485	ATT/ATTT	ATGGCTACTCCAATGCATCC	ACATGGCTCCCCCTTACTCT	59.9	962	INTERGENIC				
CaPOPI_2657	Ca4	31302749	GAAAAAAAAA/GAAAAAAAAA	CACCCACACCAAACTCTCT	GTTAGGTTGGACGGGACCTC	60.0	680	INTRON	Ca_14231		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_2658	Ca4	31303190	CTTTTTTTTT/CTTTTTTTTT	GAGGTCCCGTCCAACCTAAC	TCAGCACCGAGAGTGTC AAC	60.7	488	INTRON	Ca_14231		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_2659	Ca4	31317473	ATTTTTTTTT/ATTTTTTTTT	TGAGGCGTCATGGTAGACA	CAAATCGACATTGTTGC CAG	60.3	707	INTERGENIC				
CaPOPI_2660	Ca4	31317508	TAAAAAAAAA/TAAAAAAAAA	TTGCGCATCAGCCATATTTTG	CAAATCGACATTGTTGC CAG	59.7	509	INTERGENIC				
CaPOPI_2661	Ca4	31322894	GAAAAAAAAA/GAAAAAAAAA	CTCCTAAGGGTGGCCTTTTC	GGGTTGTTCTTGGACCTTCA	60.1	623	INTERGENIC				
CaPOPI_2662	Ca4	31406944	GTTTTTTTT/GTTTTTTTTT	CAAATTATACTCGCACAACTTGC	AAAGTGGACAAACACAA AACGA	58.9	782	INTERGENIC				
CaPOPI_2663	Ca4	31424757	GTTTTTT/GTTTTTTT	AATTGGCGAAACCACTTTT	TGCACCTGTTGGGGTTGATA	58.6	501	INTERGENIC				
CaPOPI_2664	Ca4	31445256	ATT/ATTT	AGATCTATGCATCGGCAACC	AGGGTACTACAGCTGCCCT	60.1	338	INTERGENIC				
CaPOPI_2665	Ca4	31452576	CTTTTTTT/CTTTTTTTTT	CCACTCGTGGTCCCTTA ACT	TCGGCTAAATACCATTTGTGG	59.1	566	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2666	Ca4	31529637	CTTTTTTTTT/CTTTTTTTTT	CCAAATCCGATGAGGAA AGA	TTTAAGACCCGCGATT CAG	60.0	820	INTERGENIC				
CaPOPI_2667	Ca4	31531525	G/GGT	AGGGATTGCTTGCAAA TAC	AATTCCTCAACCAATAG CCC	60.1	387	INTERGENIC				
CaPOPI_2668	Ca4	31534458	CAAAAAA/CAAAAAAA	CAAGCCAACGTGTGTT GTT	TGTGGGGGATCAATTG TTT	59.7	371	INTERGENIC				
CaPOPI_2669	Ca4	31570022	TGGGGGG/TGGGGGGG	TATTTGGATTTTGGCTC GG	AGGAAGAGTGGAGTTGC GAA	59.9	505	INTERGENIC				
CaPOPI_2670	Ca4	31609144	ATTTT/ATTT	TCGACGTTTATTTGATG GCA	TTGAGAACTTAATTGTG GGCA	60.1	651	DRR	Ca_15441	A		
CaPOPI_2671	Ca4	31611840	GTTTTTTTTT/GTTTTTTTTT	CGTTTCAGCTGAGCAA ATTC	TTGATCCATTGGGATTG TGA	60.0	392	INTERGENIC				
CaPOPI_2672	Ca4	31611867	AAT/AATAT	CGTTTCAGCTGAGCAA ATTC	TTGATCCATTGGGATTG TGA	60.0	392	INTERGENIC				
CaPOPI_2673	Ca4	31612473	TAAAAAA/TAAAAAA	TAAATCCAAACCGCA AGC	CACTTAAGCAAACGGGG TGT	60.1	462	INTERGENIC				
CaPOPI_2674	Ca4	31630531	AGG/AG	AGTTGAAGGTGCAACA CGA	AATTTACTTGAGGGTC GGG	59.3	288	INTERGENIC				
CaPOPI_2675	Ca4	31630588	TCA/TA	AAGGTGCAACACGAGA AGG	AATTTACTTGAGGGTC GGG	60.3	283	INTERGENIC				
CaPOPI_2676	Ca4	31631888	AAAA/AAAAATAA	CCAACCTGGTTCCAACA TCTG	TGGCTAATCATAGCGAA ACG	60.4	832	INTERGENIC				
CaPOPI_2677	Ca4	31633774	AG/AGG	AAATATTGTTCAATCCGC CG	CTCCTCAAGCCAAGTG AAG	59.8	491	INTERGENIC				
CaPOPI_2678	Ca4	31635242	ATTACCT/A	TCAATGTGAACGGGCAT CTA	TGGTGCCTCTACAATT TCC	60.1	778	INTERGENIC				
CaPOPI_2679	Ca4	31635868	AAT/A	GGAAATTGTAGGAGGCA CCA	GTTGCGCTACGAGATGT TGA	59.9	695	INTERGENIC				
CaPOPI_2680	Ca4	31639620	GTTTT/GTTTTT	ATTTGGAGAATGATTTG GCG	GTGTTTGGTTCAAGGGG AGA	59.9	412	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2681	Ca4	31642398	TAAAAAAAA/TAAAAAAAAA	TGTCACCTGCACTGCCAC ATA	TTTCCGGCAAAGTTCTC ATAA	59.9	482	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2682	Ca4	31644451	TA/T	AATGTCTGGGAGTTTTC TCG	GCCATCTTAGGCTTTCC CTT	59.9	953	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2683	Ca4	31646633	AA/AACA	ATGGAGAAGAGGGGGA GTGT	ACCAGTCTTTTACGGGC CTT	59.9	135	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2684	Ca4	31647747	ATT/AT	CACGTGTGAAGTCGAG AGA	AAGCTACCTGATCAATG CGG	60.0	863	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2685	Ca4	31647770	GTTTTTTTT/GTTTTTTTT	CACGTGTGAAGTCGAG AGA	AAGCTACCTGATCAATG CGG	60.0	863	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2686	Ca4	31649916	AT/A	TGAGGCATTTGGAGACA ACA	ATTGACCGGTGGAAGAC ATT	60.2	585	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2687	Ca4	31649942	CT/CTT	CGTGCCCTGCAGGTATT TAT	ATTGACCGGTGGAAGAC ATT	60.0	454	INTRON	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2688	Ca4	31652250	CTTTT/CTTTTT	CCATTACCTTTTCGTGA TGC	TGAAAGCAAAGCCACGT ATG	60.3	796	DRR	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2689	Ca4	31653241	GATAAA/GATAAAAAATAA	TTCAAACGATGGCAACA AAA	TCATGGGATTAAGCCTC CAC	60.1	268	DRR	Ca_15442	U	EIL	SPX, N-terminal
CaPOPI_2690	Ca4	31718401	AT/ATT	ATTCTCTAATGTCGGG GCT	GCCACCTTGTGAGAGT TTC	59.9	501	INTERGENIC				
CaPOPI_2691	Ca4	31757461	CTTTTTTTTT/CTTTTTTTTT	TATGCTAAACCAACCGC CTC	TTTTTCCTGACTTGGTC CTTT	60.1	383	DRR	Ca_15447	R	bZIP	
CaPOPI_2692	Ca4	31806633	ATGTGACTAATTTT/ATGTGACTAATTT GTGACTAATTTT	ACAAAAGCCTGGATAGC GAA	TCACATATACCTTAAAA TCACA	59.8	410	INTERGENIC				
CaPOPI_2693	Ca4	31816562	ATTTTTTTTTTT/ATTTTTTTTTTT	GGCTCCGATCAAAAGAA ACA	GCCCTCAGATGAGAGTC AGG	60.2	545	INTERGENIC				
CaPOPI_2694	Ca4	31837452	ATTTTTTTT/ATTTTTTTTTT	TGGAGACCATGGAATG CTT	TTTTGTGAATAGTCCATG CTTCA	60.5	456	INTERGENIC				
CaPOPI_2695	Ca4	31859597	TAAAAAAAA/TAAAAAAAAA	GTTGGAGCCCCACTTT ATT	TGCAAGCAGCATCAGAG AAC	60.2	793	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2696	Ca4	31892250	CTTTTTTT/CTTTTTTTTT	AACCGTTAACACCGAA ACA	TGCGGTCAACACACTTA GGA	60.3	520	INTERGENIC				
CaPOPI_2697	Ca4	31930111	AATATATATATA/AATATATATATATA	GAGGAGCATTGATGGAG GAA	TTTGAAGACTTTTGGG CTC	60.2	574	INTERGENIC				
CaPOPI_2698	Ca4	31931258	TAAAAAAAA/TAAAAAAAA	TCAAACCCGAGAACAAG TGA	TAACAAGCGCGCAATGT ATC	59.3	595	INTERGENIC				
CaPOPI_2699	Ca4	31937240	TGG/TGGG	CTAAGGCCCTATGTGCA AGC	CGAGACTACTCGTGGGC TTC	59.9	835	CDS (FRAME SHIFT)	Ca_15455		Dof	
CaPOPI_2700	Ca4	31967535	T/TC	TACCCTTAATGGCTGGG ATG	AAAACACTTGCGATGA CCC	59.8	510	INTRON	Ca_15456			
CaPOPI_2701	Ca4	31972811	CT/CTT	TTTGTGAAATTGGTTCC CTG	GGTCCAGCAGCATAGGA CAT	58.4	523	INTERGENIC				
CaPOPI_2702	Ca4	31974174	AC/A	GCTGAAAAAGTGGGTGT GGT	GAGAGTGCTGTTGGCTG TGA	60.0	655	INTERGENIC				
CaPOPI_2703	Ca4	31989643	CTTTTTTT/CTTTTTTTTTTT	GAAAGATTCTCCCACT CCC	TGCACATTGAAAATTG GTG	59.9	246	INTERGENIC				
CaPOPI_2704	Ca4	31991301	GTTTTTTT/GTTTTTT	AGACAACGACTTTGGCG TTC	ATTGCTCCTTCAATCATG GG	60.3	534	INTERGENIC				
CaPOPI_2705	Ca4	31994404	TAAAA/TAAAA	ATCAGCGAGGATGCAGA ACT	CATCGCTCAGTTTGAC TCA	60.0	796	DRR	Ca_15458			
CaPOPI_2706	Ca4	32008597	TAAAAA/TAAAAAA	CAGTTTGCTTGACTTCG CAA	TTCGTACAATTCATACGC GG	60.2	659	INTERGENIC				
CaPOPI_2707	Ca4	32045859	T/TA	TGGGGTTTGTATCCATT TGT	TGATGTCTTTCGATCCA CCT	60.0	607	DRR	Ca_15459			Domain of unknown function DUF828
CaPOPI_2708	Ca4	32047782	G/GT	TGGGGTTTGTATCCATT TGT	AAAGCCCAACCAACAT TGA	60.0	329	INTERGENIC				
CaPOPI_2709	Ca4	32048513	TAAAAA/TAAAAAA	CGATTTGTCGGTCAAT CTCT	TCACCGTAGGAAAGCTG GAT	59.2	355	INTERGENIC				
CaPOPI_2710	Ca4	32069410	A/AC	CCAGTGGTGTCCCTCTT GAT	GAGACGGAATTTGGGAC AGA	60.0	767	DRR	Ca_15461	R		Ankyrin repeat

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_2711	Ca4	32101684	TG/T	TCATTGCCTTGTCTGCAAAA	GCACTAACCCGACCCTACA	60.4	632	INTRON	Ca_15462			Transposase, Pta/En/Spm, plant
CaPOPI_2712	Ca4	32118643	AAAT/A	GCCAAAGGTAACAAAGGCAA	TGATTTCTTCATTGCATCGG	60.1	569	INTERGENIC				
CaPOPI_2713	Ca4	32119212	ATT/AT	TGTTTCGTTGTTGATAAGCATGT	TGTCCTCCTCCCTCCTTTT	59.6	721	INTERGENIC				
CaPOPI_2714	Ca4	32121836	AATA/AATATA	CCCCAAGCTTGTAAGCAAA	AATGAAAGCGTTGATTGGT	60.2	588	INTERGENIC				
CaPOPI_2715	Ca4	32122386	CTTTTTTTTT/CTTTTTTTTT	TGGGTTTTACCAATCAACG	CACCAGCCAAGTTCTCTCTT	60.6	359	INTERGENIC				
CaPOPI_2716	Ca4	32143759	GATATATA/GATATA	CGTTATCATTGCTTGAAACGG	TTGAGCACTTACTGGTGGGA	59.2	941	INTERGENIC				
CaPOPI_2717	Ca4	32144375	TAAAAA/TAAAAAA	TCCCACCAGTAAGTGCTCAA	GTCGTTGTTGGTCTGTGTGG	59.3	308	INTERGENIC				
CaPOPI_2718	Ca4	32156632	TAAAAA/TAAAAAA	TTCACTTGGTTGCTTTGCAG	CTTAAACCATAATCCCCGCA	60.0	692	INTERGENIC				
CaPOPI_2719	Ca4	32159052	TAAAA/TAAA	TCTCTTTAATGGGCCATGC	ATGCATGGAATCCAGCTTTC	60.0	688	INTERGENIC				
CaPOPI_2720	Ca4	32159427	ATTTTTTTTT/ATTTTTTTTT	TTCCCTTGAAAGTGCAATGA	GCTTCTATGGGCAACGTACC	59.2	224	INTERGENIC				
CaPOPI_2721	Ca4	32173778	GAAA/GAA	TGCAACACCGGAACCTTCAATA	TTTCAACCAATTGTTGCTCG	60.1	299	INTERGENIC				
CaPOPI_2722	Ca4	32179388	T/TA	TTCTTGCGCTTTGTCTCTCA	TGGAAGTGAACATAACCCCTTT	59.9	744	INTERGENIC				
CaPOPI_2723	Ca4	32179682	CAATAATCAACAAA/CAATAATCAACAAATAATCAACAAA	TTGCATACCTCATACCATCCC	TTGATGCATTACCTCCCACA	59.7	731	INTERGENIC				
CaPOPI_2724	Ca4	32180768	CAA/CA	TAAGCCAATGAAGAATCGCC	TTTTCATCCCACCCCAATA	60.2	425	INTERGENIC				
CaPOPI_2725	Ca4	32212035	CTCA/CTCATTGATGCTTATGTCA	TGAATCAACAAATGAAAGCAGTG	TCCCGCTTCGATACAGAGAT	60.2	448	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2726	Ca4	32214848	ATTTTT/ATTTTTTT	CGCATGTGTATCCCTTGTG	CGTTCTCGGAACCTTCTTTC	60.0	471	INTRON	Ca_15467	T	HB-other	Calcium-binding EF-hand
CaPOPI_2727	Ca4	32215092	AT/A	CGCATGTGTATCCCTTGTG	ATGGGAATGGAACCATTGAA	60.0	918	INTRON	Ca_15467	T	HB-other	Calcium-binding EF-hand
CaPOPI_2728	Ca4	32222918	ACTCT/ACT	TCCATCATCGTTCTCATTGG	TCGAACAAAAGGCAACACAA	59.5	225	INTERGENIC				
CaPOPI_2729	Ca4	32225876	TTAT/TT	TCGTCGCATTGGTGTAATGT	TCCGTGAGGACACAAGTGAG	60.0	506	INTERGENIC				
CaPOPI_2730	Ca4	32227293	AAAAA/AAAAATTAAAA	TCTTCACAACCCCTTGAAACC	TTCTTCCAAACGAGCCTCTC	59.9	868	INTERGENIC				
CaPOPI_2731	Ca4	32239930	TT/TTGGT	CAGGTAGAGTGCAGATTGCG	TAATGCTTGATGCCAAACCA	59.6	366	INTERGENIC				
CaPOPI_2732	Ca4	32264601	TA/TAA	GATCAAATCTCTATGCA TGTGCT	CCAATTGAAGGGTAAGTGCC	59.7	608	INTERGENIC				
CaPOPI_2733	Ca4	32264980	AAT/AATAT	GCACTTACCCTTCAATTGGG	AGGAGAGGTCCATTTCTCAGG	59.4	262	INTERGENIC				
CaPOPI_2734	Ca4	32301599	TAAAAAA/TAAAA	TGGATTGCAAACTGGT TGA	CACGAGCTTACAAACCCACA	60.1	174	DRR	Ca_15472	DO	MYB_related	WD40 repeat
CaPOPI_2735	Ca4	32335179	AAAGAAGAAGAAGAAGAA/AAAGAA GAAGAAGAAGAA	AAAGTCCGTTTGTGAATCCG	TGGGCATTCAAATCAAA CAA	60.0	507	INTERGENIC				
CaPOPI_2736	Ca4	32367636	ATTTTTTTTTTTT/ATTTTTTTTTTTT	TCCTCCTTGTGATCTTGGCT	CATTGCTCCCTCTTACTGCC	59.8	429	INTERGENIC				
CaPOPI_2737	Ca4	32369377	TA/T	TTGGTTTCGTTTGCTTGTG TG	AATAGTGCGCATGTGTG GTC	59.7	822	INTERGENIC				
CaPOPI_2738	Ca4	32395281	TA/TAA	GGTTAACAAATCTCCTAAAGGCA	TTTTGTAAAGAATTGCGACCTC	58.7	523	INTERGENIC				
CaPOPI_2739	Ca4	32396185	TCCC/TCC	TCGTCAATTTCTTGTGTTGGTTG	TCCAATTTCCGTGTCATGT	60.0	346	INTERGENIC				
CaPOPI_2740	Ca4	32410630	TA/TAA	TTATTCCACCCACCTCAAAA	CTCAGCTCATTGGTTTGTG	60.2	262	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2741	Ca4	32431643	TTAATAATAA/TTAATAA	ACCCAACCTCATCTGCA TTC	TTTCAGAAAACTACGG AACAAA	59.9	362	DRR	Ca_15476			Armadillo
CaPOPI_2742	Ca4	32460225	TAAAAAAAA/TAAAAAAAAA	CGGAGATCCATAACACG GTC	TTTGAAAGAGAAATCCA CCCA	60.3	242	INTERGENIC				
CaPOPI_2743	Ca4	32473583	TTTTTTATTTTTATTTT/TTTTTTATT TTTTATTTTTATTTT	TGATCTTAGCGATGGTT CCC	TGAGCGTTCGATTTGT TTG	60.0	687	INTERGENIC				
CaPOPI_2744	Ca4	32484353	CTTTTT/CTTTTTT	TTATCCTTTGCTGCCCA AAC	ATCATGTTGCCCTAAT CCA	60.1	753	INTERGENIC				
CaPOPI_2745	Ca4	32489291	ATT/ATTGTT	CGACAAAGAGGTGGATG GTT	CCTCCATCAATAATAA AAACCCC	60.0	423	INTERGENIC				
CaPOPI_2746	Ca4	32492742	AAGA/AA	AGTGGATTGGGTGGAAA ATG	GCCAATTTCAATTAAGC CGA	59.6	296	INTERGENIC				
CaPOPI_2747	Ca4	32494646	GAAAAAAAA/GAAAAAAAAA	CAATTCACCTTGAAACGT CTCTCAT	CACAAAATCGACAAAGA CATGC	59.7	386	INTERGENIC				
CaPOPI_2748	Ca4	32494672	TA/T	CAATTCACCTTGAAACGT CTCTCAT	CACAAAATCGACAAAGA CATGC	59.7	386	INTERGENIC				
CaPOPI_2749	Ca4	32498847	AG/A	TAGCACGGACCCCAATT AAG	TGAACCCCATCAAAGG ATA	60.0	897	INTERGENIC				
CaPOPI_2750	Ca4	32512065	AG/A	TTTCTCCGTTATGTGT CGG	TGAGTGCTGGGAATAA CCC	60.9	704	INTERGENIC				
CaPOPI_2751	Ca4	32514320	GACATTGACTTTTT/GACATTGACTTTTT TCAACATTGACTTTTT	ATTACTGGACCAGAGGC ACG	AATGTCCATTCTGGGAC GAG	60.1	510	INTERGENIC				
CaPOPI_2752	Ca4	32522290	GAAAAAAAA/GAAAAAAAAA	ACTCATTATTCCACAG CCC	TTGCTAACGGTAACACA ACGA	59.9	851	INTERGENIC				
CaPOPI_2753	Ca4	32529368	GATATATATATAT/GATATATATATATAT	GGGTGTGATTAATGGGT TCG	TCAGGGGTGCATGGTA TTT	60.1	457	INTERGENIC				
CaPOPI_2754	Ca4	32531473	TAA/T	TAAAATGGATGCATCGA GCC	ACAAATCAACCAAGTGC GCA	60.9	662	INTERGENIC				
CaPOPI_2755	Ca4	32548891	GT/GTTAT	CGAACCAAGTGAGGAAA GAGA	TGATTGGCATGAGTGCT GAC	59.5	603	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2756	Ca4	32549547	GTATA/GTA	TTGATGTCTATTGATGCA ACG	ACATTGTGCCATCCCTT GAT	57.2	747	INTERGENIC				
CaPOPI_2757	Ca4	32550360	ATTT/ATTTT	TGAATTAGCTTGGCCGT TTT	GAGAAAATCAACCAAC GTCA	59.7	530	INTERGENIC				
CaPOPI_2758	Ca4	32555948	AAAGAA/AAA	GTGTGTTTCCCATAACC ACC	TGGGAATTTTGTGTTGTG GGT	60.0	449	INTERGENIC				
CaPOPI_2759	Ca4	32559742	AAAGAAAGAAGAAAGA/AAAGAAAG AAGA	TTCATTCCAGTCTGTG GCA	ACGGCCGTTATAGTTT CCT	60.2	669	INTERGENIC				
CaPOPI_2760	Ca4	32562355	CTTTTT/CTTTTTT	AAATGGAGGAGAAGGAG GGA	CGGTGAATCCTTTACGG AGA	60.0	286	INTERGENIC				
CaPOPI_2761	Ca4	32586827	GAAAAAAAA/GAAAAAAAAA	TATTCCTTGCCGCTCCA ATC	AAGGACCAAAACCAATT GTCTC	60.2	750	INTERGENIC				
CaPOPI_2762	Ca4	32622005	T/TTAG	CATTGTTGCGCCTTAA TGA	GAATTTGAAATGCACCC GTT	59.7	525	DRR	Ca_15485	O		Peptidase S9, prolyl oligopeptidase, catalytic domain
CaPOPI_2763	Ca4	32623000	TAAAAAAAA/TAAAAAAAAA	TCGATGTTGTTGGAGAT GGA	TCCATCTTTTGAGAGAA TGG	60.0	566	DRR	Ca_15485	O		Peptidase S9, prolyl oligopeptidase, catalytic domain
CaPOPI_2764	Ca4	32634327	TTTACTTACTTA/TTTACTTA	CAGACCCGTGTGAACAC AAA	GCCTTTGGAGTTGAAGA TTGA	60.6	591	INTERGENIC				
CaPOPI_2765	Ca4	32700117	CTTTTTT/CTTTTTTTT	TACGTGTCGCTTAGGCA CTG	CGTCTTGTCGGTGTAT TTG	60.1	461	INTERGENIC				
CaPOPI_2766	Ca4	32886390	AC/ACC	AATCATCCCATGTTGCC ATT	CGAGATTTACACCAAG GGT	60.0	519	INTERGENIC				
CaPOPI_2767	Ca4	33050402	ATTTTTTTTTT/ATTTTTTTTTT	TTCCTCACACGCAAAAT GTC	AAAAGAATTTGGGTCT TTGC	59.7	531	DRR	Ca_24017	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_2768	Ca4	33054018	TAA/TAAA	GGAATGGCAAACTTCA TGC	TTTGCATTACGGATTGA TGA	60.5	520	INTERGENIC				
CaPOPI_2769	Ca4	33054232	TAAAAAAAA/TAAAAAAAAA	TCATCAATCCGTAATG CAAA	GCACATGGGTACCAGA CTT	59.0	445	INTERGENIC				
CaPOPI_2770	Ca4	33064079	ATTGTTGTTGTTGTTGTTG/ATTGT TGTGTTGTTGTTGTTGTTG	TCGGGCCACTATCTGGA TTA	GTGTGCCGTCAACAACA ATC	60.4	810	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2771	Ca4	33100738	GAAAAAAAAA/GAAAAAAAAAAA	TTGGGTTGTGAGGAATG GAT	TCATCTGTTAGGTACCC CGC	60.2	304	INTERGENIC				
CaPOPI_2772	Ca4	33145619	TAAAAAA/TAAAAAA	AAACCGTCGTTCCAGTT GTC	AGGCAACAAACATAGAA TCGC	60.0	550	INTERGENIC				
CaPOPI_2773	Ca4	33195041	T/TAGAATTCGGTGA	TTGTCCGTGAGAGACTG CAC	GAATCCTGGGCTGAAAT CAA	60.0	595	INTERGENIC				
CaPOPI_2774	Ca4	33296074	TAAAAAAAAA/TAAAAAAAAAAA	TGACCTCCCACTGCATA CAA	AAGAGACCGCATACGTG GAT	60.1	532	INTERGENIC				
CaPOPI_2775	Ca4	33308913	GAAAA/GAAA	TCATTTCCCTCGTTT TG	TTGGCCAAAACCTTTTG ATG	60.0	183	DRR	Ca_24021	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2776	Ca4	33314599	AC/A	ATGTCCATAACGCATGC AGA	CATCATGCCACTTTGGA TTG	60.1	661	INTERGENIC				
CaPOPI_2777	Ca4	33315743	CTT/CTTT	ACATGAGTCTTTGTTGC CCC	TGGCACGTGATTGTGTT GAT	60.0	477	INTERGENIC				
CaPOPI_2778	Ca4	33321015	AATATA/AATATATA	TATTGTTGCACCCCCAA TTT	ATGTCTGCCCATTTTCT TG	60.1	229	INTERGENIC				
CaPOPI_2779	Ca4	33327822	TAAAAAAAAA/TAAAAAAAAAAA	CGAAAATTCGAATGGGT AGC	GGTCAAGTGTGCGCGA AAT	59.5	516	INTERGENIC				
CaPOPI_2780	Ca4	33339958	T/TA	TGGTGACAACAAGTTT CCA	CCACATTTCTCATCCAC ACA	60.0	437	INTERGENIC				
CaPOPI_2781	Ca4	33346959	TT/TTAT	TTTTCGGTTTGTCAAG GC	GGAAAAATTGGGAAAC CCT	60.1	766	INTERGENIC				
CaPOPI_2782	Ca4	33397164	TTATATATATATATATA/TTATATATAT ATATATATATATA	ATAGGCTTGCACCTCC CCT	CCCCAACAAATGGAGC TAA	60.1	582	DRR	Ca_24022			Protein of unknown function DUF1950
CaPOPI_2783	Ca4	33397720	ATTTTTTTTTT/ATTTTTTTTTT	CTCCATTTTGTGGGGC TTA	GCCAACAAACAACCATG CTA	59.9	584	DRR	Ca_24022			Protein of unknown function DUF1950
CaPOPI_2784	Ca4	33431052	GAAAAAAAAA/GAAAAAAAAAAA	TTTATGCTCCGTTTGTG CTG	CACACCCACCTCTCCC TTT	59.9	435	INTERGENIC				
CaPOPI_2785	Ca4	33467450	CAAAAAAAAA/CAAAAAAAAAAAA	TGATGTAAAAATGATGAT GTGAAA	AATTTGAGTTGCAATTTG ATGA	57.1	558	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2786	Ca4	33467899	ATTTTT/ATTTTTTT	TCATATCATCAAATTGCA ACTCA	TGATGTTAAAAGCTACA GCAACAA	58.2	455	INTERGENIC				
CaPOPI_2787	Ca4	33615467	ATT/ATTT	GGTCCTTGTGAGTCCA ACG	CTCAAAAACCTGAGCAT GGC	60.5	646	INTERGENIC				
CaPOPI_2788	Ca4	33615658	AG/A	GGTCCTTGTGAGTCCA ACG	AATGGAATAGCGGAGTG TGC	60.5	898	INTERGENIC				
CaPOPI_2789	Ca4	33627666	TATTTAAATTTAAATTTAAATTTAA AT/TATTTAAATTTAAATTTAAAT	AGTGACATGACGGAAGT AGCA	TTGGTCCAGTGTGCAT GTT	58.4	432	INTERGENIC				
CaPOPI_2790	Ca4	33633372	GTTTTTTT/GTTTTTTT	ACGAGGAAACATATCGT CCG	ATGTCCACACATTGGGT GTC	60.0	726	INTERGENIC				
CaPOPI_2791	Ca4	33714267	T/TCTTAATC	GAACACGTTGTAGACC GGC	TGACAAAATGGGAGAA AGG	60.6	713	INTERGENIC				
CaPOPI_2792	Ca4	33714529	ATT/ATTGTT	CGTTGTTAGACCGGCTC TTG	TGGGCTGACATAATCAC CAA	60.8	940	INTERGENIC				
CaPOPI_2793	Ca4	33715942	TAAAAAAAAA/TAAAAAAAAAAAAA AA	TTGGGTACGTTGGTGTA GCA	ATTGACTGGGCACCATG ATT	60.0	634	INTERGENIC				
CaPOPI_2794	Ca4	33736905	ATTTTTTT/ATTTTTTTTT	GGCTTTTCAAAGTTCAT CGG	TTGAAGGATTGAATTC CCC	59.7	789	INTERGENIC				
CaPOPI_2795	Ca4	33738599	GAAAAAAAA/GAAAAAAAAAAAAA	ATTGTTGCGCACAAATT GAA	CACCACCAATCACAAG ACG	60.1	734	INTERGENIC				
CaPOPI_2796	Ca4	33743516	CAAAAA/CAAAAA	TGTAGCTGGTGTCACG AAG	AATGCAAGAATCCACCT TGG	59.9	435	INTERGENIC				
CaPOPI_2797	Ca4	33784625	GTAT/GTATAT	CCGGTCTCAATTTTCCT CAA	TGTACGCTAGATTTAC TTTTGGA	60.0	440	INTERGENIC				
CaPOPI_2798	Ca4	33795008	TTATATATATATATAT/TTATATATAT TAT	GTCGTGTCAATGCAACA ACC	TCGACTAAGGACATTGG GCT	60.0	514	INTERGENIC				
CaPOPI_2799	Ca4	33807474	TAAAAAA/TAAAAAA	GTCATTTGGCGGAACC TAA	TTGAGGTGGGATATGTT TGC	59.9	694	INTERGENIC				
CaPOPI_2800	Ca4	33813152	TAA/TA	AGAGAAGTTGCCGACA AAA	CTCCAATGCCCAACAA AGT	59.9	734	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2801	Ca4	33833847	TA/TAAC TGCA	GCGTCATCGTCCCTACA AAT	TCCAAC TCGCAAGGCTA TCT	60.0	375	INTERGENIC				
CaPOPI_2802	Ca4	33835234	TAAAAAA/TAAAAAAA	CCAATCAAATTGAGCAT ACCC	TGTGTTTGCTTTGCATG CTT	59.3	529	INTERGENIC				
CaPOPI_2803	Ca4	33857426	AAAAATTAAAT/AAAAATTAAATTAA AT	GTTTTGTGATGGGGAT GAC	CAAATTTGGCGTTGTTC CTT	60.0	611	INTERGENIC				
CaPOPI_2804	Ca4	33912297	ATATCT/AT	AGAATCCAAATCGAAGC CCT	ACCCGCTCTAAGTCCAA AGC	60.0	606	INTERGENIC				
CaPOPI_2805	Ca4	33921285	ATGCT/A	TGGGTGGTTGACACTTG AAA	CAGAGGAAAAATGGGTC AGA	60.0	560	INTRON	Ca_20365	O	GATA	Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2
CaPOPI_2806	Ca4	34026279	TAAAAAAAA/TAAAAAAAAA	AAACAACCGCCATCCAA CT	TTTCATGGACAACAAG CCA	60.4	213	DRR	Ca_20364			Transposase, PttA/En/Spm, plant
CaPOPI_2807	Ca4	34039084	TAAAAAAAA/TAAAAAAAA	TACCAAAGTGTCGCCAA CAA	AAAAAGGAAAGCCAGC CTC	60.1	742	INTERGENIC				
CaPOPI_2808	Ca4	34169705	CAATGA/CAATGATAATGA	TCAAAGTGGCTCACAAG TGC	TCGACTCAAGAAGGCAA GTG	60.0	781	INTERGENIC				
CaPOPI_2809	Ca4	34227066	A/AG	ACGGCAAAAACAGTGA AAT	TGAGGAAAATTGAGACC GGA	59.5	327	INTERGENIC				
CaPOPI_2810	Ca4	34240189	CC/CCTGATGC	AGCGACAGCTCTGATT TGT	GGGAGCTGCTTGATGAG AAG	60.0	168	DRR	Ca_20356	L		DNA mismatch repair protein MutS, C-terminal domain
CaPOPI_2811	Ca4	34246830	ATT/AT	CGTCTTCGTACAAAGC CTC	GATTGGGGACCATTCCA TTA	59.9	320	INTERGENIC				
CaPOPI_2812	Ca4	34254143	GTTTTTTTTT/GTTTTTTTTTTT	TTTTGCGACATTTGATC GTT	TGTTCTCGCACACCAAA AAG	59.2	454	INTERGENIC				
CaPOPI_2813	Ca4	34330740	TAAAAAAAA/TAAAAAAAAA	TGCACACATCTACCCCT GAA	GGCATGGCAACTTCACT TTT	60.1	502	INTERGENIC				
CaPOPI_2814	Ca4	34375164	ATTTTTT/ATTTTTT	CAAATCTTCTCAAATCT TGACCAT	CTATCGACCAAGCCACC ATT	59.9	768	INTERGENIC				
CaPOPI_2815	Ca4	34382417	GC/G	AAGGGGCTTTGAGGTAA GGA	TGGAAAATGGATGTTGA CGA	60.1	572	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2816	Ca4	34388082	CATATATATATATAT/CATATATATATATATATATAT	GTTGGTTCCTAGCACC GTA	CTGTCAATTGAGTTGCG ACG	60.0	484	INTERGENIC				
CaPOPI_2817	Ca4	34388181	GAAA/GAAAA	GTTGGTTCCTAGCACC GTA	CTGTCAATTGAGTTGCG ACG	60.0	484	INTERGENIC				
CaPOPI_2818	Ca4	34473954	CTTTTTTT/CTTTTTTTT	ACCCAAATCCAGTGTTCTGC	GGCCTTGTCGAATGATTGTT	60.0	839	INTERGENIC				
CaPOPI_2819	Ca4	34475378	GAAAAAAA/GAAAAAAA	CATTGTGGATGCAGTTT TGC	CGAAATAAGATGTCCAC CGC	60.1	535	INTERGENIC				
CaPOPI_2820	Ca4	34475759	GAAAA/GAAA	GCGGTGGACATCTTATT TCG	CGCATTGAAGCATAAAC CCT	60.5	446	INTERGENIC				
CaPOPI_2821	Ca4	34482261	GCCGCC/GCCGCCGTAAACGCC	ACGCCATCTGCCATATG TTT	TTTGGGGTGATGGAAAT GAT	60.4	497	INTRON	Ca_20350	R	G2-like	Domain of unknown function DUF676, hydrolase-like
CaPOPI_2822	Ca4	34518791	ATTTTTTT/ATTTTTT	CAGCTTCCCACCAAGT AAA	TCGATGTGAACAATAGG CCA	60.1	463	DRR	Ca_20349		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_2823	Ca4	34566424	ATT/AT	CCCTGAGACTCACGAAG AGG	AAAATCCAACAATCTCCC CC	60.0	612	INTERGENIC				
CaPOPI_2824	Ca4	34599013	AGGGG/AGGG	TGTGCATCGAAAAGGTG TGT	AGCCTACGGAGGACCAA AAT	60.2	568	INTERGENIC				
CaPOPI_2825	Ca4	35237197	TTTATTATTATTATTATTATTATT/TTATTATTATTATTATTATTATTATTATTATTATTA	TCACTGCTCACACCAACA	TTGAAATGGGGTTGAAG GAC	59.9	276	INTERGENIC				
CaPOPI_2826	Ca4	35295864	TAA/TAAA	CACGATGAATTAATAG CATCCA	ATTACATGGTTGTTGCG CAA	59.0	239	INTERGENIC				
CaPOPI_2827	Ca4	35319446	ATTTTTTTTT/ATTTTTTTTTT	GGTCAGTTCATCCTAGG GCA	TTTTTGTTGCCTAAGT GGG	60.1	462	INTERGENIC				
CaPOPI_2828	Ca4	35343662	TCCACAACC/TCCACAACCAACCAACC	CCACAACATGGTGCAAA CTC	AACCGGTTCAAGTTCTG TTG	60.0	679	INTRON	Ca_20018	Z	NAC	IQ motif, EF-hand binding site
CaPOPI_2829	Ca4	35369859	GATTAA/GATTAAATTAA	TTTAGTGCGCATGAATTTTACA	TTTCCACAAGCTAACAAA AATGA	59.7	494	INTERGENIC				
CaPOPI_2830	Ca4	35432013	TTAT/TTATAT	TGTTCAACATCCACGAA CAA	TGCCATACTCATGTCGG AAA	58.5	669	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2831	Ca4	35432836	TTATATATATATATATATAT/TTATATATATATATATATATAT	TTTCCGACATGAGTATGCA	TTTGGAAAGTAACACTGCACG	60.1	785	INTERGENIC				
CaPOPI_2832	Ca4	35457008	TTGC/T	AATTGCAGAAAAATGCGGTC	TTGTACCAGATATTGGCCG	60.1	776	INTERGENIC				
CaPOPI_2833	Ca4	35620689	TGA/TGAGA	ACAATCCCGACACAAAGTCA	GAAGCGAGAGGTAAGCGATG	59.0	499	INTERGENIC				
CaPOPI_2834	Ca4	35639160	ATT/ATTT	GGAAAAGATGGTATTTGCCG	CTTCCCTGCTGGCAACTTAG	59.4	339	INTERGENIC				
CaPOPI_2835	Ca4	35818039	AAATAATAATAATA/AAATAATAATA	GTTCATAACGAAGATGACAATAACA	TGCAGTCAAACTTTAAAGGAAG	57.4	728	INTERGENIC				
CaPOPI_2836	Ca4	35822348	TGG/TG	GATCAAATCGAGGACCGAAA	CGAACAAAACGATGGGAGT	60.0	695	INTERGENIC				
CaPOPI_2837	Ca4	35999977	ATTTTTTTTT/ATTTTTTTTTT	GCTGGCAGCACAAATAACA	TCGAACCAATGACCTCAAA	59.9	439	INTERGENIC				
CaPOPI_2838	Ca4	36079126	TTGTG/TTGTGTG	ATTTTGATGCTCACGGTTCC	CGGAGATGATGTTTCAGGTT	59.9	595	INTERGENIC				
CaPOPI_2839	Ca4	36094744	TAAAAAAAAA/TAAAAAAAAA	CCTACCATTGCCTGACCTGT	TTCCGAGTTGTTTGAGAGGA	60.0	427	INTERGENIC				
CaPOPI_2840	Ca4	36245892	TTATATATATATATATATATAT/TTATATATATATATATATAT	TACATGCAAGCGAAATGGAA	AGGCATGGTGTGGAGTCAT	60.2	287	DRR	Ca_14846	O		Zinc finger, RING-type
CaPOPI_2841	Ca4	36256375	ATTTTTTTTT/ATTTTTTTTTT	GATCATCGAGTTTCCCGTGT	AGTTCTGAGGGAGGCTCACAA	59.9	350	INTERGENIC				
CaPOPI_2842	Ca4	36335313	ATTTTT/ATTTTTT	TTGCGACAAGATCAAGCAAC	TCAACACCAACACAAGGGA	60.0	519	INTERGENIC				
CaPOPI_2843	Ca4	36336918	TAAA/TATAAAA	ACAACAAGGGTGACCTCAC	TGCTTGCTATTCTGCGTCAA	59.9	736	INTERGENIC				
CaPOPI_2844	Ca4	36337139	GC/G	TGCAATGTCAATATGAACCAAA	CCACAACCACTCATCACGAC	58.9	479	INTERGENIC				
CaPOPI_2845	Ca4	36337338	TT/TTATTAT	TGACGCAGAATAGACAAGCAA	CCACAACCACTCATCACGAC	59.6	341	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2846	Ca4	36472761	TAAAAAAAA/TAAAAAAAAA	CGTAGGACAGAAACCGTGGTA	TATGTAGCCCGTGTCAA GCA	60.0	679	INTERGENIC				
CaPOPI_2847	Ca4	36529935	TTATATATATATATATATATATATATA TA/TTATATATATATATATATATATATA TA	TGGTGTAAATTGATTTC TCCCT	TCTGAAAAACTTGAAC CACAA	58.9	523	INTERGENIC				
CaPOPI_2848	Ca4	36593028	TAAAAAAAAA/TAAAAAAAAA	CGCGGGGCATATTCTAG TTA	TGATTTGGCATTGTGTT GC	60.1	527	INTERGENIC				
CaPOPI_2849	Ca4	36690853	CTTTT/CTTT	TTGACAAGCGCTGTGAA ATC	CAATGTGTATTCAACGA CCGA	60.0	538	INTERGENIC				
CaPOPI_2850	Ca4	36952818	TT/TTGAAC	GGGTTTCATGTTTGAAGG GTG	ATGGGCCCTCTTTTGT TTT	60.2	846	INTRON	Ca_14797	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2851	Ca4	36953596	AATATATATAT/AATATATATATAT	AAAAGAGGGCCCATGAG ATT	TGTGCATTGGGAACAAC ACT	59.9	693	INTRON	Ca_14797	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2852	Ca4	36968194	TAAAAAAAA/TAAAAAAAAA	GGCGAAAGTACCCAAAC AAA	GACTTCTGCAAAGGACC TCG	60.0	426	INTERGENIC				
CaPOPI_2853	Ca4	36968275	G/GTTAATAC	GGCGAAAGTACCCAAAC AAA	GACTTCTGCAAAGGACC TCG	60.0	426	INTERGENIC				
CaPOPI_2854	Ca4	36969837	CTTTTTTTTT/CTTTTTTTTT	AGGTCATGCCATCAAAG ACA	GAGCTGTGGAGAAGAAA AGCA	59.1	145	INTERGENIC				
CaPOPI_2855	Ca4	36972358	CTTT/CTT	ACAACCAACAAATGCG ACA	AGCCTTGAGCGACCACT TTA	60.0	484	INTERGENIC				
CaPOPI_2856	Ca4	36972412	GTT/GTTT	ACAACCAACAAATGCG ACA	TTGAAACATTCTCAGCCT TGTT	60.0	564	INTERGENIC				
CaPOPI_2857	Ca4	37034691	ATTTT/ATTTT	CTCCATTCTTTCCACTC CA	AGGGAAAACAAGGGTTT TGG	60.0	522	INTERGENIC				
CaPOPI_2858	Ca4	37035676	GTAATAATAATAATA/GTAATAATAATA ATAATAA	TCAAACCAATGAAAGG CTC	TCCCTTTACCTTGCCTC ATT	60.1	640	INTERGENIC				
CaPOPI_2859	Ca4	37035741	TCC/TC	CCCAATGAAAGGCTCAC AAT	TCCCTTTACCTTGCCTC ATT	59.9	635	INTERGENIC				
CaPOPI_2860	Ca4	37038560	TGAGA/TGAGAGA	TGGTTTATAACCCGCT TATATTCA	AGGATTCAACCACAAAG GACA	59.0	242	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2861	Ca4	37039540	TAAAAAAAAA/TAAAAAAAAA	TTTATTGACGAGCATCGTTCC	TGGCAAGTGCAACCAATA	60.1	386	INTERGENIC				
CaPOPI_2862	Ca4	37044142	TAAAAA/TAAAAA	TGATTGTTTTGATCCCTCA	TCACGAAATTAGCCCTCAA	58.9	328	INTERGENIC				
CaPOPI_2863	Ca4	37047512	CAAA/CA	GAAGTGGGAAATGGGTTTGA	ATGATTGTGCCTCGTGAACA	59.8	662	INTERGENIC				
CaPOPI_2864	Ca4	37047776	GC/GCC	ATACTCTGCACCACACACGG	ATGATTGTGCCTCGTGAACA	59.6	241	INTERGENIC				
CaPOPI_2865	Ca4	37055713	A/AT	GCCGGACAGTGATTGTGTTT	CCATATGCCACCATTTCTT	59.9	552	INTERGENIC				
CaPOPI_2866	Ca4	37057959	TA/T	TTTGTGCTCCATACACACATGA	CACCGTCTTCAAAGAATTCCA	60.0	771	INTERGENIC				
CaPOPI_2867	Ca4	37099831	TAAAAAA/TAAAAA	TGAATAATTCGCGTACGGCT	TGTGAGGAGCTCTTTGTGGA	60.6	589	INTERGENIC				
CaPOPI_2868	Ca4	37117919	AT/A	TACGGAAATCGGCTGGATAG	GCACGATAAATGCAACCTT	60.1	496	INTERGENIC				
CaPOPI_2869	Ca4	37118197	ATTTTTTT/ATTTTTTT	AAGGGTTGCATTATATCGTGC	CCAGCTCGTTTGTTTGAAGA	60.0	237	INTERGENIC				
CaPOPI_2870	Ca4	37128543	TAAAAA/TAAAA	TGCGACTTTTGAGATTGAA	TGCATCCATCGTCAAATACAA	59.4	462	INTERGENIC				
CaPOPI_2871	Ca4	37130048	ATTTTTTTTT/ATTTTTTTTTTT	TTGCAGAAGGTTCCCAATC	TGTTGGCCATCTTTTAGCTTT	60.1	841	INTERGENIC				
CaPOPI_2872	Ca4	37131217	TC/T	TTGTGACCAAAGGTTGGAGG	AATTTGCGAGCATTACCTGC	60.9	710	INTERGENIC				
CaPOPI_2873	Ca4	37311820	GATATATATATATATATATATA/GATATATATATATATATATATA	CGCTGTAAAATGCATGTGCT	TTGGGTGAACCATTAGGCAT	59.9	528	INTERGENIC				
CaPOPI_2874	Ca4	37443931	CT/CTAT	CCGCATTTTCTTCATTAGGG	ACGTTAAGGCATGAGTTGGG	59.5	364	INTERGENIC				
CaPOPI_2875	Ca4	37519504	CTATTTATTTATTTATTTATTT/CTATTTATTTATTT	GAAAAAGGAGTTGCCACCAA	TGGGGATACGTAGGAGCAAG	60.1	306	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2891	Ca4	40508840	GAAAAAAAA/GAAAAAAAAA	GGGGAAAAAGAAAGGA GGA	GTGGCTGCAAAAGCTAA AGG	59.5	294	DRR	Ca_14874			IQ motif, EF-hand binding site
CaPOPI_2892	Ca4	40514871	AATA/AA	GGAGAACCAGCTTCCTC CTT	CGCTCTTGCTTCCTTC ACT	59.8	278	INTERGENIC				
CaPOPI_2893	Ca4	40521264	TTACTACTA/TTACTA	AGATGCGACACAATTCC ACA	CATTAATAATTTCAAAGAT TTTGCG	60.1	162	INTERGENIC				
CaPOPI_2894	Ca4	40521734	ATTTTTTTTT/ATTTTTTTTTT	TCATCGGGACAACCTTG TATG	CGGCTCATCTCAATCCT TGT	58.5	655	INTERGENIC				
CaPOPI_2895	Ca4	40522888	AAATATATATA/AAATATATATTTTA GAATATATATA	GATGGGTTGGTTTGATT TGG	CGACAATTTTGGTCTCT CCA	60.0	946	INTERGENIC				
CaPOPI_2896	Ca4	40528670	GTTTTTTTT/GTTTTTTTT	AAATGCAACAGGAAGAT GCC	TGGACTTGAAGAGAAA CGG	60.1	558	INTERGENIC				
CaPOPI_2897	Ca4	40529406	CTTTTTTTTT/CTTTTTTTTTT	CCGTTTCTCTCCAAGT CCA	CGCTAAGCACCAGTTTC CTC	60.2	608	INTERGENIC				
CaPOPI_2898	Ca4	40560588	TAAAAA/TAAAAAA	TCATTCTCCGATCTTC CAC	TTTCTGTGGACTCACGC ATC	60.0	636	INTERGENIC				
CaPOPI_2899	Ca4	40561270	TTTCAA/T	ACTGATGCGTGAGTCCA CAG	GGATGTTGGCTCCCAAG TTA	59.9	785	INTERGENIC				
CaPOPI_2900	Ca4	40573928	CAAAA/CAA	TTCGTGGAATATCACAA AAGTTC	TGGACAAAACTCATCT GCATT	58.2	895	INTERGENIC				
CaPOPI_2901	Ca4	40574863	A/AC	TGCAGATGAGTTTTGT CCA	AAAATTAAGACAAAAGG AAGTTCAACA	57.8	658	INTERGENIC				
CaPOPI_2902	Ca4	40575649	ATTTTT/ATTTTT	TTTCTCATTTTCATGACT CCTATCA	TCACCAGTGACACGTT GAT	59.2	375	INTERGENIC				
CaPOPI_2903	Ca4	40593121	CAAGT/CAAGTAAGT	CATTCCCACCATCCTTC ACT	GGCCTATCGAACCACAC AGT	59.8	932	INTRON	Ca_14867	R	BES1	Zinc finger, RING-type
CaPOPI_2904	Ca4	40593400	GTT/GTTTT	AAGGATTGCTTGCTGA TGC	GGCCTATCGAACCACAC AGT	60.4	276	INTRON	Ca_14867	R	BES1	Zinc finger, RING-type
CaPOPI_2905	Ca4	40615032	TAA/TA	GAGCCCAACGATGTTCA AAT	TGAACCCCAACGACATT ATT	59.9	793	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2906	Ca4	40620475	A/AT	TATGTGAAATTGCCACG GAA	ACCTCATCGAGCCATTG ATT	59.9	509	INTERGENIC				
CaPOPI_2907	Ca4	40622124	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	ACATACACACGTCACGG GAA	TTTGCAAATGAGATTTC TAAAGA	59.9	391	INTERGENIC				
CaPOPI_2908	Ca4	40626965	TAA/TAAA	GACGTGCTCACTGAAAG GGT	CATCGAGGCCATTATG ATT	60.3	687	INTERGENIC				
CaPOPI_2909	Ca4	40649020	ATTTTT/ATTTTTTTT	TGTGATTATCCGGTACC ACAAC	TGTATTGAGACCTCGC AGA	59.6	207	INTERGENIC				
CaPOPI_2910	Ca4	40700886	AGAC/A	TCTTGATGTAACGTTTT TTTCAGA	TGAATATTTGAGTTACGA ATTTGATGA	60.1	478	INTERGENIC				
CaPOPI_2911	Ca4	40702737	ACTCT/ACT	CCCCCATCATAAAATTGT GC	AAGATTAGTGGGCGACC CTT	60.0	392	INTERGENIC				
CaPOPI_2912	Ca4	40704105	ATTTTT/ATTTTT	GGATCTCCACTGCCAGG TTA	TTTCGTTTCCATTCTAC GC	60.1	648	INTERGENIC				
CaPOPI_2913	Ca4	40719941	CTTTTTTTTT/CTTTTTTTTT	TCCTCCCTTTTGTTTTGT GC	TCGTCATCACCCACACT CAT	60.1	410	INTRON	Ca_23911	BK	FAR1	PWWP
CaPOPI_2914	Ca4	40728044	TATTTGTAATT/TATTTGTAATTTGTAAT T	AGCATACATTGGCACCA CAA	CATGCATTTGATGGTAA CCG	60.0	502	INTERGENIC				
CaPOPI_2915	Ca4	40729597	T/TG	TTGTGAAATTGAAAAGG TTCCA	CAACCATGTGTGAGGTC CAT	59.5	817	INTERGENIC				
CaPOPI_2916	Ca4	40743968	A/AAAC	TGTTGAAAAACACCGCA AGA	GCAATGAAGTGTGTGCC AAT	60.3	575	INTERGENIC				
CaPOPI_2917	Ca4	40753856	GTATATATATATA/GTATATATA	TTACGATATTGCCGCAA CTG	GCCCTTTCTTTCAGGCT TCT	59.7	444	INTRON	Ca_23905	J		Diphthamide synthesis, DPH1/DHP2
CaPOPI_2918	Ca4	40761334	A/ATATAT	GAACTTTGTTATTGCATT CGTTTT	TGGATACACCGTCCAAA GTG	58.7	714	INTERGENIC				
CaPOPI_2919	Ca4	40767434	GTTTT/GTTTTT	CCAAGAAGTCCAGTTT GGT	AGGTACGTCCAGGCATC AAG	60.0	644	INTRON	Ca_23904	Q		Pyridine nucleotide-disulphide oxidoreductase, class-II
CaPOPI_2920	Ca4	40773929	TTAT/TTATAT	GTGTGCACCATAGGGAA GGT	ATCCTTGACATCCCAA AAA	59.9	405	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_2921	Ca4	40788340	ATTTTTTTTT/ATTTTTTTT	GCATCGGAGCATGAATGTA	TTCGCACACGATGAAGACTAA	59.7	167	INTERGENIC				
CaPOPI_2922	Ca4	40797521	ATT/AT	CAAGGTCCCCAACATCCTACT	ATGGACCATCGATTCTGGAG	59.8	610	INTERGENIC				
CaPOPI_2923	Ca4	40799151	TTAGCATA/TTA	CCAGCAATCTAATGAACGCA	ATGTCACCAATGGGGTTTGT	59.8	323	DRR	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2924	Ca4	40799742	TCCCCC/TCCCCCC	ACAAACCCCATTTGGTGACAT	TGGCTTGTAAGGCTGTGTTG	60.0	740	DRR	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2925	Ca4	40801294	AAAA/AAAATACCAGTAAA	AGCTTGCTCTGAGCTCTTG	TTTATGGCATGGGACCAAT	60.0	736	INTRON	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2926	Ca4	40802030	A/AC	CATGAAGCCAAGAAGCAACA	TTGACACCTGTACACATGCTGC	60.0	518	INTRON	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2927	Ca4	40809750	A/AC	TGCAAGAACAATCTCTCCC	GCAGCTTTTGGCAGTTCTCT	60.1	278	INTRON	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2928	Ca4	40810384	G/GAAAAAA	AAAAACGGCAGTAAAGCCA	GGGACGAGGTACATGCAGAT	59.8	298	INTRON	Ca_23902	R		DNA-directed DNA polymerase, family A, palm domain
CaPOPI_2929	Ca4	40836419	TAAAAAAA/TAAAAAAA	GTGTCGGTCACGACATTCTCAG	AGATTGAAAAGTTGCACCCG	60.2	714	INTERGENIC				
CaPOPI_2930	Ca4	40837444	TAAAAAAA/TAAAAAAA	GGAAGCAGATGGAAGGAA	TCAACTTTGAGGACCCAACA	59.2	494	INTERGENIC				
CaPOPI_2931	Ca4	40842793	TC/T	CTGGATTGAGTTGAGGCCTAT	TGGACCAACCAAGCACATA	60.1	568	INTERGENIC				
CaPOPI_2932	Ca4	40844159	TAAAAA/TAAAAAAA	AACATTAATGCAACAGCCA	GACTTCCGTCCCTTACAGAGAA	60.0	199	INTERGENIC				
CaPOPI_2933	Ca4	40887107	GAAAAAAA/GAAAAAAA	TGAATCCAATCCATCCAACA	ACTATCGACCAACTGCCCAC	59.7	705	INTERGENIC				
CaPOPI_2934	Ca4	40891579	AATATATA/AATA	GCACAAAAGCAGTGAGCCA	CCCGAACCTCTCCACAATAA	60.1	869	INTRON	Ca_11020	R	G2-like	C2 calcium-dependent membrane targeting
CaPOPI_2935	Ca4	40891712	TCC/TC	ATCGAATCCTCGTTGGATG	CCCGAACCTCTCCACAATAA	59.9	725	INTRON	Ca_11020	R	G2-like	C2 calcium-dependent membrane targeting

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2936	Ca4	40901246	AAA/AAATAA	GGGTATATTAATTTAACA ACTCCCTCC	TTAGAGGTCGCATCTT CGT	59.7	462	INTERGENIC				
CaPOPI_2937	Ca4	40907158	TATACAT/TATACATAATACAT	TGTCGTTGAAATCAAG CAAT	ATCGTTTGGGTGAAGAA TCG	58.3	334	INTERGENIC				
CaPOPI_2938	Ca4	40929080	T/TC	ATGGTGGGGTAAGCAA TCT	AAGAAGCGCGTATTGGT GTT	60.6	813	INTRON	Ca_11015		bZIP	Basic-leucine zipper (bZIP) transcription factor
CaPOPI_2939	Ca4	40931865	TCCCC/TCCC	TGCTTGGAAAACAAGCA ATTT	AACTCGTGGGAACGCAC TAC	59.8	779	INTRON	Ca_11015		bZIP	Basic-leucine zipper (bZIP) transcription factor
CaPOPI_2940	Ca4	40937505	GTTTTTTTTT/GTTTTTTTTT	TAATCCGATGGCAACAT GAA	CGGTAGGAAATGATGAA ACCA	59.9	615	INTERGENIC				
CaPOPI_2941	Ca4	40949429	TT/TTAT	CCATGTGCACCATAAAT TGC	CAGAATGTCTTTTCGGA ATGG	59.8	612	INTRON	Ca_11013			Protein of unknown function DUF599
CaPOPI_2942	Ca4	40967580	TAAAAAAAAA/TAAAAAAAAA	AATGAAAACTTTGTGC GGC	GTTTGAATCGGGTAAC GAA	60.1	748	INTERGENIC				
CaPOPI_2943	Ca4	40968955	TC/TCC	CACTGGAATGATTGCCA AAA	TTCTACCCAAGATCGGA TGG	59.5	398	INTERGENIC				
CaPOPI_2944	Ca4	40996595	GAAAAA/GAAAA	CGGTGTTAAAAATTGGG GTG	AAACGTGGAGGTGATT TGC	60.1	445	DRR	Ca_11010			Glycoside hydrolase, family 28
CaPOPI_2945	Ca4	40997097	C/CT	GCAAAATCACCTCCACG TTT	AACGGTCGTCCTCATTC ATC	60.0	762	DRR	Ca_11010			Glycoside hydrolase, family 28
CaPOPI_2946	Ca4	41016384	ATTTTTTT/ATTTTTTTT	AAACACGGGGCAACATA AAG	TGTTGGTGGTGAACGAG GTA	59.9	631	INTERGENIC				
CaPOPI_2947	Ca4	41027713	AATATATATATATATATATATATAT AT/AATATATATATATATATATATAT ATATATATAT	TGAATCCAAAATTTGAA CCA	TTTGATCGCAAGGGTTT AGG	60.2	637	INTERGENIC				
CaPOPI_2948	Ca4	41029836	AATATATATATATATA/AATATATATAT ATATA	TTTCTCTCCATCGACCC ATC	GAACCTTTGGGAAATCA GCA	60.0	760	INTERGENIC				
CaPOPI_2949	Ca4	41159362	ATTTTTTTTTT/ATTTTTTTTTT	ATGCTTGGACCAACATT CTC	CGTGTGAAACCTTTGCT GAA	59.9	891	INTERGENIC				
CaPOPI_2950	Ca4	41272417	GATTATTATTATTATTATTATTATTA TT/GATTATTATTATTATTATTATTAT T	GGTTCACATGGAACCTC ACA	AGCCTTTTGCTTCCTTC CTC	60.8	737	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2951	Ca4	41713312	TAAAAA/TAAAAA	CCATCAAAACATGCATC CAC	CATGACAACACAACCA CCA	59.8	748	INTERGENIC				
CaPOPI_2952	Ca4	42078586	AAGGCATGAAA/AAGGCATGAAACACA GGCATGAAA	TCTTTTGAACACTCCCC CTG	CCAAAGGAAACCACGAC AAT	60.1	810	INTERGENIC				
CaPOPI_2953	Ca4	42083362	CA/CAA	TTTCAAAGGTTTGATT TGA	AAAATTAACCGTATGGC CGA	59.2	327	INTERGENIC				
CaPOPI_2954	Ca4	42120439	TAAAAAAAA/TAAAAAAAA	CACAAGCATTGGAGTCC CTT	AACCTCGTGGGTTGGATT TTG	60.1	495	INTRON	Ca_10910		C2H2	Glycoside hydrolase, family 28
CaPOPI_2955	Ca4	42120489	TAAAA/TAAA	CACAAGCATTGGAGTCC CTT	AACCTCGTGGGTTGGATT TTG	60.1	495	INTRON	Ca_10910		C2H2	Glycoside hydrolase, family 28
CaPOPI_2956	Ca4	42374619	ATTTTTTT/ATTTTTTT	TTTGATGTGTTACGGC ACT	CGGCATGCATGATTATT TTG	60.2	331	INTERGENIC				
CaPOPI_2957	Ca4	42407053	GTTT/GTTTT	GCATAAGGATCGGGAA ACT	AATGATCGTCTTCGGAT TGG	60.3	392	INTERGENIC				
CaPOPI_2958	Ca4	42546801	CAAAA/CAAAA	GGTTGGTCAATTAATT CCGC	CTAATATCATGCCCTT CG	59.6	686	INTERGENIC				
CaPOPI_2959	Ca4	42548370	ATTTTTTT/ATTTTTTTT	CGTGCCCTTGTCGTCTC TTT	AGAGGCCCAATATCCTT GCT	60.4	528	INTERGENIC				
CaPOPI_2960	Ca4	42561342	AATAGAGATAGAGATAGAGATAGAGA/ ATAGAGATAGAGATAGAGA	CGGCAAAACAGAGACAA TCA	TCTCACGGTTGTGAGGA CTG	59.8	310	INTERGENIC				
CaPOPI_2961	Ca4	42633986	TATAATAATAATAATAATAATAATAA TAATA/TATAATAATAATAATAATAA TAATAATAATAATAATA	TTGCTTTAGATGAATCAA ATCCC	CGACAGGCTTAGGTTAG ACCA	59.5	362	INTERGENIC				
CaPOPI_2962	Ca4	42693293	TC/TCC	AAATGCTCGAACGAAA TGC	TCGAAGTTGGATGCTTT TGA	60.2	503	INTERGENIC				
CaPOPI_2963	Ca4	42945720	CATATATATATAT/CATATATATATATAT	TGTCAATGTTACTTTATT TCAAAACTC	TTGGGTTATCTTCATTG CAAAA	57.2	739	INTERGENIC				
CaPOPI_2964	Ca4	43005724	CTTTTTTTTT/CTTTTTTTTTT	TTGTAGTTGTATTCAATG ACGAAGA	CAGAATTAATTTATTTGA CAACTCCA	58.0	628	INTERGENIC				
CaPOPI_2965	Ca4	43222555	TTATATATATATATATATATAT/TTATA TATATATATATATAT	AAAGATTAAAGGGCAA AAAGTG	CTGGCAGCTGGGAAAGA TT	58.0	908	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2966	Ca4	43278176	GTTTTTTTT/GTTTTTTTT	ACTGCGTCTCCATGGGT AAC	TTGGAATGGGCTCTTT TTG	60.0	592	DRR	Ca_23681			
CaPOPI_2967	Ca4	43291624	TAA/TAAAA	GAGCGATTACCGGTGTT GTT	GCCTTCAAATGTAACCC CCT	60.0	946	INTERGENIC				
CaPOPI_2968	Ca4	43301091	ATAA/ATAATGTAA	ACCATAAAGGGAACAG GGG	TCATGGTCTGCAATCTC GTC	60.0	714	INTERGENIC				
CaPOPI_2969	Ca4	43301725	ATTTT/ATTT	GACGAGATTGCAGACCA TGA	TGGGCCCTTAGTCTCTT TTT	59.8	753	INTERGENIC				
CaPOPI_2970	Ca4	43362642	TG/T	AGAATCACACTGCCCCA AAC	TTGCAAGGGAATTTTGT TCA	60.0	590	DRR	Ca_23687		AP2	
CaPOPI_2971	Ca4	44040432	TAAAAAA/TAAAAAAA	GATTGCGGAATTAGCCT TCTT	TGGTTAAGTGAAGCGCA AAC	59.7	774	INTERGENIC				
CaPOPI_2972	Ca4	44098644	ATTTTTT/ATTTTTTTT	TCACCTTCATCCATCGT CAA	TGTGGTGTGCAAGATGA CTG	60.0	408	INTERGENIC				
CaPOPI_2973	Ca4	44134460	AAC/AACACAC	TACCAGATTGCCCACT TTC	GCCAAAACGGATGAAGT TGT	59.9	554	INTERGENIC				
CaPOPI_2974	Ca4	44428431	CATATATATATATATATAT/CATATAT ATATATATATAT	TGTTGCGGAATGTTAG TTCA	TTCATCCATGCAATATTC AAAAA	59.2	699	INTERGENIC				
CaPOPI_2975	Ca4	44498939	CTTT/CTT	ACCTTGGGCCTTAATTG AAA	CGGAACATCACTGTTCA CAAA	58.6	410	INTERGENIC				
CaPOPI_2976	Ca4	44507569	CTTTT/CTTT	AGCGGTTGTTCAAAATG ACC	AAAGCAAGTCCGACCAA AAA	60.0	421	INTERGENIC				
CaPOPI_2977	Ca4	44507737	TTTCTTCTT/TTTCTTCTTCTT	AGCGGTTGTTCAAAATG ACC	AAAGCAAGTCCGACCAA AAA	60.0	421	INTERGENIC				
CaPOPI_2978	Ca4	44511339	ATTTT/ATTTTT	GATGCAGGTCATGAAAC CAA	GTCCTCAACGCTTCAAG AGG	59.5	494	INTERGENIC				
CaPOPI_2979	Ca4	44522624	GAAAAA/GAAAAAA	GAAGTGCTTGCTCCGA TTC	CCCTAGCAAGTGCTAAC CCA	60.0	675	DRR	Ca_09124		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_2980	Ca4	44523921	ATTTTTTTTTT/ATTTTTTTTTTTT	GCAATGTGCTCACTTTT GTCT	AACGAAGGAGGAGGGA AGAA	59.4	651	DRR	Ca_09124		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2981	Ca4	44525230	TAAAAAAAAAAAAA/TAAAAAAAAA	ATGACGTTGGTGATTGGACA	GCGCTAGCAAAATAGCCAC	59.8	884	INTERGENIC				
CaPOPI_2982	Ca4	44526873	ACTCCAAA/ACTCCAAATGCTCCTCCAA A	TTCCATTCTTTTGCCAA GG	TTGGCTCAAGTGGGATA AGC	60.0	397	INTERGENIC				
CaPOPI_2983	Ca4	44533305	TAAAAAAAA/TAAAAAAA	CAAAATGCCGTCACAGA ATG	CCTTGGTTTCGATGCCT AAA	60.1	368	DRR	Ca_09125	L		Smr protein/MutS2 C-terminal
CaPOPI_2984	Ca4	44559914	TTATATATATAT/TTATATATATATAT	GCGGGGCATAAACTGAT AGA	CATTTCATATCACCAAA TCACG	60.1	465	INTERGENIC				
CaPOPI_2985	Ca4	44694709	TAGAGAG/TAGAG	GATTCGATCATCTGGG AAA	AGGCTTCTGGTGCTGT CTT	59.8	539	INTERGENIC				
CaPOPI_2986	Ca4	44773439	ATTTTT/ATTTTTTTT	TTGTTTCACTTTTCCAT TCCA	TAGGGTTCTTGATCCAT CGC	59.5	596	INTERGENIC				
CaPOPI_2987	Ca4	44886483	TTCT/TT	TAATGGAGGGCAATTC GAG	AAAACACCCAACCCCT AAT	60.0	349	INTERGENIC				
CaPOPI_2988	Ca4	44902733	AAGAGAGAGAGAGAGAG/AAGAGAGAG AGAGAGAGAGAG	TGTGAAGCAACAAGGAA CAGA	TCGATTCCCACATGACA CTG	59.5	133	DRR	Ca_09152		C2H2	Protein of unknown function DUF3511
CaPOPI_2989	Ca4	44953374	TACACACACA/TACACA	TCCCTCCATCACCAAA CTC	ATGTGCAGTGACCAGAG CAG	59.9	349	INTRON	Ca_09159	G		Glycoside hydrolase, family 32
CaPOPI_2990	Ca4	44965984	TTCAACTT/TTCAACTTAATTTCTCAACT T	ATCTTTCCCTCCACAC ACA	TGGTCGCATTGCATAT AAA	60.4	601	INTERGENIC				
CaPOPI_2991	Ca4	44968120	ATTCTTCT/ATATTACTTCTTCTTCT TCT	ATTCTCCCAATCCACCAT CA	GCATGTTTAAGTGGGGC CTA	60.1	184	CDS (large-effect mutations)	Ca_09160	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2992	Ca4	44970459	CAAA/CA	CATTGCACGAGCACAAC TG	TGGAACGTAATCCTCC ATT	60.0	661	DRR	Ca_09160	R	C2H2	Zinc finger, C2H2-type
CaPOPI_2993	Ca4	44987442	TG/T	TCATGAAAACGTTTGGT TAATTG	AAAAGGGATACTGAATT TCATCCA	58.9	373	INTERGENIC				
CaPOPI_2994	Ca4	44987779	GA/GAATA	ACTTTGGAACAAAAGGA GGAA	TGGTCAAGATGTGTTGA CTTTG	57.8	570	INTERGENIC				
CaPOPI_2995	Ca4	44999560	GTCTCTC/GTCTC	TTCATTTTCCACCCCTA CA	TCCCTACTCAAAGGGGT CAA	60.2	630	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_2996	Ca4	45005102	A/AAT	CTCCGTTCAAGCCTCTT GTC	GAAAGTGTGAGCAACA CGA	60.0	225	INTERGENIC				
CaPOPI_2997	Ca4	45068051	CAA/CAAA	CGTGGACTTCCCAGCTA CAT	ACAATTTACTCCCTCCG CCT	60.0	584	DRR	Ca_09168	T	WRKY	Disease resistance protein
CaPOPI_2998	Ca4	45076892	CG/CGG	GGTCCAACATTCTCCT TGA	TCCACAAATAACAGTTT TCCC	59.9	606	INTERGENIC				
CaPOPI_2999	Ca4	45350262	TTA/TTATA	AGAATCGTTTTGTGGG ATCA	GTCCTTGGTAGCGAGTT GGA	59.4	778	INTERGENIC				
CaPOPI_3000	Ca4	45366808	TT/TTAT	ACACCCCAATCCAAATT GA	ATGCTCAAATGGGTAGC AGG	60.0	771	INTRON	Ca_09200	K	MYB	SANT domain, DNA binding
CaPOPI_3001	Ca4	45369151	CTTTTT/CTTTTT	TTGCATTCAATGTCTGC ATTT	GGGCAGTCACCTCCACT AAA	59.2	575	INTERGENIC				
CaPOPI_3002	Ca4	45380400	ACTACG/A	TTGCCGTTAATCTTGG AGC	GTGGAGAAAACAACAAC GGG	60.2	774	INTERGENIC				
CaPOPI_3003	Ca4	45397379	TA/TAA	CACGTGAGTGTGACATG GTG	CAATGGCAAAATATCC CAAA	59.6	626	INTERGENIC				
CaPOPI_3004	Ca4	45399331	ATTTTTTTTTTTTT/ATTTTTTTTTT	ACCACTTCACCACAAGA GGG	ATTCCGCTTGCTGTCA AAC	60.0	445	INTERGENIC				
CaPOPI_3005	Ca4	45399782	AG/A	GTTTGACAGCAAAGCGG AAT	ACAGCTTGCAACTGATG TGG	60.3	334	INTERGENIC				
CaPOPI_3006	Ca4	45505990	AATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT A/AATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATT	GAATCACGCAGCATTCA AAA	CGGAGATTGCAAGTAAA AGAGTC	59.8	402	INTERGENIC				
CaPOPI_3007	Ca4	45567618	TTATATATATATATATAT/TTATATATA TATATATAT	TCACAAATGGCAGTTTT GTCTT	CCAATCCTAGCTTCTGA AAATG	59.7	635	INTERGENIC				
CaPOPI_3008	Ca4	45626888	ATTT/ATTTT	TATCAGCAGCACCAAT GGA	GCCTGATGTTTGTGAGG GTT	60.2	286	INTRON	Ca_09219	Z	MYB_related	Kinesin, motor domain
CaPOPI_3009	Ca4	45949230	AATTATTATTATTATTATTATTATTATTA TTATTATGATTATTATTATTAT/AATTATT ATTATTATTATTATTATTATTATTATTAT TATTATTATTATGATTATTATTATTAT	TCGAAAGAACCTCGACT CGT	TCAATATGAGGTGCGTT CCC	60.0	508	INTERGENIC				
CaPOPI_3010	Ca4	45959235	TTTATTATTATTATTATTATTAT/TTT ATTATTATTATTATTATTATTAT	GGCCTATGGCCTAGCCT ACT	ACGGCCTACCATAGGCT TTT	59.7	555	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3011	Ca4	46001807	GATAATAATAATAATAATAATAATAA TAATAATAATAATA/GATAATAATAATAA TAATAATAATAATAATAATAATAATA	TTGCTCCTACGTATCCC CAG	CTCAATCGTGGGTGACC TTT	60.1	385	INTERGENIC				
CaPOPI_3012	Ca4	46003281	TTTATTATTATTATTATTATTATTAT TATTATT/TTTATTATTATTATTATTATTA TTATTATTATTATTATT	ATTCTCTCCCCCTGGTG TCT	TGTTTGGCCTAAAATTG GGT	59.9	724	INTERGENIC				
CaPOPI_3013	Ca4	46004838	TAAAAAA/TAAAAAAA	TGATTTCATGAGAGGA TTTTGTT	GCTCGATTGATGTTAAG GGC	59.0	425	INTERGENIC				
CaPOPI_3014	Ca4	46301292	TAAAAAAAA/TAAAAAAAAA	CGCTTTTGGTCTCTAAT GATTT	ATATGTCGCAGTCTCCC ACC	57.6	184	INTERGENIC				
CaPOPI_3015	Ca4	46384693	T/TCCCTATAAAAA	GAGGAGGGTGGAGAA GGAT	GGGTGCCTGGTACAAA CTC	60.3	708	INTERGENIC				
CaPOPI_3016	Ca4	46386159	ATT/ATTT	GAGGAGGATGTCCCTAA GCC	AGAATCCAATGCTCCAC AGG	60.0	779	INTRON	Ca_19274		Dof	Aminotransferase-like, plant mobile domain
CaPOPI_3017	Ca4	46496090	TAAAAAAAA/TAAAAAAAAA	AAAGTGGGGTCAACTTT TTGAA	TGTCAAGGAGACCCACC ACT	59.9	481	INTERGENIC				
CaPOPI_3018	Ca4	46674801	A/AG	GGATGACTCGAAACGGT GTT	TTACCCAAAACCCCAAT CA	60.0	667	INTERGENIC				
CaPOPI_3019	Ca4	47188403	TTATATATATATATATATATATATAT/T TATATATATATATATATATATATATATAT	ACGTCCACTGATTGGTC ACA	ACAATAGCGCAATGCTC GTT	60.0	583	INTERGENIC				
CaPOPI_3020	Ca4	47193005	TTTAT/TTTATTAT	CAATGTGGGTGAATTTG CTG	GATTCTGGCAAATTCGT CGT	60.0	287	INTRON	Ca_10862			Protein of unknown function DUF1645
CaPOPI_3021	Ca4	47238699	ATTT/ATT	TTTTGATCGAATCTGAC CCA	TCGGCCATTTTCTTCAA TC	59.0	659	INTERGENIC				
CaPOPI_3022	Ca4	47442661	AATATATATATATATATATATATATAT/ AATATATATATATATATATATATATATAT ATAT	TGTGGGAGCAAAATCAC ACT	GACGATCAAAATCGGAAG AAAA	59.1	688	DRR	Ca_10843	U		Inositol polyphosphate-related phosphatase
CaPOPI_3023	Ca4	47705093	C/CG	TTCGCATCCGTATCAAAT CA	TCACACCCATGAAGATA TGAGC	60.0	269	INTERGENIC				
CaPOPI_3024	Ca4	47755689	CTTTTTTT/CTTTTTTT	TTTTCTTTTGGTGGAATT GG	TGTGCAACTTTCTCACC CAG	59.8	480	INTERGENIC				
CaPOPI_3025	Ca4	47793461	TATAAATAAATAAATAAATAA/TATAAA TAAATAAATAAA	TGTGCCAATGGATTGAG AAAT	CTGCAAGCACGTATGCC TTA	60.3	396	DRR	Ca_10815	C		Flavodoxin

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CaPOPI_3026	Ca4	47848250	TAAAAAAAA/TAAAAAAAAA	GACGGTGTGTAGCAG CAG	TTTCTTCCCTTTTGGG TT	59.5	273	INTERGENIC				
CaPOPI_3027	Ca4	47895561	ATTT/ATTTT	AAAGGAGGCTAAATCA AGAACC	AAAGAATGATCAAACGC AAGG	59.2	317	DRR	Ca_10803	S		
CaPOPI_3028	Ca4	47961030	TG/T	CAATTTATAACGATTCT CTCACAA	GCAATGCATAGAGCAG CAA	58.0	270	DRR	Ca_10794		ARF	Transcriptional factor B3
CaPOPI_3029	Ca4	47961387	TG/T	GCTGCTCTATGCATTTG CTG	GAGCATGGACGTTTGGG TTT	59.7	527	DRR	Ca_10794		ARF	Transcriptional factor B3
CaPOPI_3030	Ca4	47966378	CTTTTTTTTT/CTTTTTTT	AGCAAATTGGGAACCTT GTG	CGAGAAACCCATGAGGA AAA	60.0	361	DRR	Ca_10792		B3	
CaPOPI_3031	Ca4	47982618	TTTTTATTTTATTTATTTT/TTTT TATTTATTTTATTTT	CCAACTCCAATCAAAAT GGG	CAATGAGAATTTCTG GGCA	60.2	483	INTRON	Ca_10790	U	ARF	Armadillo
CaPOPI_3032	Ca4	47982672	TC/TCC	CCAACTCCAATCAAAAT GGG	CAATGAGAATTTCTG GGCA	60.2	483	INTRON	Ca_10790	U	ARF	Armadillo
CaPOPI_3033	Ca4	47983864	CTATATAT/C	GCTTTGTTTCATAAGC CCA	GGACCTCTTCTACCCC TGG	60.1	332	INTRON	Ca_10790	U	ARF	Armadillo
CaPOPI_3034	Ca4	47985512	G/GGTCAATATTGTAA	ATGGGAAGGAGCTTTT TGT	TTTGATACTATTGCGA AGTTT	59.9	383	INTRON	Ca_10790	U	ARF	Armadillo
CaPOPI_3035	Ca4	48019545	AATATTTATTTATTTATTTTATTTT ATTT/AATATTTATTTATTTATTTT	AAGCAACCCGTTATTT GTG	TTCTGACCATACCGGCA GAT	59.9	588	INTERGENIC				
CaPOPI_3036	Ca4	48116724	AATATATATATATA/AATATATATAT ATATA	TTTGACGTTGAAAAAC CAC	ATGGAACAATCGGACAC CAT	58.6	433	INTERGENIC				
CaPOPI_3037	Ca4	48196964	AATATATATATATAT/AATATATATATA TATATAT	GGGTTTTACCTAGACG GTGA	TCATGACATGGCGTGGT AGT	58.1	709	INTERGENIC				
CaPOPI_3038	Ca4	48204819	T/TAA	AAGAGGAAGAGGGCAA AGG	GCAAACCCGATAGAGA GGG	59.8	425	INTERGENIC				
CaPOPI_3039	Ca4	48207508	AGATATAGT/A	CCGCCCTTATCCTTAT TGT	TTTCAAGCAGCTAAAC GCA	60.2	568	INTERGENIC				
CaPOPI_3040	Ca4	48214982	GAAT/GAATTAAT	ATGCTTTCAAACATCATG CC	CCATCGGATAGGTCAGA ACC	60.2	525	INTERGENIC				

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CaPOPI_3041	Ca4	48227983	TTCTCT/TTCTCTCT	AAATTGATCTCGGCAGCTA	AGACATGGATTGCCACTTC	59.9	594	INTERGENIC				
CaPOPI_3042	Ca4	48230328	A/AC	TCCTTGAGGGACCAGGATAA	ATTGTGGATTTTGTGTGCGCA	59.5	431	INTERGENIC				
CaPOPI_3043	Ca4	48243356	CCTTCT/CCT	TGCATTTGTTGGACGCTTAG	AAATCGATAGTTTGGCCCC	59.9	601	INTERGENIC				
CaPOPI_3044	Ca4	48260228	GT/GTTTTAAGTT	TGTTGCCATTTTGTTCGAT	ACCTGCACCACAAGAAACC	60.0	635	INTRON	Ca_10761	K	B3	DNA-directed RNA polymerase, subunit 2, domain 6
CaPOPI_3045	Ca4	48278382	CGAGAGA/CGAGA	ATGTTCCGGAATTTGAACTCG	ACCAACGACGAGATAGGTG	59.9	604	INTERGENIC				
CaPOPI_3046	Ca4	48314680	ATTT/ATTTTT	GTAATGCGTTTGACCTGCAA	ATAGGCGCATCTCAATCACCC	59.7	649	DRR	Ca_10756		BBR-BPC	GAGA binding-like
CaPOPI_3047	Ca4	48314877	TA/T	TGCGCCTATCTCTCTGTGTG	TTCGATCCATTTTACCACCC	60.2	365	DRR	Ca_10756		BBR-BPC	GAGA binding-like
CaPOPI_3048	Ca4	48318482	AATA/AA	CAACATATTTGCGGTTACCAA	CTCACCGTTTCACGTGATTG	58.5	920	INTERGENIC				
CaPOPI_3049	Ca4	48323095	AACACACACACA/AACACACACACA	GCAGCCAAACCAGCTTAGAC	AATTTGCAAAAATTCGGCTG	60.0	515	DRR	Ca_10754	Q	GeBP	Cytochrome P450
CaPOPI_3050	Ca4	48330370	AC/A	GCAAAGGAGCTTCTCAATGG	GCATCAGGAACAACCATCCT	60.0	617	INTRON	Ca_10753	J		Ribosomal protein L13
CaPOPI_3051	Ca4	48366728	A/AGAG	CAAGGGCTGGATTGTTTGT	TTGGCTTTACACTTGGTCCC	60.0	673	DRR	Ca_10750	A	bHLH	Helicase, C-terminal
CaPOPI_3052	Ca4	48398628	GTATA/GTATATA	ATGGCCCAATTAAGCTTTGA	CTGTTCTTGCGTGACCTTCA	59.5	565	INTERGENIC				
CaPOPI_3053	Ca4	48414216	CATAT/CAT	ATGAGCATAGCATGTGCAG	GCATGGTTATCGGCTGATTTC	59.9	418	INTERGENIC				
CaPOPI_3054	Ca4	48435268	A/AG	TTGCAGTTGAATTTCGAAGAA	TGATGTGATCCTAGGGTGAAGA	59.9	610	INTERGENIC				
CaPOPI_3055	Ca4	48443839	AT/A	TGCCATAACTTTGAAAAATTGC	GAGTTTGAGAAGTGCAGGGC	59.2	955	INTERGENIC				

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CaPOPI_3056	Ca4	48454259	CTTTT/CTTT	TTGCTTTTCTACCACCA CC	CAGCAGAGTCCAATTCA GCA	60.0	376	INTERGENIC				
CaPOPI_3057	Ca4	48465859	GTTTTTTTTT/GTTTTTTTTT	TGTGTGTCTCAGTGGT GGT	GCCTTTCCTTGACAGTC TGC	60.0	619	INTRON	Ca_10746	LA		Zinc finger, CCHC-type
CaPOPI_3058	Ca4	48467313	TAG/TAGAG	CTATTTGCGTCTTTTCC CA	ACGTGAACTTTTTGTG CCC	60.1	202	INTRON	Ca_10746	LA		Zinc finger, CCHC-type
CaPOPI_3059	Ca4	48522137	TTTATTATTATTATTATTATT/TTTAT TATTATTATTATTATTATT	CATTGCAATCGGCCTCT ATC	TCCCACTTTCACTTGG GTC	60.6	657	DRR	Ca_10740		C2H2	Zinc finger, C2H2-type
CaPOPI_3060	Ca4	48541135	TAAAAAAAAA/TAAAAAAAAA	AATCCACACGTACGC TTC	GATGTTCTTGGCTTGTG GCT	60.0	723	INTERGENIC				
CaPOPI_3061	Ca4	48575054	TGGGG/TGGGGG	GCAACAATTGAATCAAC CCC	CTTCATGAATTGCACCAT GC	60.2	705	CDS (FRAME SHIFT)	Ca_23007	P		Heavy metal transport/detoxificatio n protein
CaPOPI_3062	Ca4	48576925	AT/ATT	ATCTCACCCAAGACAA CCA	TCATTCCAGAAGGAGAT GGG	60.4	211	INTRON	Ca_23007	P		Heavy metal transport/detoxificatio n protein
CaPOPI_3063	Ca4	48577228	A/AC	AACACATCCGGGATCCA TTA	TGATGACGAAGACGAAG ACG	60.0	303	INTERGENIC				
CaPOPI_3064	Ca4	48651388	AACTTTAAAGGTACTTTA/AACTTTAA	AAAACCACTCCAGACAT CGG	CTTGAATACCCGCAAA GTT	60.0	682	DRR	Ca_23016	O	LBD	Heat shock protein Hsp90
CaPOPI_3065	Ca4	48683487	TAAA/TAAAA	GTGTTTGTGCGATGATT TGG	TGGCATCATAAATTGT GTGTGTA	60.0	200	INTERGENIC				
CaPOPI_3066	Ca4	48687183	TTTACTTA/TTTACTTACTTA	TTCATAATTGCTGCACC CTG	ATGGAACCAATGATCC TGA	59.7	677	INTRON	Ca_23019	R		C2 calcium- dependent membrane targeting
CaPOPI_3067	Ca4	48766746	TAAAA/TAAAAA	ATATCCAGCCGTGTTTG CAT	TTCTCCCACCACTAAC TCG	60.4	261	INTRON	Ca_23023		FAR1	Lipase, GDSL
CaPOPI_3068	Ca4	48772701	AT/A	GGTTGGAAAACGGAAAA ACA	AAGAAATCTAAACGCC AAGG	59.8	295	DRR	Ca_23023		FAR1	Lipase, GDSL
CaPOPI_3069	Ca4	48781102	TAT/TATGAT	TCGGCATTTTCATTGTCT CA	TGTGTACCGACCGATGT TTG	60.2	190	INTERGENIC				
CaPOPI_3070	Ca4	48793555	TTCTCTCTCTCTCTCTCT/TTCTCTCT CTCTCTCTCTCTC	ACGGAGAGTTTGGGTGT GAC	GTTATTCCACCGCGAGA AAA	60.0	451	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3071	Ca4	48809672	GAAAAAAAA/GAAAAAAAA	GCGAGCGAATTAACTC ACC	GGGAACATGACTTGGTT CGT	59.9	190	INTERGENIC				
CaPOPI_3072	Ca4	48831208	GTATATA/GTATATATA	TATTTCCCAAGACCTCG TGC	ATGTGGTTGTTGTTGCC TGA	60.1	255	INTERGENIC				
CaPOPI_3073	Ca4	48846764	ACATCATCATCATCA/ACATCATCATCA	GGTAAACGTGTGTTGCA TGG	ACAGCAGTAGCCCTTTG AGC	59.9	715	INTERGENIC				
CaPOPI_3074	Ca4	48850057	GA/GATCA	GCATCAATATGAATCAC CAATCA	TGACGATTTTATTACGC CAA	59.7	857	INTERGENIC				
CaPOPI_3075	Ca4	49073579	GTT/GT	GTGACTTGGAGGGAGT GGAA	ATCCGCTAACCAATCAC AGC	60.1	453	INTERGENIC				
CaPOPI_3076	Ca4	49074099	ATTTTTTTTT/ATTTTTTTTT	GCTGTGATTGGTTAGCG GAT	CGACGCGGGTTACACAC TA	60.1	694	INTERGENIC				
CaPOPI_3077	Ca4	49135046	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATT TATTATTATTAT/ATATTATTATTATTATT ATTATTATTATTATTATTATTATTATT	TATAAAGCGGTTTGGTT CGG	ATCAACACAACATCCAC CCA	60.0	938	INTERGENIC				
CaPOPI_3078	Ca5	115778	TTCACCGGTCA/TTCA	AAAGATTGCAATTTGCCT GC	TTTTTAGGGGGCGATTG TATT	60.2	511	INTERGENIC				
CaPOPI_3079	Ca5	132937	CAA/CAAA	CCAAAGACACAGCAAAG CAA	CACTTCCACCAAGTTGCA AAA	60.0	569	INTERGENIC				
CaPOPI_3080	Ca5	133283	AATATAT/AATAT	ACCTTTACATGGTGCCA AGC	GCGTTGTGAAAACAGGA CAA	60.0	433	INTERGENIC				
CaPOPI_3081	Ca5	133428	GAACA/GAACAATTTTATAATAACA	ACCTTTACATGGTGCCA AGC	GCGTTGTGAAAACAGGA CAA	60.0	433	INTERGENIC				
CaPOPI_3082	Ca5	146635	GAAAAAAAA/GAAAAAAAA	TGCATTATTACTTCTTT ACCAACA	CGAGGAAGGTAATACCA TTTTGA	57.2	712	INTERGENIC				
CaPOPI_3083	Ca5	155645	TAAAAA/TAAAAA	GAGTGGTCACTCACGGG TTT	CCAATTTCCCACTTGG TTG	60.0	773	INTERGENIC				
CaPOPI_3084	Ca5	158794	TAAAAA/TAAAAA	TGATGCGTCATGGACAT AAA	TTTTAAAAATGTCATTT ACACCG	58.5	498	INTERGENIC				
CaPOPI_3085	Ca5	164138	T/TGTAAATG	GGTAAAAGAGACTCGCG TGG	CTGATGTGCTCGTTGTT GCT	59.9	695	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3086	Ca5	180097	ATTTTTTTTT/ATTTTTTTT	ATGACCAAGGAGGCACAGAC	GAATCAGAATGACGATTGTTGA	60.1	782	INTERGENIC				
CaPOPI_3087	Ca5	188946	CTT/CTTT	CCCCATTTTACAATCCACG	CATGTATGAGCAGCCACACC	60.0	366	INTERGENIC				
CaPOPI_3088	Ca5	191792	ACTATCTATCTATCTA/ACTATCTATCTATCTA	TCACACTTGCACTTTGGAGC	CTTGGAAATCGAAACCGTTGT	60.0	680	INTERGENIC				
CaPOPI_3089	Ca5	195971	GATAT/GATATTTTGTTAAGTGTTATAT	ATCACGGAAAGCTTGTGTCC	TTTCACCTTCATCCTCTGTC	60.1	866	INTRON	Ca_18174	L		ATPase, AAA+ type, core
CaPOPI_3090	Ca5	198698	AA/AAGA	CCGGAGCACGTAAGCTTAG	GTGGCATCCACAATGACAAA	60.0	488	DRR	Ca_18174	L		ATPase, AAA+ type, core
CaPOPI_3091	Ca5	200719	GTTT/GTTT	CGATCACCTCCAACCAAAAT	AAGTGTTTCCGCATGGTAGG	59.8	665	DRR	Ca_18175			4-diphosphocytidyl-2C-methyl-D-erythritol synthase
CaPOPI_3092	Ca5	210200	ATTTTTTTTT/ATTTTTTTTTT	TTAACACCCGTGTTGTGGA	AAATGGCTTAGGGAGGGAGA	59.9	607	DRR	Ca_18176		C2H2	F-box domain, cyclin-like
CaPOPI_3093	Ca5	210510	ATT/ATTT	TCTCCCTCCCTAAGCCATT	GAATTATCGCTGCTTGTCAT	60.0	201	DRR	Ca_18176		C2H2	F-box domain, cyclin-like
CaPOPI_3094	Ca5	217922	CTT/CTTAGTTT	AAGGACATCCACAATGGAAA	ATCACAAACCACCACGCTA	57.8	406	INTERGENIC				
CaPOPI_3095	Ca5	218592	TATAATAATAATAATA/TATAATAATAATAATAATAATA	TAGCGTGGTGGTGTGTGAT	CCTTCAAGGTCAGCCCAT	60.0	739	INTERGENIC				
CaPOPI_3096	Ca5	236073	CGAAGAAAAT/CGAAGAAAATGAAGAAAATGAAGAAAAT	TTGAATTGACCGGAGGAATC	GGGATAGGGAGGGTTGTGTT	59.9	680	INTERGENIC				
CaPOPI_3097	Ca5	241183	ATTTTTTT/ATTTTTTTTT	AAAACACAACCCTTCAAGAGACA	GGGACGTCTTCGCATACATT	60.1	129	INTERGENIC				
CaPOPI_3098	Ca5	244348	T/TAATACAAA	TTTGGCGGAGAATTGATAA	GCACTTACCACCGCTCTCTT	59.4	918	INTERGENIC				
CaPOPI_3099	Ca5	262311	CTTTT/CTTT	TCGCTCGCACAGTAAATG	GGTCGATGCGTAGTTTCAT	60.0	859	INTRON	Ca_18180	A		Tudor domain
CaPOPI_3100	Ca5	276846	T/TGCATCGGTTCA	TTGTTGCTTTTCTTCGGCT	ACAGGCACTCCAGGATCAAC	60.0	330	INTRON	Ca_18181	D		Mitotic checkpoint

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3101	Ca5	280542	AATTATTATTATT/AATTATTATTATTATT	CAAAACAAGCTTTTTCAC TTCTCA	AGGACCTCCCTTTTTCT CCA	60.0	636	DRR	Ca_18183		ARF	Protein of unknown function DUF482
CaPOPI_3102	Ca5	291054	TAAAAAAAA/TAAAAAAAAA	TGCTTCATATGCTTGAC CACA	TGGTGCTTCTTTGGCTC TTT	60.3	476	INTRON	Ca_18185	R	B3	Multi antimicrobial extrusion protein
CaPOPI_3103	Ca5	291688	ATTTTT/ATTTTTTT	AAAGAGCCAAGAAGCA CCA	AGCAAATGCGACTGTGA TTG	60.0	722	DRR	Ca_18186			
CaPOPI_3104	Ca5	291943	GCGCAACCGCAA/GCGCAACCGCAACC GCAA	TTCGTGGCTTAATCCCA CTC	GTCTGGTGCTCTTCCCA ATC	60.1	517	DRR	Ca_18186			
CaPOPI_3105	Ca5	292149	A/AC	AAAGTGCCGAAGTTTGC AGT	TGCTTTCCTTCAACAG TCA	59.9	485	DRR	Ca_18186			
CaPOPI_3106	Ca5	360986	ATTTTTTTTT/ATTTTTTTTT	TGTGAGTTTAAGGGAGG GGA	GCATCCAGGATCAGAGG TGT	59.5	390	DRR	Ca_18192	P		
CaPOPI_3107	Ca5	378415	T/TG	AGCTTTAGCTTGAGGGG GAG	TCGATTTAATCCGCAGA AGG	60.0	510	DRR	Ca_18193	E		Amino acid/polyamine transporter I
CaPOPI_3108	Ca5	435121	CA/CAAA	TGCAAATCAGGTGATCC AAA	CAGCAACCAACAATTCAA CTCA	60.0	497	DRR	Ca_18196			
CaPOPI_3109	Ca5	456196	CTTTTTTT/CTTTTTTTTT	TGCCTACAACCACACAT GCT	CGTTTTCCGATT CATGC TTT	60.2	685	INTERGENIC				
CaPOPI_3110	Ca5	456689	GGAAAACGAAAACG/GGAAAACG	TGTTGAGTTTTGCACA GGC	TGAAAGGAGTCGGTTTT GTG	59.9	257	INTERGENIC				
CaPOPI_3111	Ca5	457302	CG/CAAAGACCGTTGTG	CACAAGAAAGGGAATGA CACTG	ACCACACA ACTTTGGGC TTC	59.6	643	DRR	Ca_18199			
CaPOPI_3112	Ca5	622630	G/GGCAACTCA	CATGCTTACCCTCTGGC CTA	ACAGCAGAATGGGGTAG TGG	60.2	651	INTERGENIC				
CaPOPI_3113	Ca5	927603	TTAATAATAATAATAATAATAATAAT AATAA/TTAATAATAATAATAATAATAAT AATAATAATAATAATAA	GGTCTTTTGAAAATAATC TTAACGC	AAGGGGAAGTTAAGCC AGA	58.8	664	INTERGENIC				
CaPOPI_3114	Ca5	1065182	TAAAA/TAAAAA	AATGGCCACGAATCTGA AAG	ACCATTTTCAACTGCATC CC	60.1	634	INTERGENIC				
CaPOPI_3115	Ca5	1677289	CTATATATATATATATATATATATATA T/CTATATATATATATATATATATATAT ATAT	AAGCGCTGTAAAAGGTG CAT	ATGTGAATCCCACCAGG AAA	59.9	794	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3116	Ca5	1709760	A/ATT	TGATGGGGAAACATT TGT	AAAAAGGGCATGTGAAT GATCT	60.0	247	INTERGENIC				
CaPOPI_3117	Ca5	1970073	ATTTTTTT/ATTTTTTTTT	GATGAAATCGAGGACTG GGA	TTCGGACTAGACGAGGG CTA	60.0	596	INTERGENIC				
CaPOPI_3118	Ca5	2100697	ATTTTTTT/ATTTTTTT	TGGACACGACGGTGAAA TAA	TTCGGTTCTTGTTCCTC TCT	60.0	642	INTERGENIC				
CaPOPI_3119	Ca5	2140832	G/GC	GCCCGGATTGCAAGTAT AAA	TTTGTGAGAGGGTGGA GTC	59.9	549	INTRON	Ca_26505	B		Helicase, C-terminal
CaPOPI_3120	Ca5	2295220	GAA/GA	GCACCAGCATAAACTGC ACA	GCAGGAGTTTTCTTGC ATT	60.9	739	INTERGENIC				
CaPOPI_3121	Ca5	2323461	GAAAA/GAAAAA	GCGCCAGATTTCAAACA CTA	ACCAGCAGACCAAAATG GAC	58.9	262	INTERGENIC				
CaPOPI_3122	Ca5	2327252	TAA/TAAA	TCGAAATGAAATCGAGG ACC	ACAGACGAGGGCTAGG GATT	60.0	721	INTERGENIC				
CaPOPI_3123	Ca5	2375435	TTTA/T	ATGTTTTGGATTTTGGCT CG	AGGAAGAGTGGAGTTGC GAA	59.9	571	INTRON	Ca_18664		B3	
CaPOPI_3124	Ca5	2774211	CTCT/CTCTTCCCTTAATCT	ATCCGACATTTCTTTGG CAG	CAAAGCAAGGTGAAGTG CAA	60.1	842	INTERGENIC				
CaPOPI_3125	Ca5	3061873	GATAATAATAATAATAATAATAA TAATAATAATAATAATAATA/GATAA TAATAATAATAATAATAATAATA ATAATAATAATAATA	TTGCTCCTACGTATCCC CAG	TTATTTACCCTCGTGT CCA	60.1	332	INTERGENIC				
CaPOPI_3126	Ca5	3106419	CACA/CACATAACTACA	CAATTTTCGTGATGTGG CAG	TGAGTGATGCGAGTTGT TCG	60.1	749	INTERGENIC				
CaPOPI_3127	Ca5	3337230	CATATATATATAT/CATATATATATAT	TCATCCGAATCAGTTC ACA	GGCATGATGCAAGGGAT AGT	60.0	291	DRR	Ca_18697			
CaPOPI_3128	Ca5	3353130	A/AC	GCGGTCACCTCCACATA GTT	TGTTGGAGCCCATATG AAA	60.0	659	INTERGENIC				
CaPOPI_3129	Ca5	3742109	TT/TTACATAT	ATTTACGAGCAGCGGAA AGA	TGGTCATGCAGAACTC AGC	60.0	605	INTERGENIC				
CaPOPI_3130	Ca5	3742639	TA/TAA	TGCTGAGTTTCTGCATG ACC	CCCGTGATAGGCAGTAC GTT	60.0	597	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3131	Ca5	3850375	ATTTTTTTTTT/ATTTTTTTTTT	TTTGAATCTTGAGGGTG GAAA	GAATGATATATTGATTG GGTGTGTG	59.5	396	INTERGENIC				
CaPOPI_3132	Ca5	3862372	TAAA/TAA	TTCACATCCCCTCTAAAC CAA	TCCCAATGACTCATCGT CAA	59.4	349	INTERGENIC				
CaPOPI_3133	Ca5	3874588	AC/A	GACCTTGCTTGGGGTT GTA	CACATCCCCTCTAAACC AACC	60.0	409	INTERGENIC				
CaPOPI_3134	Ca5	4035916	CTTTTTTTTTT/CTTTTTTTTTT	GCGGTGGGTTTGAAAA GTA	ACACCAGTCAAACGCAC AAA	60.0	420	INTERGENIC				
CaPOPI_3135	Ca5	4064742	G/GC	TATGTTTGTTCGCGT CA	AGGATGTACCATTCTTG CGG	60.0	375	INTERGENIC				
CaPOPI_3136	Ca5	4176359	T/TG	TGCAATGGTCTCAATGT ATTCAA	CCCGAAACCCTAAACCC TAA	60.4	703	INTERGENIC				
CaPOPI_3137	Ca5	4179599	GATATATATATAT/GATATATATAT	CGGTTTAGGGATTGGGT TTT	TCGATTGAGTCTTTGC ACTT	60.0	166	INTERGENIC				
CaPOPI_3138	Ca5	4275629	GC/G	TTAGGGTTTAGGGTTTC GGG	TGACTTTTGCACTAATTG GACG	60.2	516	INTERGENIC				
CaPOPI_3139	Ca5	4307171	AGGTTTAGGGTTTAGGGTTT/AGGTTT GGGTTTAGGGTTTAGGGTTT	AGGGTGAAGGGTCTTG GTCT	CAAAAGCCAAATGACC TCAA	59.0	747	INTERGENIC				
CaPOPI_3140	Ca5	4470545	TGT/TGTCGCGTCGT	GATTGAACCTTGGTGGG ATT	AATTCCAACCAAACCT CC	59.9	557	INTERGENIC				
CaPOPI_3141	Ca5	4968830	AATATATATATATA/AATATATATATAT A	TTTCCAAAGTACAACGC ATCA	TTGGAGAACTTTTCCG CTG	59.2	529	INTERGENIC				
CaPOPI_3142	Ca5	5190851	CTATATATATATATATATATAT/CTAT ATATATATATATATATATATAT	AGCGCTATGTGACCCTT TTG	AATGTGAATCCCACCAG GAA	60.3	555	INTERGENIC				
CaPOPI_3143	Ca5	5318962	TC/T	ACGTTGACCAATTCAGC TCC	CACTAGGGACCCTTTGG TGA	60.1	720	INTERGENIC				
CaPOPI_3144	Ca5	5602407	CATATATATATATATATATATATAT/ CATATATATATATATATATATATAT ATAT	GTTGGTCCCTAGCAC GTA	CAATTGAGTTGCGACGA GAG	60.0	552	INTERGENIC				
CaPOPI_3145	Ca5	5836817	TACCCTAAACC/TACCCTAAACCCTAAA CCCTAAACC	GTATGAGGAGGATCTTG CGG	TCAAAATGCACCATAAAC CG	59.7	594	INTERGENIC				

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CaPOPI_3146	Ca5	5837067	ACCTAAACCCTAAACCCTAAACCCTAA/ACCTAAACCCTAAACCCTAA	AAAGAAAAACACTCGCGCTG	AGCGTTTTGGGTTTAGG GTT	60.6	825	INTERGENIC				
CaPOPI_3147	Ca5	6199138	TTTATTATTATTATTATTAT/TTTATTATTATTATTATTATTATTATTATT	GCATTCCCGTATGCGACTAT	GGCACATGTTATTGTGTTTGG	60.0	511	INTERGENIC				
CaPOPI_3148	Ca5	6200121	CT/CTT	TTGCGCAACTCCACTCTTCT	GATCCATTTTCCCCCAATC	60.0	342	INTERGENIC				
CaPOPI_3149	Ca5	6369660	TC/TCAC	GAGGAAACACGGTGAATGGT	CGTCTACTAGTCGAACGAGA	59.8	486	INTERGENIC				
CaPOPI_3150	Ca5	6401833	GAAAAAA/GAAAAAA	CCTTTTGACACAAGCTTCA	TTATGCATGTTGGGTTTCCA	60.0	551	INTERGENIC				
CaPOPI_3151	Ca5	6532288	AAAAAGAACAAAA/AAAAA	TGTCTTCAACTTCTGCGGTG	TTGCAACGTGTCATTGTCCT	60.0	831	INTERGENIC				
CaPOPI_3152	Ca5	6727251	CGG/CGGG	TTTGGATTTTGACTCGGAGG	AGGAAGAGTGAGGATTGCGAA	60.0	509	INTERGENIC				
CaPOPI_3153	Ca5	6764095	GTATATATATATATATATATAT/ATATATATATATATATATATAT	TCAATTTGGGTTTCAGGGTGT	ATGATGGGCCAGACGTTAAG	60.2	841	INTERGENIC				
CaPOPI_3154	Ca5	6765423	GCAACA/GCAACAACA	CGAAGCTGCCAGGTAAAAAG	TGAGTCCATTCTCCAAACCA	60.0	652	INTERGENIC				
CaPOPI_3155	Ca5	6772280	CTTTTTTTTTTT/CTTTTTTTTT	CCAATGGCTTCGACATTCT	AAGTCACCCCTCGTTGTTG	60.1	726	INTERGENIC				
CaPOPI_3156	Ca5	6772456	GCACACA/GCACA	TGCACAACAAAAGCACACA	TGTACCATCATAGTGGCGGA	59.9	512	INTERGENIC				
CaPOPI_3157	Ca5	6773384	AATATATATATATATAT/AAATATATATATATATATATATATATAT	TATTTTGGATTTTGCGTCGG	AAACCGGTAAATCTCCGCT	59.9	681	INTERGENIC				
CaPOPI_3158	Ca5	6833150	TTTATTATTATTATTATTATTATT/TTTATTATTATTATTATTATTATTATT	TGCTAGGAACCGAGCCTTTA	TTGGCATCGTGATTTTATGC	60.0	924	INTERGENIC				
CaPOPI_3159	Ca5	6833700	ATATT/AT	GCATAAAATCACGATGCCAA	CGATTTTTCGTCTACATGTGC	59.5	211	INTERGENIC				
CaPOPI_3160	Ca5	6833833	AATA/AATATA	AAATCACGATGCCAAAGAAAA	AAGAAAGTTGTAAATGTGTTTTATGGA	59.6	616	INTERGENIC				

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CaPOPI_3161	Ca5	6833924	ATTT/ATT	AAATCACGATGCCAAAG AAAA	AAGAAAGTTGTAAATGT GTTTATGGA	59.6	616	INTERGENIC				
CaPOPI_3162	Ca5	6834075	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTA/ATAT TATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTA	GCACATGTAGACGAAAA ATCG	ATGGCATGGTGATTTTA TGC	58.3	775	INTERGENIC				
CaPOPI_3163	Ca5	6834263	CT/C	GCTTAATCCATAAAACAC ATTTACAA	TTCTCATGCGCTTGACT AATG	57.9	526	INTERGENIC				
CaPOPI_3164	Ca5	6834706	TAAAAA/TAAAAAA	TGCATAAAATCACCATG CCA	TTGTACGTTTCTTTTCTA TGATTTGC	60.9	360	INTERGENIC				
CaPOPI_3165	Ca5	6837967	TAAAAAAAAA/TAAAAAAAAA	TCGAGAACAACCTCGTCT CGTG	AATTTGCAGTGTGCGAA AAA	61.6	254	INTERGENIC				
CaPOPI_3166	Ca5	6872599	ATTATTTATTATT/ATTATTTATTATT ATT	CGGCCATCACACAATGA TAA	TCAGGATGTCACCACGA AGA	60.3	454	INTERGENIC				
CaPOPI_3167	Ca5	6907615	A/AGTG	GGTTGTGTTATCCCTCG ACA	AGGGTGCCACATTTACT CCA	58.4	539	INTERGENIC				
CaPOPI_3168	Ca5	6907876	GA/GAATA	GGTTGTGTTATCCCTCG ACA	AGGGTGCCACATTTACT CCA	58.4	539	INTERGENIC				
CaPOPI_3169	Ca5	6908168	GTAAT/GTAATTAAT	GGAGTAAATGTGGCACG CTG	CCAACACTAGTCGCAAA GTCA	60.4	588	INTERGENIC				
CaPOPI_3170	Ca5	6909501	TATATATAATTTAAATATATAATTTAAAT/ TATATATAATTTAAAT	AATGATGGAGGGAGTGA AGC	AACTGTCCATTTGTGAG GGC	59.1	405	INTERGENIC				
CaPOPI_3171	Ca5	6910554	A/AC	CTTTCAGGAACCAACAA CCA	CCAAATTACCAACGCC AAC	58.6	328	INTERGENIC				
CaPOPI_3172	Ca5	6964667	CTAATA/CTAATAATA	CAAAATGCAGCAGCAAT CAT	CCAACGGCAAATATTGT GGTA	59.8	634	INTERGENIC				
CaPOPI_3173	Ca5	7495764	ATTTTT/ATTTTTT	AAGGGACAGGGGTAAAA TGG	TTGTCATCTGGCAATCC TGA	60.0	914	INTRON	Ca_18748	O		Peptidase C13, legumain
CaPOPI_3174	Ca5	7523624	ATTT/ATT	TGGATGAAGTTTTTCGG TGG	CCTTACCCTACCTCCA TCA	60.9	615	INTRON	Ca_18747	O		Peptidase C13, legumain
CaPOPI_3175	Ca5	7595427	CAAAAA/CAAAAAAAA	TTTTTCGATTTTCATCCG GT	GGTGACCACGATCCATA ATCA	59.4	549	INTERGENIC				

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CaPOPI_3176	Ca5	7605369	T/CAAAA	CGAAGATGGGAACCAACT	TATTTGAGCCGAACCGAATC	60.0	760	INTERGENIC				
CaPOPI_3177	Ca5	7639450	AAGTTAGTT/AAGTTAGTTAGTT	AACCAAGCCAACCTCAACAG	CCCTTTCATGCCAACAAAT	60.1	392	DRR	Ca_18738		B3	Transcriptional factor B3
CaPOPI_3178	Ca5	7661539	CA/CATA	GATAGGTGGTGGGTGGGTC	GGAACCACTGCGTTGAAAT	60.0	720	DRR	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3179	Ca5	7661611	ATTTTTTT/ATTTTTTT	CCCCAAATCTTAAATCCGA	GGAACCACTGCGTTGAAAT	58.9	327	DRR	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3180	Ca5	7662046	TAGAAG/TAG	ATTTTCAACGCACTGGTTCC	TTCGGTTTTGGGATGTGTTT	60.0	671	DRR	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3181	Ca5	7663256	GTTT/GTT	TTGTTGCACTGACCGAGTGT	GAAATTTTACTCGCCGTGGA	60.4	795	DRR	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3182	Ca5	7666528	TAAAAAAA/TAAAAAAA	CGGGACCACATTAAAGGCTA	CCAACATCCCAGCTAAAGA	60.0	648	INTRON	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3183	Ca5	7670175	CAAG/CAAGTAAG	AAATTTGCGCAATGTTGTGA	AAAGGAAGCTGAGCAAGCTG	60.1	921	INTRON	Ca_18734	A		Regulator of nonsense-mediated decay, UPF3
CaPOPI_3184	Ca5	7674333	CAAAAAAA/CAAAAAA	GCAAAAGCCACACATCAGAA	TCAAAATTTGCCTCTTTCTCTTC	59.8	252	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3185	Ca5	7680447	AG/AGG	TGTTCTCGTCAACTTCATCC	AATCAACCGCTTTAGCTTGC	60.1	867	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3186	Ca5	7682051	CAAAAAAA/CAAAAAAA	CCTCTCCCCATTTTTCAACA	TGGGATTCCAAATTTTTCACA	59.9	856	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3187	Ca5	7695472	A/AGTTG	GATGCGACAAATGACCAATG	CAAAGGGTCTTAACACATGGA	59.9	239	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3188	Ca5	7695635	T/TG	GATGCGACAAATGACCAATG	GGCAAAATTGCAAAAGGAAA	59.9	802	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3189	Ca5	7696426	TAA/TA	TGGTGGCAATGCTTGTTCTA	TCTCTTGCCACTCAATCCA	60.3	476	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3190	Ca5	7696679	AGTATGTA/AGTA	TGTCTTGTCTAGCCGTCACAA	ATGGAATTGGAAGGTGGT	59.4	904	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3191	Ca5	7696740	A/AAT	TGTCTTGTCTAGCCGTCAA	ATGCACAAGTAGGGTCGAGG	59.4	978	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3192	Ca5	7707739	A/ATCCGTCATATTGGG	CATGTGCTTGTGAGTTGGCT	TTGAGATTGTTGCCTTG CAG	59.9	344	INTRON	Ca_18733	K	MIKC	Transcription factor, K-box
CaPOPI_3193	Ca5	7786396	GAAAAAAAA/GAAAAAAAA	ACACAAATGGTACTGCCCAA	AAAGCATTGGGGTGATATGC	58.9	596	INTERGENIC				
CaPOPI_3194	Ca5	7828844	TAAA/TAA	TGAAAACTCGAAAGAGCGGT	GCCGATGCGTAGATCGTAAT	60.0	791	DRR	Ca_18728			
CaPOPI_3195	Ca5	7846426	TAAAAATAAAAA/TAAAAATAAAAAATAAAAA	GGAGCCATTCTGTTTG CAT	TTTTGTGGTGGTGATGACT	60.1	596	DRR	Ca_18725	A	MYB_related	RNA recognition motif domain
CaPOPI_3196	Ca5	7858765	TGGGGG/TGGGGGG	GGAAATTCAGCAAGGTCCA	GGCTTTTGTATCCCCCATTT	60.1	128	INTERGENIC				
CaPOPI_3197	Ca5	7866386	AAAATATA/AA	TCGAAAATATCCTTCATCGAAAA	TCAAAGGATTAGCCAAACAAAA	59.9	383	DRR	Ca_18723			Glutathione S-transferase, N-terminal
CaPOPI_3198	Ca5	7886991	ATTTTTTTTTTT/ATTTTTTTTT	GTCCAGGTGTACAGTTCCCG	TCGCATTTTCTTAGCACTTTTG	60.4	605	INTERGENIC				
CaPOPI_3199	Ca5	7892187	CTT/CT	AGTTGTCTTACATTGGCGGG	TGAAGCCTGCCCTAGTC AAT	60.0	458	INTRON	Ca_18722	R		Methyltransferase type 11
CaPOPI_3200	Ca5	7913105	TG/TGG	CCTGCCGTCCTGAAGAATA	CAGTGGATCACACAATTGCG	60.2	180	INTERGENIC				
CaPOPI_3201	Ca5	7915989	C/CG	ATTAGGGACCGATTTCTGA	GGCATGTCGGCAAAATT AAG	59.4	551	INTERGENIC				
CaPOPI_3202	Ca5	7918404	GTTTTT/GTTTTTT	TGCATCATGCGAATTCA TTT	AGAACACACATTTCTTTC TCGTT	60.0	592	INTERGENIC				
CaPOPI_3203	Ca5	7937565	GT/GTT	ATCGTTTTGTTTCGGGACTG	ATGCCCATGCATGTTTG TAA	60.0	404	INTERGENIC				
CaPOPI_3204	Ca5	7957712	CAAAAA/CAAAAAA	CTCTGCCTTGGAAGTGAAGG	GCAGAAACCTCACCCAA TGT	60.0	519	INTERGENIC				
CaPOPI_3205	Ca5	7963920	CAA/CAAAA	TTGGATTTTCTGGGCATCTC	CACATTGGAAAGACCGTCAA	60.0	321	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3206	Ca5	7966801	GTTTTTTT/GTTTTTTT	CCAAAAAGGTTGGTTG AGC	TGGCATCAAATGCCTAC AAA	59.6	387	INTERGENIC				
CaPOPI_3207	Ca5	7967489	GTTTTTTT/GTTTTTTT	TTGATGCCATTGTTGAA GGA	ACAGATCACCGTTGTTT CCC	60.0	439	INTERGENIC				
CaPOPI_3208	Ca5	7967914	AATATATATATATATATA/AATATATATAT ATATATATA	GGGAAACAACGGTGATC TGT	GGGGATATTTTGTGTG CGT	59.8	858	INTERGENIC				
CaPOPI_3209	Ca5	7978058	TTAATAATAATAATAATAATAATAAT AATAAT/TTAATAATAATAATAATAAA T	CTCCATGCTTTTGGGTG TTT	GGTTTTTGCAATGCCTG TTT	60.0	454	INTRON	Ca_18720	E		Amino acid transporter, transmembrane
CaPOPI_3210	Ca5	7982148	CC/CCTTC	CTTGATGCCATTTTTCG CGT	GGACTTTTGCCTCGGG TAA	60.1	377	INTERGENIC				
CaPOPI_3211	Ca5	8071914	ATTTT/ATTTT	TTTTCGTTTCAATAATTG TTTCTT	AATTGATTCGTGTGTTG CCA	57.6	658	INTERGENIC				
CaPOPI_3212	Ca5	8088108	CAAAAAAAAA/CAAAAAAAAAA	CACTGTACATGCAGTCC TTGC	TAGGCTGGGATGGAAAT CAG	59.4	604	DRR	Ca_18715	C		Glycerophosphoryl diester phosphodiesterase
CaPOPI_3213	Ca5	8090658	CCT/CCTGCTTT	GCATGTCGAATTTTCC CAT	GGACGCCTTCGTCAGAT AAG	59.8	604	INTERGENIC				
CaPOPI_3214	Ca5	8090888	ATTTTTTT/ATTTTTTT	TTTCCCTCAATTCCTTT CAACA	GGACGCCTTCGTCAGAT AAG	60.0	291	INTERGENIC				
CaPOPI_3215	Ca5	8097767	GAAATTTTA/GA	TGTTTCTGACAGTTCTTT CCCA	TGGAAAGTCATGCTTTG TGG	59.8	664	INTERGENIC				
CaPOPI_3216	Ca5	8098608	ATAGTACGTTA/ATA	TCGTCAATGTTTGTGCC ATT	TTTCATGTTTGCAAGAA GAAGG	60.0	378	INTERGENIC				
CaPOPI_3217	Ca5	8100992	AATAACAACCTTATAACAACCTT/AATAA CAACCTT	TTTTCCCCTAGTTGTG CAG	AATCTCCAGCCACTTAG GCA	60.1	533	INTERGENIC				
CaPOPI_3218	Ca5	8164282	TAAAAAA/TAAAAAAA	CTACAAACGGAGAAGTC GGG	TTGACTGATGTTAAGTAT GCACG	59.7	816	INTERGENIC				
CaPOPI_3219	Ca5	8199807	TTATATATATATATATATATAT/TTA TATATATATATATAT	TGCATGTTCTTACGCTC GTC	AGTTATCGGTCTGCGT GTC	60.0	704	INTERGENIC				
CaPOPI_3220	Ca5	8241804	ATTTT/ATTT	TGACAGGAGCTTCCCTG AGT	GTACGAACTTCTCCCA CGA	60.0	678	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3236	Ca5	8877960	AG/AGG	AAAGGAAAGATAAAGTG GAAGTGAGA	ATAGTGTGCCCCATT GAA	60.1	441	INTRON	Ca_20339		bZIP	Zinc finger, RING-type
CaPOPI_3237	Ca5	8929713	GA/GACA	AGTTTTGTGGCTAGGAG GCA	ATGCAAGGAGGCCATAA AAA	59.9	782	INTERGENIC				
CaPOPI_3238	Ca5	8930267	GA/GAA	TTTTATGGCCTCCTTG CAT	TGGGATTTCATTCCATT TG	59.5	721	INTERGENIC				
CaPOPI_3239	Ca5	8934749	TAAAAA/TAAAA	GGCAAGCGAAGGTAAGT GAG	AGACTGGTGAGCAAATT CGG	60.0	427	INTERGENIC				
CaPOPI_3240	Ca5	8937226	AGT/AGTGT	CCACAAGCTAGGATACT GCCA	CGTAACCCAAGTCGCTA ATCA	60.3	420	INTERGENIC				
CaPOPI_3241	Ca5	8952513	TAAAAA/TAAAAA	GCCAATCACCGCGTATA ACT	TCTTGCTTCGCCCTTAC CTA	60.0	566	INTERGENIC				
CaPOPI_3242	Ca5	8969612	TAAAAA/TAAAAAA	TGCAATGATGTTTCTC CAA	TTGCTTCGATCTTGAGG TCC	60.0	562	INTERGENIC				
CaPOPI_3243	Ca5	8970639	AATATATATATATA/AATATATATAT ATATA	GATTTTAAGCGGCCAA CAA	CGGTCGCTAGTGTA GGC	60.1	425	INTERGENIC				
CaPOPI_3244	Ca5	8975579	CAAAAAA/CAAAAAA	TCATGAGGTGTGCTCA TCG	TTGACTTTCTCCCGTT GAC	60.8	110	INTERGENIC				
CaPOPI_3245	Ca5	9002459	TTATATATATAT/TTATATATATAT	CCCAACCATGAAATGAT GAA	GCAACAACCAAAACCT CAT	59.2	377	INTERGENIC				
CaPOPI_3246	Ca5	9015474	CT/C	TCCACACCTCATTGGTT GTC	TTGGTTGATGACGTTCA AGG	59.4	548	INTERGENIC				
CaPOPI_3247	Ca5	9015926	AG/A	CCTTGAACGTCATCAAC CAA	TCACGGCATAAGAGGA TGA	59.5	413	INTERGENIC				
CaPOPI_3248	Ca5	9032003	ATAAGT/AT	TCTTCTTGAGGTTGG GTG	CAAAGCATCAAACCTCC CCT	60.1	173	DRR	Ca_19958	R		Sugar/inositol transporter
CaPOPI_3249	Ca5	9075563	T/TAC	CTCTGAAACCATGCAAG CAA	TGACGGCTGAATTGTCC ATA	60.0	676	DRR	Ca_19962	O		Prohibitin
CaPOPI_3250	Ca5	9112753	TTT/TTTATT	CCACATTCATACAAA GGGG	GGAAACTCGGGAGCCTT ATC	60.1	325	DRR	Ca_19963	IT		Diacylglycerol kinase, catalytic domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3251	Ca5	9122149	CCTCT/CCTCTCT	GCTGATGCACACCTTTCAGA	CAGAGAGTTGGTGTGCC TGA	60.0	829	INTERGENIC				
CaPOPI_3252	Ca5	9123724	AT/A	TTTAAATTGATTGCGCCTCG	CCAATTGAATCCCTGCATTT	60.0	673	DRR	Ca_19964		C2H2	Protein kinase, catalytic domain
CaPOPI_3253	Ca5	9132512	CTTTT/CTTTTTT	ACTTGCGGATAAAACCA CCA	TGGATTGGTGTTCAGC ATC	60.4	704	INTERGENIC				
CaPOPI_3254	Ca5	9133458	AAT/AATTCAT	ATTGGTTCAGTGGTTGG CTC	TTGTCAAATACTCCATTC AACCC	60.0	399	INTERGENIC				
CaPOPI_3255	Ca5	9140493	AAAGAAGAAGAAGAAGAAGAA/AAAGAAGAAGAAGAAGAAGAAAGAA	CACTAGCACCGTAGCAT GGA	AATTGCGGCGAGAGAAG ATA	59.9	378	INTERGENIC				
CaPOPI_3256	Ca5	9148867	GA/GAA	AATTCCTTGGCCTTGAG GTT	AAGTCACATCCCCATC AAA	59.9	859	INTERGENIC				
CaPOPI_3257	Ca5	9163773	AG/A	TCTGGTCATTTTCCTTG GTTG	CTCCAGCGATCTGTAAAGCC	60.0	180	INTERGENIC				
CaPOPI_3258	Ca5	9163864	CT/CTT	TCTGGTCATTTTCCTTG GTTG	TCTCTTTAAAGTCGTTGATTGG	60.0	235	INTERGENIC				
CaPOPI_3259	Ca5	9172890	TT/TTATCT	GCCTCCAAACCTGAAAC AAA	TAGCGACCACACGAAGATGT	60.1	618	INTERGENIC				
CaPOPI_3260	Ca5	9194215	CATATAT/CATAT	GTGGCGCTCTAGGGAAT ACA	TTGGTTTCATGACCTGC ATC	60.2	456	INTERGENIC				
CaPOPI_3261	Ca5	9231109	AAT/A	ATTGATGACGACGTTGCTTT	TTTTGCAATTGTGGTCC ATC	58.2	634	INTERGENIC				
CaPOPI_3262	Ca5	9233301	CAAAA/CAAAA	TTGTAATGCTTTGTAATGCTTGG	TTTTGGAGGTGTGTATT TTGGA	59.2	538	INTERGENIC				
CaPOPI_3263	Ca5	9308007	GTTTTTTTTTTTTTTT/GTTTTTTTTT	TAACCCACGGAGGAATCAAG	ATTGGTGGTGTCTATGGA TGT	59.9	720	INTERGENIC				
CaPOPI_3264	Ca5	9348625	TA/TACA	ATATCCCATGTCCGGTT TGA	CATTCGCTAACAATCTC CACA	60.0	508	INTERGENIC				
CaPOPI_3265	Ca5	9349749	TA/TAA	CATTTGAGTTGTGTGTG GTTCA	TATGGTCCATTTGGGGT GAT	59.5	846	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3266	Ca5	9352151	ATT/AT	TCAGAAAGCGCAAACGT ATG	TTTGCCACGTCTAATGC AAA	60.1	720	INTERGENIC				
CaPOPI_3267	Ca5	9360960	CAAA/CAA	GAGGGACTGCAGGGTC ATTA	TAAACCCAGTGAAGGCA ACC	60.1	421	DRR	Ca_19977	T		
CaPOPI_3268	Ca5	9361061	CACAAA/CACAAACAAA	GAGGGACTGCAGGGTC ATTA	TAAACCCAGTGAAGGCA ACC	60.1	421	DRR	Ca_19977	T		
CaPOPI_3269	Ca5	9361874	TAAAA/TAAAA	TTGCCCAAGCAATAACA TCA	GACTGCATTGGAGCTG TGA	60.1	303	DRR	Ca_19977	T		
CaPOPI_3270	Ca5	9363778	TGG/TGGG	ACCACCTTGTGTGATGA CGA	TGACCTCAATCCCATTG ACA	60.0	552	INTERGENIC				
CaPOPI_3271	Ca5	9403421	TA/TACCTTA	GGCACTTTTCACGTCCA TTT	ACAGCAGAATGGGGTAG TGG	60.0	836	INTERGENIC				
CaPOPI_3272	Ca5	9416660	TA/TAA	CCATCTTAAATCATGGT GTTGG	TTCAACTCCTTTTGTTC CG	59.2	522	INTERGENIC				
CaPOPI_3273	Ca5	9436009	TAAAAAA/TAAAAAA	TTTTCAATTCCTTTAAAA TTCGAGA	CCAAAAATTTCCAAAGCT CCA	59.6	726	INTRON	Ca_19988			Protein of unknown function DUF566
CaPOPI_3274	Ca5	9441399	AATTTTATTTT/AATTTTATTTTATTTT	TGCGATGGAGAAATCAA AGC	CTAGTTTGGCTTGACGG GAA	61.3	865	INTERGENIC				
CaPOPI_3275	Ca5	9441477	CAAAAAA/CAAAAAA	TCGTGTCTCAAAATTCAA GGAG	CTAGTTTGGCTTGACGG GAA	59.4	675	INTERGENIC				
CaPOPI_3276	Ca5	9467922	T/TAGCCAATAAAC	CCTCTTTGGTTCCATGT GCT	AAGCGTACCTGTGGGAA TTG	60.1	489	INTERGENIC				
CaPOPI_3277	Ca5	9520123	TAA/TA	TGAGACACATGACTCCA AGATTC	CAATACATTTGCATCGA ATTACA	59.2	484	INTERGENIC				
CaPOPI_3278	Ca5	9520244	CAAAAAA/CAAAAAA	TGAGACACATGACTCCA AGATTC	TCGCGTTGTTTAAAGTG TGG	59.2	754	INTERGENIC				
CaPOPI_3279	Ca5	9524095	A/AC	GTCCCAATTGCCTTCTG AAA	ATCAAATGGCGGAAGCT ATG	60.1	799	INTERGENIC				
CaPOPI_3280	Ca5	9535247	GTT/GTAAAGTCTTTT	GGAAGTGTGGAGAAGTT GCC	GCTAGTCCTGCACCCCC TAT	59.7	915	INTERGENIC				

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CaPOPI_3281	Ca5	9560422	ATTTTT/ATTTTTTT	TGTTACAATCCCATACCAAAAA	AGAGGGACGAAACAGAGCA	58.3	668	INTERGENIC				
CaPOPI_3282	Ca5	9570925	CTTT/CTTTAATTT	TGGTGAACTGATCTCAGCA	CTTAATCAACGTGCAGGCAA	59.4	458	INTERGENIC				
CaPOPI_3283	Ca5	9570971	AATCATATAT/AAT	TGGTGAACTGATCTCAGCA	CTTAATCAACGTGCAGGCAA	59.4	458	INTERGENIC				
CaPOPI_3284	Ca5	9582075	TT/TTAT	AGCTGACACCACACACACAC	TCCTGAACCTGTCCCGATC	59.6	438	DRR	Ca_23783			Pectinesterase inhibitor
CaPOPI_3285	Ca5	9583627	TT/TTGACAAATCTGT	TTGGCTAGTAGGTGGGATGG	GGTATTTTGTGTGCCATGTG	59.9	260	INTERGENIC				
CaPOPI_3286	Ca5	9615819	TAAAAA/TAAAAAA	TTGCCTTTAACTGGTTTGGG	CGGGTATGGTTTGACTTTATCC	60.0	149	DRR	Ca_23788	C		Pyridine nucleotide-disulphide oxidoreductase, NAD-binding region
CaPOPI_3287	Ca5	9620206	ATTTT/ATTT	ACCACATGGACTGGAAAGC	CTCTTCAGCATCAGCCATCA	60.0	528	INTERGENIC				
CaPOPI_3288	Ca5	9626102	CCACA/CCA	AGTTTCCTCCCCGAAACCTA	TGGCAAATCGATTGACAAA	59.9	657	INTERGENIC				
CaPOPI_3289	Ca5	9733773	AA/AACA	TGTCACTTAAGGAACGAATGAA	CAAGGAAGAATTGGATGGG	60.0	295	INTERGENIC				
CaPOPI_3290	Ca5	9767795	ATTTTTTT/ATTTTTTTT	AATACCCAAAATGCCCCTTC	CTGAACCTGGATTCACGCAAA	60.0	490	INTERGENIC				
CaPOPI_3291	Ca5	9768398	TA/T	TTTGCGTGAATCCAGTTTACG	TTTGATACGAGTGGGTTTGC	59.8	829	INTERGENIC				
CaPOPI_3292	Ca5	9768596	T/TTTCTAAATAAATGA	TTCTGAAAAATTGGTGCAT	TTTGATACGAGTGGGTTTGC	58.1	574	INTERGENIC				
CaPOPI_3293	Ca5	9774862	TAAAAAA/TAAAAAA	TGTCTTCACAGCTCAATTGAAAA	TGAGTCTGGCTCAGTGTGCT	59.9	755	INTERGENIC				
CaPOPI_3294	Ca5	9775672	CAAAAA/CAAAAAA	CAACCTGCAATTCCAACTT	GAGTAATGGATCTCGTCGCG	60.0	148	INTERGENIC				
CaPOPI_3295	Ca5	9782845	ACCC/ACC	AAACATGCTTAAGAAATTCGG	CGCAAAACACTAACCGACA	57.5	689	INTERGENIC				

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CaPOPI_3296	Ca5	9808086	TT/TTCT	GTGACGAAGAATGCCAA CAA	GACCTCAAGTTTCACAA TGTGGT	59.7	396	INTERGENIC				
CaPOPI_3297	Ca5	9809593	AATTCATTCATTCATTC/AATTCATTCAT TCATTCATTC	GCATTCAAATCTCCTTG GGA	CTGAGGGGCTTCGAAGAA ATG	60.0	542	INTRON	Ca_20501	O		Peptidase M3A/M3B, thimet/oligopeptidase F
CaPOPI_3298	Ca5	9819633	GATA/GATAGTTCATTATA	CCAAGTGGCAAGTTTGG TTT	TCGGTGCAAGTTGAGTT CTG	60.0	545	INTRON	Ca_20501	O		Peptidase M3A/M3B, thimet/oligopeptidase F
CaPOPI_3299	Ca5	9828911	CTTTTTTTTT/CTTTTTTTTT	ATGAACGCTCACACTTTT CG	TGGAGAAAACCATGGAA GGA	58.9	539	INTERGENIC				
CaPOPI_3300	Ca5	9829260	CTTAATTA/CTTAATTAATTA	ATGAACGCTCACACTTTT CG	TGGAGAAAACCATGGAA GGA	58.9	539	INTERGENIC				
CaPOPI_3301	Ca5	9836320	ATTTTTTTT/ATTTTTTTTT	CATGGTGAAACATGTGA TTCTG	CCTCTTCAAAGCTCAAC AACC	58.9	700	DRR	Ca_20502	U		Vacuolar sorting protein 9
CaPOPI_3302	Ca5	9836548	T/TGTATTGTCAA	AGCATGTGGTTGTGAG CTTT	CACACGAAATTTGAGGT GTCA	59.8	408	DRR	Ca_20502	U		Vacuolar sorting protein 9
CaPOPI_3303	Ca5	9859158	GATA/GATAATA	TTTTGCAACGGAAGTTT GGT	ATAGCTCATCCATTGTC GGC	60.5	717	INTERGENIC				
CaPOPI_3304	Ca5	9883179	TAA/TA	TCGTGGAAGGATAATCC ACA	CCTTGCCCCCTACATCT ACA	58.9	477	INTERGENIC				
CaPOPI_3305	Ca5	9884435	ATTTTT/ATTTT	TGGTGGATTGTGTTTG GAA	ATACATGCTTCGGCCCT ATG	59.8	547	INTERGENIC				
CaPOPI_3306	Ca5	9900286	C/CA	CATTTTGCTTGCATCCAT TG	TGGAATAGAGTGTGATT GCTTTC	60.1	172	INTERGENIC				
CaPOPI_3307	Ca5	9905958	AGA/AGACATTTCTTGA	GTTTCGCGATGATAACA ACC	TTTGAGTCAGGGTGCTG GAT	60.3	713	DRR	Ca_20506		STAT	Protein kinase, catalytic domain
CaPOPI_3308	Ca5	9917719	GAAAAA/GAAAAAA	TGGACAGAATCAATGCT CCA	TGAGCTACGTCCAGTCC TCA	60.2	677	INTERGENIC				
CaPOPI_3309	Ca5	9919003	TG/TGG	TGATTGGAGTGGGAATG GAT	TAAAGCCCTTGTGTGCC TCT	60.1	395	INTERGENIC				
CaPOPI_3310	Ca5	9953374	CTTTTTTT/CTTTTTTTTT	GTGACCTTACTCTTTGG CCG	AAATCACAAAATGGCTG GCT	59.7	532	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3311	Ca5	9955402	GA/G	ACAAGGCCAGCTGTAA TGA	AAGTGGGGGAGGATCAA CTT	58.4	581	INTERGENIC				
CaPOPI_3312	Ca5	9957931	AAGGTT/AAGGTTTTATTGAGGTT	TTCTTGTGTGTGGTCTC CCA	TCGGCTATTTTCCCTT CTT	60.1	366	INTRON	Ca_20508		WRKY	DNA-binding WRKY
CaPOPI_3313	Ca5	9964705	A/AT	GCCAAGGTAAGAGAAC GCA	TTGGCGCATACAAAA TGA	60.4	603	INTRON	Ca_20509	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_3314	Ca5	9965556	CTT/CTTTT	TCTCAGGCGACCTGTTT TCT	TTTCCGGATCTCAAACG AAC	60.0	385	INTRON	Ca_20509	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_3315	Ca5	9981523	TA/T	AAATCCGTGATTCCAAG CTG	GCCGTGAGTCTGATTC ATT	60.1	342	DRR	Ca_20510	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_3316	Ca5	9986447	TAAAAAA/TAAAAAA	TTCAAAATCAACCACGA CCA	AAGGCTTGGGCCATTAT ACC	59.9	589	INTRON	Ca_20511	P		Cystathionine beta-synthase, core
CaPOPI_3317	Ca5	10004188	GTTGTTGTATTGT/GTTGT	TCGCCATTCCAACACT CC	AATTTCTCCTCCACC AGT	60.1	703	INTERGENIC				
CaPOPI_3318	Ca5	10024689	TAAA/TAAA	GGGTCTTTAGGCCCTCT TGT	ACCTCGTGTGACTGATG ATGA	59.6	565	INTERGENIC				
CaPOPI_3319	Ca5	10025602	TAAAAAA/TAAAAAA	TGAGTGCTCGACGACAT TTT	AGACCTGTTGATTGTGT TTTGG	59.4	700	INTERGENIC				
CaPOPI_3320	Ca5	10054215	ACTCT/ACTCTCT	TTGCCCACTTGATGAA ACA	GCCATAGCACCTCTGTA GGC	60.1	531	DRR	Ca_20515			
CaPOPI_3321	Ca5	10084501	CTTGTTTTGTTTT/CTTGTTTTGTTTT TTGTTTTT	TTTTTGCCATTCCCATCA TT	TCATGAAATCATAAGC CACG	60.1	603	INTERGENIC				
CaPOPI_3322	Ca5	10131669	TAAAAAA/TAAAAAA	AATTAGACGACACGGGG TTG	CGTATCAATTTCTTTCA AATGG	59.9	635	DRR	Ca_20519			
CaPOPI_3323	Ca5	10132207	CTTTTT/CTTTTT	TCCATTTGAAAGAAATT GATACG	TCATCAACGGTCATTCA ACC	59.4	737	DRR	Ca_20519			
CaPOPI_3324	Ca5	10159630	TG/T	CCAACAGGCAAACTGA AAT	GCACAATGGGCTTATTC GAT	60.0	197	INTERGENIC				
CaPOPI_3325	Ca5	10176653	CA/C	CTCTCAAACGGTTGCAT TGA	TGTTTCAGCTGTGATGC AAA	59.8	571	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3326	Ca5	10191175	CTTAAATTAT/C	TCTTGTTTCGTGTGCATAGTTCG	CATTTTTCGTGTGTGTGCT	60.2	407	INTERGENIC				
CaPOPI_3327	Ca5	10223215	CATAAAAA/C	AATGGGGGTACATGGGAAT	TCAATTCACCTTGCAGCAATA	60.1	547	INTERGENIC				
CaPOPI_3328	Ca5	10289518	A/AT	TTGTGACACTTTTACCCGTG	GTTACGGTGTGCGGTTTCT	58.6	343	INTERGENIC				
CaPOPI_3329	Ca5	10299950	CAA/CAAAA	CCTTTTCAGCATTCGAATCA	GGTTAATTATTTTAATGGCGG	60.1	356	INTERGENIC				
CaPOPI_3330	Ca5	10300146	GA/GATGATTAATAA	CCTTTTCAGCATTCGAATCA	GGTTAATTATTTTAATGGCGG	60.1	356	INTERGENIC				
CaPOPI_3331	Ca5	10331676	ATTTTTTTT/ATTTTTTTTT	AATGCCAAAATCTCAACCG	GCCATGTTTGTCTTTGCACT	59.9	688	DRR	Ca_21237	O	E2F/DP	14-3-3 protein
CaPOPI_3332	Ca5	10348801	ACC/ACCC	TGTGCCTGAAATGATTGGA	CAGCTTCGTACACTTTGCCA	60.0	615	INTERGENIC				
CaPOPI_3333	Ca5	10389582	CTACGTTA/CTA	TGGTTGCTTCATTGCTGTG	GCGAAGGATATTCGACCAAG	60.8	216	INTERGENIC				
CaPOPI_3334	Ca5	10396682	TAAAAAAAAA/TAAAAAAAAA	TTGGAGGTCAAATCTGGGAG	AAAATTTTATGCCGCCACAC	60.0	310	INTERGENIC				
CaPOPI_3335	Ca5	10409173	TTGTGT/TTGTGTGT	TGGCTCTTGAAAAGAAACGAA	TCAATGGTGCTTTTGTTGGA	60.0	805	DRR	Ca_21231		WRKY	Glycoside hydrolase, family 9
CaPOPI_3336	Ca5	10413807	GTTTTTTTTTTT/GTTTTTTTTTTT	TTCTCATGCTCACTGGTTGC	TCGCATTTAACCATTACACA	60.0	569	INTERGENIC				
CaPOPI_3337	Ca5	10414029	TACCCAC/TAC	TTCTCATGCTCACTGGTTGC	TCGCATTTAACCATTACACA	60.0	569	INTERGENIC				
CaPOPI_3338	Ca5	10457260	CACAATACTC/CACAATACTCTACAATACTC	GGGGCGAGATATTCAGACAA	TGATTGTTCTAGTGGTCTCT	60.0	108	INTERGENIC				
CaPOPI_3339	Ca5	10497866	AT/ATT	GCAAACGGGTAAATTGGAGA	GTCTTATGAGCCGAAGGTCG	59.9	764	INTERGENIC				
CaPOPI_3340	Ca5	10507484	ATTTTTTTTT/ATTTTTTTTTT	TGCAAGTTAAAGAATAATTAGAGCG	GGAAACGATTGGATTGCGAGA	59.5	897	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3341	Ca5	10515370	A/AT	CGATTAAAGTCAAAGTTT CACGA	AGCAAACCAAGTTGTCC TGT	58.5	560	INTERGENIC				
CaPOPI_3342	Ca5	10516286	TTTTTATTTTATTTT/TTTTTATTTTATTT TATTTT	ATTGGGTTGAAGTGT GCC	ATTCAATGCAACTCCCT GC	59.8	598	INTERGENIC				
CaPOPI_3343	Ca5	10550017	C/CATATTTTACCATTGAT	CTCCTCATATTGCAGGC GTT	CGGCTAAACAACAAGCC ATT	60.2	703	DRR	Ca_21226			
CaPOPI_3344	Ca5	10559602	AT/ATTTATCATTCATATGT	TGTCATTTCAAATTAGAC CCAAAA	GCTTTTACGGAATGGCA AAA	59.8	250	INTERGENIC				
CaPOPI_3345	Ca5	10564601	ATTTT/ATT	TCCAAATCCCAAGCTAC CAA	GGGCTCATTTCCCTTT AAC	60.4	408	INTRON	Ca_21225			
CaPOPI_3346	Ca5	10605600	GT/GTT	AGTGAAACCAACGCCAA AAC	TCACTCAAAGGGCTACT GCC	60.0	272	DRR	Ca_21224			
CaPOPI_3347	Ca5	10625989	TAAAAAAA/TAAAAAAA	TGTAGGGGTACAGGG AAAG	AACTCCGTGTTTTTGC CA	58.9	165	INTERGENIC				
CaPOPI_3348	Ca5	10679625	TAAAAAAA/TAAAAAAA	GGGATTGTTTGAATAT GAGGG	TCACACGATCATTTGG CAT	59.6	596	INTERGENIC				
CaPOPI_3349	Ca5	10686981	TAAAAAAA/TAAAAAAA	GCTCCTTCTGCATCAAC ACA	TGCCCCACATTTTAGAC CTC	60.0	509	INTERGENIC				
CaPOPI_3350	Ca5	10689102	TAAAA/TAA	ATGGGCCACCTATTGAG ACA	TGCCAAGAAAAAGGT TCG	60.3	623	INTERGENIC				
CaPOPI_3351	Ca5	10689622	AGAAGCATG/AG	CGAAACCTTTTCTTTGG CA	AACGGATTGTCCCTTCA TTG	60.2	418	INTERGENIC				
CaPOPI_3352	Ca5	10693789	CTTGTGATTGTTTGTGTGATTG/CTT GTGATTG	CCAATTTGAATTGTCCG TCC	TTGCAAAAGCTGGGTCA AGT	60.2	406	INTERGENIC				
CaPOPI_3353	Ca5	10995810	AAATAATAATAATAATAAT/AAATAA TAATAATAATAAT	ACTTCAGGTGGTCGATG TCC	GGGAGCGACCTCACACT AGA	60.0	923	INTERGENIC				
CaPOPI_3354	Ca5	11131180	GT/GTT	CAAGTGCACAGCGGAAT TTA	TCCGATTGGATTTTCAG GAC	59.9	148	INTERGENIC				
CaPOPI_3355	Ca5	11168411	AATA/AA	TTCAAACGGAAGTATG CTTT	TTGGTTGGGGGAGTTAT TGA	59.7	954	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3356	Ca5	11168801	ACTATTAGTCTATTA/ACTATTA	TCGTTTGAGGAAAAACAA ACAAA	TTGGTTGGGGGAGTTAT TGA	59.6	557	INTERGENIC				
CaPOPI_3357	Ca5	11168904	GTCTCTCT/GTCTCT	TCAATAACTCCCCAAC CAA	TCACAATTGGGTTTGA TCA	60.2	227	INTERGENIC				
CaPOPI_3358	Ca5	11169035	CG/C	TCAATAACTCCCCAAC CAA	TGACGCCGTGAAAAACA TTA	60.2	626	INTERGENIC				
CaPOPI_3359	Ca5	11233017	TAAAAA/TAAA	ATTGGACGTATCCCGAG TTG	GTTGTGGGATGAACTGA CCC	59.8	633	INTERGENIC				
CaPOPI_3360	Ca5	11420785	TTATTA/TTACTATTA	ATTAAGTGAATGGATCG CGG	AGTGTGGAAGGACGAG CAAG	59.9	485	INTERGENIC				
CaPOPI_3361	Ca5	11505972	TTTCTTC/TTTC	GGACCTAAATTTTGCAA CAACA	GAACGCGAGATATTGGG TGT	59.0	199	INTERGENIC				
CaPOPI_3362	Ca5	11628665	CNNNNNNNNN/CNN	TATCCCCGTCCATTAA CAA	GGGAGTGGTTGAGACCT TGA	60.0	248	INTERGENIC				
CaPOPI_3363	Ca5	11729570	AAATAATAATAA/AAATAATAA	CACGGTCCCTAGACCA ATA	CGGGAGATACGTAGGA GCAA	60.1	672	INTERGENIC				
CaPOPI_3364	Ca5	11878820	CATATATATATATATATATATATAT/ CATATATATATATATATATATATAT	TATTTTGGATTTTGCTC GG	AGAGGGGTTTGTGTTTG ACG	59.9	599	INTERGENIC				
CaPOPI_3365	Ca5	11879108	TAA/TAAA	AAGATTTCTCCTCTCT CCA	CTTTAACATGCGTTTCC GGT	60.0	327	INTERGENIC				
CaPOPI_3366	Ca5	11886997	GATAATAATAATAATAATAA/GATAA TAATAATAATAATAATAATAA	TGCCTTCGGTTTTCTA TTG	AATGTTTGGAATCCCC CTC	60.1	888	INTERGENIC				
CaPOPI_3367	Ca5	11983861	GTCT/GATCTTCT	CTGCTGTCAACTCCACT CCA	TCAAAATCCCCCAATA CA	60.0	713	DRR	Ca_17106			
CaPOPI_3368	Ca5	12040897	T/TTTTAAATGAAG	TCGATGATGTTAACTCG CAA	GCGGTGTCATTTTGTTT CAA	57.9	636	INTERGENIC				
CaPOPI_3369	Ca5	12448859	ATTTT/ATTTTT	TTCTACCCGAAATTTGT GCC	GTCAGTCAGCCTCTCT GCC	59.9	361	INTERGENIC				
CaPOPI_3370	Ca5	12619050	AATATATATATATATATATATA/AATAT ATATATATATATATATATATATA	TCCTAACCTTTTGACTAA TTTTTCTTC	TCAATCCTCTTAAGATAT TTCCCTG	58.9	685	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3371	Ca5	12631984	GCGTC/GC	GGTTATCACCGTGGTGC TCT	TGGCTTCTGTTGGATT TTC	60.0	648	INTERGENIC				
CaPOPI_3372	Ca5	13636401	A/AC	ATCGACAAACCAACATG CAA	GGGAAACTCACTTGCGG TTA	60.0	735	INTERGENIC				
CaPOPI_3373	Ca5	13636921	CTGT/CT	TAACCGCAAGTGAGTTT CCC	GCGGTGGCTGAGTTTCT TAC	60.1	387	INTERGENIC				
CaPOPI_3374	Ca5	13714998	TA/T	TGATGTGAGGTGACAGG CAT	GTAGCGTGGAGAGGAG CAAC	60.1	374	INTERGENIC				
CaPOPI_3375	Ca5	13825062	ATATTATTATTATTATTATCATT ATTATTATTAATATGATTATTATTAT TATTATTATTATTATTATTATTATTA TTATTATT/ATATTATTATTATTATTA	TGGTTTCATAACGTTTGT CCA	TGATTTGGTCATTTGGT ATTCA	58.9	823	INTERGENIC				
CaPOPI_3376	Ca5	13855690	TA/TAA	CCAGGTTTGCACTCAAC TCA	GGGTGATGAGGACTCAG GAA	59.9	573	INTERGENIC				
CaPOPI_3377	Ca5	13858932	A/AC	GATTCCCCATTCTTAAC GCC	TCGCGAAGAGATAGAAG GGA	60.6	554	INTERGENIC				
CaPOPI_3378	Ca5	14022502	ATTT/ATTTT	GGAAATGGATGTCTGCC AAT	TTGCAATCTCATCAACTC GG	59.8	318	INTERGENIC				
CaPOPI_3379	Ca5	14084083	A/ACAAGGATG	TGTTGTTGTGATTGTGC CCT	TTAGCATGCACCTTGAA AGC	60.0	385	DRR	Ca_20825	K		Nascent polypeptide-associated complex NAC
CaPOPI_3380	Ca5	14307259	TTTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTAT/TT TATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT	GCTCTCCAACAACAAAT CAACA	CACTTGAAATTTTAGGC CGC	60.2	798	INTERGENIC				
CaPOPI_3381	Ca5	14330970	ATTTTTTTTT/ATTTTTTTTTT	TGATTAAGAAGTTTTGAT TTGCG	GGTTTGGACAATCTGCC TTG	58.5	795	INTERGENIC				
CaPOPI_3382	Ca5	14394852	CTTTT/CTTTT	TCTTCCACCCAGTTTCA CC	TTGAGGGCTATGTTTT CGG	59.9	337	INTERGENIC				
CaPOPI_3383	Ca5	15176756	AATATATATATATATATATATATAT/ AATATATATATATATATATATATATAT AT	ACATTTAGGGCCACTTG GTG	GTTGGTTCCTAGCACC GTA	59.9	725	INTERGENIC				
CaPOPI_3384	Ca5	15184248	AGGGGGGG/AGGGGGGGG	TCTAACCCGGAATCCTT TGA	TGAGGATTGAACGTAAC CCA	59.5	300	DRR	Ca_21631			
CaPOPI_3385	Ca5	15339602	GAAAAAAAA/GAAAAAAAA	AGGAGAGAAAAAGGGG GAAA	GGGAAACCCACCTCTTG ATT	59.1	211	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_3386	Ca5	15756736	GACAC/GAC	GC GCGATTACCAAAA TGT	TTTGAGTGGTGGGTTGT GAA	60.0	431	INTERGENIC				
CaPOPI_3387	Ca5	15773178	GATTATTATTATTATTATTATTATTA TTATTATTATTATTATT/GATTATTATTAT TATTATTATTATTATTATTATTATTA TTATTATT	GCCTTAAATTTGGCAAT GG	TCTTCGCAAATCAAAG AATGA	59.4	807	INTERGENIC				
CaPOPI_3388	Ca5	15835478	CAAAA/CAAA	TGCATGATTCCAGAATT CCA	AGCGGTGAGGAGAACTC TGA	60.0	690	INTERGENIC				
CaPOPI_3389	Ca5	15877436	GC/G	GGGCTACATCCAGTCCT CAC	TTTGGCTGTAGAGGTTCCAA	59.5	474	INTERGENIC				
CaPOPI_3390	Ca5	15918981	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTATT TTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATT	CCTCCCCATTGTCTT CTT	GCCTGATGTTCAATTT TTCA	60.3	462	INTERGENIC				
CaPOPI_3391	Ca5	15929348	ACCC/ACC	TGATGACGAAGACGAAG ACG	AACACATCCGGGATCCA TTA	60.0	416	INTERGENIC				
CaPOPI_3392	Ca5	16319965	TGGG/TGGGG	TTGTGTGCAGGATCCAC ATT	TTGACCATTGCACGAA CAT	60.0	502	INTERGENIC				
CaPOPI_3393	Ca5	16363340	GTT/GTTT	AATCCTGGTGACAGATT TTC	ACATCGCCATTACCGAA CTC	59.9	445	DRR	Ca_17921	R	MYB_rela ted	Pentatricopeptide repeat
CaPOPI_3394	Ca5	16393546	CTTTTTTTTT/CTTTTTTTTT	CACAACTCCGCCATTAC CTT	GTTGCAAGTTGCCGTGT CTA	60.0	713	INTERGENIC				
CaPOPI_3395	Ca5	16765808	TAGA/TA	CGATCGTGCTACGTCTT CAA	TGGTGGGAATGTTGTGA TTG	60.0	677	DRR	Ca_17941	R	HSF	Pentatricopeptide repeat
CaPOPI_3396	Ca5	16889364	AATATATATATATATATAT/AATATATA TATATATATATATATAT	GGAGAAAATTCATTTGG CATT	CCTTTGCATGGGACAGT TTT	58.0	985	INTERGENIC				
CaPOPI_3397	Ca5	16958294	AT/A	GGGAAGGATGGAATTT GGT	GGTGGAGAGTGAGGTG GTGT	60.0	684	INTERGENIC				
CaPOPI_3398	Ca5	17494887	CTGA/CTGACCTCCTATATGTGA	CTACGCCAAGAACTGC TCC	GTACGCGTCCAGACATA GCA	60.0	245	INTERGENIC				
CaPOPI_3399	Ca5	17612584	CATTCAAAAAATTCA/CATTCAAAAAA TTCATAAAAAATTCA	GTCTCTTGCTCTCCAC CAA	TTTATGTGGTGAATTTG CGA	60.4	769	INTERGENIC				
CaPOPI_3400	Ca5	17757862	TC/TCC	AGAGTCTTTCAAACGG CCT	TGTTGGAATCAAGTTGG TTTT	60.2	815	DRR	Ca_22474			

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									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3401		Ca5	17760753	TAATAAAATAAAATAAAATAAA/TA ATAAAATAAAATAAAATAAAATAAA A	TGAAACCGCGTTTGATT GTA	GGTGGGACCACTTCTC AAA	60.1	168	INTERGENIC				
CaPOPI_3402		Ca5	17876530	CAA/CAAA	TTTCATCCATCACCAC AAA	CTCAACGAATGCCTGAA ACA	59.9	573	INTERGENIC				
CaPOPI_3403		Ca5	17876693	CACAAA/CAA	TGTTTTCAGGCATTCGTT GAG	TCAATACCATTTTCACCG CA	59.8	471	INTERGENIC				
CaPOPI_3404		Ca5	18049660	CATATATATATAT/CATATATATAT	GCACGTTGTAAAGAGTG GACTG	AAAAGGCCACAAAGAGT TGA	59.8	694	INTERGENIC				
CaPOPI_3405		Ca5	18136111	CTTTTTTTTT/CTTTTTTTTT	CGGGTCATTTCTTTCT CCA	TTGTGGCTCTTTAAGAT GGTTG	60.0	327	INTERGENIC				
CaPOPI_3406		Ca5	18176797	TAAAAAAAAA/TAAAAAAAAA	TGGGTTGAAAGTTGGAT GTG	ATCCTGTTGGGGAAGG TAG	59.4	473	INTERGENIC				
CaPOPI_3407		Ca5	18191704	ATTTTTTT/ATTTTTTTTT	TGAAATCCGCCTAAATC CTG	TAATTGGGAACCAAAA AGC	60.0	715	INTERGENIC				
CaPOPI_3408		Ca5	18299239	GTTTTTTTT/GTTTTTTTT	ATCACAAATTTTCGCGA CCT	CGGGATTGTGAAGAAGT GGT	59.6	880	INTERGENIC				
CaPOPI_3409		Ca5	18404984	CATATATATATATATATATATA/CATA TATATATATATATATATATATATA	ATTTTGGACAACAGGTT CGC	GCAAGAACATGTGAGGA GCA	60.0	397	INTERGENIC				
CaPOPI_3410		Ca5	18589511	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTA TTATTAT/TTTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT	CACGTTCCCACTCTC TCA	TCCATTTACGGCAAATTC AA	59.9	829	INTERGENIC				
CaPOPI_3411		Ca5	18683897	AGCG/AGCGCGAGTCATCAGCTCGCG	ATGGCCGTTCTTAGTTG GTG	GTACAAAGGGCAGGGAC GTA	60.0	395	INTRAGENIC				
CaPOPI_3412		Ca5	18944656	CAAAA/CAA	TCCTGTCATGTGCTTTG AGC	CTAACCTCCCAGGACCC AAT	60.0	131	INTERGENIC				
CaPOPI_3413		Ca5	19351420	ATTTTTTT/ATTTTTTT	CAAGACCGCACAAATA CAA	AGGCAACACTTCTTGGT TGTC	59.6	618	INTERGENIC				
CaPOPI_3414		Ca5	19391673	ATTTTT/ATTTTTTT	CATGTTCGGCTGCACTT CTA	GATTTGGGCAATTTTAC GTC	60.0	663	INTERGENIC				
CaPOPI_3415		Ca5	19579350	A/AC	ACGAACGTTGAAAATCC AGC	GTATCAAGTGACACGCG GAA	60.1	489	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3431	Ca5	21152020	ATTTTTT/ATTTTTTT	AAATTGTGGGTTTCGCG TAG	GAGGTAGGTGGCAAG GACA	60.0	459	INTERGENIC				
CaPOPI_3432	Ca5	21411216	TAAAAAAA/TAAAAAAAAA	CCAAAGTGGGTCAATAA CGC	CTTCGACAGCCAGTTCA TCA	60.4	883	INTERGENIC				
CaPOPI_3433	Ca5	21623515	AAATTAATT/AAATT	AGGTCATTTTCATCCAC CCA	ACACACCTATGGGATGC ACA	60.2	678	INTERGENIC				
CaPOPI_3434	Ca5	21755455	CATAG/CATAGTATAG	TGGCTTTGTTGATCTCA TGC	ACCAATGCAAGCTGGAA GAA	59.8	363	INTERGENIC				
CaPOPI_3435	Ca5	21866481	GA/GAA	TCCGATTGGATTTTCAG GAC	GCTTCGTTCTTCGTCTT CG	59.9	437	INTERGENIC				
CaPOPI_3436	Ca5	21883868	AATATATATATATATATA/AATATATAT ATATATATATATA	GCTCCATTTGTGGTTCC AAT	CTATTTGCTATGCCGC TCC	59.8	405	INTRON	Ca_24467		C2H2	Glycoside hydrolase, family 28
CaPOPI_3437	Ca5	21899576	TAAAAAAAAAAAA/TAAAAAAAAA	TGACCTGACCTGGCCTA TTC	CCCCAACAAAGCCTTAT GGA	60.1	519	INTERGENIC				
CaPOPI_3438	Ca5	21965060	AG/AGG	ACGCTCAGAGTTCACTG GGT	GGCAAATCGATTGGACA AGT	59.9	365	INTERGENIC				
CaPOPI_3439	Ca5	22218019	TAAATTAAAATTAATAATTA/TAAATTA AAATTAAAATTAATAATTAATAA	AAATCCTGCATTTGTGA GGG	TGCTTATTGTGGCTGCT TTG	59.9	676	INTERGENIC				
CaPOPI_3440	Ca5	22631833	TGAGAGAGAGAGAGAGAGAGAGAGAG AGAGAGA/TGAGAGAGAGAGAGAGAGA GAGAGAGAGAGAGAGAGA	TGGAGAATTGGCTGGAG TTC	GCTTAAACTCATGGCGA AGC	60.2	749	INTRON	Ca_20079			Bromodomain
CaPOPI_3441	Ca5	22918447	T/TG	TTATCGGCCTTATCCAC TGC	GGATTCCACCAAATTC A GGA	60.1	721	INTERGENIC				
CaPOPI_3442	Ca5	22918526	AT/ATT	TTATCGGCCTTATCCAC TGC	TGAAATCCATGAACCG TGA	60.1	915	INTERGENIC				
CaPOPI_3443	Ca5	22919631	AG/A	GATTTGGTGGAATCTCC GAA	GCCACCGACTACTTCTC CCT	59.9	336	DRR	Ca_21962			
CaPOPI_3444	Ca5	22919722	GTT/GT	GATTTGGTGGAATCTCC GAA	GCCACCGACTACTTCTC CCT	59.9	336	DRR	Ca_21962			
CaPOPI_3445	Ca5	23051252	ATTTTTTTTT/ATTTTTTTTTT	TGGGACTAAAACATAGC GCC	ACGGATGAGTGACGTGA CAA	60.1	118	DRR	Ca_21972	U		Target SNARE coiled-coil domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3446	Ca5	23096429	TGTG/TGTGAGTG	GAATGTGCCGCCTATTG TTT	TGTCCTCCCTTAATTGC ACA	60.0	662	INTERGENIC				
CaPOPI_3447	Ca5	23111759	ACCCCC/ACCCCCC	TCTCACGGTTGTGAGGA CTG	TAGAGAAGTGTGCACCG TGG	59.9	600	INTERGENIC				
CaPOPI_3448	Ca5	23663097	TAATGAATGAATGAA/TAATGAATGAA	GAGGGTTTTGGGTCACT GAA	AGTTTTCAAGGGTAGCG GGT	59.9	789	INTERGENIC				
CaPOPI_3449	Ca5	23664574	TT/TTCCAAC	CAAGAAGGAACGAGGTG CTC	TAGCCTAGAGCAGGGGT GAA	60.0	626	INTERGENIC				
CaPOPI_3450	Ca5	23672060	TC/TCGCCC	TGAGTAAGGGGGCTGAA ATG	TGAGAGACGGTGGTTTA CCC	60.1	822	CDS (FRAME SHIFT)	Ca_17683			
CaPOPI_3451	Ca5	23770283	ATTTTT/ATTTTTT	TTGGCCTTCCTTTTACAT GC	CCATCAAGCGTCTGTG AGA	60.1	882	INTERGENIC				
CaPOPI_3452	Ca5	23812349	TAAAAAAAAA/TAAAAAAAAAAAAA AA	ATTGCTAGCCACATTT GGG	CGCTATGATAGGATGGT CCAA	60.0	664	INTERGENIC				
CaPOPI_3453	Ca5	23990846	GCCC/GCC	TTCAGCTGGTGCACCA TAG	AGTTGGAAGTCGCCATT TTG	59.9	261	INTERGENIC				
CaPOPI_3454	Ca5	24097297	AAGCTTTGGATAC/A	CAGAGCCAACACTACAG GCA	ATTTGAAGGGCCATGTG AAG	60.0	329	CDS (large-effect mutations)	Ca_17656	S		Protein of unknown function DUF3437
CaPOPI_3455	Ca5	24602434	GTAATAAATAAATAAATAAATAA/ GTAAATAAATAAATAAATAAATAA ATAAATAA	TCACATCAGTTAGGCCA CCA	GTTTCGAACACCGGACC TTA	60.1	235	INTRON	Ca_15595	G	bHLH	Protein kinase, catalytic domain
CaPOPI_3456	Ca5	24881793	TAAAAAAAAA/TAAAAAAAAAAAA	CCGAAAGAATAGCTGTT GGA	TTCAAAATCTGACGGA GGG	60.2	681	INTERGENIC				
CaPOPI_3457	Ca5	24932738	ATTTTTTT/ATTTTTTT	TGAAGAAACTTTTCGCC TGC	TGGAATTTTACGGTGC AGA	60.5	710	INTERGENIC				
CaPOPI_3458	Ca5	24982766	GTATATATATATATATATAT/ATATAT ATATATATATATATATAT	CTTGCCAGAAAATTGG AAA	CGTTGAATACGCCTAAC GGT	60.0	676	INTERGENIC				
CaPOPI_3459	Ca5	25050486	AATATATATATATATATATATATAT ATATATATAT/AAATATATATATATAT ATATATATATATATATATATATAT	AGTGGCGGAGCTTGATA GAA	GGGTCCAAGTTGAAC TAACCA	60.0	677	INTERGENIC				
CaPOPI_3460	Ca5	25186556	GAAAAAAAA/GAAAAAAAAA	TCAGAGGTACATTCGCC AGA	GTCAATTTGATAGGCC CCT	59.4	686	DRR	Ca_15627	L		Smr protein/MutS2 C-terminal

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3461	Ca5	25202952	ATTTTTTTTTTTT/ATTTTTTTTTTT	AACCAGGGTCTATTCCA TGC	TTGGTAATGCGTTGATG GTG	58.9	790	DRR	Ca_15629	O		Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
CaPOPI_3462	Ca5	25250090	ATCTT/AT	TGCTCTGACTCATTCAA CCG	TCCTTAGCTAGACGCC TGC	60.0	638	INTERGENIC				
CaPOPI_3463	Ca5	25288223	AGAAACTTGTGATTGAGGAAAC/AGAA C	TTGCTTGAAGACATGAA CGC	TGGATGTCAAGCAGTCT TGC	60.0	493	INTERGENIC				
CaPOPI_3464	Ca5	25600693	A/AT	CGTGCACTTTCACGACA AAT	TTGCTGTACTTGGTTGC TCG	59.8	801	INTRON	Ca_09030	E		Asparagine synthase
CaPOPI_3465	Ca5	25661861	TAAAAAAAA/TAAAAAAAA	GGAGTGACAATGCCCTC AAT	TCCGCTTGGGACAATTT TAG	59.9	432	INTERGENIC				
CaPOPI_3466	Ca5	25726766	AG/A	TCAAAGCGCGAGGAAAT AGT	ATTGTTGCCCAATGGAG AAG	60.0	315	INTERGENIC				
CaPOPI_3467	Ca5	25785107	CATA/CA	TGCCCGTGCTAATAATT TTG	AAGCACGGAAACAACGA TTT	58.7	580	INTERGENIC				
CaPOPI_3468	Ca5	25803856	TAAAAAAAAAAAA/TAAAAAAAAAAAA	ATCCGATAAATCGCATT GTG	CCCACAAGTCCGAGAA TTA	58.5	203	DRR	Ca_09020			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_3469	Ca5	25803970	TGGGGG/TGGGG	GGGGCGTTACATGTGGT ATC	TGTAGGGCACATTGGGT TTT	60.1	510	DRR	Ca_09020			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_3470	Ca5	25836482	AG/A	AAGGCAACAACAACAA GCC	ATGCCATTGAGCACATT GA	60.2	344	INTERGENIC				
CaPOPI_3471	Ca5	25922321	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT TATTATTATTATTA	AGGCGTTTGTGTATGGA AGG	ATTGGACAAAAGGAGGA CCC	60.0	580	INTERGENIC				
CaPOPI_3472	Ca5	26816643	AATATATATATATATATA/AATATATAT ATATATATATATA	CGCACAAAATCATGTG GAC	GGACACCCCAATTTCT CAA	60.0	896	INTERGENIC				
CaPOPI_3473	Ca5	26852877	TGAA/TGAACGTCGTCGATGTTAGGAA	CCATTGCTTGCTCGCTA AAT	CCCTCAAAGAATTTGGTT GGG	60.4	218	INTERGENIC				
CaPOPI_3474	Ca5	26889418	TAAAAAAAA/TAAAAAAAA	TCATCGCAGGTGTACCA TGT	TCCCTTTCGCAGACAAG AAT	60.0	712	INTERGENIC				
CaPOPI_3475	Ca5	26904550	GTTTTTTTTT/GTTTTTTTTT	CGTGGTAGACCTTCGGT GAT	TCCTTCACGAGTAAAT GTCTCA	60.0	786	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3476	Ca5	26995171	TAG/TAGCACAAGCACTAAG	GGAGCGGGAATATGACTGAA	GCGGCAGAAAGAACCTATTG	60.0	576	DRR	Ca_08931	R	MYB	
CaPOPI_3477	Ca5	26996806	A/AAAAGCAAAATTA	TCGTTTTGGGTGAATTGTGA	TGCCTCCTCGTTCCTTTTGA	59.9	410	INTERGENIC				
CaPOPI_3478	Ca5	27000467	AA/AAGA	TTGGCACTGAATAGTGC TCG	TCGAAGCTGTGCTAATG GTG	60.0	361	INTERGENIC				
CaPOPI_3479	Ca5	27000752	CTTTTTTTTTTTTT/CTTTTTTTTTTTT	TTGGCACTGAATAGTGC TCG	CGTCCCGAATAGACGAA CAT	60.0	698	INTERGENIC				
CaPOPI_3480	Ca5	27000834	ATCTCT/ATCT	TTGGCACTGAATAGTGC TCG	CTCAGCGGGTAGAGTAT CGC	60.0	940	INTERGENIC				
CaPOPI_3481	Ca5	27099226	GAA/GAAA	TGGCAGACAAACCAAC AAA	TGGTTTTGCCATGAGAC AGA	60.1	406	INTERGENIC				
CaPOPI_3482	Ca5	27364017	AAAAAAAAATAAAA/AAAAAAAAATAAAA AAAAATAAAA	CAAGAAGAGTCCATTGG GGA	GGTAAGACCACTCGATC AATCA	60.0	748	INTERGENIC				
CaPOPI_3483	Ca5	27389155	A/AAAAAT	CACGAGCTCAAGAGAG CCT	ATGAGATCGTTGTTGGG AGC	59.9	507	INTERGENIC				
CaPOPI_3484	Ca5	27393057	CAGTCATA/CAGTCATAGAGTAGTCATA	TGGTGCTGATGAATTTT CACTT	TGCAATTTCCCTTACGC TTT	59.6	639	INTERGENIC				
CaPOPI_3485	Ca5	27458409	ATTATATATAAAATTTTATATATAAAATT TTAT/ATTATATATAAAATTTTATATATAA AATTTTATATATAAAATTTTAT	CAATTGGTCGGCAGAGT TTT	CCCACAACCATGCAATA GAA	60.1	531	INTERGENIC				
CaPOPI_3486	Ca5	27460399	GAAAAAAAAA/GAAAAAAAAA	GCACATGTGTTGGCAAC TTT	AAAGCTCACCAATGCC ACT	59.6	456	INTERGENIC				
CaPOPI_3487	Ca5	27472549	AG/A	GCATTATGCCGTCATCA TTTT	TTCGCATTCAAATTGTT GTT	59.8	491	INTERGENIC				
CaPOPI_3488	Ca5	27477754	ATTTTTTATTTTTTTTTTATTTTTTTT/A TTTTTTTATTTTTTTTTTATTTTTTTTTT TTTTTTTT	CGGCCCTCCTTTTCTAG TCT	AAAAACCCAAATATGC CCC	59.8	678	INTRON	Ca_08905		bHLH	Protein kinase, catalytic domain
CaPOPI_3489	Ca5	27603143	GATATATATATATAT/GATATATATAT ATAT	CTTGCCCTTCATGCGAAT TTT	GATTTCAAAGATGCAGG GGA	60.2	555	DRR	Ca_08896			NAD(P)H-quinone oxidoreductase, subunit N
CaPOPI_3490	Ca5	27675113	GATATATATATATATATATATA/GATA TATATATATATATATATATA	TTGCCACTTGATACAGC AAAA	ATCGGTGGGAATAAGAG CCT	59.4	891	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3491	Ca5	27724401	GATATATATATATATATATA/GATATATATATATATATA	ACATCATTGGCATTGGGTTT	TGCAAAACTACAACGATCTCC	60.1	678	INTERGENIC				
CaPOPI_3492	Ca5	27880873	GAAAAAAAAA/GAAAAAAAAA	GGCAGCTTCTGTTTTGTCAAC	CATTCTCCTCCCAAAGGGT	59.9	786	INTERGENIC				
CaPOPI_3493	Ca5	27945125	TAATAATAA/TAATAATAAAATAATAA	TGGCTACATCCAGTCCCTTC	TTGGGCAATTTAGTTCTTGTTT	60.1	579	INTERGENIC				
CaPOPI_3494	Ca5	28012407	AATATATATATATATAT/AATATATATATATAT	TTGAAGGAAGATGAATCGTTGA	ATGCGGATACTCTCTGCCAC	59.7	622	DRR	Ca_13417	S		GIN5 complex, subunit Psf3
CaPOPI_3495	Ca5	28068856	CTATATATATATATATATATA/CTATATATATATATATATATA	GATTCGTCGGTTCACCTGTT	TGATGATGAATGTTGCACGA	60.1	139	INTERGENIC				
CaPOPI_3496	Ca5	28131912	ATTT/ATT	TGCCATATTCAGGAGTGTGC	ATGTACATTGCATGAGGCCA	59.7	850	INTERGENIC				
CaPOPI_3497	Ca5	28188039	T/TC	CAAGAAAAGTAACCATCGTAATGA	TGTGGATTCATGATCCTTGTTG	57.5	494	INTERGENIC				
CaPOPI_3498	Ca5	28234704	AATATATATATATATATATAT/AATATATATATATATATATATAT	TTTCAAGCTTTTGATGCAACG	TTTCTTTTCCAGTTCACACG	60.0	751	INTERGENIC				
CaPOPI_3499	Ca5	28342481	TTCAAAATCAAAATCAAAATCAAAATCA/TTCAAAATCAAAATCAAAATCA	CTCCTTAAGTGACGGCCCA	GGACTATTTTCGCGAATGAGTAA	60.1	329	INTERGENIC				
CaPOPI_3500	Ca5	28413401	A/AT	TTCTCCTTGAAGCTGTCTGGT	ATTGCCAACATTTCCGGTAG	60.0	252	INTERGENIC				
CaPOPI_3501	Ca5	28588926	TGGG/TGG	CAACTGCTCCTGTTCTCCAA	CTAGGAGCATGTCGCTCTCC	59.0	412	INTERGENIC				
CaPOPI_3502	Ca5	28864108	AATATATATATATATATATATAT/AATATATATATATATATATAT	AAAAGGGACGATACCTTGCCA	TCCTCTCAAAAGCCCTCAAA	59.6	787	DRR	Ca_13346		NF-YC	Histone chaperone domain CHZ
CaPOPI_3503	Ca5	28865362	TTCT/TT	TTTAGTGGTGCAAGTGCATGT	CGAAAGCTAGCCATGAGGTT	59.3	104	INTERGENIC				
CaPOPI_3504	Ca5	28974386	TAAAAAAAAA/TAAAAAAAAA	GCCATAATCGAGAGGAATGG	ATTAATCCCCGTCAAGACCC	59.5	527	INTERGENIC				
CaPOPI_3505	Ca5	29247345	ATTTTTTTTT/ATTTTTTTTTTT	CGTGGAAGAACTCCCTCAAAA	TGACGAGCGTAAGAACAATGC	60.1	853	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3521	Ca5	30128968	GATTATAATTAAAAATA/GATTATAATTA AAAATAATTATAATTAAAAATA	TGTTTCTCTCTCCGCTC ACA	CCGCCGACTATACCTGT TTT	59.7	681	INTERGENIC				
CaPOPI_3522	Ca5	30131050	AATATATATATATATATATATA/AATAT ATATATATATATATATA	CAAATTTGAGCAACAA TGC	AACACAAATGTTAAATTG CGAAGA	59.3	571	INTERGENIC				
CaPOPI_3523	Ca5	30135601	CAT/CATAT	CTGGTCCTCCTTCTGTC GAG	ATCCCATCAAAATAGCT GCG	60.0	426	DRR	Ca_04690	J	E2F/DP	Alanyl-tRNA synthetase, class IIc
CaPOPI_3524	Ca5	30355494	CATATATATATATATATATA/CATATA TATATATATATATATA	CCTTTGGTTCAAGTAAT GGCA	TGCACACCAATTCCA AGT	60.0	531	INTERGENIC				
CaPOPI_3525	Ca5	30712358	G/GGATAGAAA	TATTGGATTGGGCCAAA CAT	TTCGTTGGTTTGGGTT CTC	60.0	534	INTERGENIC				
CaPOPI_3526	Ca5	30835479	TTATATATAT/TTATATATATAT	TCGGCGATGTAAAATTC TCG	TGATAGACAAGCCACAT GCC	61.1	495	INTERGENIC				
CaPOPI_3527	Ca5	30858994	TTT/TTTATT	ATGAAGGCTGCGTTCTG ACT	GGCCCTTGGAAGTCACA TAA	60.0	214	DRR	Ca_04781		NF-YB	Protein kinase, catalytic domain
CaPOPI_3528	Ca5	30860511	CAA/CAAA	ATAGCAACACTCCATCC GCT	TTAGCAACTGATCGCCA CTG	59.7	580	INTERGENIC				
CaPOPI_3529	Ca5	30861801	TTAAT/TTAATGTAAT	TTACCTACTCCGAATGC CCA	TGATGGTGGTGAGGATC AAA	60.5	658	INTERGENIC				
CaPOPI_3530	Ca5	30864475	TAA/TAAA	TTCTGCAAGACGGTTCT GTG	CGGATGTCTACCTCGT GTT	60.0	260	INTRON	Ca_04782	T	bHLH	Protein kinase, catalytic domain
CaPOPI_3531	Ca5	30868972	AT/A	ACCATTCAATTTCTGCAG CC	ATTTCCATGTCCAACAA GGC	60.1	526	DRR	Ca_04782	T	bHLH	Protein kinase, catalytic domain
CaPOPI_3532	Ca5	30875873	ATT/ATTT	GTCGTCCAGCGTTAGG ATA	AAGAGAATTAGAGAAGA GTGCGG	60.1	318	DRR	Ca_04783		BES1	Glycoside hydrolase, family 17
CaPOPI_3533	Ca5	30886397	CTT/CTTT	GTGACATATTGAGGGTG GGG	CTCCCCAACGTAGAACC AAA	60.1	791	INTRON	Ca_04785	R		WD40 repeat
CaPOPI_3534	Ca5	30900578	AAAA/AAAAATAAA	AGTGTCACGTGAGAGTG CCA	TCAAAGGAGGCAATGG TAAA	60.5	570	DRR	Ca_04787	T	MYB_related	Protein kinase, catalytic domain
CaPOPI_3535	Ca5	30948697	CAA/CAAA	ATATTGTTGGTAGCGTC GGC	TGTGCGGAGACATCTTA TGC	60.0	601	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3536	Ca5	30959016	CTATAT/CTAT	GGGGCATACTGCTACGA TGT	TTCGCTACACCTTGACC ACA	60.0	639	INTERGENIC				
CaPOPI_3537	Ca5	30959641	AT/ATGATACT	TGTGGTCAAGGTGTAGC GAA	TGCCATGTATTCTGAGC GTC	60.3	425	INTERGENIC				
CaPOPI_3538	Ca5	30961731	A/AC	GCCTGTGCTATCTTGGC TTC	AGGATTGCTCCAGCAAA GAA	60.0	493	INTRON	Ca_04795	R		Sugar/inositol transporter
CaPOPI_3539	Ca5	30986745	GATAAAT/GATAAATTTGTCATTAATAAA T	AAAAAGACTGCAACAAG AAAAACT	TCTCATAACTGCATCCG CTG	57.9	957	INTERGENIC				
CaPOPI_3540	Ca5	30997360	GA/GAA	TTGGTGCCAAATTGGTG TAA	CTCTCGACTCTCAAATTC CGA	59.8	419	DRR	Ca_04797	K		ARID/BRIGHT DNA-binding domain
CaPOPI_3541	Ca5	31001905	AAT/AATATAT	CGACTCACGACAGAGGA TGA	CGAAGAGGAAATTTCTTG TTTGTTT	60.0	836	INTERGENIC				
CaPOPI_3542	Ca5	31038384	ATACTACT/ATACT	TCAAAACACAATCCTTCC TTCA	TGGAATAATGACGGTGA CGA	59.6	625	INTERGENIC				
CaPOPI_3543	Ca5	31045566	AT/ATT	AACTCACTTCACAATG CCC	CACTTGCAAATCAACCC CTT	60.0	231	INTRON	Ca_04803	O		Peptidase, cysteine peptidase active site
CaPOPI_3544	Ca5	31052451	TAAAAAAAAA/TAAAAAAAAA	TGGATCTTGCCATGTGG ATA	TCTGAAACCTGGTGGGA GAC	59.9	581	INTERGENIC				
CaPOPI_3545	Ca5	31065540	TATAA/TATAAATAA	GTGCATCCTTGTTTTCG GTT	GTGATGACTTCAAGGGG CAT	60.0	938	INTRON	Ca_04805	R		Sugar/inositol transporter
CaPOPI_3546	Ca5	31072835	A/AC	GTTTTTCATGCATTGCTC CCT	TTCAACCCAATGCACTT CAA	60.1	622	INTERGENIC				
CaPOPI_3547	Ca5	31084271	TAAC/TAACCAAC	GATTCGGGGCAACAAG TAA	ATTTACCCCCAACCTTA GC	59.9	524	DRR	Ca_04808			
CaPOPI_3548	Ca5	31094152	AATATATA/AATATA	TTTCATGCAATTCAAAAA TCG	CTGCCCAATGTCTAAT GCT	58.7	438	DRR	Ca_04810	O		Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain
CaPOPI_3549	Ca5	31110488	AGGATAATG/AG	GGTGAGTCAACGGCATT TTT	CCGGGTGCAAGTTCAGT AAA	60.0	279	INTERGENIC				
CaPOPI_3550	Ca5	31121983	TCAACTCCAACCTCAA/TCAACTCCAAC TCCAACCTCAA	CTGCTGCCAACTTCTC CTC	CCGTTTGTGCAGTGTTC ATC	60.1	614	INTRON	Ca_04814		NF-YC	Mlo-related protein

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3551	Ca5	31188289	TAAAA/TAAA	AAAGTGTTCCGAGCGAGAAA	GCATGAGTTCATTGGTG GTG	60.0	479	INTERGENIC				
CaPOPI_3552	Ca5	31193802	T/TTC	TTAATTCCAATGCGGAAAGC	CCTTTCCAATGCACCAAACT	60.0	367	DRR	Ca_04825	R	WOX	High mobility group, HMG1/HMG2
CaPOPI_3553	Ca5	31197193	TA/T	TTGGCTAAATACCTCTCGTTCC	GTCGGTTGAGCTAGGGCTTA	59.6	488	INTERGENIC				
CaPOPI_3554	Ca5	31229749	GATATATA/GATATATATA	TCGGCTCCTTTTCATTTACG	CTACCGATTGCAATCCAAAT	60.2	272	INTERGENIC				
CaPOPI_3555	Ca5	31241531	CTTTTTTT/CTTTTTTTTT	CGATGAACGCAAACTCAAGA	TAATCAACCAAAACCCCAAA	60.0	689	INTRON	Ca_04830	R		Bromodomain
CaPOPI_3556	Ca5	31255829	TG/T	AGACGGCAACAAATACTGGC	TGCTATTTTGGTGTGCGTAAAA	60.1	673	INTERGENIC				
CaPOPI_3557	Ca5	31256076	TA/TAA	TTTTTGTTGTAACGATGGCTAA	CGCTCAACACACGTTCAATT	57.5	672	INTERGENIC				
CaPOPI_3558	Ca5	31264749	TTATATATATAT/TTATATATATATATAT	CTGGAGCTGGTGTGTCAATTG	GGCCATTGCAAAAACCTGT	60.3	374	DRR	Ca_04832	T	WRKY	Protein kinase, catalytic domain
CaPOPI_3559	Ca5	31311316	CTTTT/CTTTTT	TTGGCACATATGGGGTTT	CCAACGCATAAGTCATGTGG	60.1	730	DRR	Ca_04834		Nin-like	Phox/Bem1p
CaPOPI_3560	Ca5	31333742	CAA/CA	GCGTTTGGGGTGACTTACAT	TGGTTCGTTCTGTGTGTGAT	59.9	780	INTRON	Ca_04835	P		Catalase
CaPOPI_3561	Ca5	31334829	TATTATAAAATT/TATT	AATGTCCCCAACCAATTTGA	ATGGGTGATAAATACCTGTTTTG	60.0	774	INTERGENIC				
CaPOPI_3562	Ca5	31375160	ATTT/ATT	TTGTCCGTTTGTTACGTGGA	TCCAAAGCCTGAAGCTCAAT	60.0	429	INTERGENIC				
CaPOPI_3563	Ca5	31412254	AATTA/AA	CACGTGTCCATCAAAATGTC	TGCAAGCGAATCAAACAAA	60.0	721	INTERGENIC				
CaPOPI_3564	Ca5	31435124	CTTTTT/CTTTTT	TTGAAATCCGATTGGTGACA	ATTTGGTGTCCCTTGTC TCG	59.9	538	INTERGENIC				
CaPOPI_3565	Ca5	31481808	TG/T	GATGTTTTGGTTGTTTTGGG	ACTACAGTCCACCGGCTTA	60.1	507	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3566	Ca5	31526667	CTTTTT/CTTTTTTT	GGATGTTTATTGGTCAT TTTTCG	TTGTGAAATGCACGAGA GAA	59.6	254	INTERGENIC				
CaPOPI_3567	Ca5	31532842	CTT/CTTT	AAGCAAAAGGGAGGGAT GAT	CCTGAAACTCAACCCA AGG	59.9	577	INTERGENIC				
CaPOPI_3568	Ca5	31539844	GTTTT/GTT	TGTTTGAAGGACCCAAT GAA	ACCGGAGAGGGCATAAA AGT	58.9	146	INTERGENIC				
CaPOPI_3569	Ca5	31585638	TTTAAATATTAAATATTAAAT/TTTAAATA TTAAATATTAAATATTAAAT	CACAGAATTTGGTGGCA TTG	TGATCATGCGTGGATTT TGT	60.0	745	DRR	Ca_04861	R		Tetracycline resistance protein, TetA
CaPOPI_3570	Ca5	31609524	T/TGTATATGAA	GCAGGCTGCCTATTTGA GTC	ATGTAGCAAACCTGCGG GTC	60.0	627	DRR	Ca_04863			
CaPOPI_3571	Ca5	31611802	TGGG/TGG	TTCTTACCTGGGCTGAA TGG	GCAGGCTGTTTCACAAC TGA	60.1	689	INTERGENIC				
CaPOPI_3572	Ca5	31621509	CTT/CTGTATATCTACTTTT	ATCCGAGTTTGCGTATG TCC	GGGACGTGGAGATTGTT GAT	60.0	635	INTERGENIC				
CaPOPI_3573	Ca5	31694006	GGAATGAATGAATGAATGA/GGAATGA ATGAATGAATGAATGAATGA	CCAAGCATGCTCATCAG AAA	TGAGAATGGGATCAGGG AAG	59.9	484	INTRON	Ca_04872		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_3574	Ca5	31710056	CA/CAGA	GCATTGAGTCAACAGC CAA	TTTTGCTTGAAGCCAGG TCT	59.8	353	DRR	Ca_04874			
CaPOPI_3575	Ca5	31716024	AAA/AAATAA	CAATGAAACCTGCAAC CTT	CACGAGAATCTCCCCTA CCA	60.0	717	INTRON	Ca_04875		FAR1	Lipase, GDSL
CaPOPI_3576	Ca5	31732127	CTGT/CT	TGCTAGCTTCTTCCAC GTT	AAAACGAACAAAATAAC ATTCTG	60.0	306	INTERGENIC				
CaPOPI_3577	Ca5	31754975	TTAT/TT	TTTGGTGCAGTACACT TCC	TGAGGATTTGGTTGAGA GGTG	58.8	261	INTERGENIC				
CaPOPI_3578	Ca5	31755077	CTTT/CT	TACACTCCGTGCACCG TTA	TGAGGATTTGGTTGAGA GGTG	60.2	250	INTERGENIC				
CaPOPI_3579	Ca5	31759396	G/GC	CCACAAGCAGCACAAAG TGT	GGATTAGCGCTGTGAC TTC	59.9	490	DRR	Ca_04880	O	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3580	Ca5	31772153	AATTAATATTAATAT/AATTAATAT	CTTGTGCCACACACAT TTT	TCCATTGTTGTTGTCGT CGT	59.5	498	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3581	Ca5	31787653	CA/C	GAACCCCAACACGCTTCTA	GCTTTAACGGCGCATATGTT	60.1	626	DRR	Ca_04883			
CaPOPI_3582	Ca5	31805131	GAAAAA/GAAAAAA	TGCAGTGGATAGATAACGGG	TCCTTTGGCAGTGTACAC	58.6	919	INTERGENIC				
CaPOPI_3583	Ca5	31807859	TCC/TC	AATCATACAGGTGGTGGTCT	TTGCATTGTTACATGCTCA	60.1	224	INTERGENIC				
CaPOPI_3584	Ca5	31809508	TAAAAAAA/TAAAAAA	TCTGTTCTCGACGTTGTTCG	CAAAGAACATGGACCA	60.0	637	INTRON	Ca_04886	Z		Tubulin
CaPOPI_3585	Ca5	31835201	TAAAAAAA/TAAAAAA	AGAGTGCATCTATGCGACC	CCAACAAAAGAGGGGA	60.2	211	INTERGENIC				
CaPOPI_3586	Ca5	31844171	CGG/CG	CAAGAACAGGGCCGTTAGA	CGGTAGCCTAATGAAC	60.2	371	INTERGENIC				
CaPOPI_3587	Ca5	31869532	TAA/TA	GCTGGAGGCACTTCAAGAGT	TTGGTCATTGAAATAATTGGGT	59.6	788	DRR	Ca_04893			
CaPOPI_3588	Ca5	31883810	AAAATTA/AAAATTATAAATTA	TGTGTTGTTGTTAAATCAGGATG	TGATTGCGGGATTTTATGGT	59.8	780	INTERGENIC				
CaPOPI_3589	Ca5	31886554	AATA/AA	AGGCTTCAAGTGCAGACAG	AATGGCTGGGCAGTAAACA	59.5	235	INTERGENIC				
CaPOPI_3590	Ca5	31887987	ATTTTTTTTT/ATTTTTTTTTTT	GTGAGGTGTGACTGGTGCAT	TTCAAGGACATGAATTTGCC	59.6	722	INTERGENIC				
CaPOPI_3591	Ca5	31932559	AAACAACA/AAACAACAACA	CAAATGGGAGGAAAAACCAA	TCATCAAAAGGGAAACCTGC	59.8	284	DRR	Ca_04898			Protein of unknown function DUF869, plant
CaPOPI_3592	Ca5	31941021	AATATATATATATATATATATATATAAATATATATATATATATATATATATA	CGTAACAAGGCCCAACAC	GCCCCCTTCAATAAATCAT	60.4	568	INTERGENIC				
CaPOPI_3593	Ca5	31967141	AATATATATATAT/AATATATATATATAT	ACGGGTCATTTTAAACACGC	TTCCGCCACCAAGTCATGATA	59.9	550	DRR	Ca_04900			Glyoxal oxidase, N-terminal
CaPOPI_3594	Ca5	31970233	CATATATATA/CATATATATATA	CGCTGTCACTAGGGAATGTGT	CTGTTTTACCACCCAA	60.2	435	INTERGENIC				
CaPOPI_3595	Ca5	31974245	GTTTTTTTTTT/GTTTTTTTTT	GGCTAAGTTTTCTTTGGGG	GCACTCCATGAATCAAGCA	59.9	696	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3596	Ca5	31999312	GA/G	AACGGTTATTTCCGGC TTT	TTACAACAGCACGTGCA ACC	59.8	433	DRR	Ca_04903		S1Fa-like	Protein kinase, catalytic domain
CaPOPI_3597	Ca5	32021738	CAAA/CA	CTTGGGAAGGTCAACA GAT	TACTGTCAGCATGGCAC CTC	60.0	659	INTRON	Ca_04906	S		Protein of unknown function DUF726
CaPOPI_3598	Ca5	32041461	CTT/CT	GAAGTAGCGGTCATGCC AAT	ATAGTGGAGGAGCTGGA GCA	60.1	338	DRR	Ca_04909	K	MIKC	Transcription factor, MADS-box
CaPOPI_3599	Ca5	32044892	T/TC	CTGTTTTTCACCGCCAA AAT	TCCTCCCTAATCACGCAT CC	60.0	763	INTERGENIC				
CaPOPI_3600	Ca5	32062989	ATATTATTATTATT/ATATTATTATTA TT	GAGGGAGAGCTCATGTG GAA	TTCGTGCATGCAAAATTG AGT	60.3	376	INTERGENIC				
CaPOPI_3601	Ca5	32068203	TT/TTGATAAATGAAT	TGAAAAATGGAATCCCA CTAGC	GAGCATTTAGTGGAGCG GAG	60.3	683	INTERGENIC				
CaPOPI_3602	Ca5	32087284	TAA/TAAA	GGATGTCACATTTTGGG ACC	TTGAGTTATACCATGCTT CTCAACA	60.0	553	DRR	Ca_04911	K	LBD	Transcription initiation factor IIF, beta subunit
CaPOPI_3603	Ca5	32087748	TAAAAA/TAAAAA	TTCTAAATGTTGAGAAG CATGG	TGTGTGTGTGGGTCAA TCT	57.1	630	DRR	Ca_04911	K	LBD	Transcription initiation factor IIF, beta subunit
CaPOPI_3604	Ca5	32096296	AGAT/AGATGAT	TTGTGGATACAAAAGA ATCTCAA	CACACCACCTCCTCCTG TTT	59.9	648	INTERGENIC				
CaPOPI_3605	Ca5	32100080	CATAT/CATATATAT	GTGGCATCAGGAATAGC GTT	CACCTAAAGGTCCCAAC CAA	60.1	480	INTRON	Ca_04912		ERF	Drug/metabolite transporter
CaPOPI_3606	Ca5	32149202	TCAC/TCACAC	AAATTCATTTTCGGGAA CC	GGTGGGAATCCTTGGA AAT	60.0	466	DRR	Ca_04917	G	C2H2	Tetrapyrrole methylase
CaPOPI_3607	Ca5	32163070	CCTTCTT/CCTTCTTCTT	CACGTGCCTTTTCTCAC TCA	GTTGATCTTTACGGCCT CCA	60.0	552	INTRON	Ca_04917	G	C2H2	Tetrapyrrole methylase
CaPOPI_3608	Ca5	32196357	TC/TCC	AGCATTTCCAAAGGGGA CTC	CCAAAACGGTGGACTGG TTA	60.4	779	INTRON	Ca_04919	K	TALE	Homeobox
CaPOPI_3609	Ca5	32201348	A/AC	ATGGAGTTGGCGTTTCT GTT	TTCTCCTGCCTCTCTCC AAA	59.6	772	INTRON	Ca_04920	M		Glycosyl transferase, group 1
CaPOPI_3610	Ca5	32226752	ACC/ACCC	TTGGGCGACGTTACTTT TAGA	GGAGTGGGTTATTCTTT TGGC	59.8	189	DRR	Ca_04923	T	WRKY	Protein kinase, catalytic domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3611	Ca5	32241464	GTAATAATAATAATA/GTAATAATAATAA TAATAATA	ATCATGGCCAAAAGAGG TTG	TCGGTTTGGTTTGGGTT AAA	59.9	724	INTERGENIC				
CaPOPI_3612	Ca5	32324347	GCTCTCTCTCTCTCTCTC/GCTCTCTCTC CTCTCTC	TGATGCCACGTGAGAAA GAG	CTGTTCAGATGCAGGC AAA	60.0	899	DRR	Ca_04930	I	bHLH	Cellular retinaldehyde binding/alpha-tocopherol transport
CaPOPI_3613	Ca5	32349699	TAAAAA/TAAAAA	AGGGGCCATGTGTAAGT ACG	CATTAACACCGATGAGG GCT	59.9	566	DRR	Ca_04933			
CaPOPI_3614	Ca5	32435142	TC/T	CCATCGCAAGGCTGTAA AAT	ACATGTCAAGTGGGGT GTT	60.1	873	INTERGENIC				
CaPOPI_3615	Ca5	32540371	TA/T	TGGTTGCTTGTGGTTT CTG	GTGAAAGAGCGTTAGAG CGG	59.7	706	INTERGENIC				
CaPOPI_3616	Ca5	32649599	ATTTTTTTTTT/ATTTTTTTTTT	TCGGACAAGTTAGCAA AACAA	CCGTATTTTGAATATCA GTGGC	59.8	561	INTERGENIC				
CaPOPI_3617	Ca5	32745764	TAAA/TAAA	AGGCATCACATTGAGGG ACT	CCTCGGTGACCCCTGAAT AAA	59.5	148	INTERGENIC				
CaPOPI_3618	Ca5	32848829	GAAAAAAAA/GAAAAAAAA	AACATTTACCAGTCCAG CGG	TCACCGTATGCAAAGAC GAG	60.0	848	INTERGENIC				
CaPOPI_3619	Ca5	32912336	AATATATATATATATATATAT/AA TATATATATATATATATATATATAT ATATATAT	ACCCCTCACCTCCTTA TTG	TTTTCTTGCCTCACTTGT TGA	60.2	499	INTERGENIC				
CaPOPI_3620	Ca5	33146690	TAAAAAAAA/TAAAAAAAA	TACCCGAACAACCTTGA CCC	TGCTTTCGTGATTCCAA CAA	59.8	731	DRR	Ca_05009	D	YABBY	Protein kinase, catalytic domain
CaPOPI_3621	Ca5	33444959	GATATA/GATATATA	TTATGGAGGCCACATTC ACA	GAAATTAAGGCCTCTTG ATCTTTTT	59.9	961	DRR	Ca_01912	O	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3622	Ca5	33456475	TTATGTTAAATATGTTAA/TTATGTTAAA TATGTTAAATATGTTAA	GATGAAGTGCTGATCAG AGGC	ACCAGGAAACATTGCCA GAC	60.0	789	DRR	Ca_01911	O	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3623	Ca5	33457018	TTTTATTATTTATTTA/TTTTATTATTTT ATTTATTTA	GCTGGCAATGTTTCCT GGT	GGTGGTGTATGTATATC TTTACGGG	60.0	430	DRR	Ca_01911	O	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3624	Ca5	33457459	ATT/ATTT	TCTTCAAATTAATTC ACCCA	GTTGAAATTTGGGTGT CGG	59.7	750	DRR	Ca_01911	O	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3625	Ca5	33457924	ATTTTTTT/ATTTTTTTT	CCGACACCCAAAATTC AAC	GCCCTCAGATGAGAGTC AGG	60.2	680	DRR	Ca_01911	O	MYB_rela ted	SANT domain, DNA binding

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3626	Ca5	33600042	CT/C	TAACCATTCCACAGCCA CAA	CTTAGAGGTCGCTTCAA CGG	60.0	680	DRR	Ca_01896			
CaPOPI_3627	Ca5	33687861	TTATATATATATATAT/TTATATATATATA T	GACTTCCTAAGGAGGGT GGC	ATTTCCACGGCAAATTC GTA	60.1	381	DRR	Ca_01887			
CaPOPI_3628	Ca5	34072036	CCCAAAGCAGAT/C	CATTGGTGTTCGTCT CGG	ACCGTTCCGTTTGTCT GAC	60.0	262	INTERGENIC				
CaPOPI_3629	Ca5	34164848	C/CA	CTTCCAGGGGATGCAAG ATA	CGTAGGCAATAAGACAC GCA	60.0	377	DRR	Ca_01832		NF-YB	FAS1 domain
CaPOPI_3630	Ca5	34629428	A/ACTTAAAAAGTTG	TTAGGTTGAGGCAGTTC GCT	TTTGGGTTTCGACCATA AAAA	60.0	587	INTERGENIC				
CaPOPI_3631	Ca5	34698063	GATAATAATAATAATAATAATAATAA TAATAA/GATAATAATAATAATAATAATA ATAATAATAATAATAA	ATGGCTTTTCCTACCTTC GG	ACCAAAACAAAACCAA CGG	60.4	560	INTERGENIC				
CaPOPI_3632	Ca5	34871969	GA/GAAATGAA	TGACGTTGCATTACCA AAT	AGGGAGGACGAAAATGA CCT	60.0	609	INTERGENIC				
CaPOPI_3633	Ca5	35072594	GATATATATATATATATATAT/GATAT ATATATATATATATATATATATAT	GGTAGAGGCACATGGG AAAA	CTTGAACCTCACATGC ATGAAC	59.9	760	INTERGENIC				
CaPOPI_3634	Ca5	35104483	TTATATATATATATATATAT/TTATATATA TATATATATATATATAT	GCTTCACCCACCTTCCA CTA	TCTTGTTTAGAGTGTG CAATGA	60.1	833	INTERGENIC				
CaPOPI_3635	Ca5	35190711	GAAAA/GAAAAA	TGTCACTTTTGTTTCGT CCT	TGAAATGTTGCCACTG TGT	57.4	454	DRR	Ca_01716	O		Proteasome component (PCI) domain
CaPOPI_3636	Ca5	35231327	ATTTTTTTT/ATTTTTTTTT	CACGAACCATAGCATGG GA	ATTGGATCGGGCCTAGT GTA	60.5	834	INTERGENIC				
CaPOPI_3637	Ca5	35328160	ATTTTTTTTT/ATTTTTTTTTT	ACCACGTGACCCCTTAA CTT	TGATGAAATTACGTTATA TTGAGGATG	58.4	204	INTERGENIC				
CaPOPI_3638	Ca5	35599782	TTATATATATATATATATATA/TTATAT ATATATATATATATA	ATTTCCAACTGTTTGGG CAG	TACTAGATCGCGTCCCA CG	60.0	665	INTERGENIC				
CaPOPI_3639	Ca5	35607633	CAATAATAATAATAATAATAATAATA AAAAATAATAATAATAAA/CAATAATAA TAATAATAATAATAATAATAATAATA AAAAATAATAATAATAAA	TCGTTTACAGCATCGAC CAA	GAACAATCTTGCACGT CCC	60.3	531	INTERGENIC				
CaPOPI_3640	Ca5	35734976	CNNNNNNNNN/CNNN	TTTTGGGCAACTTGTT AGG	TCAATATAAACGGCGAA GGG	60.0	570	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3641	Ca5	36120649	GA/GATAA	GCTTTCAGGCCAGACTA TGC	AGGGGTAGGAATAGGC CAGA	60.0	118	INTERGENIC				
CaPOPI_3642	Ca5	36176137	AATATATATATAT/AATATATATATATAT	TCATTGACATTTTGTCCC CA	TTGGTTGGAAAGGTTTG TCA	59.8	617	DRR	Ca_01608			
CaPOPI_3643	Ca5	36212540	GTT/GTTAGATT	TTTCATTGTTCCGTCAC CA	TTGAGTCAATGCAAGAG TCCTT	59.9	874	DRR	Ca_01603	I	B3	Lecithin:cholesterol acyltransferase
CaPOPI_3644	Ca5	36214320	G/GC	TACCAACCAACAATGC AGA	TGGTGATGGTGATGGAA CTG	60.0	475	DRR	Ca_01603	I	B3	Lecithin:cholesterol acyltransferase
CaPOPI_3645	Ca5	36308359	TTTATT/TTTATTGGTATTATTATTATT	GTTTGTGGCGGATTTTG TTT	CCGATACAACGGAATTG TCC	59.8	423	DRR	Ca_01593	Z		Interferon-related developmental regulator, C-terminal
CaPOPI_3646	Ca5	36583877	CATATATATATATATATAT/CATATATAT ATATATATATATAT	TCACTTTTAGGATCCGTT TGA	CACAATGGACCATGCAC TTC	57.4	809	INTERGENIC				
CaPOPI_3647	Ca5	36742914	CTTTTTTTTT/CTTTTTTTTTT	CAAATGTTGGGCTTGGA GTC	ATTTCTTTGGGGATTTTG GG	60.5	351	INTERGENIC				
CaPOPI_3648	Ca5	36897567	TTATATATATATATATATATATATATAT/T TATATATATATATATATATATATATATAT	AGTCCCATCTCAACTC GTG	TGATTTGGACGGAGAAA ACC	60.1	383	INTERGENIC				
CaPOPI_3649	Ca5	37015456	TTATATATATATATA/TTATATATATATAT ATA	TTGCATTTTGGCTCTCT CTCA	TGTCAGCATCATGCACT TCA	60.0	534	INTERGENIC				
CaPOPI_3650	Ca5	37229002	CCACACACACACACACACA/CCACA CACACACACACACA	GAGCTGCTGAGCTGGAC TTT	GCAACTGACTTGTTGTG CGT	59.9	281	INTERGENIC				
CaPOPI_3651	Ca5	37799581	CTTTTT/CTTTTTT	GCACCGTGATTTTGATG ATG	ATCAAGTCAGTGCTGCA TCG	59.9	594	DRR	Ca_01443			VQ
CaPOPI_3652	Ca5	38005397	CTCT/C	TGAGAGACCTTGATTGA TACAAATG	TCAATTTGGTTCCAACG TCAT	59.6	540	INTERGENIC				
CaPOPI_3653	Ca5	38016624	TAAGAAA/TAA	ATCCTCGAGAAGGAAGG AGC	CCTTTTCCCTCCAATGT CAA	59.9	276	INTRON	Ca_01419	A		Pseudouridine synthase, RsuA and RluB/C/D/E/F
CaPOPI_3654	Ca5	38019468	ATTTTTTT/ATTTTTTT	TTTTTCAGCTTTGGAC CAG	CAAACGTAACCATTTGTG CCA	60.2	644	DRR	Ca_01419	A		Pseudouridine synthase, RsuA and RluB/C/D/E/F
CaPOPI_3655	Ca5	38021365	AAAGCA/AAAGCAAGCA	TCTTGCATTTTCTCAGC CT	ATTTTGGCAGCTGTCTT TGG	60.0	507	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3656	Ca5	38023980	AACACAC/AACAC	CCGCAGTAAGAGTTGACCA	TTCCGAGGAATGTTGTTC	58.9	548	INTERGENIC				
CaPOPI_3657	Ca5	38032027	ATCTCTCTCTC/ATCTCTCTCTCTC	CAGTGGTGCGAGAAAAAGAA	TTCCATAATGTCCACGC AAA	60.0	429	INTERGENIC				
CaPOPI_3658	Ca5	38034605	CG/CGG	CTGCTATTGCGATCCCTCTC	TTTTGAACGCAAGAAAA CAGAA	59.9	800	INTERGENIC				
CaPOPI_3659	Ca5	38034841	TTTA/TTTAATTA	TCGTCCGATTTATACCGACA	CGACGAGGTATATGCCAACA	59.0	856	INTERGENIC				
CaPOPI_3660	Ca5	38042134	T/TA	TTGTCATAGGTTATACGTAGGTCTC	GGGGACCAAAACCACAA TTA	59.0	265	INTERGENIC				
CaPOPI_3661	Ca5	38043572	TAAAA/TAAA	AGGAGGCTAATTGAGGGAGC	TGTGGGTGCATGGTAGA AAA	59.8	519	INTERGENIC				
CaPOPI_3662	Ca5	38045991	ATT/ATTTCTT	TGACATTTTCAATGCCAG	TGAAATGCGAAAGAGGTGAA	59.5	652	INTERGENIC				
CaPOPI_3663	Ca5	38052063	CATATGAATATATGAAT/CATATGAAT	CAACAAAATTCCCAAAAATTGA	TTTTTGGCAGTTATCGA CATT	60.1	822	INTERGENIC				
CaPOPI_3664	Ca5	38067693	CTATATA/CTATATATA	GAGCACAATAATTTTCGTCAACA	GCGACAGATTCAACTCAGAGA	59.2	593	DRR	Ca_01413			
CaPOPI_3665	Ca5	38068190	GAAAAGAAAAAGA/GAAAAGAAAAAGAA AAAGA	GCAATGTGCACAATCCA AAC	CCCTTACCTGCTAAGCG AAA	60.0	580	DRR	Ca_01413			
CaPOPI_3666	Ca5	38075218	GTTTTTTTTTTTT/GTTTTTTTTTTT	ATTTTGAAGCTGTTGGTGG	TGATCCACTCCCCTCTTGTC	60.0	457	DRR	Ca_01412	O	MYB_related	Ubiquitin-associated/translation elongation factor EF1B, N-terminal
CaPOPI_3667	Ca5	38075506	TCC/TC	GACAAGAGGGGAGTGGATCA	CACAACGGCAAGACAGACAT	60.0	441	DRR	Ca_01412	O	MYB_related	Ubiquitin-associated/translation elongation factor EF1B, N-terminal
CaPOPI_3668	Ca5	38102985	TA/T	GCTGGTGGCATACTTTGGTT	GTCCATGACAGCAGCAAAA	60.0	122	CDS (FRAME SHIFT)	Ca_01408	P		
CaPOPI_3669	Ca5	38107026	AAAACAA/AAA	GGGCTTTCTTGAAGGGTTTC	TGTGCCTAATGAAGTTGCCA	60.1	564	INTERGENIC				
CaPOPI_3670	Ca5	38110715	CATATATATATATA/CATATATATATA	TATACGCAGCCCACAATCAC	GATTGTCTGCTGGATTGGT	59.6	426	DRR	Ca_01407	S		

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3686	Ca5	39872057	GATATATATATATATATATATATATA/ GATATATATATATATATATATATATAT A	AGGAAACATTGGTGGG ACA	ATCAAACAACCGAAAGT GCC	60.2	656	DRR	Ca_07512	F		Xanthine/uracil/vitamin C permease
CaPOPI_3687	Ca5	39927528	TTATATATATATATATATAT/TTATATATA TATATATAT	ATAGGGGGCAACTAGGG GCTA	AAACATGGACAAGAGAC CGC	59.9	360	INTERGENIC				
CaPOPI_3688	Ca5	39996193	ATTTTTTTTT/ATTTTTTTTT	GCATCCCAAGAATACAA CCG	AACAAACCTCTCCGCA ATG	60.3	413	INTERGENIC				
CaPOPI_3689	Ca5	40119931	GAAAAAAAAA/GAAAAAAAAA	AAATTGTTGGGAAATTG GCA	GGGAAAAGCGCTTCTAA GGT	60.2	757	INTERGENIC				
CaPOPI_3690	Ca5	40191220	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAAT/AAATAATAATA ATAATAATAATAATAATAATAATAAT AATAATAATAATAAT	TTCATGAGTGGGTGGTA GTTTG	TTGAATTTTTGTTTGGCT TGA	59.9	257	INTERGENIC				
CaPOPI_3691	Ca5	40223853	ATTGTTTGTT/ATTGTT	GTCTCTCCCAACCACC TCA	CCTTCATTGGTTGTCGT GTG	60.1	451	INTRON	Ca_07547	R		RNA recognition motif domain
CaPOPI_3692	Ca5	40392907	GTATATATATATATATATATATATATA TATAT/GTATATATATATATATATATA TATATAT	GCATTATCACGAGCAAC ACG	TCAATGTGGTTCGCAAA AGA	60.3	192	INTERGENIC				
CaPOPI_3693	Ca5	40471737	CTTTTTTTTT/CTTTTTTTTT	TGATTTTCCCTGTGCAT CAA	AATGTGGCAAAGGATT CAG	60.0	757	DRR	Ca_07567			Double-stranded RNA-binding
CaPOPI_3694	Ca5	40493832	CTATATATATATATATATATATA/CTA TATATATATATATATATATA	TGCACAAAATATCGGGA GAA	GGGACCACGGGAACAT TTT	59.1	779	DRR	Ca_07570		C3H	Leucine-rich repeat
CaPOPI_3695	Ca5	40750478	TGGGG/TGGG	ATGTTATCAACCTCGC TCG	TCAATTCCTCTTTTAA TAACGTG	60.1	510	INTERGENIC				
CaPOPI_3696	Ca5	40968327	TAAAAAAAA/TAAAAAAAA	CAAAATTTCAATCAAAA CCCA	TACATTCCCGTGGTCCC TTA	58.9	393	INTERGENIC				
CaPOPI_3697	Ca5	40970000	AATATATATATATATATATATAT/AA TATATATATATATATATATATAT	TGCATTTAATCAGAGAC GTAAAGG	TAAAGGGGCACATTCAA AGC	59.7	246	INTERGENIC				
CaPOPI_3698	Ca5	40983709	AATATATATATATATATATATATATAT ATAT/AAATATATATATATATATATAT	TTGTCAGCACATCACAA CCA	CAAAGAGTCGTCACGTT GACTT	59.7	603	INTERGENIC				
CaPOPI_3699	Ca5	41063761	CTTTTTTT/CTTTT	TTTGCAGCCACAAAAGA CAG	GCCCTCACAAACGTTGA TTT	60.0	122	INTERGENIC				
CaPOPI_3700	Ca5	41124249	TCAACA/CAACAACA	ATATTGTTCAGCACCCG AGG	CAGACGACGAATGAAG CAA	60.0	361	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3701	Ca5	41179556	AA/AAAGAGTGTGAAAAGA	GACTCAATGCAGATGGG GTT	GTCCCATACCTGCAAAA GGA	59.9	596	INTRON	Ca_07636			
CaPOPI_3702	Ca5	41226745	CAAAAAAAAA/CAAAAAAAAAAAAA	GCCCCAAATCAAAAACCT CCA	TGTGTCGTAAAAAGATG TCTAAGCA	59.9	611	INTERGENIC				
CaPOPI_3703	Ca5	41250178	TTATATATATATATATATAT/TTATATA TATATATATATAT	CAGTTGAGACTGGGCAG ACA	GCATCCCATCTTGAGTT GCT	60.0	640	DRR	Ca_07641		CO-like	Zinc finger, B-box
CaPOPI_3704	Ca5	41455567	AATATATATATATATATATATATAT/ AATATATATATATATATATATATA	TTGCCACTTGATACAGC AAAA	TGCATGTTGAAACACCG ACT	59.4	757	INTERGENIC				
CaPOPI_3705	Ca5	41459766	CTATTATTATTATTATT/CTATTATTA TTATTATTATTATT	GGACGTAGAAAATTAAT GACATGG	TAGGGAGGGCTTTGTAA GCA	58.9	479	INTERGENIC				
CaPOPI_3706	Ca5	41467556	TA/TAA	AAAGGATGCAGTATGGG TTTTT	TCACTGGGTGGAAAAA TGAG	58.9	453	INTERGENIC				
CaPOPI_3707	Ca5	41467725	CTT/CTTT	CTCATTTTTCCACCCAAG TGA	AGCGACAAGATGAAAGC TCC	60.0	529	INTERGENIC				
CaPOPI_3708	Ca5	41477742	CAA/CAAA	TGAGGCAAGCATGTGTA AGC	AATGTGCATGAGAGGCT GTG	60.0	223	DRR	Ca_19232	B	MYB_rela ted	SANT domain, DNA binding
CaPOPI_3709	Ca5	41603707	GTATATATATATATATATATAT/GT ATATATATATATATATATATATATA TAT	ACGTCCATTTCCATGT GGT	TTGCCATTTCCATCTTCC TC	60.1	444	INTERGENIC				
CaPOPI_3710	Ca5	41614182	AATATATATATATATATAT/ AATATATA TATATATATATATAT	TGTGGATTCATGATCCT TGTG	TTTAACGTCAATGCCAA CTTT	59.4	916	INTERGENIC				
CaPOPI_3711	Ca5	41678103	TCT/TCTTCCCTTAAAGGGACT	CAGTGGGTCCCTCTTCCA CAT	CCCGAACTCCTGTTACT CCA	60.0	551	INTRON	Ca_19215	J	C3H	Argonaute/Dicer protein, PAZ
CaPOPI_3712	Ca5	41795988	ATT/AT	TGGAATGCTACACAAGC TGC	TTGAGGTGCATCGATCA AAA	60.0	317	INTERGENIC				
CaPOPI_3713	Ca5	41854653	AATATATATATATATATATATA/AAT ATATATATATATATATATA	TTACGGCTACCACCGAA AAC	CTCCCACTCAAAGTTT GTTCA	60.0	488	INTERGENIC				
CaPOPI_3714	Ca5	41858516	TTATATATATATATATATATATATA TAT/TTATATATATATATATATATAT ATATATATAT	AGCAATGAACAACGCAT CAA	AAGGCATCATCATTTGA GAAAGA	60.3	614	INTERGENIC				
CaPOPI_3715	Ca5	42231500	CC/CCGAGAACGTAC	TCAAAATCCACCCCCA CTT	GCCATCTCCAATAGCAC CAT	60.2	888	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3716	Ca5	42425779	CATGTTTTATGTTTTA/CATGTTTTA	TCAATGGAATGGAGTCG TCA	CGACAATTCATTATCCG TCC	60.0	749	INTERGENIC				
CaPOPI_3717	Ca5	42427468	TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATAT	CAACTGATCGGAGTGGG ATT	AAATCCTTAAGATCGGC GGT	59.9	618	DRR	Ca_11375			Proteinase inhibitor I25, cystatin, conserved region
CaPOPI_3718	Ca5	42975249	CTTATTATTATTATTATTATTATTATTAT TATT/CTTATTATTATTATTATTATTATTA TTATT	TCTGATGAGTTGCTTGT GCC	GGCCGCAATTATTGTTT TGT	60.0	528	INTERGENIC				
CaPOPI_3719	Ca5	43073124	CA/CAA	ACACGGCTCAAGCACTT TTT	GACACCATGTCCAACAT GTCA	59.9	665	INTRON	Ca_11300	OU	WRKY	Membrane insertion protein, OxaY/YidC
CaPOPI_3720	Ca5	43722797	TAAAAAAA/TAAAAAAA	CATTGTCCAATGGCATG TTT	CGAGTGTCTGTTAACCG CTG	59.3	822	DRR	Ca_12680	P	MIKC	Sulphate transporter/antisigma-factor antagonist STAS
CaPOPI_3721	Ca5	43921147	CTATA/CTATATA	TGGGACCAAAACATGTGA AGA	TCTAATTGTTTTGATTTA TCCCTCA	59.9	583	INTERGENIC				
CaPOPI_3722	Ca5	44596809	ATT/ATTT	TTGGCACATGCATTTTT GTT	GACCAAACTCTGTGTGT GCAGA	60.0	582	INTERGENIC				
CaPOPI_3723	Ca5	44597112	CTATA/CTATATATA	GGGGTTAGTGCAAGCCA AAT	GTTCGCACGTGATGAAC AAT	61.2	862	INTERGENIC				
CaPOPI_3724	Ca5	45086826	TA/TAA	CAACGCAAAATTAAACA CACAA	AATACAGCTGGGTTTGT GGC	60.0	367	INTERGENIC				
CaPOPI_3725	Ca5	45098220	ATTTTT/ATTTTTTT	ATGTTCGAAACGCTGAT TCC	TTGCCAAGCCTTTTGAA ACT	60.1	121	INTERGENIC				
CaPOPI_3726	Ca5	45449782	GAAAAAAAAA/GAAAAAAAAA	TCCATATTCGGTAGCCG TTC	TGATGCACCCAAAATA CGA	59.9	579	INTERGENIC				
CaPOPI_3727	Ca5	45511101	TA/TAA	CAAGGTTTCTCTTCGCTGC	CTCAAATTGGTCCCCTG AAA	60.1	539	INTRON	Ca_03998	T		Protein phosphatase 2C, manganese/magnesium aspartate binding
CaPOPI_3728	Ca5	45989618	TAAAAAAAAA/TAAAAAAAAA	TTGCTCCTCTGGTCCTC ACT	GTTGGCTTTCGTACCCT CAA	60.0	325	INTRON	Ca_04045		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_3729	Ca5	46056306	GTTATTATTATTATTATTATTATTATTAT TATTATTATTATTATTATT/GTTATTATTAT TATTATTATTATTATTATTATTATTATT ATTATTATTATT	TTGTTTGGTCCACATTC CTG	GGAGCATATCAATGGAA AATCA	59.4	779	INTERGENIC				
CaPOPI_3730	Ca5	46070562	AATATATATATATATATA/AATATATAT ATATATATA	TGGCAAAATTCATACGT GGA	AAAACCGTCCAACATC CAT	59.9	515	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3731	Ca5	46132848	TTTATTATTATTATTATTATTATTAT TATTATTATT/TTTATTATTATTATTAT TTATTATTATTATTATTATTATT	TGTACCGTCACATTGCA CCT	TACTGTATCAACGCCGC AAG	60.0	771	INTERGENIC				
CaPOPI_3732	Ca5	46208612	AAT/AATAT	ATGCAGCACAAAATGCA AGT	TTCGAATCTTATTTTGAC AATTTTT	59.4	502	INTERGENIC				
CaPOPI_3733	Ca5	46212141	AATGATG/AATG	AAAAATCAATCCTTTCTC CAATG	AGTTTCAAAAACGGTGG TGG	58.6	107	INTERGENIC				
CaPOPI_3734	Ca5	46231130	ATTTTTTTT/ATTTTTTTT	GGAAGCCAAGCATTCAA GAG	TGGAAAAAGAAATGAAAT TGCTTA	60.0	849	INTERGENIC				
CaPOPI_3735	Ca5	46271953	TTTTAATT/TTTTAATTTAATT	CCATCAATGTTGGTCA CTCC	ATTCACTCGCCTTGTCT GT	60.2	352	INTERGENIC				
CaPOPI_3736	Ca5	46425096	ATT/ATTT	GCGAGAATGGACTCCAG AAA	TCTCGTATTGACGGAAT GACA	60.3	323	DRR	Ca_04100		WRKY	DNA-binding WRKY
CaPOPI_3737	Ca5	46429100	GAAAAAAAAA/GAAAAAAAAA	TGCTCACGTTCTTTGTT GG	TTGGTCTTGCTTCTTTCA AATG	59.9	501	INTERGENIC				
CaPOPI_3738	Ca5	46490687	CTTTTTTTTT/CTTTTTTTTT	CTCTGAACCCCTCTCAC CAC	CCAACTCCTTGGCAGGT TTA	59.7	481	INTERGENIC				
CaPOPI_3739	Ca5	46637208	TGAG/TGAGAG	TGGACTAGTGGGCCTA TGG	TATGGGCATGAGCTGTC AAA	59.9	361	DRR	Ca_04123	V		Dual specificity phosphatase, catalytic domain
CaPOPI_3740	Ca5	46654455	AATATATATATATATATATATATAT/ AATATATATATATATATATATATAT AT	ATGCTCTTGAATCGTG GTC	CATCGTTTTCTCGTTCAT GC	60.1	781	INTERGENIC				
CaPOPI_3741	Ca5	46661039	AATATATATATATATATATAT/AATATA TATATATATATATATAT	TGGAATTCAAGGGACCA AAA	ACTTGCGAGATAATTTA GTAGGGA	60.3	863	INTERGENIC				
CaPOPI_3742	Ca5	46886435	T/TTAACTATACTCAAAC	CAGCCATGCTCGTATGC TAA	AGAACCCCATCCAACA ATG	60.0	444	INTERGENIC				
CaPOPI_3743	Ca5	47118403	GTATTATTATTATTATTATTATT/GT ATTATTATTATTATTATTATT	ATTCGAATAATGGGTGG CAA	TTGGGTCAAGTAGGAGG TCG	60.2	515	INTERGENIC				
CaPOPI_3744	Ca5	47138535	CTATTATTATTATTATTATTATT/CT ATTATTATTATTATTATTATTATTAT TA	TGAATCTTCCGCATTG TG	CCTGAAAGACTTAGACG GCG	59.7	651	INTERGENIC				
CaPOPI_3745	Ca5	47166855	GAAAAAAAAA/GAAAAAAAAA	CGTGGAATCCATCGAAT TTT	GTGGCACCTTTTGTCTC AAT	59.8	117	DRR	Ca_04173	J		Ribosomal protein S2

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPl_3746	Ca5	47226447	TTTATATTATATTATATTATAT/TTTATATATATTATATTATATTATAT	ACCGTTACCTTTTGTCG CTG	GAGCTTTCACGTACGG AGC	60.0	449	INTERGENIC				
CaPOPl_3747	Ca5	47512183	GTTTTTTTTT/GTTTTTTTTTTT	TGGCATATCCCATCC ATA	TGTGGGTATAAATGAGG GGC	60.9	404	INTERGENIC				
CaPOPl_3748	Ca5	47553707	GAA/GAAA	ATGATGAATGTCCGACA ACG	CAAAAGACAACCAAGGG CAT	59.4	744	INTERGENIC				
CaPOPl_3749	Ca5	47588093	AT/A	TGTGGTTAGAATCCTGG CTC A	TTCGAATTCAGGACAAG ACG	60.6	385	INTERGENIC				
CaPOPl_3750	Ca5	47838081	AATATATATATATATATATATA/AATAT ATATATATATATATATATA	TACCTCATTGTAGGCC AGC	TAGTTCGGGGCAAATGG TAG	60.1	168	INTERGENIC				
CaPOPl_3751	Ca5	47945436	AATATATATATATATATATATATA/AAT ATATATATATATATATATATATA TATA	ACATCAAAGGCGGATCC ATA	TCCTCGAACACACACA TTT	60.3	392	INTERGENIC				
CaPOPl_3752	Ca5	48059653	TTCTC/TTC	CGAAACTCCACTGCAGA CAA	GCATATTTGCAAGCAC AAA	60.0	804	DRR	Ca_04266	R	ERF	Pentatricopeptide repeat
CaPOPl_3753	Ca5	48121332	TTTTATTATTATTATTATTATTATTAT TTAT/TTTTATTATTATTATTATTATTTA TTTAT	ATTTTATGGCCAACCCA ACA	ACTCGGCTTCCATTGAT GAG	60.1	178	INTERGENIC				
CaPOPl_3754	Ca5	48164734	AGG/AG	GGTTGCAATTATGGGAA ATGTT	AACTCTAAATCCCCGCA AGG	60.0	485	INTERGENIC				
CaPOPl_3755	Ca6	112870	TG/T	AACTCCTTGGGACC GTG ATT	ACCTTGCAACTGGAGCA AAT	60.7	242	INTERGENIC				
CaPOPl_3756	Ca6	233726	CTATTATTATTATTATTATTATTATT TATTATTATTATTATTATTAT/CTATT TATTATTATTATTATTATTATTATTA TTTATTATTATTATTATTATTATTATT	CGGATCCCACCACTTGA TAA	TTGATCGTTGGGTTGAT GAAT	60.7	640	INTERGENIC				
CaPOPl_3757	Ca6	472874	AT/A	TTTTCTTCTCCCTTTG AC	AGCAAGAAACAAACGAC GCT	59.3	719	DRR	Ca_13267		G2-like	Myb, DNA-binding
CaPOPl_3758	Ca6	582030	AATATATATATATATA/AATATATATAT ATATATATA	AAAACTGAAGATCTTCA CAAA	TGGCCTAATCTTTGTGG GAC	57.2	264	DRR	Ca_13279	O	SRS	Peptidase A1
CaPOPl_3759	Ca6	1239992	CATATATATA/CATATATATATA	CGAGACCAAAGTTTCT TGC	GACATGGCAATTTAGCT CAACA	59.9	684	INTERGENIC				
CaPOPl_3760	Ca6	1343859	GAAAAA/GAAAAAA	CAACGAGTTTGATTCTTA TTCTAACG	TTGGGTAGCCAAGGTTT CAC	59.7	721	INTERGENIC				

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CaPOPI_3761	Ca6	1350878	A/AGTCTGT	ACACATCAGCTTTTTGGCTG	AGCCCACTCACCTTCTTCCT	58.9	428	INTERGENIC				
CaPOPI_3762	Ca6	1353833	CAA/CAAA	TGTTTAAAGGGGTGGCATT	ACGGAAGGATCCAGTAGGCT	59.5	513	INTERGENIC				
CaPOPI_3763	Ca6	1354322	GAA/GAACCAA	AATTTGCATAGGCGGTGAAG	GGTGTACAGCTTTCATGAACAAA	60.1	420	INTERGENIC				
CaPOPI_3764	Ca6	1468628	TAAAAAAAAA/TAAAAAAAAA	AAGAATGGAGCTCAAGGGGT	GCCTCCAAAAAGTAATCCC	60.1	405	INTERGENIC				
CaPOPI_3765	Ca6	1491943	CT/CTT	TGGTTTTCGTACCGGACTCT	CAATGTCATCAAATAGCGGC	59.6	772	INTRON	Ca_27033	H		Folypolyglutamate synthetase
CaPOPI_3766	Ca6	1492206	TAAGAAGAAAAG/TAAGAAGAAAAGAAGAAAAG	CCGTGCATATGACAGAAATGA	ATGCACCGTTGAAACAA	59.6	510	INTRON	Ca_27033	H		Folypolyglutamate synthetase
CaPOPI_3767	Ca6	1492346	ATAGC/ATAGCGCCGCTGTAGC	CCGTGCATATGACAGAAATGA	ATGCACCGTTGAAACAA	59.6	510	INTRON	Ca_27033	H		Folypolyglutamate synthetase
CaPOPI_3768	Ca6	1492728	AT/ATT	TTGTTGTTTCAACGGTGCAT	ATGGTTGGGGGATAAAAGG	60.0	651	INTRON	Ca_27033	H		Folypolyglutamate synthetase
CaPOPI_3769	Ca6	1542114	ATT/ATTT	TGCACTTTGTGCACTCCTTA	GTAATGCTGCGTGCAAAACA	58.1	334	INTERGENIC				
CaPOPI_3770	Ca6	1556325	TAAA/TAAAAAAAAA	ATTGTTCTCCGTTGTCA	GTGATCGACATACTTCGGCA	60.0	864	INTERGENIC				
CaPOPI_3771	Ca6	1556869	TAAAA/TAAAAA	CAATTTGGTTGGGCGTA	TTGCTTTATACTCATATT	60.2	528	INTERGENIC				
CaPOPI_3772	Ca6	1557117	TAAAAAAAA/TAAAAAAAAA	GCTTTTCTTTCATATTGCGTT	TTTTGAGCGGAAAGAGTCGT	59.6	674	INTERGENIC				
CaPOPI_3773	Ca6	1559285	GTTA/GTTATTA	CAGAGCAGTGTGACAGCAAGA	TCAAAAATTTCAAACAAATCCA	60.4	456	INTERGENIC				
CaPOPI_3774	Ca6	1559495	GAACAAA/GA	GGATTTTGTTGAAATTTTGATG	TATTTTATTCCCACCGCTGC	58.9	445	INTERGENIC				
CaPOPI_3775	Ca6	1559581	ATTTTTTTTTTT/ATTTTTTTTTT	TGAAGTTAAATTAAGGATCGCA	TATTTTATTCCCACCGCTGC	58.0	283	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3776	Ca6	1560016	TTT/TTTAATT	AATATTACTGCAGCGTGGG	GGACCACAAGAAATCCTCCA	60.0	719	INTERGENIC				
CaPOPI_3777	Ca6	1682722	GTGCATCTGTTT/G	GAGGCATTGTCTTTGGTGGT	GCAAATGTTTGAATGGCTT	60.0	656	INTERGENIC				
CaPOPI_3778	Ca6	1683094	TATTAAC/TATTAACCATGATTAAAC	AATAAGTCCATCCGGTCTCT	TTGTGGATGGCGTTGTAA	59.9	276	DRR	Ca_10299		HB-other	Rop nucleotide exchanger, PRONE
CaPOPI_3779	Ca6	1683226	CAA/CA	AATAAGTCCATCCGGTCTCT	TTGTGGATGGCGTTGTAA	59.9	276	DRR	Ca_10299		HB-other	Rop nucleotide exchanger, PRONE
CaPOPI_3780	Ca6	1683327	AC/A	TTATCAAACGCCATCCACAA	CACTTGCCTGTGGTAGTGCT	59.9	504	DRR	Ca_10299		HB-other	Rop nucleotide exchanger, PRONE
CaPOPI_3781	Ca6	1728817	GTTTTTTTTT/GTTTTTTTTT	ATGGCTCCTTGATTTCGATG	TCAAAAAGGACAATTAAAGCCA	60.0	539	INTERGENIC				
CaPOPI_3782	Ca6	1788325	CTTTTTTTTTT/CTTTTTTTTTT	AGGGTGTAAGGCATGGATGA	CCATCAATCAAAGCAAAACCA	60.3	330	INTERGENIC				
CaPOPI_3783	Ca6	1820872	TTG/TTGGTG	CCCACGGGTAACAACCTCAAT	CGGGTTGGTTTGATTCAAGT	59.7	707	DRR	Ca_10309			Acid phosphatase (Class B)
CaPOPI_3784	Ca6	1824130	GT/GTT	TTGCAGAATGCATGGGAATA	TCCAAACTCTCCGACCAAAC	60.0	779	INTERGENIC				
CaPOPI_3785	Ca6	1824314	CA/CTCACAAAA	TTGCAGAATGCATGGGAATA	TCCAAACTCTCCGACCAAAC	60.0	779	INTERGENIC				
CaPOPI_3786	Ca6	1825931	C/CT	TCAAATCACATCACCGTTTG	AGCTCCCAATTTTGCACCTTG	57.9	508	INTERGENIC				
CaPOPI_3787	Ca6	1832442	A/AC	AAAGGTACGTGAGGTGTGCC	CGTAATTAATGATGGTGAGTGG	60.0	614	DRR	Ca_10310	G		Fructose-1,6-bisphosphatase class 1/Sedoheptulose-1,7-bisphosphatase
CaPOPI_3788	Ca6	1846516	GCC/GC	CCATAATCTGGAAGCTGGGA	AATCTTGCATGTGGCCTTTC	60.0	746	DRR	Ca_10312	R		Leucine-rich repeat, cysteine-containing subtype
CaPOPI_3789	Ca6	1846574	CAAAAAA/CAAAAAA	CCATAATCTGGAAGCTGGGA	AATCTTGCATGTGGCCTTTC	60.0	746	DRR	Ca_10312	R		Leucine-rich repeat, cysteine-containing subtype
CaPOPI_3790	Ca6	1854353	ATTTTTTTTT/ATTTTTTTTT	GCATTTTGTCTCTTTGTCG	AGAGGACGCGTACACTTCAAA	59.7	288	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3791	Ca6	1976018	AAT/AATAGAT	GAAC TAGATGCCGCAAAGC	GTACGTGGTCCTTCCTGAA	60.0	560	DRR	Ca_10322			
CaPOPI_3792	Ca6	1976736	TC/TCCC	TTATTCTCCATTGGGCATCC	TCCTGCGGGTAATGATAGC	59.7	963	DRR	Ca_10322			
CaPOPI_3793	Ca6	1977351	TTT/TTTTTT	GCTTATCATTACCCGCAAGGA	TAGCATAGTCCAAGCGGACC	60.1	465	DRR	Ca_10322			
CaPOPI_3794	Ca6	1978360	A/ATCG	CGTGGAGCATTCCGAGTATT	GGAGTTAGGGCGTGTGATGT	60.1	575	INTRON	Ca_10322			
CaPOPI_3795	Ca6	1978522	C/CCTGAGG	ACATCACACGCCCTAACTCC	CTTAGCCTTGCAAATGAGGC	60.0	197	INTRON	Ca_10322			
CaPOPI_3796	Ca6	2189256	CGG/CG	GTGTTGCGTGTTTCGAGTCTT	ATTGAAATCATCCGTGCTC	58.9	388	INTERGENIC				
CaPOPI_3797	Ca6	2478363	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TGCAATGTGGAACGAAGAAA	CATCAATTCACTCAACTGTGGAC	60.2	736	INTERGENIC				
CaPOPI_3798	Ca6	2518566	TG/TGG	TAGTCACGCTTGGTCACTCG	AATGCATTTGCCTGACTCAA	60.0	952	DRR	Ca_10384			Protein of unknown function DUF599
CaPOPI_3799	Ca6	2518811	TA/TAA	AATCTGGCTCAAAATGCAGC	AATGCATTTGCCTGACTCAA	60.4	723	DRR	Ca_10384			Protein of unknown function DUF599
CaPOPI_3800	Ca6	2528953	AATAT/AAT	TGGGTCAATGTTAAGAGGGC	CGTCAACGTCGTGCATTAC	59.9	515	INTERGENIC				
CaPOPI_3801	Ca6	2533591	AT/ATT	CTCTTATGTCGGTCGCCAAT	AACTTTGTGGAAGCTGTGGG	60.1	533	INTERGENIC				
CaPOPI_3802	Ca6	2553132	GCACACACACACACACA/GCACACACACACACACACACA	TTGCTTGCAATGCACATTTT	TGGTCTAACTTTCGGCAAA	60.3	647	INTERGENIC				
CaPOPI_3803	Ca6	2586276	GTTTTTTTTTTT/GTTTTTTTTTTTTT	GGTGCCACACATACATTGGA	TAATGCGCGGATCTTATTC	60.2	490	INTERGENIC				
CaPOPI_3804	Ca6	2674985	ATGTT/AT	GAAACTTCGTGCCTTTTTGC	ACGATAGTAGATGTGGCGGC	59.9	152	INTRON	Ca_10401	V		Protein of unknown function DUF1712, fungi
CaPOPI_3805	Ca6	2960468	CATATATATATATATAT/CATATATATATATATATATAT	AAGAAAGGGGTATTGGTGGC	CACAAATTTGACAATAAACTTTGACA	60.2	698	INTRON	Ca_10438	T	bHLH	Protein kinase, catalytic domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3806	Ca6	3176026	AGG/AGGG	GCAATGGAAGGTGAAA TGG	GCATAGGAGCGTGAAA TTG	60.3	522	INTERGENIC				
CaPOPI_3807	Ca6	3232392	ATTTATTTTATTT/ATTTATTTTATTT TATTT	ACGTGGCTCCTTATACC ACG	TTTTTGAGCCTTTTTCAC CAA	60.0	563	INTERGENIC				
CaPOPI_3808	Ca6	3255826	AATATATATATATAT/AATATATATATA TATATAT	TGGCTTGTTTGATTAG GACA	ATTCGAATGATCAGTTG CCC	58.3	547	INTERGENIC				
CaPOPI_3809	Ca6	3330798	AATTATTATTATTATTATTATTATTA TTATTATT/AATTATTATTATTATTAT TATTATTATTATTATTATT	TCAATTGATTTTCGGTAT CCTTC	GACCTCCCAAAGGCATT TTT	59.3	406	INTERGENIC				
CaPOPI_3810	Ca6	3351662	GATATAT/GATATATATAT	CGAAAATGGAACACC ACC	TCGAGTTGCGTAAGTGA CATAG	60.2	687	INTERGENIC				
CaPOPI_3811	Ca6	3351745	CATATTATATATA/CATA	GGTTGATTTAGGCTTCA CGG	TCGAGTTGCGTAAGTGA CATAG	59.6	580	INTERGENIC				
CaPOPI_3812	Ca6	3352912	AATTA/AA	AAAGTGGGTGGCAATTA ACG	TTATCCAATTCGGTTGCA CA	59.9	247	INTERGENIC				
CaPOPI_3813	Ca6	3355103	GCTATTGATCAATCTATTGAT/GCTATT GAT	TGAATAGATGTGCGCGA GAC	TCCACGGGAGTGAGAGA GAT	60.0	401	INTERGENIC				
CaPOPI_3814	Ca6	3355875	CTTT/CTTTT	AATTTGGCCCTATTGGC TTT	AGAAACGGAATGAGTCA CGG	59.8	709	INTERGENIC				
CaPOPI_3815	Ca6	3375286	AATATATATATATATATAT/AATATATA TATATATATATATATAT	GATCAGTTGACCCGCGT AGT	TTGATGCCACCTATTTCT CG	60.1	789	INTERGENIC				
CaPOPI_3816	Ca6	3377584	CTTTT/CTT	ATGCGGTGATGGTGATA TTG	TATGGCGAATATGGATG GGT	59.2	745	INTERGENIC				
CaPOPI_3817	Ca6	3382708	AA/AAGGGTTGGA	ATCACCGACCACTCAC TTC	TCAATTTTCTTCGTTGA CGG	60.0	787	INTERGENIC				
CaPOPI_3818	Ca6	3382789	CTTTT/CTTT	ATCACCGACCACTCAC TTC	GTTCAATCAGTGCAGCG TGT	60.0	810	INTERGENIC				
CaPOPI_3819	Ca6	3382946	CAAAA/CAAAA	TAACCAACAACATTCTG CCA	TGTTCCGTCCCACTCAT ACA	60.0	927	INTERGENIC				
CaPOPI_3820	Ca6	3387853	AGTACGTA/AGTA	GAGCCAACAGGATAAGA GCG	GAAAATTGAGTTCCATG ACGTTT	60.0	477	INTERGENIC				

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CaPOPI_3821	Ca6	3387937	A/AG	GAGCCAACAGGATAAGA GCG	GAAAATTGAGTTCCATG ACGTTT	60.0	477	INTERGENIC				
CaPOPI_3822	Ca6	3388065	GATATATATAT/GATATAT	GAGCCAACAGGATAAGA GCG	TTGTCTTTCACCTCTTTT TCCG	60.0	841	INTERGENIC				
CaPOPI_3823	Ca6	3420698	TTATATATATATATATATATATAT/T TATATATATATATATATATATAT	TAGCCGACAACATTGGA ACA	TGAACTCGCACATTGA GGA	60.1	386	INTERGENIC				
CaPOPI_3824	Ca6	3519049	GTTTTTTTTTTT/GTTTTTTTTTTT	AAGACTGCCCTGACCAG AGA	GTGGGGGACTAAGCTAA GGG	60.0	334	INTERGENIC				
CaPOPI_3825	Ca6	3520685	CTATATATATATAT/CTATATATATAT AT	GTTTCGCGATTTCTCGT GTT	CACGCATTTGACTCGAA AAC	60.3	249	INTERGENIC				
CaPOPI_3826	Ca6	3742066	ATATTATTATTATTATTATTATTATT ATTATT/ATATTATTATTATTATTATT TATTATTATTATTATTATTATTATTATTA	TGAAAGTTTAGCGGCAA TCA	AATTGTTGGCAGCCTTT TTC	59.4	609	INTERGENIC				
CaPOPI_3827	Ca6	3756968	TAAAAAAAA/TAAAAAAAAA	TCCGTTACCACTCACAC CAA	ACCCCTCAAATCTGTG TGC	60.0	640	INTRON	Ca_05928		bZIP	Ribosomal protein S4/S9, N-terminal
CaPOPI_3828	Ca6	3780129	CTTTTT/CTTTTTTTT	GCGTTGTCAAATTACA AATTCA	TTATTTGAATCCCCAAA ACA	59.1	693	INTERGENIC				
CaPOPI_3829	Ca6	3920180	GTTGGAATCTTTT/GTTGGAATCTTT TGGAAATCTTTT	TGGCATCCAACAATTGT CAT	TTGTGCAACCAATCACTT GAA	59.8	899	DRR	Ca_05908	R		Inositol oxygenase
CaPOPI_3830	Ca6	4290626	ACATCATCATCATCAT/ACATCATCATC ATCATCAT	CATTCCAGACATTGACG GTG	ACCTGGAACATTTTGC TCG	60.0	684	CDS (large-effect mutations)	Ca_05873		C2H2	Protein kinase, catalytic domain
CaPOPI_3831	Ca6	4363547	AT/ATAGGT	TTGCCTCTTCATTCTTTT GC	TAAAAACCGGTTTCGTT CAG	58.1	338	INTERGENIC				
CaPOPI_3832	Ca6	4432554	ATTTTTTTTT/ATTTTTTTTT	TTTCCTTTGCCAGAGAG ACG	AAGTGTCTTTGGGGACG TTG	60.5	424	INTERGENIC				
CaPOPI_3833	Ca6	4621073	ATTTTTTTTTTT/ATTTTTTTTTTTT	CCAACGCTACAACCCCT CAT	GGAGGAAACAAATTGAT CCAAA	60.0	761	INTERGENIC				
CaPOPI_3834	Ca6	4649762	AATAAGT/AATAAGTATAAGT	GGTCGAACCACTTGAGG TGT	AATCCACTCCCACTCCA CTG	60.0	389	INTERGENIC				
CaPOPI_3835	Ca6	4673406	ATTTTTTTTTTT/ATTTTTTTTTTTT	TTTTTACTCGGGTGGA ATAA	CGCCAAAGAGAAAAACA AATG	58.5	585	INTERGENIC				

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CaPOPI_3836	Ca6	4731176	ATTTTTTTTT/ATTTTTTTTT	GACACGTGCAAACCACT AGC	AAGCAACGATGATAAAA TACGACA	59.4	611	INTERGENIC				
CaPOPI_3837	Ca6	4801698	TGG/TGGG	ATAACCGACACAGACGA GGC	GTTGTTGCTTCTGCTCC TCC	60.1	278	INTERGENIC				
CaPOPI_3838	Ca6	4836563	GATACATAAT/GATACATAATACATAAT	TGGCAGCATAGTTCACCA AAA	TGGTGCAAAATAAATTATG AGTTGG	60.1	524	DRR	Ca_05811	R		High mobility group, HMG1/HMG2
CaPOPI_3839	Ca6	5295925	TTTATTATTATTA/TTTATTATTATTAT TATTATTA	TTGACATTTCAAACCGG TCTAT	TGGA AAAAGACTCCTGAA TATGGA	58.5	359	INTERGENIC				
CaPOPI_3840	Ca6	5853411	GTATTATTATTATTA/GTATTATTATTAT TATTATTA	TCGAACATAACACCTCG CAG	TCCGGTTACATTCTTCT TTTG	59.9	467	INTERGENIC				
CaPOPI_3841	Ca6	5971753	GATATATATATATATATATAT/GATATAT ATATATATATATATATATATAT	AGAGAGACGATTGTCAA GGCA	GCTTGTTTCACAAGTCA TTTCAA	60.0	737	INTERGENIC				
CaPOPI_3842	Ca6	6163420	ATTTTTTTTT/ATTTTTTTTTT	CCGTCCCTTAGCAAAAT TCA	AAGCAACTATGGCAAAT GGG	60.1	443	DRR	Ca_05680	T	G2-like	Arf GTPase activating protein
CaPOPI_3843	Ca6	6319723	CTTTTT/CTTTTTT	CATGATGGAAAACATGG GTG	CAGTGGCGTTGGTTAGC ATA	59.6	540	INTERGENIC				
CaPOPI_3844	Ca6	6409588	TTATATATATATATATAT/TTATATATATA TATATATATATAT	TCCACGGCCTCTTGTTG TAT	AGAGCAAGCAAGTTGGT GGT	60.5	581	INTERGENIC				
CaPOPI_3845	Ca6	6411336	AAT/AATAT	ATCTCGTGGTGCAACAA TCA	TTTGGGAAGGGTCAAGA AAA	60.1	628	INTERGENIC				
CaPOPI_3846	Ca6	6411391	AATTTATTTATTTATTTAT/AATTTATTTA TTTATTTATTTATTTAT	ATCTCGTGGTGCAACAA TCA	TTTGGGAAGGGTCAAGA AAA	60.1	628	INTERGENIC				
CaPOPI_3847	Ca6	6447647	TTATATATATATATATATAT/TTATATATA TATATATATATATAT	TAATTCGTGCGTCGTAT GGA	TTTTCATCAATAACATTG AGCG	60.1	219	INTERGENIC				
CaPOPI_3848	Ca6	6583135	ATTTTTTTTTT/ATTTTTTTTTT	TACGCGGATACGGGTTA TGT	AGGACAAATGTGGGAAT TGG	60.2	421	INTERGENIC				
CaPOPI_3849	Ca6	6747248	TAA/TAAA	ACATGATAACCAATGCG GGT	GGGGGTTGAAACGAGG TATT	60.1	509	DRR	Ca_16935		NF-YA	Plant self-incompatibility S1
CaPOPI_3850	Ca6	6862212	ACC/AGAATGAGTTATCC	TGATGATGAGAGGCGAG ACA	GGTGAGCTGTTTATTG GGA	60.5	198	INTERGENIC				

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CaPOPI_3851	Ca6	6918472	ATGGGTAGGGT/ATGGGTAGGGTTTGGTAGGGT	TTGTTCGCCATTGATTTGA	TGATACCCAAGAGGGTACGG	60.1	333	INTERGENIC				
CaPOPI_3852	Ca6	6954085	ATACTAACT/ATACT	ACAGCTTCGAACTTGCACT	GCATTCACTGGTCCAATGTG	60.1	482	INTRON	Ca_09688		NF-YB	Protein of unknown function DUF248, methyltransferase putative
CaPOPI_3853	Ca6	7254332	AATATATATATATATATATATAT/AATATATATATATATATATAT	TCACAGTCAAGCACGTCCTC	AGGGTTGGGTTGTGTTCAAA	60.0	708	INTERGENIC				
CaPOPI_3854	Ca6	7373908	TTATATATATATATATATATAT/TTATATATATATATATATATAT	GGAAAGGCTTCACAAAGCTG	TAGCCCTCTGCTCATAGA	60.0	696	DRR	Ca_09643	Q		Alcohol dehydrogenase superfamily, zinc-containing
CaPOPI_3855	Ca6	7548995	ATTTTTTT/ATTTTTTTT	ATTTCTCAACAGGTGTGTGC	GATCGCAAGGATGATGAAT	60.0	667	INTERGENIC				
CaPOPI_3856	Ca6	7555065	GGTCTA/GGTCTAGTCTA	GGCATCAACCCCTTTTAAT	TATCCAAGCTGGAATGAG	60.0	746	INTRON	Ca_09627	S		
CaPOPI_3857	Ca6	7568051	GACTAA/GACTAACTAA	TGGGGGAACTTTGCTACAC	TTTTGACCCATGAGGAGACC	60.0	615	INTRON	Ca_09627	S		
CaPOPI_3858	Ca6	7572118	CTTTTTTT/CTTTTTTT	CTTTGCTAAGGGCGTTTGTG	CCCATGCAAAGATTGTGTT	60.0	536	INTRON	Ca_09627	S		
CaPOPI_3859	Ca6	7587896	TTT/TTTAATT	AGTTGCGATTGTCCGAAGTT	GATGAGACTTTTCCCTAGCCTT	59.7	485	INTERGENIC				
CaPOPI_3860	Ca6	7588189	TT/TTGCAT	AAGGCTAGGGAAAAGTCTCATC	GCTCTCAGTTGAATAGCACGG	58.1	504	INTERGENIC				
CaPOPI_3861	Ca6	7592871	GAAGAAA/GAAGAAAGAAA	AGCACGAAAGTTTCCACAG	AGAGACGGTATCCGGTTG	60.3	646	INTRON	Ca_09625		ERF	Glycoside hydrolase, family 17
CaPOPI_3862	Ca6	7593280	CAAA/CAAAAA	CCTTCTTGCTGGCATTAGC	TGGCTTAAAGAGATCGGTGC	60.0	477	INTERGENIC				
CaPOPI_3863	Ca6	7606703	ATT/AT	TTTCGTGGCATGGAATACAA	CCAAAAATTGCCAGCAGTT	59.9	597	INTRON	Ca_09624	R		Domain of unknown function DUF699, exodeoxyribonuclease V alpha chain
CaPOPI_3864	Ca6	7632106	A/AACT	CGCTTTTGTGTTCAAGTTGTGA	GGAAAAATGTGAAATCCAAAA	59.9	930	INTERGENIC				
CaPOPI_3865	Ca6	7643356	ATTTTTT/ATTTTT	TTGCATTCCATAAACACGGA	TGATCAGATAGATATGTTGACCGA	59.9	695	INTERGENIC				

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CaPOPI_3866	Ca6	7644118	ATTTTTTTTT/ATTTTTTTTT	CCAGAGGTTGAATCAATGAGA	GAGGAAGCACGAACGAAGTC	57.7	674	INTERGENIC				
CaPOPI_3867	Ca6	7658418	TTAAAAATAAAAAT/TTAAAAATAAAAATAAAAAT	AGATCAGCCGCAGAATTGT	CACCCGTGAAACTGTTGATG	59.8	606	DRR	Ca_09616			
CaPOPI_3868	Ca6	7685952	AATATATATATATATATATATAT/ATAATATATATATATATATAT	CAGCGCCATAGTTGAGCATA	GGGTGGTGTGGAGTCAATTT	60.0	591	INTERGENIC				
CaPOPI_3869	Ca6	7861860	AACTTCAGGCA/AA	GGAGGCGTTGACAATAGTGAT	TATTTGGCGTCGTCTGCTG	59.1	616	INTERGENIC				
CaPOPI_3870	Ca6	7912887	GTT/GTTTTT	CCTTGAAGCTTCTCCCATCA	CTCCCTCTCTGTGGTTTGG	60.3	896	INTRON	Ca_09584	U	M-type	Inositol polyphosphate-related phosphatase
CaPOPI_3871	Ca6	7961982	A/AAT	CGTTGCAGCTGCTTTGTTTA	TTGGGGAAGAAAGTTGGAGA	60.2	841	INTERGENIC				
CaPOPI_3872	Ca6	8032854	AATATATATATATATATATATATATAT/AAATATATATATATATATATATATATATAT	TTGCAATACTTTATCCTAGAGCCC	TGGTGAGGGCATCAATT	60.0	929	INTERGENIC				
CaPOPI_3873	Ca6	8085419	ATA/ATACAGTTTA	TTTCCCCGTAGACACTGAC	TGATAAAAGACGGAATCTTTCAA	60.0	565	DRR	Ca_09563	C		Mitochondrial carrier protein
CaPOPI_3874	Ca6	8313713	GTTTTTTTTT/GTTTTTTTTTTT	TTTGACAATCTCATGTTTGCAG	GGGTCAAAAAGTGTGCAAGGT	60.2	730	INTERGENIC				
CaPOPI_3875	Ca6	8557817	TGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG/TGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	TTTGGAGACCAATGGTGACA	CTCCGTTTGTAGCGCAAAAT	59.9	783	INTERGENIC				
CaPOPI_3876	Ca6	8796967	A/AG	GCCAAACAATAGTTGAACCAA	AACGTTACGCATGAACCTCC	59.0	588	INTRON	Ca_16754	E		Amino acid transporter, transmembrane
CaPOPI_3877	Ca6	8904663	GATATATATATATATATATATATATATATATATATAT/GATATATATATATATATATATATATATATATAT	TGAATTGCTTCGAACCTGTG	TGCATTTCAGGCTCTCATGC	59.8	465	INTERGENIC				
CaPOPI_3878	Ca6	9130006	ATGATTTGATTTGATTT/ATGATTTGATTGATTTGATTTGATTT	ATTGTGATCGGAGATCGAGG	AAATGTGGTGGAGGCTTGTC	60.0	400	INTRON	Ca_08684	O	Nin-like	Rab GDI protein
CaPOPI_3879	Ca6	9203559	G/GTTATATT	TCGTGAAATAGTGGACGTG	TGAACATCAAAATGCCCAA	59.6	763	DRR	Ca_08676	OT		Peptidase, cysteine peptidase active site
CaPOPI_3880	Ca6	9257795	TAAAAAAAAA/TAAAAAAAAA	GCATCCTCGGAAAATTTCAA	CACGACAAGTCTCGTGCTA	60.0	352	INTERGENIC				

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CaPOPI_3881	Ca6	9403873	AATATATATATATATA/AATATATATATATATATA	TTTGTGCGCAATGATAGTTGA	TAGCGTTCCGAATCTTTCGT	58.4	891	INTERGENIC				
CaPOPI_3882	Ca6	9472058	CAAAAAAAAA/CAAAAAAAAA	TTCATTTGGTTCTCCCTTCG	TGTTTAGTACTTTTCCCAATGCC	60.0	498	INTERGENIC				
CaPOPI_3883	Ca6	9606829	TAAAAAAAAAAAA/TAAAAAAAAAAAAAA	CGCTACATGAACTTTGTCACTCA	AAAGGTGATGGTCGAAGGTG	60.4	567	INTERGENIC				
CaPOPI_3884	Ca6	9884658	AT/ATGT	GCCTTTGAGCGGTAATGAAA	TCGGAAATTTGGAGTCAAGC	60.2	716	INTERGENIC				
CaPOPI_3885	Ca6	9890136	CTTTTTTTTT/CTTTTTTT	AGTCTTCACGTTGGTGTCC	CCTTCTTCAGCCAAACCAA	60.0	381	INTRON	Ca_08601		FAR1	Protein kinase, catalytic domain
CaPOPI_3886	Ca6	9893250	TAA/TAAA	CCGAATCATGGAAGGAGAGA	AACCGCGAAACTTCATTCAC	60.2	774	INTERGENIC				
CaPOPI_3887	Ca6	9894814	T/TA	AAATTCGAAACGCGAGAGA	GGATCTTGCAACGTGGACTT	60.0	391	DRR	Ca_08600	O		Peptidase, cysteine peptidase active site
CaPOPI_3888	Ca6	9900963	CATGAT/CAT	ATGTTGCCAAGGCAGAGAGT	TCGTCGAGGCATCACAACTA	59.9	928	INTERGENIC				
CaPOPI_3889	Ca6	9903379	ATTT/ATTTT	TTCGATGTTGCCTAGTCCT	GTCGTCGAGGCATCAAACT	59.7	230	INTERGENIC				
CaPOPI_3890	Ca6	9925899	CATTATTATTATTATT/CATTATTATTATTATT	CCAATTTTGGTGTGCTCCT	GGTGAGGACACTTCAATGGG	60.0	448	INTERGENIC				
CaPOPI_3891	Ca6	9935576	CGAGAAAAACAGAGAAAA/CGAGAAAAACAGAGAAAAACAGAGAAAA	TTCATTTCCGTTGCAAAATG	AATGAAGAATTTGAGCGCGT	59.5	381	INTERGENIC				
CaPOPI_3892	Ca6	9957991	TAAAAAAAA/TAAAAAA	TTAGAGTTAATTTGATGGACAGTGA	AAAATTAAGTGTAAAGACAAA	57.1	525	INTERGENIC				
CaPOPI_3893	Ca6	9961842	CAAAAA/CAAAAA	ACGTTTTCGAATTGGCTCAT	AGAAATCATTCGTCCGTTC	59.6	366	DRR	Ca_08594	O		Preprotein translocase Sec, Sec61-beta subunit
CaPOPI_3894	Ca6	9987106	CA/CAA	TTGACATCAAAATTCGACAACA	TCACCACACAATCAAAACCA	59.1	337	INTERGENIC				
CaPOPI_3895	Ca6	10002215	ATT/ATTT	CCTAATGTAATGGAGGGG	CAAGAGGTTCAATTTGACCGA	58.3	291	INTERGENIC				

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CaPOPI_3896	Ca6	10002372	CAATTTATTAATTT/CAATTT	TCGGTCAAATGAACCTCTTG	TCGAATACTGTTTTGAGAACCTTT	58.7	328	INTERGENIC				
CaPOPI_3897	Ca6	10012800	A/AT	ACCATATCCCAAGCAAGCAC	CTATGCCTGGGGCATGATTA	60.0	792	DRR	Ca_08591	R	G2-like	Domain of unknown function DUF676, hydrolase-like
CaPOPI_3898	Ca6	10046135	GTTTTTTT/GTTTTTTT	CAGCCGTTGGTTCAATAGGT	TCATGCATGTTTTTATCATTTTGT	60.0	722	INTERGENIC				
CaPOPI_3899	Ca6	10050244	TTTTATTATTTATTTATTTAT/TTTATTATTTATTTATTTATTTATT	GCAAATCGACAACGAATCCT	TTTAGGGACGAAAATGATGG	60.1	560	INTERGENIC				
CaPOPI_3900	Ca6	10050426	AAT/ACGGTTTGAT	GCAAATCGACAACGAATCCT	TTTAGGGACGAAAATGATGG	60.1	560	INTERGENIC				
CaPOPI_3901	Ca6	10061419	A/AT	TTGAAATTGGTAACGAATGAGAAA	CATCTAACACAACACCGTCA	59.9	674	INTERGENIC				
CaPOPI_3902	Ca6	10061549	ATTTTTTT/ATTTTTTTT	TTGTGACAAATATGTATGTGTAATTG	TCCGTAAAGATGTTGTTGATGC	59.2	860	INTERGENIC				
CaPOPI_3903	Ca6	10107731	CTTTTTTTT/CTTTTTTTT	GCGCAAGTTGCATAAATCT	ACTCGTGCTAGCGACATTGA	60.2	766	INTERGENIC				
CaPOPI_3904	Ca6	10107926	CACAATAA/CA	TGCACATCAACCTTAAATTCCA	GTTTCCGATTGCCAGGTTTA	60.4	745	INTERGENIC				
CaPOPI_3905	Ca6	10123378	AAGTA/AA	TTTCTTTCCGTCACAAGCTG	TTTTTGATTTTCGCAGACG	59.0	175	INTERGENIC				
CaPOPI_3906	Ca6	10135848	TTTTTTT/TTTTTTTATTTTTT	TTCCAAGGATCCCATTAACA	TATTTTGTGCGTGTGACCCA	60.1	440	INTERGENIC				
CaPOPI_3907	Ca6	10163284	ATTTTTTT/ATTTTTT	CCACAACAAAGGACGAGACA	CATGGACACAAATTGCAAGG	59.7	827	INTERGENIC				
CaPOPI_3908	Ca6	10178382	TC/T	TATCTAACGTGCCCCCTCAC	ACAGGGGAAACTAGACCCGT	60.0	635	INTRON	Ca_08573		ERF	Glycoside hydrolase, family 17
CaPOPI_3909	Ca6	10178910	TA/T	ACGGGTCTAGTTTCCCCTGT	TTAATGCCTAGATCCTGCGG	59.9	166	INTRON	Ca_08573		ERF	Glycoside hydrolase, family 17
CaPOPI_3910	Ca6	10180510	CTCTTCTTTC/CTCTTTC	GAGACAACTGAAGGCCGAG	GGTTGGTCTCGAATAAGGCA	60.0	561	DRR	Ca_08573		ERF	Glycoside hydrolase, family 17

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3911	Ca6	10185405	TAAA/TAAAA	TTTTTGACGAGATTGGCAATTA	AGGCCACAACCTGTTCATTTG	59.6	528	INTERGENIC				
CaPOPI_3912	Ca6	10190857	C/CT	AGGGTATTTTCACGCAGGTG	CGAACGCACACACTTTTCAT	60.0	433	INTRON	Ca_08570	I		AMP-dependent synthetase/ligase
CaPOPI_3913	Ca6	10208472	ATTTT/ATTTT	TGATCGCATTAACTTTGACTG	AGAAAATCCCTCTTCCCAC	60.1	656	INTERGENIC				
CaPOPI_3914	Ca6	10209877	ACTCTCTCT/ACTCTCT	AGGGAGAGTCGTATTCGGGT	CAGGGTTTTGGGTTTGAAGA	60.0	137	INTERGENIC				
CaPOPI_3915	Ca6	10224803	TC/TCC	CCCCGCAGTTTGTGTTTGTAT	GATGCTATTGTGGGCATGTG	59.9	641	DRR	Ca_08566	T	FAR1	Metallo-dependent phosphatase
CaPOPI_3916	Ca6	10250923	CAAAA/CAAAAA	TTATAAGCACTCGCGTTCCA	AAATCCGCGATTGGTTTCTA	59.5	409	DRR	Ca_08565	R	bZIP	
CaPOPI_3917	Ca6	10251637	TTTCAATAATT/TTTCAATAATTCAATAATT	GGATTGCAGGAAGATACCCA	TCGTAAACGGTTTCTTTGGC	59.9	640	INTERGENIC				
CaPOPI_3918	Ca6	10251944	CTCATCATCATCATC/CTCATCATCATCATC	CATATAGGGTGGGGTTGTG	ATCCAAAACGACGACGATC	59.9	344	INTERGENIC				
CaPOPI_3919	Ca6	10259432	GTTTTTTT/GTTTTTTTTT	ATTCGCTAGTCGTCGTACC	AAGGCAGCGTTGAAGGTAGA	60.0	505	INTERGENIC				
CaPOPI_3920	Ca6	10265158	ACATGTCTAACTACTTCA/ACATGTCTAACTACTCATGTCTAACTACTTCA	TTGATTTGTGCATTGGTGCT	TCCCTTGATTGTTTCTTTTGG	60.1	199	DRR	Ca_08562	S		YL1 nuclear, C-terminal
CaPOPI_3921	Ca6	10272224	G/GGCGTATAT	TAGGGTGCTAGCGGATTGTTG	AAGGCACCCATTAGTTGACG	60.2	550	DRR	Ca_08561			Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor
CaPOPI_3922	Ca6	10275563	CTTT/CTTTT	AGGTCTAGGCCAATCAGAAA	ATGTGCCATGTCGTAGGCTT	57.9	497	DRR	Ca_08560	R		
CaPOPI_3923	Ca6	10316984	C/CG	TGCAGAACACAAACATGGC	ATTGCATCCGATTGTTCTCC	60.7	613	INTERGENIC				
CaPOPI_3924	Ca6	10318872	CTTTTTTTTTTT/CTTTTTTTTTTT	TTAACCAACCCGGTTCTCAAG	TGACATGGTTGGCTGTGAAT	60.0	724	INTERGENIC				
CaPOPI_3925	Ca6	10377538	ATA/ATATTATTATTA	CTCGATTTGGGCGAAAAATAA	TTGGCGCATCAATTTTTGTA	60.0	549	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3926	Ca6	10377821	ATGT/AT	CTCGATTGGGCGAAAA TAA	TTGGCGCATCAATTTT GTA	60.0	549	INTERGENIC				
CaPOPI_3927	Ca6	10395343	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	GTGTGTGGGTTTTGGC TTT	TTTGACAGCAAGGCAACA TAG	59.9	565	INTRON	Ca_08553	R	MYB_rela ted	Small ubiquitin-related modifier, SUMO
CaPOPI_3928	Ca6	10412258	GAAAAA/GAAAAA	AGGGCCAAACTTGGATC TTT	TTTTCACAAGCTCACAG GGA	59.9	374	INTERGENIC				
CaPOPI_3929	Ca6	10417732	TGG/T	CTCACTTGTGGGTTTC CTCT	CCCCCTCGAACAACAAA ATA	58.3	369	INTERGENIC				
CaPOPI_3930	Ca6	10438851	CA/C	TCTCTTGAACCTCTCG ACAA	ATTGGTCCTCTACCCCC ATT	60.0	302	DRR	Ca_08552	R		Rab-GAP/TBC domain
CaPOPI_3931	Ca6	10457521	TA/TCCTTTTCTAAGTCA	TTCTTCGGTCTTGCT GCT	ATTTGGATCATGCAAC ACA	60.0	551	INTRON	Ca_08551			
CaPOPI_3932	Ca6	10458622	TGGATG/T	CAGAGTTGGAGTGGTGC AAA	TTTTCAGTTTCGCCATG GAT	59.9	567	INTRON	Ca_08551			
CaPOPI_3933	Ca6	10472712	TAAAAAA/TAAAAAA	AACCAGATCAGATTGTC GCC	TGGGATGAATTTGGATC ATTT	60.1	852	INTERGENIC				
CaPOPI_3934	Ca6	10476151	TA/T	GCCCATTTATGGGGTA TTT	GCTCTGTGGGAACGAG GAG	59.8	595	INTERGENIC				
CaPOPI_3935	Ca6	10482318	CA/C	CAAGTGGGAAATGGCA AGT	ATTGGATTGAGTTGGGC TTG	60.0	535	INTRON	Ca_08548	E	CAMTA	Spermine synthase
CaPOPI_3936	Ca6	10486008	ATTT/ATTTTT	AATCAAGTATTTGTCCG GCG	TCTGTGGAAGCAAGATG CAC	60.0	650	DRR	Ca_08548	E	CAMTA	Spermine synthase
CaPOPI_3937	Ca6	10497132	CAATAAATAAATAAATAA/CAAA TAAATAAATAAATAA	ACCACCTTTGAGACAAA CCG	GTTTGCAGTGGTTCCC TGT	60.0	291	INTRON	Ca_08547	G	C2H2	D-galactoside/L- rhamnose binding SUEL lectin domain
CaPOPI_3938	Ca6	10514411	CAAAAAAAAA/CAAAAAAAAA	TTCGCAATCTGTGTTTT CG	CAAGAATTCGTATCGTC TAAATGC	59.8	642	INTERGENIC				
CaPOPI_3939	Ca6	10559368	T/TG	CGCCCTAGGTGCTGTT TTA	TGGATGGATGTTTGCAA TGT	60.3	417	INTERGENIC				
CaPOPI_3940	Ca6	10564033	AATATAT/AAT	GAAATCCCAATCCAAT TTCA	GCAGCACACAGCATAGG AAA	60.0	567	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3941	Ca6	10564108	ATTTTTTTTT/ATTTTTT	GAAATCCCAATCCAAATTCA	GCAGCACACAGCATAGGAAA	60.0	567	INTERGENIC				
CaPOPI_3942	Ca6	10564399	CTT/CTTT	TTTCCTATGCTGTGTGCTGC	CTTTTCACCCCTTGATCGGAA	60.0	611	INTERGENIC				
CaPOPI_3943	Ca6	10576490	CTTTT/CTTTTTT	TTGCCAAAGGTTAATGCA	ATGGTGTTGCTAGGTTTGC	60.1	888	INTERGENIC				
CaPOPI_3944	Ca6	10587047	A/AC	CACCCAGTCGCTCACAACTTA	CACGACCTTCCTTTGGTTGT	59.7	824	INTERGENIC				
CaPOPI_3945	Ca6	10604574	TTAT/TTATTTATTTATCTAT	GCAAAGGCTTGTGGTTT	AAAGCGAGATCTGAACCGAA	60.2	264	INTRON	Ca_08537	H		Adenosylhomocysteinase
CaPOPI_3946	Ca6	10608315	TG/TGG	ACCCGCTTAATTGTGGCTAA	ACATTACCCGCATCCACTA	59.6	383	INTERGENIC				
CaPOPI_3947	Ca6	10611247	TAATAAATAAATAAATAA/TAATAAATAAATAAATAA	TCTGACATGACAAATGTGG	TCGGAATTGGTCCGAAATTA	59.4	409	DRR	Ca_08536	K	HSF	Heat shock factor (HSF)-type, DNA-binding
CaPOPI_3948	Ca6	10642500	C/CCTATAGA	CGATTGACAGCAAAGCAA	GACAACCTTCGTTGCCCTAA	60.0	437	INTERGENIC				
CaPOPI_3949	Ca6	10649918	GTTTGTTTTGTTTTGTTTT/GTTTGTTTTGTTTGTTTTGTTTT	GACGGTTATGGAGCCTTCAA	TTGATATCTTGTGCCTCCC	60.1	363	DRR	Ca_08531	I		AMP-dependent synthetase/ligase
CaPOPI_3950	Ca6	10657533	C/CTT	ACATCTCTCATTGCCATCC	ATCAGTGCTTTGCTGCTTT	59.9	769	INTRON	Ca_08531	I		AMP-dependent synthetase/ligase
CaPOPI_3951	Ca6	10660162	TTAT/TT	CTAGTGAGCATTGCGAGCAG	CTTGTGAGGCAGTCCAACTA	59.9	372	INTRON	Ca_08531	I		AMP-dependent synthetase/ligase
CaPOPI_3952	Ca6	10664790	TC/T	TGCTTGGTACCACAAGACAAA	AAAATTCGTTTCAAAAATCTTGT	60.6	767	INTERGENIC				
CaPOPI_3953	Ca6	10665216	ATTTTTTT/ATTTTTTTTT	CAAAAACAAGATTTTGAACGAA	TCAAAAGTTTCGAGCAATACGA	59.6	398	INTERGENIC				
CaPOPI_3954	Ca6	10677110	TCCCC/TCCCCC	TTCAACACGTGCATGGAAT	GCTAACACATGATTTCGCA	60.0	581	INTRON	Ca_08530		bHLH	Aspartate/glutamate/uridylyl transferase
CaPOPI_3955	Ca6	10686252	TACAC/TAC	CCAGCTTCTTGTGTGTGGA	CAGAGGCAACAAGCTCAGTG	59.9	609	INTRON	Ca_08529		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolisin

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CaPOPI_3956	Ca6	11315858	ATTT/ATTTT	GTTTGTGTGGTTGCAGTGG	GCTGATTGGTTGCCTCTCTC	60.0	399	INTERGENIC				
CaPOPI_3957	Ca6	11344092	CTTTTTTTTT/CTTTTTTTTTT	TTGACATGTTTTATTGGTGTGAA	CGTGGATGTAGGCAAGAGGT	58.0	652	INTERGENIC				
CaPOPI_3958	Ca6	11367342	CAAAAAAAAA/CAAAAAAAAA	TAGATCCACCTTCAAACCG	AAAAGCGGTGACAGATGAC	59.9	667	INTRON	Ca_23422	K	ARR-B	Signal transduction response regulator, receiver domain
CaPOPI_3959	Ca6	11464290	TAAAA/TAA	AGGAAAAGGAGGAGGATGGA	GTGCCAAAACAAATGACGTG	60.0	638	INTERGENIC				
CaPOPI_3960	Ca6	11546492	GTA AAA/G	TCGGAAAGGTCATTCAAAGC	TTTGTGTCCAAAGCATTCTCC	60.2	472	INTERGENIC				
CaPOPI_3961	Ca6	11569101	T/TAAGTAA	CAAAGGGGGTATTTTGTTTC	CGTTCAATTCCTGCCAAT	59.6	499	INTERGENIC				
CaPOPI_3962	Ca6	11617529	GA/GAA	TTGGGAGTTCATTGCAATCA	TTTGTGAAGATATTGTTTCCTCG	60.0	905	INTERGENIC				
CaPOPI_3963	Ca6	11617707	AATATATATATATATATATATATATAT/ AATATATATATATATATATATATATATATATATATAT	GAGGCATCGTTTCACAAATGA	AGGTTTGCAGGACTGTGTT	59.7	809	INTERGENIC				
CaPOPI_3964	Ca6	11630320	AAGTAGT/AAGT	TGCATATGTGTGGGGGATA	GCTTGATACTTGGCAAGCC	59.6	621	INTERGENIC				
CaPOPI_3965	Ca6	11650123	TTAA/T	GGAAGGGTCCACGCATAGTA	GCTTTTGTGGTGCACTTTT	60.0	827	DRR	Ca_25059	J		Ribosomal protein S7
CaPOPI_3966	Ca6	11655132	TAAAACTAAAACTAAAACTAAAACT A/TAAAACTAAAACTAAAACTA	GCATGGATGAAATCAAAAGC	TTGGGATGATCCAACAA CAA	58.2	333	DRR	Ca_25060		FAR1	
CaPOPI_3967	Ca6	11655226	AATAACTTTT/TA/AA	GCATGGATGAAATCAAAAGC	TTGGGATGATCCAACAA CAA	58.2	333	DRR	Ca_25060		FAR1	
CaPOPI_3968	Ca6	11680950	C/CA	TAATCCATGGCGAACACAAA	TCCAAGTTTGACAGCAT TCA	59.9	581	INTERGENIC				
CaPOPI_3969	Ca6	11681178	TTGTGTGTGTGTGTGT/TTGTGTGTGT GTGTGTGTGTGTGT	ATCAATTGCCATTGCA TCA	TAGCATTTTGTAGGGGG AAA	59.9	692	INTERGENIC				
CaPOPI_3970	Ca6	11688551	GAAAA/GAAAAA	TCTCCTCCTCCTCTCTCC	TGTTGCCCAAAACCATC ATA	59.9	557	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_3971	Ca6	11691624	T/TA	CTTTGCAGCAAGTCATTGGA	CCTAACTGGGGAGAAA CAA	60.0	871	INTERGENIC				
CaPOPI_3972	Ca6	11722419	TATATT/TATATTAATATT	CCTTCGCCGTATATGAT TCC	AAGCAAAGGTCTGAGC AAA	59.4	185	INTERGENIC				
CaPOPI_3973	Ca6	11737556	CTATATATATATATAT/CTATATATATAT ATATATATATAT	GCAAGCGCTATGTACCTTT	AATGTGAATCCCACCAG GAA	60.4	770	INTERGENIC				
CaPOPI_3974	Ca6	11742023	ATTTTTTT/ATTTTTTTT	GCGCTTCAATTTACAAC GCT	TTTTGCACGAAATCAAT CA	60.4	614	INTERGENIC				
CaPOPI_3975	Ca6	11785408	ATTTT/ATTT	TGCAAACGCACATATAC ACG	AATTTGAGGCGTGTGGG TAG	59.2	711	INTERGENIC				
CaPOPI_3976	Ca6	11792161	AAT/A	TGTTGGACGGACAATTG AAA	CAAAATGCCATAAAATC GGC	59.9	408	INTERGENIC				
CaPOPI_3977	Ca6	11806357	CATATATATATATATAT/CATATATAT ATATATATATAT	TCACCTAGGAATTCGCG ATC	CGAGGTTGGAGTTGGAT CAC	60.0	711	INTERGENIC				
CaPOPI_3978	Ca6	12253200	AATATATATATATATATATATATATAT ATATATATATATAT/AATATATATATATAT ATATATATATATATATATATATATATA TATATATAT	CTCCGTTTATCTCCGTT GGA	CGTGATGATTGATGCAT TTCA	60.1	746	INTERGENIC				
CaPOPI_3979	Ca6	12254420	AATATATATATATATATATATATATAT ATATA/AATATATATATATATATATATATA TATATATATATA	CCTGTGGTTGGTTGTAG CCT	CTGGAGGTCACCTTCGA CAT	60.0	703	INTERGENIC				
CaPOPI_3980	Ca6	12335628	TGAAG/TG	GGAAGGGTGTTGGTGT GTTT	TTGGTCACTAAGGGGGT GAG	59.7	968	DRR	Ca_24849			Protein of unknown function DUF688
CaPOPI_3981	Ca6	12543039	TTATATATATATATATATATATATATA TATATATATATATATA/TTATATATATA TATATATATATATATATATATATATAT ATATATATATATA	TTTCGACATAGGTTGTTA AGCTTTT	GAAACCAGTGAAGTTCT CCCC	59.7	590	INTERGENIC				
CaPOPI_3982	Ca6	12663993	TAAA/TAAAA	ATTGCCTTGCACACAG TAA	CGGCTCGAACGGTACAT ATT	60.2	636	INTERGENIC				
CaPOPI_3983	Ca6	12787897	AATATATATATATATATATATAT/AATATA TATATATATATATATAT	ATCAAACAATGTTGCG AGC	CAAAACCCATTTTTGTG ATTGA	58.8	749	INTERGENIC				
CaPOPI_3984	Ca6	12853638	TAAAA/TAAA	CTCATCCATCACACCAA AGC	CTCAGATTCTGCGTCCA TCA	59.1	875	INTRON	Ca_05058	T	TALE	Protein kinase, catalytic domain
CaPOPI_3985	Ca6	12856182	TC/TCAAGTTCGAC	TCCAATGCTGGATTAGG CTC	GCATTTATGAACATAAC GCCAA	60.2	512	DRR	Ca_05058	T	TALE	Protein kinase, catalytic domain

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CaPOPI_3986	Ca6	12865294	ATTGT/ATTGTATATTTATTTTTGT	CAAAATGGACACTTAAGGGGA	CTTCCACCCATTATGCCACT	58.9	948	DRR	Ca_05059	O	MYB_related	Ubiquitin-conjugating enzyme, E2
CaPOPI_3987	Ca6	12877302	CG/CGCTTTTTTG	GTTTCGTAAAGGACGGGATGA	CTTTTACAGCGCTTTCTGGG	59.9	235	INTERGENIC				
CaPOPI_3988	Ca6	12879345	TAAAAAAAA/TAAAAAAAA	TAAAGGACCAAGTCGGGAAA	ATCCAAAGGAAAGCATCGTG	59.5	599	INTERGENIC				
CaPOPI_3989	Ca6	12891974	GAAAAAAAA/GAAAAAAAA	GGTAAAGCCCACTTGGTGA	CCCTGTATTGCTCTCCGAA	60.0	552	INTERGENIC				
CaPOPI_3990	Ca6	12899744	TAAAAAAAA/TAAAAAAAA	TTGGATGTATACGGCGACA	CAATCCACCTGAATGAATCC	60.0	881	INTERGENIC				
CaPOPI_3991	Ca6	12909901	AT/ATT	TGGACAGGTGAAGACCAACA	TTCTTCTCTCCAATCAATGC	60.1	696	DRR	Ca_05064	T	bHLH	Protein kinase, catalytic domain
CaPOPI_3992	Ca6	12920553	TAAAAAA/TAAAAAA	GGAAGGAAGGAGGTTCTCAA	TGCACTGGTTTATTTTGA	59.7	585	INTERGENIC				
CaPOPI_3993	Ca6	12922857	A/AC	TTTTACCGCGAAACAAATC	CAGAAACAGCAGAGACAGCG	59.9	686	INTERGENIC				
CaPOPI_3994	Ca6	12934565	ATTTTTTT/ATTTTTTT	CGGTTTGAAGATGAGGTTACAC	TATTCAAGCAACGGCTGTGT	59.6	691	INTERGENIC				
CaPOPI_3995	Ca6	12934614	GAAAAAAAA/GAAAAAAAA	CGGTTTGAAGATGAGGTTACAC	ATTATTCAAGCAACGGCTGG	59.6	693	INTERGENIC				
CaPOPI_3996	Ca6	12935007	TA/T	GCAAACAATCTAGAGGGAGGAA	GGGGGCACAAAGACAACATA	59.7	362	INTERGENIC				
CaPOPI_3997	Ca6	12940701	TAAAAAA/TAAAAAA	TAGCCTCTCTCCCAACCTT	ATTCATGGATTGGCATTGGT	60.2	665	DRR	Ca_05066			Protein of unknown function DUF1423, plant
CaPOPI_3998	Ca6	12950692	AATATATATAT/AATATATATATAT	ATCATCGAAGAAGCATTGGG	TCAATTGAGCGAGTGTA	60.0	633	INTERGENIC				
CaPOPI_3999	Ca6	12954436	TAAAAA/TAAAAA	TGAAATGATGAGGGGGAGAC	CCCTTCATCCCTTACCCCTA	59.9	716	INTERGENIC				
CaPOPI_4000	Ca6	12957093	TAAAAAAAA/TAAAAAAAA	TGAATCCCAGAAATTGACAT	AAAAGCAAACAGGTGAACCG	60.1	404	INTERGENIC				

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CaPOPI_4001	Ca6	12957392	ATTTT/ATTT	TGAATCCCAGAAATTGACAT	AACTTTTGGCACTTAAAA GGGA	60.1	919	INTERGENIC				
CaPOPI_4002	Ca6	12961933	GCA/GCATGTCATAGAATTTTAACA	TGGGCTTCCAAGTATTGACC	CAGGGGATACGACCTCTCAA	59.9	693	DRR	Ca_05068		MYB_related	Glycoside hydrolase, family 16
CaPOPI_4003	Ca6	12963634	CAAAAA/CAAAAAA	TTTATTTTCCCCTTTCGGCT	AAAGAGAACCATGCCACGAG	59.9	612	INTERGENIC				
CaPOPI_4004	Ca6	12965366	ATTTTTTTTTT/ATTTTTTTTTT	TTTCAACTGGACACTATTCTCTCA	ATGATTGGATGAAAGAGCGG	59.4	341	INTERGENIC				
CaPOPI_4005	Ca6	12965600	CAAAAA/CAAAA	CCGCTCTTTCATCCAATCAT	ACATTTTGGCCTCATTTG	60.0	657	INTERGENIC				
CaPOPI_4006	Ca6	12972982	GTTTTTTTTT/GTTTTTTTTT	AGTTGGTGAGAGGAAGCGAA	GTCCAACCCAGTGGAGAAA	60.0	487	INTRON	Ca_05069	S		Oxoglutarate/iron-dependent oxygenase
CaPOPI_4007	Ca6	12981169	T/TA	ATTGAAATGCACCAGACA	GGAATTTGGTGGGGAGAA	60.0	417	INTRON	Ca_05071	O	E2F/DP	Metallo-dependent phosphatase
CaPOPI_4008	Ca6	13007668	AT/A	TTGAACCTCATTGTGGCAAA	ATAAGTTTGGCTCCCCACC	60.1	116	DRR	Ca_05074	U	M-type	Inositol polyphosphate-related phosphatase
CaPOPI_4009	Ca6	13019215	GAAAAAAAA/GAAAAAAAAA	TAGGCCTATGCCATCAAAACC	ACGTGACACCACGCAAA GTA	59.9	627	INTERGENIC				
CaPOPI_4010	Ca6	13292268	AATATATATATATATATAT/AATATATATATATATATAT	AAATGATGACGTGGGATGTTT	TGCGATTTCATCCACTACATTC	59.2	686	INTERGENIC				
CaPOPI_4011	Ca6	13330838	A/ATTATTATTATTATAT	TTTCAATTTGGCTTGATGGA	GCAACTCACAACCACTCAA	59.1	567	DRR	Ca_05104			Zinc finger, RING-type
CaPOPI_4012	Ca6	13394015	GATATATATATATATATATATA/GATATATATATATATATATA	TTGCCACTTGATACAGCAAAA	TGCAACTTGCCTCTAGGATG	59.4	771	DRR	Ca_05112	Q	B3	Cytochrome P450
CaPOPI_4013	Ca6	13422865	CAAAAAAAAA/CAAAAAAAAAA	CATCGTCGTCAACCACTGTT	TGTGAGCCTGCTCATTGTTC	59.6	550	INTERGENIC				
CaPOPI_4014	Ca6	13428719	CTATTTATTTATTTATTT/CTATTTATTTATTTATTTATTTATTT	GTCTGCGAAAAAGAGATGTC	TTTCCCTATTGCACCTGGAG	60.0	329	INTERGENIC				
CaPOPI_4015	Ca6	13481060	GAAAAAAAA/GAAAAAAAAA	AAAGGTGCTGCCTGTCTTA	GGAGTTGGAACCTCGGAACAA	59.9	483	INTRON	Ca_05119	S		Mitochondrial matrix Mmp37

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4031	Ca6	15727514	ATTTATTTTATTTTATTTTATTT/ATTTATTTTATTTTATTTTATTTT	TTAGTTTGGGCTTGGT TTT	TTGCTCTACGTATCTC CCG	58.6	911	INTERGENIC				
CaPOPI_4032	Ca6	15728024	AA/AAATA	CGGAGATACGTAGGA GCAA	TCGATTATGCGTAGGGA AGG	60.2	248	INTERGENIC				
CaPOPI_4033	Ca6	15730699	TAAA/TAA	ATTTGAACCTGGCAGCA AAA	GGTTTGAAAAAGGGTG ATG	60.6	175	INTERGENIC				
CaPOPI_4034	Ca6	15731057	TAAAA/TAA	ATTTGAACCTGGCAGCA AAA	GGGACAAAAGGCTAGTT TGG	60.6	909	INTERGENIC				
CaPOPI_4035	Ca6	15732116	TAAAAA/TAAAAAA	AGAGTGTTAGCGGCTC AATG	TCAACCCCCCTCTTAG GTG	59.5	472	INTERGENIC				
CaPOPI_4036	Ca6	15877864	GTATA/GTA	TGAGAATAAATGCATG CCG	GGTCTTCAACGGAGATG GAA	59.8	216	DRR	Ca_22023	R		Sugar/inositol transporter
CaPOPI_4037	Ca6	15999975	A/AG	AAGTGTGGCATTTCCT TTG	ATGGACCTCTGTATTCG CCA	60.0	137	INTERGENIC				
CaPOPI_4038	Ca6	16012701	TA/TAA	TAAGAGTTTGGTCCGG TGG	TGTGCAGATAAATGGCC AAA	60.0	397	INTERGENIC				
CaPOPI_4039	Ca6	16286125	CTTACTTTTT/CTTACTTTTACTTTTT	TGTTGGGATATTCCTT GGA	CTTGAAAGAGCCGCAAG AAG	59.3	576	INTERGENIC				
CaPOPI_4040	Ca6	16322518	GTT/GTTT	AGAAGGGAAAAAGAGAG GCG	TCAAAGGAAATCCCTG ACG	60.0	160	DRR	Ca_19667	FP	bHLH	Inositol monophosphatase
CaPOPI_4041	Ca6	16413106	GTTATTATTATTATTATTAT/GTTATTATTATTATTAT	AGAGAGGAGATGCCAAA TGC	GGGGCAAGGGTATGA TATT	59.4	177	INTERGENIC				
CaPOPI_4042	Ca6	16476384	AGAGAA/AGAGAAATGACGAGAA	CTTGATGTTCCGATGT GGA	TCTCTAAGGGACACCA TCG	59.5	671	INTERGENIC				
CaPOPI_4043	Ca6	16547931	GA/GAGAGCTTA	TTCTTCTGCTCGTGC TAT	TTCTTTGGCTGAAATGG TCC	60.0	640	INTRON	Ca_06284	A		PSP, proline-rich
CaPOPI_4044	Ca6	16548981	CAT/CATAT	CTTCCAAGTCACCCAG TGT	GGTCTTATGTGCACGG TGT	60.0	460	INTRON	Ca_06284	A		
CaPOPI_4045	Ca6	16723215	C/CA	GCGAGGATTAGGTTTG TGA	GTGGCCAGGTGAGAGA AGAG	60.1	208	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4046	Ca6	16866680	TATAATAATAATAATAATAATAATAA TAATAATAA/TATAATAATAATAATA ATAATAATAATAATAA	TGTCTACCGGTCCATAC AAAAA	CACATTACAGATGATCC TTGCAT	59.4	816	INTERGENIC				
CaPOPI_4047	Ca6	17086650	GTATATATATATATATATATATA/GTA TATATATATATATATATATATATATAT ATA	AACGGTGAACAAATGCA CAA	ACAAGCCACATTCCTCA TAC	60.0	520	INTERGENIC				
CaPOPI_4048	Ca6	17100171	AATATATATATATATATATAT/AATATATA TATATATATATATAT	CTCGAAACCAGCAAACC ATT	TTTTCTTTGTTGTCATCG ACATTT	60.1	562	INTERGENIC				
CaPOPI_4049	Ca6	17249239	CTTATTATTATTATTATTATTATT/C TTATTATTATTATTATTATTATTATT A	CCCTTTGACCATCAATC ACA	GCACAAATGCAAACGAG AGA	59.3	257	INTERGENIC				
CaPOPI_4050	Ca6	17312806	CT/C	ACCACAATCAGTTTGCC TCC	TTCCCGCTCAAATTAGG ATG	60.0	720	INTERGENIC				
CaPOPI_4051	Ca6	17914426	CAA/CAAA	ATCTTTTGGTGGAAATT GCG	CGCGAAAACAGCGTTAT GTA	59.9	744	INTERGENIC				
CaPOPI_4052	Ca6	18382715	TAAAAAAAA/TAAAAAAAA	GTGGCAACCTTCTCTTC GAC	GGCTACCTCGCGTGTA CAT	59.9	664	DRR	Ca_06453			
CaPOPI_4053	Ca6	18526506	CATATATATATATATATATATATAT ATATATA/CATATATATATATATATAT ATATATATATATA	ATTTATGGTTTCTTGGC CCC	TGATTTTGTGTTGTGGG CA	60.0	719	INTERGENIC				
CaPOPI_4054	Ca6	18790835	TCCGTTGAG/T	TGCATGGTACGCCAAAT AAA	AGCGGGTGGTTGCTAAA GTA	60.0	869	INTERGENIC				
CaPOPI_4055	Ca6	18932008	ATTTTTTTTTT/ATTTTTTTTTT	GCAATTTCCAGGCTATT CCA	GGTTCTGGTGAGACGAA GGA	60.0	754	DRR	Ca_06500	U		WD40 repeat
CaPOPI_4056	Ca6	19172700	TTTTTAAATTAATTTTTATTTTAA/TTTT TAAATTAATTTTTATTTTAAATTAATTT TTTTTTTTAA	GTGGCACAGTAGACCCC ATT	CGTGACATTAACTTGG CCT	59.9	712	DRR	Ca_06524	R		Ribokinase
CaPOPI_4057	Ca6	19355099	CTTTTTTTTT/CTTTTTTTTT	TTGTTTCATGAAGTCTTG GCA	CCGTGATCATATTTCAA ACCA	59.3	400	INTERGENIC				
CaPOPI_4058	Ca6	19591689	CATATATATATATATATATATATATAT CATATATATATATATATATATATATAT AT	TGGAACACACATTGTG ATTGAT	TGTGCATATCTGCAGTT TCATTT	60.1	709	INTERGENIC				
CaPOPI_4059	Ca6	19680352	TTATATATATATATATATAT/TTATATA TATATATATATATATAT	GGGAAATGAACATGTC ACAGA	CTTTGATAAGTGCGGT GGT	59.8	654	INTERGENIC				
CaPOPI_4060	Ca6	20531282	CTTTTTTTTT/CTTTTTTTTTT	TTGGTGGAACTCTTGAA AATGA	CCTTTTCAGCAAAAACTC CG	59.6	630	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4061	Ca6	20851411	TTTCTTCTTCTT/TTTCTTCTTCTTCTT	ACACAAACTGCCGATC CAT	CTTGAAACGAATTGGG ACC	60.4	335	INTERGENIC				
CaPOPI_4062	Ca6	20852278	TAAAA/TAA	TGCAATTTCAGGGACA AGA	CAAGGATGATAGGCGAT GTG	59.2	731	INTERGENIC				
CaPOPI_4063	Ca6	20853701	GA/GAATAAGCA	TCTTGAGGAACATTCTC CGT	AAGCAACAAAAGACAT CACACA	59.7	327	INTERGENIC				
CaPOPI_4064	Ca6	20920548	CATATT/CATATTATATT	TTCTGGAACCTGCAAA ATC	AAAGACCAGCACCATCA ACC	60.1	353	INTRON	Ca_16338	U		Domain of unknown function DUF1692
CaPOPI_4065	Ca6	21021586	CTATTTATTTATTTATTTATTT/CTA TTTATTTATTTATTTATTT	CACCGTCGTGTTTCATC GTC	TTATTTACCGTCGTGT CCA	60.2	458	INTERGENIC				
CaPOPI_4066	Ca6	21139884	ATTTTTTT/ATTTTTTTTT	CAGAAGGATTGCTCGTG TGA	TGCATAGGCCAAAAATGA TTGA	60.0	528	INTERGENIC				
CaPOPI_4067	Ca6	21141563	GTTTTTT/GTTTTTT	TCCGATAGGAGAGCCA ATG	ACGTTTATTTTCGGACC CC	60.2	697	INTERGENIC				
CaPOPI_4068	Ca6	21146689	AT/A	CACACCTTTTGGATGCA CAC	TGGTCATTTTCGTCATC CCT	60.0	379	INTERGENIC				
CaPOPI_4069	Ca6	21353236	GTTTTTTTTT/GTTTTTTTTT	TTATCGGTGACGGAGCT AGG	TGCATTATTTCTCAGCG GGT	60.2	548	INTERGENIC				
CaPOPI_4070	Ca6	21399662	AAATAATAATAATAATAA/AAATAAT AATAATAATAA	TCCCTAGTTGGAGGTCG ATG	GTCCACCTAAATGCCCT TGA	60.1	447	INTERGENIC				
CaPOPI_4071	Ca6	21401312	C/CT	AGCTCAGTCCTCACAAC CGT	TTAGATCGGACAAGAAA CCGA	59.9	344	INTERGENIC				
CaPOPI_4072	Ca6	21401897	ATATTACACTATTA/ATA	TCGGTTTCTTGTCGAT CTAA	ATTCATGGATGCGGGTA TGT	59.7	721	DRR	Ca_19861	E		Serine hydroxymethyltransferase
CaPOPI_4073	Ca6	21408015	ATTTTTTT/ATTTTTTT	AGGCCTTTTATTTTCGTT GCC	TTGAATCGCAAAACAAC CAA	60.4	897	DRR	Ca_19860			Methyltransferase type 11
CaPOPI_4074	Ca6	21485595	GTTTTTTT/GTTTTTTTT	TGCGGGCTAGCTCACTT AAT	TCAAAACAAATAGGCAG GGG	60.0	115	INTERGENIC				
CaPOPI_4075	Ca6	21605985	CTATATATATATATATA/CTATATATA TATATATATATA	GATTTTCGCAGTGAACG GAT	TCCCCTTCTATTTCCCTT GAA	60.1	437	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4091	Ca6	24232847	TTATATATATATATATATAT/TTATATATATATATATAT	TGAGGTGCTGTCCAAT TGT	ATAAATCCGCAACCGA TCA	59.1	521	INTERGENIC				
CaPOPI_4092	Ca6	24296638	CATATATATATATATATATATA/CATATATATATATATATATATA	GAGAAGGAGGGAAAAAT GGC	ATGTTTGGATTTTGGCT CG	60.0	421	INTERGENIC				
CaPOPI_4093	Ca6	24459206	TTATATATATATATATATATAT/TTATATATATATATATATATAT	ATCGAGCGGTGGAGTGA ATA	TTTGGTATACATGGTCG GTAAGG	60.6	831	INTERGENIC				
CaPOPI_4094	Ca6	24637049	TTTCTTCTTCTTCTTCTTCTTCTTCT/TTCTTCTTCTTCTTCTTCTTCT	TGTTTTGGTGAAACGT GGA	AGGATGAATGTGGTGT GAAGA	60.0	376	INTERGENIC				
CaPOPI_4095	Ca6	24647579	ATTTTTTTTT/ATTTTTTTTT	GTTCTGGATGTGTTTGG CCT	ATTCAACTGCATGTCGC ATC	60.0	485	INTERGENIC				
CaPOPI_4096	Ca6	24730447	GTAATAATAATAATAATAATAATAA/GTAATAATAATAATAATAATAATAAT AA	TGAGGACTGGACGTAGC CTT	ACCCCAATTTCAACCAT CA	59.9	498	INTERGENIC				
CaPOPI_4097	Ca6	25002657	AATATATATATATATAT/AAATATATATATATATATATAT	CTACATATGCAAAAGCG GCA	GGATGTGTTTCCCTT CAA	59.9	400	INTERGENIC				
CaPOPI_4098	Ca6	25594919	AATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATA	TATTTTGATTTTGGCTC GG	CGAAAAAGAAACGGGA GAA	59.9	293	INTERGENIC				
CaPOPI_4099	Ca6	25682308	GTTTAGGTTTTAGGTTTTAGG/GTTTAG GTTTAGGTTTTAGGTTTTAGG	TGGGCTTGGGCTGTTT TAG	CCCTTAACCTTAACCC CAA	60.1	838	INTERGENIC				
CaPOPI_4100	Ca6	25762575	TTATATATATATATATATATAT/TTATATATATATATATAT	TCTCTTCGCGAAACGAA TCT	TTGGTATTGAACCTCAGG GGC	60.1	576	INTERGENIC				
CaPOPI_4101	Ca6	25959668	TACATCAAA/TACATCAATATATGACAT CAAA	TGTCATCCCAACACGT CAT	TTTTCCCATGCAAGGT TAG	59.8	339	DRR	Ca_25499	R	C2H2	Pentatricopeptide repeat
CaPOPI_4102	Ca6	26092614	GATATATATATATATATATATAT/GATATATATATATATATATATATATAT	ATGTTTGGATTTTGGCT CG	AATTCCTTCCACACAA CCA	59.9	716	INTERGENIC				
CaPOPI_4103	Ca6	26277672	T/TG	TTAGGTGCGCTTGACTG ATG	GTTTGGCGTTGGTTTCACT	60.0	558	INTERGENIC				
CaPOPI_4104	Ca6	26590044	GATAATAATAATAATAATA/GATAATAATAATAATAATA	CCTTTGTGAGGGCTAAA AGC	TTGTTGTTGACCAAGCT AGGAA	59.0	731	INTERGENIC				
CaPOPI_4105	Ca6	26764661	TAGAGAGAGAGAGAGAGAGAGA/TAGAGAGAGAGAGAGAGAGAGA	CCATAGGATGAATGCT GGC	GCAGCCATGAACCTTCA ACT	60.4	436	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4121	Ca6	28326755	AT/ATT	TTTGGGCTTGAAGATGAAA	TTTAAAAGCAAGGTGGTGG	58.3	336	DRR	Ca_25968	A		Ribonuclease T2
CaPOPI_4122	Ca6	28327723	CATATATATATATAT/CATATATATATAT	CAAGAGCATCGTGTCAGGA	GTCCTGGCGTGACAAGAAAT	60.0	424	DRR	Ca_25968	A		Ribonuclease T2
CaPOPI_4123	Ca6	28332319	ATTTT/ATTTT	TTTCAAAAAGTCCCAATCGC	GGTTTGAGAGAAGAAGACGAAA	60.1	751	INTERGENIC				
CaPOPI_4124	Ca6	28332579	A/AG	GTCGGAGCTCTGCCATAAAA	GGTTTGAGAGAAGAAGACGAAA	60.4	599	INTERGENIC				
CaPOPI_4125	Ca6	28332651	C/CT	GTCGGAGCTCTGCCATAAAA	GGTTTGAGAGAAGAAGACGAAA	60.4	599	INTERGENIC				
CaPOPI_4126	Ca6	28332758	TAA/TAAAA	TTTCGTCTTCTCTCCAAACC	CCCAACATATTACCTGTTACCCA	58.4	502	INTERGENIC				
CaPOPI_4127	Ca6	28332811	A/AG	TTTCGTCTTCTCTCCAAACC	CCCAACATATTACCTGTTACCCA	58.4	502	INTERGENIC				
CaPOPI_4128	Ca6	28332973	A/AT	TTTCGTCTTCTCTCCAAACC	CGTGCAAAGTCGAAGCGTAT	58.4	669	INTERGENIC				
CaPOPI_4129	Ca6	28336699	ATTTT/ATTT	TCTCCCATTTTACCATGCC	TTTGGCTTTGGTTGATTCCT	59.8	980	INTERGENIC				
CaPOPI_4130	Ca6	28443583	CTCTTTTGTGTTA/CTCTTTTGTGTTATATCTTTTGTGTTA	AAAAACACCAAAAGCCCCTC	CATAAAATGCCATTGATCCCT	60.3	499	INTERGENIC				
CaPOPI_4131	Ca6	28444744	GATAATAATAATAATAAA/GATAATAATAATAATAATAATAATAA	TCCCAACAGCCTAACCAACC	CAACGCAATCTGAACAATAA	60.0	509	INTERGENIC				
CaPOPI_4132	Ca6	28503466	ATAAT/ATAATTAAT	TTTGTGCCTCCATTCCTTC	TTTTTAACATAATTGATCACCGCT	60.1	497	DRR	Ca_25961			
CaPOPI_4133	Ca6	28513162	TATCTTCAACTTCCCTACCA	CCCACACCTTCTTACCAAGA	GGGACCCAAATTGTCGATAG	60.0	492	INTERGENIC				
CaPOPI_4134	Ca6	28513941	ANNNNNNNNN/ANNNNN	TGAAGAAAATTTAAAGGACAGAA	GTGTTGCATCTCATTGGTGG	59.2	569	INTERGENIC				
CaPOPI_4135	Ca6	28515482	GAAAAAAA/GAAAAAAA	GGCATAGGTGAGATGACCGT	GCTCCTTATCAAACATTGTC	60.0	507	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4136	Ca6	28520924	CAA/CAATTAAA	TTAGAAACAGGGACCCC TCC	TTGTCTGTGAACCGAAG CTG	60.3	577	INTERGENIC				
CaPOPI_4137	Ca6	28521027	A/ACATAG	TCTCATTCTTGCCTTGC CTT	TTGTCTGTGAACCGAAG CTG	60.0	172	INTERGENIC				
CaPOPI_4138	Ca6	28521076	AACTAT/A	TCTCATTCTTGCCTTGC CTT	TTGTCTGTGAACCGAAG CTG	60.0	172	INTERGENIC				
CaPOPI_4139	Ca6	28537234	ATT/AT	ATTCTCTAAAGCCCTCA CCT	TTCCACTTCTCTTTCCAC CA	60.1	436	INTERGENIC				
CaPOPI_4140	Ca6	28610431	CT/C	AGGATTTGGTTCAAGGG TCC	TGTCCTGACTCTTGCGCA GTG	60.2	643	DRR	Ca_17488	K		
CaPOPI_4141	Ca6	28832556	AAAATAATAAAATAAAATAATAAAT AAATA/AAAATAAAATAAAATAAAATA ATA	GCTTTCTTGATCAAGT GCGAA	TGCAATTGTGGTTTCTG TCTG	59.4	648	INTERGENIC				
CaPOPI_4142	Ca6	29148934	GTTATTATTATTATTATTATTATT/GT TATTATTATTATTATTATTATTATT	TTGTGTCGTGTTGCTGT TCA	TCGTGTTTCAAAAATTCAA GGA	59.9	871	INTERGENIC				
CaPOPI_4143	Ca6	29174756	AATATATATATATA/AATATATATATAT A	ACCAGCTCCTTTTTGTG ACC	CAGCCCCCAATACTCCT ACA	59.2	595	INTERGENIC				
CaPOPI_4144	Ca6	29231459	AAAGTCTCAAGTCTCAAGTCTCAA/AAA GTCTCAAGTCTCAAGTCTCAAGTCTCA A	ACTCCCACACCTCAA AGG	TTTCAAGTCTAGTCGAA GTTCATCA	60.0	834	INTERGENIC				
CaPOPI_4145	Ca6	29640665	AATATATATATATATATATATATAT/AA TATATATATATATATATATATAT	CACACATCGCGAGTAAT GATG	AACTTCTCGAGGACGCA AAA	60.2	541	INTERGENIC				
CaPOPI_4146	Ca6	29833274	A/AG	GCCGAATAAAACCTCA CAA	CAAAGCAACCACAAAAA GCA	59.9	561	INTERGENIC				
CaPOPI_4147	Ca6	30102387	ATTTTTTTTTTT/ATTTTTTTTTTT	TTGGGAGATGCATGTAT TGG	TTAGACGTAACCCACCT TGGA	59.4	596	INTERGENIC				
CaPOPI_4148	Ca6	30588229	AATCGC/A	GGACGTCTACAACATTG GGG	CCACATGAGTGTGTTGA GGG	60.2	948	DRR	Ca_16461		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_4149	Ca6	30816682	GTTTTTTTTT/GTTTTTTTTT	ATAAACCTTCGGAGGGG AAA	ACCCCTCTCAAAGCACA AGA	59.8	518	INTERGENIC				
CaPOPI_4150	Ca6	30901162	ACT/ACTCT	CACTCCAAAAGGCACTG GTT	CACAGATGATGGGCAGA AGA	60.1	341	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4151	Ca6	31097180	ATTT/ATTTTT	TCCCAATTGAGTGACATCTTTC	CTTATAGCCGAATGGCCAAA	59.0	587	INTERGENIC				
CaPOPI_4152	Ca6	31099504	TA/T	TGGGATGATGTTGGGAAGT	TTGCAAGAAAACCTCGCTT	60.2	129	INTERGENIC				
CaPOPI_4153	Ca6	31132134	TAAA/TA	CACTCCAGGTTCCATTCCTC	GCTGGTGGCTAATTATCCATT	59.5	708	INTERGENIC				
CaPOPI_4154	Ca6	31335349	TTATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT	TCGGTTCATAAAACGAGTTAAAA	GAAGCTTCTATGGTCCCGTG	58.0	392	INTERGENIC				
CaPOPI_4155	Ca6	31413696	CAAAAA/CAAAAA	GAACGGTGATGACAGCTTGA	GGCCTCCTTGTAACCTCCTCT	59.8	491	INTERGENIC				
CaPOPI_4156	Ca6	31769480	A/AT	CGGGAGATACGTAGGAGCAA	TCGATTATGCGTAGGGAAGG	60.2	250	DRR	Ca_15194			
CaPOPI_4157	Ca6	31950641	ATTTTTTTT/ATTTTTTTT	CCACTTCAGCGTGCAATCTA	TTCTTGGGTAGAAAATGCGG	60.0	612	INTERGENIC				
CaPOPI_4158	Ca6	32372827	CAA/CA	GAATACGCGGCTGATTCATT	CGCCCCGTTTTAACTCATTA	60.1	613	INTERGENIC				
CaPOPI_4159	Ca6	32391786	AATATATATATATATA/AATATATATATATATATA	CGCTATGCCCCATTAGATGT	TTTGATTGACTCATTGCGTG	59.9	294	INTERGENIC				
CaPOPI_4160	Ca6	32519592	AG/A	CGCATGCCACTCACTCTAAA	CGCTGCCACTTTCTACATCA	60.0	611	INTERGENIC				
CaPOPI_4161	Ca6	32521477	GACATGATAC/GAC	TTGCCAACGTGTCAATCACTACT	TTTTCCCTACTATTTTGCAGCC	60.2	259	INTERGENIC				
CaPOPI_4162	Ca6	32521795	ATTTTGTGTTTT/ATTTT	TTGCCAACGTGTCAATCACTACT	TGCTAGGACCAACGATCATGT	60.2	902	INTERGENIC				
CaPOPI_4163	Ca6	32522263	CA/CAA	TTGTTCATTTTGTGTCGTCA	CCTTGGCGGATATAGGGAAT	59.0	347	INTERGENIC				
CaPOPI_4164	Ca6	32540181	TATATAT/TATATACATATAT	GTTTATCAATGGACGCGGAC	TTCCCCTAAAAACGGTTGTG	60.3	341	INTERGENIC				
CaPOPI_4165	Ca6	32540257	TACATAA/TACATAAGAAACATAA	GTTTATCAATGGACGCGGAC	TTCCCCTAAAAACGGTTGTG	60.3	341	INTERGENIC				

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CaPOPI_4166	Ca6	32540480	GTTTTTTTT/GTTTTTTT	CACAACCGTTTTTAGGG GAA	GAGGATTGCTATGGACA ACCA	59.8	214	INTERGENIC				
CaPOPI_4167	Ca6	32617100	AAA/AAATAA	GAACGGTCCATGCAAAA GTT	CCCCCGATCCTTATACG ACT	60.0	554	INTERGENIC				
CaPOPI_4168	Ca6	32630124	TAAA/TAAAA	TTTGAGGGAGGGAATTA GGG	TAGTGATTGGAAGGAC GGC	60.3	583	INTERGENIC				
CaPOPI_4169	Ca6	32759448	AATATATATATATATATATATAT/AATATA TATATATATATATATAT	AATTTTGAAGTGGCCGT GAC	TCGACCTTCATTTTCATAC ATTTTT	60.0	701	INTERGENIC				
CaPOPI_4170	Ca6	32839696	TTATATATATATATATATATATATATATATA TATATATATATA/TTATATATATATATATA TATATATATATATATATATA	CCATATTAAACCGTGCA CACA	CAAACGCTGTTCCACAA GAA	59.4	863	INTERGENIC				
CaPOPI_4171	Ca6	32932244	TTATATATATATATATATATATATATATA T/TTATATATATATATATATATATATATA TATATATATA	GCAAATGGCGATTTCCT TTA	GTAATGTTGGGCTTCGG AGA	60.0	713	DRR	Ca_22231		ARF	Transferase
CaPOPI_4172	Ca6	32971894	CTTTTTTTTTT/CTTTTTTTTTT	TTAACCTACCAATTGCAA TACCA	TTAATGCATCTTGATGGT GG	57.7	257	INTERGENIC				
CaPOPI_4173	Ca6	32974504	AAT/AATGAT	TCGAGATGTGTTTGGGT GAA	TTTTACGATGGACAACC GTG	60.1	940	INTERGENIC				
CaPOPI_4174	Ca6	33094621	ATTT/ATT	TCAAAATGTAGCGGGTT TCC	AAGCCTTCCTCAAAATC CAA	59.9	398	INTERGENIC				
CaPOPI_4175	Ca6	33094845	CAAAAA/CAAAAAA	TCAAAATGTAGCGGGTT TCC	AAGTTGGACAAAATTGG GGT	59.9	950	INTERGENIC				
CaPOPI_4176	Ca6	33229235	CTT/CTTT	GCTTTTATCCAAATTAT GGCG	AAATTTTAGACCGCGAC ACG	59.8	758	INTERGENIC				
CaPOPI_4177	Ca6	33229272	GAAAA/GAAA	TGTTGACGGTGTTTTT TAAGG	AAATTTTAGACCGCGAC ACG	59.9	477	INTERGENIC				
CaPOPI_4178	Ca6	33229296	TG/TGG	CGGTGTGTTTTTAAGGA TTGG	AAATTTTAGACCGCGAC ACG	59.4	471	INTERGENIC				
CaPOPI_4179	Ca6	33229369	ATTTTTTTTTTTTTT/AATGTTTTTTTTTTT TTTT	CGGTGTGTTTTTAAGGA TTGG	AAATTTTAGACCGCGAC ACG	59.4	471	INTERGENIC				
CaPOPI_4180	Ca6	33229523	AAAAACGAAAA/AAAAA	CGGTGTGTTTTTAAGGA TTGG	GCGGATATCGTAGGGTG CTA	59.4	644	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4181	Ca6	33229803	TAAAAAAAA/TAAAAA	AAGCAAGCCAAAAACGA AAA	GCGGATATCGTAGGGTG CTA	59.9	382	INTERGENIC				
CaPOPI_4182	Ca6	33231576	AT/ATT	TGGTGTATTGGGTGCTG ATG	GACCCATCGATTGAAG CAT	60.4	975	INTERGENIC				
CaPOPI_4183	Ca6	33233620	G/GAA	CCGCCCACTAAAAAGTT GAA	AATCGCCATAACTTGAA ATGC	60.1	935	INTERGENIC				
CaPOPI_4184	Ca6	33240261	A/AAAGAG	GTTTGGTATTGGGCTCC CTT	CACAATTCCTCCCTCTC CAA	60.2	314	INTERGENIC				
CaPOPI_4185	Ca6	33240380	A/AG	GTTTGGTATTGGGCTCC CTT	CGAAACTCACCCCTTGT TGT	60.2	750	INTERGENIC				
CaPOPI_4186	Ca6	33240742	AA/AATATA	TTGGAGAGGGAGGAATT GTG	CGAAACTCACCCCTTGT TGT	60.0	456	INTERGENIC				
CaPOPI_4187	Ca6	33256778	ATATTATTATTATTATTATTATT ATTATTATTATTATTATTATTA/ATATTAT TATTATTATTATTATTATTATTATTA TTATTA	TGGCTATTTATGGCAGC ACA	TAATGTGGAACCCCT CAA	60.1	596	INTERGENIC				
CaPOPI_4188	Ca6	33337104	ATTT/ATT	CCAATTTTGATTCCCTC CA	TTAGGCTCCTGCTTCAT GCT	59.7	527	INTERGENIC				
CaPOPI_4189	Ca6	33340808	GTTTTTTT/GTTTTTTTT	TTCAATGTCATACACAG GCCA	ATGATAACGCATGAATG GCA	60.0	841	INTERGENIC				
CaPOPI_4190	Ca6	33488777	GATATATATATATATATAT/GATATAT ATATATATATATAT	TTACCCAACCCCAATTTT CA	AAGTTTTGGGAAAGGGG AAA	60.0	641	INTERGENIC				
CaPOPI_4191	Ca6	33780561	ATTTT/ATTTT	TGGGAGCTTCAGGAATC ACT	TGCATGTTTGATAATGC GGT	59.8	250	DRR	Ca_22060	G	C3H	Metallo-dependent phosphatase
CaPOPI_4192	Ca6	34222252	CATATATATATATAT/CATATATATAT ATATATAT	TGCCTTTTGTGTTCCCT TC	AGTTTAATGTCGTGACC GGC	60.1	496	INTERGENIC				
CaPOPI_4193	Ca6	34570118	TTTTTG/T	TGGTCGACAAGCAACTG AAG	AACAATCTCCCCCTTTT GG	60.0	583	DRR	Ca_15816			
CaPOPI_4194	Ca6	34728984	TTATATATATATATATATAT/TTATATA TATATATATATATAT	TAGGCACATCAAGTCAA CCG	TCAGACCATCCGATAGA GGC	59.7	570	INTERGENIC				
CaPOPI_4195	Ca6	34775621	T/TCAATTCAC	AAATGAACCTGTACGG GCT	TCCCAACATTAGCTGAT CCC	59.6	702	INTRON	Ca_15807	R		

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4196	Ca6	34859064	GATATATATATATATATATATATA/GATATATATATATATATATATATATA	GAAAGAGTTTGTGACCA CCG	AAGTCCAATCTCGGTCA AACTT	59.9	625	INTERGENIC				
CaPOPI_4197	Ca6	34936983	AATATATATATATATATATA/AATATATATATATATA	TCATCTTGCACTTGGCT TTG	TCGCGTCGAAAAGTAGA TCA	60.0	708	INTERGENIC				
CaPOPI_4198	Ca6	35161798	TATAAATATAA/TGAATATAAAATAAATA TAA	AGGAAGAGTGGAGTTGC GAA	CGGTTGAGAACCAAGGA TGT	60.0	649	INTERGENIC				
CaPOPI_4199	Ca6	35399356	GTTT/GAATTT	TTGAAGCTCAGATGGCA CAC	CTCCCCCTTTTGGCAT AAT	60.0	718	INTERGENIC				
CaPOPI_4200	Ca6	35528115	AACA/AACACA	AAGACCATCTCCAGCA CAC	CACCCATCGGATAATGC TTC	60.1	783	INTERGENIC				
CaPOPI_4201	Ca6	35616799	C/CCTT	GTTTCTGAGGCAAAATC CCA	TGCATTGTCTTCCATT GA	60.1	537	INTERGENIC				
CaPOPI_4202	Ca6	35719325	AATAGAATACTTTATTAT/AATAGAATAC TTTATTATAGAATACTTTATTAT	TGCATCGTTTTTCATCTT TCA	GCGGCTAATTTCAACCA AAT	59.3	630	INTRON	Ca_15773			
CaPOPI_4203	Ca6	35801189	AAATAATAATAATAATAATAA/AAAT AATAATAATAATAATAA	CTTCATAAGCCGCATT GTT	TTGAACAATAAAATTA TCGCAA	60.1	548	INTERGENIC				
CaPOPI_4204	Ca6	35802672	TTTCT/TT	GAGCCTTAGAGTTGGGA GCA	ACCCAACCTGTCGAACC AAC	59.6	778	INTERGENIC				
CaPOPI_4205	Ca6	35810337	C/CT	TCATCGATTGCAACTTG CTT	CCCTAAATTTTGTGGG CTT	59.4	672	INTERGENIC				
CaPOPI_4206	Ca6	36029920	CTTT/CTTTT	TTTGGAACCAAAACTTC TTCAA	GGAGAAAAAGAAATTA AATCCTCTAA	60.0	520	INTERGENIC				
CaPOPI_4207	Ca6	36039668	CATAA/C	CAAGTCGTCGCTTCCAA AGT	AATTGCGGCGAGAGAAG ATA	60.4	394	INTERGENIC				
CaPOPI_4208	Ca6	36237842	CATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTAT AT/CATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTA	TCTACCCCCAATCCCTC TCT	ATTGCCCTGATGTTTT GG	59.9	573	INTERGENIC				
CaPOPI_4209	Ca6	36281940	CATATATATATATATATA/CATATATA TATATATATA	AGTGACCATCTCCCAAG GTG	ATTTTAACGGATGTCGT GGG	60.0	646	INTERGENIC				
CaPOPI_4210	Ca6	36452738	AATATATATATATATA/AATATATATAT ATATATATATA	CAATCCCATTCCCATTT TG	AATGGGCGCTGTAAAT GTC	60.0	778	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4211	Ca6	36722414	ACCC/ACC	CTTAGGTTTGCACTCAGCCC	TCGCGGATCTGCTCTTA AAT	59.9	685	INTERGENIC				
CaPOPI_4212	Ca6	36722630	TA/TAA	TTGCTCCTACGTATCCC CAG	TCGCGGATCTGCTCTTA AAT	60.1	295	INTERGENIC				
CaPOPI_4213	Ca6	36880735	AATATATATATATATAT/ AATATATATA TATATAT	GGGCCAAGCCCATATTT TAT	TTGTTTGCAAATACTCCC CT	60.0	177	INTERGENIC				
CaPOPI_4214	Ca6	36898169	AATATATATATAT/ AATATATATATATAT	AAGAGAGGTCACTTTGG CGA	CAATCCCACAGGTACG CTT	60.0	692	INTERGENIC				
CaPOPI_4215	Ca6	36951265	TTTATTATTATTATTATTATTATTAT TATTATTAT/TTTATTATTATTATTATTAT TATTATTATTATTATTATTAT	TGGGCAGAATTGATAAA TCG	CTCCCTCTCATCTGTTC AAAAA	58.6	578	INTERGENIC				
CaPOPI_4216	Ca6	37640608	CAAAATTTAAAAATTTAAAAATTTAAAA/ CAAAATTTAAAAATTTAAAAATTTAAAAA TTTAAAA	TTTGCGTGTGTGACTTGC	CTCGTGAGGGGAAGCAT AAG	59.9	308	INTERGENIC				
CaPOPI_4217	Ca6	37714381	CATATATATATATATA/ CATATATATA TATATATATA	TCGATCTCACCAGCAAC AAC	TGGTGTCTATGACCAAAA TGG	59.8	352	INTERGENIC				
CaPOPI_4218	Ca6	37788611	GTATATATATATATATAT/ GTATATAT ATATATATAT	AATGGAGGAAGGAGGG AGAA	TTTGGATTTTGACTCGG AGG	60.0	435	INTERGENIC				
CaPOPI_4219	Ca6	37849692	CAAAA/CAAAA	TCGAAACCATGACGTT GTA	GAATCCTGGGCTGAAAT CAA	60.0	547	INTERGENIC				
CaPOPI_4220	Ca6	37890277	AATATATATATATAT/ AATATATATATATA TAT	TCACGGCGAATATGAAA TGA	TGCTATGCGTTTGGATC TTG	60.0	652	INTERGENIC				
CaPOPI_4221	Ca6	37902107	TT/TTGATAT	GTTTTGACAGGCCCGAA TAA	ATGGTGGTTCGGTCACA TTT	59.9	462	INTERGENIC				
CaPOPI_4222	Ca6	37981858	TAAA/TAA	TGCAATGACCTTGAAAT CG	CTTTAGCCTTCATCGC CAG	59.7	817	INTERGENIC				
CaPOPI_4223	Ca6	37982172	AATGAT/AAT	GGTACACTTTCCCATCA GCAA	CTTTAGCCTTCATCGC CAG	60.0	468	INTERGENIC				
CaPOPI_4224	Ca6	38201434	GTTTTTTT/ GTTTTTTTT	GGTTCGTAATGGATGGG ATG	AAGGCCTTTTACAACGC TCA	60.0	609	INTERGENIC				
CaPOPI_4225	Ca6	38317090	ACC/ACCAAAATGCC	CAATCACAACCTTTGCC CTT	GTGGGAAGTCGCCATTT AGA	60.0	531	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4226	Ca6	38822653	T/TCGTTTACATTGTTCA	TGAGAAAGGGGAAAGG GAAT	TGAGGTTGTTGCTTTGA CCA	59.9	737	INTERGENIC				
CaPOPI_4227	Ca6	39182715	GAAAAAAAA/GAAAAAAAAA	TGGACGAAGTCAATGGT CAA	TCAATGGAATTTTTCGA GTCAA	60.1	843	DRR	Ca_15911	P	ERF	SPX, N-terminal
CaPOPI_4228	Ca6	39781733	CATATATATATATATATATATATA/ CATATATATATATATATATATATAT A	TCTCCGCATAAGCTTTC GAT	TGCTTCGACACAGTAGC ACC	59.9	478	DRR	Ca_15927			
CaPOPI_4229	Ca6	40508760	GAAAA/GAAAAA	AATTGACGTGCAACCT GTC	CGTAGCGAAGTCGGATG AAT	60.0	364	INTERGENIC				
CaPOPI_4230	Ca6	41139265	AA/AAACAGGA	TTCGGGCTTAACCAAA ATG	AGCTGCAAGTGCAGAGC ATA	59.9	534	INTERGENIC				
CaPOPI_4231	Ca6	41432949	GAATTAATTAA/GAATTAATTAAATTA A	TCGAATTTTGAGACGGA AAGA	GGTTCGAGTGTGTGCCA TAA	59.8	684	INTERGENIC				
CaPOPI_4232	Ca6	41493875	TTATATATATATATATATAT/TTATATA TATATATATATATAT	GGATCCAAATCTTCTCG TTAAA	AGTGGACGGTCTCAACT TGG	57.4	993	INTERGENIC				
CaPOPI_4233	Ca6	41520820	AATATATATATATATATAT/AATATATA TATATATATATATAT	GCATTTTGTTGAAGATT TTGATG	ATTCAATCACCCAAACC GAA	59.9	414	INTERGENIC				
CaPOPI_4234	Ca6	41574227	CATAATAATAATAAT/CATAATAATA ATAATAATAAT	TGATTAATCGCAAATTGT CCA	TTTTTGGGGTCGTTTTAT GC	59.0	471	INTERGENIC				
CaPOPI_4235	Ca6	41574282	TTTATTATTATTATT/TTTATTATTAT TATTATTATT	TGATTAATCGCAAATTGT CCA	TTTTTGGGGTCGTTTTAT GC	59.0	471	INTERGENIC				
CaPOPI_4236	Ca6	41654561	GAAAAAAAAA/GAAAAAAAAA	CCTTTTGTGAAAGAGGC AGC	CACGGGGAAAGTTGTTT TGT	60.0	623	INTERGENIC				
CaPOPI_4237	Ca6	41659483	CAAAA/CAAAA	CCATCAGAACTGGGAT GGT	TGGCCCTTCATTTTCAA TC	59.8	495	INTERGENIC				
CaPOPI_4238	Ca6	41669872	ATT/ATTT	TGTAGAATCCACCAATG TCCA	ACCAATCATGTTTCGTG GAA	58.8	651	INTERGENIC				
CaPOPI_4239	Ca6	41875891	ATTTTT/ATTTTT	GGATCTATGATTTCCCT CTTGC	AGTCCCCATGTAATTGT CACG	59.1	568	INTERGENIC				
CaPOPI_4240	Ca6	41957220	CTATATATATAT/CTATATATAT	TCCCCAACTTTTGAATTT GC	TGCTTCAGTCAATGGGA CAG	59.9	877	DRR	Ca_21949	O		Armadillo

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4241	Ca6	42309198	AATATATATATATATATA/AATATATATATATATATATA	AGGAAGCCCAAGTTCCA AAT	CCAAGAGAGGTGCAACC AAT	59.9	569	INTERGENIC				
CaPOPI_4242	Ca6	42398678	ATTTTTTT/ATTTTTTT	GGTTTGGGAGAGAAAA GGAA	TGTTTAAACTCATTGG TCCC	59.6	900	INTERGENIC				
CaPOPI_4243	Ca6	42869037	TAA/TAAA	TTGTCGTGATTATTAGG GGACA	TTGTCAAACATATGCC GTTTC	59.3	263	INTERGENIC				
CaPOPI_4244	Ca6	42907383	A/AAGAGGG	ACTGGCTGACCACTCTC GTT	CAGCGCTTATTTGGGAA AAA	59.9	840	INTERGENIC				
CaPOPI_4245	Ca6	43017644	ACATCAT/ACATCATCAT	GGAAGGATTTTGAAGAA ACCA	GCCGTGCCTTTTAAATG TGT	58.1	529	INTERGENIC				
CaPOPI_4246	Ca6	43043105	CA/C	TGATTGGTCGCAACAG CTA	AAAATTGTGCCAAAGTT ATGTGA	60.4	556	INTERGENIC				
CaPOPI_4247	Ca6	43064353	A/AACTG	CGCCACAACCTCTACTC CTT	GAGGTGCGACAACAGAT GAA	59.4	785	INTERGENIC				
CaPOPI_4248	Ca6	43116900	AATATATATATATATATATATATATA ATA/AATATATATATATATATATATATA TATATATA	GTTTGGGGTTACTCATG GGA	ATTCCCAACATTGGCA AAA	59.6	195	INTERGENIC				
CaPOPI_4249	Ca6	43138332	GAAAA/GAAA	GTTCCCTTTGGAATGCT TGA	TCTTTGGGCCAGTGAAA ATC	60.1	741	INTERGENIC				
CaPOPI_4250	Ca6	43144384	TTTCTTCTTCTTCTTCTTCTTCT/TT TCTTCTTCTTCTTCTTCTTCTTCTT CT	TCATGTGGACTAAATGG GCA	ACAGCTCAAGCGAAACC CTA	59.9	399	INTERGENIC				
CaPOPI_4251	Ca6	43144709	TTTATTATTATTATTATTATTATTAT TATTATTATTATAATTATAATTATTATTA TTATTATTATTATTATTATTATTATT ATT/TTTATTATTATTATTATTATTAT	TAGGGTTTCGCTTGAGC TGT	TCCGGATCCTTCAGATT CAC	60.0	656	INTERGENIC				
CaPOPI_4252	Ca6	43901335	GCCC/GCCCCC	GACCTTTGAGGGTTCC CAT	ATTGACAACCTTCCAC TGC	60.2	260	INTERGENIC				
CaPOPI_4253	Ca6	43909185	TTGAAG/TTGAAGCAAGTACAACCTCATG AAG	TGATTGGGTTTGGGTTT ATT	ACATAGATGCCGCCTTC ATT	60.0	445	INTERGENIC				
CaPOPI_4254	Ca6	44072205	TTATATATATATATATATATATATAT/T TATATATATATATATATATATATAT	GACATTTCGAACTTGAAT TTCTT	TTTGGAATTGCGACTTC CTT	58.7	363	INTERGENIC				
CaPOPI_4255	Ca6	44266489	AATATATATATATATATATATATATAT A/AATATATATATATATATATATATA	CCGCATTATAATTCCGC TGT	GTGCCGAGAAAATGTGG ATT	60.0	819	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4256	Ca6	44386840	GAT/G	ACCCAGTGCCTTTCT CTT	GCGTCAGAGGAAGAAT CAG	60.1	577	INTERGENIC				
CaPOPI_4257	Ca6	44418513	CCTCTCTCTCTCTCTCTCT/CCTCTCTC TCTCTCTCTCTCT	ATAGGTGGCCATTGTTCA A	TGTGGAGTGAAAGCATG AGG	60.2	543	INTRON	Ca_24238		MYB_rela ted	Toll-Interleukin receptor
CaPOPI_4258	Ca6	45018203	AA/AAGTAACA	TCAAGACGGGAATTGGA AAG	TTGCAAAGGATGTATTG GCA	60.0	433	INTERGENIC				
CaPOPI_4259	Ca6	45329060	T/TTTAAAA	TTTTTGCTATTTTATCT CGTGG	TCGATTATGCGTAGGGA AGG	57.6	762	INTERGENIC				
CaPOPI_4260	Ca6	45469975	TGTTCA GTTCAGTTCA GTTCAGTTCA	TGCGAAAAATGGGTTTG AGT	ATGTGAATCCCACCAGG AAA	60.5	637	INTERGENIC				
CaPOPI_4261	Ca6	45484176	GTTTTTTTTTTTT/TTTTTTTTTTTTTT	CACCAAAAATTGTACCA CTGTC	GAGGCAACGACTCAAAC CTC	59.4	864	INTERGENIC				
CaPOPI_4262	Ca6	45922563	GTTTTTTTTTTTT/TTTTTTTTTTTTTT	GTGGCCACTCACCAAAA GAT	TGAACAAAACCACCAAA CCA	60.0	564	INTERGENIC				
CaPOPI_4263	Ca6	46031146	G/GGA	GGAAATGGATGTCTGCC AAT	AGCCTCGTAGGTTCGAC TGA	59.8	551	INTERGENIC				
CaPOPI_4264	Ca6	46128884	AAATAATAATAATAATAATAATAATA ATAATAATAATAAAT/AAATAATAATA ATAATAATAATAATAATAATAATAAT AATAATAAT	ATGCCAGCTTGGACAAT GTT	TGGAGATGCGACCGTCT ACT	60.5	741	INTERGENIC				
CaPOPI_4265	Ca6	46391549	ATTTTTTTT/ATTTTTTTTTT	GAACATGAAAAGGGTCA CCG	GGAGGAATCTTTGTG CCA	60.4	564	INTERGENIC				
CaPOPI_4266	Ca6	46517053	T/TAAATAATAATAATAA	TCTTCGTCGTCACATG AGC	AGCAACGGAAAGGATAC ACG	60.0	574	INTERGENIC				
CaPOPI_4267	Ca6	46772986	A/ATT	GATTATTCTGCCTCCCG TCA	AAACGCAATCCTTGAGT TCG	60.0	633	INTERGENIC				
CaPOPI_4268	Ca6	46804307	AATATATATATATATATATATATAT/ AATATATATATATATATATATATAT	TAAACCAAGTTCCCCGT CAG	CAATGGCTAAGAGCAAA GGG	60.0	799	INTERGENIC				
CaPOPI_4269	Ca6	46855085	AATATATATATATATATATA/AATATAT ATATATATATATA	CTGTATCACGTGGACAA CGG	CGATCAGGCCGGATATT AGA	60.0	699	INTERGENIC				
CaPOPI_4270	Ca6	46877609	TTTATTATTATTATTATTATTATTAT/ TTATTATTATTATTATTATTATTA	TGGATGGATTGGTTGAA TGA	TGAAGGAGGGACCAAAA CTG	59.7	198	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4271	Ca6	47001052	A/AG	GAAGCGGTACTTCCCAT TGA	GGTTACAATGTGGGGAC GAG	60.1	417	INTERGENIC				
CaPOPI_4272	Ca6	47040606	TTTATTATTATTATTATTATTATTAT TATTATTATTATTAT/TTTATTATTATTAT TATTATTATTATTATTATTATTAT	TATCATCACCTCACCCC CAT	TCCAGTCAATGTGCAAA AACA	60.0	550	INTERGENIC				
CaPOPI_4273	Ca6	47149113	TAAAA/TAAAA	AAACGGGAACCTCCAGAA TGA	TTTCCACCCAGAAAGCA ATC	59.5	617	INTERGENIC				
CaPOPI_4274	Ca6	47312521	GTT/GTTT	TATCTGTGGTCGTGTGG GAA	TCACGGGTCAACACGAT TTA	60.0	822	INTERGENIC				
CaPOPI_4275	Ca6	47393714	AAATATCAATA/AAATATCAATCAATA	TTATCTGCCGCTACCCA AAG	TCTTGAGCTTTTGCT TGT	60.2	755	INTERGENIC				
CaPOPI_4276	Ca6	47697947	GTTCTGATTAAATTTTCTG/GTTCTG ATTAATTTATTTCTGATTAAATTTT CTG	TATTTGGGGTTATCGA GCG	TTGGTTTATTTGGGTG GGA	59.9	801	INTERGENIC				
CaPOPI_4277	Ca6	47816277	AATATATATATATATATATATATA/A ATATATATATATATATATATATA	TGGGAATAGGCCAGACT TTG	TTCCGAGTTGTTTGAGA GGA	60.1	748	INTERGENIC				
CaPOPI_4278	Ca6	48011269	GATATATATATATAT/GATATATATATAT ATAT	TTTGTTCGTAATGTT GTTGA	TAGCTGTTGCGACCAA TCA	59.2	665	INTERGENIC				
CaPOPI_4279	Ca6	48260819	GAAAAATATAAAATA/GAAAAATATAA AATAAAATTAATAAAATA	GTGGATGGTGGGGAATA GTG	CTGAGGTCCCAAGCTAC GTC	60.1	504	INTERGENIC				
CaPOPI_4280	Ca6	48271447	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTA T/TTTATTATTATTATTATTATTATTA TTATTATTATTATTATTAT	TGACTAATTGGTCGCCC TTC	GGATGCGATCATGTGAA GAA	60.1	685	INTERGENIC				
CaPOPI_4281	Ca6	48271722	CATATATATATATATATATATATAT/C ATATATATATATATATATATAT	TGGACCAAAGCAGTGAT GAG	TGACATTTTCAGGAGGC ACA	59.8	804	INTERGENIC				
CaPOPI_4282	Ca6	48271982	GTATATATATATATATATATATAT/GT ATATATATATATATATATAT	GAGGATGCGACCTCCTA CTG	TGACATTTTCAGGAGGC ACA	59.8	337	INTERGENIC				
CaPOPI_4283	Ca6	48279188	T/TA	TCAAGAACGTTTCGACC ACA	GCAACTCGCGGGTTAGT ATC	60.3	562	INTERGENIC				
CaPOPI_4284	Ca6	48279626	ATTTTTT/ATTTTTT	AACCAGATACTAACCCG CGA	TCTGGAAGTTTCTTGAC CGTG	59.6	620	INTERGENIC				
CaPOPI_4285	Ca6	48280097	GAAAAAAA/GAAAAAAA	GACACGGTCAAGAACT TCCA	TGCGTTGACTCTTCAAT ACACA	60.1	376	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4286	Ca6	48280225	GTAT/GT	GACACGGTCAAGAAACTTCCA	TGTGGCACATTCCAAATTAT	60.1	601	INTERGENIC				
CaPOPI_4287	Ca6	48280286	ATTTTTTTTTTTTT/ATTTTTTTTTTT	GACACGGTCAAGAAACTTCCA	TGTGGCACATTCCAAATTAT	60.1	601	INTERGENIC				
CaPOPI_4288	Ca6	48280766	TCTA/TCTAAACTA	TGTATTGATGAGTCGTTGAATGAT	GGAGACGTTAAAGTCCCACA	58.5	902	INTERGENIC				
CaPOPI_4289	Ca6	48281397	TAAAAAAA/TGAAAAA	GGGACTTTAACGTCTCCAATACA	CTTGAGAACGATCTGCCACA	59.4	473	INTERGENIC				
CaPOPI_4290	Ca6	48281570	TA/TAATTAA	TAGGCAATTGTGCACATGA	CTCCAGGTAACGGTTGGT	61.1	335	INTERGENIC				
CaPOPI_4291	Ca6	48316872	T/TAGCC	AGGAGGTGTCACCGTCAATC	TGTTTAGGGTACAATGCGA	60.0	164	DRR	Ca_24607	Q		Multicopper oxidase, type 1
CaPOPI_4292	Ca6	48788599	CATATAT/CATATATATAT	TACAATTGATTGGCGGCATA	ATTGTGGTGGAGGTTGTGGT	59.9	738	INTERGENIC				
CaPOPI_4293	Ca6	48905266	CTAAATAAATAAATAA/CTAAATAAATAAATAAATAAATAA	CACGGTCCCTAGAGCCAATA	ATCGACTCCCGAACTCAAAA	60.1	666	INTERGENIC				
CaPOPI_4294	Ca6	49178234	TTCTCTCTCTCTCTCTCTCT/TTCTCTCTCTCTCTCTCTCT	CATAACCCCTTTTGTGCGT	CTTGGACGACCTTGGAAGA	59.9	280	INTERGENIC				
CaPOPI_4295	Ca6	49218883	TAAAAA/TAAAAA	CCCCTTCATATGCTTCCAGA	GTGCTTGCTTTTACTTCGCC	60.0	446	INTERGENIC				
CaPOPI_4296	Ca6	49733827	TCC/TC	TTGCAATCTCATCAACTCGG	GTAAAAAGAAGCGCTTTCGC	59.8	810	INTERGENIC				
CaPOPI_4297	Ca6	50818138	AAAAATTTATA/AA	CACATACTTACATTTTGCAATTGA	TGTAACCCCTTACC GTGTGTC	59.9	682	INTERGENIC				
CaPOPI_4298	Ca6	51012538	TTAATAATAATAATAATAAT/TTAATAATAATAATAATAAT	TGGCACATCTATTCAAC CACA	CATGCGATGCAAACATG TAA	60.0	540	INTERGENIC				
CaPOPI_4299	Ca6	51337603	AG/AGG	TGATGGGGTGCAAATTATGA	CAGGGACCAAGAAATTCAGG	59.7	877	INTRON	Ca_19171	R		Tetratricopeptide repeat-containing
CaPOPI_4300	Ca6	51429120	AATATATATATATATATATA/ATATATATATATATATATATA	CATGACCCCAATTTTTCAGG	TGGACAACGAATCTAACGGA	60.2	943	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4301	Ca6	51482572	TAAAAAAAA/TAAAAAAAAA	TGCACAATTGTTTATGATGT TTTT	ACACTCCCAAAATCGTCAG	58.5	552	INTERGENIC				
CaPOPI_4302	Ca6	51672087	AT/AATATATAACCT	ATGGAATGAATCCACACGGT	TCTTCCACCCAGTTTTGACC	60.1	360	INTERGENIC				
CaPOPI_4303	Ca6	51675507	A/AG	GGAAGGGATTTTTGTGGTGA	TTCGTAATGGACGGGATGAT	59.8	596	INTERGENIC				
CaPOPI_4304	Ca6	51771487	AATAAAATAAAATATA/AATAAAATATA	CGACCCACATGTTGAAGTTG	TCCCCCTTTGTCTTCTTTGTG	60.0	685	INTERGENIC				
CaPOPI_4305	Ca6	51776432	AATATATATATATATATATATATATAT/ AATATATATATATATATATATATAT	ATTTTTCTGTTGAAACGCCA CC	GGCCTATAGCCTGGCCTACT	60.0	481	INTERGENIC				
CaPOPI_4306	Ca6	51959426	CAA/CAAAA	TAATGGTTTTACGCCACA	ACCGGAAACGCATGTTAAAG	60.0	586	INTERGENIC				
CaPOPI_4307	Ca6	52074906	TTTATTAAGCGATTATTATTACGCGAT TTATTATTA/TTTATTCAGCGATTATTATTA TTA	TCCTGAAGATGAGATGCTGTG	GGCTATCGCTTATGCAGGAC	59.9	797	DRR	Ca_17514		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_4308	Ca6	52075058	GTTATTATTATT/GTTATTATTATTATT	GC GTGTCTTATTGGAGA GAGC	GGCTATCGCTTATGCAGGAC	59.1	782	DRR	Ca_17514		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_4309	Ca6	52104833	A/AC	CAGAAAAAGTGCAACCAACA	TCCTCCAACCACCATTT CAT	59.7	793	INTERGENIC				
CaPOPI_4310	Ca6	52477923	TTTATTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT/TTTA TTATTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATT	TGCGATTGAATAGATGTGCC	ACTTTGGAGGAACGACTTGG	59.7	733	INTERGENIC				
CaPOPI_4311	Ca6	52486383	GTTTTTTTTTTTTTTTT/GTTTTTTTTTT	GTTCCATGCTGCCTTTT CAT	AGAGGAAGCAGCCACTGTGT	60.1	271	INTERGENIC				
CaPOPI_4312	Ca6	52486696	ATTTTTTTTTTT/ATTTTTTTTT	AGGCCATCACATTCCTTTTG	CACTTTGGGGACGTCAA GTT	59.9	449	INTERGENIC				
CaPOPI_4313	Ca6	52522417	CTTTTTTTTT/CTTTTTTTTT	TGCAAAATCAATTTCAATCAGG	GGGCCTTTTAGGTCCAT ACC	59.9	480	INTERGENIC				
CaPOPI_4314	Ca6	52529525	TAAAAAAAAAAAA/TAAAAAAAAAAAAA	CCCCAGGTGCAATAGAGAAA	TCGCCTACTCACGGATT TTT	60.1	278	INTERGENIC				
CaPOPI_4315	Ca6	52669647	TTTATTATTATTATTATTATTATTATT/TT TATTATTATTATTATTATTATT	TGATGATAATCGGTGTC CCA	AGTTGGAGTCACTAGC CCA	59.7	372	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4316		Ca6	52676255	GATATATATATATATATATATAT/GAT ATATATATATATATATATATATAT	ATGGGTATAAGTACCCG CGA	TGTTGCCATCCCTAAAA CGA	59.3	223	INTERGENIC				
CaPOPI_4317		Ca6	52848807	ACTCGCT/A	CTGCCAAATACTGCGAC TCA	TCAATTTTGCTTGTAGGA TGGA	60.0	381	INTERGENIC				
CaPOPI_4318		Ca6	52850074	ACTAATTTCTAATT/ACTAATTTCTAATT TCTAATT	TCTGATTCGTTAATGACA ACCTTT	CGTGGGAGCAATTATGT CCT	59.1	218	INTERGENIC				
CaPOPI_4319		Ca6	52850184	TA/T	AGGACATAATTGCTCCC ACG	TCCATCTCCAACAACAT CAAA	60.0	305	INTERGENIC				
CaPOPI_4320		Ca6	52862596	T/TTATAA	ACATGAAGGCTTGGGTT GAC	GAGGAGCATGATAGCAA GGC	60.0	193	INTERGENIC				
CaPOPI_4321		Ca6	52889876	ATT/ATTT	TAAAGGACCAAGTCGGG AAA	TGCTCATGGAGTTAGAA GCAA	59.5	471	INTERGENIC				
CaPOPI_4322		Ca6	52890257	TT/TTTGT	TTGCTTCTAACTCCATGA GCA	TTATTTGGGTGCATGAG CAA	58.7	413	INTERGENIC				
CaPOPI_4323		Ca6	53305336	ATTTTTTTT/ATTTTTTTTT	CAAGATTTCGTGGTGCA AGA	TTGAGGACAAAAGCTGC TGA	59.8	660	INTRON	Ca_22925	G		Major intrinsic protein
CaPOPI_4324		Ca6	53311252	AT/ATT	GATGGTGGCCATTGAAG AGT	CAACAGTGTATGCACCT GCC	59.9	721	INTERGENIC				
CaPOPI_4325		Ca6	53312302	AAAAATAAAATAAAATAAAATAAA/AAA AATAAAATAAAATAAAATAAAATAAA	ATAGCAATTGGTGCATC CCT	ATGACCAAGGCATTGAG GAC	59.4	761	INTERGENIC				
CaPOPI_4326		Ca6	53413835	ATT/ATTT	CGTCATTTGGGGGACTA AAA	GAGTTCGGGAGTAGGG AAGG	59.8	978	INTERGENIC				
CaPOPI_4327		Ca6	53680637	CATATATATATATATATATATATAT/C ATATATATATATATATATATATATATAT	TCTATGGCACTTGGAGC CTT	AATTTGCATGTCITTTTGC CC	59.8	667	INTRON	Ca_18901			
CaPOPI_4328		Ca6	53780329	GATTAATTAATTAATTAATTAATTAATTA ATTAATTAATTAATT/GATTAATTAATTA ATTAATTAATTAATTAATTAATTAATT	CACACCCTCTCAAGGTG GAT	TCGAATGGTTGATAAAAT TAACG	60.0	723	INTERGENIC				
CaPOPI_4329		Ca6	53799025	ATTT/ATTTT	GGCCCAATATTTGAAAC CCT	CAACTTGCAAAGACCCA TCA	60.0	704	INTERGENIC				
CaPOPI_4330		Ca6	54068748	CCATCAT/CCAT	GTAAGTGAAAGCGGGAG TGC	ACCACCACTTGCTTGC TCT	59.9	527	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4331	Ca6	54068881	TAATATAAAAA/TAATATAAAAAATATAAA AA	GATCCCAACCATCATTTG TCC	ACCACCAACTTGCTTGC TCT	60.0	258	INTERGENIC				
CaPOPI_4332	Ca6	54068968	GA/GATA	GATCCCAACCATCATTTG TCC	ACCACCAACTTGCTTGC TCT	60.0	258	INTERGENIC				
CaPOPI_4333	Ca6	54069131	ATTTT/ATTTTT	GATCCCAACCATCATTTG TCC	AATTACCACGGCTCTT GTG	60.0	824	INTERGENIC				
CaPOPI_4334	Ca6	54070088	ATT/ATTT	GCAATTGTCGTGATTTTA TTTTTG	TTTTGGTGGGTCCACT TTT	59.8	379	INTERGENIC				
CaPOPI_4335	Ca6	54070236	TAAAA/TAA	TTTCTTTCTCATGCTTT AGAGG	TTTTGGTGGGTCCACT TTT	59.1	123	INTERGENIC				
CaPOPI_4336	Ca6	54143384	T/TAA	CCAAGAGATATACGGGG CAA	TGAAAGTCTGATCCGAT CTAATAGT	59.9	623	INTERGENIC				
CaPOPI_4337	Ca6	54143633	AATATATA/AATATATATA	CCAAGAGATATACGGGG CAA	CGACAAAACAAACCGCA TAA	59.9	907	INTERGENIC				
CaPOPI_4338	Ca6	54158111	CTTTT/CTTT	ATTCGAAACCATCGGAA CTG	TTGGTGTGCAAAATGA AAA	59.9	588	INTERGENIC				
CaPOPI_4339	Ca6	54158243	ATTTTGAATTTTT/ATTTT	ATTCGAAACCATCGGAA CTG	TTGGTGTGCAAAATGA AAA	59.9	588	INTERGENIC				
CaPOPI_4340	Ca6	54160975	AAATAT/AAATATTAATAT	TTGATTTGACAATTTTCA TTGCTT	TCAGTTTTCCGGTTTCTT GC	59.9	703	INTERGENIC				
CaPOPI_4341	Ca6	54192734	ATTTTTTTT/ATTTTTTTTT	GGACGGCGAAAATAAAA CAA	TTGAAAATGGCTAAGGC AAAA	59.9	642	INTERGENIC				
CaPOPI_4342	Ca6	54339604	GAGGATCA/GA	ATCATGCGTTTCTCACAT GC	TACGGGGTTGGGGATAA TTT	59.7	216	DRR	Ca_16289	O	WRKY	Peptidase M41
CaPOPI_4343	Ca6	54339840	CAAAAA/CAAAA	TAAATTATCCCCAACCC CGT	CTGATGAGCTTTCGGTG CTT	60.3	205	INTERGENIC				
CaPOPI_4344	Ca6	54339929	TC/T	AAATTATCCCCAACCCC GTA	TCATTGGACTCTCATCC TCTCA	60.3	628	INTERGENIC				
CaPOPI_4345	Ca6	54341513	T/TCTCTC	GATGTTGGGTGCTTTC AAT	AAAACCAACACTGCCAA AGG	59.9	688	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4346	Ca6	54344134	ATTTTTTT/ATTTTTTTT	AAGTCACAAATGGAAAC GGC	AGGAACTGTAGCAGCCT CCA	60.0	564	INTRON	Ca_16290	R		
CaPOPI_4347	Ca6	54712565	AAAACAA/AAAACAAACAA	GCATACCCTTGGTAAAT TGCTC	TGCTAGAAATAGAATTG GCACA	59.9	352	INTERGENIC				
CaPOPI_4348	Ca6	54952283	TTATATATATATATATATATATATA T/TTATATATATATATATATATATAT	CCATTGTAAACACCCAA ATTTTA	TTTCCTCCATTCTTCGT GG	59.9	937	INTERGENIC				
CaPOPI_4349	Ca6	55143076	A/AAAGAGTGTAAAGGTAAT	ATAAGCCTCGCGATGA AGA	CACCAATACGGGTTAC GTC	59.9	466	INTERGENIC				
CaPOPI_4350	Ca6	55490894	T/TTAATAC	TGAAGAGACGCACATTG GAG	TGTCGGTTACTAAACAT GATGGA	60.0	542	INTERGENIC				
CaPOPI_4351	Ca6	55540809	TAAAAAAAA/TAAAAAAAAA	TGTTTGAGACAACGA GAGA	ACTTCCTCTCACTACGC CGA	59.8	548	INTERGENIC				
CaPOPI_4352	Ca6	55769150	C/CT	TCGATTATGCGTAGGGA AGG	TTTTTCCTTTGTAGGCC CAA	60.1	943	INTERGENIC				
CaPOPI_4353	Ca6	55771133	GTC/GTCTTC	GGAAACGTGTGAACGGA AGT	GGTAACCAATCCGAAGA CGA	60.0	575	INTERGENIC				
CaPOPI_4354	Ca6	55771190	TAT/TATCGTCTTCGGAT	TTACCGATGCATTGATC GAC	GGTAACCAATCCGAAGA CGA	59.5	143	INTERGENIC				
CaPOPI_4355	Ca6	55781099	GTTTTT/GTTTT	AGAAGGCTACCACTACG CGA	ATCGACTCCCGAACTCA AAA	60.0	500	INTERGENIC				
CaPOPI_4356	Ca6	55876495	TTAATAATAATAATAATAATAATAAT AATAATAATAA/TTAATAATAATAATA ATAATAATAATAATAATAATAATAAT AATA	ACATCTGCCACATTGA TGA	CTTTCAAAGTCAGCGGG AAC	59.9	567	INTERGENIC				
CaPOPI_4357	Ca6	56087656	CTTT/CTTTT	TTGTGAGCATGAGAAGT GTTG	TGAAAAATTATTGAAAA GTTACTTCC	59.0	737	INTERGENIC				
CaPOPI_4358	Ca6	56191156	CAAATAAATAAATAAATAAATAAA/ CAAATAAATAAATAAATAAATAA	TCGATTATGCGTAGGGA AGG	TCCTTGAGTTTTTGGGAC ACA	60.1	482	INTERGENIC				
CaPOPI_4359	Ca6	56504001	ATTTTT/ATTTT	GTTGGCGCAAACCTCTT TTC	TGCAACTTTCAGGTCCC TTT	60.0	583	INTERGENIC				
CaPOPI_4360	Ca6	56504140	AAAAGAAA/AAAA	AAATGCAAAGTCGGATG GTC	TGCGAAGAAGAATGATC ACG	59.9	896	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4361	Ca6	56504753	ATTTTTTTTTTT/ATTTTTTTTTT	CGTGATCATTCTTCTTC GCA	TCGGTCACCAAGTTACC ACA	59.9	614	INTERGENIC				
CaPOPI_4362	Ca6	56505598	AC/A	TGGTAACTTGGTGACCG ACA	AATTTTGCAGAAGAAA GAAAAAG	60.0	485	INTERGENIC				
CaPOPI_4363	Ca6	56507452	TATCA/TA	CGTGATCATTCTTCTTC GCA	ATCCAACATTGGCCAT TTC	59.9	685	INTERGENIC				
CaPOPI_4364	Ca6	56507723	GTTTTTTTTTTTT/GTTTTTTTTTTTTT	CGTGATCATTCTTCTTC GCA	CTCCCAATTGCAGTGT CCT	59.9	966	INTERGENIC				
CaPOPI_4365	Ca6	56507798	CA/CAA	AAATTCAAGTCTCGACG CAAA	CTCCCAATTGCAGTGT CCT	59.9	511	INTERGENIC				
CaPOPI_4366	Ca6	56727392	TAA/TAAA	AGGCAAAACATGTTCCC TCA	AATGTTAGTGCACCGTG TCG	60.5	706	INTERGENIC				
CaPOPI_4367	Ca6	56775193	TTTATTATTATTATTATTATTATT/TTATTATTATTATTATTATTATT A	CGTGTGCGAACTTGCTT AAA	GAATCCCTGGTTCACAG CAT	60.1	279	INTERGENIC				
CaPOPI_4368	Ca6	57055878	ATTTTTTT/ATTTTTTTTT	TCCAAATGAAGCAAGAT CAAAA	GCGGAAAGAAACAAATC TCAA	59.7	600	INTERGENIC				
CaPOPI_4369	Ca6	57058024	TAAAAAAA/TAAAAAAA	AGGTTACGCTTAAATT TGGA	CAGATCGAATCGGATTT TGAA	58.5	351	INTERGENIC				
CaPOPI_4370	Ca6	57132721	CAAAAAAAAA/CAAAAAAAAA	ACAAGATCGGAGGAG GAGT	TTTTGTGGTTTGGTTC GTG	60.1	580	INTRON	Ca_17439			Glycosyl-phosphatidyl inositol-anchored, plant
CaPOPI_4371	Ca6	58084151	TAAAAAAA/TAAAAAAA	GGCTACATCGCCATCAT CTT	TCAAGTCGATCCCATCA AATC	60.1	770	INTERGENIC				
CaPOPI_4372	Ca6	58373671	GATATATATATATATATATA/GATA TATATATATATATATATATATA	TCACGCAAAAGATTCA TAAAAAGA	AGTTTGAAGCTGTGCG TCG	58.9	500	INTERGENIC				
CaPOPI_4373	Ca6	58523123	TTATATATATATATATATATA/TTATAT ATATATATATATATATATA	TTTTGGAACAAATCTAA CGGAA	GACACGAGCCTCACCAA AGT	59.9	238	INTERGENIC				
CaPOPI_4374	Ca6	58597676	CG/C	CGATCATGCTGCTTGT TTTG	TCGTTTCATCTGAATGT GACAA	60.4	737	DRR	Ca_15402			Pectinesterase inhibitor
CaPOPI_4375	Ca6	58834846	GTTTTTTTTT/GTTTTTTTTTTT	TGAAACGTCACCTTTTC GGA	AGGACTTCACCATCAAT TCCA	59.3	292	INTERGENIC				

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CaPOPI_4376	Ca6	58966264	AATATATATATATATATATAT/AATATATATATATATATATAT	TCAGCCTAAGCAGATGC AAA	CAATTCCCACAGGTACG CTT	59.7	414	INTERGENIC				
CaPOPI_4377	Ca6	59059948	CT/CTTT	ATAGGACGCAAGAAAG CCA	TCCACAACAACCTACGT CCA	59.8	263	INTERGENIC				
CaPOPI_4378	Ca6	59093194	ATTTTTTTTTT/ATTTTTTTTTT	GGAGGCAACCCAACCTC ATG	TCGCATAATTGGAACGT CAA	59.6	271	INTERGENIC				
CaPOPI_4379	Ca6	59184042	TGAAGAAGAAGAAGAAGAAGAA/T GAAGAAGAAGAAGAAGAAGAA GAAGAAGAA	CAAAACTGCCTAATCCC CAA	CGTTTGAGTGGGATGAG GTT	59.9	157	INTERGENIC				
CaPOPI_4380	Ca6	59193085	CTTTTTTTTT/CTTTTTTTTTT	ATGGGGTTTACCATT GAA	ACATGATGGCAAGACCA AGA	59.0	511	INTERGENIC				
CaPOPI_4381	Ca6	59273276	TA/TAAA	TGAAGCTTGTGCCAAG GTA	GGTGGAATGAAACGG AGA	59.5	754	INTERGENIC				
CaPOPI_4382	Ca6	59273311	TA/T	TTTTGGGCTGAAGCCA TAC	GGTGGAATGAAACGG AGA	60.1	359	INTERGENIC				
CaPOPI_4383	Ca6	59349983	AATATATATATATATATATATAT A/AATATATATATATATATATATATA	TTTCCATTGCACTCACTC CA	CCTATCATGGCCTGACC TGT	60.2	777	INTERGENIC				
CaPOPI_4384	Ca6	59422588	TTATATATATATATATATAT/TTATA TATATATATATATATATAT	CGGTCAAACCTCATTGT TGC	AGCGAGTCTGCTCCTAA ACG	59.2	702	INTERGENIC				
CaPOPI_4385	Ca7	180428	T/TGAGGCAA	TCAACAGCAGCTTTGCA TTC	TTTCGCAGCTGGTATGT GAG	60.1	280	INTERGENIC				
CaPOPI_4386	Ca7	357521	CITT/CTTTT	TATTGGTTCCTTATGGG GCA	AGCTCTGGAGACCTCCT TCC	60.1	581	INTERGENIC				
CaPOPI_4387	Ca7	509621	ATTTTTTTT/ATTTTTTTTTT	AGCATCAGCTGCTGGTT TTT	GCACCAAACCAAGCCTA TGT	60.0	646	INTERGENIC				
CaPOPI_4388	Ca7	540192	C/CAT	TGAGGCAATTTGGTGA CAA	ATACCCTCATGCCACAT GGT	60.1	421	INTERGENIC				
CaPOPI_4389	Ca7	586986	AA/AATTA	TTCCATTTCTCCACAAA GC	CAACCGCATTGTCACTA TTC	60.1	531	DRR	Ca_24415			
CaPOPI_4390	Ca7	760518	AACACACACA/AACACACA	TCTAGCGACGGGTCTGA TCT	CAATGCCAACAAAGCGT TTA	60.0	365	DRR	Ca_03403	R		Short-chain dehydrogenase/reduct ase SDR

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4391	Ca7	760856	GTTGAAGATTG/GTTGAAGATTGAAGAT TG	TAAACGCTTGTGGCAT TTG	AGTTCGCAGGCTCTGTT GTT	59.7	445	DRR	Ca_03403	R		Short-chain dehydrogenase/reduct ase SDR
CaPOPI_4392	Ca7	819442	ATTAG/A	TTCACGAAATTTGTTCCC CT	TGTACATTTCTCTAAAAAC ACATTGA	59.4	784	INTERGENIC				
CaPOPI_4393	Ca7	1018745	C/CT	TTGCAACATGATAGCT GCC	TTGTTGGCATTGTTGTG GTT	59.8	467	INTERGENIC				
CaPOPI_4394	Ca7	1018777	ATTGCAT/ATTGCATATTTGCAT	TTGTTCCCGTAAAAGAT CGC	TTGTTGGCATTGTTGTG GTT	60.1	233	INTERGENIC				
CaPOPI_4395	Ca7	1038892	TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATATATATATAT	GTACGAGATGACGACGC CTT	ATGAATGCAGTTACGTG GCA	60.3	717	INTERGENIC				
CaPOPI_4396	Ca7	1176487	TTATATATATATATAT/TTATATATATATA T	GGGATGGGTGGATTCT TCT	TGGTCGGGACTTCAAGA AAC	60.1	542	DRR	Ca_03355	R	bHLH	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_4397	Ca7	1219494	TG/T	GGAGGGATGAATTTGGT TGA	CATCCACATGTATGCTTT CCA	59.7	442	INTERGENIC				
CaPOPI_4398	Ca7	1245279	A/AATTTTCAT	TGCACAAAACACACAAC CCT	TCGCTCCTGTGTCAGTT TTG	60.0	468	INTERGENIC				
CaPOPI_4399	Ca7	1307924	A/AGAT	CAAAAATAAGGCATAGT GTTGA	TAGTTTGAACCCCGTG CGT	58.3	260	INTERGENIC				
CaPOPI_4400	Ca7	1807047	CAAAAAAAAA/CAAAAAAAAAA	TGTTGTCACCACACTC TTGC	GCTTGGTCCCATTTGAG AGA	59.8	846	DRR	Ca_03288			Zinc finger, RING-type
CaPOPI_4401	Ca7	1919879	TTATATATATATATATATAT/TTATATATA TATATATATATATAT	TGAATTTGGGGTCAAC CAT	ACACAGCCCCAAAAGTT GTC	60.0	435	DRR	Ca_03281			BNR repeat
CaPOPI_4402	Ca7	2047396	TTATATATATATATATATATATAT/TTA TATATATATATATATATATATATATAT	ATGGGACTAGGCAACAC GTC	TTTCAACCGTAAATCATA CTTGG	60.0	630	DRR	Ca_03268	GC	HSF	UDP- glucuronosyl/UDP- glucosyltransferase
CaPOPI_4403	Ca7	2168224	CATA/CATATA	TTCTGAGATTGGCAAAA GGG	CGCGATCGTTCACTGAT ATG	60.2	820	INTRON	Ca_03253	P		Porin, eukaryotic type
CaPOPI_4404	Ca7	2169830	AAT/A	CAGGGCCTTACTGCTAC AGG	CAACGGAAAACATCGTT CAA	59.9	397	CDS (FRAME SHIFT)	Ca_03253	P		Porin, eukaryotic type
CaPOPI_4405	Ca7	2169903	T/TA	CAGGGCCTTACTGCTAC AGG	CAACGGAAAACATCGTT CAA	59.9	397	INTRON	Ca_03253	P		Porin, eukaryotic type

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4406	Ca7	2380600	ATTTAATTTGTTTAA/ATTTAATTTGTTT AATTTGTTTAA	CCACCATTTTGTATGAC GTG	TGGAAAAACCACAAATAT TACATTG	59.8	593	INTERGENIC				
CaPOPI_4407	Ca7	2432614	TTATATATATATATATATAT/TTATATA TATATATATATATAT	CAAATGGATTGGTGAGA CGA	GGCATGAGTGAGTATGG CCT	59.5	640	INTERGENIC				
CaPOPI_4408	Ca7	2525335	CAATACAATTGATTAATA/CAATACAATT GATTAATACAATTGATTAATA	TGGTGGAAAAATAGCAT TTGG	CCTCTCCGAATGACTC AAG	59.8	868	INTERGENIC				
CaPOPI_4409	Ca7	2639799	CTCATCATCATCATCATC/CTCATC ATCATCATCATCATCATC	TTCAAGACAAAGAGGGG GTG	CAATGCAGCAATGAGAG CAT	60.1	382	CDS (large-effect mutations)	Ca_03214	O		
CaPOPI_4410	Ca7	2940930	AAATAATAATAATAATAATAATAATA ATAATAATAATAATA/AAATAATAATAAT AATAATAATAATAATAATAATAATAA TAATAATA	TCTTCAGACCAAAAATG GGC	TGCAAGTTTTCTGTCC AAA	60.1	581	DRR	Ca_03181		FAR1	
CaPOPI_4411	Ca7	2974132	CTATA/CTA	ATTACCTCCCTCTCCT CCA	AAACAGTGAACGGAACC AGG	59.9	465	DRR	Ca_03176	R		WD40 repeat
CaPOPI_4412	Ca7	3243289	AGTTATTTGATTTTGTTATTTTGATTT GT/AGTTATTTTGATTTGT	TGAGTTTGGATATCGTT TTTACAC	CATTTTGTCTAGCCAC GCA	57.4	350	INTERGENIC				
CaPOPI_4413	Ca7	3259173	TCCC/TCCCC	TAGAAAGGAATTGGCGG TGA	TCATTTTCATTAGAAGC ATGAGC	60.6	767	INTERGENIC				
CaPOPI_4414	Ca7	3317609	GTTT/GTTTT	CCACGGTTCTGAAGTT GTT	TGGGAAGTTGGTCTGTG TGA	60.0	599	INTERGENIC				
CaPOPI_4415	Ca7	3523561	CAAAAA/CAAAAAA	TTGGATGGGAAGACCTT CTG	TCATTGCAAGAAGATCA CGC	60.0	405	INTRON	Ca_03116	I		Synaptojanin, N-terminal
CaPOPI_4416	Ca7	3528666	CTATAT/CTATATAT	GGGGAACACATCAAAAC CAC	TTATTTTCTACTAATTTT GATCTCTCA	60.1	778	INTERGENIC				
CaPOPI_4417	Ca7	3540216	GTTTTT/GTTTTTTT	TCAACAATGAAGCAACA CATCA	CATTGCGCAAGAGAATA CGA	60.2	634	INTERGENIC				
CaPOPI_4418	Ca7	3552289	TAAA/TAAAA	CCTGCTTCAATTATTC TCTCA	TGTTCTGTTGGCACAGAT GTT	59.7	586	INTERGENIC				
CaPOPI_4419	Ca7	3613493	CTTT/CTTTT	GCAAGTGCTCCCATTTT ATT	ACTTGGCAATGCAAGAG TCC	60.1	297	INTERGENIC				
CaPOPI_4420	Ca7	3617634	TAAA/TAA	CCGCTACTTTTTCGAAC ACTTC	TCAAACCACCCCCAAAA ATA	60.3	626	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4421	Ca7	3629960	TTTATTA/TTTA	ATTGCCATGTGGGTGAG AGT	TGGCAACATAATGTCCA TGC	60.4	390	INTRON	Ca_03106	E		Saccharopine dehydrogenase / Homospermidine synthase
CaPOPI_4422	Ca7	3670558	A/AT	AAGGCAATAGGTGATGG TGG	TCACTATTCACACGCGG AAG	59.8	717	DRR	Ca_03102	TU		Zinc finger, FYVE-type
CaPOPI_4423	Ca7	3672046	AT/A	ACATAGGTCGGCATACT CGG	TACAGTTTCAGCCTGGG TCC	60.0	330	DRR	Ca_03102	TU		Zinc finger, FYVE-type
CaPOPI_4424	Ca7	3676987	ACTC/ACTCTC	TTGAGTGGCATTTCAGC AAG	TCCTTCTCCAAAATCGAA GG	60.0	492	INTERGENIC				
CaPOPI_4425	Ca7	3683696	TA/T	CCATGAAATCACCTTAA TGACA	CCGACAAGGCGACAAGT AAT	58.9	451	DRR	Ca_03101			Tify
CaPOPI_4426	Ca7	3689798	TAGAGAG/TAGAG	ATGGTAGGGGGAAGAG GAGT	CTTTTCGTTTGCCCAAT GTT	58.9	381	DRR	Ca_03100	S		Uncharacterised protein family UPF0136, Transmembrane
CaPOPI_4427	Ca7	3691358	TAAA/TAA	GCACAAAAGGAATGCA TCA	AAGAAGGATCGGACGGA GAT	59.7	963	INTRON	Ca_03100	S		Uncharacterised protein family UPF0136, Transmembrane
CaPOPI_4428	Ca7	3905558	TG/T	ACTCTGTGTTGAGGTG GGG	TGAGGGATGAAGAGGAC AAAA	60.0	468	INTERGENIC				
CaPOPI_4429	Ca7	3934957	AATATATATATATATATATATAT/AATA TATATATATATATATATATATATAT	TTCCATATTGGGTGCC ATT	TGTGCATCTTTTCCAAT GC	60.0	547	INTERGENIC				
CaPOPI_4430	Ca7	4001096	CATATATATATATATATA/CATATATA TATATATATATATA	AAAATTAAGGGTTGCC CC	TTCAAAACAGTACGTGC GGA	60.0	922	INTERGENIC				
CaPOPI_4431	Ca7	4233766	TTCTCTCTCTCTCTCT/TTCTCTCTCTCT CTCTCT	TATGTTCTGCCACAAGC AGC	CGCCACTCAAAACATG CTA	60.0	740	INTERGENIC				
CaPOPI_4432	Ca7	4329744	AATATATATATATATATA/AATATATAT ATATATATATATA	TTCATGAAGTGGATGTG GTGA	AAACAAAAGTTGCTTTT ACGAA	60.0	561	INTERGENIC				
CaPOPI_4433	Ca7	4351119	TAAAAAAAAAAAA/TAAAAAAAAAAAAA	AGCGCTCAACCATAAAT TCG	TGTGGAGGTCGGTGTTT GTA	60.2	223	DRR	Ca_03023	T	HB-other	Calcium-binding EF-hand
CaPOPI_4434	Ca7	4369825	ATTTTTTT/ATTTTTTT	GATCGCGGTTGACGAGT ATT	TGGTCCTCTAAATTTGC CA	60.1	912	INTERGENIC				
CaPOPI_4435	Ca7	4385687	GAAAAA/GAAAAA	TTTAATGGGGCTAAGG GAG	GTGAGAGAGTGCCCCCA ATA	60.3	776	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4436	Ca7	4418125	A/ATC	CAAGTCAGCACCCGACAAAGA	ATAAAGGGTGACGTGCAG	60.0	592	INTERGENIC				
CaPOPI_4437	Ca7	4674504	AATATATATATATATATATATAT/AATATATATATATATATATAT	GCCCAATTTTACCACA CAT	GCCACCTATGTGCTATT TGC	59.6	679	INTERGENIC				
CaPOPI_4438	Ca7	4805132	ATTTTT/ATT	AAATTTGTGCATCTCAA TCG	TGCACCTCCA AATTGT ACC	60.1	371	INTERGENIC				
CaPOPI_4439	Ca7	4867122	AATATATATATATATATATATATATAT TTATATATATATAT/AATATATATATAT ATATATATATATATTTATATATATATAT T	AGGTGGTGAGCGTTTT GAA	TTGATGATGTGAAGGAA TGACAG	60.7	670	INTERGENIC				
CaPOPI_4440	Ca7	4999972	GAAAAAAAAA/GAAAAAAAAA	CCTCAGATGAGAGCCAG GAC	TTGGTTGTAACACCCCG TTT	59.9	453	INTERGENIC				
CaPOPI_4441	Ca7	5014340	CAA/CAA	AATACCACCACCGACCA CAT	AATGAGCTCCAACGGTC ATC	60.0	787	INTERGENIC				
CaPOPI_4442	Ca7	5024464	ATTTTT/ATTTTTT	CCCCGCATGTATTATG GAG	ACCCACATCCGTTTCAT AGC	60.2	294	INTERGENIC				
CaPOPI_4443	Ca7	5033957	AATATATATATATATATAT/AATATATA TATATATATATATATATATATAT	TGGATCGTGCTTTGATC ATTG	AATAAACCGTTGCAAGT GGG	59.5	592	INTERGENIC				
CaPOPI_4444	Ca7	5034485	ATTTTTTTT/ATTTTTTTTTT	CCCAC TTGCAACGGTTT ATT	TGAGGTAAGCTTTGCAT CATGT	59.9	837	INTERGENIC				
CaPOPI_4445	Ca7	5140984	GTTTTTTTTT/GTTTTTTTTTTT	CCCCTTCTATT CAGCTT CCC	TTGAGCCAATTGACCTA CCC	60.0	612	INTERGENIC				
CaPOPI_4446	Ca7	5342023	CTTTTTTT/CTTTTTTT	GGCATAACCGCGAAACT TTA	CATGAAATCAAACAACA CCACA	60.1	506	INTERGENIC				
CaPOPI_4447	Ca7	5343899	CTTTTTTTTT/CTTTTTTTTTT	TGAGGTGATGTGCCAT TGAG	TGCAGAGAACAAGCACA TTG	59.5	477	INTERGENIC				
CaPOPI_4448	Ca7	5398943	TAATAA/TAATAACAATAA	CTTTTCCTTG TCTGCA TGA	TCGCTTCACTCCATCT TCT	60.0	348	INTRON	Ca_06830	R		Kelch repeat type 1
CaPOPI_4449	Ca7	5399126	CAAAA/CAAAA	CTTTTCCTTG TCTGCA TGA	AGGTGAGTGGGCTATGT TGG	60.0	819	INTRON	Ca_06830	R		Kelch repeat type 1
CaPOPI_4450	Ca7	5405233	AC/A	TGGCCTCTCTGAAACCA TCT	TCCTTTCCAGAATTGG ATG	59.8	905	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4451	Ca7	5434245	ATTTTTTT/ATTTTTTTT	CCAATTATGCCATTGGA ATTT	TCAAATTCAAAATCACAA CGCT	58.7	685	INTERGENIC				
CaPOPI_4452	Ca7	5434750	AG/A	GCGTTGTGATTTTGAAT TTGA	CATGGTCCACTTCGAGG AAT	58.7	524	DRR	Ca_06825			
CaPOPI_4453	Ca7	5434792	CTTTT/CTTT	GAAAGAGGATCAACCCG ACA	CATGGTCCACTTCGAGG AAT	60.1	466	DRR	Ca_06825			
CaPOPI_4454	Ca7	5436041	GTTTTTTTTT/GTTTTTTTTTT	TGTTTAGATGTGGTGGT GCTG	CAAGCAGGTATGTGAGG GGT	59.6	721	DRR	Ca_06825			
CaPOPI_4455	Ca7	5443791	TATAAATAAATAAATAA/TATAAATAAT AA	TATTTGCGAGCGTGCT TCA	TTTTGATGCTTTTCCAC CA	60.5	516	INTERGENIC				
CaPOPI_4456	Ca7	5443871	TAAAA/TAAAAA	TATTTGCGAGCGTGCT TCA	TTTTGATGCTTTTCCAC CA	60.5	516	INTERGENIC				
CaPOPI_4457	Ca7	5446544	ATATTTATTTATTTATTTATTTATTTATTT TATT/ATATTTATTTATTTATTTATTTATTT	CCCCTTTCGGAATTTCA TTT	CACAAAGCCTTCTTTCT GC	60.1	527	INTRON	Ca_06824			
CaPOPI_4458	Ca7	5459177	ATTTTTTTTT/ATTTTTTTTTT	GAAAAAGGTTGCAATCC GAA	TCAAGGTGTTTGGGTTT GTG	60.1	817	INTERGENIC				
CaPOPI_4459	Ca7	5465549	TAACCGGAA/TAA	AGTCCTAATGCGGCTGT GAT	ATGTGGGAATTGTGGCA TTT	59.7	207	DRR	Ca_06821			Uncharacterised protein family UPF0497, trans-membrane plant
CaPOPI_4460	Ca7	5470006	TTATATATATATAT/TTATATATATAT	GGGATCTATTAACCA GAACCA	TGGAATTGCCACCACA ACA	60.4	632	INTERGENIC				
CaPOPI_4461	Ca7	5482693	TATT/TATTTTATAATT	TTCGTGTAGTTGATTCAA ACCAT	AACAAAAGGCAATAAAT GAACGA	58.6	576	INTERGENIC				
CaPOPI_4462	Ca7	5482708	ATTTT/ATTT	TTCGTGTAGTTGATTCAA ACCAT	AACAAAAGGCAATAAAT GAACGA	58.6	576	INTERGENIC				
CaPOPI_4463	Ca7	5524631	ATACAATTTTACAATTT/ATACAATTTT TACAATTTTACAATTT	CTTGTTTACACGGTTC CTT	CAAAACGCGAATTGCTA TGA	60.0	840	DRR	Ca_06814		TCP	Heat shock protein DnaJ, N-terminal
CaPOPI_4464	Ca7	5540728	TC/T	TCAATGTTGGAGTTTGT GCAT	CGCATATCAACATTGC AGC	59.0	569	DRR	Ca_06810	R	G2-like	Sugar/inositol transporter
CaPOPI_4465	Ca7	5540919	T/TTATTA	TCAATGTTGGAGTTTGT GCAT	GCCAATTGCCTAGCAGT AGC	59.0	645	DRR	Ca_06810	R	G2-like	Sugar/inositol transporter

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CaPOPI_4466	Ca7	5572652	ATTTTTTTT/ATTTTTTTTTT	AAAAATGCGTTCATCA AATG	TTTGCCAATTTTAGGGA CC	59.8	502	INTERGENIC				
CaPOPI_4467	Ca7	5572728	GTTTAATTTTAATTTTAATTTA/GTTTA ATTTTAATTTTA	ATGGGTCCCTAAAAATT GGC	GCTTGTTACTTATATTCA GAGGGCA	60.0	559	INTERGENIC				
CaPOPI_4468	Ca7	5575534	ATTTTTTTT/ATTTTTTTT	GGTGAAGGAGAAATGCA AGAA	TTATTAACGTGGGTGTG GGC	59.3	556	INTERGENIC				
CaPOPI_4469	Ca7	5578208	AG/AGAATGAATG	ATGGGAAATTGTGAATG GGA	TGCCCGTTAGTCAATGT TTG	60.0	435	DRR	Ca_06805			
CaPOPI_4470	Ca7	5582721	AATATATATATATATATATATATATAT/ATATATATATATATATATATATATATATATATAT	TGCCCACTCATTTGGCT ATT	AAGACGGTCTGGAACG ACG	60.5	494	INTERGENIC				
CaPOPI_4471	Ca7	5585752	TAAAAAAAAA/TAAAAAAAAA	ATTCACACGACCAAAAA CCT	TGATGAGATGTATTCGA TGCAA	57.0	496	DRR	Ca_06804			Protein of unknown function DUF679
CaPOPI_4472	Ca7	5633058	T/TAAG	GCAAGCCAAACCACAAA AAT	ACAGGCGCTTCCTTCTT GTA	60.0	386	DRR	Ca_06796	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_4473	Ca7	5648526	TAAAAAAAAA/TAAAAAAAAA	TGTGCACCAACAACA TCA	TGGGGGATGACATGTAC CTT	59.6	448	INTERGENIC				
CaPOPI_4474	Ca7	5649774	CTTTTTTTTT/CTTTTTTTTT	AAGGGAATGCATTGTCT CTCA	TTTGTTATGTGTGGCTT GTAGTGA	59.7	359	INTERGENIC				
CaPOPI_4475	Ca7	5650363	AAATAATAATAATA/AAATAATAATAATA ATA	TCGTTCCCTCTGAAATG AAA	TCGAGTGAACGTGGAAG ATG	58.3	239	INTERGENIC				
CaPOPI_4476	Ca7	5668000	TAAAAAAAAA/TAAAAAAAAA	TCATACTCGTATTCGTG CCG	CAGGGTCCTTGTCGTGA TTT	59.7	764	INTERGENIC				
CaPOPI_4477	Ca7	5684395	TTAT/TTATAT	CGTTCAAGCTTGTCGTG AAA	GAGATGTTCAATGGCCT GGT	60.0	716	DRR	Ca_06789	K		RNA polymerase I specific transcription initiation factor RRN3
CaPOPI_4478	Ca7	5694761	TAAAAA/TAAAAA	GGAATCTGTTTGCAAG GGA	AACCCATCACTTGCTGA TCC	60.1	627	INTERGENIC				
CaPOPI_4479	Ca7	5698697	ATT/ATTTT	AAGTCGATTACGATCCA CGC	CCCCCTTAAAGACAAT TCAAA	60.1	430	INTERGENIC				
CaPOPI_4480	Ca7	5702622	GTATATATA/GTATATA	TATGCCACGCCATAAGA TGA	GGCCCAACAAGAAGTT ATCC	60.1	726	INTERGENIC				

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CaPOPI_4481	Ca7	5778254	AAACAA/AAACAACAA	CAAATCCATCCACTCTTCA ACAA	CTGCAAAAACCTCTCTC TCG	60.0	910	INTERGENIC				
CaPOPI_4482	Ca7	5779009	ATTTTTTT/ATTTTTTTTT	GCTGAAGCCAGTTCTG GAC	CACACCAAACCAAGCAA CAC	60.0	458	INTRON	Ca_06780	F		Ribonucleotide reductase
CaPOPI_4483	Ca7	5785096	GTCATCATCA/GTCATCA	TTTGCAACTTGTGTCA CTCT	CGCTCTCTATCTCTCG CAC	58.4	789	INTERGENIC				
CaPOPI_4484	Ca7	5785418	GTCT/GT	TGCGGAGAGATAGAGAG CGT	GGGTGATTTGATTGTT TTGC	60.3	206	INTERGENIC				
CaPOPI_4485	Ca7	5799102	TTATAAATATAAA/TTATAAATATAAATA TAAA	ATGACATGTCTCGAGCT CCC	TTGGCCCTCTTTTCTCT CAA	60.2	312	DRR	Ca_06778	R		RNA recognition motif domain
CaPOPI_4486	Ca7	5800832	TTTCTT/TTT	AAAAGCGGGCCATTCTA GTT	TTCTAGCATTGTGGCTG TGC	60.1	375	DRR	Ca_06778	R		RNA recognition motif domain
CaPOPI_4487	Ca7	5841878	CTT/CT	TGCAACTTTGAAGGTGC TTG	CAACAAAGCCACAAAAG CAA	60.0	731	DRR	Ca_06775			
CaPOPI_4488	Ca7	5843643	AT/ATT	GGTGAGTTTCTCTCC CCC	TTTCATCGTCTGAAGTCA CGG	59.9	501	INTERGENIC				
CaPOPI_4489	Ca7	5858608	TACTAA/TA	TGTTTAGTCATGCGGTG ATTG	CCCGTCAAAGGGTATTT GAA	59.6	846	INTERGENIC				
CaPOPI_4490	Ca7	5870900	GAAAAAA/GAAAAAAA	TTGTGGCTAATATTTG GTCAA	CACAACTCTCCAGAGCC AAA	59.5	485	INTERGENIC				
CaPOPI_4491	Ca7	5871833	TAAAAAA/TAAAAA	AATTGTGGTTCTTCATG CCC	TTCGTATTGTTATTGCG GGA	59.8	487	INTERGENIC				
CaPOPI_4492	Ca7	5874667	CAAA/CAA	AAGCTGATGTGACAAGC CAA	TTATAACATGGGCGAA CCC	59.4	391	INTERGENIC				
CaPOPI_4493	Ca7	5884631	ATTTTT/ATTTTTTTTT	TCTTGTTGCTGTCTC GTG	ATGCGAAGGAGCAATTA TGG	60.0	832	INTERGENIC				
CaPOPI_4494	Ca7	5889222	CTTT/CTT	ATTGGCAAGAGTGTTAC GGG	GTGTGACTTTGGCCACC TTA	60.0	520	DRR	Ca_06769	O		Peptidase A1
CaPOPI_4495	Ca7	5890273	TTATATATATAT/TTATATATATATAT	TGTTCATATACATGCA TCGC	TGAGAGTGAGATGGTGG TCA	59.5	127	DRR	Ca_06769	O		Peptidase A1

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CaPOPI_4496	Ca7	5893840	CAAAAAAAAA/CAAAAAAAAA	AAATGAAAGCAGGCCTC AAA	CGGTGTTGTCCGTTTT CTT	59.8	411	INTERGENIC				
CaPOPI_4497	Ca7	5894005	GTTTTTTTTT/GTTTTTTTTT	AAGAAAAACGGACAACA CCG	TGTTGTGCATGACTTGA AGG	60.0	375	INTERGENIC				
CaPOPI_4498	Ca7	5894787	TTTTAAAA/TTTTAAAAATTTAAAA	CGGTTCAATCAGGTTGA CATT	TGGCCCCAAAATTGATA CAT	59.8	421	INTERGENIC				
CaPOPI_4499	Ca7	5895013	CAAAAAAAAA/CAAAAA	CGGTTCAATCAGGTTGA CATT	TGGCCCCAAAATTGATA CAT	59.8	421	INTERGENIC				
CaPOPI_4500	Ca7	5916457	TATCATCATCATCATCATCA/TATCA TCATCATCATCATCATCA	CATGCAATCATGTATCC CCA	CTACCTGCACCCCTAT TGA	60.2	475	CDS (large-effect mutations)	Ca_06766	G	G2-like	Glycoside hydrolase, family 18, catalytic domain
CaPOPI_4501	Ca7	5934199	GTATATATATA/GTATATATA	TTGAAAACAATTTGCAG GC	CACGAGCGCTTTAAAAA TCC	58.8	903	DRR	Ca_06764	P	GRAS	ATPase, P-type, H ⁺ transporting proton pump
CaPOPI_4502	Ca7	5955426	CA/C	TTCCCAATCATTGGC TTC	ATTGTGGCACTAGTGGA GGG	60.1	947	INTRON	Ca_06761	A	AP2	Ribonuclease III
CaPOPI_4503	Ca7	5975269	TTATATATATAT/TTATATATAT	AGAGCAGAATGGAACAC GCT	TGCAATTTTAATTTTCAT ATTTTCG	60.0	472	INTERGENIC				
CaPOPI_4504	Ca7	5977012	GTATATAT/GTATAT	TGAAACCACATTGCTCA CCT	CCTCCACTTTTGAGCAC CAT	59.1	481	INTERGENIC				
CaPOPI_4505	Ca7	5978931	TTAGATACTAG/TTAG	TGCCAAATGTTTGGTT GTG	CTGGGGACTCGATTGAG AAA	60.4	843	DRR	Ca_06760			Lipid-binding START
CaPOPI_4506	Ca7	5989176	GATACA/GA	TGCTCTAACTGAAGGG GGA	GTTTCGTGGACAAGACG GAT	59.8	311	INTRON	Ca_06760			Lipid-binding START
CaPOPI_4507	Ca7	5992633	GC/G	AACGCAATCCATGACAA ACA	GTATGCTCTGTTCCCC CAA	60.0	497	INTRON	Ca_06760			Lipid-binding START
CaPOPI_4508	Ca7	5995821	ATGT/AT	GACCGTCAAGGGGTTGT TTA	AGTTTATTGGCGACCA GAG	59.8	916	INTERGENIC				
CaPOPI_4509	Ca7	6008667	ATTTT/ATTT	CCATCCCGATTGTATT GG	CCCTTCGGTCATCAACG TAT	60.0	486	DRR	Ca_06759			
CaPOPI_4510	Ca7	6016711	ATTTTTTTTT/ATTTTTTTT	GCCTTTTCITTTTCAAGC CC	CATTTTGACAAGTGATA GTTTGA	60.2	306	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4511	Ca7	6018232	CTAA/C	GAGCCAACCTGTGTCT ACGG	CGAGGTGACACACATT TCG	59.8	271	INTERGENIC				
CaPOPI_4512	Ca7	6020433	TAAAAAA/TAAAAAAA	AATCCGTTGAGATTGGG ATG	TTTTGTTCATTGGTGT TTATTTT	59.8	677	DRR	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4513	Ca7	6020761	TCA/TA	AAACAAAGGAAAGGACA AAAATG	TGACGTTTAGTTTTCTG TTTTATTG	58.6	826	DRR	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4514	Ca7	6021501	CTTCTTT/CTT	CAATAAAACAGAAAACT AAACGTCA	TTTTGTTCCAATTCACG GA	58.1	786	DRR	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4515	Ca7	6021592	GTTTTTTTTT/GTTTTTTTTT	TCTTGCAAAAACAGTTT CAA	TTTTGTTCCAATTCACG GA	59.4	366	DRR	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4516	Ca7	6021693	ATTTTTTTTT/ATTTTTTTTT	TCTTGCAAAAACAGTTT CAA	TTTTGTTCCAATTCACG GA	59.4	366	DRR	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4517	Ca7	6024790	GAAAAAA/GAAAAAAA	TCTCGATAGAAAACGTG GAAA	TTTCGACCCCTCTCTTT AGG	57.5	918	INTRON	Ca_06757	R		Sugar/inositol transporter
CaPOPI_4518	Ca7	6033948	ATTTTTT/ATTTTTTT	ACTTCAGCATCAAGCCA GGT	AAAATTTTGCAAGTTGG TTGTT	59.9	291	DRR	Ca_06755	A		D111/G-patch
CaPOPI_4519	Ca7	6044320	A/AATT	TCACCCACTTTGGTTGC ATA	CAATTAAGTGAAGTGGC CAAA	60.0	339	INTERGENIC				
CaPOPI_4520	Ca7	6055513	TA/TTTAGTATGA	TTTGTGTCTTCCAGGT CCC	AGAAGGTCGCATCCAGA CAC	59.9	507	INTERGENIC				
CaPOPI_4521	Ca7	6056347	GTATACACTATACA/GTATACA	CCATCGATTAAAAATGA GCA	TATGGGGGCGGATAATT ACA	57.8	517	INTERGENIC				
CaPOPI_4522	Ca7	6060869	ACT/ACTCT	CCTTGGTCTGTCCACT TGT	GAACACGGACATGTTGT TGC	60.0	454	INTRON	Ca_06754	K	TALE	Homeobox
CaPOPI_4523	Ca7	6062336	GTTAT/GTTATATTAT	CAAAGGAAAGGAATTG GCA	TGCTTTCACCTGCACTG TTC	60.0	188	DRR	Ca_06753			
CaPOPI_4524	Ca7	6081820	CTTTTTTTTTT/CTTTTTTTT	GATTTCTCGGTTTTGT GGA	AACGAGAGTCTAACGCC TTCC	59.9	825	INTERGENIC				
CaPOPI_4525	Ca7	6083464	AATATA/AATATATA	GGACCGTTTTGCTGTCA AAT	CACATTCCTGGCTTCCA ACT	60.0	548	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4526	Ca7	6097018	AG/A	CTCAGCAGCACAAATCCAAA	GCACAACATCACCATATCGC	60.0	472	DRR	Ca_06748			
CaPOPI_4527	Ca7	6100952	CTTTTTTTT/CTTTTTTTT	TATTGCATGTTTGACGGCAT	CGGACTCCCCCTTTTATTC	60.0	558	INTRON	Ca_06748			
CaPOPI_4528	Ca7	6104896	AG/A	TTGAACTCCCCAAGGAAACA	TCGGTTGAATTTTGAATCATCA	60.5	315	INTERGENIC				
CaPOPI_4529	Ca7	6106310	TTAT/TT	ACATCCTGGACCTGCTCATC	ATTCGAACGCGAATTTTCAG	60.1	546	DRR	Ca_06747			
CaPOPI_4530	Ca7	6107406	AAAAATTTAAATTT/AAAAATTTAAATTTAAATTT	TGTTCCACTTTCACCATTTCA	TGGGTGTTTTATTTTTCAGATTACTG	60.4	204	DRR	Ca_06747			
CaPOPI_4531	Ca7	6107658	TG/T	TGTTCCACTTTCACCATTTCA	GAGCAGTGTGGGGTTTTAGG	60.4	703	DRR	Ca_06747			
CaPOPI_4532	Ca7	6122129	GTTTTT/GTTTTTTT	TGGGTTTCGAGCCTAATTTTG	CCGATTTCATCCAAGCCCTTA	60.1	435	INTERGENIC				
CaPOPI_4533	Ca7	6125384	TAAATTC/TAAATTCAAATTC	TCAACTTCCACACTTGCTTAAA	TCAACTATCATCCCTTGCTCTTT	57.6	902	INTERGENIC				
CaPOPI_4534	Ca7	6126281	TAAAA/TAAAA	TTTCTGCCTAGAAAAGTCCAT	TGTAGCCACGTAAGGAAACCT	57.2	246	DRR	Ca_06744	O		Ubiquitin
CaPOPI_4535	Ca7	6162985	TTT/TTTATT	CTACCCCACTTGCCATGATT	TCACAAACGCGGTTGATTTA	59.8	624	INTERGENIC				
CaPOPI_4536	Ca7	6195527	GTATATATATATATATAT/ATATATATATATATATATATATATAT	GATCTAACGGCTGAGCGAAC	CAGAAGCTCCAAGAACTGCC	60.0	156	DRR	Ca_06738			
CaPOPI_4537	Ca7	6314366	GTTTTTTTTT/GTTTTTTTTT	TGACGTCAAAGATCCCAAAA	TGCTCCCTTAATTTGCATGA	59.1	567	INTERGENIC				
CaPOPI_4538	Ca7	6347731	ATAATTA/ATAATTAATTA	TGTTAATCACCCCGGAAAAA	GCTGCATTTCAGAAGCATCA	60.2	521	DRR	Ca_06721	R	NAC	Pentatricopeptide repeat
CaPOPI_4539	Ca7	6481476	ATTTT/ATTT	TCCTCGCTGTTGACAATCAC	TTGTTAAGTGGTGGGAAGGC	59.8	454	INTERGENIC				
CaPOPI_4540	Ca7	6686273	TAAAAAAA/TAAAAAAA	TGCCATAAATGTCAAGATGTGA	CCAATTTGTGAAGGAGGGA	59.0	887	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4541	Ca7	6842219	GA/GAAA	CCAATTCGGGGGATAAA GTT	TGGGATGACAAACGAG TCA	60.0	124	INTERGENIC				
CaPOPI_4542	Ca7	6854971	ATTTTTTTTT/ATTTTTTTTTT	TATGAGGAGTGTGCTGC TGG	ACTCGCGACTTAACTT CCA	60.0	348	INTRON	Ca_06677	T	YABBY	Protein kinase, catalytic domain
CaPOPI_4543	Ca7	6912264	TTATATATATATATATATAT/TTATA TATATATATATATATATAT	TGCACCTGCACATGTGG AATAA	AATCCCTGCAATTGTGG AAG	60.2	560	INTERGENIC				
CaPOPI_4544	Ca7	7243214	CTATATATATATATATATA/CTATATATA TATATATATATA	CGTCCGTGAAAGGTTTC CTA	TGACCGACTATACAATC TTACATGC	60.1	669	INTERGENIC				
CaPOPI_4545	Ca7	7284443	AATATATATATATATATATATATATAT ATATA/AATATATATATATATATATATA TATATATATATATATATA	TTGAATTCGGAGTTTTC CTTTT	CCTCACTTCATTGCTGC TCA	59.1	992	INTERGENIC				
CaPOPI_4546	Ca7	7332178	TC/T	TCGACAGTTTTGGTCAC TGCTCT	TCTCATCTCCTCCAATCT CTCA	59.8	592	INTERGENIC				
CaPOPI_4547	Ca7	7332238	CATATAATTATAT/CATATAATTATATAA TTATAT	TCGACAGTTTTGGTCAC TGCTCT	TCTCATCTCCTCCAATCT CTCA	59.8	592	INTERGENIC				
CaPOPI_4548	Ca7	7335750	TAAAAAAAAAAAAA/TAAAAAAAAAA	GTGTTTGGGATTGCGTT CTT	CTCCCCAAATTGAAAA TGT	60.0	583	INTERGENIC				
CaPOPI_4549	Ca7	7380960	AAT/AATTAT	GGTGAACCCATTGCAAT TTT	TCAGGCCAAGAAAGGAG AAA	59.7	766	INTERGENIC				
CaPOPI_4550	Ca7	7385094	GGT/GGTGT	ATTCAATTCAAGTTTGC GG	CAAATGAGCAGCTCGGT GTA	59.9	750	INTRON	Ca_06620	S		Protein of unknown function DUF92, TMEM19
CaPOPI_4551	Ca7	7404264	TAAAAAA/TAAAAA	GGTGGGCTCAGAAAACA GAG	TCCAGGTATTGCATTG TGA	59.8	603	DRR	Ca_06618			Acyl-ACP thioesterase
CaPOPI_4552	Ca7	7411561	TAA/TAA	AGTTACCCGATGTGCAT GGT	TGCAAACTTTGGTGTGG GTA	60.3	631	INTERGENIC				
CaPOPI_4553	Ca7	7411632	TAAGTCA/TA	AGTTACCCGATGTGCAT GGT	TGCAAACTTTGGTGTGG GTA	60.3	631	INTERGENIC				
CaPOPI_4554	Ca7	7411899	TAAAAAA/TAAAAA	AGTTACCCGATGTGCAT GGT	TGCAAACTTTGGTGTGG GTA	60.3	631	INTERGENIC				
CaPOPI_4555	Ca7	7440742	GGAG/GGAGAG	ATCATCCACGACCCAAT CAT	CACAAACAGAATGTGCA CCC	60.0	562	INTRON	Ca_06616		bHLH	Protein of unknown function DUF936, plant

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4556	Ca7	7458735	A/AT	TTTGTCAATTTGACCGTCTT	GACCCACATAGTGAGGGGTG	59.6	693	INTERGENIC				
CaPOPI_4557	Ca7	7459713	TACA/T	TTTTTGTCTTAACTGGGCCG	TGGAGGTCTCCTCGTTCTACT	60.1	541	INTERGENIC				
CaPOPI_4558	Ca7	7462087	TTTACTTACTT/TTTACTTACTTACTT	TTGAAGCTGCTGCTGAAGA	CAGATGTCCAACACCGACAC	60.0	323	INTRON	Ca_06613	B	NAC	Histone deacetylase superfamily
CaPOPI_4559	Ca7	7491994	AAAGAA/AAAGAAGAA	GCAAAGCTTGCTTTTTGTCC	ATAGAGGGCGCATGTCACTT	60.0	411	INTRON	Ca_06610	L	GeBP	DNA mismatch repair protein MutS, C-terminal domain
CaPOPI_4560	Ca7	7510196	TC/TCC	TTGGAAGGGAAAAAGCAAGA	TGCATTTTATTCTGCACCTGA	59.8	555	DRR	Ca_06609		TCP	Transcription factor, TCP
CaPOPI_4561	Ca7	7543253	AG/A	ATTAATATGCCAACTGGCCG	ACCACTACCAATTCTTGCG	59.8	596	INTRON	Ca_06607	K	C2H2	Transcription factor TFIIIE, alpha subunit
CaPOPI_4562	Ca7	7547228	CTGAACATGAACAT/CTGAACAT	TGACGATTGTTGTGAAGGG	TTTCATCAACCTTCTCTCCAG	59.5	746	INTERGENIC				
CaPOPI_4563	Ca7	7550729	ATTTTT/ATTTTT	CCGTGAATTTGGGTTCAACT	CTCGCGTAATCCACGTATT	59.8	602	INTERGENIC				
CaPOPI_4564	Ca7	7597807	A/AT	TCCTTTATGATCAGCCCAACC	CGTTCAACGGAGCAATTTT	59.9	356	DRR	Ca_06600	A		RNA helicase, ATP-dependent, DEAD-box, conserved site
CaPOPI_4565	Ca7	7626364	CTTTTT/CTTTTTT	AGTCAGCTGCAAACCAAGT	GGGAAGGTCATGCCAACCTTA	59.9	819	DRR	Ca_06598	Z	MYB_related	Kinesin, motor domain
CaPOPI_4566	Ca7	7668650	ATTT/ATTTT	CATTTTCCATCCAATTTTGAG	CCACTTTCTCATTTTGTGTGG	58.5	501	DRR	Ca_06594	R		ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter
CaPOPI_4567	Ca7	7671749	AA/AATA	TGCACCATTTATGTGAGGCT	TTCCAAATTCACATGCATCC	59.2	571	DRR	Ca_06593	J	MYB_related	Translation elongation factor IF5A
CaPOPI_4568	Ca7	7683130	TAA/TAAA	TTCGATAAACCGCTAATGCAC	GTACTTGGCTGCTTTGGAGC	60.1	847	INTERGENIC				
CaPOPI_4569	Ca7	7688075	TGGG/TGG	TTGTGTCATGGATGATGGTGCT	CCTCCATGGGTGAAAGTTTG	59.9	664	INTERGENIC				
CaPOPI_4570	Ca7	7689690	GTTTTTTTTT/GTTTTTTTTT	TCAGAAACATCATCAACGCA	TGGTTTCAAAACAAAAATGCAG	60.3	952	INTERGENIC				

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CaPOPI_4571	Ca7	7694767	AATAGATAGATA/AATAGATA	TCTCATTGATGACCCAAAGG	CACAATCACAAAGTGGGACG	58.5	722	INTERGENIC				
CaPOPI_4572	Ca7	7701750	CA/CAA	CCGATTCTATTTGTTGAAAGC	TAACCCCTCCAACGCTACAC	58.7	492	INTERGENIC				
CaPOPI_4573	Ca7	7703445	AA/AATATGGATTAGTAGACA	TCCAAAAGGTTCTTGCAATCC	AACATGGAGAATGAAACGCG	60.1	641	INTRON	Ca_06588			Protein of unknown function DUF3353
CaPOPI_4574	Ca7	7724983	GTTT/GTT	TCAACAAAGCTTAATTGGCG	ACACTGCCGAAAGTTTTGCT	59.0	724	DRR	Ca_06585	J		Phenylalanyl-tRNA synthetase
CaPOPI_4575	Ca7	7738038	TC/T	GATTCCATTGGGATTGGTTG	CACGTTTTAGAGATGTCATTTTTG	60.0	505	INTERGENIC				
CaPOPI_4576	Ca7	7738595	GTATATATATATATATATATATA/GTATATATATATATATATATATA	CAAAATGGACATCTCTAAACGTG	TCTCTACCCAATCACCAAA	59.9	583	INTERGENIC				
CaPOPI_4577	Ca7	7753007	GTTTTT/GTTTTTTTT	GGAGAATCGCCAACCAGATA	GGGGAAAACAATGCAGGTAA	60.0	542	CDS (FRAME SHIFT)	Ca_13243	KL	G2-like	SNF2-related
CaPOPI_4578	Ca7	7850911	CAAAAAAAAAAAAA/CAAAAAAAAA	TCGATGATATTTTGTTCGCTT	TGGAGCTTGCAGCTCATACA	58.8	440	INTERGENIC				
CaPOPI_4579	Ca7	7861934	ATTT/ATTTT	TCGCTTGGTGTGTGATAGGTG	TTCTAATGCTTCGGCAATCC	60.1	452	INTERGENIC				
CaPOPI_4580	Ca7	7875761	ATT/ATTT	CTTTCACCAAGGATAGGCA	GGCTTTCTGCCACTCATCTC	60.1	820	INTRON	Ca_13230		MIKC	GDP-fucose protein O-fucosyltransferase
CaPOPI_4581	Ca7	7880271	A/ACTGTTAG	TGGATATTCACACAGCATTAAG	TTGGAACCTGTCTCAACCGA	59.0	727	INTERGENIC				
CaPOPI_4582	Ca7	7881505	CTTTTT/CTTTT	ACCTTCTGGATATGCCATGC	GAGATGGGATCTCCAACATCA	59.9	189	INTERGENIC				
CaPOPI_4583	Ca7	7888043	A/AC	TAACTGAGACCCAGGAGGGA	TTCAACACAGCCCATAACCA	59.6	645	DRR	Ca_13229			BSD
CaPOPI_4584	Ca7	7910843	ATA/ATACTTA	AACACACGTTACAGCAATCTC	AAGCATGTTTTACCTTTTACACACA	59.8	477	INTERGENIC				
CaPOPI_4585	Ca7	7944979	TATGAAATGAAAT/TATGAAAT	ATTTAATGGCTTCCACAGC	CGTACTCAACAGAGTTGGATCG	60.0	640	DRR	Ca_13222	K	MIKC	Transcription factor, MADS-box

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CaPOPI_4586	Ca7	7950061	CATTGCAATTGCAATTGCA/CATTGCAATTGCAATTGCAATTGCA	GCCACAGCCTTTTCTCTTG	TGCTGAAGTTGCTCTCATCG	60.0	442	INTRON	Ca_13222	K	MIKC	Transcription factor, MADS-box
CaPOPI_4587	Ca7	7952171	AGGGG/AGGG	TATCCAAATTGCGTCGGATT	ACTCGGATGTCTCAATGCAA	60.3	307	INTERGENIC				
CaPOPI_4588	Ca7	7954760	AAATAATAATAATAATAATAAT/AAATAATAATAATAAT	TGCAATTTTGGATCTCCCAT	TGGAATAATCAAGGTGTCCAT	60.3	422	INTERGENIC				
CaPOPI_4589	Ca7	7958075	CAATGGTAAT/CAATGGTAATGGTAAT	CGAGCATCAAAGGTGAGGAT	ATTGGGGAGGATTCTTTGGA	60.2	321	INTERGENIC				
CaPOPI_4590	Ca7	7962835	A/ATTCT	TGGAATAAACTCTGTGCCCC	CGATGACGACAACATAACGG	59.9	283	INTERGENIC				
CaPOPI_4591	Ca7	7962974	AACAGAGTTTGTTAG/A	TGGAATAAACTCTGTGCCCC	GACGGCGACAAAAACAAAG	59.9	365	INTERGENIC				
CaPOPI_4592	Ca7	8010935	TAAAAAA/TAAAAAA	AGGCCACAAATGCAGCTTAG	CAAGTCAGCTTTTCCAGGC	60.4	586	DRR	Ca_13217	R	NF-YA	Kelch repeat type 1
CaPOPI_4593	Ca7	8016813	TAATAATAATAATAATAATAAT/TAATAATAATAATAATAATAAT	TGACCTCTGCAACCTTTTCC	GGTGGACGTGCTACTTGTGA	60.2	200	INTERGENIC				
CaPOPI_4594	Ca7	8019951	ACTACAT/ACTACATAGTCTACAT	TAATGTATAGGGGGAGGGG	CTGTGTCATCACATCTTGCT	59.9	305	INTERGENIC				
CaPOPI_4595	Ca7	8023022	TAAA/TATAAAA	GGAACCACGAGAGAAGGAGA	GGGTGAGATCTTGCACTGGT	59.4	468	INTERGENIC				
CaPOPI_4596	Ca7	8028807	AT/ATT	TCAAAGGTTTCTCCACAC	GGTGGCTTCTTGTGGTGTT	59.9	608	DRR	Ca_13215			
CaPOPI_4597	Ca7	8032032	GAAAAAAA/GAAAAAA	CAAGAAATCCGATCACATCCA	CACAACACGATGACTCTCC	60.1	639	INTERGENIC				
CaPOPI_4598	Ca7	8082220	TC/T	CGATTCAATCTTGATTCCGT	CGTGCAATTTTCTCTATTGGT	57.6	491	INTERGENIC				
CaPOPI_4599	Ca7	8107965	G/GTT	CACAAAATTTAGGGGCT	AGAAAGGGGATCAAGGAAA	60.2	679	INTERGENIC				
CaPOPI_4600	Ca7	8147843	CT/C	ATGTACCGACTCTCCGCTG	GTTGTGGGATGAATTGACCA	60.3	752	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4601	Ca7	8158726	ATTATTTTATT/ATTATTTTATTTTAT T	TTCGACCACTACTGCCA TCA	TTTCTCTCCGTTTCATGA GG	60.3	677	INTERGENIC				
CaPOPI_4602	Ca7	8160639	CATAT/CATATAT	TCCCTCCTTCCCCCTAT CTA	GTGGATCATTACCATGG CCT	59.9	443	INTERGENIC				
CaPOPI_4603	Ca7	8168245	TCC/TCCC	GAAAGAGAGATGGTGG GTGC	ATCCTTCAGCAACGATC CAC	59.7	568	DRR	Ca_13197	S		Uncharacterised protein family, transmembrane-40
CaPOPI_4604	Ca7	8215292	AG/AGG	CACTAACGCCAACCATG AGA	AAAAGTTACAAAGCGGA GATGC	59.7	345	DRR	Ca_13193			
CaPOPI_4605	Ca7	8216237	TGG/TGGG	TTCTTGAACCTTGGGCA TTC	CAATTGTTGGGAGGAA ATG	60.1	766	DRR	Ca_13193			
CaPOPI_4606	Ca7	8241298	CATATATATATATA/CATATATATATA TATATATATATA	ATGCATAAATGACCTTG GCA	ATGGTCCATGTGTTAGG GGA	59.0	298	INTERGENIC				
CaPOPI_4607	Ca7	8246509	CTAGAAAAT/CTAGAAAATAGAAAAT	TGATTTGGGGGTATCAC GTT	AAAAGCCTCTTGCTATG CCA	60.1	634	INTERGENIC				
CaPOPI_4608	Ca7	8250120	TATATTGATATTG/TATATTGATATTGAT ATTG	GCAGCTGGTGTGTTTC TGA	TGCAAGAAGTGAAGTGG GTG	60.0	546	DRR	Ca_13190	R	C2H2	Zinc finger, C2H2-type
CaPOPI_4609	Ca7	8303689	CTTTTTTTTTT/CTTTTTTTTT	TTTTGGACCACTTTGCT GTG	ACGAGGCTTGACCTC ATT	59.7	326	DRR	Ca_13182		FAR1	Protein kinase, catalytic domain
CaPOPI_4610	Ca7	8310630	ATTTTT/ATTTTTTTT	TTGGTGGTGAAAGTGA CAA	TGAACCCACAAACACA AGG	60.0	562	DRR	Ca_13181			Protein of unknown function DUF827, plant
CaPOPI_4611	Ca7	8311161	AT/ATGT	CCTTGTGTTGTGGGTGT TCA	TCATCCCCGAAACTAC ACC	60.5	670	DRR	Ca_13181			Protein of unknown function DUF827, plant
CaPOPI_4612	Ca7	8315825	CAATCATTT/CAATCATTTACTAATCATT T	GCCATATCACCTTTGAT CAAGTC	TGCCATGACACAAACAA CAC	59.9	142	INTERGENIC				
CaPOPI_4613	Ca7	8363466	CCTTT/CCTTTCTTT	GCAACCACAGACACAGA ACG	TCAAATGTGGTGTAGGG GGT	60.4	599	INTERGENIC				
CaPOPI_4614	Ca7	8366630	G/GTAT	AAGCAGTGATCCAATC CTCA	TGGAATTATAAACCGAT TAAGGTG	59.9	210	INTERGENIC				
CaPOPI_4615	Ca7	8384302	CTAATAATAATAATAATAATAATAAT AATAATAATAATA/CTAATAATAATA ATAATAATAATAATAATAATAATA	AAGAAATGCAGGCAATC ACC	AAAAGGCTTCGCGTGAG TTA	60.1	386	INTRON	Ca_13172			Actin-binding FH2/DRF autoregulatory

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4616	Ca7	8409838	CGGG/CGGGG	TGCAGCCTTTTCACCTTCTT	CGGTGCACAACCTTATCTTGC	60.0	122	INTERGENIC				
CaPOPI_4617	Ca7	8437623	CT/CTTT	TTTGACTACTTGCGTGGCAG	ATGTTGCCTGGGTTGCTATC	60.1	534	DRR	Ca_13163	O	TCP	Zinc finger, RING-type
CaPOPI_4618	Ca7	8438347	AGGGG/AGGGGG	GATAGCAACCCAGGCAACAT	ACATCGTGATGCAATGGA AAA	60.0	510	DRR	Ca_13163	O	TCP	Zinc finger, RING-type
CaPOPI_4619	Ca7	8440281	T/TG	TTTAGTCTCCAGGCTTTTCA	CATCAAAGCAGGAGCTGACA	60.0	608	INTRON	Ca_13162	G	MYB	Ribulose-phosphate 3-epimerase
CaPOPI_4620	Ca7	8442048	GGTTA/GGTTATTAGTGAGTTA	TTGGCGATTCTGTGGTGTAGTA	TTTGAAGCACAGATGGCTGCTG	60.1	597	INTRON	Ca_13162	G	MYB	Ribulose-phosphate 3-epimerase
CaPOPI_4621	Ca7	8445186	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	GCATGCCATTGGTTTAAGTTT	GGACTAAACGTTGCCTGAAA	59.0	443	INTERGENIC				
CaPOPI_4622	Ca7	8466786	TAA/TAATAAA	GTTTTATTGCAACCCGTGG	CTATCCTTCGCCGACAAACAT	60.2	186	INTERGENIC				
CaPOPI_4623	Ca7	8467239	GC/G	ATGTTGTGCGCGAAGGATAG	TCCGTCCTAAATTGTATGCCA	60.1	918	INTERGENIC				
CaPOPI_4624	Ca7	8473510	CATTATTTCTTGTGTGTA/CATTATTTCTTGTGTAATTATTTCTTGTGTA	CGAAGTTGGGTACAACACATGA	CCCACCACAACATAGACCCT	60.9	409	INTERGENIC				
CaPOPI_4625	Ca7	8477670	GA/GAA	CATCAGTTGCTTTTGGAACA	CGATTTGTCGATGGGAATCT	60.0	624	INTERGENIC				
CaPOPI_4626	Ca7	8492749	TAA/TA	GACTCTCTGCGGGAGATTG	TTCCGGCTGATGATCTTTTC	60.0	690	INTERGENIC				
CaPOPI_4627	Ca7	8492888	TAAA/TAA	TACCGTGATCCTTTTCTCC	TTCCGGCTGATGATCTTTTC	60.1	455	INTERGENIC				
CaPOPI_4628	Ca7	8522491	CAA/CAAA	GGATTCTGTTTTCCCCA AAT	TTCGCAACTCCACTCTTCCT	60.0	343	INTERGENIC				
CaPOPI_4629	Ca7	8529147	TAAAAAA/TAAAAAA	CACAAACCAAAACAACCTGTG	AATGAGTCATCCCTTTTGCG	59.0	459	DRR	Ca_13150			Protein of unknown function DUF3223
CaPOPI_4630	Ca7	8529891	TATAAA/TA	CATGAATTCAGGATTTTCCA	TTCCACCCCAATTTGTATA	59.7	489	DRR	Ca_13150			Protein of unknown function DUF3223

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4631	Ca7	8597223	CTG/CTGTG	AGTGACAAGCGGTGGAAATC	GGTAGGACCAAGAACACAACC	60.1	931	INTERGENIC				
CaPOPI_4632	Ca7	8601211	TC/T	AGCGGTTTTTGCGAGAGATA	CACCTCACACCTAACCCTCA	60.0	769	INTERGENIC				
CaPOPI_4633	Ca7	8619938	TAG/TAGAG	TTCCATGGTTTTCTCCAGAG	TCTAATAAATGGCAACGGGC	59.9	218	INTERGENIC				
CaPOPI_4634	Ca7	8633845	TA/TAA	TTATGTTTGTGGTGGTTGCG	AAATGTGCGGTGGAATGAGC	60.4	618	DRR	Ca_15354	DZ	C2H2	Calponin homology domain
CaPOPI_4635	Ca7	8634841	ATTTT/ATTT	TACAAAGGGAGAAATGGGCAG	GCACCCTCCTATGTCGTCTAA	60.1	536	DRR	Ca_15354	DZ	C2H2	Calponin homology domain
CaPOPI_4636	Ca7	8662282	AGTGTG/AGTG	TGAGAATAGTTTTACGGTAGTTTTGG	CATTGGCAACACTTCCTCCT	59.2	641	DRR	Ca_15350	R	bZIP	Kelch repeat type 1
CaPOPI_4637	Ca7	8662645	AATA/AA	CTTCTGCAGATGTTTTGCA	TGCATTGACACGTGGTTT	60.0	374	DRR	Ca_15350	R	bZIP	Kelch repeat type 1
CaPOPI_4638	Ca7	8666289	ATTTTTTCTTT/ATTT	TCACTCCAACAACCAATGACA	CAACAATCAACAAGGCTCCA	60.0	566	INTERGENIC				
CaPOPI_4639	Ca7	8670801	AA/AAAAGA	CACATGCGGACCCTTAACCTT	GCCCAATTGGTCGCTTATA	60.0	798	INTERGENIC				
CaPOPI_4640	Ca7	8673839	CC/CCGTAAAAATGAAC	TCGAGCTTTGGAGTTAAGGTTT	TGAAATCGCCCCAAATTAAA	59.4	442	INTERGENIC				
CaPOPI_4641	Ca7	8678324	CTTATTTTATTTTATTTT/CTTATTTTATTATTTTATTTT	AAAAAGGGTTGGTTGGTTCC	TGTCCCCCTCTGATCTTGGA	60.1	679	INTRON	Ca_15349	T	WRKY	Protein kinase, catalytic domain
CaPOPI_4642	Ca7	8681581	AT/ATT	ATAATTGCGTGGCTTGCATT	ATTGCTTTGGAGACACAGGG	60.5	488	DRR	Ca_15348	G		Aldose 1-epimerase
CaPOPI_4643	Ca7	8709902	CAAAA/CAA	ATCAATCATGCGTCAAAACG	AAACACAAGCAGGGTTGGTC	59.5	392	INTERGENIC				
CaPOPI_4644	Ca7	8737215	TAAATAAAAATAAAAATAA/TAAATAAAAATAAAAATAAAAATAA	TTTTGACACTCTAGCCTTGTG	TGGGATTTTGTTGTGCTTTTT	57.2	575	INTERGENIC				
CaPOPI_4645	Ca7	8761317	CTTT/CTT	GGGCAATGCTTTTAAAGGTG	ACGCATGCACATTGATTGT	59.6	818	INTRON	Ca_15340		HD-ZIP	Pectate lyase/Amb allergen

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4646	Ca7	8762041	GTTTTTTTT/GTTTTTTTTT	ACAAATCAATGTGCATG CGT	TCTCACATTGCACAAATC TCG	60.0	484	INTERGENIC				
CaPOPI_4647	Ca7	8792391	TTATAT/TTAT	TTTTGTTTGCACTTCCTT GAAA	CGGCAGACGCTTCTTAA TTT	59.8	772	INTERGENIC				
CaPOPI_4648	Ca7	8793998	TAAAAAAAA/TAAAAAAAAA	TCATTGGTTATTGGTTG GGAA	GAAGGAACCAAGGGAG ACC	60.0	823	INTERGENIC				
CaPOPI_4649	Ca7	8839299	C/CAA	CCAATTGCCCCAAAATA AAA	GTTTCCCTTTGAGTCC GAT	59.6	450	DRR	Ca_15328	E	BBR-BPC	Oligopeptide transporter
CaPOPI_4650	Ca7	8841846	TATAATAAATAAATAA/TATAATAA TAAATAAATAAATAA	TTCATTTTGCCTCAACA CG	AATGGGTGATTGCATGC TG	59.7	399	DRR	Ca_15327	P	GRAS	ATPase, P-type, H+ transporting proton pump
CaPOPI_4651	Ca7	8859288	TAA/TAA	CCTATTGATGTCCTGT TCA	GGTACGATTGCCTTTTC CAA	59.4	191	INTERGENIC				
CaPOPI_4652	Ca7	8875146	TTT/TTTAAATT	CATTATACACCCTGGAC AAATGG	TTAATGAAATTTGGTCC GTG	60.4	304	INTERGENIC				
CaPOPI_4653	Ca7	8898762	GAGAAGAAGA/GAGAAGA	TGCCACGTCATTGAAA TGT	CTGCGTCGAAATTTAGG GAA	60.0	859	INTRON	Ca_15325		C2H2	Domain of unknown function DUF629
CaPOPI_4654	Ca7	8907832	TATCAT/TAT	TCATGACAATGAGTCAA TTTGC	GACTCTCGCCAGAATCA TGTC	58.6	656	INTERGENIC				
CaPOPI_4655	Ca7	8955893	CTTTT/CTTT	CATACCAGTGGGAGGCA GTT	TTGCTTCCCATTAAGC ATC	60.0	636	INTRON	Ca_15319			
CaPOPI_4656	Ca7	8967220	AAATTAATTAATTA/AAATTAATTA	TTATTTGGCTCACACCC TCA	ACAACAGGCTGAGCCAA GTC	59.1	539	INTERGENIC				
CaPOPI_4657	Ca7	8973095	TA/T	GGCGGTGTTGTTAGCAA TTT	TGTGGAACAAGTTCCCA AGG	60.0	626	INTERGENIC				
CaPOPI_4658	Ca7	8974976	ATTTTT/ATTTTT	TAGAAGCCCAAGGCTC AAA	GGTACAGAACGTGGTGC AAA	60.0	918	INTERGENIC				
CaPOPI_4659	Ca7	8994610	CTTTTTT/CTTTTTTTTTT	CTGCTGCGTTTCTGATT GAA	AACGAAAAAGACCGCAA CAT	60.1	471	INTERGENIC				
CaPOPI_4660	Ca7	9020687	AC/A	ATTACTTTGAAGCCCTG GCA	TGGCACACATGACAACT TGA	59.7	489	INTRON	Ca_15313	U	bHLH	Exportin-1/Importin-beta-like

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4661	Ca7	9023557	CTT/CTTT	GACAGAGGGGGAGCTA ATCC	AGAACCGCCTTCCCAGT TAT	60.0	621	INTRON	Ca_15313	U	bHLH	Exportin-1/Importin-beta-like
CaPOPI_4662	Ca7	9030127	GAAATATAAATATAAAT/GAAATATAAAT ATAAATATAAAT	CACGATAGCGTTGGAGC TAA	TTGCACCTAAGTTTGT CCG	59.1	755	DRR	Ca_15313	U	bHLH	Exportin-1/Importin-beta-like
CaPOPI_4663	Ca7	9031079	CTTTTT/CTTTTTTT	ACCCTCCATTTTCTCCCA CT	ACTGCGCCATGAATGAT TTC	59.8	703	DRR	Ca_15313	U	bHLH	Exportin-1/Importin-beta-like
CaPOPI_4664	Ca7	9032345	ATTCTATCTTT/ATT	ACCACCTGAATTGCTTTT GG	TCTCGCACCTTGACAGT TTG	60.0	936	INTRON	Ca_15312	R		Tubby, C-terminal
CaPOPI_4665	Ca7	9034671	CAAA/CAAAA	TTTCATGGTGGTGGTAC TGG	TTCGCAAAGGTGTCAA CTG	59.3	463	DRR	Ca_15312	R		Tubby, C-terminal
CaPOPI_4666	Ca7	9037363	GTTT/GTT	CCACAAAGGAGTGGGAC CTA	GTGGTGTCTTGGCCCT AGT	60.0	295	INTERGENIC				
CaPOPI_4667	Ca7	9044478	GTT/GTTTT	AAGTTGCAGGGTTTCT TGA	TGAATTTATTGCGATT ATGAATG	59.7	247	INTERGENIC				
CaPOPI_4668	Ca7	9051626	A/AT	TGAGAGGATCTCCTTCC AACTT	TTCAAAAATTGGTCCC ATT	59.3	120	INTERGENIC				
CaPOPI_4669	Ca7	9064807	TGA/T	CAGGAACGTGAACCAAA CAA	AATGCTACGTCCAAACC TGG	59.6	785	DRR	Ca_15308	R	AP2	Smr protein/MutS2 C-terminal
CaPOPI_4670	Ca7	9075277	TA/T	AGGCACGGTCTTCTCTT TTT	ATTGCTAGGGGTGTTGA TGG	60.1	355	INTERGENIC				
CaPOPI_4671	Ca7	9084742	TTAT/TT	TGAGATCATGAAATGC CCA	GGAGTTGATTTGATTTG CGG	60.0	975	INTERGENIC				
CaPOPI_4672	Ca7	9101816	AAGA/AA	CAAGTGGTCATTCAAAA GCAAA	TTTAAGTGGACCACGCC ATT	60.1	549	INTERGENIC				
CaPOPI_4673	Ca7	9109063	AG/AGG	TGGACCTATTGGCTAC GTT	TCGTTCAAAAAGGAAAC ATCG	59.5	904	INTERGENIC				
CaPOPI_4674	Ca7	9129170	GAGCTA/GAGCTAGCTA	TTGTGAGGCGGAGAGA GTTT	AGCATCCGACAATGTCA CAA	60.0	480	DRR	Ca_15303	K	ARR-B	Signal transduction response regulator, receiver domain
CaPOPI_4675	Ca7	9134590	CATAAAAA/CATAAAAAATAAAAAA	TTTTCTGGGAGATGGAT AAAAA	ACATTGCGAGTCCAAC ACA	57.7	503	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4676	Ca7	9180941	TA/TAGA	ATGATTTCCACGAGCCA AAC	TGCAACATTCTCTGATG AGC	59.9	322	INTERGENIC				
CaPOPI_4677	Ca7	9181192	AGT/AGTCGT	ATGATTTCCACGAGCCA AAC	ACGACATGCCAATGTCT CAA	59.9	641	INTERGENIC				
CaPOPI_4678	Ca7	9181858	CT/C	TATTACCCAACCAAGCC AGC	TGAACTTTGATTGCCGC TAA	60.0	554	INTERGENIC				
CaPOPI_4679	Ca7	9183560	CCACA/CCA	CGATTGCCAAATATGCC TTT	GTGTTGGCATTGTCTTC CCT	59.9	337	INTERGENIC				
CaPOPI_4680	Ca7	9210664	CTTTTTTT/CTTTTTTTTT	GTGTGCCACATATCCAC AGC	GGACCAAATTGAGGAAC CAA	60.0	539	INTERGENIC				
CaPOPI_4681	Ca7	9232233	GAAAAA/GAAAA	GAAACGTTGGTGGACAT TCA	ATGCCATATTCTCGAGT CGG	59.4	546	INTRON	Ca_17335			rRNA small subunit methyltransferase G
CaPOPI_4682	Ca7	9255165	CACCTACTTACTTACTTAC/CACCTACTT AC	AATTTGCAACCAATTACC GC	ATCCACCAACACAGCA ACA	59.8	220	INTERGENIC				
CaPOPI_4683	Ca7	9259824	AATTTTTTGA/AATTTTTTGATTTTTTGA	AGTGGGAGAGCAGCTG AGAG	ATCGGTGCAAGACACAT TGA	59.9	352	INTERGENIC				
CaPOPI_4684	Ca7	9261954	ATGA/ATGACGATACTGA	GGGAAAGTCTTACTGTG TGCG	TGGACCAAATTGATGAA CCA	59.8	808	INTERGENIC				
CaPOPI_4685	Ca7	9276938	TAA/TCGAATCGAAA	GGAGCCTGATAATTCGG TGA	GCAATTCGATTTTCTGC GAT	60.0	241	INTERGENIC				
CaPOPI_4686	Ca7	9312827	A/AC	TTTTGGCCTGGGTCA TAG	AGACGGAAGCAACACAA CAA	59.9	520	DRR	Ca_17329		C2H2	HhH-GPD domain
CaPOPI_4687	Ca7	9367031	CGATTAAATTTAT/C	TCAGCTTATTGTGCGAG ACG	CACACAACAAGTCCAC AGG	60.2	391	INTRON	Ca_17324			Gibberellin regulated protein
CaPOPI_4688	Ca7	9386132	G/GC	TCCTCCAGTGGAACTCA TGTC	TTTTTCTCATGGCCATT GT	60.1	509	DRR	Ca_17321		WRKY	
CaPOPI_4689	Ca7	9401104	AT/ATTT	AATAGGGTCCGATGTT TCC	TTGAACGGAGAAAAC TCT	60.0	345	INTERGENIC				
CaPOPI_4690	Ca7	9406189	AAATAATAATAATAATAA/AAATAAT AATAATAATAA	CGCTCAATACTCTTCAA GTTCA	TTCCCTTGTCATTTC GTG	58.7	545	INTERGENIC				

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CaPOPI_4691	Ca7	9421127	TGGG/TGG	ATTGTGATGAAATGGGGACA	GTGGGTGGGATGCATAATTC	58.6	569	INTERGENIC				
CaPOPI_4692	Ca7	9421758	A/AT	CTTCGCAAAAATGCGAAACT	GCTATCGCGCTATTCCAAC	60.4	486	INTERGENIC				
CaPOPI_4693	Ca7	9422013	AATAT/AATATAT	CTTCGCAAAAATGCGAAACT	CATGATGATGCAGAAAACGG	60.4	573	INTERGENIC				
CaPOPI_4694	Ca7	9440061	TTACT/TTACTACT	GGGTGTTGATTCCCTTGATT	ATTTCCAGTTGGAGTGGTCG	60.0	867	DRR	Ca_17315	O	TCP	Zinc finger, RING-type
CaPOPI_4695	Ca7	9452345	CTTCA/CTTCAATTCA	GCTTCACATTAGGCCTCTGC	CCACGAGTAAGCTAAAGCCG	60.0	129	CDS (FRAME SHIFT)	Ca_17312			Ribonuclease III
CaPOPI_4696	Ca7	9459566	ATT/ATTT	TGGCGATAATGTTGCA TGT	AGAGCAAACGGGAAAGTGTG	60.0	131	DRR	Ca_17311			
CaPOPI_4697	Ca7	9465063	TAAAA/TAAA	TGAGTGGGATTGGTAGGAG	GCAACCATGACACGAAATTC	59.9	917	DRR	Ca_17310	C	bHLH	Aldehyde dehydrogenase domain
CaPOPI_4698	Ca7	9468329	TTA/T	TTTGAGCAATGTTCCCA AAT	TTTGAGGAGTGGCCTCAAGT	60.3	642	INTERGENIC				
CaPOPI_4699	Ca7	9494173	AACA/AACACA	TACGCAGCCTACTGTTGTGC	TTGTGTCTGACCACGCTATC	60.1	594	INTERGENIC				
CaPOPI_4700	Ca7	9495205	TTTATTAT/TTTAT	TCTCGCTATCCACTTTTGG	CCCCAGAGAACAACTTCCA	60.2	801	INTERGENIC				
CaPOPI_4701	Ca7	9542781	ATTT/ATT	ATTTTTGGCCTCGTTTTCT	TTGAAGTTGGTGAATGATGGA	59.9	759	INTERGENIC				
CaPOPI_4702	Ca7	9559628	A/AAAC	CCAAATTGTAACCGTAAATGAA	TTTATCCAATCTTCCGCGT	59.3	420	INTERGENIC				
CaPOPI_4703	Ca7	9586429	AA/AAGGA	ACATGCGCATTGTGTGTTT	GAAGGTTTTCCGAAGAGGG	60.0	439	INTERGENIC				
CaPOPI_4704	Ca7	9593254	TA/TAA	CTCCTTGTGGCAAATGGTT	GGTGTACCGTTGTTATGCC	60.0	586	INTERGENIC				
CaPOPI_4705	Ca7	9624778	GA/G	GAACAGCCAGTGCTTCTTCC	TGGGTCATGTTGCCAGTTTA	60.0	580	INTRON	Ca_17293			UvrB/UvrC protein

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CaPOPI_4706	Ca7	9639157	T/TTA	ATTTACCCAATTTCTGGC CC	AAATGGTGGGTAGCCTT CCT	60.0	123	INTRON	Ca_17292	A		Mpp10 protein
CaPOPI_4707	Ca7	9648140	CA/CAA	CAAGTTCGTGCTTGCAT CAT	TTCTACGGGTGCTATTT GCC	59.9	694	INTERGENIC				
CaPOPI_4708	Ca7	9655480	TA/TAA	GAGTTGGACTTGATGCA CGA	ACATAGGCAAAGCTAGG CGA	59.8	508	INTRON	Ca_17290		TALE	Protein kinase, catalytic domain
CaPOPI_4709	Ca7	9665800	TA/T	CTGGGGTGGCAACATCT TAT	TTGCATAGCTCACAAC GGC	59.8	223	INTRON	Ca_17290		TALE	Protein kinase, catalytic domain
CaPOPI_4710	Ca7	9672464	TAAA/TAA	TAATGGAATGTGCGTGT GGT	ACTTGTGTCGCCATTTT CCT	59.8	294	INTERGENIC				
CaPOPI_4711	Ca7	9676622	CAA/CAAA	CCGTTAGGAAACTTGTG GGA	GGGACTGAGGTCTTAAG CAAA	60.0	113	INTERGENIC				
CaPOPI_4712	Ca7	9699894	TA/T	AACTCTATCCCACACG CAC	CAAACACGTCGGATTG TAA	60.0	476	INTERGENIC				
CaPOPI_4713	Ca7	9701171	GAAAA/GAAA	CCCAACACACACACAC AAA	ATGCAATTGTTGACGT GAC	58.9	817	INTERGENIC				
CaPOPI_4714	Ca7	9705402	GAAAAA/GAAAAAA	TGGAGACATACAGTTAA GAAAACAA	CACATGTGCTGATTGCC ATA	57.2	240	INTERGENIC				
CaPOPI_4715	Ca7	9710850	ACCCC/ACCC	TGAACCAAATTGAAAC CCT	GAATTGTGCACGATGGA TTG	59.3	595	INTERGENIC				
CaPOPI_4716	Ca7	9711096	TG/TGG	CTGAACCAAATTGAAA CCC	ATAGGCATGCAATGATG CAA	59.3	667	INTERGENIC				
CaPOPI_4717	Ca7	9774600	GGTT/G	GAAGTCCACTTTTCAA TACG	GGAAGTCCACTTTTAAA TGACG	58.7	299	INTERGENIC				
CaPOPI_4718	Ca7	9814381	CTA/CTATA	TGCTTTATGGTTGCGTT GAG	TGACAAATTGTGATTGG TTGG	59.9	109	DRR	Ca_12746	S		Cwf15/Cwc15 cell cycle control protein
CaPOPI_4719	Ca7	9814956	TAAAA/TAAAA	GAACGCAACCTTTAAAA ACGA	TGACTGTTCCACACGG AAG	59.3	252	DRR	Ca_12746	S		Cwf15/Cwc15 cell cycle control protein
CaPOPI_4720	Ca7	9821392	CCTCT/CCTCTCT	ATTGCTTCCGTTGATGT TCC	CATCCCCACAAACCCAT AAG	59.9	402	INTRON	Ca_12747	G		Glycosyl transferase, family 8

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CaPOPI_4721	Ca7	9843413	C/CCTGATTA	TGACAAGGGTGTTCAC TGC	TGGCTTTGGAGGACTGA ATC	59.7	532	INTERGENIC				
CaPOPI_4722	Ca7	9843838	AA/AATAATA	TTGAAATTTCCCGAAGAT GC	CAACTGCCTCCTATTTTT ATTTTGA	60.0	304	INTERGENIC				
CaPOPI_4723	Ca7	9843850	AT/A	TTGAAATTTCCCGAAGAT GC	CAACTGCCTCCTATTTTT ATTTTGA	60.0	304	INTERGENIC				
CaPOPI_4724	Ca7	9844158	TTTT/TTTTATTT	TTGAAATTTCCCGAAGAT GC	GCAACGAGGCCTTAGAA CTG	60.0	787	INTERGENIC				
CaPOPI_4725	Ca7	9844646	ATGTT/ATGTTGTT	GCAGTTCTAAGGCCTCG TTG	CCCATCCACCTACGAAC ATC	60.0	672	DRR	Ca_12750	JO		Ribosomal protein S30
CaPOPI_4726	Ca7	9868243	TAA/TAAA	CATTCTTCCTCCACCA AAA	ACGCGTATACCAACTTT GCC	59.9	568	INTERGENIC				
CaPOPI_4727	Ca7	9927302	CTT/CT	TATCACTAACCGCACAC CCA	TGTTGAAAAATAGTACA AGCCG	60.0	525	INTERGENIC				
CaPOPI_4728	Ca7	9941741	TCC/TC	ACGAAGATGGAGCGAAA AGA	AAAGTGAGAAGATGTC GTCA	60.0	688	INTERGENIC				
CaPOPI_4729	Ca7	9951203	GAAAAA/GAAAAAAA	AATTGCTTGTCTCCGATT GC	TCTTTTGGCATGTGTATT GGA	60.2	865	INTERGENIC				
CaPOPI_4730	Ca7	9960561	TTCTGAAAA/T	GGTTTGAAGCACGGGAA ATA	GGTTGGTTGAGTGGTTC TTTG	59.9	359	INTRON	Ca_12761	GMW	ERF	Exostosin-like
CaPOPI_4731	Ca7	9967617	ATTTTTTT/ATTTTTTTTTT	TCAATGTAATGTTGGTTC GCA	GAATGCGCCAATACGTT TCT	60.0	576	DRR	Ca_12763		MYB	
CaPOPI_4732	Ca7	9968032	TTAAATATAAAT/TTAAATATAAATATAA AT	GCGGGAGTTTCTCAAC TAA	GTGCTGCTTCTCTGGGT TTC	59.3	822	DRR	Ca_12763		MYB	
CaPOPI_4733	Ca7	9975017	TGG/TG	ACTTTCCATACCAACG AGG	CGGGGTTAAGCCATCAA CTA	60.0	688	INTERGENIC				
CaPOPI_4734	Ca7	9992899	ACCCCC/ACCCC	GATTTGTCGGATGCTTT GGT	GGGGTTTGTTTGAAATT TTTG	59.9	406	INTERGENIC				
CaPOPI_4735	Ca7	10007202	TG/T	CGCAACATCTCTTACA CCG	AAACCATAAACA CTGCA GCC	59.3	853	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4736	Ca7	10016031	CAAA/CAAAA	TAAAAACGCGTACCGAA TCC	GTCGGCTTTTCAAGCAA CTC	60.0	588	DRR	Ca_12767		MYB_related	SANT domain, DNA binding
CaPOPI_4737	Ca7	10058702	A/AC	TCGCTTTCAAAAATGAG CAA	TTATAGGGCCAGCTTGG TTG	59.6	519	INTERGENIC				
CaPOPI_4738	Ca7	10081345	GGT/GGTATGT	TGATCATGTGCTCCAAC ACTC	CCACGGCTGCATACATA CAC	59.7	820	INTERGENIC				
CaPOPI_4739	Ca7	10111639	TGG/TG	AAATGATTTTCATGGTAA TGGAAT	GAAGCAACTGTATCGTG GGG	57.8	494	INTERGENIC				
CaPOPI_4740	Ca7	10112519	GAGAAAGAAAAA/GAGAAAGAAAAATAA GAAAGAAAAA	GGCCGACCCAAGAATTA GAT	TGTTGCTTTTTCCCAAT CA	60.3	923	INTERGENIC				
CaPOPI_4741	Ca7	10119011	TTTT/TTTCTTT	TTTGGCCCGACTTATCT TTG	TAAATCAGGCGGTTTTG GTC	60.1	516	INTERGENIC				
CaPOPI_4742	Ca7	10129752	TTC/T	AAACACATGCATTCCT CAA	GAACATGAGAGGCCAC AAT	59.0	387	INTERGENIC				
CaPOPI_4743	Ca7	10138374	AAA/AAAGTTGAAACAA	CTACCCCTTCTTTTG CCA	TCCACCAACTACTTTCAC CG	60.1	551	DRR	Ca_12775		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_4744	Ca7	10192729	TTTTTTTCATATA/TTTTTTTCATATAATG TTTTTTTCATATA	CCCATTCCGAATACATT GCT	GAGTTGGGTGCACGATT TTT	59.8	624	INTERGENIC				
CaPOPI_4745	Ca7	10194004	ATAATTAATT/ATAATT	TTGCTCGATAGAGTTAA ATTCCG	CATTTGCCAAGTTTTCAT TTTT	59.8	672	INTERGENIC				
CaPOPI_4746	Ca7	10204089	CTTTTT/CTTTTTT	GATGGGATGACTTTTGT TTGC	GGTTTGTTCCCGTGAGT GTT	59.4	475	INTERGENIC				
CaPOPI_4747	Ca7	10208171	GAAA/GAAAA	GCATGATGTGGGAGAG GAGT	CAAACCTCCAAAAGGC AGC	60.1	482	DRR	Ca_12782	TU	bHLH	Ras GTPase
CaPOPI_4748	Ca7	10213506	AAAAT/A	ACCGGTATCAGAGATCG TCG	TGGATTTACATAAAATC CGTC	60.1	639	INTERGENIC				
CaPOPI_4749	Ca7	10214018	AATGTATATATTATGTATATATTAT /AATGTATATATTAT	TCTCACCTAAAGTAAAGT GACGGA	AAACAAGTGCTTTTCGTT GGAA	59.4	741	INTERGENIC				
CaPOPI_4750	Ca7	10224561	AT/ATGTT	GCAGAAATCCCGCAGT AAA	GCAGCATGCAAAAACATA GCA	60.2	851	INTRON	Ca_12784	U	B3	Major sperm protein

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4751	Ca7	10247426	AT/ATATTT	TTCAATCACCTTAACCTT TGATCG	TTTTAAGAAATTATGTAC GATGTCCAA	59.6	579	INTERGENIC				
CaPOPI_4752	Ca7	10260220	TTTTATTTATTTATTT/TTTTATTTATTTA TTTTATTT	GATGATCAATCCTAACAT GCCA	AAGTCCCCGCACCTCTA CTT	59.9	486	INTERGENIC				
CaPOPI_4753	Ca7	10289954	TA/TAA	TGACACGGTACAAGGTG GAA	ATGGAATGTGTTAGCCC TGC	60.0	870	INTERGENIC				
CaPOPI_4754	Ca7	10313209	TAATTTCTAAATTTCTAAATT/TAATTTCT TAAATT	TTTCCATGCATTGATCTC CA	TCCCTAAGATGCATTCC TCC	60.0	620	INTRON	Ca_12794	A		tRNA/rRNA methyltransferase, SpoU
CaPOPI_4755	Ca7	10339253	AAACAAAA/AAACAAAAAGAACAAAA	GAAGCATCCCCATTGAA AGA	GGTGCATTTTGTCACTC CCT	60.0	549	INTRON	Ca_12794	A		tRNA/rRNA methyltransferase, SpoU
CaPOPI_4756	Ca7	10343265	TAAAAA/TAAAAA	AAGCGCTTCTTTTAGT TTAACA	TGATCAAATGGAAGGAC AAAAA	59.9	132	INTERGENIC				
CaPOPI_4757	Ca7	10351925	CATATATATAT/CATATATATATAT	TTGTGTGGTATCAAGCC CAA	AAGCTAAAGCCTCCTCG GTC	60.0	663	DRR	Ca_12795			Cupin 2, conserved barrel
CaPOPI_4758	Ca7	10380474	TAAAAA/TAAAAA	TGATTCTGGATGTCGTT TTGG	GCAGAACTTGGCTGGTT TGA	60.9	646	INTERGENIC				
CaPOPI_4759	Ca7	10393062	ATTT/ATTTT	TCCTCCATGTCAACCTC CTC	CGTTGCCCTCTTTTGGT ATC	60.0	653	INTERGENIC				
CaPOPI_4760	Ca7	10395585	GGA/G	TGGGTTTGACGAAAGGA GAG	CTGGATCGTGGGACTCC TAA	60.2	559	INTERGENIC				
CaPOPI_4761	Ca7	10396287	TAAA/TAAAA	TGACAAATAAGCTAACG GTGC	TCGAGGTCAATTTTACC ATCAAT	58.0	413	INTERGENIC				
CaPOPI_4762	Ca7	10405924	TC/TCC	ATTGCTGGTTGGCAAGG TAG	CCATAATCACATTGCGG GAT	60.1	669	INTRON	Ca_12799	T		Recoverin
CaPOPI_4763	Ca7	10415974	T/TTATA	GACATTGACATATGGAG GCG	TGCTTCTGCCCTTTTCT GTT	59.0	743	INTERGENIC				
CaPOPI_4764	Ca7	10423937	ATTT/ATTTT	TTCATTGATGCTTGTG ACC	GAGGTGAAGCCTCCATG TGT	59.7	607	INTERGENIC				
CaPOPI_4765	Ca7	10434123	AGTTTG/A	TACAACTTTTGAATGG GCA	ACCCTCTCCCTAGATGG GAA	60.1	783	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4766	Ca7	10447170	GTA/GTATA	AGGATTTATTGTGCCG TCA	TGCCCTTGAAGTGTG GTT	60.3	679	INTERGENIC				
CaPOPI_4767	Ca7	10449940	AA/AAGA	TTGACTTCACAGGTTCA AACAA	CTCCCTCGTGAATGGTG ATT	58.3	664	INTERGENIC				
CaPOPI_4768	Ca7	10459620	TA/T	GATAATGGACCCGCGAC TTA	CGCCATTGAATGACGT ATG	59.9	680	DRR	Ca_12806	T	WRKY	Protein kinase, catalytic domain
CaPOPI_4769	Ca7	10464523	CAAA/CAAAA	ATTCGGAACAACTGCAA TCC	GCTGAAGCTGCTCTTGT GTG	59.9	879	DRR	Ca_12807			
CaPOPI_4770	Ca7	10471583	GAA/GAATCGCTTTTAAAA	ATCTCGGATGGGTTTCT TCA	TTTCATCTCTTCCACTCA ACACA	59.5	228	INTERGENIC				
CaPOPI_4771	Ca7	10473226	TA/TAA	GGTAACTCCACCGAA ACA	TCCCAAGTCTTTGATTT GC	59.8	648	DRR	Ca_12809	R		Endoribonuclease XendoU
CaPOPI_4772	Ca7	10482051	TTCTCTCT/TTCTCT	CAAGAGGTAGCAGGCAC ACA	TTATGGCTCCGGGTAGA CAG	60.0	383	INTRON	Ca_12810		SRS	Protein of unknown function DUF702
CaPOPI_4773	Ca7	10490031	TC/T	AGAGTTTAAAGTTAATTT TTACGGTTG	TATGCCTCCAATAGGC CAG	57.1	687	INTERGENIC				
CaPOPI_4774	Ca7	10515194	ATTTTTTT/ATTTTTTTT	TGAAGGGTTATCAAGAA ATTTGG	TTGCTCCCTTAAATGAC CG	59.4	626	INTERGENIC				
CaPOPI_4775	Ca7	10517966	TTATATATATATATAT/TTATATATATATA T	AGCATTGTCATGCCTAG AACCC	ACAGGTAGGTCAGGGTG CAG	59.2	382	INTERGENIC				
CaPOPI_4776	Ca7	10552099	CAA/CAAA	GCAGCTTCACCCAAAA ATA	AAACGGGGTTGTTTCATC AAA	60.1	139	INTERGENIC				
CaPOPI_4777	Ca7	10557993	A/ACAC	GCGGCTAAATCAGGTCC ATA	AAGAAAAAGGCGACAGG ACA	60.1	685	DRR	Ca_12813	O		Peptidase S16, Lon protease, C-terminal
CaPOPI_4778	Ca7	10568493	TTATATATATATATATATATATATATATA T/TTATATATATATATATATATATAT	ACGATGGAGGCCAAAGT ATG	AAAATAAGGCATGGTGT TGGA	60.0	487	INTERGENIC				
CaPOPI_4779	Ca7	10572777	TCTAC/T	TCAAAATGTGACCAGGT GAAAC	CCTGGCCCAACTTGTCATAC	59.9	650	INTERGENIC				
CaPOPI_4780	Ca7	10579803	ATT/AT	TGACATTTATGCCTCACT AGCC	AATGCTTGTGGGTCTGT GGT	59.3	489	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4781	Ca7	10591717	TAAA/TAAAA	TCTGCTCCAATTAATG GTGTTT	CACCGTTCCTTCTGAC AGT	59.9	764	INTERGENIC				
CaPOPI_4782	Ca7	10607434	GAAA/GAA	TATATGGAGACCCGTGC CTT	CTCCATTGCTGTTGCTT TGA	59.4	526	INTRON	Ca_12815	O		Peptidase S16, Lon protease, C-terminal
CaPOPI_4783	Ca7	10613236	CTTT/CTT	TCCCTCTGAGCTGTATG CCT	GGCAACAAGGTCATCCT CAT	60.0	649	INTRON	Ca_12815	O		Peptidase S16, Lon protease, C-terminal
CaPOPI_4784	Ca7	10620555	CATG/CATGATG	GCAACTGCATCATCTTG CTC	TACCCCTGATTTCCGTC AAA	59.6	604	DRR	Ca_12815	O		Peptidase S16, Lon protease, C-terminal
CaPOPI_4785	Ca7	10631442	TTGCAACATGCAACAT/TTGCAACAT	AGAGAGATATGCCTGGC GAA	CTTCAGCAAGGGGAAAA CAA	59.9	136	INTRON	Ca_12818	U	Trihelix	Ras GTPase
CaPOPI_4786	Ca7	10672753	TTAT/TT	TGGTGTGAGATGGGAA TGA	GGATACAAATGTTGGCC CAT	59.9	583	DRR	Ca_12824		NF-YB	Protein of unknown function DUF248, methyltransferase putative
CaPOPI_4787	Ca7	10672818	TCC/TC	TGGTGTGAGATGGGAA TGA	GGATACAAATGTTGGCC CAT	59.9	583	DRR	Ca_12824		NF-YB	Protein of unknown function DUF248, methyltransferase putative
CaPOPI_4788	Ca7	10676593	TGATCGAT/TGATCGATCGAT	AAAACCGGAGCAACAAT TAAGA	ACCCGGGAAAAGAGTTT TGT	60.0	557	INTERGENIC				
CaPOPI_4789	Ca7	10680712	ATTTTT/ATTTTTTT	TGGTGGAGGAAGAGGA CGTA	TTCATGGTTCACACATT GGC	60.6	497	INTERGENIC				
CaPOPI_4790	Ca7	10681107	GTAT/GTATATAT	TGGTGGAGGAAGAGGA CGTA	TTCCCTCGGTCACAAAC ATT	60.6	801	INTERGENIC				
CaPOPI_4791	Ca7	10694557	TAAAA/TAA	TGTGGATTCAACATCG CAA	TGCCAAAATTTAAAGGA CGAA	61.1	582	DRR	Ca_12826	K	MYB	SANT domain, DNA binding
CaPOPI_4792	Ca7	10718905	T/TC	ATTGTTCTGGGCTGCAAA TAG	AGGAATCTTTTGGGGAA GGA	60.1	399	INTRON	Ca_12827			Tetraspanin
CaPOPI_4793	Ca7	10731505	AAG/AAGAG	CAGAACCTGTCGGGATT CAT	TCGGCAACTTCAATTC CTC	59.9	417	DRR	Ca_12828	U	M-type	Inositol polyphosphate related phosphatase
CaPOPI_4794	Ca7	10732290	A/ATT	GCAGTGAAAGAAGAAAT CTCCG	AGAAGTACCCGCGAAGA TGA	60.4	482	INTERGENIC				
CaPOPI_4795	Ca7	10741982	ATCAATTT/AT	TTTGAAAGATGAATTCG GGG	AAAATACATCCCGCGAT CCT	59.9	855	DRR	Ca_12829	FE		Phosphoribosyltransferase

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CaPOPI_4796	Ca7	10838599	GAAAAA/GAAAA	TGGAAGGACGAGGAAAGTTG	CTTGAAGTGCTCCTTGAGACAA	60.2	453	INTERGENIC				
CaPOPI_4797	Ca7	10839999	CTTTT/CTTTT	CACATTTGCCCATGAAATTTG	ACAATTTGGAACTTTGCG	59.8	395	INTERGENIC				
CaPOPI_4798	Ca7	10896204	GTTT/GTTT	TCCGATTTATGCTTTGTTG	TTTAGGCTAATTGATCCGCTG	58.8	121	INTERGENIC				
CaPOPI_4799	Ca7	10899870	ATCT/AT	TTCCAGTGTCATCCATTCA	ATATGGAGCTGGTGGTGAG	59.9	594	INTERGENIC				
CaPOPI_4800	Ca7	10904696	AT/A	CAGGTGCATCCTCTCCAAT	TGCAGCATCGACACTTTAGG	60.1	333	DRR	Ca_12847			Ferredoxin
CaPOPI_4801	Ca7	10905837	ATTT/ATT	TGCACGGCCAACAAATATAA	ACTCCAGCTAGCCCAAGTCA	60.0	383	INTRON	Ca_12847			Ferredoxin
CaPOPI_4802	Ca7	10910160	GATATATATATATAT/GATATATATAT	AGCGCAAAACATTGACAT	TTCTTGCTTCTTGCAATTTT	59.2	779	INTERGENIC				
CaPOPI_4803	Ca7	10925493	CATATTTATCCAATATTTA/CATATTTA	TTGCATGATTGATTGTTGGG	CCGGCATAGAGATCGAAGAC	60.3	517	INTERGENIC				
CaPOPI_4804	Ca7	10937736	TCAACACAACACA/TCAACACA	TGCCACGTCAACTGATGTTT	CAAAGATCTCGCAGCAATGA	60.2	681	INTERGENIC				
CaPOPI_4805	Ca7	10938162	TAA/TAAAA	AACACAACACACGGGTAGCA	TATTCATCCCTCCGACAAC	60.1	661	INTERGENIC				
CaPOPI_4806	Ca7	11034555	GTGTA/GTGATGTA	TGTCAATGTCAACCATGCT	TCAAAAGGCCACCTCTTCAT	60.0	270	INTERGENIC				
CaPOPI_4807	Ca7	11065887	AC/ACTTAACTTC	ACCGTGGCTAGACAAAGTGG	TTGGGGTTGAGACACTGACA	60.2	768	INTRON	Ca_09379		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_4808	Ca7	11070487	AATATATATATATATATATAT/AATATATATATATAT	GGCCTGCCAATTCTGTTTAT	GTTTCGATTCTGGGGATCTA	59.0	290	INTERGENIC				
CaPOPI_4809	Ca7	11074298	TAAATTAATAATTAATAAATTAATAA	TACCGATTGCCATCCTTAGC	TTTTCAAGTAGGGTACCTCAATTTTT	60.1	831	INTERGENIC				
CaPOPI_4810	Ca7	11075792	ATATTACTATTA/ATATTA	ATGCAAAAGTCGGTCATCCT	GATTTGGAATGAGTGGGT	59.6	544	INTERGENIC				

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CaPOPI_4811	Ca7	11079201	CAAA/CAAAA	AAAGAAGGGTTGAGAGGGA	GAGCAGAAAGGTGGAAGTGC	60.0	553	DRR	Ca_09378		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_4812	Ca7	11092070	CATAT/CATATAT	CGTCCGGTCAAAATGAAGTT	CCGAACCCAATTTCCCTAAT	60.0	497	INTERGENIC				
CaPOPI_4813	Ca7	11118723	CAAA/CAAAA	TGCATCCAAGAACACCGTAA	AATGTCGTTTTGGTTCCAGC	60.1	774	INTERGENIC				
CaPOPI_4814	Ca7	11120511	TA/TAATTTAAA	CCACTCACTGCTTGCTTATCC	TCGGGAAATGTTGTTGTCA	59.9	913	INTERGENIC				
CaPOPI_4815	Ca7	11122293	CTTTTT/CTTTTTT	GTAGCCCACTCAATTGGCAT	TTTTTGCAATCCAGCTTCT	60.0	634	INTERGENIC				
CaPOPI_4816	Ca7	11154403	AACCGCA/AACCGCACCGCA	ATCGACCGAAATCAATCCA	AAAGAGTGAGCCGACCATTG	60.3	317	INTERGENIC				
CaPOPI_4817	Ca7	11166262	ATTTTTTTTT/ATTTTTTTTTTTTT	TTCCAATTCAATGGCATGAG	CATTGACACGCCAAACTGTC	59.5	830	INTERGENIC				
CaPOPI_4818	Ca7	11180939	TCCGG/T	TTCCAAACCGAGATGAATCC	CCCCTCATTTACACAAATCC	59.9	659	INTERGENIC				
CaPOPI_4819	Ca7	11205713	AA/AAATA	ACCATGTCACTCCCCATGTT	TTCCATTGTCTCTGCTGCC	60.1	395	INTERGENIC				
CaPOPI_4820	Ca7	11224360	TGATCTTAA/TGATCTTAAGATCTTAA	AACCAAAGTGTGTGCAGCAG	AGGGTGGCCTCCAGTAGTTT	59.9	534	INTRON	Ca_09369			
CaPOPI_4821	Ca7	11229799	TATCAATGTTTCTAAT/TAT	TCCGCACAAAAGACAGACAA	CCTGGTGACAGTTTGATCTT	60.4	473	INTERGENIC				
CaPOPI_4822	Ca7	11230451	GAGAAA/GA	CAGAGCCGGAACACAAAGAT	AGCCCTCCCATGTTTTAAT	60.3	953	INTERGENIC				
CaPOPI_4823	Ca7	11246939	GAAAAA/GAAAAAA	ATTTACGCCGCTGATTTCAA	AATTGCATACCACCGGAATAA	60.6	747	INTERGENIC				
CaPOPI_4824	Ca7	11268569	CATATATATATAT/CATATATATATATAT	TTTTAACTCGTCGGGTACAC	TCTCCCAAATCTTACCCCTCC	60.0	486	DRR	Ca_09366			Methionine biosynthesis MetW
CaPOPI_4825	Ca7	11272809	TAAA/TAAATAAAA	ACGTCTCGTGAACITGCTT	ACGGAGTTCGTAGTGCGTTT	59.9	516	INTERGENIC				

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CaPOPI_4826	Ca7	11286406	GAAATAAATAAATAAATAAA/GAAATAAATAAATAAATAAATAA	GTAGCAATCCCCACCAAGAA	TCATGCAAGCAAGAAGATGG	59.9	460	INTRON	Ca_09365		AP2	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_4827	Ca7	11313507	CTTTTT/CTTTTT	TGGACAAATATTGCATCATGG	CCTTCACCTGTTTAAGGAAAATATAA	59.2	593	INTERGENIC				
CaPOPI_4828	Ca7	11343583	ATTCACCTCACTTC/ATTCACCTC	TGTTCCATACACCCACCTT	TGCAGTTCAACATTGTGTCC	60.1	531	DRR	Ca_09360			VQ
CaPOPI_4829	Ca7	11345461	CTTTTTTTTT/CTTTTTTTT	CCACTGGTGCTTCTTCAT	GATGCTCCAAATTCTTCCA	60.1	401	INTERGENIC				
CaPOPI_4830	Ca7	11375539	TA/T	CAGATTGTTCGGAAGGT	GGTCGACACATCTCACCTT	60.0	759	INTERGENIC				
CaPOPI_4831	Ca7	11397404	GTTTTTTTT/GTTTTTTTTT	TCAAGGTGCGTTTTTCTT	CAACGTTAAGAATCGATGGGA	59.7	670	DRR	Ca_09356	C		NADH dehydrogenase ubiquinone Fe-S protein 4, mitochondrial
CaPOPI_4832	Ca7	11413494	TA/TAA	AAGTCCCCTGCAAATACCAA	GGAAGCATGGAAGGAAATGA	59.4	598	DRR	Ca_09355		MYB_related	SANT domain, DNA binding
CaPOPI_4833	Ca7	11428616	GAAAA/GAAAA	CCATGCAACTTCGACTTCAA	GGTGGTCAATGACACAGTGC	59.8	658	DRR	Ca_09352		GRAS	Transcription factor GRAS
CaPOPI_4834	Ca7	11430402	CTTGTTGTTGTTGTTG/CTTGTTGTGTTGTTG	TCTTGGGGAGGTGAGAAAGA	CTCAACTCCACCACCACCTT	59.8	308	CDS (large-effect mutations)	Ca_09352		GRAS	Transcription factor GRAS
CaPOPI_4835	Ca7	11438197	ATTT/ATT	CTGTGCGTCATTTCTTCCA	TTGGCAATGTTCCCAAGAAT	59.8	802	INTERGENIC				
CaPOPI_4836	Ca7	11441772	ACTCT/ACT	GTGGAGGGCATTACATTTT	TTCATGTTTAATGCGAAGTGAGA	59.8	265	INTERGENIC				
CaPOPI_4837	Ca7	11481982	ATT/AT	GGAGGGACGATGTTACTCCA	TCCACCAATTGCGTTGATC	59.9	257	INTERGENIC				
CaPOPI_4838	Ca7	11487806	T/TG	TTGATGTTGAAGGGGGAAG	GTCATTGGATATGGCCTCGT	59.9	631	INTERGENIC				
CaPOPI_4839	Ca7	11494762	CCTT/CCTTCTT	AGGAGCAGTTTGTGAGGTGC	GAAAGGTGACTTCCTCAGCG	60.5	223	DRR	Ca_09346			GCN5-related N-acetyltransferase (GNAT) domain
CaPOPI_4840	Ca7	11511673	C/CCCGCAAACCTT	TGACCCCTAAGAACCCACAG	GGATGGGGTAACATTGTCC	60.0	514	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4841	Ca7	11517081	CTATA/CTA	GGTGACGTACACGACCTCAA	GGATGAGGGAACAATGTGCT	59.8	487	INTERGENIC				
CaPOPI_4842	Ca7	11518406	TTTAAAGACACATATTAAAGA/TTTAAAGA	CCTCAAGTGTGGCGTAGACA	ACGTGGCATGTGTTGTGAAT	59.9	796	INTERGENIC				
CaPOPI_4843	Ca7	11542682	ATTTTTTTTT/ATTTTTTT	AACTGCCATGGAGCTAGGAA	TTTTTGGTTTGAGTATTATGCGA	59.8	737	INTERGENIC				
CaPOPI_4844	Ca7	11543117	ATGTGTGTGT/ATGTGTGTGTGT	TCGCATAATACTCAAACCAAAAA	TTCAATCTCCGAGTCCGTTC	58.7	432	INTERGENIC				
CaPOPI_4845	Ca7	11545129	CTTAA/CTTAAGAAAGTAAGGCATTAA	CCAAACGTTTATAAGCATGCAA	TGTGAAAGGGAAGGAGATGG	60.0	311	INTERGENIC				
CaPOPI_4846	Ca7	11580871	GTTTTT/GTTTTTT	TGGTGGGCCACAGTTATGTA	GCATGTCCAAAATCATTCCC	59.8	694	INTERGENIC				
CaPOPI_4847	Ca7	11585943	CTTTT/CTTTTT	CTTAACCCACACGTGCC TTT	ATGCGAATTGAAGACGG AAC	60.0	212	INTERGENIC				
CaPOPI_4848	Ca7	11600742	CAT/CATAT	AGCTTCGCGCATGAATAGAA	ATCGACCATCTTCATGCTCA	59.9	734	INTERGENIC				
CaPOPI_4849	Ca7	11624553	TATTAATTAAT/TATTAAT	AGACTCCTTTTGGGGTTTCC	GCAAGACATTGACAAAACTTTCA	59.4	303	INTERGENIC				
CaPOPI_4850	Ca7	11678977	TTTTATT/TTTTATTATTTATT	CCCAGCTCATTTCAAGAGAA	AATTGCGTGAGAGCTTTTGG	58.0	732	INTERGENIC				
CaPOPI_4851	Ca7	11691921	TA/TAA	GTGGAAAAGGAAGTCGCAAG	GTTGGGGATTTGGGGTTTTA	59.9	654	INTERGENIC				
CaPOPI_4852	Ca7	11692218	AA/AATA	GGATGCACATTAGAGCGACA	GCTGAAGACACGTATGCGAA	59.8	759	INTERGENIC				
CaPOPI_4853	Ca7	11714431	ATTTT/ATTT	AACGATGAGATGGCAAAAGG	GGCTTTGGTGCTAAGTCAG	60.1	598	INTERGENIC				
CaPOPI_4854	Ca7	11729720	CAAAAA/CAAAAAA	AACAAATCTTGCCATGAG	GGCGTGTGCTTGTAAGAGT	59.9	711	INTRON	Ca_09324	O	NAC	Peptidase A1
CaPOPI_4855	Ca7	11732346	TC/TCC	TTTTCAGGCCAGACCAAACT	GGTTCTTGATCCCATGCCAGT	59.7	324	DRR	Ca_09323		ERF	Frigida-like

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4856	Ca7	11751654	CTTT/CTT	CATGTTGACCACTCCAATG	AGCCAAATTGGTTTCCACAT	59.8	428	DRR	Ca_09321		C2H2	Zinc finger, C2H2-type
CaPOPI_4857	Ca7	11756608	ATAT/ATATAATTAT	CTTTGGGACAGTCTGGTGGT	CAAGACGGACTAGTGGGATGA	60.0	476	INTERGENIC				
CaPOPI_4858	Ca7	11757918	ATTTT/ATTATTTTT	TTTCCCAAAATGCTGTTCTT	CTTCCGATTCTCCGTGTGAT	59.6	588	INTERGENIC				
CaPOPI_4859	Ca7	11757957	A/AG	TTTCCCAAAATGCTGTTCTT	CTTCCGATTCTCCGTGTGAT	59.6	588	INTERGENIC				
CaPOPI_4860	Ca7	11834363	GTATATATAT/GTATATATATAT	TGTTGCTGACGGACATTGAT	CATCCCCAATTTCTTTGACA	60.1	542	INTERGENIC				
CaPOPI_4861	Ca7	11884796	GAT/G	AAGGGAAAGACTCCCTTCA	AGGGCTGCATGAACAAATTC	60.0	566	INTRON	Ca_09310	P	C3H	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter
CaPOPI_4862	Ca7	11892192	TATTACTA/TATTACTAATATATAAATTA CTA	ATTAGGGAGAAACGGAGGGA	TTTTGTGCCCTAACACTTAGCA	59.9	441	INTERGENIC				
CaPOPI_4863	Ca7	11902508	TAAAAA/TAAAAA	CCATTGCACAAGTCCTCAAA	CCATGCGGATTGAAAACTT	59.7	757	INTERGENIC				
CaPOPI_4864	Ca7	11911166	AAGA/AAGAGA	CAAATACAATGGCAGCTGGA	TGCAGGAGCATATGACC AAC	59.7	305	INTERGENIC				
CaPOPI_4865	Ca7	11960847	ATAT/ATGTATGGATGTAT	TGATGGCACATCATTGTCCT	AACCCCATCCCCAAAT AAG	59.9	221	INTERGENIC				
CaPOPI_4866	Ca7	11961138	CAAA/CAA	AGAGCCCCACTGGGTTACTT	ATTGAATAGGGAAGGGGTGG	60.0	645	INTERGENIC				
CaPOPI_4867	Ca7	11979039	AAATAATAATAATAAT/AAATAATAA TAAT	TCACTTGCCCAATCATTCA	CATGCCTAGGATGAAGGAAGA	60.0	558	INTERGENIC				
CaPOPI_4868	Ca7	11990830	TATAAAATAAA/TATAAAATAAAATAAA	TGATCGCATGAATAAAATGGTT	TCACTTGCCATGTGTACGCT	59.3	193	INTERGENIC				
CaPOPI_4869	Ca7	11990906	CTA/CTATATA	TGATCGCATGAATAAAATGGTT	TCACTTGCCATGTGTACGCT	59.3	193	INTERGENIC				
CaPOPI_4870	Ca7	12006713	AT/ATGT	CCAATCAGTGGCAGAACTT	TGGCTCTACAATGGATGCAG	60.1	720	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4871	Ca7	12024461	AATATATATATATA/AATATATATATATATA	TGGTTCACAAATCAGATGGG	GATGCATCCCGATGAAA	59.3	260	DRR	Ca_09302		WRKY	DNA-binding WRKY
CaPOPI_4872	Ca7	12024656	TGAAGAAGAAGAAGAAGAA/TGAAGAA GAAGAAGAA	TGGTTCACAAATCAGATGGG	CACACTAATAAGTGCTCTAAGGACCA	59.3	746	INTERGENIC				
CaPOPI_4873	Ca7	12092590	GAAAAAAGATAAA/GAAAAAAGATAA AAAAAAGATAAA	AAATTGGAGTTGCCAAACAGA	TCGTCTTAAATCCACAAACCC	59.6	757	INTERGENIC				
CaPOPI_4874	Ca7	12106813	T/TATACCCAAAAA	ATTGGGAGGAGATTGTGTC	ATTGGAGATCAGCATTTGCC	59.9	567	INTERGENIC				
CaPOPI_4875	Ca7	12125579	C/CG	AGATGGAGGCAGAGGAAAT	AAGAAATGCAGTTGGA	60.0	689	DRR	Ca_09295		AP2	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_4876	Ca7	12138547	TG/T	TGAGTTGTGTCAAAGGCAGAA	TGAAGCAAATTCGTCAATCAA	59.5	710	INTERGENIC				
CaPOPI_4877	Ca7	12143576	ATTTTTTT/ATTTTTTTTT	AAACCAATATTTTCGGCC	TTTGTTTACAAGGTATTC	60.0	454	INTERGENIC				
CaPOPI_4878	Ca7	12145921	TTTATT/TTT	TTTCAATCCACACAGAAA	TCCTTGGGTCAAACTT	59.2	646	INTERGENIC				
CaPOPI_4879	Ca7	12210192	TTGTGTGTGTGTGT/TTGTGTGTGTGTGTGTGT	TGAAAATATGTGCTCCGTCT	ACGAAGGGCAACAACAA	59.6	823	INTRON	Ca_09287	Q		O-methyltransferase, family 3
CaPOPI_4880	Ca7	12212766	ATTTTT/ATTTTTTT	GGGCAATTGGAAATCAGAA	TCGCTTTTGATGATGACACC	59.9	719	INTERGENIC				
CaPOPI_4881	Ca7	12212967	TTAAACCA/T	ATCACCATCGTCCCTAAA	CAAAGGCTTGGACAAAGAGC	57.9	754	INTERGENIC				
CaPOPI_4882	Ca7	12227697	ATT/AT	TCTTGTAGTCAACGAATCTTCATCA	GTCAACGAGAATTGTTGCCA	60.2	431	INTERGENIC				
CaPOPI_4883	Ca7	12234527	AA/AATA	AGACGACGAACAACACAACG	ATTTTCGATTTCCGAGGACC	59.8	353	INTERGENIC				
CaPOPI_4884	Ca7	12266841	CATT/CATTGAAAAGTATATT	GTTGCAACATCGGAGGTTT	AAAAAGCGGGGATTTAGAA	60.0	508	INTERGENIC				
CaPOPI_4885	Ca7	12280015	TAAAA/TAAAAA	TGGTTTTAATGTGTTGCGGA	TTTGGGATAATTTCAACCCTTTG	60.0	501	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4886	Ca7	12283477	C/CGACACATAATT	ATAGCCCCTCGTACAA CCC	GGGTCTATCTCGAATTG GCA	60.2	943	INTERGENIC				
CaPOPI_4887	Ca7	12285646	TTCTC/T	TTGAAACCTCATTTGGG AGG	CTTCGGTTTGTGGTGGT CTT	59.9	269	INTERGENIC				
CaPOPI_4888	Ca7	12291131	TCC/TCCC	TAAAGCCAACAACCACA CCA	GGCCCAATTATTTGCCT CTT	60.0	190	INTERGENIC				
CaPOPI_4889	Ca7	12300332	GTAATTCCTA/GTA	TTTTCATCCATCGGTCAT CA	TGGAAGGCCTTTTTATA GCAAC	59.9	665	INTERGENIC				
CaPOPI_4890	Ca7	12321093	GTT/GT	GAGCGAAAATGAAACGA AGC	GATGGGTTAGCCAGCTT TCA	60.0	854	INTRON	Ca_09281	R	G2-like	RNA recognition motif domain
CaPOPI_4891	Ca7	12332691	TCACAC/TCAC	CATGGGAGATCGATTGG GAC	CCTGCAACAAGTACCCG AAT	60.3	659	INTERGENIC				
CaPOPI_4892	Ca7	12339660	CAAA/CAAAA	AAATGTGGGTTGAGGGT CAG	GTGTCGTGTCTGGCTGA GAA	59.8	280	DRR	Ca_09278			
CaPOPI_4893	Ca7	12347854	CATATATATAT/CATATATATATAT	AATCATGCAACTACACC ACCA	AACGTCGTTCCAGACAC TCC	58.9	434	INTERGENIC				
CaPOPI_4894	Ca7	12348225	TA/T	TTTTGAAAAGGACGGGA TTG	GCCAAATGGTTTGTTC TCT	59.9	534	INTERGENIC				
CaPOPI_4895	Ca7	12361782	TAA/TAAA	GACAAAAATGATGCGGT CAA	GAAAACTTAGGCAACC CCC	59.5	300	INTERGENIC				
CaPOPI_4896	Ca7	12422509	GATGTATA/GATGTATATGTATA	TTCAAAAGCAAAAATTAT TTCCAA	TGTTGATGTGGTTTGCC ATT	59.1	464	INTERGENIC				
CaPOPI_4897	Ca7	12432563	GTTT/GTTTT	GCCATAGTTGGTGTGG CTT	CCAAAGCCTTTTCTGAA GCA	60.0	819	INTRON	Ca_09272			
CaPOPI_4898	Ca7	12477809	ATTT/ATTTT	AATAGTTGCAGTTGGT CGG	CGCAACACATAAGACAT GGG	60.0	849	INTRON	Ca_09269	Z		CTLH, C-terminal LisH motif
CaPOPI_4899	Ca7	12483012	T/TAAGGAG	GCGCAAACTGCAAGTC ATA	CCTTTTCGGACAGGAAA TCA	60.0	723	DRR	Ca_09268	R	bHLH	Pentatricopeptide repeat
CaPOPI_4900	Ca7	12489580	CG/C	CATGCTTCTCAGTCCC ATT	TTCTCCTTCAACGCACA CTG	60.1	748	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4901	Ca7	12495945	TA/T	GATTTCCAATCCCATTGC	AAAATGGAAGTGCCATGAGG	60.1	961	INTERGENIC				
CaPOPI_4902	Ca7	12506632	TTATCATATCATATCATATCA/TTATCATATCATATCA	AAGAAGCATGTTAGCCCCACG	GGACTGTGACCAGGGTC TGT	60.3	686	INTERGENIC				
CaPOPI_4903	Ca7	12520999	GAAA/GAAAA	AGCGCTCAAAATTGCA TCT	TGTGTGCGGTCATAAT TGG	60.0	377	DRR	Ca_09264			
CaPOPI_4904	Ca7	12524095	TG/T	TGAGATTGGAGGGATGA AGG	ATGCAAAAATTCATCGC AAA	60.0	334	INTERGENIC				
CaPOPI_4905	Ca7	12550642	TAATTAT/TAATTATGCAAGAATTAT	TTTTAGGCCCACAACTC CTG	ATTTGACCATCACCCCCA AAA	60.1	419	INTERGENIC				
CaPOPI_4906	Ca7	12583983	TC/T	GCCATTCCAAATGACGA CTT	GGAGCGTGTGTTTATG TCA	59.9	204	INTERGENIC				
CaPOPI_4907	Ca7	12585103	TATTTAATTTAAT/TATTTAAT	ACCCGTGCACATCAATT AAA	TCACCATACGTTTGTGT ACGG	58.9	762	INTERGENIC				
CaPOPI_4908	Ca7	12608444	GGTGTG/GGTG	ATGCATTGAAGGAAGGG AAA	TCCAAAATGTATGCCAC CAA	59.5	311	DRR	Ca_09260		SBP	Domain of unknown function DUF547
CaPOPI_4909	Ca7	12609027	TTATAT/TTAT	TTGGTGGCATACATTTT GGA	ACAAGCATGATAGAGGC AAAA	59.8	780	DRR	Ca_09260		SBP	Domain of unknown function DUF547
CaPOPI_4910	Ca7	12645517	TAAATTAATAATAATAA/TAAATTAATA ATTAATAATAATAA	TGGACCAAAGCAGAACACAG	GGAGGCAGTCATTAGTT GGG	59.9	500	INTERGENIC				
CaPOPI_4911	Ca7	12653885	TTTAATTAAT/TTTAAT	AAGTGTGTTGAAGATGA AGCGA	ATGCACTTGCACTGCCA TAA	59.9	400	INTERGENIC				
CaPOPI_4912	Ca7	12663192	AGGGG/AGGGGG	AAC TTCCCATCCTCTC AAC	GGAGCTAGCAGAAGCAG CAT	60.2	906	DRR	Ca_09255	T	FAR1	Protein kinase, catalytic domain
CaPOPI_4913	Ca7	12689465	AATGA/AA	GCACGTTGCAAGTCAGAGA	GTTGTGGTTTCGTCATGG TCA	60.2	496	INTRON	Ca_09253	G		Phosphoglycerate/bis phosphoglycerate mutase, active site
CaPOPI_4914	Ca7	12712927	AAAAGAA/AAAAGAAAGAGGAACAAAGAA	CAGGGGTTTTAGGATTT GGG	CTGTGTGTTGCTGGGTC CTA	60.5	610	INTERGENIC				
CaPOPI_4915	Ca7	12724633	AATATATATAT/AATATATATATAT	GTGCATTTTCCCATGTCTT	ACGAAATACGATGAAAG CCG	59.8	571	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database	
CaPOPI_4916	Ca7	12730150	TGAAGAG/TG	CGCAGCTGTCAATTTCT TCA	TTCGACGCAGATACTTG CAC	60.1	426	INTRON	Ca_09247			LBD	Lateral organ boundaries, LOB
CaPOPI_4917	Ca7	12745134	AAACTT/AAACTTGAATTATATAACTT	TTTGGAACACAACAAC TCCA	GTAGGGTTAAAGGGGAC CGA	59.1	206	INTERGENIC					
CaPOPI_4918	Ca7	12762980	ATATTATT/ATATT	CGTTGTGTTTTGCAATG ACC	GTTCACCATTGGACCGA GTT	60.0	516	DRR	Ca_09243	H			Tetrapyrrole methylase
CaPOPI_4919	Ca7	12773412	GT/GTT	TTGGAAGTGTGAAAGGT GGG	TTGTGTTGACTGGTTTG GGA	60.1	747	INTRON	Ca_09242			LBD	Disease resistance protein
CaPOPI_4920	Ca7	12808768	AATATATATATATATATATATAT/AATATA TATATATATATATAT	AATCATGAGCCCAACGT TTC	GGCGGCATATACCGTCA TAA	59.9	874	DRR	Ca_09239	Q			Multicopper oxidase, type 1
CaPOPI_4921	Ca7	12810410	A/AC	GGTAGATCGGCTCAAGA ACG	AAAGTGTTCCACAAC GGC	59.8	391	DRR	Ca_09238			Dof	Zinc finger, Dof-type
CaPOPI_4922	Ca7	12810847	CATATATATATATATATATATA/CATATA TATATATATATATATATA	GCCGTTTGTGGAACAC TTT	ATGCTGCAAGTTTCGAT TGT	60.0	509	DRR	Ca_09238			Dof	Zinc finger, Dof-type
CaPOPI_4923	Ca7	12844900	CTTATTTTTATTTTTATTTTTATTTTTAT TTTTATTTTTATTTTTATTTTA/CTTATT TTTATTTTTATTTTTATTTTTATTTTTATT TTTATTTTTATTTTTATTTTTA	TGCTCTTCAAAGTAATT GTTCC	AGATCGACTGTCCCAA ATG	57.6	458	INTRON	Ca_09236				Alpha/beta hydrolase fold-1
CaPOPI_4924	Ca7	12848385	C/CTAG	AGGTTCCCAACGGGAAT ATC	TGCTCGAATCTTATGTC CCC	60.0	367	DRR	Ca_09235				
CaPOPI_4925	Ca7	12850002	AATTTACAACAT/A	CGTATCTGCAGCTCAGC AAG	ACTCTGACTTGTCGGT TGG	59.9	622	INTRON	Ca_09235				
CaPOPI_4926	Ca7	12853842	GTTT/GTTTT	CCAAACGTGGAAGTGGA ACT	GCTTGGTCGACGAATCT CTC	60.0	589	INTRON	Ca_09235				
CaPOPI_4927	Ca7	12858631	CT/CTAT	AATGAAGTAGGGTGGCG ATG	TGAGAGAGAGAGAAAGT AGCACCA	60.0	487	INTERGENIC					
CaPOPI_4928	Ca7	12865284	TTAA/T	TGACACTCATTGTGTCA CGG	CGGACAGATTGTTGTG TTG	59.1	177	INTERGENIC					
CaPOPI_4929	Ca7	12897407	ACCCC/ACCCCC	TGATGTTTTTCCATCCAG CA	ACCTCACAAATGCACTC GAA	60.0	707	DRR	Ca_09230	O			Peptidase S9, prolyl oligopeptidase, catalytic domain
CaPOPI_4930	Ca7	12921443	T/TAG	TCAGAGTTCTCTCCACC GCT	AGGGAGGTGTTGGTGTG GAG	60.1	526	DRR	Ca_09228				

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CaPOPI_4931	Ca7	12923877	AC/A	GAAGTGTAGCCTTTCAG GCG	CCTGGACTCGACAAAAG GAA	60.0	556	INTERGENIC				
CaPOPI_4932	Ca7	13032221	TG/T	GGCAGTACAAGCATCAA GCA	AACGCTATCACACCA CGA	60.0	480	INTERGENIC				
CaPOPI_4933	Ca7	13032927	GAAAAA/GAAAA	TTGAATGCAACCTTGGT GTC	GTTTGGAGACCTGTGCC CTA	59.5	602	INTERGENIC				
CaPOPI_4934	Ca7	13033158	AAAA/AAAAGAAA	TAGGGCACAGGTCTCCA AAC	GAATATGTCGAGTCGCG CTT	60.1	145	INTERGENIC				
CaPOPI_4935	Ca7	13037732	TA/TAA	AAATGTGCTGATCGGGT TTC	GGCCGATACGATAATGG GTA	59.9	715	INTERGENIC				
CaPOPI_4936	Ca7	13060580	TCGTGACC/TCGTGACCGTGACC	CCCTTCACGTGAGGATT GTT	CCAGTTTTGCCACCCTA CAT	60.0	767	DRR	Ca_09222		MYB_rela ted	BTB/POZ-like
CaPOPI_4937	Ca7	13066626	CAGTTAGTTAGTTAGTT/CAGTTAGTTA GTT	GGAAAGGTGCACACAAG TGA	GAGACCGAATCCGACTT GAA	59.7	442	INTERGENIC				
CaPOPI_4938	Ca7	13071654	GAAGTAAG/GAAG	ACTCGCGATTCTCAAC CTT	TTTGTGGCTAGAGGCTA TGACA	59.7	445	DRR	Ca_09221			Cold acclimation WCOR413
CaPOPI_4939	Ca7	13178303	TCAT/TCATATCAAACAT	GGATCTGCTGCTGTTTC ACA	AAAACACTGGACCCACC ATC	60.0	338	INTRON	Ca_16019			Uncharacterised protein family UPF0497, trans- membrane plant
CaPOPI_4940	Ca7	13188851	TTAAATAAA/TTAAATAAATAAA	CTGCAGCAAAAACAGGA CAA	TGCATCGTACCGTCGTG TAT	60.0	424	INTERGENIC				
CaPOPI_4941	Ca7	13193883	CG/CGG	TTCGACATACTAAATTAG CCTCACA	TCTTAAACCGAGACGAA CAAAA	59.3	412	INTERGENIC				
CaPOPI_4942	Ca7	13283430	TAAAAAAA/TAAAAAAA	ACATCAGGCTGTCTGGG AAT	CCATATTCATCCATCGC CAC	59.5	747	INTERGENIC				
CaPOPI_4943	Ca7	13285824	AAAAACAAT/AAAAACAATTCTCAAAACA AT	AACGACGGTCTTGTAAGCAA	CACAAGACCCGAAAAAG GAA	59.8	628	INTERGENIC				
CaPOPI_4944	Ca7	13299994	GC/G	CCCTAAGATTTTGAGAC GCG	GAAGGTGGGCTTGACTA TGC	60.0	213	INTERGENIC				
CaPOPI_4945	Ca7	13306728	AAGAGAGA/AAGAGA	TGTGTTTGGATAAGAGG GAAAAA	TTTCTGGACCATTGCAG TTATG	59.9	185	INTERGENIC				

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CaPOPI_4946	Ca7	13313904	TAAAA/TAAAAA	ACCCTGGCATTATGAA CCA	TCGCATTTGATTCTTTG GA	60.2	694	INTRON	Ca_16026	K	TALE	Homeobox
CaPOPI_4947	Ca7	13321942	TTT/TTTGTT	CTTTGCTCTTCAACC TCC	GTTGGTTCCCAAAGGAC GTA	59.8	774	INTERGENIC				
CaPOPI_4948	Ca7	13381675	GTTTTT/GTTTTTT	AAGCCATCAAGCGAACC TTA	CTCTAGACACGCGGTGA ACA	59.8	310	DRR	Ca_16030		HD-ZIP	Pectate lyase/Amb allergen
CaPOPI_4949	Ca7	13456910	GA/G	ATTGGACAACCGGTAA AAT	CCCATGAAATCACAATAA AATCC	59.3	630	INTERGENIC				
CaPOPI_4950	Ca7	13467995	TA/TAAA	TGCACCTGGAAAATACA CCG	TTCTTATTCTCCACCGA CG	59.6	545	DRR	Ca_16035	I		GNS1/SUR4 membrane protein
CaPOPI_4951	Ca7	13468281	TA/TAATGA	AACAAGCGCGATGTTT TTC	TTCTTATTCTCCACCGA CG	60.3	268	DRR	Ca_16035	I		GNS1/SUR4 membrane protein
CaPOPI_4952	Ca7	13479302	AGA/AGAGGA	AATGCACATACCAGCAT CCA	TAGGGCCAATGAAAATG AGG	60.0	505	INTERGENIC				
CaPOPI_4953	Ca7	13495702	ATAA/ATAAGTAA	TGGACATTTTCGTAAA GGGA	CTCACTGAGGTGGGTT GGT	59.4	581	INTERGENIC				
CaPOPI_4954	Ca7	13497952	CTATATA/CTATATATA	TTGGCATTCGGGTTCT ATC	GCCTACTAGACGCCACC ATC	59.9	552	INTERGENIC				
CaPOPI_4955	Ca7	13500441	TAAAAAAA/TAAAAA	GGGACAAGCATTGCTCA CTT	TGTCATTTCTGGCGTAG TGTG	60.3	994	INTERGENIC				
CaPOPI_4956	Ca7	13522224	TTATATATATATATAT/TTATATATATA TATATATAT	AAGGGTTTGTGGTTTTG CAG	ACCACCACACTCCCTCT CAC	60.0	314	INTERGENIC				
CaPOPI_4957	Ca7	13599607	TCAATTAATA/T	TGTGGTGTATGGAGGT TTCC	ATGTGGTGTGCGAATA ACA	59.7	127	INTERGENIC				
CaPOPI_4958	Ca7	13622541	GCCCC/GCCC	TTTCTTCATCCGCGTTAT CC	CCGGGATGTTTCTCTTG GTA	60.0	661	INTERGENIC				
CaPOPI_4959	Ca7	13655144	TAAAAAAA/TAAAAA	CGAGACATTGAGGTAAC ACGG	TTGGCATCGTTGTGTG ATT	60.6	597	DRR	Ca_16047	DR		Leucine-rich repeat
CaPOPI_4960	Ca7	13656688	GTAATACT/GTAATACTAATACT	GGAAGAGGTGGCAGAG ACAG	ATGATCCATCAGCGTCA TCA	60.0	688	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4961	Ca7	13676108	ATTTT/ATTT	AAC TTTCAGGAAGCAGC CAA	TTTTGCCCGTACATTGT GA	60.0	651	INTRON	Ca_16049			Protein of unknown function DUF81
CaPOPI_4962	Ca7	13684363	AAGA/AA	TAGCATTTCCATTGTG GCA	TGAGTTTGTTGTTTCTC AAATTCT	60.1	485	INTERGENIC				
CaPOPI_4963	Ca7	13684569	TA/T	AGGTTGGCAAAC TTGAG GAT	CGAGGTGCCATAACA AA TGA	58.6	776	INTERGENIC				
CaPOPI_4964	Ca7	13686933	ATTATTATTTATTATTTATTATTTA/ATTA TTATTTATTATTTATTATTTATTATTTA	CGAAGTTCGAACCTTGA AGC	TTAATCTGCGGGGATTT TTG	60.0	363	INTERGENIC				
CaPOPI_4965	Ca7	13690598	CT/CTGTATCGGAGTT	GCGCGAGAGATGAGTTT TCA	TGTGTATCGTTGTCCCT TCG	60.3	890	INTERGENIC				
CaPOPI_4966	Ca7	13800047	TTATATATATATATATATATATATATATA TATA/TTATATATATATATATATATATATA TATA	ATGGTGGAGGTGGATG GTAG	TTGACTCAATTTATTCGT TATGCAA	59.7	649	INTERGENIC				
CaPOPI_4967	Ca7	13909902	AATATATATATATATA/AATATATATAT ATATATATATA	TCGTCATTTGAAACAGC GAC	GAAAAC TCGGCAATGT GGT	59.8	611	INTERGENIC				
CaPOPI_4968	Ca7	14026857	GAAAA/GAAAA	TACAAATTGGATGCGGT TGA	TCTTCCACCCAGTTTTCA CC	59.9	233	INTERGENIC				
CaPOPI_4969	Ca7	14075293	CATATATATATATAT/CATATATATAT ATAT	TTTGT TTAGCCACA CTT TTGA	CGTGCTCGGGATTTATT TGT	57.6	862	INTERGENIC				
CaPOPI_4970	Ca7	14157143	T/TTCC	TGTTTAGATCAACAATTC CCCA	CAAAGGCAGCTGTCAAC AAA	59.3	522	INTERGENIC				
CaPOPI_4971	Ca7	14317932	A/AT	CGAAAAGCGACAAAGAA AGG	GCTTCGGAGTAGTCACT GCC	60.0	938	INTERGENIC				
CaPOPI_4972	Ca7	14352764	CAATAAATAAATAAATAAATAAATA AATAAATAAATAAA/CAATAAATAAATAA ATAAATAAATAAATAAATAAATAA	GCCTCTTCCTTCTTTTG CCT	TTTATT CATCCCCGAA GAC	60.0	165	INTERGENIC				
CaPOPI_4973	Ca7	14379603	ACC/AC	TTCCCCATTCTTAACGCT CA	GGTAAGGGCTCCTTCCA AAC	60.6	452	INTERGENIC				
CaPOPI_4974	Ca7	14780927	ATTTT/ATTTT	AAATGAAATTTCCGGGA AGG	AGGGATGGAAAACACAC GAC	60.1	473	DRR	Ca_09968	O	bHLH	Heat shock protein DnaJ, N-terminal
CaPOPI_4975	Ca7	14803293	CTATTATTATTATTATTATTATTATT ATTATTATTATTAT/CTATTATTATTATTA TTATTATTATTATTATTATTATTATT ATTAT	CGACAGTTGATTGCGTA TGG	ACGTAGGAGCAAGATCG CAT	60.1	196	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_4991	Ca7	15902473	TTATATATATATATATAT/TTATATATATATATATATAT	TTGATAGGTGTTTGAGCCC	GGACAACAAAGCGAGCC TAA	59.9	593	INTERGENIC				
CaPOPI_4992	Ca7	16001405	AATTATTATTATTATTATTATTATTAT/AA TTATTATTATTATTATTATTATTAT	AAAACACAACGTGCAAA CGA	GGGTACCAAGCACAGT TTT	60.2	679	INTERGENIC				
CaPOPI_4993	Ca7	16122158	AAATAATAATAATAATAATAATA/AA ATAATAATAATAATAATAATA	TCATTAGAAATTTCGTTT GGTC A	GGGTGAAATTGGTTTAC AACG	58.7	620	INTERGENIC				
CaPOPI_4994	Ca7	16240640	TCAACAACAA/TCAACAACAACAA	AACCCAAAGTTAGGGAT CCAA	CAC TTCACGTAGAGGAC GCA	59.7	306	INTERGENIC				
CaPOPI_4995	Ca7	16354763	ATTTTTTTTTTT/ATTTTTTTTTTT	TATACCGGTTTTCCATC CCA	TCAA ACTCATACCAATTCAATCAA	60.0	902	INTERGENIC				
CaPOPI_4996	Ca7	16405742	ATTTTTTTTTTT/ATTTTTTTTTTT	TTGACTGCAATGCTTCG TTC	TGTA ACTCCGGGATTAA AAGATG	60.0	661	INTERGENIC				
CaPOPI_4997	Ca7	16414718	TGTCATAAAAT/TGTCATAAAATATTA TAGTCAATAAAAT	GTGGTTCTTTTGTGGC GTT	GATAGCTGACGTTTGCG ACA	60.0	607	INTRON	Ca_09848			Glucose-methanol-choline oxidoreductase, N-terminal
CaPOPI_4998	Ca7	16453107	CTATATATATATATATATATATATAT/CTATATATATATATATATATATATATATATATAT	TTGGGTTTCGTGGTTTTCAAT	GCCGCATTTCAAATTCA CTT	60.2	259	INTERGENIC				
CaPOPI_4999	Ca7	16548666	TG/T	TCCCTTCTACTTGGTGG TGG	GTGATTCATGCTCCAAG GCT	60.0	624	DRR	Ca_20555	R		Sugar/inositol transporter
CaPOPI_5000	Ca7	16610320	TAAAAAAA/TAAAAAAA	CCACATCTCGTCTCCCT CAT	TTGCAGGTCATGTGGCT AAC	60.1	247	INTERGENIC				
CaPOPI_5001	Ca7	16941588	TAAA/TAAAA	TGCCGTAGTATTCACCA CCA	TGCCATGAAATTCTGCC ATA	60.0	852	INTERGENIC				
CaPOPI_5002	Ca7	17133790	ATTTTTTT/ATTTTTTT	GACACTACCCGGCATCA AGT	CCAACCCAAATAATGA AAATCA	60.0	530	INTERGENIC				
CaPOPI_5003	Ca7	17139267	GATTATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATT/GATTATTAT TATTATTATTATTATTATTATTATTATTA TTAATT	AAAAAGCGCTGTTGTGT CCT	CCAAGTGAACAGTACGT GCC	59.9	517	INTERGENIC				
CaPOPI_5004	Ca7	17172621	AATCATAT/AATCATATCATAT	GGCTAAACCTTGTCTTT GGC	AGACTCTGCTTGACCGG AAA	58.8	541	INTERGENIC				
CaPOPI_5005	Ca7	17374590	CTTTTTTTTTTT/CTTTTTTTTTTT	GCATCTGTAAAAACAAGA CCGG	ACATCGATAAGAGGCAG CGT	59.6	525	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5006	Ca7	17922655	TGGGGGG/TGGGGG	AAGTCGAGTGCTTGAGC CAT	TCCTTGC GTGCGTGCTA TAC	60.0	606	DRR	Ca_15831		bHLH	Protein kinase, catalytic domain
CaPOPI_5007	Ca7	18121209	TAAAA/TAAAAA	TGAAAAGCAATCCCAA TGT	AATGGGCATTCTGAAAT CGT	58.1	429	INTERGENIC				
CaPOPI_5008	Ca7	18417161	A/AG	TGGTGAACTGCACTTC TGC	TCGGGGTGTTACACTTC ACA	60.0	593	DRR	Ca_22130			
CaPOPI_5009	Ca7	18587623	AAAGCGGAAGGCGG/AAAGGCGG	CGATGATGACTGATTGG GGT	TGTTTGTGTTTGTAGGC GTT	60.7	374	INTERGENIC				
CaPOPI_5010	Ca7	18587996	CTTTTTTTTT/CTTTTTTT	GAGTGTACAAAGGCGGA AGG	GGGTGTTACAAGGAGTC TTGG	59.7	865	INTERGENIC				
CaPOPI_5011	Ca7	18588675	TTATAT/TTATATAT	CCAAGACTCCTTGTAAC ACCC	GCACATATATACAGTA AAATCGCA	58.6	299	INTERGENIC				
CaPOPI_5012	Ca7	18588937	ACTATATAT/AATATAT	CCAAGACTCCTTGTAAC ACCC	TTCTCCGTTTTCGTAAGA CCA	58.6	792	INTERGENIC				
CaPOPI_5013	Ca7	18918117	C/CG	TGAGTGATTCGGTGGGT TTT	CAACAACCTCTCATGCT CGC	60.4	374	INTERGENIC				
CaPOPI_5014	Ca7	18918765	TAA/TAAA	TGTTTGTGCAATTGAAT ATAGTTATG	CCCACATCAGCCAAAA GAT	58.6	971	INTERGENIC				
CaPOPI_5015	Ca7	18928675	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	AGCTCACAGAAAAACAC GGG	TGTCCCGTGCGATTTTT AAT	60.3	392	INTERGENIC				
CaPOPI_5016	Ca7	19290788	TTATATATATATATATA/TTATATATATAT ATATATA	CTGCCATGTTCAAGTGC CTA	TCAACTGGGTGTGACGA GGA	59.9	475	INTERGENIC				
CaPOPI_5017	Ca7	19359942	TA/TATGCCATTGA	ACGAGTGCGGGTATCAA TGT	GAGAAATGGAGGCAATG GAA	60.4	456	INTERGENIC				
CaPOPI_5018	Ca7	19393876	CAAAAAAAAAAAAA/CAAAAAAAAAAAAA	TGCGGAAAGCCATCTTA ACT	TTAGTGGCGCATTTTAT CCC	59.8	385	DRR	Ca_12340		bHLH	Protein kinase, catalytic domain
CaPOPI_5019	Ca7	19589201	TTATATATATATATATATATAT/TTATA TATATATATATATATAT	GGTCGTCCAAATAGTAC CCG	AGGAAGCCCAAGTTCCA AAT	59.3	828	INTERGENIC				
CaPOPI_5020	Ca7	19614333	TTATATATATATATATA/TTATATATATAT ATATATA	TCTGCTAAAGAGCTGGA GGG	CCAATTTGATACGCACC CTT	59.7	176	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5036	Ca7	20495725	CACAACAACAAC/CACAACAAC	TCCCATTAATAATTGTAGC GTGTT	GTATGATTGCAATGCGG CTT	59.8	843	DRR	Ca_12400		AP2	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_5037	Ca7	20501449	AA/AAATA	TAATGCACCTTCCGTGT CAA	GACTCCTTCGGTATCCT TGG	60.1	245	INTERGENIC				
CaPOPI_5038	Ca7	20501733	TGTA/TGTAGTA	TAATGCACCTTCCGTGT CAA	TTATAGGAAAAAGAAG AAGGAAA	60.1	636	INTERGENIC				
CaPOPI_5039	Ca7	20502385	TAAA/TAAAA	TTCCGATTTACTTCTCT AAAATGA	GCTTCCTCTATTCTATG CGT	59.6	456	INTERGENIC				
CaPOPI_5040	Ca7	20502470	CAAAAA/CAAAAAA	TTCCGATTTACTTCTCT AAAATGA	GCTTCCTCTATTCTATG CGT	59.6	456	INTERGENIC				
CaPOPI_5041	Ca7	20503526	T/TCAC	TTGAAGGTTTTTGGGA TATGG	ATGAAGGAGTGGAGCGA GAA	60.0	141	INTERGENIC				
CaPOPI_5042	Ca7	20503738	GTTTTTTT/GTTTTTT	TTCTCGCTCCACTCCTT CAT	CGAAACTAAAAGAGGGA GGCT	60.0	571	INTERGENIC				
CaPOPI_5043	Ca7	20505830	TAAAAAAA/TAAAAAAA	GGCATGGAAAATTCTGA AAAA	AAGAAGCGACGAAGAGA ATTTG	59.0	732	INTERGENIC				
CaPOPI_5044	Ca7	20505889	ATA/ATAGAAATTA	GGCATGGAAAATTCTGA AAAA	TTCATTCTCGATTGAG GGC	59.0	803	INTERGENIC				
CaPOPI_5045	Ca7	20508181	TTATT/TTATTATATT	TCAAAAGCAGTCGTTCT TGG	AAGGTTGCCCTCCAGC TTT	59.0	558	INTERGENIC				
CaPOPI_5046	Ca7	20510109	ATTTT/ATTT	GAACAATGCAAGAGCCA CAA	AATGCACTGGCTTCTCG TTT	59.8	575	INTERGENIC				
CaPOPI_5047	Ca7	20510427	TTT/TTTATTAGTGATTAAAT	TGCATTGCTCCCTAGAC ACA	GGCACTGCTTTATGCAC TCA	60.4	503	INTERGENIC				
CaPOPI_5048	Ca7	20517567	GAAAAAAAAA/GAAAAAAAAA	GAACTGACCCAACAAC CGT	ACCACCTCGAAATGGAC ATC	59.9	277	INTERGENIC				
CaPOPI_5049	Ca7	20518314	TTATATATATATA/TTATATATATAT ATA	TGCAAGCAGCTCTGT ACG	CAGTTTACCCACCTAGC CCA	60.3	588	INTERGENIC				
CaPOPI_5050	Ca7	20530900	AACG/AACGACG	GCAAACTCTAGTTGCT GAGG	CGAGTGTCACATAGATG GCAA	59.1	890	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_5066	Ca7	21598915	TTATATATATATATAT/TTATATATATATAT	TTTCATGTTTCGCATCAT	AACCCCATGTGTGAAATGCT	59.9	242	INTERGENIC				
CaPOPI_5067	Ca7	21670841	A/AAGAT	TGACAAATCTTTGCAACCA	ATTGCTCATTTTCATGCCCTC	60.1	217	INTERGENIC				
CaPOPI_5068	Ca7	21675444	AAAATAA/AAA	TTTGATGCGTGAAGAGGTTG	TGGACTGTGACTGCACCAT	59.8	510	INTERGENIC				
CaPOPI_5069	Ca7	21685577	TT/TTAT	TTTATAAATTGGCCCCATCG	TAGGGGGACCAAGAAAC TGG	59.6	501	INTERGENIC				
CaPOPI_5070	Ca7	21728387	CAAAA/CAAA	ATCTCTGCGCAATATCGCTT	AGCCGACTTTTCTACCAACA	60.0	674	INTERGENIC				
CaPOPI_5071	Ca7	21729097	TAAAAA/TAAAA	TGCTCAAAAGGGGAAGAAA	GCCACGTGGTTGAAAGAGT	59.8	240	INTERGENIC				
CaPOPI_5072	Ca7	21729303	T/TC	TTGCTCAAAAGGGGAAGAAA	TTGTATTTTCTTTATGCGTTG	59.8	426	INTERGENIC				
CaPOPI_5073	Ca7	21743270	CAA/CA	TTGCCCTCTAAATTCCTTGG	TCCCTCGTATTTAGCCCTCA	59.2	686	DRR	Ca_14521			Transposase, PttA/En/Spm, plant
CaPOPI_5074	Ca7	21743627	ATTTTTTT/ATTTTTTTT	TGAGGGCTAAATACGAGGGA	GGGATTGAGCGCCTATACAA	59.7	461	DRR	Ca_14521			Transposase, PttA/En/Spm, plant
CaPOPI_5075	Ca7	21743947	AA/AAATA	CCTGGTGTGCATTGAAAGAGA	AATTGCGGTTTTTGGTTC AAG	59.7	410	DRR	Ca_14521			Transposase, PttA/En/Spm, plant
CaPOPI_5076	Ca7	21745626	TTTTATATTTAT/TTTTAT	ATAGGGCCCATTTTACAGCG	CCAGTTGCCCTGTCCATACT	61.2	455	INTRON	Ca_14522	O	MYB	SANT domain, DNA binding
CaPOPI_5077	Ca7	21838175	TAAT/TAATAAAT	CCCTGCCTCAATTGTTTTGT	AGCATATATTGTTCCGCGT	60.0	300	INTERGENIC				
CaPOPI_5078	Ca7	22014557	GTGT/GTGTGT	AAC TTGCAGCAAAGAACCGT	CACTACCCGCTACTTCGCAT	59.9	419	INTERGENIC				
CaPOPI_5079	Ca7	22028394	G/GA	TCATCAAAATCCGTAACGCAA	TCCATGTTTTGCTCTATTGGC	60.1	271	DRR	Ca_14536	R	MYB	Integrase, catalytic core
CaPOPI_5080	Ca7	22036269	GCTC/G	GCTCAGCCTTGAAATCGAAC	TTCATCATCATCTTCAAA CAAAA	60.0	627	INTERGENIC				

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CaPOPI_5081	Ca7	22038011	C/CT	CTCCAAATTTCCAGCCA AAA	ACACGGACGGGTCTTGT ATC	60.0	822	INTERGENIC				
CaPOPI_5082	Ca7	22043317	T/TG	TGGTTCAAATGCTGTAA TCTTCTC	ATTCGCTCAATACACGG GTC	59.7	884	INTERGENIC				
CaPOPI_5083	Ca7	22045478	ATTTTTTT/ATTTTTTT	TGTGGTGTTCCTCCAAAAG ACA	CAAAGCGAAGTGCAAAA TGA	60.0	246	INTERGENIC				
CaPOPI_5084	Ca7	22046891	CATAATAATAATAATAATAATAA TAATAATAATAAT/CATAATAATAAT AATAATAATAATAATAATAATAA TAATAAT	ATAATTTGCCTTTGCGG TTG	TTCTGTGAGCAAGGCTG ATG	60.0	319	INTERGENIC				
CaPOPI_5085	Ca7	22046957	CTATATATATATATATATATAT/CT ATATATATATATATATATATAT	ATAATTTGCCTTTGCGG TTG	TTCTGTGAGCAAGGCTG ATG	60.0	319	INTERGENIC				
CaPOPI_5086	Ca7	22046996	TGCGCGC/TGC	ATAATTTGCCTTTGCGG TTG	ACCTGGTCGTAGATGCC ACT	60.0	414	INTERGENIC				
CaPOPI_5087	Ca7	22049141	TTATATATATATATAT/TTATATATATA TATATATAT	ATTTTGGAAATCCCGC TCT	TTGGTTGAGGCTAAAAT GGTG	59.9	521	INTERGENIC				
CaPOPI_5088	Ca7	22336659	CGTGT/CGT	CCTGGAAATTCGTTGA TGG	TTAGTTGCAGCGTCTT CG	60.3	592	INTRON	Ca_14549	K		Transcription initiation factor TFIIID component TAF4
CaPOPI_5089	Ca7	22380060	CATATATATATATATATATATA/CATA TATATATATATATATA	GCGAATTGCGATTAATG TGA	GCCACTTGTTTGTGTT GATG	59.7	510	INTERGENIC				
CaPOPI_5090	Ca7	22440146	TAATATA/TAATATAAAATATA	GAGTTGTAATCGGAGG CCA	GGCAGAGATGGAGGTG ATGT	60.1	542	INTERGENIC				
CaPOPI_5091	Ca7	22519524	TTAATAATAATAATAATAATAATAAT AATAA/TTAATAATAATAATAATAAT AATAATAA	ATGATCTTCCTTCTCGG CCT	CCGTTTCTTCTCTCCC TCT	60.2	257	INTERGENIC				
CaPOPI_5092	Ca7	22587400	TTATATATATATATATATATATATA T/TTATATATATATATATATATATAT ATATAT	AAGGAACAAAACGTCAT TTTCAA	AGTCAGACGCTACTCGG CAT	59.9	519	INTERGENIC				
CaPOPI_5093	Ca7	22658192	GTATATATATATATATATATATAT/GT ATATATATATATATATATATAT	TACACCTGAGTCCGCTA CCC	TCCCAAGTTTCAAATGCT GA	60.1	494	INTERGENIC				
CaPOPI_5094	Ca7	22678046	AG/AGG	ACCAGTCAACAAATGCC CTC	CCACCAACTTTAGCTCC GAA	60.0	314	INTERGENIC				
CaPOPI_5095	Ca7	22745128	G/GGTAGTTAGTGAT	GGAGTTGGTCGCTACAC CAT	CGAGGCATTCTTCACA AAT	60.0	634	INTRON	Ca_19530	R		Haloacid dehalogenase-like hydrolase

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CaPOPI_5096	Ca7	22886024	G/GCTAC	GCCCTTCTATGCTTGTCAGC	TTGGAAGGTATGAAGGCAG	60.0	728	CDS (FRAME SHIFT)	Ca_19525	S	ARF	G-protein, beta subunit
CaPOPI_5097	Ca7	22890324	A/AT	GTATCACACCCCTGCAACCT	TGTGGTGTGGGTACTTCAGG	59.9	705	DRR	Ca_19524	S		WD40 repeat
CaPOPI_5098	Ca7	22950306	TTATATATATATATATATAT/TTATATATATATATAT	ACCCAAGAGAGGTGCGACTA	AATGGCGACTTACCAAGGA	59.9	832	INTERGENIC				
CaPOPI_5099	Ca7	23038315	TCCCCC/TCCCCCCCCC	CTAATTTAGAGGGGAGCGG	TGATGTTGTGCCTCTCTGC	60.0	825	INTERGENIC				
CaPOPI_5100	Ca7	23667025	AAATAATAATAATAATA/AAATAATAATAATAATAATA	ACACTGATTTCCCAAAACGC	TTTCCTTCCCTTCTCATTGC	60.0	728	DRR	Ca_26877	G	FAR1	NAD-dependent epimerase/dehydratase
CaPOPI_5101	Ca7	23688628	TTAATAATAATAATAATAATA/TAATAATAATAATAATAATAATAATA	CCACAAAGACAATCGAGCAA	CGTGCAATCTGCTTGGA GTA	59.8	308	INTERGENIC				
CaPOPI_5102	Ca7	23780060	TTATATATATATATAT/TTATATATATATAT	CGCTCGTCTATGCGATTGTA	TAAATCTCCGCTCGCAACT	60.0	946	INTERGENIC				
CaPOPI_5103	Ca7	23797195	AATATATATATATATATATATATATAA/AATATATATATATATATATATATATATA	AAGAAATCGCGAGTCACAGG	TTAATAGACGCGCCAAAGG	60.4	652	INTERGENIC				
CaPOPI_5104	Ca7	23907440	AATATATATAT/AATATATATATAT	TTGGAGAATTCAAAAAAGGCA	CGTGACAAAGCACGAAGAA	60.0	513	INTERGENIC				
CaPOPI_5105	Ca7	23984802	AGTTGTTG/AGTTG	AAGCTGGCATGATGAGGACT	GGGAATTGAGCCTAAAGC	59.8	359	INTERGENIC				
CaPOPI_5106	Ca7	24096310	TCCCCC/TCCCCC	CTTGCCACCACTAATGCTCA	ACAACCGATTCAAGCCATC	59.9	818	DRR	Ca_19914			
CaPOPI_5107	Ca7	24260186	ATTTTT/ATTTTT	TCAGCTTTTGGCTGATGTG	TTTCTTTCAATTTATGTC AACCCA	60.0	667	INTERGENIC				
CaPOPI_5108	Ca7	24260251	CTTTTT/CTTTTT	AGAATGAGGTGACATTCGGG	TCTCCTTCAATCCTCCTCTCA	59.9	978	INTERGENIC				
CaPOPI_5109	Ca7	24347972	TAAAA/TAAAA	CTCTCATCTGAGGGCAAGC	CGATTGAATTAAGCCCA GGA	60.1	356	INTERGENIC				
CaPOPI_5110	Ca7	24348355	TAA/TAAA	TCCTGGGCTTAATTCAATCG	CGTTCCTGAGGGAATTGTGT	60.0	378	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5111	Ca7	24421160	AATATATATATATATATATA/AATATATATATATATATA	AGGAAGCCCAAGTTCCA AAT	ACAGCCAACAACCACAT CAA	59.9	469	INTERGENIC				
CaPOPI_5112	Ca7	24450388	TTATATATATATATATAT/TTATATATATATATATATAT	TTGTTAGTTTGACGAGG GCA	TGGGTGCTATTTGCAAT CAA	59.3	380	INTERGENIC				
CaPOPI_5113	Ca7	24485265	C/CAACTTT	GTCCACCCCTAGGAGCT TTC	CGGACCAAAAATTAAAG CGA	60.1	986	INTERGENIC				
CaPOPI_5114	Ca7	24495058	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT/T TTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATT	TCCGTCGTAGCTTTTTG ACA	TCTGAATCCGACATAGT GCG	59.5	625	INTERGENIC				
CaPOPI_5115	Ca7	24660866	CTTTT/CT	ACGTTCTCCATTTTCGTT GC	AATCCGCTCCTTAGGGA AAA	60.1	838	INTERGENIC				
CaPOPI_5116	Ca7	24876128	TAA/TA	GCTTTAGAGGCAACAAC CGA	CTCCAAGAACCAACTCC TGC	60.4	686	INTERGENIC				
CaPOPI_5117	Ca7	25111194	AATATATATATATATA/AATATATATATAT ATATA	GGGATTGAGAGGAGAG GGTC	ATTTAAATGTCGTGACC GGC	60.0	489	INTERGENIC				
CaPOPI_5118	Ca7	25240070	CTATATATATATATATAT/CTATATAT ATATAT	GTTGTAGCCGGTCCAAG GTA	GTTTAAGCCCCTTTGAG CCT	60.0	406	INTERGENIC				
CaPOPI_5119	Ca7	25613830	TAAAAAAAA/TAAAAAAAA	TCGATGGCTACCTCAAA TCC	GGTGGTCCTCTGCTCTT ACG	60.0	512	INTERGENIC				
CaPOPI_5120	Ca7	25626892	CGG/CGGG	TTGGCCAAGTCCCTGTT TAC	CCCGTGATAGGCAGTAC GTT	60.0	420	INTERGENIC				
CaPOPI_5121	Ca7	25834002	GTTTTTTTT/GTTTTTTTTT	TGCTCTTAGTGGTGACC GTG	CATCGTCATCGTTGCAA TTC	59.9	461	INTERGENIC				
CaPOPI_5122	Ca7	26035041	TAAAAAAAA/TAAAAAAAA	TAAAGAGATTCGACGCG GTT	CATGTTTTCGAAGCTCA CCA	60.0	407	INTERGENIC				
CaPOPI_5123	Ca7	26056806	CTTTTT/CTTTTTTTTT	GTTGCCACTTGGCGTAA AAT	GGCCGATTTACTGCTCA CAT	60.0	393	INTERGENIC				
CaPOPI_5124	Ca7	26160184	AG/A	GTGGCTACCTTCTTGGG TGA	TTTCATCGCCGAAACCT ATC	60.1	141	INTERGENIC				
CaPOPI_5125	Ca7	26179604	AT/ATT	TCAGGATGAGTTTCAC TTCG	TTGGGAAGTTGGGAGAC TTG	60.2	625	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5126	Ca7	26221720	AATATATATATATATATATAT/AATATATATATATATAT	CTTGGGAATTGGAGAGCAAG	GGGTTTCTTCTCTTGAA GCC	59.8	671	INTERGENIC				
CaPOPI_5127	Ca7	26228410	GAAAAAAAA/GAAAAAAAAAAAA	ATGGTGCAAAATGGTGA CAA	GAAAGTCGGTGCATGGA AGT	59.8	304	INTERGENIC				
CaPOPI_5128	Ca7	26233274	TAAAAAA/TAAAAAA	TACGCCATCCAAAAATG TGA	CCCTCATCCGAAAAGAT GAA	59.9	945	INTERGENIC				
CaPOPI_5129	Ca7	26235537	TTATATATATATA/TTATATATATATATA	TGCGACCTCAGTTTCTC AAA	GGGGTCATAGCATCCCC TAT	59.6	157	INTERGENIC				
CaPOPI_5130	Ca7	26240583	G/GTAACATATT	GTTTCCACATCCAGAG GAA	GAGATCAACGTGAATTG GTCA	59.9	330	INTRON	Ca_23643		HD-ZIP	Lipid-binding START
CaPOPI_5131	Ca7	26326487	GTATATATATATATATATATATA/GTATATATATATATATATATA	GGTGGTAGCTGGTAGG GTGA	TGACAACTACGAGGTTG CTTG	60.0	657	INTERGENIC				
CaPOPI_5132	Ca7	26662956	CAA/CA	TCCAAGCTTCCTTCAAT GGT	CTCAAAAGCGCTCCAAT TTC	59.7	542	INTERGENIC				
CaPOPI_5133	Ca7	26694675	ACC/ACCCCCC	CTCGGCCATCCGAGATA TAA	GCTCACTAACTCTGCCT GGG	60.0	881	CDS (FRAME SHIFT)	Ca_16250			
CaPOPI_5134	Ca7	26699922	A/AACTAG	AAACTCCAGCCCGGTAA ACT	AACCCATTGAGGTGAC TGC	60.0	465	DRR	Ca_16249			
CaPOPI_5135	Ca7	26701106	A/ACTAGGAATTACTCCC	CAATAGGGCGAGTCGAA TGT	AAGTCCAGTAGCCGAAA GCA	60.1	838	DRR	Ca_16249			
CaPOPI_5136	Ca7	26701534	C/CG	AAGCTTCATCCTGGTCA TGG	AAGTCCAGTAGCCGAAA GCA	60.1	381	DRR	Ca_16249			
CaPOPI_5137	Ca7	26906603	ATTTT/ATTTT	TGGAGTTCCAACACGCA CTA	CAAGGTAATTTGCATTG AAGGA	60.3	112	INTERGENIC				
CaPOPI_5138	Ca7	27115436	GATATATATATATAT/GATATATATAT	CAATCCCACAGGTACG CTT	CAAACCTAATTTTCAA ACACG	60.0	347	INTERGENIC				
CaPOPI_5139	Ca7	27346895	TTATATATATATATATATAT/TTATATATATATATATATATATATAT	TGCTTGATTGCTTGAGT TCC	CGCGCAGATTGTCAAAT AGA	59.0	641	INTERGENIC				
CaPOPI_5140	Ca7	27520803	AATATATATATATAT/AATATATATATATAT	GCCGCAAGGAATTTAAC TCA	GGAGAAAGAGGGAATTT GGC	60.2	618	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5141	Ca7	27521328	CAAA/CAA	GCCAAATTCCTCTTTCTCC	CCTTCCACACAACCACAGA	60.0	393	INTERGENIC				
CaPOPI_5142	Ca7	27521551	TC/T	GGTAAGGGCTCCTTCCAAC	GATTCCTCCCTCTTAACGTC	59.9	576	INTERGENIC				
CaPOPI_5143	Ca7	27935917	AGGGG/AGG	GGCTGTTAGCCCAGTTTGTG	GTTGGTTCCTAGCACCATA	59.7	664	INTERGENIC				
CaPOPI_5144	Ca7	28056896	TAAAAAAA/TAAAAAAA	TCCAAAAGATATGGCCGAC	GTATTAGCTGGTGCGCTGGT	59.9	406	INTERGENIC				
CaPOPI_5145	Ca7	28190197	AGTTTATTGG/AGTTTATTGGTTATTGG	TTGGTTTATTGGTTGGGA	ACCAGGAAAAGAAGAAGGGC	60.0	519	INTERGENIC				
CaPOPI_5146	Ca7	28335175	AAAATATA/AA	GGTACTGTTCACTGCGCAAA	TCAACCAAATCCCCCAATA	59.9	236	INTRON	Ca_18921			GOLD
CaPOPI_5147	Ca7	28355456	AATATATATATATATATA/AATATATATATATATATA	GCCAACTCATCAAATCGTGA	ATGGAACAATCGGACACAT	59.7	521	INTERGENIC				
CaPOPI_5148	Ca7	28400317	AATATATATAT/AATATATATATAT	CTGACCAAAATCCAAAAGACA	TCGGTTTTGAAACCAAAATG	59.1	637	INTERGENIC				
CaPOPI_5149	Ca7	28454557	GTT/GTTACTT	TGTCGGTCAATCCACTTTT	CCCAAACCATTCATTTTGTG	58.0	411	INTERGENIC				
CaPOPI_5150	Ca7	28561460	CCAC/CCACAC	CACTGCTTTAGCAACCACTCA	TTCTAGAAGCGGCGTTGTTT	59.9	678	DRR	Ca_18943	L	C3H	Domain of unknown function DUF223
CaPOPI_5151	Ca7	28702659	ATCCTCC/ATCC	TCCATTAAACCCTCTTGAGGAAA	TCAGGATGAAGAAGGGGAGA	59.9	531	INTERGENIC				
CaPOPI_5152	Ca7	28707261	ATTT/AT	TGATGGTGGATATGCGAATA	TTGGTTTTGATGGTGGGAT	59.9	314	INTERGENIC				
CaPOPI_5153	Ca7	28707412	GAAATAACAATAAAAAACAATAACAATA AAA/GAAATAACAATAAAAAACAATAACA ATAAAAAACAATAACAATAAAA	ATCCCACCATCAAAAACCAA	GATATGTTCCGAGTGCCGTT	60.0	491	INTERGENIC				
CaPOPI_5154	Ca7	28914738	TAAAAA/TAAAAAAA	TGAACCCAAAACACAAACACA	AACATTCGTGCCTTTTCGT	59.9	827	DRR	Ca_11811	QR	B3	Oxoglutarate/iron-dependent oxygenase
CaPOPI_5155	Ca7	28918944	GTGCT/GT	TGCCGTCAAAATTGTAGCAG	TCCCATCCATTTCAATTTGT	59.9	505	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5156	Ca7	28925485	AAGTAGTAG/AAGTAG	TCATCAAAAGACCGAAAGCA	ACCACCACTTAGAGAGGCCA	59.4	410	INTERGENIC				
CaPOPI_5157	Ca7	28935886	GTTATATCA/G	TGGAACCACTCCCTTAGACG	TCCATCATGGCAAGTTTCT	60.1	797	INTERGENIC				
CaPOPI_5158	Ca7	28936338	TAAAAAA/TAA	TTCGGAATTCAACCGATAAA	TAAAGAGGGTGCAAGGTCC	58.1	866	INTERGENIC				
CaPOPI_5159	Ca7	28937372	ATT/ATTTT	AACCTCATGTTCCCTTTCC	TGGGTCATGGCCATCTATTT	60.2	702	INTERGENIC				
CaPOPI_5160	Ca7	28941166	TAT/TATATACAAT	TCAACCACATGTGAAGATGGA	TTGGCTCCCTACATTTTCTTC	60.0	752	INTERGENIC				
CaPOPI_5161	Ca7	28942484	AATTA/AA	AGCTTGTGAAGGTTTGGTGG	CAAGAGCCGGTGAATGAGT	60.1	559	INTERGENIC				
CaPOPI_5162	Ca7	28949507	TTATA/TTATATA	CCACCATTGGCATTCTTCT	GCTGCTCAAATTCGACACACA	59.9	599	INTERGENIC				
CaPOPI_5163	Ca7	28979318	TA/TATATTCAACA	TTCTGGCCCGTTAGCATTAC	CTCAGCCTTCCCACCAATA	60.1	453	DRR	Ca_11805	C		Malic oxidoreductase
CaPOPI_5164	Ca7	28999036	CAAAAAA/CAAAAAA	CGTGGACAAAGATCGTGATG	ATTCCCCGTGGTCTTGATA	60.1	447	INTERGENIC				
CaPOPI_5165	Ca7	29001394	TA/TATAAATATTTTATGA	TTGACTTGCAATTCATCGTGC	ATGCTTCCTCCCGAAATCT	59.7	569	INTERGENIC				
CaPOPI_5166	Ca7	29001560	ATTTT/ATTTT	ACTTGCATTCCATCGTGCAT	ATGCTTCCTCCCGAAATCT	60.3	566	INTERGENIC				
CaPOPI_5167	Ca7	29004077	ATGA/ATGACACTGA	CGTCGGTGGTCAGGTAAAT	TCACAATCCCTGCAATTCAA	59.9	681	INTRON	Ca_11804	UR	HB-other	Dynamin central domain
CaPOPI_5168	Ca7	29006131	AATATA/AATA	TTTCTCATCCTCCTGGTTG	TGAGGGATCAACTTCCCTTG	60.0	752	INTRON	Ca_11804	UR	HB-other	Dynamin central domain
CaPOPI_5169	Ca7	29010477	CAAAAA/CAAAAA	TTTTCATCGGGTCACAGTCA	TGGATATGACCGTGCTTTT	60.1	738	DRR	Ca_11804	UR	HB-other	Dynamin central domain
CaPOPI_5170	Ca7	29012088	TAA/TAAA	TTTGCCCTCAAGATTGTTC	ATTGGTGGCTCATGACCTGT	60.1	102	INTRON	Ca_11803	F		Adenylate kinase

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5171	Ca7	29014917	TCCC/T	TTTGGCATACACTCCCC TTC	GGGAGCTGATGAGTGT GGT	59.9	225	INTERGENIC				
CaPOPI_5172	Ca7	29020483	TATAAA/TATAAATAAA	TGGTATAAGCATTCGGT AGACG	CAACGCTAAGTTTGTA GCAACA	59.2	982	INTERGENIC				
CaPOPI_5173	Ca7	29021071	TTA/TTATA	TTAGCCAAAATTGTGGT CCC	TCATGACGTAGTCATCG CGT	59.8	209	INTERGENIC				
CaPOPI_5174	Ca7	29021112	TAAAAAAAAAAAA/TAAAAAA	GTCCGCAACTGGAACCT TTA	TCATGACGTAGTCATCG CGT	60.1	148	INTERGENIC				
CaPOPI_5175	Ca7	29022459	TAAAAAAA/TAAAAAA	TTAGAACAATGCGACGT GAA	TCACCCGAAACATCTCC TTC	57.9	261	INTERGENIC				
CaPOPI_5176	Ca7	29022601	AGG/AG	TTAGAACAATGCGACGT GAA	TCACCCGAAACATCTCC TTC	57.9	261	INTERGENIC				
CaPOPI_5177	Ca7	29023514	AAGA/AA	GGACCACGTGTGTATT AGCC	TCACCAGCAATGATCTG AGC	59.4	482	INTERGENIC				
CaPOPI_5178	Ca7	29067406	ATTAAATTTA/ATTAAATTTAAATTTA	AGCTTTTGGCTGACATT GTG	AAAACTGCGTGGCCT TTG	58.9	522	INTERGENIC				
CaPOPI_5179	Ca7	29069731	AG/A	AGTCTTCCCTTCCCTC CAA	CATACACCACCAATCC ACG	60.0	369	DRR	Ca_11799			Uncharacterised protein, Wax2 C-terminal
CaPOPI_5180	Ca7	29069848	AGG/AG	AGTCTTCCCTTCCCTC CAA	CAACATGGCTTCCAACC TCT	60.0	875	DRR	Ca_11799			Uncharacterised protein, Wax2 C-terminal
CaPOPI_5181	Ca7	29070532	TATTAGATACCAT/TAT	TCATTACCCTCCTTGGC AAC	AAACCCGCAAGGATTG TTC	59.9	265	INTRON	Ca_11799			Uncharacterised protein, Wax2 C-terminal
CaPOPI_5182	Ca7	29085797	TAAAAA/TAAAAAA	CCAAATTATCCTCTCTT TTCCC	GAATTGGACCGAATGCA AGT	59.4	656	INTERGENIC				
CaPOPI_5183	Ca7	29090138	GTATA/GTA	TGTCCTGTTTGTAAC TTGC	ATCAAGTCAAACCTACC ACAA	58.8	745	INTERGENIC				
CaPOPI_5184	Ca7	29095794	ATTTTTTTTT/ATTTTTTTT	CATTGAATCTATTGTCC GCAA	CTTTGGTAGGACAGCAA AAGC	60.0	390	INTERGENIC				
CaPOPI_5185	Ca7	29104256	AC/ACTC	TTTTGATTTACAGCCTC CAC	TCGTATTGATGCAGCTC CTG	60.1	573	INTRON	Ca_11798	Q		ABC transporter, transmembrane domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5186	Ca7	29118994	CATTTAATTTAATTTAATTT/CATTTAATTTAATTTAATTTAATTT	TTTAACCTCTCCGCGGAATTC	CTCCCAACGCTCTCGTAAG	59.3	490	INTRON	Ca_11796	FE		Phosphoribosyltransferase
CaPOPI_5187	Ca7	29121824	GATAATAAATAAATAA/GATAATAAATAAATAA	TTAGTGCCAACAAATGCAG	TTGCCACGTCATTGAAAG	59.9	492	INTRON	Ca_11795	S		NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3
CaPOPI_5188	Ca7	29127420	CT/CTTT	GCAGTGTCCAGACCCTCAT	CACAACCACAAAGATGGCAC	60.1	460	INTRON	Ca_11794	R		tRNA (guanine-N-7) methyltransferase
CaPOPI_5189	Ca7	29128437	TC/T	TCTATAATCCCGTGTGCG	ACCTGCAATTTTGGATGAGC	58.7	599	DRR	Ca_11794	R		tRNA (guanine-N-7) methyltransferase
CaPOPI_5190	Ca7	29133168	CAAA/CAAAAA	AGAGCAGCTTTTCCCAT	GAAGAAAAGTATTGCACGTTTGAA	60.2	720	DRR	Ca_11793			
CaPOPI_5191	Ca7	29135633	ATTAATTTTAATTTAATTT/ATTAATTTTAATTTAATTTAATTT	CGACGATTCGACAATCAAA	AAATGCAAACCAACTCAC	59.7	955	INTERGENIC				
CaPOPI_5192	Ca7	29164762	CAAT/CAATAAAAT	ATGGTCATGTCAAATGGACG	GGAAAAAGTGGATTGGGGTT	59.2	610	INTERGENIC				
CaPOPI_5193	Ca7	29172192	GAAAAA/AAAAA	CACCACCACTACCCCAT	TGCTTGTTCCTCACTTGTGC	60.1	628	INTERGENIC				
CaPOPI_5194	Ca7	29177568	CAAAA/CAAA	GCTTATTCCTGGTCCCCATT	TGATACAAAGCAACCCAGCA	60.2	381	INTRON	Ca_11788			EF-HAND 2
CaPOPI_5195	Ca7	29179462	CTTT/CTT	CTGAAGGTGTCCCTGGTGTT	GCGGCTACCAAACTTGACTC	60.0	489	DRR	Ca_11788			EF-HAND 2
CaPOPI_5196	Ca7	29191236	GAAA/GAA	TACCGGAAAACCTCACGAC	GAACCAATGAGCATGAGCAA	60.0	611	DRR	Ca_11786	J		Glutamyl/glutamyl-tRNA synthetase, class Ic
CaPOPI_5197	Ca7	29196375	CTT/CTTT	CTTCTCGGAAACTGACAGGG	CCACATGAGCGTGAACAATC	59.8	359	DRR	Ca_11785			
CaPOPI_5198	Ca7	29208189	CTTT/CTT	AAACTTTCACGACCTCCCT	CACCGGGTTACAAATCTGC	60.0	307	INTERGENIC				
CaPOPI_5199	Ca7	29219777	CT/CTCACGAT	TGAAGTTGTAGGGCTTGCT	TGCTTAGAGCCTTTTGGCAT	59.9	588	CDS (large-effect mutations)	Ca_11784			Protein of unknown function DUF3550/UPF0682
CaPOPI_5200	Ca7	29221906	CTTTTT/CTT	TATCGCCAATCTCCCATCTC	CTCGATGACAGTGGCAAATAA	60.0	429	DRR	Ca_11783	C		NADH:ubiquinone oxidoreductase, 17.2kDa subunit

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CaPOPI_5201	Ca7	29223450	CA/CAA	AGGCCTCAAGAAGGTG TGA	ATTTTCATGGGGTGGAA ACA	59.8	414	DRR	Ca_11783	C		NADH:ubiquinone oxidoreductase, 17.2kDa subunit
CaPOPI_5202	Ca7	29226958	AATTGATA/AATTGATATTGATA	TTCCATCTGGAAGGCAT CTC	TCCTGTTTGAGGGGGTG TAA	60.2	577	INTRON	Ca_11783	C		NADH:ubiquinone oxidoreductase, 17.2kDa subunit
CaPOPI_5203	Ca7	29240073	CAAA/CAAAAAA	GCAGAGGTCCGAGAGAA ATG	GCATCCACTACCGCTGA AAT	60.0	583	INTERGENIC				
CaPOPI_5204	Ca7	29265546	T/TA	ATTGTACCTTCGCGAAC ACC	TAGCAATGTCACGAAAT GCC	60.0	707	INTRON	Ca_11779		C2H2	Glycoside hydrolase, family 28
CaPOPI_5205	Ca7	29280548	ATATTATTATTATTATTATTATT ATT/ATATTATTATTATTATTATT ATT	TTGTTTGA AAAACCAATA TGACA	TTGCAACTACCAAAATAA ACAATTTC	57.2	875	INTERGENIC				
CaPOPI_5206	Ca7	29296655	AATTATTATTATTAT/AATTATTATTATTA TTATTAT	TGCATGTCTTCTAAGGG TATTTTTC	AGGGAGCTGGTAGGGG ATTA	59.9	837	INTERGENIC				
CaPOPI_5207	Ca7	29322502	TATTTTGAT/TATTTTGATTTTGAT	AAACGCTCTTAAAAACAT TCTTCC	CTCGTACAATGGCCAG ATT	59.3	852	INTERGENIC				
CaPOPI_5208	Ca7	29324634	TTT/TTTATT	TGGCAAATGCCTACAAT TCA	TTTTTCCCATATTTTTC GTTG	60.1	865	INTERGENIC				
CaPOPI_5209	Ca7	29326662	CAAAAA/CAAA	AAGTCAACGGAATCTCA TCCA	GCAAAGCGATTAAATGAC AGG	59.5	978	INTERGENIC				
CaPOPI_5210	Ca7	29334299	ACATCATCA/ACATCATCATCATCA	AATCCCCACCTGGATAC CTC	GCTCGCTACGTACGACA ACA	60.0	609	INTERGENIC				
CaPOPI_5211	Ca7	29344358	TTA/TTAGAGTATTTATA	TTATCATCATGTAACCAT GTGTCTT	CACGCTCCCACTAATCT TACA	57.5	227	INTERGENIC				
CaPOPI_5212	Ca7	29346372	G/GC	CAAAAGGGAAGATGCAA TTTTT	TTTGCGGGATGAATTCT TTT	59.5	206	INTERGENIC				
CaPOPI_5213	Ca7	29347288	CAAT/CAATTAAT	TTCAAATCCACGATTAG GGTG	CATCAGCTATGCCATCT CCA	59.8	829	INTERGENIC				
CaPOPI_5214	Ca7	29357883	TTTATT/TTT	ATGAATGATTGCGTCCA TGA	GGGACCACCGGTGTTAT TTA	59.9	517	INTERGENIC				
CaPOPI_5215	Ca7	29388652	GTTTTT/GTTTTT	AATAATCTTCGGCATG CAA	ACATCAGTCAAGCGCAC AAA	58.3	832	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5216	Ca7	29392132	TAAAAAA/TAAAAAA	TCAATTGAGGACATTCTG	CGATTCTGATAATTCACCA	59.6	542	INTERGENIC				
CaPOPI_5217	Ca7	29410137	GTCT/GT	TTGTAGGGCGGATCTGGTTA	GGGCATTCTACATGCAAT	60.5	541	INTERGENIC				
CaPOPI_5218	Ca7	29416537	ATATAAATTATAAATTATAAATTAT/ATAAATTATAAATTATAAATTATAAATTAT	AAAATCATTACTCACCAATAAGTGGA	TGCTCTCCTCCTCAACAACAACT	59.3	436	INTERGENIC				
CaPOPI_5219	Ca7	29418151	GT/G	CATGTACACGTCACATCGGA	TTGTAGGCTGGACATCATGC	59.0	329	INTERGENIC				
CaPOPI_5220	Ca7	29446111	CATT/CATTGATT	GTCTCCGCTCAATCAGAAGG	TCATTCCCAACATTATTCGTG	60.0	763	DRR	Ca_11775	R		Alpha/beta hydrolase fold-1
CaPOPI_5221	Ca7	29446201	ATTTTTTTTT/ATTTTTTTTTT	CGTTGCGCATGTGTAATTG	TCATTCCCAACATTATTCGTG	61.1	639	DRR	Ca_11775	R		Alpha/beta hydrolase fold-1
CaPOPI_5222	Ca7	29458658	GCA/GCAATCA	CACTGTGGTATGACCGGAAG	GCCCTTTGATCATGCAACTT	59.0	460	INTRON	Ca_11773	S		Autophagy-related protein 3
CaPOPI_5223	Ca7	29465694	GCTC/GCTCTC	AATCATTTCACCCACCTGC	GGGATATGGTCTCGAGTCA	59.8	807	DRR	Ca_11772		ERF	Frigida-like
CaPOPI_5224	Ca7	29489393	C/CT	TCGACCGGTAAGTATGAAA	AAATGATAAGCCTCGTTGCG	59.1	280	INTERGENIC				
CaPOPI_5225	Ca7	29496210	TG/T	TTTTTCTTTCAAATGCAAGCC	TGTGCTTCTGAGCTTCAATGG	59.4	300	INTERGENIC				
CaPOPI_5226	Ca7	29535944	CTT/CT	AGGTTGATCTGGACTGGTGG	TGGTTACCCCAATTCAGGTT	60.0	109	INTERGENIC				
CaPOPI_5227	Ca7	29537259	T/TG	TTTGACCACACCTTGGTTA	GAACAAAAGGAAAGGGGAAA	60.0	528	INTERGENIC				
CaPOPI_5228	Ca7	29550695	AT/A	AAGCATCCCAATTCGTCTG	AGAAGTTGAGGCGACCAAGAA	60.1	466	DRR	Ca_11767		SBP	Profilin/allergen
CaPOPI_5229	Ca7	29552593	TATTAATTA/TATTA	TTTGACCACACCTTGGTTA	GCTTTTGAAGGGGATTATGATAGG	60.0	586	INTERGENIC				
CaPOPI_5230	Ca7	29572407	GT/GTTT	CGTCCAAGACCATTCACCT	CGCTCCATTCGCTTTCTTAC	60.0	324	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5231	Ca7	29580185	TAAAAA/TAAAAAA	GTTACACACGTAGGCCAAA	TCATGTGCGTTTGACTGATG	59.6	537	INTERGENIC				
CaPOPI_5232	Ca7	29582004	AA/AATAAATA	GCAATGTGATTTTCATTCGTGA	AGCCCAATCTTTTGTTTCA	59.5	297	INTERGENIC				
CaPOPI_5233	Ca7	29582896	ATTTTTTT/ATTTTTTTTT	ATGGCTAAATAACACCCGCA	TAACCAAGGTGTGGTGCAAA	60.3	377	INTERGENIC				
CaPOPI_5234	Ca7	29584512	ATTTTT/ATTTTTTTTT	GGTATGAAGGTGCAATGGCT	TGAAGCTCAATTCATTGGAGA	60.0	771	INTERGENIC				
CaPOPI_5235	Ca7	29595027	AAAGAAGAAGAAGAAGAAGAA/AAAGAAGAAGAAGAAGAA	TCCAAGTGGTGAAAATGTGTG	CAACCTTGGCAAAGGAGAA	59.5	254	INTERGENIC				
CaPOPI_5236	Ca7	29609973	TAAAAAAAAA/TAAAAAAAAA	AATCACATTCAACTGCCGTG	TGAGTTAAGCCCGCTAGAA	59.6	702	DRR	Ca_11764			F-box domain, cyclin-like
CaPOPI_5237	Ca7	29610103	ATTTTT/ATTTTTTTTT	AACAGAAAGAAGGCCGTGTTG	TGAGTTAAGCCCGCTAGAA	59.4	134	DRR	Ca_11764			F-box domain, cyclin-like
CaPOPI_5238	Ca7	29615212	ATTTT/ATTTT	TGCCAATCCACAATGAAA	AGTGAAACCAACGCCAAAC	59.9	474	INTERGENIC				
CaPOPI_5239	Ca7	29615433	AA/AATCGATCTAACTCGA	TGCCAATCCACAATGAAA	AGTGAAACCAACGCCAAAC	59.9	474	INTERGENIC				
CaPOPI_5240	Ca7	29615700	TA/TAA	GGCGTTGGTTTCACTCAAT	ATGAAGCTTACGGCCATCAC	60.0	277	INTERGENIC				
CaPOPI_5241	Ca7	29616903	ATTTTTTTTT/ATTTTTTTTTT	GGGGTGTACACTTGAGGCA	TCGGAGAAAAATAGGAGCAAA	61.0	551	INTERGENIC				
CaPOPI_5242	Ca7	29617184	TTTTTTATTTTTATTT/TTTTTTATTTTATTTTTTTTATTT	TTTGCTCCTATTTTCTCCGA	GTAAGTCATGCCATAGGCC	59.0	378	INTERGENIC				
CaPOPI_5243	Ca7	29645650	ATA/ATATAAATCTTA	GCCTCATCTACGATTACGTCG	CTTGCAAAGCATTTGGATCA	59.7	693	INTERGENIC				
CaPOPI_5244	Ca7	29645891	CAA/CAAA	GAAAGCGAGAAAGAGGGAAAA	CTTGCAAAGCATTTGGATCA	60.0	483	INTERGENIC				
CaPOPI_5245	Ca7	29672845	AA/AATA	TTTCTCAATTACGGGAGCATC	TCATCAAATTCGTAACGCAAA	59.2	834	DRR	Ca_11757	P	MIKC	Heavy metal transport/detoxification protein

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5261	Ca7	29866869	TAAAAAAAA/TAAAAAAAAAAAA	AGGTGAACTTCCGAAA TGC	AAATAGGGCCTCACCT GCT	59.2	548	DRR	Ca_11737	R		Protein kinase, catalytic domain
CaPOPI_5262	Ca7	29969276	ATTTT/ATTTT	ATAGGCACAACAATTG CCC	AGTCACGTTTCATCGAGA GACAA	60.0	681	DRR	Ca_11731			
CaPOPI_5263	Ca7	29969403	CAT/C	CGTCGTAGAGCCATTGA TGA	TGGCTATGAAACCCGGA TAC	59.8	729	DRR	Ca_11731			
CaPOPI_5264	Ca7	29969461	TG/T	CGTCGTAGAGCCATTGA TGA	GGGAGGATGGACAATG CTTA	59.8	871	DRR	Ca_11731			
CaPOPI_5265	Ca7	29972956	TAAAAA/TAAAAAA	ATGGATCCCAGTATCCC ACA	TAACAAGCTTGGAATGC ACG	60.0	269	INTERGENIC				
CaPOPI_5266	Ca7	29976341	CAA/CA	CCCCAATTGTTTCATGTT CC	TGGCTCAACTGCACAA AAC	60.0	288	DRR	Ca_11730	KR		Mitochondrial transcription termination factor-related
CaPOPI_5267	Ca7	29979176	A/AGAGTT	ATTACGCAACGAGGGAC AAC	TATGCATGCTTTTAC CGT	60.0	445	INTERGENIC				
CaPOPI_5268	Ca7	29979856	TTT/TTTTATT	CAATGAAAAGAAGAGA CATTCCA	TTGAGAACCAACAAC TTCTT	59.6	888	INTERGENIC				
CaPOPI_5269	Ca7	29980723	CAAAAA/CAAAA	CACATTTTGTGTCCAATC TGTTG	ATCCTGTCCATCAAACG AGC	60.3	756	INTERGENIC				
CaPOPI_5270	Ca7	29980870	T/TC	CAACCGCAATCTTAACA AAAA	ATCCTGTCCATCAAACG AGC	57.9	402	INTERGENIC				
CaPOPI_5271	Ca7	29982388	ATTT/ATT	TCTCCACCCAATTTTTCG AC	GTGCGAATTCAGTTTCG ATT	59.9	397	DRR	Ca_11729			Protein of unknown function DUF506, plant
CaPOPI_5272	Ca7	29983649	TAAAAAAAA/TAAAAAA	TCAATGGAGCTCAATCT TCAAA	TTGGATTGGGTCGATTT TGT	59.8	619	DRR	Ca_11729			Protein of unknown function DUF506, plant
CaPOPI_5273	Ca7	29986240	A/AT	AAATGAACGGCACCAAC ATT	CCAATTCCAAATGCCAA ATC	60.2	536	INTERGENIC				
CaPOPI_5274	Ca7	29994584	TTATA/TTA	CTCCGCAATTGTATGCA GAA	CGTCGGTGCTGTAATGT GTC	59.8	315	INTERGENIC				
CaPOPI_5275	Ca7	30002970	ATTTTTTT/ATTTTTT	CGAAATTACCGGTTTGC CTA	CGTTGTCGGGTTACAT AGA	60.0	495	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5276	Ca7	30007344	AAACAAC/AAACAACAAC	CCTTTTCTTGAACATCCC TCC	TTGATCCGTTGACTTTTC CC	59.9	385	INTERGENIC				
CaPOPI_5277	Ca7	30007406	GAAAAA/GAAAA	CCTTTTCTTGAACATCCC TCC	TTGATCCGTTGACTTTTC CC	59.9	385	INTERGENIC				
CaPOPI_5278	Ca7	30009218	ATTATTAT/ATTATTATTAT	AATTGTGGTTGTGGTTC GGT	GATGGTGCTGGGGAATC TAA	60.1	881	INTRON	Ca_11728		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_5279	Ca7	30009540	T/TTTG	ACGGAGGGAGAAAATCA GTG	GATGGTGCTGGGGAATC TAA	59.1	580	INTRON	Ca_11728		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_5280	Ca7	30015362	CTTTTT/CTTTTTTTT	CCAAAATTAGAAAAGCTT TGAACG	CCCCAAGCAAAAGAAAC AAA	60.5	562	INTERGENIC				
CaPOPI_5281	Ca7	30026336	AATGATG/AATG	GAGCTGAGGAAGGGTT GATG	TCCTTGCCCACTAACCT GG	59.8	507	INTRON	Ca_11727			Glycosyl transferase, family 2
CaPOPI_5282	Ca7	30041676	CA/C	ATGCGTGAAGAAGAGG ATG	AATCGGACAAGGGACAC AAA	60.2	428	INTERGENIC				
CaPOPI_5283	Ca7	30048460	GAAAAAAAAAAAAA/GAAAAAAAAA AA	TGTGTGTGTGTGTAAT GGCA	AAGAGCGGGGACGTATT TTT	59.5	585	DRR	Ca_11723	O	GeBP	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain
CaPOPI_5284	Ca7	30053126	TAA/TA	AAAGAGAGAACGGACAT AATCCA	TCGCATATTTTCTTTTC AGTCC	59.1	550	INTERGENIC				
CaPOPI_5285	Ca7	30053648	CAAAGT/C	GGA CTGAAAAGAAAAT ATGCGA	GTGCTCTCTTTTGCCGA TTC	59.6	774	INTERGENIC				
CaPOPI_5286	Ca7	30072638	GATAATTACAAA/GATAATTACAAAT TACAAA	TGAGATTTGGAAC TAAC GGTGA	AAAGGATCAAATCGGAG AAAA	59.6	349	INTERGENIC				
CaPOPI_5287	Ca7	30073842	AGTGT/AGTGTGT	CGGACAACGAGTGTAT TTAGC	GCCAATGGGTGCTGATT ATT	58.8	944	DRR	Ca_11719		NAC	Uncharacterised protein domain XH
CaPOPI_5288	Ca7	30091306	ATTTT/ATTT	ACATTCCACGGTCTAGC TGC	GATGAATTTCCAGGCCT CAC	60.3	888	INTERGENIC				
CaPOPI_5289	Ca7	30099390	TA/TAA	TGGGCACATGTCACAAA ACT	TGAGGTATGGGAAGGT GAG	60.0	840	INTERGENIC				
CaPOPI_5290	Ca7	30107818	TA/TAACCAGTTTATAA	GAAGGCTGCAACTCCTT GAC	AACGTGAAACCCACCAA AAC	60.0	764	INTRON	Ca_11716	T	WRKY	Protein kinase, catalytic domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5291	Ca7	30129775	AATGAT/AATGATGATGAT	CCACGTGAGTTACCATGCTG	AATGCATTCAATTCGGAACC	60.2	203	INTRON	Ca_11715	U		Citron-like
CaPOPI_5292	Ca7	30137991	AAAAGC/AAAAGCTCTTAATTAAGC	TGGCTATTTTGTGTTC	TTCCCTCTGCCAACAATTTC	60.1	424	DRR	Ca_11715	U		Citron-like
CaPOPI_5293	Ca7	30140331	TAAA/TAA	CTTTGGCCAGAAGGGACATA	TTTATGCTGGTGGGATGAT	60.1	522	INTRON	Ca_11714	H		GTP cyclohydrolase I/Nitrile oxidoreductase
CaPOPI_5294	Ca7	30154601	ATCTTCTTC/ATCTTC	TGGGTTGTAAACATAATTGAATG	CTTAACCCACCAACCACAG	59.1	293	INTERGENIC				
CaPOPI_5295	Ca7	30157722	CG/C	CCGAGATGAATGGGAAGAAA	AACACCTAGGAGGAGAAGAAAAACA	60.0	354	INTERGENIC				
CaPOPI_5296	Ca7	30157868	GA/GAA	CCGAGATGAATGGGAAGAAA	GCTCCTGTCAATAGAGTGCAT	60.0	716	INTERGENIC				
CaPOPI_5297	Ca7	30166196	CAA/CTTAAA	TGAGCCATAATGTGCAAGAA	CTTTTTGAAAGGGCATCAGC	60.2	520	DRR	Ca_11711	Q	B3	Cytochrome P450
CaPOPI_5298	Ca7	30173467	ATTTTTTTTT/ATTTTTTTTT	TGGTCAATTCACCTGCAAAA	TTCCITGTGAACCAATTCGC	60.1	542	INTERGENIC				
CaPOPI_5299	Ca7	30192100	A/ATT	CATCGTTGGTTGTTGGTTG	TGCAAAAATGACTCGGAACA	59.9	279	INTRON	Ca_11709	U		ER lumen protein retaining receptor
CaPOPI_5300	Ca7	30192636	ATAAGCATT/AT	CCTTCAGCAATTTGGCAGT	TCCCATGGTTCAAAGTTGT	60.2	594	INTRON	Ca_11709	U		ER lumen protein retaining receptor
CaPOPI_5301	Ca7	30208302	CGA/C	TTGGACGATGTGGATTGAAA	CCATCTCAGCATGTGTTTGG	59.9	642	INTRON	Ca_11706			Mitochondrial inner membrane translocase complex, subunit Tim17/22
CaPOPI_5302	Ca7	30208770	ATTT/ATT	CCAAACACATGCTGAGATGG	CTTCCTTTGCACGACCGTAT	60.1	707	INTRON	Ca_11706			Mitochondrial inner membrane translocase complex, subunit Tim17/22
CaPOPI_5303	Ca7	30221695	T/TGAA	CTTGTTGATGCAATGTTGGC	TTTGCCACACAAAAACAAA	60.1	538	INTERGENIC				
CaPOPI_5304	Ca7	30228676	TTTTAA/TTTAACTTTAA	AGACATGTCGCATCATGGAA	TGCTTTGAACTTTGGAAACG	60.1	408	INTERGENIC				
CaPOPI_5305	Ca7	30235069	TTTCTTCTTCTTCT/TTTCTTCTTCT	TGCGTGTTTCGAGTTGTAGG	AACGTGCCAAAAACCACATTC	59.9	606	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5306	Ca7	30240282	ACGT/ACGTGATCGT	TAAATGCGGCAATGTCAAAA	TCCATTTCGTGAGTAAAA CATCA	60.1	219	INTERGENIC				
CaPOPI_5307	Ca7	30269288	AAAT/A	ATTTAATTCGGCTTTGCGTG	AAAACGGGTGGCACAATAGA	60.1	620	INTERGENIC				
CaPOPI_5308	Ca7	30276513	AAAT/AAATAAT	TTTCCATCATCAATTCCTTTTG	GAGGTATGGTGCAACCTGCT	58.9	686	INTERGENIC				
CaPOPI_5309	Ca7	30278558	ATT/ATTT	CCCGTGGTTATTGCATTTC	AATACCAGATTTGGGCGTTTG	60.2	529	DRR	Ca_11700	C		Ribosomal protein/NADH dehydrogenase domain
CaPOPI_5310	Ca7	30279217	T/TCTAGGCC	CAACGCCCAATCTGGTATT	TGCTAATCAGCATTTTCCCC	59.8	517	INTRON	Ca_11700	C		Ribosomal protein/NADH dehydrogenase domain
CaPOPI_5311	Ca7	30280166	GAAA/GAAAA	GATGTCCTCTCCATGCCATT	ATGTGAAGCATAGGCTTGGG	59.9	300	INTERGENIC				
CaPOPI_5312	Ca7	30294894	A/AT	GTCGTGGTCCTACTCCGAAA	AAAGTCGCATCCTCTCAAAAA	60.1	320	INTRON	Ca_11698	QI	bHLH	Cytochrome P450
CaPOPI_5313	Ca7	30298307	GATATATATA/GATATATA	GCTTGGTGTCCCAACAAGT	TGGGACCAAAACAGAAGAGAA	60.0	583	INTRON	Ca_11698	QI	bHLH	Cytochrome P450
CaPOPI_5314	Ca7	30298620	CTATATATATATA/CTATATATATA	GCTTGGTGTCCCAACAAGT	CTTTCATGCATGCCGATTTA	60.0	923	INTRON	Ca_11698	QI	bHLH	Cytochrome P450
CaPOPI_5315	Ca7	30303300	AACACACACACA/AACACACACA	GAACCGATGGTTACACTCCAA	CGTCATCGGATTGAAGGAAT	59.8	666	INTERGENIC				
CaPOPI_5316	Ca7	30308260	GAAAAAAAA/GAAAAAAAA	ACCCATGTCGTCATCCATTT	ATCATGGCTCCTATGGTTGG	60.1	602	INTRON	Ca_11697	QI	B3	Cytochrome P450
CaPOPI_5317	Ca7	30309875	GTTACTTACTT/GTTACTT	CAAAAAGACAAGGGAGAAATGA	TGGGATGGCCTATTATTGGA	59.6	125	CDS (FRAME SHIFT)	Ca_11697	QI	B3	Cytochrome P450
CaPOPI_5318	Ca7	30317892	T/TTG	CATTGCACGAAAATGTGGTC	TTGCCTTTTCAATTTTTCGG	60.0	633	INTRON	Ca_11696	QI	B3	Cytochrome P450
CaPOPI_5319	Ca7	30359172	CT/CTTT	CGGATAAGCACGCTCTTAGG	GAGATTGAAGGGTTTTGCCA	60.0	349	DRR	Ca_11693	O	C2H2	PUG domain
CaPOPI_5320	Ca7	30365181	CAAAA/CAA	TTTTCTTCTGCGATTCTTCTT	CGGTCACATTGGAACACAAG	60.1	610	INTRON	Ca_11693	O	C2H2	PUG domain

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CaPOPI_5321	Ca7	30365537	GAAAAAAAA/GAAAAAAAA	CTTGTGTTCCAATGTGACCG	GCAATACCAGCTTAGAGGAAGC	60.0	299	INTRON	Ca_11693	O	C2H2	PUG domain
CaPOPI_5322	Ca7	30366631	CTCTTCT/CTCTTCTTCT	TCACTTTTGGAACAGCCATTT	AAAAATCCTGTGCGATTCCA	59.6	867	INTERGENIC				
CaPOPI_5323	Ca7	30394719	TATA/T	TCATCTTCGATGCAATCA	TGTCGTCGGATTAAATGTTTT	60.2	375	INTRON	Ca_11690		MYB_related	Glycoside hydrolase, family 16
CaPOPI_5324	Ca7	30394911	TAAAAAA/TAAAAA	TCATCTTCGATGCAATCA	TTTTCTCACCAATCAAGCTGTC	60.2	783	INTRON	Ca_11690		MYB_related	Glycoside hydrolase, family 16
CaPOPI_5325	Ca7	30395077	AAGAGTTTA/AA	AAAGGTGCTCGCATCTATGTA	TTTTCTCACCAATCAAGCTGTC	57.6	540	INTRON	Ca_11690		MYB_related	Glycoside hydrolase, family 16
CaPOPI_5326	Ca7	30395813	CTATATATATAT/CTATATATATAT	TCGATTCTCTCCCATGAATC	AGGGAACGAAATTCTGCTCA	59.1	556	INTRON	Ca_11690		MYB_related	Glycoside hydrolase, family 16
CaPOPI_5327	Ca7	30415401	ATG/A	GGAGTCATTCTCTCCCATGAA	GTCCTCGTCCCTCATGTGT	59.1	683	INTERGENIC				
CaPOPI_5328	Ca7	30420041	AATGTATCTA/AA	ATGCAGGGATTAGGCAGTTG	CCGATTCTATCATCGGC AAT	60.1	667	INTERGENIC				
CaPOPI_5329	Ca7	30662891	TAAAAAAA/TAAAAAA	TTGGGGTAGTAAACCTCAAGAGT	GGTCTGGGTGTCAAACCTGT	59.5	275	INTERGENIC				
CaPOPI_5330	Ca7	30668720	ATTTTAATTATAATAATTTTAATTATAA T/ATTTTAATTATAATAATTTTAATTATA ATAATTTTAATTATAAT	TTGACACCAACGGAACGTAA	CAAGGTAGCATCCCCCACTA	60.0	905	INTERGENIC				
CaPOPI_5331	Ca7	30709199	T/TA	GCTGCAATTTCTGAAGCAT	TTTGGAGGCTCAATTTTGCT	60.2	724	INTERGENIC				
CaPOPI_5332	Ca7	30744719	GAAAATTAAAAAA/GAAAATTAAAAAA ATTAAAAAA	ACTCCATGAATCACGAAGGC	CCCACACTCATATTCCC ACTC	60.1	668	INTERGENIC				
CaPOPI_5333	Ca7	30746774	TAAAAA/TAAAAA	GTTTTCACCCAATCAACA	ATCGTGTTCTGTAGGGGAGTT	59.4	588	INTERGENIC				
CaPOPI_5334	Ca7	30760339	AA/AACA	TCAGCCAGAATTCATTTCC	CGCGTATGAGTTGTTGTCGT	60.0	399	INTERGENIC				
CaPOPI_5335	Ca7	30763146	C/CAG	CTTAGCCAGAGATTGACCG	CCATTGCCAAAGGACAGATT	60.1	237	INTRON	Ca_23324		HD-ZIP	Homeobox

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5336	Ca7	30770470	GAA/GAAA	GAAAAAGTTGGGCCGACATA	CCATGGCTGATAATGGTGTG	59.9	488	INTERGENIC				
CaPOPI_5337	Ca7	30778209	CTATAAATAGAAT/CTATAAATAGAATTA TAAATAGAAT	CAACATCAATTACATCTCTTCG	CAACCAAGCTTACGATGCAAA	59.6	178	INTERGENIC				
CaPOPI_5338	Ca7	30795636	A/AAAC	AAAGCTGAGAAGCAATC CAAA	CATGGCGTCTCACCTACCTT	59.1	354	INTERGENIC				
CaPOPI_5339	Ca7	30805803	AAGAAATAGAAATAGAAATAGAAA/AAG AAATAGAAATAGAAA	CCTCGCTTTGCTACTCTGGT	CTGCGGCAGACTGTAAACAA	59.6	771	INTRON	Ca_23321	O		Peptidase M16, N-terminal
CaPOPI_5340	Ca7	30806501	TG/T	GCTCGTCATGGGGAGTAAA	GAAATACCCCGCCAGTGTTA	60.1	673	INTRON	Ca_23321	O		Peptidase M16, N-terminal
CaPOPI_5341	Ca7	30807395	T/TA	TAACTGCGGGGGTATTTC	CTCGTCAAGACGGACATGAA	59.8	720	INTRON	Ca_23321	O		Peptidase M16, N-terminal
CaPOPI_5342	Ca7	30824955	TTTGGGT/TT	CCAAAATTTAAGCGCCA AAC	TGACTCGGATTCTTTTC CAGA	59.6	577	INTRON	Ca_23321	O		Peptidase M16, N-terminal
CaPOPI_5343	Ca7	30840351	TAAAAAAAA/TAAAAAAAAA	TTGAGACGCTAACAATTATATGCAA	CAAATTTGGGTACACCAATCA	60.1	554	DRR	Ca_23320			
CaPOPI_5344	Ca7	30858655	TCATAACATA/T	TTGGGTGCAAAATTGAA AAA	CGTTGTTCCAACATACAGGTTA	59.0	860	DRR	Ca_23319	T	HB-other	Protein kinase, catalytic domain
CaPOPI_5345	Ca7	30869621	CA/CAA	CAAACCGATGTGTCATT CCA	CCAATTCTCACGGATT TGT	60.4	492	INTERGENIC				
CaPOPI_5346	Ca7	30870269	GTTGAATACACTTGAATACACTTGAATA CACTTGAA/GTTGAATACACTTGAATAC ACTTGAA	TTAAGATTGGTTGGGCTGC	GAACCAGACCCAGCAGTTGT	60.1	307	INTERGENIC				
CaPOPI_5347	Ca7	30874290	TAA/TAAA	TTGTCTCAACAATCTCCC CC	ACCACCTCACTGCCCTACAC	59.9	734	DRR	Ca_23317			
CaPOPI_5348	Ca7	30930614	TCC/TC	CCACTCAAGGCCAGTGATTT	ATGAGCAGCACCAACATCAA	60.1	222	DRR	Ca_23314			
CaPOPI_5349	Ca7	30967683	ATTTT/ATTTT	CCCCATGATCTTCCCTTTT	GCAACAAACCTATGGCAGGT	60.1	355	DRR	Ca_23312			
CaPOPI_5350	Ca7	31087270	TAAAAAA/TAAAAAA	ACAGGGAGCTCCATTTCTT	TGCAATGCAATGTCCATTTT	60.1	190	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5351	Ca7	31112471	TGG/TG	GCAAAGGCACTCATTCC ATT	GCAAAAACACGAGAAGG AGG	60.1	493	INTERGENIC				
CaPOPI_5352	Ca7	31133335	GTTTT/GTTTTT	TTCTCAATCATTACTCCG ACCA	TCACCGATCACTTACGT TGC	59.6	562	INTERGENIC				
CaPOPI_5353	Ca7	31146442	TTATATATAT/TTATAT	TAGGGATTGAGCTGGCT CTG	TAGAAGACCTTGACCGT GCC	60.5	765	INTERGENIC				
CaPOPI_5354	Ca7	31152594	CA/CAAA	TGAACACTTAGACCGTG TTGG	CAGCGTAATGCCGACCT ATT	60.1	540	INTERGENIC				
CaPOPI_5355	Ca7	31154886	ATTTTTTT/ATTTTTTTT	CTGCGATAATGACGATG ACG	TGTAACCTCTTGACTTTG TCCTTTTG	60.2	627	INTERGENIC				
CaPOPI_5356	Ca7	31167770	TATAGA/TA	TCGAGATGTCATCGCAA ATAA	TTTTGTCTCCCTCACTC CG	59.3	316	DRR	Ca_10142	Q	E2F/DP	ABC transporter-like
CaPOPI_5357	Ca7	31175781	ATT/ATTT	TTGCACCATAAAAGTGC AGC	CTCACCCACCATAGCA TTT	59.9	592	DRR	Ca_10141	C		Malic oxidoreductase
CaPOPI_5358	Ca7	31181804	T/TCAAAA	TCACACACAAATTGAA GATGGA	CCATTGCTTGCATTGATT TG	60.4	600	INTERGENIC				
CaPOPI_5359	Ca7	31188755	TAAAA/TAAAA	TTAACCAATGACACTGG AAGG	CCCTCAAATCATCTTCAA ATCA	57.6	848	INTERGENIC				
CaPOPI_5360	Ca7	31188947	ATTTTT/ATTTT	TTGCACGTTGAATTAAAA ACTCTT	TCACGCTTTCTTCGTTTC CT	59.3	501	INTERGENIC				
CaPOPI_5361	Ca7	31196149	ATTTT/ATTT	CAACCAAGATTTTGATG AGTCG	CACGAGGGTAGTTTTGT CTTTC	59.6	622	DRR	Ca_10138			
CaPOPI_5362	Ca7	31199747	TGG/TG	TCAAGCGATTCACGAC AAG	TGGTCGTGTGCGTTTA AGA	60.0	406	DRR	Ca_10137		bHLH	Protein kinase, catalytic domain
CaPOPI_5363	Ca7	31202147	TA/TAA	CATGCTCATGGAATCAG GTG	ATTTGGCGTTGTCCTTTT TG	60.1	370	INTRON	Ca_10137		bHLH	Protein kinase, catalytic domain
CaPOPI_5364	Ca7	31204267	TAAATTAAACAAAT/TAAAT	TCCTAAGCCACCAATGA TCC	CTGGTGATCCTTTTCCT CCA	59.9	267	INTRON	Ca_10137		bHLH	Protein kinase, catalytic domain
CaPOPI_5365	Ca7	31205971	CAAAAAAAAAAAAA/CAAAAAAAAAA	ACCTGGCAACACATCAA ACA	TGCAAGTCGCTTTCTCC TTT	60.0	785	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5366	Ca7	31210939	CTC/CTCAATC	CCTTTCTCAGCCCATAT CCA	TCAACAATGCAAACGAA GGA	60.0	306	DRR	Ca_10136		ARF	AUX/IAA protein
CaPOPI_5367	Ca7	31213637	TAAAAAA/TAAAAAA	GTTTGCATGCACCACAA TTC	AAAGAAGCCACGAAAAG GGT	60.0	356	INTRON	Ca_10136		ARF	AUX/IAA protein
CaPOPI_5368	Ca7	31215378	GAAAAAAA/GAAAAAAA	GTTGTGCCGCTTAAGTT GGT	ATGGGACCACTTGGTGG TAA	60.2	854	DRR	Ca_10135	G		Hexokinase
CaPOPI_5369	Ca7	31215551	AT/ATT	GCACTGGATTGGAAAT TGG	ATGGGACCACTTGGTGG TAA	60.3	496	DRR	Ca_10135	G		Hexokinase
CaPOPI_5370	Ca7	31231997	CATATATATATATATATAT/CATATAT ATAT	TCGTTGAAACCATACGA CCA	TCCTTGTAATTTGATTA CCCCA	60.0	909	INTERGENIC				
CaPOPI_5371	Ca7	31252978	GTTATTTATTTATTTA/GTTATTTATTTAT TTATTTA	TCCATTGACTGCTCCT TTT	TTGCAACACTTTCTGGA GCA	59.7	567	INTERGENIC				
CaPOPI_5372	Ca7	31257051	TAAAA/TAAAA	ACAATGAGGCTGAGGGA GAG	GCCTTCACAAAGTAGCT GGC	59.4	178	DRR	Ca_10132			IQ motif, EF-hand binding site
CaPOPI_5373	Ca7	31277211	TAAAAAA/TAAAAAAA	GGTGCAATTGAGTTTGC TGA	CCACAAGTTCTGGGGA AAA	59.8	336	INTERGENIC				
CaPOPI_5374	Ca7	31294686	AA/AAACA	ACGAAAACCAATCCAAT CCA	TGAATCTGTGAACCGCA TGT	60.2	753	DRR	Ca_10130	O		Peptidase M16, zinc-binding site
CaPOPI_5375	Ca7	31300454	TTAAA/TTAAATAAA	CAGGCCATAAAGTCGAT GGT	CAACATTTAATGGATGG GGG	60.0	592	DRR	Ca_10129		C2H2	ATPase, AAA+ type, core
CaPOPI_5376	Ca7	31302590	CAATGTCAGA/CAATGTCAGAGTAGAAA AATGTCAGA	CATGTTCTTGGAGACGC AGA	GCTGTTTCAAATGCCAG TGA	60.0	691	INTRON	Ca_10129		C2H2	ATPase, AAA+ type, core
CaPOPI_5377	Ca7	31313382	GTTT/GTT	ATTTCCTTTGAAGCACAC GG	ACCCCTGTAGCACCCA CAC	60.1	799	INTRON	Ca_10128			
CaPOPI_5378	Ca7	31330956	AT/ATT	TTGTTCTCCTTTGCCAC CTT	TGTGATGATGTCATGGG GAC	59.7	156	INTRON	Ca_10126	R		Inositol oxygenase
CaPOPI_5379	Ca7	31335294	CAAG/CAAGGAAG	TTTCTTTCCGTTTCCAAT GC	ACAGCCTGTGCACTGTT TTG	60.1	605	INTERGENIC				
CaPOPI_5380	Ca7	31352192	CAAAA/CAA	GCGAGCAAAATCTGAAC CAT	TGTTAGGGTCAGTTCTG CCA	60.2	245	DRR	Ca_10122	U		Vacuolar protein sorting-associated protein 26

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5396	Ca7	32650059	TAATAATGTAAAAA/T	ATGGGACTGTGGGAGA GAGA	GAAAAAGGCTTCAACA TCAAA	59.6	398	INTERGENIC				
CaPOPI_5397	Ca7	32653182	G/GA	TTTTCAAATTTCCGGTT GC	CCAATTCCTGTGGAAAT GCT	59.9	582	INTERGENIC				
CaPOPI_5398	Ca7	32654894	AAATAATAATAATAAT/AAATAATAA TAATAATAATAATAAT	AACGAAGTGAGACGTGA GCA	TGATGGCTATGGTGGAA CAA	59.6	618	INTERGENIC				
CaPOPI_5399	Ca7	32655163	TTAATA/TTA	AACGAAGTGAGACGTGA GCA	TGATGGCTATGGTGGAA CAA	59.6	618	INTERGENIC				
CaPOPI_5400	Ca7	32655249	TATTAATTAA/TATTAA	TGTTGTTCCAAATTTTAC CTGAA	TACAGACCGGGCTCAAA ATC	58.6	935	INTERGENIC				
CaPOPI_5401	Ca7	33055618	CTGTG/CTG	TCTCAAGGTGAATCTG ACAAA	TTATCATGCGCTGAAAA ACG	59.7	345	INTERGENIC				
CaPOPI_5402	Ca7	33061943	TA/T	CGATCAATGACTGTCCA ACG	TCCCTTTAGAATTGACG CTTTT	60.1	252	INTERGENIC				
CaPOPI_5403	Ca7	33068212	ATTT/ATT	CTTCTTCGTATCCATTG GC	AAGCCTATCACTCATCC AATCAA	60.6	624	INTERGENIC				
CaPOPI_5404	Ca7	33069173	ATTTT/ATTTT	TGACATGCATGATTCAA CTGG	TTTGAATTGGTCCCTGA TTTT	60.5	617	INTERGENIC				
CaPOPI_5405	Ca7	33102819	ATT/AT	AACAGTCCCGCATTGGA TAG	CAGCACTGTCCAAATTG TGC	60.0	447	INTERGENIC				
CaPOPI_5406	Ca7	33211070	TAA/TAAA	ACCTGCCATCTTTTGAG CAT	AATTTCCGTCGGGTCTT TTT	59.7	622	INTERGENIC				
CaPOPI_5407	Ca7	33237657	GATATAT/GATATATATAT	TTTGGCCTTATCACCCA AAC	CAACTTGGTTCAACGCA AAA	59.8	171	INTERGENIC				
CaPOPI_5408	Ca7	33247703	ATCTCT/ATCTCTCT	TGTAACGCGTAGGGTAA GGG	TAAGCATCCGCTTCTTC AGG	60.0	136	INTERGENIC				
CaPOPI_5409	Ca7	33251332	AAATAAT/AAAT	TGTTGATAAATGATAATT GGTTGTTG	GACTATCGCTCCCCTAA GCC	59.2	836	DRR	Ca_16152	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_5410	Ca7	33275253	TAAAAA/TAAAAAAA	TTTAATGTATTGGATCAC TCCTCC	CTGGCTCTCTCACATG ACA	58.5	393	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5411	Ca7	33288649	ATTT/ATTTT	TCCCCTTCTCGTATTG CAC	TTTTGGACCGAATATGA TTATGC	60.1	442	INTERGENIC				
CaPOPI_5412	Ca7	33295433	GTTAATTA/GTTA	CGACCACGAGTTTAATC GAA	AAAAGGAACAACCGTCG TCA	58.8	510	INTERGENIC				
CaPOPI_5413	Ca7	33298775	AAG/AAGAG	TGGAAAACCCCTGCATT AAG	CACCCAACCATTTGATG TCA	59.9	571	INTRON	Ca_16157			Tify
CaPOPI_5414	Ca7	33329178	GTTTTT/GTTTTTTT	TCACCTTCTGACCTTGA ATGAA	TGGTGGGCTATGAACAA ACA	59.7	619	INTERGENIC				
CaPOPI_5415	Ca7	33343840	TA/T	TGGTGACTGGTGAGTT CAA	CGTCGATTTCAAGCACT CAA	60.1	519	DRR	Ca_16160			
CaPOPI_5416	Ca7	33350171	TG/T	TGTGGCTGAAGTCAATG AGC	AATTTGTCTCAACAACC CG	60.0	547	INTRON	Ca_16161	YU		Nuclear pore protein 84/107
CaPOPI_5417	Ca7	33358560	CTTGT/CTGTGTGT	AACAAGGGCAAGTTGGT TTG	GGGTTTTTCCCCTTCAC AAT	60.0	397	INTRON	Ca_16161	YU		Nuclear pore protein 84/107
CaPOPI_5418	Ca7	33412820	ACATATCGAATT/ACATATCGAATTTCC ATATCGAATT	TTTCTTGCTTTCAACTCG CA	CCAGTTTCTCAATCCCTT GG	59.7	548	INTRON	Ca_16164		C3H	Zinc finger, CCCH-type
CaPOPI_5419	Ca7	33413065	CA/CAAA	AATTTGACAACCTTGGC ACC	ATGGTGGAGGGGAGAA AAAG	59.8	508	INTRON	Ca_16164		C3H	Zinc finger, CCCH-type
CaPOPI_5420	Ca7	33472559	ATTTTT/ATTTT	GCTGCAAAGGATTGAGG ATT	TGTCTCGTCATCGTTTT CCA	59.3	532	INTERGENIC				
CaPOPI_5421	Ca7	33473339	TAAAAA/TAAAAA	TTAAAGTCAGTGGGTAG CTCAAA	TTGCCAAAATTATGCATG TGA	58.1	185	INTERGENIC				
CaPOPI_5422	Ca7	33473368	TAAAAAAA/TAAAAAAA	TTAAAGTCAGTGGGTAG CTCAAA	TTGCCAAAATTATGCATG TGA	58.1	185	INTERGENIC				
CaPOPI_5423	Ca7	33519406	ATTTTTTT/ATTTTTTTTT	CGCCGCCATTTTATTAT CAC	TTTGCCTTTTGTATGGAA CA	60.3	802	INTERGENIC				
CaPOPI_5424	Ca7	33524828	A/AAATGTC	CCGAGAACACGAGATGG ATT	ACCAAGTCTTGCTGAGC ACT	60.1	316	INTRON	Ca_16172	S	M-type	NADH:ubiquinone oxidoreductase intermediate-associated protein 30
CaPOPI_5425	Ca7	33528371	ATTTTTTT/ATTTTTT	GAATATTTGGTGAGAT CGCA	AATGGAGCGGAATTTTC CTT	59.9	482	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5426	Ca7	33532784	T/TG	GCCTAGCTCAGAAGACA AGTCC	CGATGCTTCATTATAAT CAACTCTT	59.7	534	INTERGENIC				
CaPOPI_5427	Ca7	33539636	GTTT/GTTT	AAATTGGACGGTGCTAA TCC	CACGAAAGGTTTCATCA CAAA	58.9	243	INTERGENIC				
CaPOPI_5428	Ca7	33558611	TTTG/TTGTAGTTTTTG	TTCAAGGACATTGCCAA TTTAT	TGCATTTTCCTTCTTCC ACTT	58.5	492	INTERGENIC				
CaPOPI_5429	Ca7	33559679	CTTTTT/CTTTTTT	GCTCATTGCAAGAAGAG GATG	TCTCAAAGTGACAATGG TGTGA	60.0	417	DRR	Ca_16175	QI	B3	Cytochrome P450
CaPOPI_5430	Ca7	33561063	GTACTATTCATAC/GTACTATTCATACTA TTCATAC	CGTGTACTCCCCTTCC CTT	GGCCATTTGTGCAGAT TTT	60.4	431	DRR	Ca_16175	QI	B3	Cytochrome P450
CaPOPI_5431	Ca7	33561157	TATCATCATCAT/TATCATCAT	CGTGTACTCCCCTTCC CTT	GGCCATTTGTGCAGAT TTT	60.4	431	DRR	Ca_16175	QI	B3	Cytochrome P450
CaPOPI_5432	Ca7	33576122	GTTTTTTTTT/GTTTTTTTTT	TAATTTAACGAACGGCC GAG	TTGGGTGACTCATGGTG AGA	60.1	410	DRR	Ca_16178	I		Synaptotagmin, N-terminal
CaPOPI_5433	Ca7	33597364	CTAATTAATT/CTAATT	GATGTTAACGCACCTCC ACC	CACACTTCGATCTCCGA TCA	60.4	483	INTERGENIC				
CaPOPI_5434	Ca7	33605853	TATAATTAAATAAAT/TATAATTAAAT AATAATTAAATAAAT	CCACACACCCTCATAGC CTT	TTTAAACCCCGTCAACA CCT	60.0	665	INTERGENIC				
CaPOPI_5435	Ca7	33606263	TT/TTCT	TTTCAAGACAGGTGTTG ACG	AAGTGTTCATTTGTTTG TGATTTT	59.9	529	INTERGENIC				
CaPOPI_5436	Ca7	33619410	TTTCCTTCCTT/TTTCCTT	TCGTGGCTCATTCCACA TTA	GGGTTGTGTCCCAAAAG CTA	60.1	431	DRR	Ca_16179	J		Ribosomal protein/NADH dehydrogenase domain
CaPOPI_5437	Ca7	33638562	AATGAAT/AATGAATATGAAT	TCGCAAGAGTTTGACCT TTT	TTCTAAAACGGAAAGC TATTTTGA	59.9	643	INTERGENIC				
CaPOPI_5438	Ca7	33638744	A/AC	TCGCAAGAGTTTGACCT TTT	GCACATGGTTTGAATG TTG	59.9	882	INTERGENIC				
CaPOPI_5439	Ca7	33640082	TAA/TAAA	CCAAATCGTCGGTGTGA ATA	CCTTTGTTTGTGGGAT CAT	59.4	614	DRR	Ca_16180		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_5440	Ca7	33640133	CAAA/CAAAAATAAAA	CCAAATCGTCGGTGTGA ATA	CCTTTGTTTGTGGGAT CAT	59.4	614	DRR	Ca_16180		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5441	Ca7	33644014	TTTTT/TTTTCTTTT	GTGCCCCACAACCTCTGTTT	TGTTTTTATCCAATCCAAATCA	60.0	489	INTERGENIC				
CaPOPI_5442	Ca7	33644686	TTTA/TTTATTA	TTTTCTCAATCAAGAGGCCA	CAATATGACATGACGGCTGG	58.4	581	INTERGENIC				
CaPOPI_5443	Ca7	33645082	CTT/CTTT	TTGACATTGCGCTTCTCAAG	CAATATGACATGACGGCTGG	60.1	202	INTERGENIC				
CaPOPI_5444	Ca7	33662614	ATTTTTTT/ATTTTTTTTT	AAGGCACTCAAAACAATGGG	GGGAACTAATTAATGTGAACATTGTC	60.0	528	INTERGENIC				
CaPOPI_5445	Ca7	33662685	TTATATATAT/TTATATAT	AAGGCACTCAAAACAATGGG	TGAATTTGGATTGTCAAATGATG	60.0	662	INTERGENIC				
CaPOPI_5446	Ca7	33662861	CAAAAAA/CAAAAAAA	AAGGCACTCAAAACAATGGG	TGAATTTGGATTGTCAAATGATG	60.0	662	INTERGENIC				
CaPOPI_5447	Ca7	33662912	ATTTTTTTTT/ATTTTTTTTT	AAGGCACTCAAAACAATGGG	TGAATTTGGATTGTCAAATGATG	60.0	662	INTERGENIC				
CaPOPI_5448	Ca7	33663454	TA/TAA	GGTCCAACAAGTCACTCATGTC	AGTCAACTCAACAGCTCATGGA	60.6	137	INTERGENIC				
CaPOPI_5449	Ca7	33672380	CATTA/CATTAATTA	CTCTGTGTTGGGCCAAGATT	TCACAGGAGACACGTAGATGAAA	60.1	347	DRR	Ca_16181		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_5450	Ca7	33683185	GCAAGTCA/GCA	GGGCATTTCAAGGAATATGTTTT	GATTGAGCCGAAAGTGAAGC	59.2	919	INTERGENIC				
CaPOPI_5451	Ca7	33713974	ATTTTT/ATTTT	CTATGGGCCGACCTTGAATTA	CCAATTGGTCCCTCAGAAA	59.9	699	INTERGENIC				
CaPOPI_5452	Ca7	33726416	T/TC	TAAATTGCCGTGACGATGA	TCGATTCAGATTGAAGGCTTTT	60.1	366	INTERGENIC				
CaPOPI_5453	Ca7	33766122	ATTT/ATTTT	AATATTTGGCTCCACCAACA	GGGTACAAACTTCTGCTCCA	60.2	564	INTRON	Ca_16185			Initiation factor 2B-related
CaPOPI_5454	Ca7	33768691	TAAA/TAAAA	TCATGTGGGGAAGAAATCA	AAAAAGACAAAACCTACCCTTGTA	58.9	577	INTERGENIC				
CaPOPI_5455	Ca7	33770972	ATTTTTTTTT/ATTTTTTTTT	TTTCTTTCTTCCGATTTAGTCC	TGGCTCGTTGGGCTAGATTA	60.0	639	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5456	Ca7	33774070	CAAA/CA	TTATGGCCCGCTAAATGAC	TGCTTGACAGAGTTGGATA	59.9	776	INTERGENIC				
CaPOPI_5457	Ca7	33781250	AA/AATA	TTGAGGTGACTAAAGCTCCGA	TCGAACCACACAGAATCCA	60.0	379	INTERGENIC				
CaPOPI_5458	Ca7	33781676	ATT/ATTATTT	ATGGAATTCTGTGTGTTTCG	TCGTAAATACCAGCATCATCAA	58.4	508	INTERGENIC				
CaPOPI_5459	Ca7	33795392	GAAAAAAAAA/GAAAAAAAAA	TGGCCCTTCATCATATCTT	TAAACGAAGCTATGCCCCAC	59.3	441	INTRON	Ca_16187			
CaPOPI_5460	Ca7	33806939	AAAAAATTAATAA/AAAAAATTAATAA	AGGCATAGGCACAGGAAGA	TTCGATAGTCGCACAACAC	59.8	842	INTERGENIC				
CaPOPI_5461	Ca7	33810289	ATT/ATTT	AACTCAACGCCAAACCAACGAC	CCATGCTTGGATTTTGTCTT	60.2	232	INTRON	Ca_16189		C3H	Remorin, C-terminal
CaPOPI_5462	Ca7	33812293	TCACA/TCACACA	TTGGATGAAAGAGACAAACGAAA	GTATCCATGAATTGGGGGTG	59.9	687	DRR	Ca_16189		C3H	Remorin, C-terminal
CaPOPI_5463	Ca7	33813164	TAA/TA	TAAAGAATTGCATTGGCCC	GGAAGAGTGATCCTCAACCC	59.9	471	INTERGENIC				
CaPOPI_5464	Ca7	33814827	TAT/TATTATAGTTTTTAACCAT	TGTTTGATGGCGTTAATGTGA	TCTTTAATCTTTGCAAAATCAATGG	60.0	422	DRR	Ca_16190	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_5465	Ca7	33815491	GT/GTT	TTTGTTTTTCATGCATGTGTCC	TCTGCATGGCAGTGAATAGC	59.4	162	DRR	Ca_16190	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_5466	Ca7	33815769	TAAA/TA	ATGGCTATTCACCTGCCATGC	ATCATCCTTGGTCCCGATA	61.0	434	DRR	Ca_16190	E		1-aminocyclopropane-1-carboxylate synthase
CaPOPI_5467	Ca7	33843751	TTTCTATTTCTCCTCT/TT	TAGAGCATGGCATTTCACCA	GGCCTTTAAATTGGGCTTTC	60.2	229	DRR	Ca_16192		NAC	Pectinesterase, catalytic
CaPOPI_5468	Ca7	33855265	GTTTTT/GTTTT	TCCAGAAGATGGTGAGAGTGG	ACTTGATTGCACATGGATCG	60.2	578	INTERGENIC				
CaPOPI_5469	Ca7	33855439	CA/CA	TCCAGAAGATGGTGAGAGTGG	ACTTGATTGCACATGGATCG	60.2	578	INTERGENIC				
CaPOPI_5470	Ca7	33855544	CT/C	TGCAACATTTTACTCAATCCG	ACTTGATTGCACATGGATCG	58.7	137	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5471	Ca7	33855578	ATTTTTTT/ATTTTTT	CGATCCATGTGCAATCAAGT	TCCAACAAGCGATTTCCTT	59.5	497	INTERGENIC				
CaPOPI_5472	Ca7	33856959	GAAAAAAA/GAAAAAA	TCCCATCATAAATCTTGTGCC	ACTTTTGCTCTGGCTTCAA	59.8	161	INTERGENIC				
CaPOPI_5473	Ca7	33859459	AAG/A	AAAATGCGAAGATGTTTACGG	CTTCACCTCTCGTAGCACCC	59.1	768	INTERGENIC				
CaPOPI_5474	Ca7	33872304	T/TG	TCATGCCACTTTAATGCTG	TGCCAACCTTAACCACAGA	59.7	507	INTERGENIC				
CaPOPI_5475	Ca7	33880924	TAAAAAAA/TAAAAA	TTTTTGTAATGATTGCTTGAATTT	CCGTTTCACTTTACCTTCGC	57.1	711	DRR	Ca_16194	O		Ubiquitin-conjugating enzyme, E2
CaPOPI_5476	Ca7	34109983	GAAA/GAAAA	TCGGGACCCACTTATTTGAC	AAAATTGTGTGGTGGTGGT	59.8	497	INTERGENIC				
CaPOPI_5477	Ca7	34136390	T/TA	TGCCCATTAATCTTGTGCTC	AGGCTGATTCTCCCTTGAT	60.0	458	INTRON	Ca_21006	K	ERF	DNA-directed RNA polymerase, subunit 2, domain 6
CaPOPI_5478	Ca7	34138307	GTTTTTTTT/GTTTTTTTTT	CAAGATGCACAGGAGTGGA	GGACAAAGCATTCCTCCCTA	59.8	451	INTRON	Ca_21006	K	ERF	DNA-directed RNA polymerase, subunit 2, domain 6
CaPOPI_5479	Ca7	34173121	TAAAAAAA/TAAAAA	TCGGCAACCTAATTCAACCC	AATGCGTAACATTTGACCCC	59.9	609	INTERGENIC				
CaPOPI_5480	Ca7	34173546	GT/GTATCT	TGGGGTCAAATGTTACGCAT	TTTGATCTTCTTCGGTCGCT	61.1	499	INTERGENIC				
CaPOPI_5481	Ca7	34174102	CTTTTTTT/CTTTTTTTTT	AGCGACCGAAGAAGATCAAAA	GCTTGCAATTTGGGTGAT	60.0	509	INTERGENIC				
CaPOPI_5482	Ca7	34176709	TTTTATTT/TTTT	AGCGTTGAAATTATGGACCG	TCGTTTGTGTGCAATTGTTTC	60.0	682	INTERGENIC				
CaPOPI_5483	Ca7	34187425	GAA/GAAA	AGGTCTGGATTCGTGGTTTG	ACATCCGTGCAAGGAAAG	60.0	646	INTRON	Ca_21004	S		
CaPOPI_5484	Ca7	34189872	AATAT/AAT	CATTCAGGCATTTGTTCC	AAAACTAGGGCTATTTGGAGC	60.3	594	DRR	Ca_21004	S		
CaPOPI_5485	Ca7	34213991	TCAGAATTACAGAATTACAG/TCAGAATACAG	TGCGCGATCTCTAATCAATG	CGGCAACCTTACCTCAATCTC	59.9	763	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5486	Ca7	34238786	TAAA/TAA	ACACAAATTTAATATGGA TTGAGTACA	CAAAGCAAAACAAAGTG CCA	57.3	426	INTERGENIC				
CaPOPI_5487	Ca7	34241485	CTTTT/CTT	TGGTTGTTCCATCACAT GTCT	CAAAGCTACCACACCTT ACTTGC	58.8	536	INTERGENIC				
CaPOPI_5488	Ca7	34251183	AAT/A	AACCATGGGAACCAATT GAA	TGGCCCAATGGATCATT TAT	60.0	748	INTERGENIC				
CaPOPI_5489	Ca7	34256619	TCA/TCACA	CGGAGTGGACTCTAACC CAA	TTAGGTGATTCTATGCG CCC	60.1	532	DRR	Ca_20996	S		Basic helix-loop-helix, Nulp1-type
CaPOPI_5490	Ca7	34274334	AAATTATTTTCAA/AAA	AAAACCAACCGAGTCATC AGC	AGCCCGTTTGCTACCTT TTT	60.1	555	DRR	Ca_20991		M-type	Chlorophyll A-B binding protein, plant
CaPOPI_5491	Ca7	34274392	TAAAA/TAAA	ACCACCGAGTCATCAGC TCT	AGCCCGTTTGCTACCTT TTT	59.9	552	DRR	Ca_20991		M-type	Chlorophyll A-B binding protein, plant
CaPOPI_5492	Ca7	34276465	ATTCAC/A	ACACTTTGTTGTGGCAG CAG	CGTTGCCACAGTGATTT TGT	59.9	493	INTRON	Ca_20991		M-type	Chlorophyll A-B binding protein, plant
CaPOPI_5493	Ca7	34277307	T/TG	CAATGGCAGAAGAAGCA CAA	TTTGTGGTGCCAGTGTG AAT	60.0	335	INTERGENIC				
CaPOPI_5494	Ca7	34278471	T/TAAATAC	TTTGACCCATCAAATCAT CAAA	CCTTCGCCATTTAATTTT GG	60.2	102	INTERGENIC				
CaPOPI_5495	Ca7	34283992	GAAAAAAAA/GAAAAAAAA	CATAACCCATATGCGAG CAA	TCCATGAATTTGTCAACC GA	59.5	662	DRR	Ca_20990	A		Brix domain
CaPOPI_5496	Ca7	34286263	TAAAAAAAA/TAAAAA	ACGTCAGACATTGGATG TGC	TTGTTTTCAAGGAGTTG CGA	59.6	666	INTERGENIC				
CaPOPI_5497	Ca7	34286533	AAG/AAGAG	CCTCTAAAAATGGAAAT GACCA	GTCTCTGCCGCTGAAC CTT	59.4	793	INTERGENIC				
CaPOPI_5498	Ca7	34295146	AATTTGT/AATTTGTTATCTATTTGT	CCAACCTGGCCTAGGATG AAA	TGGGAGAAAAACAAGCA AGG	60.1	579	INTERGENIC				
CaPOPI_5499	Ca7	34305236	AATCATAACCATCATAACCATCATA/AATCATAACCATCATA	ACCGATGCATTGATGAA GGT	CAATGGTGTGCTTGTA CCG	60.3	806	INTERGENIC				
CaPOPI_5500	Ca7	34305420	CT/CTT	TGCAACTCTAGATGTGA GCCA	CAATGGTGTGCTTGTA CCG	59.6	727	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5501	Ca7	34312118	AAATTAAT/AAAT	TTGCTAATTGCTAATTGCTTG	TGGAGTGAGTGAGAAAGGAG	57.4	388	INTERGENIC				
CaPOPI_5502	Ca7	34312433	GATAAATA/GATA	CTCCTTTCTCACACTCATTCCA	TTGGTGGACTTCCCAACTTC	59.5	515	INTERGENIC				
CaPOPI_5503	Ca7	34312678	ATTTTTTTTT/ATTTTTTTT	CTCCTTTCTCACACTCATTCCA	TTGGTGGACTTCCCAACTTC	59.5	515	INTERGENIC				
CaPOPI_5504	Ca7	34314534	ATTTTTTT/ATTTTTTT	AAAGATGGCCTCAACCTATTCA	TTGACAATTGTTAGAAGTGATTCCA	60.0	453	INTERGENIC				
CaPOPI_5505	Ca7	34318595	CATTATTACAGATTT/CATTATTACAGATTATTATTACAGATTT	TCAATGACTGTGACAAATCCA	GCTAGCAGCCACCTTCTTTC	59.0	503	INTERGENIC				
CaPOPI_5506	Ca7	34319877	CTTGTTGTTGTTGTTGTTGTTGT/CCTTGTTGTTGTTGTTGTTGT	CCCACTCCATGTTCACTACC	AGCACCACCATCAATGTCAA	59.8	246	INTERGENIC				
CaPOPI_5507	Ca7	34321138	GAAAAAA/GAAAAAA	AAATTGGGGAGGGAAAAATG	TGAAGGCACCGACTCTTACA	60.0	247	INTERGENIC				
CaPOPI_5508	Ca7	34323694	TAAAA/TAAA	TATGAGCGGGTTGGATTGTT	ATGGGTACGGGTAATCCACA	60.3	402	INTERGENIC				
CaPOPI_5509	Ca7	34328524	TCC/TCCC	AGGGAGGCACCTTCGGAGTAT	TCAATTGCACAAACATCTGTA	60.1	433	INTERGENIC				
CaPOPI_5510	Ca7	34336122	T/TTTA	TATTTGACCCGTGAGACGTG	CAACCACAATTCAATTTATGCAA	59.6	539	INTERGENIC				
CaPOPI_5511	Ca7	34337758	TAAAA/TAAA	TGCAAAACAACTGCAAAAG	TGCAACATCCATTGATGACC	59.9	755	INTERGENIC				
CaPOPI_5512	Ca7	34342253	TTTT/TTTTATTTT	AATGATAGGTGGACGTTCAAA	GGGTAACCTCGCCACAACTA	57.1	725	INTERGENIC				
CaPOPI_5513	Ca7	34350011	AC/ACC	TTGAGTGTGGATGGCTTCA	GGAGATTCGTCGCTTCTTTC	60.2	439	INTRON	Ca_20986	C		Inorganic pyrophosphatase
CaPOPI_5514	Ca7	34383642	TTCT/TT	TTAATTCAGTCGATGCCACG	TCTGGAAAATACACGTTGAATACAT	59.7	841	INTERGENIC				
CaPOPI_5515	Ca7	34391793	CTTTTTTTTT/CTTTTTTTTTTTT	GGCGAGCATGAAATACCAAT	CAATTGATGCAGGCACACTAA	59.9	256	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5516	Ca7	34408338	GTTTT/GTTT	TTCCCCGGTGACATAACAGT	CACTGCATAAGCCTGCAAAA	60.2	758	INTERGENIC				
CaPOPI_5517	Ca7	34509865	AGAGAGAGAGAGAG/AGAGAGAGAGAGAGGGGAGAGAGAGAGAG	TTTGTGGTTCTTCCTCGACC	GGGTGGATACAAATGACCAA	60.1	173	INTERGENIC				
CaPOPI_5518	Ca7	34903171	AATATATATATATATATATATA/AATATATATATATATATATATATA	AAAGGCTCGAGGCATTTTAA	TGTCTGCATTTTAAGCAACGA	59.0	790	DRR	Ca_17624		ARF	Transcriptional factor B3
CaPOPI_5519	Ca7	35020588	GATATATATATATATATATATATA/GATATATATATATATATATATATATATATATA	ATACTCGCGTTTGCTTTTG	TACATGCATTGCTGGCATTAA	60.3	476	INTERGENIC				
CaPOPI_5520	Ca7	35121887	GAAAAAAAA/GAAAAAAAAA	AAAAATAATTGGCACAAACCA	GGGCAATTTTCTGTCTCCAA	58.5	851	INTERGENIC				
CaPOPI_5521	Ca7	35131579	T/TA	TCGTGGTCGATTGAACTTA	GAATCAAAATGGAGCGGAAA	60.3	376	INTERGENIC				
CaPOPI_5522	Ca7	35138981	ATTTTTTTTT/ATTTTTTTT	ATGGGTGCGTTTCTTTTTCAG	TCGCTCTCATCAATCACATCA	60.1	171	INTERGENIC				
CaPOPI_5523	Ca7	35148641	ATCTCT/ATCT	GTTGCCAAATGTTAGCCGTT	GTCTTTGTCAGGGGAGTGGA	60.0	221	INTERGENIC				
CaPOPI_5524	Ca7	35150109	TTTTATTTATTTATTTATTT/TTTTATTTATTTATTTATTTATTT	GGGGAAACTTTGGGGAGTA	CACCTTCGCCAATTTTCATCT	60.2	820	INTERGENIC				
CaPOPI_5525	Ca7	35154545	ATTT/ATTTT	TCCATGTCAGATTCGGAAGA	CAATGTCCATTTACGATGG	60.0	749	INTERGENIC				
CaPOPI_5526	Ca7	35154835	TTATATATATAT/TTATATATATAT	CAAAACGATAGAAAGATAATGCAAGA	CAATGTCCATTTACGATGG	60.0	374	INTERGENIC				
CaPOPI_5527	Ca7	35166389	CATGT/CATGTTATTTTATGT	ATCAAGGTGGGGATTGTGA	TTGTAGTTTTTCACGTGTGTC	60.2	781	INTERGENIC				
CaPOPI_5528	Ca7	35166415	TC/T	ATCAAGGTGGGGATTGTGA	TTGTAGTTTTTCACGTGTGTC	60.2	781	INTERGENIC				
CaPOPI_5529	Ca7	35166612	GAAAAAA/GAAAAA	TTCAATTTTGTGTTGTTGGAAA	TTGTAGTTTTTCACGTGTGTC	59.4	571	INTERGENIC				
CaPOPI_5530	Ca7	35175468	CC/CCTTC	TACTTTGCGTGTCTCGTCG	CCCATGAAGGAAAAATACGC	60.1	657	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5531	Ca7	35175572	AAATA/AA	GGCCATGGGAACATAA CTG	CCCATGAAGGAAAAATA GCG	59.4	239	INTERGENIC				
CaPOPI_5532	Ca7	35177660	AATA/ATAAAATAAATATA	GCCAACCGACTCCATCT TTA	TTTAGCAGTTTTCAATT TCCAA	60.1	690	INTERGENIC				
CaPOPI_5533	Ca7	35180198	AAAGAACAGAACAAGA/AAAGAACAG AACAAGACAAGA	GGGTTTTAGGTTGGGT GAT	TGTAACACGGTCCAATC CAA	59.9	203	CDS (large-effect mutations)	Ca_17639		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_5534	Ca7	35206628	GT/GTAT	CGGACATCTGTTGTCC TTG	TCCCATTTTATTTGTCCC CA	59.1	334	INTERGENIC				
CaPOPI_5535	Ca7	35206915	CATATA/CATA	TTGGGGACAATAAAAT GGG	AAACGTGTTTCGTATTT TGATG	59.5	548	INTERGENIC				
CaPOPI_5536	Ca7	35213604	CTTTTT/CTTTT	TTGGAGCAGTACCACT GACA	GCAATGTGTCAAAGGCT CAA	59.4	681	INTERGENIC				
CaPOPI_5537	Ca7	35217866	ATTTTT/ATTTTTTT	AAGGCTAGGATTCTCGG GAT	ATGCGGGATGTTCTTT CAT	59.2	369	INTERGENIC				
CaPOPI_5538	Ca7	35227195	GA/GACA	AAAGCGAACGCCATTTT AGA	TCAGAGCAACTGCACTT CAA	59.9	809	INTERGENIC				
CaPOPI_5539	Ca7	35230535	C/CAT	TCAAAATGGAAATGGG AAGA	TGGGTGAGGCTTTGCTA CTT	59.4	320	DRR	Ca_17641			
CaPOPI_5540	Ca7	35230825	ATTTTTTTTT/ATTTTTTTT	AAGTAGCAAAGCCTCAC CCA	CGGATAATTCAAATGG ATCACT	59.9	401	INTERGENIC				
CaPOPI_5541	Ca7	35275008	AGGTGGTG/AGGTG	CAACCTTGGTGTTGGC TTT	CTTCTTCATTGCGCTGG AAC	60.0	262	DRR	Ca_17646	R		
CaPOPI_5542	Ca7	35283537	T/TCCACGATGAA	GCCCAATTGTTTCAGTC AGT	CATCCTGAGGGCAGTGA TTT	60.0	770	INTRON	Ca_17646	R		
CaPOPI_5543	Ca7	35289806	CAAAAA/CAAAAA	ATTGGGAAAACCTTTGG TCA	GAAGGCAGTTGGGGAC ATA	59.3	315	INTRON	Ca_17646	R		
CaPOPI_5544	Ca7	35290233	TC/TCC	TATGTCCCAAACTGCC TTC	CCCAATTTTGAATTTTC TGT	59.9	442	INTRON	Ca_17646	R		
CaPOPI_5545	Ca7	35292570	GT/GTT	TGAACCAAAATTCATAT GGGA	GACCCCTCTTTGTAACG CAA	59.6	692	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5546	Ca7	35292736	ATTTTTTTT/ATTTTTTTTT	TGAACCAAAATTCTATATGGGA	GACCCCTCTTTGTAACGCAA	59.6	692	INTERGENIC				
CaPOPI_5547	Ca7	35292837	AGG/AGGG	TGCAGGATTAGTGGTGTG	GACCCCTCTTTGTAACGCAA	59.6	154	INTERGENIC				
CaPOPI_5548	Ca7	35313643	TC/T	TTCGATAAAGCAAAAGCTCCA	AACTGAATATGGGCCAGTCG	60.0	805	INTERGENIC				
CaPOPI_5549	Ca7	35317473	ATTTT/ATTTTT	CGATGCACACTCATTTTTGC	TGGTTCATTGCAATGGTTG	60.3	535	INTERGENIC				
CaPOPI_5550	Ca7	35330032	TTCT/TTCTCTCT	TCACGTGCACATATGCCTCTC	TCGGTGATGGGTATTTGACA	60.0	421	INTRON	Ca_17647	BK	FAR1	PWWP
CaPOPI_5551	Ca7	35333033	C/CT	TGCAAAGCACCCAATTGTAG	CTTTTCCATGCCACGGTACT	59.7	974	DRR	Ca_17647	BK	FAR1	PWWP
CaPOPI_5552	Ca7	35337950	C/CT	CATGATTGCTTTCCATGCAG	GGCTAGGGATGAACACCC	60.2	345	INTRON	Ca_17648		TCP	Zinc finger, RING-type
CaPOPI_5553	Ca7	35347410	T/TTATTTTA	AGTTTCCACATGTGATAAATTGC	CCTCCTATCCAACCCATGAA	58.1	749	INTERGENIC				
CaPOPI_5554	Ca7	35348488	GAAAAA/GAAAAA	GTGGGTGGTACAAGGTGGAG	AAGCAAATAACAAGGTGTGCC	60.3	669	INTERGENIC				
CaPOPI_5555	Ca7	35364737	AGATTAGGA/AGA	CGCATTCTCTCGAAAAGTC	TTGGAGAAAGATCTCCGGTT	60.0	439	INTERGENIC				
CaPOPI_5556	Ca7	35366366	CA/CAA	GCAGTGCACGGGTCTAA AAT	AGTAGTTGGGTGGACATGCG	60.1	877	INTERGENIC				
CaPOPI_5557	Ca7	35379781	ATTT/ATT	TCCTCATCACCTGCACAATC	TCCTCTACCCACCAAACCAA	59.6	445	INTERGENIC				
CaPOPI_5558	Ca7	35379825	CTTTTT/CTTTTTTTT	TCCTCATCACCTGCACAATC	TCCTCTACCCACCAAACCAA	59.6	445	INTERGENIC				
CaPOPI_5559	Ca7	35379938	G/GTGAGTT	TCCTCATCACCTGCACAATC	TCCTCTACCCACCAAACCAA	59.6	445	INTERGENIC				
CaPOPI_5560	Ca7	35385155	GT/GTT	TGCGAAATGTGAGAAATGAA	AAGTCAAGATGGCTTGGTGG	59.3	225	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5561	Ca7	35386085	CAAAAAAAAAAAAA/CAAAAAAAAA	TTGTTTCAAAGCTCCAG CAA	CATCGACAAAAGGAGT TTGA	59.6	505	INTERGENIC				
CaPOPI_5562	Ca7	35389419	TAAAA/TAAAAA	TTCGGTTCTGTCTGCC TCT	GCCGCGACCATTAATTC TAA	60.0	796	INTERGENIC				
CaPOPI_5563	Ca7	35442260	AG/A	TATGCTGTCCACCCATC AAA	CAAGCGCATGCATTTTC TAA	59.9	628	INTERGENIC				
CaPOPI_5564	Ca7	35535446	CTTTGTGTTTGTGTTTGT/CTTTG TTTGTTTTGTTTTGTTTTGT	CAGGCATGTAGAGCATT GGA	AGTTTGGCTCGTGATGG TTC	59.8	528	DRR	Ca_17760			Protein of unknown function DUF2358
CaPOPI_5565	Ca7	35684957	ATTTTT/ATTTTT	CCCCCTCTTAGGACCA TGT	TATCGCACTCCGACAAC AAA	60.4	592	DRR	Ca_17775	O	ERF	Glutathione S-transferase, N-terminal
CaPOPI_5566	Ca7	35794267	CTTT/CTTT	ATGTAGACGATTGCTTC CCG	GCAACAACTTTGCACT CCA	60.1	700	INTERGENIC				
CaPOPI_5567	Ca7	35921881	CTTTTTTTTT/CTTTTTTTTTT	TGCAATAAGATGAAAA CACCAA	GCATTGGAGCTGAAAAG GAG	59.5	332	INTRON	Ca_17797	A		Ribonuclease T2
CaPOPI_5568	Ca7	36117059	CTTTA/CTTTCTTTATTTTA	TGGATTGGGCTTTCCAA TAA	TGCCTTAACGTACCCAA ACA	60.3	435	DRR	Ca_13721	G	Trihelix	Protein of unknown function DUF604
CaPOPI_5569	Ca7	36244087	GTCTCTCTCTCTCTCTCTCTCT/G TCTCTCTCTCTCTCTCTCTCTCT	TCCATGAAACCAAGCA TGA	TGAATTTTCGGCAATCA CAA	60.0	681	INTERGENIC				
CaPOPI_5570	Ca7	36353585	TTAATTAATAAT/TTAATTAATAATTAA ATAAT	CACCGATGTGAATCTC TATTTTT	GCGTTTCAGCCAACTTG TGT	58.6	996	INTERGENIC				
CaPOPI_5571	Ca7	36358822	AAGAGAGAGAGAGAGAGAGA/AAGA GAGAGAGAGAGAGAGA	AAAACCCCAACTCAACC GTA	TCGCGCTTTCTTTCTCT CTC	59.3	587	INTERGENIC				
CaPOPI_5572	Ca7	36475569	GA/GAA	GAAATGTGAGTTTAATT CCCC	TGGCCTATGTGCTTCTA TTGG	59.3	235	INTERGENIC				
CaPOPI_5573	Ca7	36636517	AC/A	ACATAAGCCAAACAACC CCA	TGGCAACTTTGCTCGTC ATA	60.2	722	INTERGENIC				
CaPOPI_5574	Ca7	36803710	TTT/TTTTATT	AAGTGATCATTTGATGC ACAGG	TGACATGTGCAAAATTGA AAGG	60.0	720	INTERGENIC				
CaPOPI_5575	Ca7	36871436	AAGAGAGAGAGAGAGAGAGAGA/AA GAGAGAGAGAGAGAGAGAGA	TGAGCTGAAACAACATG CGT	TGTCGGGAACCATTTCC TTA	60.5	893	DRR	Ca_13774	R		Lipopolysaccharide-modifying protein

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5576	Ca7	36884880	TTTCTTCTTCTTCTTCTTC/TTTCTTCTTCTTCTTC	TTGGGGTAAGTTGGCTCTTG	TTCTACACGTTTGCAAGG	60.1	570	DRR	Ca_13775			
CaPOPI_5577	Ca7	37205527	A/AAT	TTGAAATAATTGCGTTGCCA	TGTGCCGATGATGATGTCT	60.1	666	INTERGENIC				
CaPOPI_5578	Ca7	37282057	GAATAAATAAATAAT/GAATAAATAAATAAATAAATAAATAAAT	GCGAGGGAATTATAGCCACA	TCGTGTAGCCAATAGCTTTGTT	60.1	374	INTERGENIC				
CaPOPI_5579	Ca7	37568106	CT/C	TGTGTTGCAAGTGTGCTTGA	CCAAGTCTCATCTGGAAAGCC	60.1	259	INTERGENIC				
CaPOPI_5580	Ca7	37569442	TCTGATGCTGATGCTGT/TCTGATGCTG	CCAACTGAGAAGCTTTTGGC	GATGCCTCCAACATGTTTCT	60.0	698	INTERGENIC				
CaPOPI_5581	Ca7	37595168	ATGTGTGTGTGTGTGTGTGT/ATGTGTGTGTGTGTGT	CGTTTTGCCTCCTTTTCAGTC	TGGAACCCGGTAGATACTTTG	59.9	805	INTERGENIC				
CaPOPI_5582	Ca7	37622315	TAAAAAAAA/TAAAAAAAAA	TACCCACGGTAGCTCTTTG	TTCGATCATCACCTCTACA	60.1	722	INTERGENIC				
CaPOPI_5583	Ca7	37711486	TG/T	TACCCTGTGGATGGGAATGT	TTGTCGATCCGAAATGTGAA	60.1	870	DRR	Ca_22800			
CaPOPI_5584	Ca7	37752611	ATTTTTTT/ATTTTTTTT	TCGACAAAATGCAATGTCGTA	CTGGTCCCTTATGACCA	60.1	860	INTERGENIC				
CaPOPI_5585	Ca7	37928727	GATATATATATATATATATATATA/GATATATATATATATATATATA	ATTGTGTCCGCAGGAATATC	GTGTGTGTTCCACTGCCATC	59.9	329	INTERGENIC				
CaPOPI_5586	Ca7	37964071	T/TTTCAA	CCACCATGCAAGGAGTTT	GCACGTGTGAATGAACGTG	60.0	470	DRR	Ca_16386		HD-ZIP	Homeobox
CaPOPI_5587	Ca7	38073484	GATAATAATAATAATAATAATAATAA TAATAATA/GATAATAATAATAATAATAA TAATAATAATAATAATAATAA	TGGAGAGAAACAAAATCGGG	TCTGTCTCGCTCACATACCG	60.0	424	INTERGENIC				
CaPOPI_5588	Ca7	38331525	AAGAGAGAGAG/AAGAGAGAGAGAG	TGTGCAACACCAAAACCTA	CATATCTGCTGCACCTTCC	60.0	174	INTERGENIC				
CaPOPI_5589	Ca7	38383093	ATTTTT/ATTTTTT	TTTCGACGACGATAAAACAATG	ATTTTGTGGTGATGTGCA	60.0	170	DRR	Ca_16412			
CaPOPI_5590	Ca7	38449321	ATA/ATATAATTA	GCGACTTTCACGTGGTTT	CCGATTTCCAAAGGTTT	60.2	501	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5591		Ca7	38457330	CATATATATATATA/CATATATATATATA TA	TCATGATGAGGCAATTT GGA	TTGGTTTATTTGGGTTG GGA	60.0	385	INTERGENIC				
CaPOPI_5592		Ca7	38539687	AATATATATATATATATATATATATA/A ATATATATATATATATATATATATATA	TGGCCATAAAATATGCC TGA	AGACCGAGTTATAGTTG TGTCG	59.0	635	INTERGENIC				
CaPOPI_5593		Ca7	38579414	TTATATATATATATATATATATATATA TATATATATATAT/TTATATATATATAT ATATATATATATATATATATATATA TAT	AGCCATGACTTCATAGT GCATC	CATTAGATGAAAGACAA AGTCCCA	59.2	859	INTERGENIC				
CaPOPI_5594		Ca7	38613431	CA/CATTAAGAA	TTGAGTGGGCTCTATAC CCG	CAAACTGCCGGTACTG GAT	60.1	796	INTERGENIC				
CaPOPI_5595		Ca7	38626397	GATAATAATAATAATAATAATAATAA TAATAATAATA/GATAATAATAATAATA TAATAATAATAATAATAATAATAATA	CCAAGCCCAATAAAACC CTT	GGACTCACTCCCCAAAT TGA	60.2	131	INTERGENIC				
CaPOPI_5596		Ca7	38669981	TTTTATTATTTATTTATT/TTTTATTTAT TTATTTATTTATT	CCTGCCGGTTTATTTTTC TTC	GCGATCGAATGGCAATA TCT	59.5	657	INTERGENIC				
CaPOPI_5597		Ca7	38743655	CTATTTATTTATTTATTTATTTATTTATT T/CTATTTATTTATTTATTTATTTATTTAT TTATTTATTT	CTTAGGTTTGCACTCAG CCC	CTCAATCGTGGGTGACC TTT	59.9	932	INTERGENIC				
CaPOPI_5598		Ca7	38744999	TTTATTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTATTA TTATTATT/TTTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATTAT	TCTTCTGTGGCCGACT CTT	TTGCAAAACCAAAAGG GAA	60.0	765	INTERGENIC				
CaPOPI_5599		Ca7	39149719	AT/ATT	GCACTAAGTCAGGGGCT CAG	TGGAACCCATTACACA AGA	60.0	577	INTERGENIC				
CaPOPI_5600		Ca7	39282936	GATATATATATATATATATATATAT/GAT ATATATATATATATATATATATATATATA TAT	TTCAATGTGAGCAAAGT CGAT	TCCCCAAATTCAATATC CA	58.4	391	INTERGENIC				
CaPOPI_5601		Ca7	39409758	TTATATATATATATATA/TTATATATATAT ATATATA	TTCAAACCTCAAACCAAT TCAA	GAACCAAAATCCCCCTC CAT	59.5	485	INTERGENIC				
CaPOPI_5602		Ca7	39525063	ATTTTTTTTT/ATTTTTTTTTTT	AACGACCAACTTGGGAA AAA	GGAGTGGGTCACCGAG AATA	59.4	520	INTERGENIC				
CaPOPI_5603		Ca7	39830592	AGGGGGGG/AGGGGGGG	CCTGCTCAAAGCACAG TTA	TAATCATCTCGGGTTG AGG	60.1	636	DRR	Ca_25100			
CaPOPI_5604		Ca7	39852561	AAAAATGTTAAAA/AAAAATGTTAAAATG TTAAAA	TTAATCCAACCATCACAC AAAA	CAAGCGCAGGTGTATGA AAA	57.9	749	INTERGENIC				
CaPOPI_5605		Ca7	39987914	ATTTT/ATTTT	CAAATAATGCACCACTC CCA	CAAGTCTGCCCACTAA ACC	59.4	141	INTERGENIC				

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									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5606		Ca7	40086967	A/ATTTGCTACC	GGTGAAACTGGGTGGA AGA	ATACAATTGTGCCTGCT CCC	59.9	880	INTERGENIC				
CaPOPI_5607		Ca7	40196153	AATATATATATATATATA/AATATATATAT ATATATATATA	TGAATGCCTACATATGG CGA	TTTGACCTTTATGGCGG TTC	60.1	741	INTERGENIC				
CaPOPI_5608		Ca7	40418637	TATAATAATAATAAAT/TATAATAATA ATAATAATAAT	CGGATTCACAAACGGAC TTT	GCATTCGATTATGCCGA TCT	60.0	888	INTERGENIC				
CaPOPI_5609		Ca7	40430153	AAGTAAGTA/AAGTAAGTAGTAAGTA	GTTGGTTCAAAAGCAAC CGT	ACAAGGATACGTGCAGG GAC	60.0	493	CDS (FRAME SHIFT)	Ca_20258		Trihelix	Transposase, Pta/En/Spm, plant
CaPOPI_5610		Ca7	40591240	AAATAATAATAATAATAATAATAATA ATAATAATAATA/AAATAATAATAAAT AATAATAATAATAATAATAATAATAA TAATAATA	TTGTTGGAATTGCATAG AATTGA	CACCGACCTCAAATTCA ACA	59.5	852	INTERGENIC				
CaPOPI_5611		Ca7	40985025	TAAAA/TAAAAA	GCAACTGCCTTAAAAAT GGAA	GGAACGTGCGTACATTG TTG	59.2	303	INTERGENIC				
CaPOPI_5612		Ca7	41008241	CAAAAAAAAAAAAA/CAAAAAAAAAAA	GCCAAATCAGGACACATC TCA	TCAGAACATTCCATCGG TGA	59.6	563	INTERGENIC				
CaPOPI_5613		Ca7	41009960	ATTTTTTTT/ATTTTTTTTTT	CATGACCTCGGTTTTC ATAA	CCCTCACATTTTAAAGG CACA	57.6	814	INTERGENIC				
CaPOPI_5614		Ca7	41010142	CAA/CAAAA	TGCAATGAATGAAAGTA TGCTACC	GAAAAAGCGCTGTAAAT GGC	60.4	815	INTERGENIC				
CaPOPI_5615		Ca7	41170096	T/TA	TAAGGTTGTCTGGGGAG GTG	CGGCGAATTTGTTTTCT TTT	60.0	667	INTERGENIC				
CaPOPI_5616		Ca7	41226170	AATATATATATATATATATA/AATATATAT ATATATATATATA	TTTCATCAATGGCACAAAG AAAA	TCCTTGGGGATTTTGTG AAA	59.1	500	INTERGENIC				
CaPOPI_5617		Ca7	41250872	AT/ATTATT	GTGATATTGGGGGTGCGA ATG	AAGGGTCCTCTTGAAGC GTT	60.0	680	INTERGENIC				
CaPOPI_5618		Ca7	41251256	AG/A	CCAATAGTTTAGTGGGC CAAA	AAGGGTCCTCTTGAAGC GTT	59.0	213	INTERGENIC				
CaPOPI_5619		Ca7	41252327	TTAT/TT	TGCAATGCAATGTCCAT TTT	TTTTTCCTCATGGTGCA GTG	59.9	324	INTERGENIC				
CaPOPI_5620		Ca7	41283416	A/AAG	GGTAAACCAATAGCAGC GGA	GAAAAACAGCCCCAATT CAA	60.1	566	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5621	Ca7	41429174	TAA/TA	TGAGACCGGGTTTGAGT ACC	CTGCTGCTCTTGCATCT CAG	60.0	385	INTERGENIC				
CaPOPI_5622	Ca7	41484126	GTATATATATATATATATAT/ATATATATATAT	AGATTTCGAGGAGTTG AGT	CGAGAGAGTGTACGCA TGT	60.0	701	INTERGENIC				
CaPOPI_5623	Ca7	41564191	CTATATATATATATATATATAT/CTATATATATATATATATATATAT	TGCACTCACTCCAACAC ACA	CCTATCATGGTTTGCC TGT	59.9	762	INTERGENIC				
CaPOPI_5624	Ca7	42085502	ATTTTTTTTTT/ATTTTTTTTTT	TGCTCAACCTCAACGAA ATG	GGACATTTGAAGGGCAA AAA	59.8	227	INTERGENIC				
CaPOPI_5625	Ca7	42364254	AATATATATATATATATATATAT/ATATAT/ATATATATATATATATATATATATATAT	CATCTCGGGTTGCTGAA AAT	TTTGAAGCCCTAACA CCG	60.1	363	INTERGENIC				
CaPOPI_5626	Ca7	42487577	AATATATATATATATATATATAT/ATATATATATATATATATATATATAT	TGATTGATTGGGTGCTC TGT	TAAGGCCCATGTTCAAG GTT	59.1	489	INTERGENIC				
CaPOPI_5627	Ca7	42568760	AT/A	GCAAGGTTTGCACGTCA CTA	AAATTTGTCTTCGCATTT CCA	59.9	293	DRR	Ca_20212	K		Protein of unknown function DUF667
CaPOPI_5628	Ca7	42582021	TTATATATATATATATATATATATATATAT/TTATATATATATATATATATATATATATATAT	TCAATCGGAAGGAGAG GTG	TGCCACCTTATACAGCA AAGG	60.2	740	DRR	Ca_20211			
CaPOPI_5629	Ca7	42603074	GTATATATATATATATAT/ATATATATAT	GGGCAACCGTTCTTTCT ACA	AAATTTCAGCGATCAAA CGA	60.1	741	INTERGENIC				
CaPOPI_5630	Ca7	42738535	TAAAAAAA/TAAAAAAA	TCCCGCTACACTTTGAG GAC	TCAAAAGCAAGTGTTC AGG	60.3	592	INTERGENIC				
CaPOPI_5631	Ca7	42757617	T/TGGTTTGAAGTTTGC	TTTGCTCTGAAAGCCCA AAT	AGTTCCTGCAACTCCGA AGA	59.8	527	INTRON	Ca_20201			Domain of unknown function DUF239, plant
CaPOPI_5632	Ca7	42834810	AATATATATATATATATATATATATATAT/AATATATATATATATATATATATAT	TTTCTTCGCGTTTGACTA ATG	GACATAAGAATGGAGGC GGA	58.1	691	INTERGENIC				
CaPOPI_5633	Ca7	43011755	TTATATATATATATATATAT/TTATATATATATATAT	TGCCAATTTTCAAAGGT TTTT	GCCCAAGTTCGAAATGT TGT	59.9	351	INTERGENIC				
CaPOPI_5634	Ca7	43375115	CAAAA/CAAA	CCAATATCTCGTGTTC CGT	CATTTCAAGTTGGGCA GTT	59.8	335	INTERGENIC				
CaPOPI_5635	Ca7	43487665	GTT/GT	AGCTTTTCATTCCACACC GA	CGCACTGCAGATGCAAT TTA	60.6	636	INTERGENIC				

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									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	Tfs	NCBI-nr database
CaPOPI_5636		Ca7	43554492	GA/GATA	CCGTAATCCCCATGTTTG	CAAGGTCTTCGAGGTGATCC	60.0	759	INTRON	Ca_25034	QI	bHLH	Cytochrome P450
CaPOPI_5637		Ca7	43606803	TATAAATAAAATAAA/TATAATAAA TAAATAAAATAA	TTTTGCCATGTCTCAGCTTG	TCTCCTCATTCCTCCAAAGTGG	60.0	814	INTERGENIC				
CaPOPI_5638		Ca7	43621219	GTATATATATATATATATATATA/GTATATATATATATATATATA	TGCATGTAAAACCTGGTGGGA	AGCTGAACGCCTGAACA TCT	60.0	412	INTERGENIC				
CaPOPI_5639		Ca7	43811202	CAAA/CAA	GGGTCTGGGATCAACTCTGA	TTGAACCTGAATGCAAGC CAC	60.0	630	INTRON	Ca_21355	S		GINS complex, subunit Psf2
CaPOPI_5640		Ca7	44001613	T/TG	TGAAACTGCCATTGGAC AAA	CAATTTCTTTGCGTGTG GTG	60.1	476	INTERGENIC				
CaPOPI_5641		Ca7	44083169	T/TTC	ATGCTCTGCACTTGCGACCTA	GACGAAATCTTTTAAGA GGCG	59.9	734	INTERGENIC				
CaPOPI_5642		Ca7	44150096	T/TTTA	AGTCTTACCAGCGCCAC ACT	TCCCAACTACAACGAGG ACC	59.9	567	DRR	Ca_21366	O		Prohibitin
CaPOPI_5643		Ca7	44372091	GAATAATAATAATAATAATAATA /GAATAATAATAATAATAATAATAAT AATA	CGGAGAGTTGATTTCAC ACA	CGTCAAGACGTTCTCTC AATCA	58.8	498	DRR	Ca_21371			Plant lipid transfer protein/Par allergen
CaPOPI_5644		Ca7	44396434	ACC/ACCC	ATGCATGTGAAGTAAGGCC	ACTCAGCCTCTCTCCAA CCA	60.0	458	INTERGENIC				
CaPOPI_5645		Ca7	44474070	AT/ATT	TAGCAACAAAAATGGGG GAG	TGGTAGCGTACCGTTTG ACA	59.9	634	INTERGENIC				
CaPOPI_5646		Ca7	44488959	ATATTATTATTATTATTATTATT ATTATTATT/ATATTATTATTATTATT ATTATTATTATTATTATTATT	GAGGGGAGGGGAGTAT TCTG	GATTGTGCGAAGAGGAG GAG	59.9	588	INTERGENIC				
CaPOPI_5647		Ca7	44822805	GATATATATATATATATATAT/GATAT ATATATATATATATATATATAT	CTTTCGGTTGTACTGAGGC	TTGGTCGTTTGAGCCTT TCT	59.7	529	INTERGENIC				
CaPOPI_5648		Ca7	44825811	TAAAA/TAAAAA	TAGGGCACAAAGTCTCCC AAG	GCAGTGCTGAATTTTGG TGA	60.2	385	INTERGENIC				
CaPOPI_5649		Ca7	45088200	GCTTCTTCTTCTTCTTCTTCTTCT CTTC/GCTTCTTCTTCTTCTTCTTCT TCTTCTTCTC	AACCAAGACCGGCTTTA TCA	TTTGAGACCAATGGTG ACA	59.6	900	INTERGENIC				
CaPOPI_5650		Ca7	45206871	GTATATATATATATA/GTATATATATATA TATA	AGGAGGTTTGTTTGA CGG	TTTGATTTTGACTCGG AGG	60.0	617	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5651	Ca7	45219689	GTAATAATAATAATAATAATAATAAT AATAATAATAATAA/GTAATAATAAT AATAATAATAATAATAATAATAA TAATAATAATAATAATAA	TGCCACAAGTGTTTAT TGC	TTTCTCTTTTGGTGGTTG CC	59.6	769	INTERGENIC				
CaPOPI_5652	Ca7	45241482	AATATATATATATATATATATATATAT ATAT/AATATATATATATATATATATAT ATATATATATAT	TTTACCCCAACACGTAA GCC	CAGATCGGCGCTACACT ACA	59.9	554	INTERGENIC				
CaPOPI_5653	Ca7	45247821	GAAA/GAAAA	CAAAGACCTAGCGGAAC TCG	AACCTGCTCAACTTGC ACT	60.0	767	INTRON	Ca_15725	I	bHLH	Alpha/beta hydrolase fold-1
CaPOPI_5654	Ca7	45829437	TA/TAGTAGGGGTTTTCAAA	TCGTGAGTTTGAGGGGA ACT	CGAAAAATCCTTCGCC ATA	59.7	536	INTERGENIC				
CaPOPI_5655	Ca7	46075915	CTATATATATATATATA/CTATATATA TATATATATATA	AAACAATCCAGACCACT GGC	TCAAGCCAAACCTTAT CTTTT	60.0	543	INTERGENIC				
CaPOPI_5656	Ca7	46332309	GAACACAA/GAACACAATCAACACAA	AACGTACTGCCTATCAC GGG	TTGCAACTCCACTCTT CCT	60.0	649	INTERGENIC				
CaPOPI_5657	Ca7	46560466	AATATATATATATATATA/AACATATA TATATATATATATATA	GGAGGCATTGTTTCCTC AAA	AGGAAGAGTGAGATTGC GAA	60.1	658	INTERGENIC				
CaPOPI_5658	Ca7	46868801	TATAATAATAATAATAATAATAATAA /TATAATAATAATAATAATAATAATA ATAATAA	GTACGAAGGTTTGATCC CGA	AACCCACCGTGAAACA AAC	59.9	276	INTERGENIC				
CaPOPI_5659	Ca7	47130515	CAT/CATAT	TCGTGTCCCAAAATGTG AAA	TGAAATGGGGCAGGTTT AAG	59.9	189	DRR	Ca_19486			
CaPOPI_5660	Ca7	47359557	ATTTTT/AT	TGTGCCATGAGGTTCTT TTG	TGCTACGTACGAACCTT CCC	59.7	867	INTERGENIC				
CaPOPI_5661	Ca7	47396377	ATATTATTATTATTATTATTATTATT ATTATTATT/ATATTATTATTATTATT ATTATTATTATTATTATTATT	AAAAATTAACGGCATAG AGTTTTCA	GGAAATGAAAGGGGACA TCA	59.5	483	INTERGENIC				
CaPOPI_5662	Ca7	48210281	TTTCATTCAATTCATTCAATTC/TTTC ATTCATTCAATTC	TCTTGGTAGCGAGCACA TCC	CAAGGGATTCCAGAAAC GAA	61.3	171	INTERGENIC				
CaPOPI_5663	Ca7	48234648	AT/ATT	TTGCAAAAGTCAAACCC ACA	ATACTTCTCGCGCAGAG TCC	60.1	660	INTERGENIC				
CaPOPI_5664	Ca7	48311764	GAAA/GAA	TTCAGATCTGGGATGCC TCT	GGTACGTCCAGTCTCT TGC	59.8	402	INTERGENIC				
CaPOPI_5665	Ca7	48312616	ATC/ATATCTC	CGAAGCACAAAGGAGATG ACA	TTTCCGAGTGCTGTCAA ATG	60.0	382	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5666	Ca7	48390576	CTTTATTTATTTATTTATTTATTT/CTTATTTATTTATTTATTTATTTATT	TGTC AATGGCAACCATGTCT	TTGCTCCTACGTATTTCCCG	60.0	938	INTERGENIC				
CaPOPI_5667	Ca7	48392684	TAAAAAAAA/TAAAAAAAAA	TGATCCCCAACATCCA ACT	ATGATATTGGAGTTTGCGCC	60.2	165	INTERGENIC				
CaPOPI_5668	Ca7	48703820	CAAAAAAAAA/CAAAAAAAAA	TCAGTCAAACGCACACA AAA	TTCGGTTTGAGGGAAGT CAC	58.9	496	DRR	Ca_26166			Domain of unknown function DUF239, plant
CaPOPI_5669	Ca7	48775188	ATTTTTT/ATTTTTTT	CAGATGCAAAAGATGCG AAA	CCAAGTTC CCCAGAGTCAAAA	60.0	191	INTERGENIC				
CaPOPI_5670	Ca7	48835104	A/AC	TGCCACCCAAACTATCC AAT	TGTTGAGCTCCCATTTTT CC	60.2	743	INTERGENIC				
CaPOPI_5671	Ca7	48845811	TAAAAAAAA/TAAAAAAAAA	GACTTGACGGATATTTCA CGC	TACATCCCTAGGATGCG ACC	59.6	421	INTERGENIC				
CaPOPI_5672	Ca7	48879159	TTATATATATATATATATAT/TTATATATA TATATATATATAT	AGTTGATTGGATTCGGT TCG	AGCAAATTCGATCACCC AAC	59.9	408	INTERGENIC				
CaPOPI_5673	Ca8	4957	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATA/AAATAATAA TAATAATAATAATAATAATAATAATAATA ATAATAATAATAATAA	TTGGTTTCAAGAAGGAT GGC	CGGGTTGAGTTGTTGTT CCT	60.1	738	INTERGENIC				
CaPOPI_5674	Ca8	13774	CAAAAA/CAAAA	CGAGGCACAACATCATC ATC	TGGTGCTTCAATGAACT TGG	60.1	616	INTERGENIC				
CaPOPI_5675	Ca8	104807	TTATATATATATATATATATAT/TTATATA TATATATATATAT	AACCACTAAATCGCATT GCTC	CGGGAAGAAAAAGATA AAGGA	59.2	278	INTERGENIC				
CaPOPI_5676	Ca8	419332	TAAAAAAAA/TAAAAAAAAA	AAGGTGACAACAGGCCA CAT	ATCGATTTTGTCCGTT GAA	60.4	410	INTERGENIC				
CaPOPI_5677	Ca8	465058	TAAAAAAA/TAAAAAAA	CCCAAAC TCAACGTTCAACC	ACATGGGACATGTGCAA AAA	60.4	863	INTERGENIC				
CaPOPI_5678	Ca8	610757	CAAAAAAAAA/CAAAAAAAAA	TTTTCCGACTTGGTCA TT	TTTGC GTTACGAATTTGA TGA	57.2	178	DRR	Ca_11875	O		Heat shock protein Hsp70
CaPOPI_5679	Ca8	728618	GTATATATATATATATATATATATAT/ GTATATATATATATATATATATATATA T	TGAGGGGCATCTAGAAG GAA	GCAAGTTAAAACCATCTT TCGG	59.8	504	INTERGENIC				
CaPOPI_5680	Ca8	763423	TTATATATATATATATAT/TTATATATATA TATATATAT	AAACTGCATTTGTAAATG ACGAC	CGTTGGACTTGTGAACG AGA	58.2	729	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5681	Ca8	807972	AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGA/AAGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGAGA	CCCTTTCACGCCAATAA AGA	AATCCTTAACCTCCCT CCA	60.1	565	INTERGENIC				
CaPOPI_5682	Ca8	813049	ACGCG/ACG	ACTTTCACCAGAAACCG GAA	AGAAGTCAAGCGCAACG AAA	59.6	372	INTERGENIC				
CaPOPI_5683	Ca8	1050452	GTT/GTTT	AAAGCCGAGAAAATAGG GGA	TTGAGGCTGAATTGAA GGG	60.0	273	DRR	Ca_15081			PWWP
CaPOPI_5684	Ca8	1079907	AC/A	ATTAGGTAGCCATGAGC CCC	TTCTCAGATTTGGCATG CTG	60.3	638	INTRON	Ca_15076	CR	NAC	NADH:flavin oxidoreductase/NADH oxidase, N-terminal
CaPOPI_5685	Ca8	1080030	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	ACATGATTTGCAAAAAG CCC	AAGGTATCCAACACAG CGG	59.9	457	INTRON	Ca_15076	CR	NAC	NADH:flavin oxidoreductase/NADH oxidase, N-terminal
CaPOPI_5686	Ca8	1184414	GAAAAAAAAAAAAA/GAAAAAAAAAAAAA	TTCGTACCGTTCTCTCC TCAA	TTGTACACAACCTCCCT GCG	59.9	563	INTERGENIC				
CaPOPI_5687	Ca8	1342981	CAAAA/CAAAAA	CCTCTAGGAAACCATCA ACATCA	CCTTGCCACCTCATCTC ATT	60.4	423	INTERGENIC				
CaPOPI_5688	Ca8	1343227	AAAAGAAAGAAAGAAA/AAAAGAAAGAA AGAAAGAAA	TGAGAAATTAAGCTTGT GGGG	CCTTGCCACCTCATCTC ATT	59.2	206	INTERGENIC				
CaPOPI_5689	Ca8	1779502	AATATATATATATATATATATATAT/AA TATATATATATATATATATATAT	TTGTCAACTCTCCATGT GTGG	TGAGTTGTTGGGTGTGG AGA	59.6	536	INTERGENIC				
CaPOPI_5690	Ca8	1993541	A/AGGGAATAATAAT	ATTTTCATCCCCAACCGT GTA	GGACTCCAAGGAAATG CAA	60.1	666	DRR	Ca_02403	R		Glucose-methanol-choline oxidoreductase, N-terminal
CaPOPI_5691	Ca8	2033135	TC/TCC	ACGCTCGATTTCCGAGA GTA	CACGTGTGGGTTGTTC GAC	60.0	828	INTERGENIC				
CaPOPI_5692	Ca8	2037724	ATTTTTTTTTCTTTTTTTTCTT/ATTTTT TTTTCTTTTTTTTTCTTTTTTTTCTT	TTTTGAGGACTTTCGGG TTG	CATTTGCTAGCCCTTG AGC	60.1	448	INTERGENIC				
CaPOPI_5693	Ca8	2172364	GT/GTT	TGGGAGCTACCACGCTT TAC	GCTGTGATCATCGTTTC GTG	60.3	830	DRR	Ca_02379	R		
CaPOPI_5694	Ca8	2755315	GT/GTAGAGCGGTAGATAAT	GGTTGCCCTACAACACT GCT	TACTCCGCATCAAATGG ACT	60.2	602	INTERGENIC				
CaPOPI_5695	Ca8	3128241	GTTTCGAAAGTTTCGAAAGTTTCGAAAG TTT/GTTTCGAAAGTTTCGAAAGTTT	CAGTTGTCCACCCTCCA CTT	CACTTTAACCTCCACC CCC	60.0	856	DRR	Ca_02267	E		Peptidase M20

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5696		Ca8	3313290	TTATATATATATATATATATAT/TTATATATATATATATATATAT	TGGCGTATTGTCATTTC CAA	AAAAATCTGTTTGGGG ACC	59.9	674	INTERGENIC				
CaPOPI_5697		Ca8	3556737	AATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATATATATATA	GTGAGGGCGGTTATTT AGA	TGGACAATTCCTCTAAG CTCG	60.1	803	INTERGENIC				
CaPOPI_5698		Ca8	4049374	AG/AGG	TTGCAGTGACAGTGAGG AGG	GAAAAGCAAAGCTCGT AGG	60.0	416	INTRON	Ca_02166	K	GRAS	SET domain
CaPOPI_5699		Ca8	4534293	CTTTTTTTTT/CTTTTTTTTTT	CAGAGGGAGGAATTGTG GAA	GCAGAAAAGAATCACAC GCA	60.0	607	INTERGENIC				
CaPOPI_5700		Ca8	4630639	GATATATATATATATATATATATATA/GATATATATATATATATATA	TGAAGCATGAACGGTGA GAA	ATGGGTACCGGTCAAAA ACC	59.3	265	INTERGENIC				
CaPOPI_5701		Ca8	4841766	AATATATATATATATATAT/AAATATATATATATATATAT	TGCAACTCAGCTATGCA TCC	GAGAAATGGCAATGAGGT GGT	60.0	719	INTERGENIC				
CaPOPI_5702		Ca8	4937020	ATTTTTTT/ATTTTTTTT	AGGTCATTCCATTCAAC GTC	ATGCTGGTTGTCCTCCT GTC	59.8	845	INTRON	Ca_02063			Protein of unknown function DUF620
CaPOPI_5703		Ca8	5016373	TAAAAAA/TAAAAAA	TTGTCCGTTATAACATTA AACACTTT	GAAAAGACAACCCCGCA TTA	57.5	279	INTERGENIC				
CaPOPI_5704		Ca8	5069926	GTTTT/GTTT	AGGTTTCACATCGGAGG TTG	TGGAAGTAGCCATCTTT GGG	60.0	454	INTERGENIC				
CaPOPI_5705		Ca8	5203286	TATAAAAAATAAAAAATAAAAAATAAA/ TATAAAAAATAAAAAATAAAAAATAAA ATAAAA	TGTAGAGAAAGTGATTG ACCACC	AATTTGGCATGGGAGAC TTG	58.2	643	DRR	Ca_02032	O	FAR1	ATPase, AAA+ type, core
CaPOPI_5706		Ca8	5269336	GG/GGGTCAGG	ATCCAGAATGGAGCAAC TGG	CCACGAGATTCCCTGGT AAA	60.1	478	INTRON	Ca_02025	R		Cytidylyltransferase
CaPOPI_5707		Ca8	5667391	TTCTCTCTCTCTCTCTCTC/TTCTCTCTCTCTCTCTC	TTCAACCAACAAACACC TGA	AGATCCCATGGTTCGAT ACG	60.0	423	INTERGENIC				
CaPOPI_5708		Ca8	5862916	CTT/CTTT	GGCCTTGTAACATTTGA GGG	GCTCGCCTTTGCTATGA GTC	59.4	643	INTERGENIC				
CaPOPI_5709		Ca8	6036137	CAAAAAAAAA/CAAAAAAAAA	CACACACATAAATGAAA CGAACG	CATGCTTTGACCATCAG GTG	60.3	576	DRR	Ca_01945	O	NAC	SKP1 component
CaPOPI_5710		Ca8	6056579	TTATATATATATATAT/TTATATATATATA T	TATTCAAGTCCCTTGCC CAG	TGCACGGCAATTACAAC AAT	60.0	493	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5711	Ca8	6100294	TAAAAAAAAAAAAAAAAA	TGCAAAAACCTTAAACG TATGG	TTAGATGCAACCCAAA GGG	59.1	792	INTERGENIC				
CaPOPI_5712	Ca8	6253206	TTATATATATATATATATAT/TTATATA TATATATATATAT	ACCCGTTATGAAACGAG TGC	CAGTAATCGGAGAAAAAC CCG	60.0	602	INTERGENIC				
CaPOPI_5713	Ca8	6307106	TATACATATAATACAT/TATACAT	GCAATTCAACGAAATG CAA	CCACTAAGTCATTTGCA AGGC	59.7	942	INTERGENIC				
CaPOPI_5714	Ca8	6492029	A/ATCAACC	TCTGTTTTGCCAACCTT TC	ATCTCAACGATCCAACG GTC	60.1	455	INTRON	Ca_10739	D		
CaPOPI_5715	Ca8	6492546	CAAAA/CAAA	CGTAAGCAACCCACCAA TCT	TTGTCAACAACCTCAGCG TAAAAA	60.0	142	INTERGENIC				
CaPOPI_5716	Ca8	6492603	ATTTTTTTTTTT/ATTTTTTTTTT	CGTAAGCAACCCACCAA TCT	TTGTCAACAACCTCAGCG TAAAAA	60.0	142	INTERGENIC				
CaPOPI_5717	Ca8	6492758	ATTTTTTT/ATTTTTTTT	CGTAAGCAACCCACCAA TCT	TGGACATCATACGTTAT CAATCG	60.0	672	INTERGENIC				
CaPOPI_5718	Ca8	6493315	TAAAAAAAA/TAAAAAAAAAAAA	TTTCAAAAGTGAAATTTG GTTGAA	GAGTCAGAAAACAAACG CTCTT	59.9	570	INTERGENIC				
CaPOPI_5719	Ca8	6850537	GTTTT/GTTTTTT	AAAGCAAGACGCGTCAG AAT	CAAGAGGATATCAAAGC AACAA	60.0	925	INTRON	Ca_10703	O		
CaPOPI_5720	Ca8	7065316	AATATATATATATATATATAT/AAATA TATATATATATATATATATAT	TGGACCACAATTTAAGT GCAA	GGTTGAGTGAAGGATG GAA	59.1	448	INTERGENIC				
CaPOPI_5721	Ca8	7211763	AATATATATATATAT/AAATATATATATA TAT	GTTGTTTCCGTTTGGAC CAC	TTGGCATTTGGCCTATT CTC	60.3	350	INTERGENIC				
CaPOPI_5722	Ca8	7288711	TTATATATATATATATATATATATATA TATATATAT/TTATATATATATATATAT ATATATATATATATATATATATAT	TACACCTGAGTCCGCTA CCC	CAAACGACGACTTCCCA AAT	60.1	633	INTERGENIC				
CaPOPI_5723	Ca8	7323946	GA/GAACAA	CAGTAATTCGCCATCC ACC	ACGTGAAAGCAGTTGAA GGA	60.3	911	INTERGENIC				
CaPOPI_5724	Ca8	7741922	A/AG	TGTGCTCCAATGTAAC GGC	GAGCATAGGAGCTGGCT TGA	59.7	511	DRR	Ca_10611	J		Ribosomal protein L35A
CaPOPI_5725	Ca8	7777713	CACATAACATA/CACATA	TCCAGTGGCACCATAAC AAA	CTCCCAAGAACCCTTCT TCC	60.0	744	INTRON	Ca_10607	Z	MYB_rela ted	Kinesin, motor domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5726	Ca8	7896482	TC/T	TTTGATATGTTGCTTCC GCA	CGATGCAGCCTCTTAGG TGT	60.2	689	INTERGENIC				
CaPOPI_5727	Ca8	7910743	CAAAAAAAAA/CAAAAAAAAA	ATGATTGGGCTCGTTTG TTC	CCAAAATCAACTGCAAC CCT	59.9	390	INTERGENIC				
CaPOPI_5728	Ca8	7913547	A/AT	CCGATATGTCAGAAAAC ATCACA	GGCCTTCAACTTCAACT TGCT	59.9	685	INTERGENIC				
CaPOPI_5729	Ca8	7927288	CAAA/CAAAA	AGGACCGTGCAAATGTT TCT	TGGCCTACTTATGGTCT GGC	59.6	349	DRR	Ca_11431	J		Protein synthesis factor, GTP-binding
CaPOPI_5730	Ca8	7927539	GTATTGCTTTTAT/GTATTGCTTTTATTG CTTTTAT	GCCAGACCATAAGTAGG CCA	GCAACTGGATTGCTGGA TTT	60.1	509	DRR	Ca_11430	J		Translation elongation factor EFTw/EF1A, C-terminal
CaPOPI_5731	Ca8	7927639	ATT/AT	GCCAGACCATAAGTAGG CCA	GCAACTGGATTGCTGGA TTT	60.1	509	DRR	Ca_11430	J		Translation elongation factor EFTw/EF1A, C-terminal
CaPOPI_5732	Ca8	7948182	TCA/TCACA	GCCGCAAGAAGAGAAG AGA	TGCCCAAGTCACTAATG CTG	59.8	443	INTERGENIC				
CaPOPI_5733	Ca8	7948249	ACTCTCT/ACTCT	GCCGCAAGAAGAGAAG AGA	TGCCCAAGTCACTAATG CTG	59.8	443	INTERGENIC				
CaPOPI_5734	Ca8	7950561	CAAAAA/CAAAA	GTCTTTGGCCTCCAATC AAA	TGGAGTTGGGCCAATAA TTT	60.1	359	INTERGENIC				
CaPOPI_5735	Ca8	7951970	TAAAAAAAA/TAAAAAAAA	GCAACCATAAAGAGCA AGTTGA	AGAGCAACACCATTTTG AAGG	60.6	377	INTERGENIC				
CaPOPI_5736	Ca8	7952607	GAAAAA/GAAAAAAA	CCTTCAAAATGGTGTG CTCT	GTCATTTTGCCGATCAC CTT	59.2	676	INTERGENIC				
CaPOPI_5737	Ca8	7953093	T/TC	AAGGTGATCGGCAAAAT GAC	CAGCCCTTCAGTGTCAT GAGT	59.9	609	INTERGENIC				
CaPOPI_5738	Ca8	7953809	TACCTCAA/TACCTCAAACCTCAA	ACCTGCGACACGTGAAC ATA	GAAAACGAGGCGTAAAC GAG	60.2	360	INTERGENIC				
CaPOPI_5739	Ca8	7954393	TAA/TA	CTCGTTTACGCCTCGTT TTC	CCGTAGCATGAGAGTGA CCA	59.9	561	INTERGENIC				
CaPOPI_5740	Ca8	7954496	CATATA/CATATATA	TTTCGTCGTATAAAGAC GGAGAG	CCGTAGCATGAGAGTGA CCA	59.8	545	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5741	Ca8	7955526	TCTC/T	CATGCAAGAGAAGGGAAAGAA	GTGTGGGAGAGAAAGCA TCC	59.4	296	INTERGENIC				
CaPOPI_5742	Ca8	7955567	TTCTCTCTCTCT/TTCTCTCTCTCTCTCT	CATGCAAGAGAAGGGAAAGAA	GTGTGGGAGAGAAAGCA TCC	59.4	296	INTERGENIC				
CaPOPI_5743	Ca8	7956165	GTTATATAATATTA/GTTATATAATATTA TTATATAATATTA	TTGATTTGTCTAGAAGC AGCACA	CACTTCTTGGCTGAGTT GGA	60.1	476	DRR	Ca_11432		G2-like	Myb, DNA-binding
CaPOPI_5744	Ca8	8003394	CAAAAAAAAA/CAAAAAAAAA	TCTCTCAATTCATGCTAT GGAAAA	ACCCGCATGTGATCATG TTT	60.1	703	INTERGENIC				
CaPOPI_5745	Ca8	8041385	TAGAGAGAGAGAGAGAGAGA/TAGAGAGAGAGAGAGAGA	CGGCGCGAATTTAGAGT TAG	GTTTCTGCCACTCTCTT CGG	60.0	212	INTRON	Ca_11441	U	M-type	SCAMP
CaPOPI_5746	Ca8	8075837	ATACT/ATACTTACT	TTGAGCCAAAAGCCTCC TTA	TTTTCAACAAAATGTGCG GA	60.0	824	INTERGENIC				
CaPOPI_5747	Ca8	8084688	CATA/CA	TCACCTTACAACATGAC CGA	ATGGATGCAACACCAAA ATG	60.0	977	INTERGENIC				
CaPOPI_5748	Ca8	8240879	TC/TCC	GTCGCGCTACGAGATA AAC	TTTGTGCTGATGGTGAT GGT	59.9	729	INTERGENIC				
CaPOPI_5749	Ca8	8272916	TTAT/TT	TGGCACAGAACTTCGA TTG	TTACCGCCTCTTCTTTT CA	59.8	727	INTERGENIC				
CaPOPI_5750	Ca8	8273148	GT/GTGAT	GTCACCACTACCAAGTC ACG	TTACCGCCTCTTCTTTT CA	60.2	550	INTERGENIC				
CaPOPI_5751	Ca8	8312325	AAATAGGAATGTTTA/AAATAGGAATGT TTAATAGGAATGTTTA	CGGCGATCATTAAGGAG AAA	ATTTTGAACAAGCGGAC CTG	60.2	561	INTERGENIC				
CaPOPI_5752	Ca8	8427403	TAAAA/TAAAA	TGCCATGCAAGTGTTC AAT	GTCCACGATGTTGACGT GAC	60.1	456	INTERGENIC				
CaPOPI_5753	Ca8	8623323	ATTTTTTTT/ATTTTTTTT	GGGGTGATTATGGAGCA AGA	GGTCACGTGTGTTCCAA GAA	59.9	963	INTERGENIC				
CaPOPI_5754	Ca8	8624257	ATTAAAAGC/ATTAAAAGCTCAACTTTAA AAGC	CTTTGATTGGGGTTTG GAA	TGGTGACAATTATTTTC CCGT	59.8	664	INTERGENIC				
CaPOPI_5755	Ca8	8624418	CAAAAATTTAGAAAAAT/CAAAAATTTAG AAAAAATTTAGAAAAAT	TCCTTTCAATGGACTGG TGA	GTCCCGAGCATGACGTT TAT	59.1	888	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5756	Ca8	8771102	AATTAATTTA/AATTAATTTATTAATTTA	TCATAGAAATTTGGAGG CGG	GTGCTGTTATTTGCACC CCT	60.0	742	INTERGENIC				
CaPOPI_5757	Ca8	8845260	ATTTTTTTTT/ATTTTTTTTT	TTTGCTCCTCCTCTTTCT GC	TCGTGTTATCCAACCA CTCT	59.7	697	INTERGENIC				
CaPOPI_5758	Ca8	8848853	TAAAAAAAA/TAAAAAAAA	GTTGGGTCTAGTGGGT TTG	TGTACTTTTAGGTGCC GGG	59.3	589	INTERGENIC				
CaPOPI_5759	Ca8	8848887	TAAAAAAAA/TAAAAA	GTTGGGTCTAGTGGGT TTG	TGTACTTTTAGGTGCC GGG	59.3	589	INTERGENIC				
CaPOPI_5760	Ca8	8857167	ATTTTT/ATTTTT	GCCCAATTTGTTCTTG GAA	ACTTGCCAATCTGTTT CG	59.9	929	INTERGENIC				
CaPOPI_5761	Ca8	8858935	TAA/TA	TTATTGGACCATCCGA TTT	TTTTGGGTACCTTGGC TTG	60.2	750	INTERGENIC				
CaPOPI_5762	Ca8	8860779	TAA/TA	TCTGGGACACAACAAA ACA	CAATTGCATGTGATTCA GCC	60.0	517	INTERGENIC				
CaPOPI_5763	Ca8	8862222	TAAAAAAAA/TAAAAA	AGGTTTCGAACCATGCA TTT	TGCGAGTCACATGAATT TCG	59.4	753	INTERGENIC				
CaPOPI_5764	Ca8	8868822	TATTTATTAATTTATT/TATTTATT	TGGTGGTCAAAGGTAA GGG	AAAACGACGGTGTGACA TATTTT	59.8	830	INTERGENIC				
CaPOPI_5765	Ca8	8869164	TAAAAAAAA/TAAAAA	TGAGATGCTCTCCATCT CCAT	AAAACGACGGTGTGACA TATTTT	59.8	575	INTERGENIC				
CaPOPI_5766	Ca8	8871176	T/TA	AGGACAAGCTCCACCA CAT	TTACTTGATGCCCCAC TTC	59.6	271	INTERGENIC				
CaPOPI_5767	Ca8	8873400	TTA/TTATTATTCATA	TTTCTGTGCTGGCTTA CCA	TGCATCACGTATATGAC CCATT	59.3	797	INTERGENIC				
CaPOPI_5768	Ca8	8881428	CA/CAA	CCAAAGTCAACTGGTCA AAGG	TCGTGAAGTGTGCTGAAT TGG	59.6	790	INTERGENIC				
CaPOPI_5769	Ca8	8882090	T/TTCCAAAC	ATCATTCCACGGATTTT CA	TGAAAAACAAAGAAA CAGAAA	60.1	108	DRR	Ca_11519			
CaPOPI_5770	Ca8	8885048	ATTTTT/ATTTTTT	GGTGGAAGCAGAGAC AGA	AAAGGAACATTGTTGA CCG	60.0	723	DRR	Ca_11520	C		Mitochondrial substrate/solute carrier

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5771	Ca8	8886584	ACA/ACATATAAAAATCTGTTCA	CATTTCACCTACAAC ACG	AAGGTTTTGGTCCTGCA ATG	60.0	536	DRR	Ca_11520	C		Mitochondrial substrate/solute carrier
CaPOPI_5772	Ca8	8901973	TCTCTCTCTCAC/TC	TTGCAATGGTTCAAGCT ACG	TCATTTATCACCTACGG CCC	59.9	393	INTRON	Ca_11521	G		Major facilitator superfamily MFS-1
CaPOPI_5773	Ca8	8907150	ATT/AT	ATTCTTCGTCCAACATG GC	GGAGGGGGAAAACCTTG GTA	59.9	866	INTERGENIC				
CaPOPI_5774	Ca8	8910515	GAAAAAAAA/GAAAAAAAAA	TTTCATCAATGGCAAGG TCA	CGATTGTTCTGGTTGTC CCT	60.0	530	DRR	Ca_11522			Starch synthase, catalytic domain
CaPOPI_5775	Ca8	8924623	GTTTTTTTT/GTTTTTTTTT	TAAGCGTAAATAGCGCG CAG	GGGAGGAAAAGAGGAG GTTG	60.4	188	INTRON	Ca_11523			Chromatin SPT2
CaPOPI_5776	Ca8	8938717	G/GATA	GGTGTGAGGGTGACG ATTT	GCAAGACATTCACGTTG CAC	60.0	751	INTERGENIC				
CaPOPI_5777	Ca8	8940349	TAAAAAAAA/TAAAAAAAA	TGCATTTTAACCTTGTTA CATCG	TACCGGAGAAAGCCACA AAC	59.1	770	INTERGENIC				
CaPOPI_5778	Ca8	8954679	TAAAAAAAA/TAAAAAAAA	ATCCATCGAGCAAGTCG TTC	TTGTCCTCCTGTACTTC CTCC	60.2	425	INTERGENIC				
CaPOPI_5779	Ca8	8964218	AGG/AGGG	GGCTGGCCTCTACAAC TAT	AGGGCCACAACACTCCC TAT	60.0	221	INTERGENIC				
CaPOPI_5780	Ca8	8964234	A/AT	GGCTGGCCTCTACAAC TAT	AGGGCCACAACACTCCC TAT	60.0	221	INTERGENIC				
CaPOPI_5781	Ca8	8969277	TAAAAA/TAAAAAA	GCAACATTGGCAAAAG TGA	CACATGGCCGTGGGTAA AT	59.7	534	INTERGENIC				
CaPOPI_5782	Ca8	8994344	A/AGG	TTCACTTCAACGGTTGT GGA	CGAAAAATCAAAATGAA GGAACA	60.1	665	INTERGENIC				
CaPOPI_5783	Ca8	8995565	CCTCT/CCTCTCT	GTTGCAAAGTCAACGGG TTT	TGAAAAATTGAAATGTTG ATTCATCT	60.0	330	INTERGENIC				
CaPOPI_5784	Ca8	8998721	TCC/TC	TTAACGACGAAAATGAA TTAAAA	AAGTATGCATTGTTGC CTTCA	57.2	546	INTERGENIC				
CaPOPI_5785	Ca8	9004500	TA/TAA	CAATTTGCACCTTGATAG CCAA	GTGCTGCGTAGTGACCG TTA	60.1	233	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5786	Ca8	9005048	GTTTTTTTT/GTTTTTTT	TAACGGTCACTACGCAGCAC	CGGTGGCCACATTACATACA	59.9	809	INTERGENIC				
CaPOPI_5787	Ca8	9057136	TAAAAAA/TAAAAAAA	GCGGAGACGCAACTACTGTT	TGGCTTTGTGAATCCAAGA	60.5	599	DRR	Ca_11528			
CaPOPI_5788	Ca8	9081856	ATT/AT	TGGCACCACTCATATTCA	CCTTTCCACCTTGTCATCAT	59.9	322	INTERGENIC				
CaPOPI_5789	Ca8	9084472	TACTTCA/TA	GGGCCAAAAGTTTCACAAA	TCCATTCCCCTAATTTCC	60.0	661	INTERGENIC				
CaPOPI_5790	Ca8	9087628	ATATTATTATTAT/ATATTATTATTATT	TTGGACCCCATCTTACTTGG	TGTAGCATCCCATTTCCTACT	59.8	741	INTERGENIC				
CaPOPI_5791	Ca8	9088156	TAAAAA/TAAAAA	AGTGGAATGGGATGCTACA	CACAAATTTCAACGACAAATCG	59.4	534	INTERGENIC				
CaPOPI_5792	Ca8	9088516	CTTT/CTT	CGATTGTGCTTGAAATTGTG	CCATACAAAACACAAGGTGTCG	60.4	479	INTERGENIC				
CaPOPI_5793	Ca8	9089194	TAATAAAATAAAATAAAATAAA/TAATAAAATAAAATAAA	CGCGTTCCCAAATGTTAAT	CCCTAATCTTCAACACCGA	59.8	513	INTERGENIC				
CaPOPI_5794	Ca8	9101623	CT/CTTT	CAAGGTTCTCCAGAAACCA	ACACGTGTGCGCTCAAAATA	60.1	671	DRR	Ca_11533		C2H2	Glycoside hydrolase, family 3, N-terminal
CaPOPI_5795	Ca8	9129065	TAG/TAGAAG	TCCATGGACCTTCACTCTC	GCCTTCTTCACTTGTGCTC	60.0	619	CDS (large-effect mutations)	Ca_11536	Q	Nin-like	ABC transporter-like
CaPOPI_5796	Ca8	9131797	AAGA/AA	TTCGCTTCAGATTCCCTTT	TCAACTCTTTCAACCACTGGC	58.9	447	DRR	Ca_11536	Q	Nin-like	ABC transporter-like
CaPOPI_5797	Ca8	9137514	GTTTT/GTTTTT	TTTTGGGTATCATTGAGCC	TCGTTGGGAGATTTGAGT	59.8	536	INTERGENIC				
CaPOPI_5798	Ca8	9149110	CTTTTTT/CTTTTTT	GCAAAAAGTGAAGGATTCGC	TGCATGCAGTAAAAAGTATCCA	59.8	557	INTERGENIC				
CaPOPI_5799	Ca8	9152450	ATT/ATTT	CAGCCTGTTCAAAAATGCAA	GCATTTGAGGATGCTGGATT	59.8	257	INTRON	Ca_11539	O		Peptidase M3A/M3B, thimet/oligopeptidase F
CaPOPI_5800	Ca8	9153262	CA/CAAGTA	CAGAACTCTGCGGTACAACA	TGCTGCCAGAACTTATCTGTG	60.0	431	INTRON	Ca_11539	O		Peptidase M3A/M3B, thimet/oligopeptidase F

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5801	Ca8	9153702	AAAGAAG/AAAG	CAGCACGATAAGTTCTG GCA	GGGGAATAGAGTGGGAT GCT	60.0	420	INTRON	Ca_11539	O		Peptidase M3A/M3B, thimet/oligopeptidase F
CaPOPI_5802	Ca8	9199467	ATT/AT	AGCTCCCAAGGACAGAT TCA	GCAAAGATATGATTGGG CGT	59.8	692	INTERGENIC				
CaPOPI_5803	Ca8	9201647	CA/CAA	GTCTCGATCGCAAGTCA CAA	GATATATACGGCTGACG GCG	60.0	300	INTERGENIC				
CaPOPI_5804	Ca8	9215036	GTTTTTTT/GTTTTTTT	CATCCTCTGGTTGGACG ACT	TTTTTCCCCGACACATA AG	60.1	837	INTERGENIC				
CaPOPI_5805	Ca8	9220067	C/CTA	AAAATTAGGGGGAACAC AGGA	GTATGTGTGGTGCCATT TGC	59.7	909	DRR	Ca_11542			Legume lectin, beta chain
CaPOPI_5806	Ca8	9274060	AA/AATA	AACAACAGAGCCTGCGA ACT	TCCATGTTCCGGTTTT CAT	60.1	486	INTRON	Ca_11549		NAC	Protein kinase, catalytic domain
CaPOPI_5807	Ca8	9327905	GTCTC/GTC	GCATGGAAGTATGCCTC CTC	AATTGAGAACCATTTTGC CG	59.7	698	DRR	Ca_11554	Z	B3	Kinesin, motor domain
CaPOPI_5808	Ca8	9355298	TTCT/TT	GAAAGCTAACAGTTGG CGG	GGGAATTGGCAAGTAGT GGA	60.0	431	INTRON	Ca_11556	AR		K Homology
CaPOPI_5809	Ca8	9357060	TATTA/T	CTTTGTTGCGTTGTTCC GTT	CATCATCCACGGGTGAC ATA	60.0	620	INTERGENIC				
CaPOPI_5810	Ca8	9364522	ATT/ATTT	TTGTCGGTGAGATTGTG TGAA	AAAGATTGTGATTTTGG CGG	60.1	802	INTERGENIC				
CaPOPI_5811	Ca8	9953316	TTGTGT/TTGTGTGT	AGCAGCAACAACCGTCT TTT	AAAAATCGATCGGGTGC ATA	59.9	312	DRR	Ca_18394			Protein of unknown function DUF1442
CaPOPI_5812	Ca8	9960024	CATAATAATAAAT/CATAATAATAATAATAATAAT	CCATTGGGATGTTTGCT TTT	GCTCATGTGGTGGTGTT TTG	59.8	280	INTRON	Ca_18395			Stress up-regulated Nod 19
CaPOPI_5813	Ca8	10161190	GAAAAAAAAA/GAAAAAAAAA	GCAGATGTGCTCATTGC TTT	GCTCCAGCCCAACTAT TTT	59.0	554	INTERGENIC				
CaPOPI_5814	Ca8	10357104	ATTTT/ATTTT	AATGTTACCTTGCAAG CCG	TGAGTGACCGAGCTGAC AAC	60.0	763	INTERGENIC				
CaPOPI_5815	Ca8	10366674	CTT/CT	CAAGAAGACGCCGATGA AAT	GTCGAACGTTCTCCGTT TGT	60.2	571	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5816	Ca8	10484577	GCCC/GCC	TGAGGAGTATCCATGTG GCA	GAGTTCGGAAGTGAGCC AAG	60.1	939	INTERGENIC				
CaPOPI_5817	Ca8	10509590	GA/GAA	GCCATGTCAACCGAAGA GAT	ATGCCAAGCGTTTCACT TTT	60.1	596	DRR	Ca_18435			Stress up-regulated Nod 19
CaPOPI_5818	Ca8	10590161	ATTTTT/ATTTTTTT	AACGGAGGAGGAACAA CAC	TTAGAAGGCCTTGCATA CGA	59.0	212	INTERGENIC				
CaPOPI_5819	Ca8	10591114	AAA/AAAGAA	TCCCGAGCATATCAACA TCA	TGTGGGAGTTTGTCTTG CAG	60.0	555	INTERGENIC				
CaPOPI_5820	Ca8	10612849	CTTTT/CTTT	AGTGGGAGTTTCGTCCA TTG	AGCACATGGAACCAAAG AGG	60.0	299	INTERGENIC				
CaPOPI_5821	Ca8	10684139	TAAAA/TAAA	AAAAAGAAAGGAACGGT CATAAA	AAAGTCCACTCTGCAAT ATGATCT	58.3	403	INTERGENIC				
CaPOPI_5822	Ca8	10686546	ATTTT/ATTT	TGCTATCGGTACCAATT TTGC	TCCGTTGTCTCATTCGA TCA	60.0	628	INTERGENIC				
CaPOPI_5823	Ca8	10701972	ATGTT/AT	TCAACGGTTATACGGCA ACA	TTTTATCTATGAAAAATG CCTCACA	60.0	373	INTERGENIC				
CaPOPI_5824	Ca8	10727907	GAAAA/GAAAA	GGTAGGCATTGGAGCAT TGT	CATCTTTTGCAGCATGG CTA	60.0	581	INTERGENIC				
CaPOPI_5825	Ca8	10934374	AT/ATT	TCCGATTCATCCTCTTG GTC	AATGAAAAAGCGGGGAA ACT	60.0	368	DRR	Ca_19747	R	NAC	Pentatricopeptide repeat
CaPOPI_5826	Ca8	10973766	TATA/TATAATAAATAAATAAATA	CGGACGTATGCATCAAA TTC	GGACTCGCTCGATGTAC GTT	59.0	387	INTERGENIC				
CaPOPI_5827	Ca8	11019474	TTATATATATATATATATATATAT/T TATATATATATATATATATATATATAT	CGTCGCACGGATACAAA ATA	AAAGAGTGGTGCAGGAG TCG	59.6	234	INTERGENIC				
CaPOPI_5828	Ca8	11070760	AG/A	GCTTCTAGCTGGTGCTG CTT	AGGGAATCAATTGTAGG GGG	59.9	900	INTERGENIC				
CaPOPI_5829	Ca8	11113946	GA/GAATA	CCAGAAAACGAAACCA AACA	TTTGATTTTGAGGCAGA GCA	60.0	480	INTERGENIC				
CaPOPI_5830	Ca8	11144283	A/ATTTAATC	TTGCCATGCCTACTTAA GGG	AATGACATTGAATCCC CGA	60.1	292	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/Pf)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	Tfs	NCBI-nr database
CaPOPI_5831	Ca8	11145618	TTTATTA/TTTATTATTA	TCCTTCTGGTTGCAAAAT GTITT	CATGCTTTAAGAGCCA ATGC	60.0	758	INTERGENIC				
CaPOPI_5832	Ca8	11145831	TCC/TC	TCTTTCTGGTTGCAAAAT GTITT	AAATTGAAGCAAACGGA ACC	60.0	980	INTERGENIC				
CaPOPI_5833	Ca8	11146284	TGTGTCTTAGGT/TGT	TGTGATTGAGGCACTAT CAAGC	CCGGTGAAATGGTTAT TTG	60.3	280	INTERGENIC				
CaPOPI_5834	Ca8	11146309	ATTTTTTTTTTT/ATTTTTTTTTT	TGGTTTGCTGGAATTGT GTG	CCGGTGAAATGGTTAT TTG	60.6	167	INTERGENIC				
CaPOPI_5835	Ca8	11146772	TAAA/TAAAA	TAACCTGTGCGCTATTG GTG	TGCAATAATTCTCATC ATTTTT	59.9	329	INTERGENIC				
CaPOPI_5836	Ca8	11151543	GAAAAAAAA/GAAAAAAAAA	TCCTATTGCCGCTATGT TGA	TTGAGCATCGTGTTGGA GAG	59.3	805	INTERGENIC				
CaPOPI_5837	Ca8	11193555	ATTTTTTTT/AATTTTTTTTTT	TAGCCGTAATGTTTTG GGG	ATTGTGATCACCTTCGC ACA	59.8	523	INTERGENIC				
CaPOPI_5838	Ca8	11206549	GT/GTCTATTAT	GGTTTTTCACTTTCGGT GGA	TTTGCTGACCTGACAT TTTT	59.9	464	INTERGENIC				
CaPOPI_5839	Ca8	11212615	TT/TTTTATCCCTCT	TTCTCTCCTCGATTTCG CC	TTGCACGTGTATTTTT GGA	59.5	715	INTERGENIC				
CaPOPI_5840	Ca8	11356172	GT/GTT	TTGCGTGATTGTGTTC GTT	TCACCTATCACGGGTCA ACA	60.2	771	INTRON	Ca_16822	G	NAC	Glycoside hydrolase, family 1
CaPOPI_5841	Ca8	11536143	CATTATTATTATTATT/CATTATTATT ATTATTATTATT	TCTTACACTGCAGCAAT AAAAATCA	TGTTTGATGCCCAAGTA CAA	60.2	576	DRR	Ca_16812	R	MYB	Integrase, catalytic core
CaPOPI_5842	Ca8	11545234	CTAATAATAATAATAATAATAATAAT/ CTAATAATAATAATAATAATAATAATAA TAAT	CTGGTCATTACCTGCA CCT	TTGTTTCTGTCATTTC CC	60.0	125	CDS (large-effect mutations)	Ca_16811			Auxin efflux carrier
CaPOPI_5843	Ca8	11875776	ATCTCTCTCTCTCTCTCTCTCTCTCT CTCTCTC/ATCTCTCTCTCTCTCTCTCT CTCTCTCTCTCTCTCTC	GTCAACACTCTTGGCCA CCT	TTTAGCCCCAAATCATC AGC	60.2	483	INTERGENIC				
CaPOPI_5844	Ca8	11946471	CTTTTTTTT/CTTTTTTTTT	AAATGCGAACCTACATG GCA	TTCCCCATGAATCTGCT CTC	59.2	785	INTERGENIC				
CaPOPI_5845	Ca8	11955442	T/TG	GGCCGATTACTGCTCA CAT	GTTGCCACTTGGCGTAA AAT	60.1	430	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5846	Ca8	11955768	CTAATAATAA/CTAATAA	CTAATGCCCCCACTCAT	TTGTTTGGTGAAGGCTCTTG	59.8	307	INTERGENIC				
CaPOPI_5847	Ca8	11975713	CT/C	TATACTCGTGCACTACGCGG	GGATGGAGACAATGATGAGGA	59.9	135	INTERGENIC				
CaPOPI_5848	Ca8	11975949	AATTTATGTGTAGATGATTTAT/AATTTATGTGTAGATGATTTATGTGTAGATGATTTAT	TATACTCGTGCACTACGCGG	TTGTTGGGGTGAACCTTATCG	59.9	663	INTERGENIC				
CaPOPI_5849	Ca8	11976112	AATAT/AAT	TATACTCGTGCACTACGCGG	TTGTTGGGGTGAACCTTATCG	59.9	663	INTERGENIC				
CaPOPI_5850	Ca8	11976190	TA/T	CACTACGCGGGTTAGCATCT	TTGTTGGGGTGAACCTTATCG	60.3	653	INTERGENIC				
CaPOPI_5851	Ca8	12016131	ACCCC/ACCCCC	CAACTCTCGTCGCAACTCAA	ATGCAACTTGGGAATTGGAG	60.2	362	INTRON	Ca_23846	T		Apoptosis inhibitory 5
CaPOPI_5852	Ca8	12046116	GTTTTTTTT/GTTTTTTTTT	GTAGTTCGATCCTGCATGGG	TGGATAACTTGCAATTTGGC	60.5	327	INTERGENIC				
CaPOPI_5853	Ca8	12048312	TA/TTATGGATCCTACA	TTCCCCCTAAAACAGAA CCA	TGGAAGAAGGTGGGAAAGAA	59.4	269	INTERGENIC				
CaPOPI_5854	Ca8	12048375	ACC/ACCC	TTCCCCCTAAAACAGAA CCA	GTTGTTGCTGCCCTTTGTTT	59.4	723	INTERGENIC				
CaPOPI_5855	Ca8	12072367	GAAAAAAAAA/GAAAAAAAAA	TGGAGAGGTTGTGATGTCCT	ACGGGCATCTTGATCTTCTG	60.9	782	INTERGENIC				
CaPOPI_5856	Ca8	12979016	C/CG	ATATGTTGGGGGTGATGGA	GGGGTCGGACATTACTAGC	59.9	921	INTERGENIC				
CaPOPI_5857	Ca8	12979079	TTTA/TTTAATTA	CGTGCAGTTTAGGGAAGGAT	GGGGTCGGACATTACTAGC	59.2	873	INTERGENIC				
CaPOPI_5858	Ca8	12980984	TC/T	ATCCACTGCAAACTCCACC	GAAAAATGATGCAAGAGACAAGAA	60.0	659	INTERGENIC				
CaPOPI_5859	Ca8	12983474	ATTTTT/ATTTT	TGCAGATGCACGAATCTCTT	TGCACTAATTTATCGGGACCA	59.6	496	INTERGENIC				
CaPOPI_5860	Ca8	12983910	TAA/TA	TTGGTCCCGATAAATTGTGC	GCCCAAGTTAAGACAACCCA	59.0	442	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5861	Ca8	12984097	CGTGTGT/CGTGT	AGTGTTAACCGGGATCA AACA	GCCCAAGTTAAGACAAC CCA	59.3	301	INTERGENIC				
CaPOPI_5862	Ca8	12990010	CTA/CTATA	TGGCTAATAAATTGTGC CCAT	TCATGTCCCCTCCTTGA ATC	59.3	552	INTERGENIC				
CaPOPI_5863	Ca8	13297997	TA/TAA	AAATTGATTGGATGGTG GGA	AAATGCAGAGGCACCAC TCT	60.0	442	INTERGENIC				
CaPOPI_5864	Ca8	13476730	AA/AAGA	GATGTTCCAGCTCTCTT GGC	TGGGAAATCGATTAAGC CTG	60.0	504	DRR	Ca_20118			Protein of unknown function DUF819
CaPOPI_5865	Ca8	13776463	GTT/GT	TACGGTGCTAGGGAACC AAC	TAATGTTTTTCAGCCA ACA	60.0	534	INTERGENIC				
CaPOPI_5866	Ca8	13940610	AG/A	ATTGGGTCAGTTGGTTT TGC	TTAGTCGCCTCACTCCA TCA	59.8	924	INTERGENIC				
CaPOPI_5867	Ca8	13993907	GTTTTT/GTTTT	CTCCTCAACCTCAATCC CAA	TCACCGGTCAATCAATT AAAAA	60.0	228	DRR	Ca_22739	K		CASP, C-terminal
CaPOPI_5868	Ca8	14042124	ATTTTTTT/ATTTTTTT	TTTCGGTCGTTTGTAAATG GTG	CTCAACCAACCACCAC TCT	59.4	932	INTERGENIC				
CaPOPI_5869	Ca8	14064085	CATATATATATATATA/CATATATATA TATATA	TGTGTGTGTGTGCCAG AGG	GGTATCCATGGGAGCTT TGA	59.1	804	INTERGENIC				
CaPOPI_5870	Ca8	14064157	C/CTTCATAT	TTAACCCATGGGGGTT GATT	GGTATCCATGGGAGCTT TGA	59.4	467	INTERGENIC				
CaPOPI_5871	Ca8	14073516	A/AT	TTCTTCTCAACCAACA GGC	GAAGTTGATGAACCCGT CGT	60.2	578	INTERGENIC				
CaPOPI_5872	Ca8	14074282	CCGCG/CCG	AAACAAAATCCACCGCA CTC	TAGGTTCCAAAGGTGCC AAC	60.0	606	CDS (FRAME SHIFT)	Ca_22744	U		Clathrin/coatomer adaptor, adaptin-like, N-terminal
CaPOPI_5873	Ca8	14076848	CTT/CTTGCTATTTTT	CCCAGGCCTATAGTGGT GAA	ACCGGGGATGACATATC AAA	59.9	491	CDS (large-effect mutations)	Ca_22744	U		Clathrin/coatomer adaptor, adaptin-like, N-terminal
CaPOPI_5874	Ca8	14077330	TAGAGAAAAGAAGAGAAA/TAGAGAAA	TTGATATGTCATCCCCG GTT	TTCTTTCCACCCCTCTT CC	60.0	696	DRR	Ca_22744	U		Clathrin/coatomer adaptor, adaptin-like, N-terminal
CaPOPI_5875	Ca8	14077398	GA/GAAA	TTGATATGTCATCCCCG GTT	AGCTGCATCTTCCACGA TTT	60.0	940	DRR	Ca_22744	U		Clathrin/coatomer adaptor, adaptin-like, N-terminal

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5876	Ca8	14113684	TAAAAA/TAAAAA	AACACGCCTCACACCACATA	CCAATTCACAAATCGGTCC	60.0	447	INTERGENIC				
CaPOPI_5877	Ca8	14121923	GAAAAAAA/GAAAAAAA	TGGTCTTTGATTCTCTGACGA	GCTTTTGTTGAGTCCACTTGC	59.2	690	INTRON	Ca_13048		GRAS	Drug/metabolite transporter
CaPOPI_5878	Ca8	14127063	A/AC	TCCAAGTGAACACAGCACAG	TGGCCTTCTCTGGAGATTG	59.9	154	INTRON	Ca_13047	T	B3	Protein phosphatase 2C-like
CaPOPI_5879	Ca8	14130339	CATATA/CATA	TTGTCGTTCAATGCTTTTCA	TTGGACAACGAGCTCACAAAC	59.3	240	INTERGENIC				
CaPOPI_5880	Ca8	14159846	AATATA/AATATATA	AAATGCAACATCAATGCCA	GAAAATTAAGAGGGAGGGAGGA	59.9	290	INTERGENIC				
CaPOPI_5881	Ca8	14165620	AAATTAA/AAATTAAATTAA	TTTTTCCGACTTGGTCCTTT	TGGGGGTATTGACAGGTGTT	58.7	752	INTERGENIC				
CaPOPI_5882	Ca8	14218237	A/AT	TCTCCACAAATGCAAGGAAA	AAGCCTGGCCCAACTAAATTT	59.2	465	INTERGENIC				
CaPOPI_5883	Ca8	14231465	T/TATA	TGCGTTTATTCTTGGTGGTT	AATGGTACTCCCTCCATCCC	59.5	701	INTERGENIC				
CaPOPI_5884	Ca8	14238334	AT/A	AGGGTTGGAATCCATATGTCA	TGGCTCGTGAAGAAAAACAA	59.1	713	INTERGENIC				
CaPOPI_5885	Ca8	14245101	TAAAAAAA/TAAAAAAA	AAAGGGATGGACACCATTTGA	AGCAGAGTGAAACAGGGGA	60.2	786	INTERGENIC				
CaPOPI_5886	Ca8	14250642	GAAAAAAA/GAAAAAAA	TGTCGTTTTGGTGCAACATT	TCTTCAACACTTGCTCGCAG	60.0	642	INTERGENIC				
CaPOPI_5887	Ca8	14261406	ATTTTTTTTT/ATTTTTTTTT	TGGAGATTGTGGATTTGCAG	GATTCACCATCCCATTTGATTT	59.6	592	INTERGENIC				
CaPOPI_5888	Ca8	14264326	GATATATATA/GATATATA	GTTGGTTGGATTGATTTGGG	TGAAACCCACGCACATTAAA	60.0	406	INTERGENIC				
CaPOPI_5889	Ca8	14287691	CTTTATCTTTTATCTTTTAT/CTTTATCTTTTAT	AGTGGTTTTGTTTGGTGGG	GGTTGGCAAGACTGTGGTT	59.7	467	DRR	Ca_13035			
CaPOPI_5890	Ca8	14302503	AG/A	CCTAACACCTCACACCCC	CGTCTTTGACCAAATTGAAAA	59.3	842	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5891	Ca8	14306794	ATT/AT	TATTGAAC TTGGGAGG CTG	CCCTTTAAATGTGGCAA AAA	60.1	839	INTERGENIC				
CaPOPI_5892	Ca8	14307818	CTTTT/CTTTT	CATGGGCAGCAACAAAG TAA	GAGGACCAATGAAGGCA AAA	59.7	819	INTERGENIC				
CaPOPI_5893	Ca8	14345244	GAAAAATGAAAAATGAAA/GAAAAATGAAA AATGAAAAATGAAAAATGAAA	TTTCCAAC TCCAGCTC AAC	GCAAGGTCGTGGAGAAA CAT	60.2	726	INTRON	Ca_13030	T	bHLH	Protein kinase, catalytic domain
CaPOPI_5894	Ca8	14355037	CTTT/CT	TTTGAGGGTTAGGTGGT TCG	TGGGAAAATAGTCTCCT TCATGT	60.0	369	INTERGENIC				
CaPOPI_5895	Ca8	14362355	ATATTATTATTAT/ATATTATTATT	ATCTTTCGTGCAATTC A CC	TGACAGAGATTAGGATT GAAAGGA	60.1	506	INTERGENIC				
CaPOPI_5896	Ca8	14363844	CTATATA/CTATA	GTTGCCACTTGACCTTG GAT	TGGACTTCATCCAAAA GGG	60.0	351	INTERGENIC				
CaPOPI_5897	Ca8	14370547	TAA/TAAAAA	GGCCAATCAATTTTTGAT GC	TGGGAGATTGGAGCATG ATT	60.3	590	INTERGENIC				
CaPOPI_5898	Ca8	14370711	A/AAAT	GGCCAATCAATTTTTGAT GC	TGGGAGATTGGAGCATG ATT	60.3	590	INTERGENIC				
CaPOPI_5899	Ca8	14373850	AGAAAAATGAAAAATGAAAA/AGAAAAATGA AAATGAAAAATGAAAAATGAAAA	GGAAATTTGGCGTGTA CTT	GTTTCGTTGTTGTGGCA ATG	60.0	373	INTERGENIC				
CaPOPI_5900	Ca8	14404073	GTTTTTTTTT/GTTTTTTTTT	AGATGTGTGATTGGGCC TTC	CCACTCCCTTTGTAGCA TCA	59.9	597	INTERGENIC				
CaPOPI_5901	Ca8	14408424	AT/A	GTTTGGCCACCCCTACA CAC	GTCCCGTGAAGACTTTC AGC	60.3	684	INTERGENIC				
CaPOPI_5902	Ca8	14516248	GNNNNNNNNN/GNNNNNNN	GGCAAAACATTCATCCG TTT	ATCTTTGGCTTCTCCTG CAA	59.8	679	INTERGENIC				
CaPOPI_5903	Ca8	14568462	TATATAT/TATATATATAGATATAGATAT AT	TTGCACCATGTTTGTTAT TCAA	GGCAAAGGGTTTTTGCA ATC	59.0	198	INTERGENIC				
CaPOPI_5904	Ca8	14580122	GAAAAAAAAA/GAAAAAAAAA	TCCAAATCCAAGACCTC CAC	TTTGAAATGATGCAGCTG AGG	59.9	499	INTRON	Ca_13009	Z	MYB_rela ted	Kinesin, motor domain
CaPOPI_5905	Ca8	14603641	GCA/GCACTATACCA	AATGCCGTTAAGTTGAT GGG	CGTATTGCGGAACAACA ATG	59.8	268	DRR	Ca_13007	C		NADH-ubiquinone oxidoreductase, subunit 10

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5906	Ca8	14603917	TA/T	CATTGTTGTTCCGCAAT ACG	TAAACTTCCCTGCACG AGG	60.0	310	DRR	Ca_13007	C		NADH-ubiquinone oxidoreductase, subunit 10
CaPOPI_5907	Ca8	14613573	ATTTTTT/ATTTTTT	CGTGGTGACATCAAAC TGG	CCAATCCCTCAGACCAG AAA	60.0	144	INTRON	Ca_13006	K	C3H	Endonuclease/exonuclease/phosphatase
CaPOPI_5908	Ca8	14617610	CATTAT/CATTATATTAT	GCTCCAACCGTAAAC AAA	TGCAGGGAGAAGAGGG AGTA	60.0	670	INTERGENIC				
CaPOPI_5909	Ca8	14623218	CTTTTTTTTTTT/CTTTTTTTTTT	CAGCAGCAACTTTTGG TGA	TGCTGCTGCTATTCTT TGA	60.0	531	INTRON	Ca_13005	U		SNARE-complex protein Syntaxin-18 N-terminal
CaPOPI_5910	Ca8	14625324	TC/T	GCGTCAACACTTCAAC ACA	TAAGGACTGGACGTAAC CCG	60.8	682	DRR	Ca_13005	U		SNARE-complex protein Syntaxin-18 N-terminal
CaPOPI_5911	Ca8	14645402	A/AAATAATTATAAT	TTTGAGAATCAATGTCAT ATCCG	GGACCCTAAGCATTCTG TGC	59.0	568	INTERGENIC				
CaPOPI_5912	Ca8	14647157	GTTT/GTTTT	TTGCTTGTCATGACGT AGG	TCTGCAACGAAGATTAA ACCAA	59.7	297	INTERGENIC				
CaPOPI_5913	Ca8	14659373	AT/ATT	AATTTGGAAGCACATCG ACC	CACACATTCTTGGCCC TCT	59.9	401	INTERGENIC				
CaPOPI_5914	Ca8	14659986	TAAAAAAAAA/TAAAAAAAAA	AGAGGGCCAAGAAATGT GTG	GCATGCATAACAATTTG TGTA	60.1	551	INTERGENIC				
CaPOPI_5915	Ca8	14662169	GAA/G	CTTCCTTTGGCCACCTA ACA	CATCATAACATTTAGCCC CTCA	60.1	150	INTERGENIC				
CaPOPI_5916	Ca8	14662220	GTTTTTTTTTTT/GTTTTTTTTTT	CTTCCTTTGGCCACCTA ACA	TTTAAATGCACATTTGAT TCTCC	60.1	617	INTERGENIC				
CaPOPI_5917	Ca8	14671445	TAAAAAAAAA/TAAAAAAAAA	CCTTCCCGATTGATCC TTT	TCGACAACTTACATTCA TCATCC	60.3	831	INTERGENIC				
CaPOPI_5918	Ca8	14688273	AAACA/AA	GATTTAATTTGTTGGG GATTTTT	TGCGTGATCGATGCATA TAGA	58.7	446	INTERGENIC				
CaPOPI_5919	Ca8	14707819	AGT/A	TCATGGCTATGCATGGA TGT	ACCGCATCTGCAATAGG TTC	59.9	407	INTRON	Ca_12998	R	SBP	Malate transporter, aluminium tolerance
CaPOPI_5920	Ca8	14722667	TA/TAGA	TTCATTGCACCCACACT TC	TCGGAAACAAATGGTGG ATT	59.5	578	INTRON	Ca_12995	O	NAC	Peptidase A1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5921	Ca8	14733700	ATTTTTTTTT/ATTTTTTTTT	TCTGAACGAAGTTGGAGCAA	GGTATGTTTGTGTTGAAAGGGG	59.6	787	INTRON	Ca_12995	O	NAC	Peptidase A1
CaPOPI_5922	Ca8	14742163	T/TGA	TGGTGGTTGATCATACGAGAG	GCCAAGAAATAGCCACTTGC	58.6	644	INTRON	Ca_12995	O	NAC	Peptidase A1
CaPOPI_5923	Ca8	14746760	ATTCA/ATTCATTATTTTCA	TGGATCTCATCCTCATCCT	TTGAAGTGCTTTTGGTGCTG	59.4	573	INTRON	Ca_12994			Uncharacterised protein family Cys-rich
CaPOPI_5924	Ca8	14751128	TC/T	TGATGCGTTGATAGTGTGG	GGCACTTGGTTGGTCTTCAT	58.1	619	INTRON	Ca_12994			Uncharacterised protein family Cys-rich
CaPOPI_5925	Ca8	14764445	TGG/TG	GGCATCATAGTGTGAGACCA	ACGCGCCAGAAATATAACG	58.6	609	INTERGENIC				
CaPOPI_5926	Ca8	14770790	ACC/AC	TAAAGAGTTGGTGCTTGCT	TTTGGCAAACACTTGTAATAATGA	59.9	461	INTERGENIC				
CaPOPI_5927	Ca8	14778020	AACTAT/AACTATAATACTAT	TTGGCATTATATGTGGCACC	TGACTCACGATCAGTTTGGC	59.3	750	DRR	Ca_12990			Adaptor protein ClpS, core
CaPOPI_5928	Ca8	14780556	TAAAAAAA/TAAAAAAA	CTCCAACAAACCACCACCTT	GTCCATGACGTGTCAACGTA	59.9	531	INTRON	Ca_12990			Adaptor protein ClpS, core
CaPOPI_5929	Ca8	14781231	T/TG	ATCGTTGGTCCTTGTTTGG	AAATGGCAGGACACATTGTT	59.8	608	INTERGENIC				
CaPOPI_5930	Ca8	14783369	ATTTT/ATTTT	GCAACAATTGTGCAGATGAA	AGGCCTTCAGAAAAGCAACA	58.3	216	INTERGENIC				
CaPOPI_5931	Ca8	14808806	TG/T	TTCCCAACCCAAAGTACCTC	TTTGATATTGTTGTTGGCAG	58.9	553	INTERGENIC				
CaPOPI_5932	Ca8	14815482	GTTT/GTTTTT	CTTGAGAGAAGCACCAAGGAG	GTGCCACACAAATGACAAAT	60.0	568	INTERGENIC				
CaPOPI_5933	Ca8	14820833	TTATATATATATA/TTATATATATATATA	ACATCCGTGATGGTCACACA	GGGAATGGTGAAATCAATGC	60.9	530	DRR	Ca_12987	D	bHLH	Mrp, conserved site
CaPOPI_5934	Ca8	14921456	TAAAAAAA/TAAAAAAA	CCATGGTTGAGTTGACCAAA	ATGTGTGGAGGAGTTGGGAG	59.4	626	INTERGENIC				
CaPOPI_5935	Ca8	14924927	GAAAAAAAAA/GAAAAAAAAA	AGCCACCATGACGAAAAATGTC	GTCCTCGTCAACATTCGACA	60.1	484	DRR	Ca_12980	P	MIKC	Sulphate transporter/antisigma-factor antagonist STAS

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5936	Ca8	14932583	GAAAAAAAAA/GAAAAAAAAA	CACCATTCTCCTTCAAC CAAA	AACCACGCGACTCATAC ACA	60.0	716	INTRON	Ca_12980	P	MIKC	Sulphate transporter/antisigma-factor antagonist STAS
CaPOPI_5937	Ca8	14984060	T/TGCTGCTAATCC	GCTCGAATGGACCTTGA AAC	AATATTGGTCCCCTGCA TGG	59.7	235	DRR	Ca_12975	K		Helix-turn-helix type 3
CaPOPI_5938	Ca8	15048107	TAAAAAAAAA/TAAAAAAAAA	ATGGCGGATATTCAAA CAA	TTGTTGAGATCCCTCTCT TGC	60.2	627	INTERGENIC				
CaPOPI_5939	Ca8	15162330	TTAATAATAATAATAATAA/TTAATA ATAATAATAATAA	TTCTGTCGTAGGTCCA GTG	GGGAAACCCACCTCTTG ATT	59.7	757	INTERGENIC				
CaPOPI_5940	Ca8	15315884	TCC/TC	ATTCATCTCATGCTCC CTG	CAAAGTCAAGACTGCC AAA	60.0	345	INTERGENIC				
CaPOPI_5941	Ca8	15360832	GTTTTTTTTT/GTTTTTTTTT	TGATCGACTGCCAAACA CAC	ATGCCACATCATACCATT CG	60.7	684	INTERGENIC				
CaPOPI_5942	Ca8	15435370	TTTAATTAATTAATTAATTAATTA TTAAT/TTTAATTAATTAATTAATTA ATTAATTAATTAAT	AATGGGGAACAAGCTG ATG	TGGGGCAATGAAGAAAG CTA	59.9	549	INTRON	Ca_17897		bHLH	
CaPOPI_5943	Ca8	15439013	CTTTTTTTTT/CTTTTTTTTT	GCTAAATTACATTCGTG GTCCC	TTTCATCAAATCCGTAA ACAAA	59.7	155	INTERGENIC				
CaPOPI_5944	Ca8	15558716	GAAAAAAAAA/GAAAAAAAAA	TTCTTTGTCACTGCTTC CA	CATGCTTTCAAAGATG CCA	59.4	490	INTERGENIC				
CaPOPI_5945	Ca8	15577896	CCA/CCATCA	TTTTTCAGCAACCCCAA AAG	TAGAGGCTTGTCAATCG GCT	60.1	665	CDS (large-effect mutations)	Ca_17886	T	EIL	Protein phosphatase 2C, manganese/magnesium aspartate binding
CaPOPI_5946	Ca8	15580121	A/AATTTAATTT	TCCTCAATTTGAGCACA CG	TGGACACCACACTTCAA ATCA	59.8	657	INTERGENIC				
CaPOPI_5947	Ca8	15642015	ATTTTTTTTT/ATTTTTTTTT	GGGGTGGGATGACAAAT AGA	TGAGCCCTCAAACCCCT AAA	59.6	656	DRR	Ca_17880			Polyketide cyclase/dehydrase
CaPOPI_5948	Ca8	15685177	AGG/AG	GCCCAACAACAGAACCA AGT	GACTCCAAACCCCTGTG CAT	60.0	420	INTERGENIC				
CaPOPI_5949	Ca8	15685323	TAAAAAA/TAAAAAA	GCCCAACAACAGAACCA AGT	GACTCCAAACCCCTGTG CAT	60.0	420	INTERGENIC				
CaPOPI_5950	Ca8	15685626	T/TA	ATGCACAGGGTTTGGGA GTC	ACTTGGTTCTGTTGTTG GGC	60.0	416	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5951	Ca8	15685828	TAAAAAAAA/TAAAAAAAAA	ATGCACAGGGTTTGGAGTC	ACTTGTTCTGTTGTGGGC	60.0	416	INTERGENIC				
CaPOPI_5952	Ca8	15685888	A/AG	ATGCACAGGGTTTGGAGTC	ACTTGTTCTGTTGTGGGC	60.0	416	INTERGENIC				
CaPOPI_5953	Ca8	15694311	GTATATATATATATATATATATATATATATA/GTATATATATATATATATATATATATATATATA	CCGTCTCTTTCACATGGTT	AAAGGCTCGGGTCAGTCATA	60.0	438	INTRON	Ca_17876	A		RNA-dependent RNA polymerase, eukaryotic-type
CaPOPI_5954	Ca8	15788537	TAAAAAAAA/TAAAAAAAAA	TCGGTTCCTTCAACTTTGG	ATCAATGCTTCCACCCTTTG	60.1	588	INTERGENIC				
CaPOPI_5955	Ca8	15850345	AATA/AATATGTGTTATA	TTATTGTTCCCTCTTGGG	TCTTCAAATTACTCCCTCATCA	60.1	527	INTERGENIC				
CaPOPI_5956	Ca8	15891448	GTTTTTTTTT/GTTTTTTTTTTTTTT	TGCAAGAAAGTTGTGTGGG	GTTCATGCACCTTCTTGGGT	59.7	385	INTERGENIC				
CaPOPI_5957	Ca8	15892786	AAAGA/AAAGAAGA	AGCAGTTGAAC TTGCCTCGT	CGATGATTCATTCCCAAACCC	60.1	513	INTERGENIC				
CaPOPI_5958	Ca8	15918262	A/ATTAATTCTC	AAACGTCAGAAAACATCGGG	TGCCCCGAGACATAAAGTTC	60.0	243	INTERGENIC				
CaPOPI_5959	Ca8	15918552	TAAAAAAAA/TAAAAAAAAA	AAACGTCAGAAAACATCGGG	GAGTCAACTTTGCTGAGGGC	60.0	717	INTERGENIC				
CaPOPI_5960	Ca8	16066420	AATATATATATATATATATAT/AATATATATATATATAT	TATTTTGGGATTTTGGCTCG	AGGAAGAGTGAGATTGCGAA	59.9	512	INTERGENIC				
CaPOPI_5961	Ca8	16315020	TAAAA/TAAA	AATGCAAAGCAACAAGTTTC	TTGTATGCATGTGTGATGTGTG	59.3	504	INTERGENIC				
CaPOPI_5962	Ca8	16315069	CTGATGAT/CT	AATGCAAAGCAACAAGTTTC	GCACATTGAACCCCATACAA	59.3	605	INTERGENIC				
CaPOPI_5963	Ca8	16315111	GAT/G	AATGCAAAGCAACAAGTTTC	GCACATTGAACCCCATACAA	59.3	605	INTERGENIC				
CaPOPI_5964	Ca8	16316035	CAAAA/CAAAAA	GGCATCACCCCCAAGACATAG	CCCTTGATTTTCAATCACTCC	60.3	352	INTERGENIC				
CaPOPI_5965	Ca8	16360078	T/TA	GAAAAATGAAGGAGGTGGCA	GGAAAGAATGTTACGCC TGC	60.1	159	INTRON	Ca_15558	I		Prenyltransferase/squalene oxidase

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_5966	scaffold10	68796	GATAATAATAATAATAATAATAATAA TAATAA/GATAATAATAATAATAATAA ATAATAATAATAATAA	AAAGCAAACCAATGGGC ATA	ATGAATGGAAGACGTGA CGA	60.3	657	INTERGENIC				
CaPOPI_5967	scaffold1003	13636	GAAGTAAAG/GAAG	TGCCACTATCGGGCTAA TTT	ATTTTCGCATCCAATTAC CG	59.6	885	DRR	Ca_27802	QR	B3	Oxoglutarate/iron-dependent oxygenase
CaPOPI_5968	scaffold1003	41332	G/GAGCGGT	GGGATTTGAAGGTGCTG AAA	TAGTGGCCACAACCAAC TCA	60.1	452	INTERGENIC				
CaPOPI_5969	scaffold1003	41466	AAAGA/AAAGAAGA	GGGATTTGAAGGTGCTG AAA	TAGTGGCCACAACCAAC TCA	60.1	452	INTERGENIC				
CaPOPI_5970	scaffold1006	109456	T/TC	TTGATTTAGCCAGGA TTC	TTTACAAGCAGCGGAA AGT	60.0	493	INTERGENIC				
CaPOPI_5971	scaffold1006	212542	AATATATATATATATAT/AATATATATA TATATATATAT	TTTAAGGAGGGAGCGAG TTG	TTCTATGTGCACCGCTT AGG	59.4	477	INTERGENIC				
CaPOPI_5972	scaffold1006	403767	GTTATTATTATTATTATTATTATTAT T/GTTATTATTATTATTATTATTATT	CGCGAGACAACCTTCCC TAA	AATGGTGTTTTCTGGTT GCC	60.4	520	INTERGENIC				
CaPOPI_5973	scaffold1006	520865	ATTTTTT/ATTTTTTT	TGGAGTGTGCCAAAAAG TTG	CAACCTCCCTTTGTTTTG CT	59.7	567	DRR	Ca_18036	M	HB-other	Sucrose synthase
CaPOPI_5974	scaffold1006	624934	CT/CTTAAAGAATT	TCCATTGCATAAAAGTTT TGTTT	TCATTTCTTGCCTCTCC CTT	57.8	123	INTERGENIC				
CaPOPI_5975	scaffold1006	655490	GTTTTTTTT/GTTTTTTTTT	CTTTTGGTTGTGCAATG GTG	ATGCCTTCATCAACTTTG GG	60.0	615	INTERGENIC				
CaPOPI_5976	scaffold1008	12678	TC/T	TCTTGGTTGTAACCTT GGC	GGGCTGATGCCATAAAC ACT	60.0	727	INTERGENIC				
CaPOPI_5977	scaffold1008	20458	T/TATA	TGTTTGACTGATGTTAA GTGTGC	GGGGTGCAGATTTCTGA TGT	57.9	562	INTERGENIC				
CaPOPI_5978	scaffold1010	21084	ATGC/ATGCTGC	TGTAACCCGTGTTGGAT GAA	ACCGGTTTGTGATTGTC CTC	59.8	729	INTERGENIC				
CaPOPI_5979	scaffold1013	39772	AATATATATATATATATATATATAT AT/AATATATATATATATATATATAT AT	ACGAAACAGGGAGGTTT GTG	CGGTGAATCCTTTACGG AGA	60.0	624	INTERGENIC				
CaPOPI_5980	scaffold10158	16048	TC/TCC	CTGTGGGGGCTATTCTG AAA	AAACGATCAAATCCAAC CCA	60.1	487	INTERGENIC				

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CaPOPI_5981	scaffold1017	10794	AT/A	GTTTGGACATTTACGGC GAT	GTTTCGGGTTCCACGTT AGA	59.9	725	INTERGENIC				
CaPOPI_5982	scaffold10180	748	AT/ATT	GGTGAGTTTGTGTCGTT GGA	AGGGAGGACGAAGATGA CCT	59.6	448	INTERGENIC				
CaPOPI_5983	scaffold10227	6464	AATATATATATATATATATATATATATATATATATA/AATATATATATATATATATATATATA	GGGAACGTGAAGAACTC AGC	TGCAACAACCACAACCA CTT	59.9	518	INTRON	Ca_28086		bHLH	Helix-loop-helix DNA-binding domain
CaPOPI_5984	scaffold1027	152594	CAA/CA	TGAGTGCACGGATTGT AAA	CTCAGCCCCTGACTTAA TGC	60.3	692	INTERGENIC				
CaPOPI_5985	scaffold10285	986	CTAGGAAAAAA/CTAGGAAAAAATTAGG AAAAAA	CGAAAACCTCAGAAAGGC GAC	GCCTTATGTGGAAGAC ACCA	60.0	513	INTERGENIC				
CaPOPI_5986	scaffold1038	720	TGG/TG	CGAAAATCGCCAGAAA ATA	TCCTGGTCCTCGATTTC ATC	60.0	842	INTERGENIC				
CaPOPI_5987	scaffold1039	3089	ATTTT/ATTT	CGAAGTTCCTTCAGCC AAC	CCCATCCTTCTTCTTGA CCA	59.9	358	INTERGENIC				
CaPOPI_5988	scaffold1039	32679	T/TGTTG	TTCCCTAGATCCTTCGC AGA	TGGATGGTAATCCAACG TGA	59.9	623	INTERGENIC				
CaPOPI_5989	scaffold1039	41739	AATATATATATATATATATA/AATATATATATATATATA	CTTGGGAACCTGGAGAGC AAG	ACCTTCACGTCGATTAC CGG	60.0	809	INTERGENIC				
CaPOPI_5990	scaffold1039	48817	ATTTTTTTTTTT/ATTTTTTTTT	CGACATGCATGCCTTAT TTG	CATGAGGAAACAATTGT GCAG	60.1	571	INTERGENIC				
CaPOPI_5991	scaffold1039	59288	CAAAAAAAAA/CAAAAAAAAA	GCAATCTCCTCAACTCG GTC	TACTGTGCGGCCATCTA CTG	59.8	610	INTERGENIC				
CaPOPI_5992	scaffold10412	1146	GCTC/GC	TGATTCCATTGGGGTTT CAT	ATTGTTTTCTCGAGGTT GCG	60.0	611	INTERGENIC				
CaPOPI_5993	scaffold10415	1018	AT/ATT	GAGGAAGATGCCACCAG AAA	TTTGATCCACAGAAG CCT	60.2	774	INTERGENIC				
CaPOPI_5994	scaffold10415	1060	TTGTG/TTGTGTG	GAGGAAGATGCCACCAG AAA	TTTGATCCACAGAAG CCT	60.2	774	INTERGENIC				
CaPOPI_5995	scaffold10419	1064	TAAAAA/TAAAAAA	TTTTGGCTGATGTGGAT GAA	GTTTGGGTTTGCTTGTT TGG	60.0	537	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Anneling temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_5996	scaffold1043	1901	GTATATATATATATATATATATATATATATATATATAT/GTATATATATATATATATATATATATATATATATATATATATATATAT	CGAAGCAAAAGAAGAA CCG	TGGATTACGGGTGAAAT GGT	60.0	321	INTERGENIC				
CaPOPI_5997	scaffold1045	12241	CAAA/CAA	TGTGCATCAAAATAGTG CGT	GCGGACGAAAATGACCT AAA	60.1	650	INTERGENIC				
CaPOPI_5998	scaffold1046	11369	GA/G	AGCCTAGGGAGGACGAA TGT	TACCAATCCTGTGCATC CAA	60.1	464	INTERGENIC				
CaPOPI_5999	scaffold1046	17706	ACC/AC	CATTGGATGCACAAGAT TGG	AGGTCATTTTCGTCC TC CT	59.9	871	INTERGENIC				
CaPOPI_6000	scaffold1046	20332	TAAAAAAA/TAAAAAAA	GCGCAACAAACCTATG TGA	TCAGGTCATTTTCGTCC TCC	59.7	788	INTERGENIC				
CaPOPI_6001	scaffold1046	21076	GAAA/GAAAA	GGAGGACGAAAATGACC TGA	ACCGATCTTGTGCATCC AAT	60.1	671	INTERGENIC				
CaPOPI_6002	scaffold1047	43221	ATTTT/ATTTTT	AAGTTTAATGGGTTTGG CCC	GGCAATTTTGT TTGGTC GTT	60.1	771	INTERGENIC				
CaPOPI_6003	scaffold1047	59966	TTATAT/TTATATATAT	GGGTCTTCAAGTCCATT CCA	TGCCCATATTGAAGCTT TCC	59.9	266	CDS (FRAME SHIFT)	Ca_17176	G		Glycoside hydrolase, family 32
CaPOPI_6004	scaffold1047	72978	CAAGAAG/CAAG	TCCCCAGCCACTACTTA TGC	ACCAACATTGATCAGTG GCA	60.1	409	DRR	Ca_17177	Z	Dof	Actin-like
CaPOPI_6005	scaffold1047	93852	ATT/AT	GGCTCCTTTGGTGGTAG TGA	TCATCATCCTATTGCAG CCA	60.1	484	INTRON	Ca_17178		bZIP	RNA recognition motif domain
CaPOPI_6006	scaffold1047	132182	TTTGC/T	TTTCTTTTGGGCCCTCC TAT	AGTTTCCTTTGTGCGCCC TTT	59.9	705	INTERGENIC				
CaPOPI_6007	scaffold1047	282094	TTATATATATATATATATATAT/TTATATA TATATATATATATATAT	GTCACGGGAGACAATCC ACT	TTGAGGGGTGGGAGTTA AAA	60.0	280	INTERGENIC				
CaPOPI_6008	scaffold1047	313122	GAAAAAAAA/GAAAAAAAAA	AAAATCCACACGTCCG AAG	TCAAAAGATCGCAGTTG TG TG	60.0	354	INTRON	Ca_17199	I		Patatin/Phospholipase A2-related
CaPOPI_6009	scaffold1047	419626	C/CAAACATG	CCGATGAAAATCACCC ATC	CCATTGATAAAGCGTGT ACGG	60.1	327	INTERGENIC				
CaPOPI_6010	scaffold1047	461378	TTATATATATATATATATAT/TTATATAT ATATATATATATATATATA	TATATGCTTGACGAGG CTG	ACTCCAAAAGCACCGAC AAT	60.0	514	INTERGENIC				

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CaPOPI_6011	scaffold1047	527453	GTTTTTTTTT/GTTTTTTTTT	ATCAGAGGCAAAGTGCC AAT	TACCCAGGCTTTTCTCA TGG	59.7	378	INTERGENIC				
CaPOPI_6012	scaffold1047	595067	GTT/GTTT	AGGAACGCCTGGAGAAA GAT	CGCACCTAAACCTCCTT TCA	60.2	507	INTRON	Ca_17227	Z		Actin-like
CaPOPI_6013	scaffold1049	75199	ACC/AC	ACGTTCTGAGGGAATT GTG	GTAAAGGGTCACCAACC GAA	60.0	828	INTERGENIC				
CaPOPI_6014	scaffold1049	293719	TCC/TCCC	CGTTTTTCAAAGCGAGG GTA	GCCCTCAGATGAGAGTC AGG	60.2	439	INTERGENIC				
CaPOPI_6015	scaffold1052	11395	GTATATAT/GTATATATAT	GGTAACCAATCCGAAGA CGA	GCCCTCAGATGAGAGTC AGG	59.9	518	INTERGENIC				
CaPOPI_6016	scaffold1052	16411	ATT/AT	CCGTTGTTTCAACTTCC ACC	GCAGCAGCCATTCTAC AGA	60.4	323	INTERGENIC				
CaPOPI_6017	scaffold1052	16426	T/TG	CCGTTGTTTCAACTTCC ACC	GCAGCAGCCATTCTAC AGA	60.4	323	INTERGENIC				
CaPOPI_6018	scaffold1052	20929	TAAAAAAAA/TAAAAAAAAA	TGTACCACCACAAGTCC ATCA	TGCAATTTTGCATGGTT GTT	59.9	238	INTERGENIC				
CaPOPI_6019	scaffold1052	48422	TAAAAAAAAA/TAAAAAAAAA	TGTGTTGCGTTGTGGAT TCT	CCCAACACTCGCTAT TCA	60.2	686	INTERGENIC				
CaPOPI_6020	scaffold1052	51298	AGTG/AGTGTG	GGGAGAATTGTAACACC CCA	AACCAACACACAAGGA AATATGA	59.6	337	INTERGENIC				
CaPOPI_6021	scaffold1052	147202	TGGGG/TGGGGG	AACCAACCCGTTTTTCAT CA	TCATCAACCTCCATCATC TTCA	60.2	506	INTRON	Ca_27109	J		Protein synthesis factor, GTP-binding
CaPOPI_6022	scaffold1052	186937	TC/TCC	ATTCCTGATGTTCACT CGG	ATGCCACTACAAAAGTG GGC	59.9	588	INTERGENIC				
CaPOPI_6023	scaffold1055	16854	TAAAAA/TAAAAA	CACCAAGTCCCTAAACC AAG	TCCCTTGAAAGTGTGA TGG	59.4	379	INTERGENIC				
CaPOPI_6024	scaffold1055	56180	GGGAGGAG/GGGAGGAGGAG	GCACCTGAGTAAATTC GGT	CTTGGGCTGCTAAGAAT TGC	60.0	577	INTERGENIC				
CaPOPI_6025	scaffold1055	56306	CATATATATATATATAT/CATATATAT ATATATATATATAT	GCACCTGAGTAAATTC GGT	CTTGGGCTGCTAAGAAT TGC	60.0	577	INTERGENIC				

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									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6026		scaffold1055	157848	TTATATATATATATATATATATATATATATATATATATA TATATATA/TTATATATATATATATATATATA TA	CGGAACTCATTGTTCA CCA	TCATAAACGGAGAAATC GGG	59.5	625	INTERGENIC				
CaPOPI_6027		scaffold1055	206130	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATT/AT TATATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTAT	TTTATTGCCTGCCCAA CTC	GGAACAGCAACTGCAA AAT	60.1	608	INTERGENIC				
CaPOPI_6028		scaffold1055	339319	ATTTTT/ATTT	TTTAAGGTGTGGGACCA AGC	GGAAACAATAAACCGAG GCA	60.0	540	INTERGENIC				
CaPOPI_6029		scaffold1055	340051	GAAAAAAA/GAAAAAAA	TGTTGTTCTGGCATACGA CAT	TGCACATACATAATGGA CCACA	60.0	516	INTERGENIC				
CaPOPI_6030		scaffold1055	340491	T/TATC	TGCAATAAAGCTTTTGAA GTGG	ACATACTCCCTCACTCC CCC	59.4	413	INTERGENIC				
CaPOPI_6031		scaffold1055	340641	ATGGGGGAGTG/ATG	TGCAATAAAGCTTTTGAA GTGG	AAGTTGTGTCACCATTG CCA	59.4	813	INTERGENIC				
CaPOPI_6032		scaffold1056	72718	GAA/GAAA	TTCTCCGCATATTTGAAT TCCT	TTCGCATGACCAACAA ATG	59.9	206	INTERGENIC				
CaPOPI_6033		scaffold1056	116197	ACCGAGCCGAGCCGA/ACCGAGCCGA GCCGAGCCGAGCCGA	ACCTTGTGGATGGCACT TTC	TGGCATTGATGATGGCT TTA	60.0	342	INTERGENIC				
CaPOPI_6034		scaffold1056	135454	TG/T	GCTACGGTGTTAGGGAA CCA	CTATCACGGGTCTCCAC GAT	60.0	879	INTERGENIC				
CaPOPI_6035		scaffold1056	142810	TAAAAAAAAA/TAAAAAAAAA	TTGCTCCTACGTATCCC CAG	TGGCCACAAGAAGACAA TGA	60.1	705	INTERGENIC				
CaPOPI_6036		scaffold1056	142961	ATTTTTTTTT/ATTTTTTTTT	CCGACGGCGGTAATAAT AAG	TGGCCACAAGAAGACAA TGA	59.5	404	INTERGENIC				
CaPOPI_6037		scaffold1056	148159	TTAGATAGA/TTAGA	TGAAAGAATGTGAAAG ACATGG	AAATGGTATTGGGACGA ACG	59.1	493	INTERGENIC				
CaPOPI_6038		scaffold1060	591	TAAAA/TAAAA	GTGATAAAGGCGTCAAC GGT	CCAAGGCAGACAAAGAA AGC	60.0	410	INTRON	Ca_21773		ERF	Pathogenesis-related transcriptional factor/ERF, DNA- binding
CaPOPI_6039		scaffold1060	10684	TAGAGAGAGAGAGAGAGAGAGA/TA GAGAGAGAGAGAGAGAGAGAGA	CTCCAAAGGGACAAACA TGA	AGTTGCACTGGGGTTAA TGG	58.5	738	INTRON	Ca_21773		ERF	
CaPOPI_6040		scaffold1060	51771	CTTTTTTTTT/CTTTTTTTTT	CACATGAAGCCAAGGGA AGT	GGAATCACACCATGTCA CCA	60.1	758	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6041	scaffold1060	389867	CAT/CATAT	ACCAGGATCCTCCGAAC TCT	CAAACGCAAAATTAAACA CACAA	60.1	414	INTRON	Ca_21793			Transposase, Pta/En/Spm, plant
CaPOPI_6042	scaffold1061	27664	CAAA/CAA	GCCAGATCTTTCGATTG AGC	GGAACATGGCCTCAGTT GAT	59.9	302	INTERGENIC				
CaPOPI_6043	scaffold1061	32882	T/TC	ACTAACCATCGTTTGGC CTG	GCAATTTTCGTACCCCT TGA	60.0	227	INTERGENIC				
CaPOPI_6044	scaffold1061	49764	TAAA/TAA	CCTTGTACACAGTTGG CTG	TCCTGGTTGTAACCCCTT GGC	60.3	150	INTERGENIC				
CaPOPI_6045	scaffold1061	76996	CGG/CG	TATTTGGACCAGAGGAT GGC	CCCAACAGTAGGACCA GGA	59.9	109	INTERGENIC				
CaPOPI_6046	scaffold1067	190632	GTTT/GTTTTT	TCGCGTAGTGGTAGCCT TCT	TCACAAGGGAGGCTCTA TGG	60.0	182	INTERGENIC				
CaPOPI_6047	scaffold1067	202690	AC/ACC	GCAGCCCATTTACGTTT TGT	CGAATTCTCTTCTCCT CCC	60.0	595	DRR	Ca_24425			
CaPOPI_6048	scaffold1067	203101	ATTTTTTTT/AATTTTTTTT	TGAAACTGGGAGGAGGA AGA	CAGTGCGATGGAGAAAT CAA	59.8	418	DRR	Ca_24425			
CaPOPI_6049	scaffold1067	214347	A/AGCAGTGCGG	GATAGGAGCATTGCGTG GAA	TCAAAGCGAAAACCAT TTC	60.0	658	INTERGENIC				
CaPOPI_6050	scaffold1067	229129	CTTTT/CTTTTT	ACATGGTTCGGAAACGT AGG	TCCATGCAAGAAGAGCT CAA	59.9	341	INTERGENIC				
CaPOPI_6051	scaffold1067	242965	CAT/CATAT	TTTCTTCGCTAGCCGTT GTT	TCCTGTGTTGGGTTAAG GGC	60.0	941	INTERGENIC				
CaPOPI_6052	scaffold1067	243320	TATCCAAAT/TATCCAAATCCAAAT	TTATTGTTGTTGCTTGG GCA	TCTTGTGTTGGGTTAAG GGC	60.1	447	INTERGENIC				
CaPOPI_6053	scaffold1067	243540	AGGGTTGGG/AGGG	GCCCTTAACCCAACACA AGA	CTCCCGTTGTGGAAGT ATT	60.0	594	INTERGENIC				
CaPOPI_6054	scaffold1067	243805	CAAGCCT/CAAGCCTAAAGCCT	GCCCTTAACCCAACACA AGA	AGGCGACCCTATACCGA AGT	60.0	643	INTERGENIC				
CaPOPI_6055	scaffold1067	263503	AA/AGCTAGTCAGCA	CAGTGAGTAGCAAGCAA GCG	CCCAGCCTAGTGACATC CAT	60.0	445	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6056	scaffold1067	266043	CTTTTTTT/CTTTTTTT	ATCCAGAATGAGCAAC TGG	CGGAGAAATCCGTTTTG CTA	60.1	575	INTERGENIC				
CaPOPI_6057	scaffold1081	39164	T/TC	TTCAAATTCACCACCAT TCA	GGCCGTTGTTACTGCAA AAT	58.9	774	INTERGENIC				
CaPOPI_6058	scaffold1081	86270	GAAAAAA/GTAAAAAAA	TTATTCGGGCTGTCAA AAC	CATGCGTTCCTTGTTG GTT	59.9	251	INTERGENIC				
CaPOPI_6059	scaffold1081	88052	TT/TTGT	TGAGCATGGCTAAGTTG CAC	AAGGGAAGGGCATAAT GTT	60.0	522	INTERGENIC				
CaPOPI_6060	scaffold1082	21212	ACCTAAACCCTAAACCCTAA/ACCTAA CCCTAA	TTGGACGAAGTCAATG AAT	GCGTTTCGGGTTTATG TTA	59.1	687	INTERGENIC				
CaPOPI_6061	scaffold1083	74707	AATATATATATATATATATATATATAT ATATAT/AATATATATATATATATATAT ATATAT	ATCTCGGGTGCTGAAAA TTG	GGTCCCTAGCACCATG GCA	60.1	546	INTERGENIC				
CaPOPI_6062	scaffold1083	122050	C/CT	AAGCCTAGGAGGACGA AAA	AACGAATCATGTGCATC CAA	60.2	772	INTERGENIC				
CaPOPI_6063	scaffold1087	12601	CTT/CTTT	GCTTAGGCAGCACAAA ATC	CGGTTATTTGATATCAC GGGTT	59.9	732	INTERGENIC				
CaPOPI_6064	scaffold1087	13529	TTTTATTTATTTATTTAT/TTTTATTTAT TTATT	TTCCGCATAACACTAAG TGGC	CCATGCTAATGGATGCT GTG	60.1	521	INTERGENIC				
CaPOPI_6065	scaffold1087	14399	CGAGAGA/CGAGA	TGGGTTGTACCGTTAAT TGG	ACCCCAAATATTGCCAT GAA	58.3	810	INTERGENIC				
CaPOPI_6066	scaffold1087	23029	CTTTTTTTTT/CTTTTTTTTT	TGCACCACGAGATCTTG AAA	CGTTGATACATAACAAAA ATACAAACA	60.4	597	INTERGENIC				
CaPOPI_6067	scaffold1087	23220	T/TG	TGTGGGATATCAAGTTT TGGA	AAAAATGCACGGGACAA ATA	57.9	704	INTERGENIC				
CaPOPI_6068	scaffold1092	65384	GTTTTTTTT/GTTTTTTTT	AACCAATCTTGTGCATC CAA	AACCCTAGGGAGGACGA AAA	59.0	778	INTERGENIC				
CaPOPI_6069	scaffold1092	108212	AGGG/AGG	TCCTCCCCAGGCTTATT CTT	TTGCCTAAAAACCGAA TTG	60.0	544	INTERGENIC				
CaPOPI_6070	scaffold1092	121415	AT/A	AGTTCATTTTCGTCTC CT	AATCCAATGGCACAAAC ACA	59.9	648	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6071	scaffold1092	146775	GTTT/GTT	CTTCCTCCCTCGGCTTA TTC	AGGGAGGACGAAATGA CCT	60.2	365	INTERGENIC				
CaPOPI_6072	scaffold1101	3795	TCC/TC	TTGGCTCATTGCTTGAG TTG	AGCCAAGGGAGGATGAA AAT	60.0	214	INTERGENIC				
CaPOPI_6073	scaffold1102	7455	CAAAA/CAAAA	AGGGAGGACGAAATGA CCT	AACCAATGTTGTGCATC CAA	59.9	470	INTERGENIC				
CaPOPI_6074	scaffold1109	14028	ATTTTTTTTTTTT/ATTTTTTTT	TTTGAAACCTCACCAAG GGG	TAAACTGTCAGGGGCGA AGA	59.9	416	INTERGENIC				
CaPOPI_6075	scaffold1109	14081	GTT/GTTAATT	TTTGAAACCTCACCAAG GGG	TATAAACTGTCAGGGGC GAA	59.9	418	INTERGENIC				
CaPOPI_6076	scaffold1109	109368	GCAGAAATAAATTAATCAGAAATAAA TTAATCAGAA/GCAGAAATAAATTAAT CAGAAATAAATTAATCAGAAATAAAT TAATCAGAA	TTGGTTTATTGGGTGG GGA	AATAGGGTGGGATGCAA AGA	60.0	753	INTERGENIC				
CaPOPI_6077	scaffold1109	114315	ATTT/ATT	TCCCTACTCGTAATCGA CGC	ACTCAGCCCGGGTATAG AGC	60.2	392	INTERGENIC				
CaPOPI_6078	scaffold111	98560	GATATATATATATATATATATATAT ATATATA/GATATATATATATATATAT ATATATATATATATA	CGAGTCTCGGATATCTG CTC	TCGATGCACTTTGGTCT GAA	58.4	509	INTERGENIC				
CaPOPI_6079	scaffold111	128540	ATTTTTTTTTTT/ATTTTTTTTTTTT	AACGGGAATGGACTTTA CGA	TATGACAATCCCCGACA ACA	59.4	507	INTERGENIC				
CaPOPI_6080	scaffold1115	3807	ATATATTTA/ATA	TTCTTCATTAAATGTCAAT CCATTTTT	GCGAGCATGAGAAGTTG TTG	59.3	340	INTERGENIC				
CaPOPI_6081	scaffold1116	16701	TG/T	GGCTTGTGATCTTCACG ACA	CCTCAGATGAGAGCCAG GAC	59.8	673	INTERGENIC				
CaPOPI_6082	scaffold1116	30008	AATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT/ AATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT	AAGGTGCCAACACGATA AGG	CAAGTGGATTGGCCCTT TTA	60.0	775	INTERGENIC				
CaPOPI_6083	scaffold1116	42811	TC/TCC	GATGAAACCGAGGACCA AGA	GTGTTTTCGACCAGAC GAT	60.1	599	INTERGENIC				
CaPOPI_6084	scaffold1116	94918	TATAATAATAATA/TATAATAATAAAT A	TCTTCGTTATGCAGTCA AACCT	ACCCAACAAAAATGGAC CAA	58.9	728	INTERGENIC				
CaPOPI_6085	scaffold1120	11138	C/CA	TTCATCCAAGAATCTG GGC	TGCAAGAGGAGTGCCTT TCT	60.0	486	URR	Ca_27900			

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6086	scaffold1128	45001	CAAAAAAAAA/CAAAAAAAAAA	ATGGGAAGGAACAACAA TGC	CACAAATTAACCCAAA TTGACA	59.8	453	INTERGENIC				
CaPOPI_6087	scaffold1128	46039	ATTTTTTTTT/ATTTTTTTTT	CGAATGCAAGTTCGTGG TAA	TGTCAATTGGGCAGACA CAT	59.7	510	INTERGENIC				
CaPOPI_6088	scaffold1128	151757	CTTTTTTTTT/CTTTTTTTTT	TTTGACTCCCACCTAT GGC	TGTTTCGCCTCTTTGGA GTC	59.9	597	INTERGENIC				
CaPOPI_6089	scaffold1128	198535	CAAAAAAAAA/CAAAAAAAAAA	TAGGGGACTGTCTCGGA TTG	GGATCCTCACTTGCAAG ACC	60.1	653	INTERGENIC				
CaPOPI_6090	scaffold1128	348170	TAAAAAAAA/TAAAAAAAAA	GGTATGGTCCCGATTG AAG	GCCTAGCCTGACCTATT CCC	59.2	678	INTERGENIC				
CaPOPI_6091	scaffold1128	413406	TAA/TA	GACCTCCCAAGGCATT TTT	CCGGTCATCCAACAGAA AGT	60.3	600	DRR	Ca_23739			
CaPOPI_6092	scaffold1128	483765	GTCAAACTAACTAAAT/GTCAAAC TAACTAAATCAAACTAACTAAAT	CAGGATCCTCCGTATT GGA	TTCTTTCCGGCATGATT TC	59.9	639	INTERGENIC				
CaPOPI_6093	scaffold1135	9704	GTTGTGCT/GT	TTTCGGTTGGGTTTGCT TAC	TACCCGTGCTCAACATC AAG	60.0	704	INTERGENIC				
CaPOPI_6094	scaffold1135	14111	TTAAATAAATAAATA/TTAAATAATA ATAATAA	TCTGGCACATGAACCTC AGC	CACTCGACAATTGGGAG GTT	60.0	532	INTRON	Ca_26843		SAP	Aminotransferase-like, plant mobile domain
CaPOPI_6095	scaffold1135	67023	TAAAAAAAA/TAAAAAAAAA	TTTTGCCATGTGTATGAA TTG	TCAAGTATGAATCACGG CTGA	57.0	773	INTERGENIC				
CaPOPI_6096	scaffold1135	72246	ACTT/ACTTCTT	AAACCGAAAACCGAAAA CCT	CAATGTAGTTTGTCTAA GAAGTGCAA	59.9	667	INTERGENIC				
CaPOPI_6097	scaffold1135	74034	AAACCCT/AAACCCTTAACCT	CAAACCTTAACCCAAA CCC	AGGTCATTTTGGTCTTT GGTG	60.4	358	INTERGENIC				
CaPOPI_6098	scaffold1139	1257	CT/CTTT	TCTCAACGGAGCGGTA ATC	AAACTCCACATGGATGG GTC	60.2	388	INTERGENIC				
CaPOPI_6099	scaffold1139	1393	CT/CTTT	TCATCCAGTGGGGTA CAA	TTGTGTGTGGGATG GAGC	59.8	313	INTERGENIC				
CaPOPI_6100	scaffold1139	1605	TAACAACAA/TAACAACAA	TCATCCAGTGGGGTA CAA	TTTGAGAATTTGGGATG GAAA	59.8	785	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6101	scaffold1142	4296	T/TGA	AGGTCATTTTCGTCCTCCT	TTGCATGCACAAGATTGGTT	59.9	268	INTERGENIC				
CaPOPI_6102	scaffold1145	3948	ACTTCT/ACTTCTTCT	AATCCTCAAAGCCCTCCT	TTTTGGAACCTTCGTCC TTT	60.1	750	INTERGENIC				
CaPOPI_6103	scaffold1145	7358	TAAAAA/TAAAAAA	TGAATTTTCCAAGTATTGCATCC	GTAAAGGGACCGCAAGAACA	60.2	614	INTERGENIC				
CaPOPI_6104	scaffold1145	15770	ATATTATTATTATTATTATTATT/ATATTATTATTATTATTA	TGGCACAACATCATCATCATT	GCGCATTCTTCATCTTCTCC	59.8	496	INTERGENIC				
CaPOPI_6105	scaffold1145	16689	AAAGTAAATAAGTAAAA/AAAGTAAAT AAGTAAATAAGTAAAA	GGCCAAATGCCAAATCTCTA	TAGGAAAAGGGAACCCACC	60.0	683	INTERGENIC				
CaPOPI_6106	scaffold1145	67865	AT/A	AAGCGTACCTGTGGGAATTG	TTTACCGCGCTGAAAAGACT	60.0	921	INTERGENIC				
CaPOPI_6107	scaffold115	52073	GA/GACTA	CAATTAACACAACGCCCT	TTGGCCTCCCTAGGCTTATT	59.9	577	INTERGENIC				
CaPOPI_6108	scaffold1151	18791	CTTT/CTTTT	AGCCGTCATGACTTTGTCC	ACGGACCCTTTGTGAGACA	60.1	392	INTERGENIC				
CaPOPI_6109	scaffold1153	18767	GAAAAA/GAAAAAA	TTGGAGACGAAAACATGAGTCT	AGTTTCATCAACACCACATCAGTG	58.8	472	INTERGENIC				
CaPOPI_6110	scaffold1159	27402	TG/TGG	AGGGAGGACGAAAATGACCT	CCTTCCTTGGCTTGTTCTTG	59.9	345	INTERGENIC				
CaPOPI_6111	scaffold118	104154	AATATATATATATATATATATATA/AATATATATATATATATATATATATATA	CTCGAGCAGGAGGATCAAAC	TCCGGTACCGCAAGTAAATC	60.0	861	INTERGENIC				
CaPOPI_6112	scaffold118	173557	TTATATATATATATA/TTATATATATATATATA	TGTCATGCTAATATCCGCCA	TGGATGGATTCTAGTTGCCTT	60.1	489	INTERGENIC				
CaPOPI_6113	scaffold1180	2599	ATT/ATTTT	GAGAGGTCATGGCACCCCTTA	GAGCAACACATTGCATGTCC	60.1	166	INTERGENIC				
CaPOPI_6114	scaffold1180	2913	A/AC	GAGAGGTCATGGCACCCCTTA	TCTTGCCCAACGTTTTACAT	60.1	513	INTERGENIC				
CaPOPI_6115	scaffold1180	3744	GA/G	GTGCACGAAAGTGTGGCTTA	ACTTTACCATTGCCTTCCC	59.9	766	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6116	scaffold1180	36749	CTATTTATTTATTTATTTATTTATTTATTTCT/CTATTTATTTATTTATTTATTTATTT	TACGGTTCGATCTCATG CAA	TGCCTCTTCCCTGTTT CTA	60.2	419	DRR	Ca_25737		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_6117	scaffold1180	82368	GAAAAAAAA/GAAAAAAAAA	AATCCCATTCAGGTAAC CGT	CATGCTATAAATTTTCAG CTGTTTT	58.2	742	INTERGENIC				
CaPOPI_6118	scaffold1180	102429	TAAAAAA/TAAAAA	ACAAATCGGCCAGTGA ATC	TCTTTGCCACAACGGA TAA	59.9	663	INTERGENIC				
CaPOPI_6119	scaffold1180	135503	TTATAT/TTATATAT	TTGTGTGCGTTTGACTG ACA	AAGCGGAGAAGTCGGA GATT	59.9	789	INTERGENIC				
CaPOPI_6120	scaffold1180	206096	AATATATATATATATATA/AATATATATAT ATATATATA	CCATGTGGTTCTTTTGC ATTT	AACTTCGCCATTTGTCA TCC	59.9	548	INTERGENIC				
CaPOPI_6121	scaffold1180	208476	TA/T	TAAGAGGGGCTTGTTAC CCC	CCAACCTAATATTCATGC CACA	60.3	216	INTERGENIC				
CaPOPI_6122	scaffold1180	209213	ACTAT/ACTATTCAT	TTGATTTTTGACATGTGTG CTCT	TTGAGGGGTGGCAAGTT TAG	59.5	607	INTERGENIC				
CaPOPI_6123	scaffold1180	216830	TTATATATATATATATATATAT/TTATA TATATATATATATATAT	AAGCGTCTCTTTTGGG GAT	CATATGCACGTAAATC GCCT	60.1	345	INTERGENIC				
CaPOPI_6124	scaffold1180	241101	ATTTTTTTTTTTTT/ATTTTTTTTTTT	AAAACAAGAAGGGGCAA CCT	TAAATCAGAGGATGCGG GTC	60.0	760	INTERGENIC				
CaPOPI_6125	scaffold1180	247801	TATTCATTCATTCATTCATT/TATTCATT CATTCAATTCATTCATT	TGAAAACCTGAAAGGGC AAC	CTTCAATATGCGGGTCG TTT	60.1	413	INTERGENIC				
CaPOPI_6126	scaffold1181	6020	AACAAATAC/AAC	AAACCCTAAATCCCAA CCC	TTTAGGTCATTTTGCC TTTTT	59.0	465	INTERGENIC				
CaPOPI_6127	scaffold1181	6839	GAAAAAAAA/GAAAAAAAA	GACCCTAGACCCTTAAC CCTT	TCAATTTTGTCTGTGTC CA	57.7	176	INTERGENIC				
CaPOPI_6128	scaffold1183	131590	AATATATATATATATATATATATATAT ATAT/AATATATATATATATATATATAT ATATATATATAT	GAAATGGGTTTCGCGTA GAG	TTTGCTCGAAGGCTTT TTA	59.7	428	INTERGENIC				
CaPOPI_6129	scaffold1183	142757	TAAAAAAAAA/TAAAAAAAAA	TCAATCCATTGGTCCC TTT	AAAGATGCATTTGCCAG GAC	59.2	916	INTERGENIC				
CaPOPI_6130	scaffold1183	239750	CTTTTTTTTT/CTTTTTTTTTTT	CCCTTCGTGAGGTTAC AAA	CCGGTGATATGATGAG CTT	60.0	403	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6131	scaffold1185	47365	AAATAATAATAATAATAATAATAATA /AAATAATAATAATAATAATAATAATA	TTCCTTATAGGCATGATTCTTGA	TCGTTTTGGTGTTGGTTCA	59.2	809	INTERGENIC				
CaPOPI_6132	scaffold1185	67322	GATATATATATAT/GATATATATAT	CAATTCCCACAGGTACGCTT	GACGCGAAAAACAACATTCA	60.0	683	INTERGENIC				
CaPOPI_6133	scaffold1185	67468	T/TAGGGTGA	CAATTCCCACAGGTACGCTT	GACGCGAAAAACAACATTCA	60.0	683	INTERGENIC				
CaPOPI_6134	scaffold119	16292	AACA/AACACACA	AGGAAGAGTGGAGTTGCGAA	TATTTTGGATTTTGGCTCGG	60.0	513	INTERGENIC				
CaPOPI_6135	scaffold119	16337	T/TAA	AGGAAGAGTGGAGTTGCGAA	TATTTTGGATTTTGGCTCGG	60.0	513	INTERGENIC				
CaPOPI_6136	scaffold119	35751	A/AG	ACTCATATGCAAAATGCCCC	TTATGCTGGAGATGGGAAGG	59.8	444	INTERGENIC				
CaPOPI_6137	scaffold1193	7288	TCAA/CAATTTAAGCAA	AATGCTTTCCAGAAAAACGA	TGATCTGATGGCTGACTTTCA	59.7	367	INTERGENIC				
CaPOPI_6138	scaffold1193	51363	CTATTATTATTATTATTATTATTATT ATTATTA/CTATTATTATTATTATTATT TATTATTATTATTATTATTATTATTA	ATACACGCAAAATCGCATGA	TGCCAAACTACCTTCCCATC	60.1	351	INTERGENIC				
CaPOPI_6139	scaffold1195	21554	CTTATTATTATTATTATTATTATT/CT TATTATTATTATTATTATTATT	AAGGGTGCAACCGTATTGAG	GAAAGGCTCAAACGACCAAA	60.0	594	INTERGENIC				
CaPOPI_6140	scaffold1196	44249	TTATATATATATATATATATAT/TTATATA TATATATATATATATATATATATAT	ACCCCAATAGAGGTGCACCA	CCATTTGGAATTGCGACATT	60.4	593	INTERGENIC				
CaPOPI_6141	scaffold1196	112009	AGGGGGGGG/AGGGGGGG	GTTCTCCCTTCCATCGTTCA	TGTTAGGTGTTTGGTGGCA	60.1	525	INTERGENIC				
CaPOPI_6142	scaffold1196	182114	CTTTTTTTT/CTTTTTTTTT	GGGGGAGGATGAAGATGAAT	TTGTGTGCTCTAGGAACCGA	60.1	650	INTERGENIC				
CaPOPI_6143	scaffold1196	184515	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATT/TTTA TTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT	AGAGGCAAAACAAGAACC GAA	TGCTGTCGTAGCGGAATACA	59.9	376	INTERGENIC				
CaPOPI_6144	scaffold1197	5120	GT/GTT	TCGCAGCTCAATTGGTAGTG	GAGAGCTACCGTGCAACACA	60.0	486	INTERGENIC				
CaPOPI_6145	scaffold1197	75749	TTTATTATTATTATTATTATTATTAT/ TTTATTATTATTATTATTATTATTAT TAT	TAACCCAAAAATCCCAACCA	TGGATCGCATAACTCCATGA	60.0	396	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6146	scaffold1197	87034	GATATATATATATATATATATATATAT /GATATATATATATATATATATATAT	CCGATCAACCCGTAAATC	ATCTTCAGGGTGGAGGCTCT	59.3	310	INTERGENIC				
CaPOPI_6147	scaffold1197	209617	ATTTT/ATTT	GCCCTCAGATGAGAGTGAGG	AATGTGAAC TCGCCAAGAC	59.9	514	INTERGENIC				
CaPOPI_6148	scaffold1197	244953	TAAAAAAA/TAAAAAAA	CAC TTTTT GTTTCATCGCCA	ACTGTGATCCGGTGATTGA	59.7	574	INTERGENIC				
CaPOPI_6149	scaffold1197	285281	ATTTTTTTTT/ATTTTTTTTT	AGTTTGCCATTCCAACCATC	TCCCACAACAAATTCTGTC A	59.8	467	INTERGENIC				
CaPOPI_6150	scaffold1197	540966	ACCC/ACC	TAACTGGGCGTTAAGAACGG	TTGAGGGACATATTTTGGC	60.1	901	INTERGENIC				
CaPOPI_6151	scaffold12	154021	AATATATATATATATATATATATATAT ATATATATAT/AATATATATATATATATAT ATATATATATATATATAT	TCGAGTTTGCAAAGGCAC	ATGCCAATTTGCCAAGCTAA	60.0	350	INTERGENIC				
CaPOPI_6152	scaffold12	271141	TACA/TA	TGATGATTTTGATGCGGAAA	CCGTGTAAACTTCGGACAGAG	60.0	854	INTERGENIC				
CaPOPI_6153	scaffold12	352195	GAAA/GAAAAA	GTTGTCCGGCGTATATTGCT	TCATCAAAGGCATGCAATC	60.0	572	INTERGENIC				
CaPOPI_6154	scaffold1202	6534	TAAAAAAA/TAAAAA	AGTGCCCTCGTCAACA AAC	TTACAGCGCGTGTTGA AAAG	60.2	824	DRR	Ca_24658			
CaPOPI_6155	scaffold1202	25847	CTTTTCTTTTTTTTTC/CTTTTCTTTT TTTTCTTTTTTTTC	TTGTCCACAGTGGCATATTGA	TGGCAGATATGGGGGTGTAT	60.0	737	INTERGENIC				
CaPOPI_6156	scaffold1202	82238	AATATATATATATATA/AATATATATATAT ATATA	AACACATCCGGGTCCATT A	TTTGATCCATTTGCCCTAGC	60.1	739	INTERGENIC				
CaPOPI_6157	scaffold1202	83479	GTATATATATATATATAT/GTATATATAT ATATAT	ACGGTGTAGGCAAGATGAC	AGGATGCATGGGATGA AAG	60.0	458	INTERGENIC				
CaPOPI_6158	scaffold1202	177457	TAT/TATCATTTAGAGGAAT	CAGGCCTGGGTAATCTTTGA	CACACTTGGGTGTCCTCTT	60.1	397	DRR	Ca_24666			
CaPOPI_6159	scaffold1202	178836	CCG/CCGTAAGGCG	TCTGACATGTGTGCGAGTCA	GCCACACCGTGCTACCTATT	60.0	406	CDS (FRAME SHIFT)	Ca_24666			
CaPOPI_6160	scaffold1202	179607	AG/AGG	AATAGGTAGCACGGTGTGGC	TCCCTTGCCTACATTGTTCC	60.0	814	INTRON	Ca_24666			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6161	scaffold1202	184065	C/CATGATTGGTT	CATCGAGTCTTTGAACG CAA	TCACAAATGGCAACGTG TTT	60.0	319	DRR	Ca_24667			Transposase, PttA/En/Spm, plant
CaPOPI_6162	scaffold1206	920	A/AC	TATCACCTATCAGAGCG GGG	GAGTTATTCGGGTGGGG AAT	60.1	546	INTERGENIC				
CaPOPI_6163	scaffold1215	12684	TAAAAAAAA/TAAAAAAAAA	TCTCTCCGATTGTC ATT	TTTGCTCCTCTTCTCTG GC	59.5	588	INTERGENIC				
CaPOPI_6164	scaffold1215	12961	GAAAAAAAA/GAAAAAA	GCCAGAAGAAGAGGAG CAAA	AAACATTCAATCACCAAG GGA	59.7	470	INTERGENIC				
CaPOPI_6165	scaffold1215	13648	TAAAAA/TAAAAA	TCGTGGGACTAAAACG AGGA	CGCACATATGAATGATC CCA	59.7	576	INTERGENIC				
CaPOPI_6166	scaffold1215	14063	GGGATCAT/G	AATTGAAGGAAGATGGA AAACA	ACAACTGGAGGGCAAC AAC	57.7	822	INTERGENIC				
CaPOPI_6167	scaffold1215	41563	GATATATATATATATATATA/GATA TATATATATATATATA	CCCTTCATTTCTTCGC ATA	GAAGCAGGCTTCGATGG ATA	60.0	415	INTRON	Ca_28164		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_6168	scaffold1215	44629	TAAAA/TAAAA	AAACATCTCCTTTGTGT GTGTGA	AATCTTCGCTCAACAAT GCT	59.6	391	URR	Ca_28164		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolis in
CaPOPI_6169	scaffold1215	45663	ATT/ATTT	TGGCTTTGTATTTTCAGA GTTGG	AGTGGGACCATGATTTT TGAA	60.5	492	INTERGENIC				
CaPOPI_6170	scaffold1215	45939	ATTTT/ATTT	TTTCAAAATCATGGTCC CAC	GGGGTGGTGTCTATCTT TGC	59.7	337	INTERGENIC				
CaPOPI_6171	scaffold1219	7175	AT/ATT	GGAAACCTCACCTACC ACA	TGGGTCTGTTCTTTTGG AGT	59.8	925	INTERGENIC				
CaPOPI_6172	scaffold1219	7693	CAA/CAAA	ACTCCAAAAGAACGAC CCA	GGACATTCTCACCTGC AAC	59.6	104	INTERGENIC				
CaPOPI_6173	scaffold1219	40006	GTATATATATATATAT/GTATATATAT ATATAT	TGGTTTAATGTTGGCAA ATGG	ATCCAGTTGGTGAGGAA AAA	60.6	317	INTERGENIC				
CaPOPI_6174	scaffold1221	73998	AATATATATATATATATATATATATAT ATATATAT/AATATATATATATATATAT ATATATATATATATATAT	ACGGCACCGTGAGTAAA TTC	GAAACTACCGAGCAAAAT GGC	60.0	840	INTERGENIC				
CaPOPI_6175	scaffold123	361645	TCA/TCAAAGAACTCTTTCCAACA	ATCCACCCACCTTTCTT TC	CAGAGCAACCAGGAACA ACA	60.2	293	CDS (large-effect mutations)	Ca_24703	QR	B3	Oxoglutarate/iron-dependent oxygenase

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPl_6191	scaffold1272	125862	CAAA/CAA	CTCTCATCTGAGGCCAA AGC	ATTTGGCAACACAGGGA CTC	60.1	387	DRR	Ca_26855		Trihelix	
CaPOPl_6192	scaffold1274	6685	T/TGTG	TCATTTTCGTCCTTCC TT GG	ACACACCTATTGGACGC ACA	60.0	272	INTERGENIC				
CaPOPl_6193	scaffold1275	6195	CAA/CAAGAGATAA	TGTTGCCTCGTAATTCA ACG	CAGGGACTAAAAGTGT TGCTG	59.7	556	INTERGENIC				
CaPOPl_6194	scaffold1276	1178	CTTTTT/CTTTTTT	TCAGCCATGACTTGAGG T TG	CTCACTTTGGTCCCATG CTT	59.8	361	INTERGENIC				
CaPOPl_6195	scaffold1276	1671	TT/TTATAT	AAGCATGGGACCAAAG T GAG	TTTCCCAATCGATTTGCT TC	60.1	942	INTERGENIC				
CaPOPl_6196	scaffold1278	29766	CAAAAA/CAAAA	GAGAATTCCGGGAAGGA GAC	TTTCTTCTCTCTCAGGC CG	60.0	320	INTERGENIC				
CaPOPl_6197	scaffold1278	45110	CATATATATATATATATATAT/CATAT ATATATATATATATAT	TATTTGCTCGCAACACA ACC	GTTTAAGCCCCTTTGAG CCT	59.7	253	INTERGENIC				
CaPOPl_6198	scaffold1278	60991	GTATATATATATATATATATAT/GTAT ATATATATATATATATATAT	TTAAAGAGATTGCGAGC GGT	TTTCAGGTTATCGATTG GGG	60.0	359	INTERGENIC				
CaPOPl_6199	scaffold1278	63103	GAAAAA/GAAAA	ACGAAGGGGTAGGAC GATG	ATTTGTTTGCCGATCGC TAC	60.0	611	INTERGENIC				
CaPOPl_6200	scaffold1278	63247	TAAAAAAAA/TAAAAAAA	ACGAAGGGGTAGGAC GATG	ATTTGTTTGCCGATCGC TAC	60.0	611	INTERGENIC				
CaPOPl_6201	scaffold1278	63301	ATT/ATTT	ACGAAGGGGTAGGAC GATG	ATTTGTTTGCCGATCGC TAC	60.0	611	INTERGENIC				
CaPOPl_6202	scaffold1278	63474	TTATATATATATATATATATAT/TTA GTTATATATATATATATATATATAT	CCTTTGATCCGCTTTCT GAG	TGCCATTATTACTGCTAC CCA	59.9	598	INTERGENIC				
CaPOPl_6203	scaffold1278	65072	TTTATTATTATTATTATTATTATTAT TATTATTA/TTTATTATTATTATTATT ATTATTATTATTATTATTA	TGGGTAGCAGTAATAAT GGCA	TGAGCAAGATGTGTTTT GTGG	58.2	341	INTERGENIC				
CaPOPl_6204	scaffold1278	107077	CCT/CCTACTATCACT	GCGATTATGGCACCAAA GTT	ACCGTCAAACACAAACC TTC	60.0	114	INTERGENIC				
CaPOPl_6205	scaffold128	43105	AATATATATATATATATATATATAT ATA/AATATATATATATATATATATA TA	CCTGATTTTCTCCGTCC AAA	ACTCGCAGCAAACATCC TCT	60.0	691	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6206	scaffold128	437260	ATTTTTTT/ATTTTTT	TGTGCGTATATACACGT AAAATCGT	GCACTTTCTGGAAACCT TGC	59.8	526	INTERGENIC				
CaPOPI_6207	scaffold128	547816	CAAA/CAA	CAACGCAACATAACACC CAG	GGAAAGTTGCTCACCAC CAT	60.0	361	INTERGENIC				
CaPOPI_6208	scaffold128	588046	TAA/TAAA	AGTACTGAGCCCCCTGG TTT	ATGATGTTGTAGCGATT GCG	60.0	308	INTERGENIC				
CaPOPI_6209	scaffold128	732668	A/ATAAAC	GCTCAAAGCACATGACA GGA	CATTTTGAACCAAAGCA GCA	60.0	479	INTERGENIC				
CaPOPI_6210	scaffold128	747239	TCCC/TCC	GGTGTGTTTGTGACGTT GGA	GGAGGACGAAAATGATC GAA	60.5	646	INTERGENIC				
CaPOPI_6211	scaffold128	747253	G/GT	GGTGTGTTTGTGACGTT GGA	GGAGGACGAAAATGATC GAA	60.5	646	INTERGENIC				
CaPOPI_6212	scaffold1281	46557	T/TTTGC	CAATTCGACATGCATT GCT	AATTCATGCACCGTCA ATTT	59.7	650	DRR	Ca_21505	K		Bromodomain
CaPOPI_6213	scaffold1281	376337	GTTTTTTTTT/GTTTTTTTT	TGTTTAGCGCTAGTTT GGC	TCGATTATGCGTAGGGA AGG	60.4	665	INTERGENIC				
CaPOPI_6214	scaffold1281	381985	CAATAAATAAATAAATAA/CAATAA ATAAATAAATAAATAA	GGTAGGGTCCCCCACTT TTA	AGGATCCGAATTAATGG CAG	60.2	845	INTERGENIC				
CaPOPI_6215	scaffold1281	440047	CTTTTTTTTT/CTTTTTTTTT	TTGGTTGGTAGAGTTGT GCG	CTCACCGCTGCTTCAAT TTT	59.8	190	INTERGENIC				
CaPOPI_6216	scaffold1281	469460	GAAAAAAAAA/GAAAAAAAAA	TCTCTGGCAACCGTTCT TCT	ACCTCGTTGAGACACGC TTT	60.0	566	INTERGENIC				
CaPOPI_6217	scaffold1281	471713	AATATATATATA/AATATATATATAT A	GAGCATTGTGACAAAAT TGAGC	CGGGAATTCTTGATGAA TCG	59.8	541	INTERGENIC				
CaPOPI_6218	scaffold1281	472602	CATA/CATATATA	CAAATGGAGGTTATTGC ATTG	AGCAGTGCTTCAACTCA TGC	58.0	569	INTERGENIC				
CaPOPI_6219	scaffold1281	473339	GATATATATATATATATA/GATATA TATATATATATA	ACGCATGGATATTGCAG TCA	TCCGATTGTTGACCAGT TTTT	60.1	783	INTERGENIC				
CaPOPI_6220	scaffold1281	492209	TAAAA/TAAAA	GGAATGGAAAACACATT CAACA	GAATGCTTGAGAACTT TGGG	59.7	499	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6236	scaffold1312	78884	TAAGAAGAAGAAGAAGAA/TAAGAAGAA GAAGAA	ATTTGACCTCGACACAA CGG	GCCGCTTGATCGTTAAT TGT	61.0	425	INTERGENIC				
CaPOPI_6237	scaffold1312	78931	CG/C	TCGACACAACGGACAAG AGT	GCCGCTTGATCGTTAAT TGT	59.3	417	INTERGENIC				
CaPOPI_6238	scaffold1312	80040	GAAAAAAAA/GAAAAAAAAA	GCATTGGCCTTTTATTC CAA	TGGCCATGTTACAACCT GAA	59.9	639	INTERGENIC				
CaPOPI_6239	scaffold1312	80554	ATTT/ATTTTTT	GCCAAGGTAAGGGTGA GACA	ATGAATTGTCCAATCTC GG	60.1	322	INTERGENIC				
CaPOPI_6240	scaffold1312	81111	TAA/TAAA	CCGAGATTGGGACAATT CAT	TTGGAAAAGCCACCTA CAC	59.8	661	INTERGENIC				
CaPOPI_6241	scaffold1312	82340	CAAA/CAAAA	GTGGGCCAAAAGAACT TGA	AACTGAGATTGATCCGG TGG	60.1	455	INTERGENIC				
CaPOPI_6242	scaffold1312	83212	T/TC	TCTAGCGGATGCATGAT GAG	ATACTTGACGGTTGGC TGG	59.9	461	INTERGENIC				
CaPOPI_6243	scaffold1312	89732	ATTTTTTT/ATTTTTTTT	TTTATTACGCCATTGACA CTTT	ACAATGTGTGCCAACA AAA	59.5	457	INTERGENIC				
CaPOPI_6244	scaffold1313	102532	AATATA/AATA	GCTGTCTTTCTGCTTC GCT	CACCAATGCGTTGTAG CAC	59.9	396	INTERGENIC				
CaPOPI_6245	scaffold1313	155204	GTCAAACCTAGCGAGATCAA/GTCAA CTCTAGCGAGATCAAACCTAGCGAGA TCAA	AGCGTCACAGCCTATCC ATC	TGCATAATCGATTGGCA CAT	60.2	385	INTERGENIC				
CaPOPI_6246	scaffold1313	180679	ATTTTTTTTT/ATTTTTTTTT	TCAGGGTTAGGTCATCA GGG	AGGGAGGCAAAATTCGC TAT	59.9	554	INTERGENIC				
CaPOPI_6247	scaffold1315	121793	TG/TGG	TACGTGTTAACGTGGTC GGA	TCCATTGATCCGCCTTC TAC	60.0	312	INTERGENIC				
CaPOPI_6248	scaffold1315	172506	TTATATATATATATATAT/TTATATATATA TATATATAT	TTTCCCTTTTGTTCGGA TG	CATGGTTTGAAAAGTGG TTTCG	59.9	528	URR	Ca_26616	R		Sugar/inositol transporter
CaPOPI_6249	scaffold1316	4181	TA/TAA	GTAAGGGTCACCAACC GAA	TTGTCCGTGAGAGACTG CAC	59.8	813	INTERGENIC				
CaPOPI_6250	scaffold1316	13036	AATTTATTTATTTATTTATTTATTT/AATTT ATTTATTTATTTATTTATTT	ACATGCACAGAGAATGC CAA	GTGCCAGTCGATTGCCT AAT	60.3	631	DRR	Ca_28021			

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CaPOPI_6251	scaffold1317	46249	AC/A	CATGGGTGAAGACTGTG GTG	ACCACTGTTGCATGCCT AAA	60.0	134	INTERGENIC				
CaPOPI_6252	scaffold1317	59870	AAAGAG/AAAGAGAAAGCAAGAG	AAAATCAGCCAAATCCA ACG	TTGGAATCTCATTAAAG CCAGA	59.9	930	INTERGENIC				
CaPOPI_6253	scaffold1317	63682	AAGAGAGAGAGGAGAGAGAGAGAGA GAGAGA/AAGAGAGAGAGAGGAGAG AGAGAGAGAGAGAGA	TTTCAAGCTCAAACCTCC CC	CATGTGTTGGATGAAG GGTT	59.3	364	INTERGENIC				
CaPOPI_6254	scaffold1317	69339	AC/A	TGGGCTTATAGGATTGG TCG	TGCGAAAGTCACATCCA CAT	59.9	668	INTERGENIC				
CaPOPI_6255	scaffold132	44427	TA/TAGAA	CATCGTCACGTCTTCCA TTC	TGTTACACACTTTAAGA TGAAGAGTT	59.1	427	INTERGENIC				
CaPOPI_6256	scaffold1323	6638	ATTT/ATTTT	GGCCACTGACTTGCAGT GTA	TTGTGCATCCAATACGT GTG	59.9	717	INTERGENIC				
CaPOPI_6257	scaffold1324	8519	ATTTT/ATTT	ATTTGTTGCATTGTCGG TCA	CTGCCTCACGATTTCAC TCA	60.0	899	INTERGENIC				
CaPOPI_6258	scaffold1324	49560	AT/ATT	ATTTTTCGGTTTGAAG CAA	CGATCAAGATTTCGTTC CTG	59.6	602	DRR	Ca_19753	P		Heavy metal transport/detoxification protein
CaPOPI_6259	scaffold1324	53855	GATATATATATATATATATATA/GATA TATATATATATATATA	TAGCTTCGCAAGCTCAA CAA	ACGCTTTTCCACAAAGC ACT	59.9	655	INTERGENIC				
CaPOPI_6260	scaffold1324	108053	AATATATATATATATATATATA/AAT ATATATATATATATATATA	TAGACGCATGAACACT TGC	ACCCGATTTTACCCTG ACC	59.9	249	INTERGENIC				
CaPOPI_6261	scaffold1324	215253	ATCTTCTTCTTCTT/ATCTTCTTCTTCTT CTT	CCAAATCAAATTGCAA GACC	CAATCGCCTTTTATTGG GA	59.4	219	INTERGENIC				
CaPOPI_6262	scaffold1324	227334	TG/T	TTGGTGACATTTAGCATT TCTCA	GTCCTTTGTGTCGTGGG TCT	59.6	511	INTERGENIC				
CaPOPI_6263	scaffold1324	235091	CGTTGT/CGT	TCTTGGTTGTAACCTT GGC	TTTCGACAAAAGTTCT CCG	60.0	431	INTERGENIC				
CaPOPI_6264	scaffold1324	236638	GAAAAA/GAAAA	ATGCACCTTGAAAGGTT TTG	TTCGAGGAGGTTTTGA TTG	60.0	597	INTERGENIC				
CaPOPI_6265	scaffold1324	244504	CATATATATATATATATATATATAT ATATATAT/CACACACATATATATATA TATATATATATATATATATATATAT	TTGTTTTCTAACCCGCC AAG	CGATTGAGTGCACGA GAG	60.1	370	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6266	scaffold1324	252648	T/TTCTTTCAAC	CCTATAGGCCCACTAAGCCC	TTGCAAGCAAACCTTCACGAT	59.9	587	INTERGENIC				
CaPOPI_6267	scaffold1324	252816	CGTGAAGT/CGT	TGTTAACATGATCAGGCCA	ACATAGCGCCACAACATGAA	59.9	789	INTERGENIC				
CaPOPI_6268	scaffold1324	253776	ATTTTTTTTTTT/ATTTTTTTTTT	GAGTGCTCCTTGACATCGAA	ATGAAGACCAAGCCATCCAC	60.0	514	INTERGENIC				
CaPOPI_6269	scaffold1324	255649	CTTTTTTTTTTT/CTTTTTTTTTT	CCTTGGAGGCAGTGATTGT	GAGTACCCCAATGGTTGAA	60.1	613	INTERGENIC				
CaPOPI_6270	scaffold1324	255844	GAAAAA/GAAAAAA	CCTTGGAGGCAGTGATTGT	GAGTACCCCAATGGTTGAA	60.1	613	INTERGENIC				
CaPOPI_6271	scaffold1324	255890	ATTTT/ATTTT	CCTTGGAGGCAGTGATTGT	GAGTACCCCAATGGTTGAA	60.1	613	INTERGENIC				
CaPOPI_6272	scaffold1324	256337	CAAAA/CAAA	TTCAACCAATTGGGGTAGCTC	TTCACTTGAATATTTTGTGGCA	59.9	474	INTERGENIC				
CaPOPI_6273	scaffold1324	266713	AATCTATTATCTATTATCTATTAT/AATCTATTATCTATTAT	TGTATGCATCAACAATGTCAAGA	TCAGAGGATGTGGCATA GAGG	59.1	160	INTERGENIC				
CaPOPI_6274	scaffold1324	266796	CA/CAA	TCCTCTATGCCACATCCTCTG	CACAAATAGTTGTACATTGGTTGC	60.2	238	INTERGENIC				
CaPOPI_6275	scaffold1324	267973	A/AT	CCAAGGCACACACAAATGAA	AGAGAATAACCCGCACGTTG	60.6	344	INTERGENIC				
CaPOPI_6276	scaffold1324	268436	A/AGTTCTG	CAACGTGCGGGTTATCTCT	GGCACGTGAAGTCCACTTTT	60.1	358	INTERGENIC				
CaPOPI_6277	scaffold1324	270833	GTT/GT	ACAAAATCGGCCACTGATC	TCCC GTTCATCTCTCTCACC	59.9	500	INTERGENIC				
CaPOPI_6278	scaffold1324	272116	TGGGG/TGGG	CCCCGCTCTGATAGGTGATA	TGTTTGTATGCGAGCATTTT	60.1	767	INTERGENIC				
CaPOPI_6279	scaffold1324	504029	AATATATATATATATATATAT/AATATATATATATATATAT	TCCATTGAGTTTCTCCACC	CATCCGCCTCGGAAGTATA	60.1	249	INTERGENIC				
CaPOPI_6280	scaffold1324	514795	TTATATATATATATATATATATA/TTATATATATATATATATATATA	ATCAGCGAGGATGCAGAACT	GATGACATGGATGTGTTGAG	60.0	557	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6281		scaffold1324	516063	ATTTTTTTTTTT/ATTTTTTTTTT	AAAACACGCTAGGCTCC AAT	TGGTCATGTGGTTTTG CAT	58.9	642	INTERGENIC				
CaPOPI_6282		scaffold1324	520260	AATTATTATTATTATTATTATTATTA TTATTATT/AATTATTATTATTATTAT TATTATTATTATTATTATT	TTCTTTTCGCTATTTTAT TTTCGTG	TCTTACGTATCTCCCGG TGC	60.0	734	INTERGENIC				
CaPOPI_6283		scaffold1324	642408	ATTTTTT/ATTTTTTT	CCTTGCCCTTTTATTTG GT	TCCTAGAACATGCATCA CGC	60.3	496	INTERGENIC				
CaPOPI_6284		scaffold1324	698355	GTTTTATTTTTATTTTT/GTTTTATTTTA TTTTATTTTT	TTTCACATACGCCGCAT AGA	TAAGCAGTCGGTTTGCA ATG	60.2	311	DRR	Ca_19785	T		Peptidase S54, rhomboid
CaPOPI_6285		scaffold1328	11774	C/CCT	GGTTTCGAGGAAACTG ACA	AGGGAGGACGAAAATGA CCT	60.1	958	INTERGENIC				
CaPOPI_6286		scaffold1331	50640	GT/GTT	AATGGGCGCTGTTAAAT GTC	TGGTGTCTGTTGGCACTC TAC	60.0	411	INTERGENIC				
CaPOPI_6287		scaffold1331	50773	AAT/AATAGGAT	AATGGGCGCTGTTAAAT GTC	TGGTGTCTGTTGGCACTC TAC	60.0	411	INTERGENIC				
CaPOPI_6288		scaffold1331	83953	AG/AGG	TCCTTTCACTATAAACTC TTCCGC	AGCGGTTCTGTAGGATAT TGA	60.1	471	INTERGENIC				
CaPOPI_6289		scaffold1332	500	TAAAAAAAA/TAAAAAAAAA	CCAAAATTTGAAGTCGG GAG	ACACGGGTCGTACAACT TGA	59.5	443	INTERGENIC				
CaPOPI_6290		scaffold1332	8212	CTTTTTTT/CTTTTTTTTTT	ACGAACTCAACTACAAC TCTTGG	TCAGACACTACCCGACA TCAA	57.6	624	INTERGENIC				
CaPOPI_6291		scaffold1332	8473	ATTTTTTT/ATTTTTTTTT	CACAATTCTTTTCTATG TGTGGA	AACCCGTCACACAGGAA GTC	58.2	894	INTERGENIC				
CaPOPI_6292		scaffold1332	9986	ATGTTGTTGT/ATGTTGT	CCAATTCTCCGGTACTC CAA	GACGATTCTCCACCCT TGA	59.9	808	INTERGENIC				
CaPOPI_6293		scaffold1335	46272	TC/T	TTCTGTGCAACTGACGCT AAC	CCATTGGATTAAAGA AGCC	60.1	345	DRR	Ca_28106	S		
CaPOPI_6294		scaffold1337	40902	ATTT/ATTTTCAACTTTT	TAGCATGCAAAATCAGGT TGC	CCCGACAAAAATAGACC GAA	59.8	425	INTERGENIC				
CaPOPI_6295		scaffold1337	46228	AAAACCTTAACCTTAAA/AAAACCTTA AACCTTAACCTTAAA	AAACCCCAACCTTAA CCC	TTGGGACATTTTCGGTTT TTG	59.1	353	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6296	scaffold134	60134	AATATATATATATATATATAT/AATATATATATATATATATATAT	TGCACATTGGAGTTTGATG	TCTAAGGCCTAACCAACGGA	59.7	541	INTRON	Ca_22578	O	C2H2	Peptidase A1
CaPOPI_6297	scaffold134	276694	GAA/GA	GAGCAGCACATTTTTCATCA	TTGATTGGGGTTGTACCCA	60.1	567	DRR	Ca_22585		ERF	Pathogenesis-related transcriptional factor/ERF, DNA-binding
CaPOPI_6298	scaffold134	357959	CAGCAGGAGCAGGA/CAGCAGGA	GGAGATCAACAGCAGCAACA	CTTCCTGAACAAACCCAAA	60.0	805	CDS (large-effect mutations)	Ca_22591			
CaPOPI_6299	scaffold135	113512	A/AG	GCTTATTGGGAGAAGCGTTG	GCCCTCAGATGAGAGTCAAGG	59.8	514	INTERGENIC				
CaPOPI_6300	scaffold1351	275138	TTTTATTATTTATTT/TTTTATTT	TCATCGCAGGTGTACCATGT	GAACAAGTGGGTGAAGGCAT	60.0	544	INTERGENIC				
CaPOPI_6301	scaffold1358	778	AC/A	TCCACAAGAAAACCTCCATTG	AGTGAAACCAACGCCAAAC	60.0	522	INTERGENIC				
CaPOPI_6302	scaffold1359	74591	ATTTTTTT/ATTTTTTTTT	TGGGTGGGAGTAATTTTCG	TTAAAGAGATTCGCTGCGGT	59.8	297	DRR	Ca_26683	KR	G2-like	Mitochondrial transcription termination factor-related
CaPOPI_6303	scaffold136	12993	CTTTTTTTT/CTTTTTTTTT	TTTGGAGTCACCGGAAC	CACGATACGAACCATTTCCC	59.9	165	INTERGENIC				
CaPOPI_6304	scaffold1360	17330	AAATAAT/AAAT	CGCCGTAATGAACTATGCA	AACCGCTGCGAATCTCTTTA	59.6	729	INTERGENIC				
CaPOPI_6305	scaffold1365	59505	G/GTTTGAAAACAAAGGAT	ACGTGGTGAAATCTTTTCGG	ATTTTCACCAACATCCCACA	60.0	480	INTERGENIC				
CaPOPI_6306	scaffold1365	74375	CATG/CATGATG	TATTGTGAAGAGGCGTGTGC	TGTTGGGATTTGGTTGTGAA	59.9	351	INTERGENIC				
CaPOPI_6307	scaffold1371	80775	TTATATATATATATATATAT/TTATATATATATATATATATAT	TGTCGCACGGATACAATGAT	AGGCATGGTGTGGAGTCAT	60.0	234	INTERGENIC				
CaPOPI_6308	scaffold1376	39940	TNNNNNNNNNNNNN/TN	CCTGAATCGGTCAACCTTGT	GGGTTTTGCATCTTGCACTCT	60.0	612	INTERGENIC				
CaPOPI_6309	scaffold1380	5644	ATTTTTTT/ATTTTTTTTT	TTTTAGCGGATGTCGTAGGG	TCACAAGGGGACTCTATGG	60.1	719	INTERGENIC				
CaPOPI_6310	scaffold1380	9721	CTGTGTGT/CTGTGT	CGTTGACAACTGAACCAAGGA	GCACATTCAGTCCAAGAGA	59.7	429	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6311	scaffold1382	29087	TAAA/TAAAAA	TGCTTTTGT CGTATAATT GAGCA	TGATGGACCAGTAGAC ACCT	59.8	317	INTERGENIC				
CaPOPI_6312	scaffold1382	183210	GTTTTTT/GTTTTTT	CAAAGGTTTGAAAGGC ATCA	GGATATGGCACAAAGCGA ACT	60.1	343	INTERGENIC				
CaPOPI_6313	scaffold1382	225615	GTTTT/GTTTTT	AGGTCATTTTCGTCCT CCT	CCCCCTAGGGTGTAAT GGT	59.9	805	INTERGENIC				
CaPOPI_6314	scaffold1382	339331	CCTT/CCTTCTT	TCAACCCACTTTCACCAT CA	CAGGTCCTGAATTGCCG TAT	59.9	712	INTERGENIC				
CaPOPI_6315	scaffold1386	8928	ATTTTTT/ATTTTTTTT	GTGGTGCCTACATTGG ATT	GTGCAAACGACACCTGA AGA	60.9	558	INTERGENIC				
CaPOPI_6316	scaffold1386	9543	TAAAAAAAA/TAAAAAAAAA	TCCATTGAATTGTTTGTG CAT	ATAAATTACACCCGCGC AAG	58.9	421	INTERGENIC				
CaPOPI_6317	scaffold1386	13609	CAAAA/CAAAA	TTTGTGGTAATTATGTG TGCTACA	TTTCGGTTTCCTTTGTTT GC	59.7	424	INTERGENIC				
CaPOPI_6318	scaffold1386	59518	TAAAAAA/TAAAAAA	GCAAACAGGACCATTAC GCT	GAGAGGATTGAGGGAG ATTTGA	60.1	909	INTERGENIC				
CaPOPI_6319	scaffold140	2406	CATATATATATATATATATATATAT ATAT/CATATATATATATATATATATAT	CTTGTA AAATCTCCGCT CGC	TTGGTATTGAACTCGGA GGC	60.0	665	INTERGENIC				
CaPOPI_6320	scaffold140	7449	ATT/AT	TGTCAATTTTGGCGTAG TGG	AACGTGCATTTTCGGTT GCC	59.6	362	INTERGENIC				
CaPOPI_6321	scaffold140	25774	AATTT/A	TCCTAGAACATGCATCA CGC	CTCAAGTCGACAAGCCT TCC	59.8	666	INTERGENIC				
CaPOPI_6322	scaffold1401	26858	CATATATATATATATATATAT/CATAT ATATATATATATAT	CATTGCAGGTGCTATGG TTG	TTCTCTTACGAAGCGGA GGA	60.1	648	INTERGENIC				
CaPOPI_6323	scaffold1408	24952	GTTTTT/GTTTTT	TGTGCGTCCAATAGTGG TGT	GACACGAATAAGCCAAG GGA	60.0	478	INTERGENIC				
CaPOPI_6324	scaffold1408	26856	TC/T	AACCAATGTTGTGCATC CAA	AGGGAGGACGAAAATGA CCT	59.8	571	INTERGENIC				
CaPOPI_6325	scaffold1408	92293	GTTTT/GTTTTT	AGGTCATTTTCGTCCTC CCT	TAATTGGGCAAGAATGA GCC	59.9	640	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6341	scaffold1418	38513	CTTTTATTTTTATTT/CTTTTATTTTTA TTTTTATTT	CTTTCCTAAAGCCAA TCC	TTGCTCCCTTTACTCATC TGC	59.9	811	INTRON	Ca_25262	S		Domain of unknown function DUF21
CaPOPI_6342	scaffold1418	106529	AATATATATATATATATATATATA/A ATATATATATATATATATATATA	AATATCGCTCGCTGACA CCT	AGCAGCAGGACCTTAC AAT	59.9	762	INTERGENIC				
CaPOPI_6343	scaffold1419	10604	ATTTTTTTTTTT/ATTTTTTTTTT	CCTCTTGCTGCAAAAC AAA	AACTTTTCCGCTGCTT GAA	60.0	294	INTERGENIC				
CaPOPI_6344	scaffold1419	22458	AT/A	TCATGCGCATCAAATAC ACA	TTTCAAAATTCGTCGTTG GA	59.7	265	INTERGENIC				
CaPOPI_6345	scaffold1419	30683	T/TG	TCCATCTCCAACAACAT CCA	TAATTGCTCTTGCGGTC CTT	59.9	306	INTERGENIC				
CaPOPI_6346	scaffold1419	33257	TTATA/TTA	TGCATTTTCTTGAAATTG ATGG	AAAGGTCGTGAGCAGAG GAA	59.9	595	INTERGENIC				
CaPOPI_6347	scaffold1419	49527	TGTAAACC/TGTAAACCGTAAACC	AACCCTTATCGCAGAAC CCT	GGTATTGGGTTTGGGGT TTC	60.0	609	INTERGENIC				
CaPOPI_6348	scaffold1422	687	TT/TATGTCAT	AGGTCATTTTCGTCCTC CCT	CAATGAACCTATTGGAT GCACA	59.9	274	INTERGENIC				
CaPOPI_6349	scaffold1424	15042	TC/T	CGACTCACGTTGAGGAG ACA	CCCCCTTTTGCATAAG TGA	60.0	668	INTERGENIC				
CaPOPI_6350	scaffold1424	48624	A/AT	TAGGTCATTGTCGTCCT CCC	TGGATGCACAAGATCGG TTA	59.9	272	INTERGENIC				
CaPOPI_6351	scaffold1426	5555	AG/A	CCTCAGATGAGAGCCAG GAC	ACACCCCGTTTTTCAAA GTG	59.9	434	INTERGENIC				
CaPOPI_6352	scaffold1426	5828	T/TTC	AACGGGGTGTACAATG AGC	CTGGTTTGACAATGCGT TTG	59.9	623	INTERGENIC				
CaPOPI_6353	scaffold1426	6734	TCATCAC/TCATCACCATCAC	TTGATACTATGCCACCA CGC	GCATTTTGCTTGTTGGAC TCA	59.6	635	INTERGENIC				
CaPOPI_6354	scaffold1426	7221	TAAAAA/TAAAAAA	TGAGTCCACAAGCAAAA TGC	GGTTCCTCTTGTTTTG GGT	59.8	494	INTERGENIC				
CaPOPI_6355	scaffold143	67526	TA/TAA	GGATTGTTGGTTCAATT GGG	TTAGGAAATCGATTGGG GTG	60.0	495	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6356	scaffold143	68109	CATT/CATTTTAATT	CACCCCAATCGATTTCC TAA	ACATCTGTTCCCTCCGT GAC	59.8	472	INTERGENIC				
CaPOPI_6357	scaffold1430	1269	ATTTTT/ATTTT	TCATGTGCATTTCTACCA CCA	TGATTCGAGTCAAACCA CCA	60.0	315	INTERGENIC				
CaPOPI_6358	scaffold1432	2456	TAAAAAAAA/TAAAAAAA	CCATGACATGACCTTAG GGG	CAATGTAATTTGCATCAT AAAGGC	60.2	234	INTERGENIC				
CaPOPI_6359	scaffold1432	59960	TTATATATATATATATATATATATAT/T TATATATATATATATATATATATATAT	TGCTTCAATGGTTCAAT CAAA	GAGGTGCATTAGAGATC ACGG	59.1	705	INTERGENIC				
CaPOPI_6360	scaffold1432	80163	ATTT/ATTTT	TCTTTGGATGGGTTCCA TGT	TGAAATGTTGTTGGTA GTGGC	60.2	522	INTERGENIC				
CaPOPI_6361	scaffold1432	80490	CTTTTTTT/CTTTTTTT	GCCACTACCAACAACAT TTTCA	ATTTGTGTTTGTGGGG AAA	59.9	713	INTERGENIC				
CaPOPI_6362	scaffold1432	80541	AAATAATAATAATAATAATAAT/AAA TAATAATAATAATAATAATAAT	GCCACTACCAACAACAT TTTCA	ATTTGTGTTTGTGGGG AAA	59.9	713	INTERGENIC				
CaPOPI_6363	scaffold1433	21153	A/AG	TTCCGGGTCAGATTTCA AAC	GGTCCTCGATTCATCT GGA	59.9	417	INTERGENIC				
CaPOPI_6364	scaffold1433	21769	AGCATTATTTTC/A	TCCAGATGAAATCGAGG ACC	TCATATGTACGTTTCGG GCA	60.0	498	INTERGENIC				
CaPOPI_6365	scaffold1433	21950	TAAAAA/TAAAAA	GATGAAATGGAGGACCG AGA	TCATATGTACGTTTCGG GCA	60.0	332	INTERGENIC				
CaPOPI_6366	scaffold1433	33630	CAAAA/CAAAA	AGGCGATTTTCGTACCA CAC	CGTGTCAATTATGTCGG GTG	60.0	112	INTERGENIC				
CaPOPI_6367	scaffold1439	105314	GAAAGAGAAAAAGAAA/GAAAAGAAAA AAAGAAAAAAGAAA	AGACCACCATCAGAAGC CAC	TGAGAGGCACGAACGAA AAT	60.1	643	INTERGENIC				
CaPOPI_6368	scaffold1446	21277	TATATA/TATATACATATA	GGCGTTGGAGTCATGTT TTT	TTCTCAACTGACGCATG AGG	60.0	362	INTERGENIC				
CaPOPI_6369	scaffold1448	11427	CAAA/CAA	AATCCAATGACGCAAC ACA	AGGTCATTTTCGTCCTC CCT	60.0	792	INTERGENIC				
CaPOPI_6370	scaffold1448	34387	CAAAAAAAAA/CAAAAAAAAAAA	CACACATTCACTTAACC CCC	TTCAAAGTTGTGTGTCT GCG	60.1	867	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6371	scaffold1448	99427	GAATTTAATATAAATTAATTTAATATAAA TT/GAATTTAATATAAATTAATTTAATAT AAATTAATTTAATATAAAAT	CCAGGAAATGACCCCT ATT	TTTATTTTAGCGCGGTG TCC	60.0	774	DRR	Ca_26688			
CaPOPI_6372	scaffold1448	133221	GTTTTTTTTTTT/GTTTTTTTTTTT	AACCCACCCTCGAAAGA GTT	CGTCGGATATTGGAGGA AAA	60.0	170	INTERGENIC				
CaPOPI_6373	scaffold1449	3971	AATATATATATATATATATATATATATAT/ AATATATATATATATATATATATATAT	AGGAAGAGTGGAGTTGC GAA	CTGTAACTGAAGCGCC CTC	60.0	456	INTERGENIC				
CaPOPI_6374	scaffold1452	1227	GTATATATATATATATATATAT/GTAT ATATATATATATATATATATAT	CGAAATCTTTGGGTTTT GGA	ACCTAAATTGGGAGCT CGT	59.9	618	INTERGENIC				
CaPOPI_6375	scaffold1452	29608	C/CAG	GAAGCCTTTTCAGCAGG TTG	TAGTGTGCCACCACTCC AAA	60.0	648	URR	Ca_27551	R	ZF-HD	Pentatricopeptide repeat
CaPOPI_6376	scaffold1452	29738	ATTT/ATTTT	GAAGCCTTTTCAGCAGG TTG	TAGTGTGCCACCACTCC AAA	60.0	648	URR	Ca_27551	R	ZF-HD	Pentatricopeptide repeat
CaPOPI_6377	scaffold1452	30210	TAAA/TAAAA	TGCCCAATTACCACAAT CAA	ACCAACCCTTCATTCC CTC	59.8	465	INTERGENIC				
CaPOPI_6378	scaffold1452	30615	AGC/AAAAATCTTGC	TCCATTTTCATGAACCG ATT	TGTACATTGTTCCGTC CGA	60.1	662	INTERGENIC				
CaPOPI_6379	scaffold1455	12569	TCACCTCCACCTCCACCTCCACCTCC/ CACCTCCACCTCCACCTCC	TTATAGCCGTTGGAAGT GGG	TCAGGAAGGAAGAAGGC AGA	60.0	594	INTERGENIC				
CaPOPI_6380	scaffold1455	19091	CG/C	TATTGGGTGCACCGTTT ACA	TTAGGTGGTACGGAAT CGC	59.8	438	DRR	Ca_27725			
CaPOPI_6381	scaffold1457	19983	G/GA	TGGCTTTCAAATCCACA CA	GCGAGCAGAGATTTTTA CCG	60.1	468	INTERGENIC				
CaPOPI_6382	scaffold146	9554	GTTCTT/GTT	GGTGTGCAAGAGGACTG GAT	AAAAACGAGCCTAGCGT GAA	60.1	508	INTERGENIC				
CaPOPI_6383	scaffold146	71228	ATATTATTATTATT/ATATTATTATTA TT	TGAAATAAAACCATAAAA CGACGA	CATTTTAATGTTTGACTG CATAATGA	59.8	450	INTERGENIC				
CaPOPI_6384	scaffold1462	12436	TGG/TGGG	TCAGCCAAAAAGCTGAT GTG	TTGTCCATGAAAGGATG ATATTT	60.0	380	INTERGENIC				
CaPOPI_6385	scaffold1462	14707	CAAA/CAAAA	TTTCGTCAAATAAATACA AATACCATT	ATCAGTGGTCCCGTGAG AAG	58.5	360	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_6386	scaffold1465	3149	AATATATATATATATATATAT/AATATATATATATATATATATAT	AAGGCTCAACCTTACGTGGT	TTTTTAGCAATGGCACAACTT	58.7	558	INTERGENIC				
CaPOPI_6387	scaffold1465	11699	CTTT/CTTTT	CGAGGCATTTAGCTAGCTG	CACCCCTTACCTCGACTGAA	60.1	647	INTERGENIC				
CaPOPI_6388	scaffold1465	20135	TTA/TTAGATA	ATAGATCCCTCAGCCCAAC	TTTCGGTAGTCCCGTTCATC	60.3	604	INTERGENIC				
CaPOPI_6389	scaffold1465	22512	ATTT/ATTTT	TTGCTTTGTCTTGGCAAGTG	AACCTCCCATCGAGAAGGAT	60.0	735	INTERGENIC				
CaPOPI_6390	scaffold1465	36700	CAAAAAAAAA/CAAAAAAAAA	CTTTCGTTTCGCCTCGTTAG	CCGAAACAACATGTCAAAAA	60.0	393	INTERGENIC				
CaPOPI_6391	scaffold1466	216791	CTCAACCTTCAACCTT/CTCAACCTT	GTCACCCAAGCCAACCTTGT	CTTCCCCCTATCCCTACCAA	60.0	810	INTERGENIC				
CaPOPI_6392	scaffold1467	11911	AATATATATATATATATATATAT/AA TATATATATATATATATATATATAT	TCGCAGCTGTGATGCTAAGT	ATGGGAGGTCTTGTGCAATT	59.8	359	DRR	Ca_26807	Q	GeBP	Cytochrome P450
CaPOPI_6393	scaffold1467	16133	GTC/GTCAATC	ACTTTCAAACGGTCAATCCG	ACATTATGTGAGGGCGCTTC	60.0	596	INTERGENIC				
CaPOPI_6394	scaffold1467	55724	TTTATTATTATTATTATTATTATTAT T/TTTATTATTATTATTATTATTATT	TGCGATCAATATACCCACA	CCGGAGATGCAACCATTAT	59.8	812	INTERGENIC				
CaPOPI_6395	scaffold1483	6428	TAAAAAAAAAAAA/TAAAAAAAA	TAACTTGCATGCCATTGTC	CAAAAGACACATATTTGGCA	59.5	573	INTERGENIC				
CaPOPI_6396	scaffold1483	6873	ATGT/ATGTGT	GCACCACGTGCGATAACA	TGTGTGAGCGTTATTGGTTTG	60.3	984	INTERGENIC				
CaPOPI_6397	scaffold1483	44049	GAAAAA/GAAAAA	CATCTTCAGGGGCATGATCT	TGATGGATTGTTAAAGCGTG	60.0	211	INTRON	Ca_26253	R		Aldo/keto reductase
CaPOPI_6398	scaffold1483	57089	GTGAGATTGAGATTGAGATTG/GTGAG ATTGAGATTGAGATTGAGATTG	ACCCAACAAGCAACATCTCC	CATCTTCTCCATTTCTCCGC	60.0	751	INTERGENIC				
CaPOPI_6399	scaffold1483	72991	G/GT	TCAGAAATGGCGTTCTCTAG	CATTAGTGATTGTGTGCCCG	60.2	815	URR	Ca_26256	R	NAC	Pentatricopeptide repeat
CaPOPI_6400	scaffold1488	9466	CAAAAAAAAA/CAAAAAAAAA	TCCATTAAATGCGTTGAGACTTTT	TTAGGGTTTAGGGTTTGGGG	60.0	238	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6401	scaffold1490	1256	GAAAAA/GAAAAAA	CAAACACACCTGTGGA TGG	AGGTCATTTTCGTCTC CCT	59.8	281	INTERGENIC				
CaPOPI_6402	scaffold1493	65515	AC/A	AGGCAATTGGGATTCC TCT	GGCTGCTTTGAGTTCTT TTTT	59.9	372	INTERGENIC				
CaPOPI_6403	scaffold1496	126659	AATATATATATATATATA/AATATATAT ATATATATA	TCGGGGACGAAATCTT TTA	ACGCTTCATTTTACTGC GCT	59.5	490	INTERGENIC				
CaPOPI_6404	scaffold1496	233940	ATTTTT/ATTTTTTT	CATTGCCAATCATTATCC CC	TGACAACGACATCAAAG GGA	60.0	620	INTERGENIC				
CaPOPI_6405	scaffold1496	236426	AATATATATATATATA/AATATATATAT ATATA	TTCAACCTCGAATTTCA CA	AGCGGTGGAGAGAACTC TGA	59.4	764	INTERGENIC				
CaPOPI_6406	scaffold1496	292609	GTATA/GTA	GGCTCCATGAGTTGATT GGT	GATGTTCCGTCGTCAA GGT	59.9	460	INTERGENIC				
CaPOPI_6407	scaffold1496	307581	T/TA	TGGGTGCACAAGATTGG TTA	AGGTCATTTTTGCCCTC CTT	60.0	467	INTERGENIC				
CaPOPI_6408	scaffold1499	931	TAAAAA/TAAAA	TTCTTATTACCTGGTTC CTTTT	TTGAAGGATACATTACG AGATTCA	58.3	734	INTERGENIC				
CaPOPI_6409	scaffold1499	9817	CTTTTTTTTT/CTTTTTTTTTT	TGCATTTTCTGCACCTC TG	TGGTTGAGGCACTAGCC TTT	60.0	214	INTERGENIC				
CaPOPI_6410	scaffold1499	17023	TG/TGG	GAGGTTGGTGCTTGGAC AAT	AATTTTCAGCCCCCAATA CC	60.0	676	INTERGENIC				
CaPOPI_6411	scaffold1499	48638	AAAATAAATAAATAAATAA/AAAATAAA TAAATAAA	CCGGGTGTAAGGTTCCA CTA	TTTGCAAAAACCAATGAA TACTT	59.8	284	INTERGENIC				
CaPOPI_6412	scaffold1499	62316	ATTTT/ATTT	ATGATTGGCTTGGTAGT GCC	ATGCCCCCAAGCTTCTT ATT	60.0	573	INTERGENIC				
CaPOPI_6413	scaffold1499	74379	ATTTTTTTTTT/ATTTTTTTTTTT	CTGCTCGTGCACCAT TGA	TTTTCTGTTTGGTCCTTG GG	60.0	802	INTERGENIC				
CaPOPI_6414	scaffold1499	85779	CAAAAAAAAA/CAAAAAAAAAA	TGGATCACTAGCACCA TCG	CCACCAAAACCAAGG TTA	59.7	606	INTERGENIC				
CaPOPI_6415	scaffold1499	112672	CTTTGTCAATT/CTTTGTCAATTTGT CAATT	CGGTTACGTTTTTGT ACG	ACCTCCTTCTCGTGTT GC	59.1	391	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6416	scaffold1499	129736	GTTTTTTTT/GTTTTTTTT	CAAGTGAACGTTACAAA AACGTG	CCCTGAGTCATTACAC CCT	59.6	318	INTERGENIC				
CaPOPI_6417	scaffold15	144204	CAA/CAAA	AGGTTTGAGGATCGGG GTAT	CAAGATTTGGGCAATCT GCT	59.7	757	INTERGENIC				
CaPOPI_6418	scaffold150	4518	ATT/ATTT	TGGACAAGAATTAGCCC AGG	AGGTCATTTTCGTCTC CCT	60.1	436	INTERGENIC				
CaPOPI_6419	scaffold1504	55137	ATTTTTTTTT/ATTTTTTTTT	GGAACAAGTCCCATGA AGG	AATCCAACCTTCATTCGC CAT	59.4	375	INTERGENIC				
CaPOPI_6420	scaffold1504	129111	TTATATATATATATATATATATA/TTAT ATATATATATATATATATATA	TGGAATGGCGACTTCCT AAA	ACTGGCCATACTCGAAA ACG	60.6	206	INTRON	Ca_24092		Trihelix	
CaPOPI_6421	scaffold1504	200103	CATATATATATATATATATA/CATATA TATATATATATATATA	TCTCCGCATAAGCTTTC GAT	CCGTACCGTTTCTGGGA TTA	59.9	685	INTERGENIC				
CaPOPI_6422	scaffold1504	290680	CATATATATATATATATATATATAT AT/CATATATATATATATATATATAT ATATATAT	CACGTTAGCACTTTCTG GCA	AGCAAATATCCACGAGA CAAA	60.1	736	INTERGENIC				
CaPOPI_6423	scaffold1506	37155	GTATTATTATTATTATTATTATTATT A/GTATTATTATTATTATTATTATTA	TTTGTGCCCTGAAATTG CTG	ATGAAGACCAGAGGAGC GAA	59.8	559	INTERGENIC				
CaPOPI_6424	scaffold1508	60830	T/TACA	TCACGGGTCAACACGAT TTA	AGTACATGGCGACCGGA TAG	60.0	247	INTERGENIC				
CaPOPI_6425	scaffold1508	85452	TTATATATATAT/TTATATATATATAT	GTTGGTCCCTAGCAC GTA	CACCCTGGGATTCTTGC TAC	60.0	850	INTERGENIC				
CaPOPI_6426	scaffold151	814	ATTTTTTTTT/ATTTTTTTTT	GGAGACTCCCATACATT GGC	TGCTATCCCACTTTGAG CCT	59.4	332	INTERGENIC				
CaPOPI_6427	scaffold151	1987	GAAAA/GAAAAA	GGACATTTGTGAACAAG GCA	TTGGAGCTTATGTGTC CTCAA	59.5	732	INTERGENIC				
CaPOPI_6428	scaffold151	4221	AGG/AG	TATAAGCCGAAAATGGC AGG	ATGGCGTTTGGATTGAT GAT	60.1	520	INTERGENIC				
CaPOPI_6429	scaffold151	4988	G/GT	ATCATCAATCCAACGC CAT	TCGAGAGCACAATCGAA GTTT	60.2	385	INTERGENIC				
CaPOPI_6430	scaffold151	7801	CT/CGAACATTAAAAATT	GGTGAAAACGGGTGGA AGA	CCCTCTGCAATGTCGGT AAT	59.9	277	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6431	scaffold151	35903	AAT/AATAT	ACACACGCATAACACAC GAG	TTGGAGTGCATGTGACC ATT	58.2	459	INTERGENIC				
CaPOPI_6432	scaffold151	57230	A/ATTAGAGACCTAC	ATGCAATGCGTATATGC CAA	TTCGTGTGGATTTGTG GAA	59.9	577	INTERGENIC				
CaPOPI_6433	scaffold151	68819	ATATTATTATTATTATTATTATTATT ATTATTATTATT/ATATTATTATTATTATT ATTATTATTATTATTATTATTATTATT	AAATGAATGGAAGACGC GAT	AAAATTCTCTTGAATCCC CATT	59.5	851	INTERGENIC				
CaPOPI_6434	scaffold151	221306	TCCCC/TCCCCC	TTCAAAGGAGATGGTTT GCC	ATGACAATTCCAATGCA CCC	60.1	738	INTERGENIC				
CaPOPI_6435	scaffold151	294117	ATTTTTTTTT/ATTTTTTTTT	CATTTCTTTTCTCGCGC AT	CCAAGTCCCCAGAGTC AAA	60.3	656	INTERGENIC				
CaPOPI_6436	scaffold1511	36830	ATTTTTTTTT/ATTTTTTTTT	CCGAGTTGGATTGGGTA TTG	TGGTCAACTGTTTCCT CCA	60.2	447	INTERGENIC				
CaPOPI_6437	scaffold1511	110106	TAA/TAAA	TTAATGCAGGGTTTGT GCT	ATTGAAGCCCACTATGG CTG	60.5	396	INTERGENIC				
CaPOPI_6438	scaffold1511	135714	GAAAAAAAA/GAAAAAAAAA	AGGGGCTAGCAAAGGG TAAA	GGGAGGCAACCAATTT TAT	60.1	875	INTERGENIC				
CaPOPI_6439	scaffold1511	136948	CAATAAAATAAAA/CAATAAAATAAAA TAAAA	TCAAGATTGCCCTCA ATC	AAACGCAATCCTTGAGT TCG	60.0	357	INTERGENIC				
CaPOPI_6440	scaffold1511	167354	T/TA	GGCCTGGCCTACTTAAG GTC	GCATGTTCTTGCCAT TAT	60.1	759	INTERGENIC				
CaPOPI_6441	scaffold1521	1157	CA/C	TCATGTGAACAATGCAA CCA	AACTAGGCGCTATACGG GGT	59.5	394	DRR	Ca_26976			
CaPOPI_6442	scaffold1521	10780	CA/CATCGA	TCATGTGAACAATGCAA CCA	CCACAGCTTGCTGTGCG GTA	59.5	296	DRR	Ca_26977		bHLH	Protein kinase, catalytic domain
CaPOPI_6443	scaffold1521	15206	T/TTTGAAATAAATTAT	GGGGTTAGGGCTCATAC GAT	GTTGCAGCGTGTGTTC TGT	60.2	821	INTERGENIC				
CaPOPI_6444	scaffold1521	15603	GAA/GAAA	TCGTGGTTCAATAATTG GCA	CAAATAACGATTCGGG CTC	59.9	228	INTERGENIC				
CaPOPI_6445	scaffold1521	15896	TAAAAAA/TAAAAAAA	TCGTGGTTCAATAATTG GCA	AAATTAGGCATACAGAA ATGAAGGA	59.9	403	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6446	scaffold153	28056	GAAA/GAA	AATGGCCACGAATCTGA AAG	TGTTTGAATATGACGC GGA	60.1	518	DRR	Ca_27484			
CaPOPI_6447	scaffold1530	16153	ACCCCC/ACCCCCC	TCTCACGGTTGTGAGGA CTG	ACCGTTCTTGGTTTCTG ACC	59.9	746	INTERGENIC				
CaPOPI_6448	scaffold1530	17519	TA/T	GTGCAGTTGAATGAGCC AGA	TTGGAACCTTCTCCAA CAC	60.0	508	INTERGENIC				
CaPOPI_6449	scaffold1530	19122	AA/AAGA	CATCGCCATTCACTGT TTG	CTTGCTTCCATGAATCAA CAA	60.1	623	INTERGENIC				
CaPOPI_6450	scaffold1530	21107	TC/TCC	TCTAAAAGATTTTGAACC CCAAA	TCCAAGGGTGTAGAAA CGG	59.1	812	INTERGENIC				
CaPOPI_6451	scaffold1530	23128	AATATATATATATATATA/AATATATAT ATATATATATATATATATATA	TCTCCATTGCACCCCA ATA	GGTGCTGAAATCGGAAA ATC	59.9	189	INTERGENIC				
CaPOPI_6452	scaffold1530	24452	AC/A	AGAAGGAGAATGTCACG ATGG	GACGTGTGCTGAACCTC CCA	59.2	261	INTERGENIC				
CaPOPI_6453	scaffold1530	24697	CTTTTTTT/CTTTTTTTTT	TGGAGAGTTCAGCACAC GTC	CCTCCGGTACCATAAAC CCT	60.0	249	INTERGENIC				
CaPOPI_6454	scaffold1530	25494	TAT/TATGTCAAAT	CTTTTTCCGTTTTCAGCC AC	TTTACCCCTCGGTAAAA CCTC	59.7	607	INTERGENIC				
CaPOPI_6455	scaffold1530	25850	TTTTTTATTTTTATTT/TTTTTTATTT	TCGATCTTGAGCGAATT TGA	CAATACCAATTCACGAA AATTCA	59.5	482	INTERGENIC				
CaPOPI_6456	scaffold1530	26727	CT/CTT	TGCTTTTGGTAAAGGTG CTT	ATTCGCAAAACCAACTC GAT	57.6	742	INTERGENIC				
CaPOPI_6457	scaffold1530	27039	T/TCA	CGTTTTCGACATCAAGA TGGTA	TCGCAAAACCAACTCGA TAA	60.0	134	INTERGENIC				
CaPOPI_6458	scaffold1530	27186	CTATTAT/CTTAT	TCGAGTTTGGTTTGCGA ATA	CGATTGCTCATAAAATC GCTC	59.3	538	INTERGENIC				
CaPOPI_6459	scaffold1530	27815	ATTTTTTT/ATTTTTTTTT	TTTGAGAGGGCCTTTGG TAA	TCGACAGGTTTGTGTG TCG	59.7	405	INTERGENIC				
CaPOPI_6460	scaffold1530	27996	CCTATGGTG/C	TTTGAGAGGGCCTTTGG TAA	TCGACAGGTTTGTGTG TCG	59.7	405	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6461	scaffold1530	28367	CAATTAA/CAA	GGCCCTATGGTGTTATG GTG	TTCGAAGCCATTATGTTT GATG	60.1	817	INTERGENIC				
CaPOPI_6462	scaffold1530	28720	ATTTTTTTTTTTT/ATTTTTTTTTT	CAAATCTGAGCACACAC GAGA	ATAGTGACATCGGGTTG GGA	60.0	510	INTERGENIC				
CaPOPI_6463	scaffold1531	24929	AT/ATTCT	TCAGGATTTTGGGTTTA GGG	TTTTGTAGTTGTACTCAA TAACAAGGA	58.9	482	INTERGENIC				
CaPOPI_6464	scaffold1531	27008	AC/A	CCTGAAAAGTCCCGATG AAA	CTAACGCAGAACCTGCA ACA	60.0	376	INTERGENIC				
CaPOPI_6465	scaffold1531	29443	AG/AGGG	TCCAGATGAAATCGAGG ACC	GATTTTCGTTCCACCCTT CA	60.0	621	INTERGENIC				
CaPOPI_6466	scaffold1532	69027	TAAAAATAAAAAATAAAAA/TAAAAATAA AAAAATAAAAAATAAAAA	ACCCAATCTTGGGGGAT AAA	TCITTGCTCACAACACA GCC	60.4	220	INTERGENIC				
CaPOPI_6467	scaffold1533	39114	CTATATATATATATATATATATATATATA TAT/CTATATATATATATATATATATATAT AT	TCCGCGAGAGAGTTATA GCC	CACGAAACCACAATTC TGC	59.6	790	INTERGENIC				
CaPOPI_6468	scaffold1533	40798	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATTAA TATTATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATTA	GGCACGACATCATCATC ATC	TTTTCACAAGGCTCAACT AATTACA	59.9	575	INTERGENIC				
CaPOPI_6469	scaffold1544	14620	CTTT/CTT	CCACTGGATGAATCTCG GTT	TAGAAGGAACGGAGGG GTTT	59.9	794	INTERGENIC				
CaPOPI_6470	scaffold1545	95527	ATCTACACATGT/AT	AAGGTTACCGTGTTTT TGG	CATCAAAAGTTGCATCA CCG	59.9	874	INTERGENIC				
CaPOPI_6471	scaffold1548	1087	GCTCTCTCTCTC/GCTCTCTCTC	AAATGGCTTGGTTATGG CTG	TGTAATGCCGCAAATTC AAA	60.0	432	DRR	Ca_27706	QI		
CaPOPI_6472	scaffold1550	44368	TAAAA/TAAAAA	TGGACTTTTCGAGCGAC TTT	AGTTATGACGTAGAACT ATAAACGGT	60.0	381	INTERGENIC				
CaPOPI_6473	scaffold1550	56017	TAAAA/TAAA	AGGCGATTTTCGTACCA CAC	TCCAGATGAAATCGAGG ACC	60.0	322	INTERGENIC				
CaPOPI_6474	scaffold1552	1897	AGG/AGGG	ACCAAGAATGTCCCTGC AAC	TCTTGTGGAAGGAAGCT CGT	60.0	223	INTERGENIC				
CaPOPI_6475	scaffold1552	2208	CCCGACGCTAA/CCCGACGCTAATCCG ACGCTAA	ACGAGCTTCCTTCACA AGA	GGGCTGTTGTTTCGTCA AAT	60.0	736	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6476	scaffold1559	551	GTTTTTTT/GTTTTTTT	AGGTGTTTTTCGCTCCCT	TTCGATGCACATGATTGGTT	60.0	473	INTERGENIC				
CaPOPI_6477	scaffold1569	32526	ACC/ACCC	CAGGGCCTTAAACCATGAAA	GGTTTGGGGTTTGGGATTTA	59.9	601	INTERGENIC				
CaPOPI_6478	scaffold1569	32980	TAA/TA	ATAAACCGAACCGCAAAACA	GGTTTTATGGTTTAACGGCCT	60.4	714	INTERGENIC				
CaPOPI_6479	scaffold1569	33746	T/TC	AAACCCATAACCTAACCCC	ATGGTTTAAGGCCTTGTA	58.2	612	INTERGENIC				
CaPOPI_6480	scaffold157	127896	A/AGG	TCCTGTAGATTTCTGCGG	GTGCAGATTTTCATCGGAGA	60.2	276	INTERGENIC				
CaPOPI_6481	scaffold157	212151	AATATATATATATATATATA/AATATATATATATATATATATATA	CTTAGGGTGAGGGAAGGGAG	CATCTAAGGGCAAAACGCTC	60.1	542	INTRON	Ca_21071	C	GATA	Mitochondrial substrate/solute carrier
CaPOPI_6482	scaffold157	248333	CAA/CA	TTGTATTGCCTCCATCTCAAAA	TGGAAGTTGTGGATGCAATG	59.6	483	INTERGENIC				
CaPOPI_6483	scaffold157	254639	GTTT/GTTTTT	TGGGATGAAAAGGGAGTTTG	TTGACTCTGATGAACGTGCC	59.9	605	INTERGENIC				
CaPOPI_6484	scaffold157	255873	GAT/GATAT	TTTGGTCTTGCCTTTGATGA	TGCGGTTAAGGTTGGTCTC	59.2	888	INTERGENIC				
CaPOPI_6485	scaffold157	289273	T/TATC	GCACATTCAGTGCCAAGAGA	ATTGAGGGCATTGTCACTCC	60.0	492	INTERGENIC				
CaPOPI_6486	scaffold157	308958	A/AC	ATGTGGACATGGCACAAAGAA	TTTATCTTTCGGATCACC GC	60.0	677	INTERGENIC				
CaPOPI_6487	scaffold157	335191	GAAAAAA/GAAAAAAA	TTCGAAGTTTCGGTAGGGTG	GTGCAATGAAACCCCAACAC	60.1	543	INTERGENIC				
CaPOPI_6488	scaffold157	349077	TAT	TGCCAATCCCCAACTTTA	GCGGGACATAACACCTAACG	60.3	369	INTERGENIC				
CaPOPI_6489	scaffold157	355168	GAAA/GAAAA	CTGTTGAGGTCGGGAAACAG	CTTCACTTTTGCTGATGCA	60.7	575	INTRON	Ca_21079		SBP	DEP domain
CaPOPI_6490	scaffold157	358753	ATTTTT/ATTTT	ATTTAGATCGGCGGTTGAGA	AACGTAGCTTTTGTGCGCTA	59.7	216	DRR	Ca_21079		SBP	DEP domain

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6491	scaffold1578	76566	CATATATATAT/CATATATATATAT	TCATTGTTTGTGTTTGGCGT	CTTGTTTTCTCCATGGT CGC	60.0	816	INTERGENIC				
CaPOPI_6492	scaffold1578	76623	AGG/AG	TCATTGTTTGTGTTTGGCGT	CTTGTTTTCTCCATGGT CGC	60.0	816	INTERGENIC				
CaPOPI_6493	scaffold1578	76801	ATCTCT/ATCTCTCT	CTGATAGTGACACCGGTTTG	CTTGTTTTCTCCATGGT CGC	59.0	664	INTERGENIC				
CaPOPI_6494	scaffold1578	77306	T/TG	GCGACCATTGGAGAAAAC AAG	TTGGTTGAATCCACAC AAAT	60.6	563	INTERGENIC				
CaPOPI_6495	scaffold1578	79075	CT/C	CCAGACCTCATAGATCC CCA	CATGTAAATCGCCGAA ATC	59.9	467	INTERGENIC				
CaPOPI_6496	scaffold1579	35194	CAAAAA/CAAAA	CATTTTTAATTGACAACT CAATTTTCT	TGAAATAAAACCATAAAA CGAAGA	58.3	240	INTERGENIC				
CaPOPI_6497	scaffold1579	64472	A/AT	GAGCGAATTGAGAAACG AGG	TTTTCAAATAAAGTAACA TTGACAACA	60.0	927	INTERGENIC				
CaPOPI_6498	scaffold158	131634	T/TAAC	GTGACTGGTGACTGGG GACT	TTATGCCTGCTGTTCTG CAC	60.0	227	INTRAGENIC				
CaPOPI_6499	scaffold158	132271	TAAACGTGAGGGACAAAAC/TAAACGT GAGGGACAAAACGTGAGGGACAAAAC	GTGCAGAACAGCAGGCA TAA	CGTGGCGTGACTACATT GAG	60.0	753	INTERGENIC				
CaPOPI_6500	scaffold1580	61955	AAA/AAATAA	AAGAACGCGATAACCAA AGC	TTGGACCGATGGATCAT TTT	59.4	894	INTERGENIC				
CaPOPI_6501	scaffold1580	69955	ATTTT/ATTTT	ATCACCGCCACTTAGG CAA	TCCCTTATGACAATTCAT GGTG	60.7	639	INTERGENIC				
CaPOPI_6502	scaffold1580	99509	AAATAATAATAATAATAATAATAATAATAA/AAATAATAATAATAATAATAATAA TAATAA	TACCCAGAAGTGAGAT CGG	ATCATCAATGTCGTGCC TCA	60.1	709	INTERGENIC				
CaPOPI_6503	scaffold1580	251123	CNNNNNNNNN/C	TGTTCTCTTAGGGGGTG GTG	GGCCATCTTTTAAACCC CTT	60.0	569	CDS (FRAME SHIFT)	Ca_20799	B		DEK, C-terminal
CaPOPI_6504	scaffold1580	472285	TC/T	TGATGCAAGAAGCCACA TCT	CTTGAAAGCCATTGGAG AGC	59.4	677	INTERGENIC				
CaPOPI_6505	scaffold1580	472375	CATA/CATATA	TTTTGGTCAGGGGAAGG TTT	CTTGAAAGCCATTGGAG AGC	60.7	578	INTERGENIC				

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CaPOPI_6506	scaffold1580	472426	CT/CTT	TTTGTGTCAGGGGAAGGTTT	CTTGAAAGCCATTGGAGAGC	60.7	578	INTERGENIC				
CaPOPI_6507	scaffold1586	1838	AC/ACC	AGGGAGGACGAAAATGACCT	TGACCAATTTTGAGCATCCA	59.9	471	INTERGENIC				
CaPOPI_6508	scaffold1607	47435	CAA/CA	TCACCGATGTTGGATTGTA	CGATTATCGCATCTTGTT	59.9	806	INTERGENIC				
CaPOPI_6509	scaffold1607	61142	ACTCTCTCTCTCTCTCTCTCT/ACTCTCTCTCTCTCTCTCTCTCT	AGACCAGCAAGAAGCATTGG	CCTTAAAGCAACCGTCCAAA	60.4	473	INTERGENIC				
CaPOPI_6510	scaffold1607	117990	CAA/CAAA	TGGGATGTTAACTCCATACCC	ATATTGAAACCCGTGTGGA	59.9	347	INTERGENIC				
CaPOPI_6511	scaffold1609	2922	A/AAGTTCATTT	TGTGTGTTTGTGTCATCGGA	ATCCTTGGGAGGACGAAAT	59.5	546	INTERGENIC				
CaPOPI_6512	scaffold1613	98233	TAT/TATAAAGGTAAGGAT	GACGCGTAGTTTCGAGGATG	TGGCAAGGAGCAACTTCTT	60.8	651	INTERGENIC				
CaPOPI_6513	scaffold1613	98434	A/AG	AAGAAAGTTGCTCCTTGCCA	AGGAGCACTTACCTCCGTTG	60.0	133	INTERGENIC				
CaPOPI_6514	scaffold1613	106669	C/CGATATCATAGCCAAG	ACAATTTACGCCACCGAAG	AGAAGCGACCCCATAGGTTT	60.0	549	INTERGENIC				
CaPOPI_6515	scaffold1614	8293	ATATATATATATAT/ATATATATATATATGTATATATATATATAT	CTTCTGATGCCCCGATTAAA	AAGATGGAGGAAATGCGATG	60.0	436	INTERGENIC				
CaPOPI_6516	scaffold1614	131511	AATATATATATAT/AATATATATATATAT	CCGCGAGTAATTCCGATAAA	ATCAGCCTAAGGGGGAAAGAA	60.1	875	INTERGENIC				
CaPOPI_6517	scaffold1614	188751	GTTTTTTTTT/GTTTTTTTTTTT	TGAAAGCCAATTCCACTTCC	ACTGGAAGGACAGGCTGATG	60.1	703	INTERGENIC				
CaPOPI_6518	scaffold1626	121557	TTTATTATTATTATTATTATT/TTTATTATTATTATTATTATTATT	AGAGGCAACAAGAACCAGAA	AGCCGAGAAAATAACTCGCA	59.9	311	INTERGENIC				
CaPOPI_6519	scaffold1630	6306	T/TA	GTACCACCCGACAAAAATGG	TCCAGATGAAATCGAGGACC	60.1	530	INTERGENIC				
CaPOPI_6520	scaffold1631	32889	TGGTTTAAAAA/T	GTCCACTTCCGTTTCGGTAA	GTCGCTTCAAAAGTTGGCTC	60.0	625	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_6521	scaffold1632	26463	AAGTAG/AAG	ACGTTTGTTCGACG GTT	ATCCAATCCACTTCTTC CG	60.5	554	DRR	Ca_26993			Domain of unknown function DUF239, plant
CaPOPI_6522	scaffold1635	74246	TCCC/TCCCC	GGTAACGTGTGTGCA TGG	GGAGTACCATAGGCCAA CGA	59.9	258	INTERGENIC				
CaPOPI_6523	scaffold1643	107792	TTATATATATATATATATATAT/TTATA TATATATATATATATAT	GGCGATTTTACATTATA CGTGAG	ACATATGGGTCAAACCC GTC	59.0	402	INTERGENIC				
CaPOPI_6524	scaffold1643	109664	CTATATATATATATATATATATATATA TATATATATAT/CTATATATATATATATAT ATATATATATATATATATATAT	TTATGCTTTGTGTCATG GGC	CCAACCCAAATTGAACA GGT	59.5	550	INTERGENIC				
CaPOPI_6525	scaffold1643	147473	AAATAATAATAATAATAATA/AAAT AATAATAATAATAATAATAA	ATGGTGGTGCAAACTCA ACA	CAAGCGTAGTGCAAGT GTGA	60.0	677	INTERGENIC				
CaPOPI_6526	scaffold1643	152357	GGGAAATAGAGGAA/GGGAAA	AGGAGGATGACTCAGTG ACCA	TTTGAATTCATCCCTGC AA	59.7	680	INTERGENIC				
CaPOPI_6527	scaffold1643	163768	AATATATATATATATATATATATATAT AATATATATATATATATATATATA	ATTTCCAGCATGCCAATT TC	CTTCCAGAACTAGCCG CAC	59.9	719	INTERGENIC				
CaPOPI_6528	scaffold1643	166873	CAAAAAAA/CAAAAAAA	GCAACTAGGGGTGTTC A GGA	ATGCACACTTGTGCAC CTT	60.1	610	INTERGENIC				
CaPOPI_6529	scaffold1643	167442	AC/A	GCCGTTTACAGTGCTTT TTCA	AAGCAGCGCGTTTTTAG AAG	60.3	123	INTERGENIC				
CaPOPI_6530	scaffold1643	169454	CAAAAAAAAA/CAAAAAAAAA	GTCATTTTGGCGTAGT GGG	TTTCCGGTCAACACTCA TCA	60.4	133	INTERGENIC				
CaPOPI_6531	scaffold1643	171022	TTTA/TTTAATTA	TAACCCCATCAAATTTG GGA	TCTTGAAGGAGCGGGTA GAA	60.0	563	INTERGENIC				
CaPOPI_6532	scaffold1643	180974	ATGATGAATCTTGATGAATCTTGATGAA T/ATGATGAATCTTGATGAAT	CCCACGCTTCTTTAGCA GTC	TTTCACTTCCCGCTTCT GT	60.0	859	INTERGENIC				
CaPOPI_6533	scaffold1643	192850	TATAAATA/TATA	GAGGGGGAGAAAGCTG AGAG	TGCTGACATGATTGTTG ATGTG	60.5	535	INTERGENIC				
CaPOPI_6534	scaffold1643	192933	CG/C	GAGGGGGAGAAAGCTG AGAG	TAGCATGCTGGAATTG CTG	60.5	604	INTERGENIC				
CaPOPI_6535	scaffold1643	204405	TCC/TC	TGCGAAATCGCAGTTGT TAC	ACAAATGGAGGGACGAT GAA	59.9	712	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6536	scaffold1643	207973	TAAA/TAAAA	CGAATATTGCTTTTCAAAACACC	GGCGAAAACAAGATTTCAT	59.9	327	INTERGENIC				
CaPOPI_6537	scaffold1643	210197	ATTTTT/ATTTTTTT	AATACAGCGAAAAAGCTCGC	TCGAAAAGAAATCGAGACCG	59.6	710	INTERGENIC				
CaPOPI_6538	scaffold1643	210540	ATTTTTTT/ATTTTTTTTT	CACACAATCACAAATTTTCTCAA	AAAGAAATCGAGACCGTTGC	59.1	419	INTERGENIC				
CaPOPI_6539	scaffold1643	211018	TGTA/T	TTCTCTCCACCGCTAACTCG	ATGGTGGGGGTATGAATGAA	60.5	611	INTERGENIC				
CaPOPI_6540	scaffold1643	211096	TTCT/TT	ACGGTCTCGATTTCTTTTCG	ATGGTGGGGGTATGAATGAA	59.3	585	INTERGENIC				
CaPOPI_6541	scaffold1643	213932	TAAAAAAA/TATAAAAAAAA	CGGATTTCGTCTCTTGAAGC	CATTGGTGCAGTTGTTGTC	60.0	662	INTERGENIC				
CaPOPI_6542	scaffold1651	5134	GAAAAAAA/GAAAAAAA	ATGGCACAGTCTCCCAACT	GGGGCCACTTAGGGTTGTAT	59.6	276	INTERGENIC				
CaPOPI_6543	scaffold1651	9845	TAAAAAAA/TAAAAAAA	AACGGAGGAAGAACATGTGG	TCACACAAGCATTCCCAAAA	60.0	364	DRR	Ca_27410			
CaPOPI_6544	scaffold1651	11557	GAAAAAAA/GAAAAAAA	TTCTAAGTTGGGGTGGTGG	ATCATGCTCCAAGGTTGCTT	59.8	426	INTERGENIC				
CaPOPI_6545	scaffold1651	12361	GTTTTTTT/GTTTTTTT	AAATTGTTGCTTGGGGAACA	TGACGTCATGACCTGCAATTT	60.3	882	INTERGENIC				
CaPOPI_6546	scaffold1651	13370	TATTAATTAATTAATT/TATTAATTAATTAATTAATT	CCTTGAGTTCGACACTCGGT	TGGTGACCGTGTAATTGTTG	60.3	337	INTERGENIC				
CaPOPI_6547	scaffold1651	13586	CAAAAA/CAAAAA	CCTTGAGTTCGACACTCGGT	CAGGATGTGAACCGTAATCTTC	60.3	547	INTERGENIC				
CaPOPI_6548	scaffold1651	14250	ATATTTAAGGTATTTAAGGTAT/ATATTTAAGGTAT	AAAAATGGAGAGATCGAAAGTG	TTGATGCTAGGGGGATTGTTG	57.5	553	INTERGENIC				
CaPOPI_6549	scaffold1651	16309	CATA/CATATA	TGCCAAGCATTGTTCTCAC	TCCCTTTTACATCCCTTCC	59.8	497	INTERGENIC				
CaPOPI_6550	scaffold1651	16500	CA/CAAA	GGGAAGGGATGTAAAGGGA	ACGTCGTGATTTGTGCTTCA	60.1	231	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6551	scaffold1651	16843	GACC/GACCACC	GGGAAGGGATGTAAAGGGA	AAATCTGGCCTGGACCTG	60.1	510	INTERGENIC				
CaPOPI_6552	scaffold1651	16898	TAAAA/TAAA	TAAGGCATGGTATGGGAAA	CTAAGCCTGAGTTTGGCCTG	60.1	921	INTERGENIC				
CaPOPI_6553	scaffold1651	17729	GATAT/GATATAT	TCTCTGGGTGATTTTGGG	ACACCCAAACTCTTGTTGGC	60.0	561	INTERGENIC				
CaPOPI_6554	scaffold1651	18006	A/AG	TGATTGGGGCATACTTTT	ACACCCAAACTCTTGTTGGC	60.0	171	INTERGENIC				
CaPOPI_6555	scaffold1651	18574	CA/C	CTGGATTGGAATTGTCA GCA	TCACGCACACTCCACTCTC	59.6	679	INTERGENIC				
CaPOPI_6556	scaffold1651	18823	AG/A	GAGAGATGGAGTGTGCGTGA	AACCCAGAACTCGAGCTGAA	60.0	461	INTERGENIC				
CaPOPI_6557	scaffold1651	22832	CA/CAAAA	GTCCAGCAAAAGTCGTGTGA	TTGAAGGCATTTCTCCATCC	59.9	675	INTERGENIC				
CaPOPI_6558	scaffold1659	96268	GTTT/GTTTT	TTGCTCACTACCACGCTACG	CACCAAGCACATCCATTCA	60.1	382	INTERGENIC				
CaPOPI_6559	scaffold1659	269627	AATATATATATATATATAT/AATATATATATATATATATATATAT	CACCGTAGTGTGGTGGTGAG	CGGTGAATCCTTTACGGAGA	60.1	531	INTERGENIC				
CaPOPI_6560	scaffold1661	70196	A/AGT	CAGCTTATGCGGAGACAGAGA	AACATGGACAACAACGACGA	59.2	303	INTRON	Ca_27588			
CaPOPI_6561	scaffold1661	91058	AATATATATATATATAT/AATATATATATATATATAT	GTTGGATCCCTAGCACCGTA	AAAAATGAAAAGGGGAGCGT	60.0	905	INTERGENIC				
CaPOPI_6562	scaffold1664	9660	GAAAAAAAAAAAAA/GAAAAAAAAAAAAA	TGGTCACCACGTGTCATTTT	ATGATTGCTTCGGATTACGG	59.9	584	INTERGENIC				
CaPOPI_6563	scaffold1664	59110	AAAAGAGAAAGAGAAAGAGAAAGAGA/AAAAGAGAAAGAGAAAGAGA	TTGTTTGGACCAACATTCCA	TGAATTGGGTCTGGTGAAATTT	59.8	294	INTERGENIC				
CaPOPI_6564	scaffold167	12696	AT/ATCAATATGTTTGT	TTTTTGTGTTGCCATTGGA	AGGGAGGACGAAAATGACCT	59.9	465	INTERGENIC				
CaPOPI_6565	scaffold167	29049	CTTT/CTT	TTACCGGCTATTTCATGCTC	TCCCTTAATTTTCTGCCCCT	60.1	508	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6566	scaffold167	342564	CATATATATATATA/CATATATATATA TATATA	GCGCAAATTGCCAGAT GAT	CGACATTGTAGCACCCC TTT	60.2	508	DRR	Ca_24157			
CaPOPI_6567	scaffold167	353330	A/AGTTCTCCCATC	CATGCAGTTTCAAATGG TGC	TGCTAAGTTGATGCAGC AGG	60.1	472	INTERGENIC				
CaPOPI_6568	scaffold1679	2481	CGGGTTTAGGGTTTAGGGTTAGGGTT /CGGGTTTAGGGTTTAGGGTT	TTACGGTTTTGCGTTTA GGG	AACCAAAATCCGACACC CTT	60.0	503	INTERGENIC				
CaPOPI_6569	scaffold1681	934	ATTTT/ATTTT	GAGATTTTCGTACCACC CGA	TCCAGATGAAATCGAGG ACC	59.9	797	INTERGENIC				
CaPOPI_6570	scaffold1682	8324	TTGTGT/TTGT	AGGTCGTTTTCGTCCTT CCT	CACCCAATGACACCAAT GAA	60.1	693	INTERGENIC				
CaPOPI_6571	scaffold1684	69381	TAA/TA	CGGGTTGTACAAAATC GCT	CAGCGATGGCTAGTGTT TGA	60.0	458	INTERGENIC				
CaPOPI_6572	scaffold1687	165898	ATAGTA/ATA	TACCCACACTCATGCTC CAA	GGTTGTAGAGAAAACAT CCAGACA	60.1	428	INTERGENIC				
CaPOPI_6573	scaffold1696	4415	ATTTTTTTTT/ATTTTTTTTT	ATAACCCGAACCTCAAA CCC	TGTTTGAAATATGACGC CGA	60.1	645	INTERGENIC				
CaPOPI_6574	scaffold1696	5390	TGTTTCGGGTTTCGGGTTTCG/TGTTTC GGGTTTCG	TTGAAGTACGAAAATCG CCC	TTCGTTATCGGTCAAA CCT	60.1	813	INTERGENIC				
CaPOPI_6575	scaffold1701	101096	TT/TTCT	AGGTCATTTTCGTCCTC CCT	GCCCTCAGATGAGAGTC AGG	59.9	515	INTERGENIC				
CaPOPI_6576	scaffold1703	131019	TGAAGAAGAAGAAGAAGAAG/TGA AGAAGAAGAAGAAGAAGAAG	CCAAAACGATTTCCCTT CAA	TTTCCAAAAGTGACCGA ACC	59.9	234	INTERGENIC				
CaPOPI_6577	scaffold1703	243731	TTATATATATATATATATA/TTATATAT ATATATATATATA	GAGAAAGGAGGGAATTT GGC	TATTTTGGATTTTGCTC GG	60.0	296	INTERGENIC				
CaPOPI_6578	scaffold1704	9054	ATTTTTTT/ATTTTTTT	TGTGACATCTCTGCCTC CTG	AACATCAGTCAAGCACA CAAAAA	60.0	356	INTERGENIC				
CaPOPI_6579	scaffold1704	11771	AATATA/AATATATA	AACGATCAAGAGTCGCA AAA	ACCCTAAACCCTAAAGC CCA	58.5	347	INTERGENIC				
CaPOPI_6580	scaffold1708	11531	AATATAATTTATT/AATATAATTTATTATA TAATTTATT	TCACCTTCTTCGTTGTTT GC	GCGCATAAGTCACAAGT CCA	58.9	734	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6581	scaffold1708	11960	ATTTTT/ATTTTTTT	TGAGTTGCTTGTCAGCC TTG	TGGTACAACCACAAATA GGTAAGG	60.2	444	INTERGENIC				
CaPOPI_6582	scaffold1708	14932	GTTT/GT	GCCATTGGGTGTTGA TAG	CTGCTTGAGGACAAGCA ACA	60.2	901	INTERGENIC				
CaPOPI_6583	scaffold1708	40978	ATTTTTTTTT/ATTTTTTTTT	GACACCCTAACGCCAA AAA	GCGTTTGCGAAATCGTA GTT	60.0	395	INTERGENIC				
CaPOPI_6584	scaffold1708	49501	AATATATATATATA/AATATATATATA	TTCCAACAATGACGATC TGC	TTTGAACGAAATTGAAAA CCG	59.7	659	INTERGENIC				
CaPOPI_6585	scaffold1708	68435	TCC/TCCC	GAAAAAGCGCTGTAAT GGC	CATTGAGACGTGAGCA AAA	59.9	510	DRR	Ca_27642			RNA polymerase Rpb1, domain 5
CaPOPI_6586	scaffold1708	87295	AG/A	TGACTGTTGCGTGTC TCC	ATCCCATGGTGGGAATT GTA	59.9	336	INTERGENIC				
CaPOPI_6587	scaffold1708	88337	AATATATATATATA/AATATATATATAT ATA	TTTGCCACTGACTTGCT TTG	GAGAAAGGAGGGAATTT GGC	60.0	567	INTERGENIC				
CaPOPI_6588	scaffold1708	88410	GAAGGAAAAGGAAAAGGAAAAG/GAAG GAAAAGGAAAAGGAAAAGGAAAAG	TTTGCCACTGACTTGCT TTG	GAGAAAGGAGGGAATTT GGC	60.0	567	INTERGENIC				
CaPOPI_6589	scaffold171	130237	GAA/GAAAA	CATGCGTGTCTAGGCAT TTG	TGAATTCATGCCAGCA TAA	60.3	341	INTERGENIC				
CaPOPI_6590	scaffold171	150122	CAATAATAATAATAAT/CAATAATAA TAATAAT	CGAGTTGAGGTTCTTTC GGT	GGCACAGTGGGATATTG CTT	59.3	770	INTERGENIC				
CaPOPI_6591	scaffold171	190541	GAA/GAAA	CTCTGATCAGCTCCATT CCC	CTAGGGCTCCTCCTTCG ACT	59.8	160	CDS (FRAME SHIFT)	Ca_25949			Transposase, PttA/En/Spm, plant
CaPOPI_6592	scaffold171	224792	TAAA/TAAAA	AAAAATCGATCCCCTATC ACAT	TAGCAGCTGGAGGAACA TGA	57.4	348	INTERGENIC				
CaPOPI_6593	scaffold1710	13152	CATTATTATTATTATTATTATTATTAT TTATT/CATTATTATTATTATTATTAT TATTATTATTATTATT	GGTCGCATCCTTGTA CT GTG	AACAACCTCCTCGGATT GG	59.2	540	INTERGENIC				
CaPOPI_6594	scaffold1710	43434	AT/ATT	TCGCTTTTGTGTTGAG CAG	ATGGCTCTCTCCCGGT AAT	60.2	813	INTRON	Ca_25722			
CaPOPI_6595	scaffold1710	177159	AAGAGAGAGAGAGAGAGAGAGAGAGA GAGAG/AAGAGAGAGAGAGAGAGAGA GAGAGAGAG	TCCAAACAGCTTCTAAC CGC	GCCGTCGTTTCAACCAC TAT	60.4	271	INTRON	Ca_25728	O		Abortive infection protein

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CaPOPI_6596	scaffold1722	65936	A/AT	CGTAGCGATAAAACCTGGGA	CGGGCCAGAACTACTTACAGC	60.1	802	INTRON	Ca_26630	G		Ribulose-phosphate 3-epimerase
CaPOPI_6597	scaffold1722	132942	TGG/TG	ATGGTGGATACTTGGGTGGA	CCCTGTAAGAAACGTGCAT	60.1	206	INTERGENIC				
CaPOPI_6598	scaffold1723	1064	ACTCTC/ACTC	CCTCATAGGTCGACTGGGA	GCGCCCTCACATAATGTTT	60.1	467	INTERGENIC				
CaPOPI_6599	scaffold1725	28680	TTT/TTTATT	GATTCACTGGCCGATTTGT	TTGGACGAAAAAGGAGGAAA	59.9	917	INTERGENIC				
CaPOPI_6600	scaffold1730	64331	ACATATGATTTTTCATAT/ACATAT	TTGGATGTTTTCGCTTACCA	CAAGTTAGTGGTGAACCGGG	59.2	882	INTERGENIC				
CaPOPI_6601	scaffold1730	87897	T/TTA	TTGAGGCGTCAAGCTAATGA	CGAGCAACCCCAAACTTAGA	59.6	707	INTERGENIC				
CaPOPI_6602	scaffold1730	100035	TAAAAAAAAA/TAAAAAAAAA	ACGGGACGGCTATCAATGATG	GGCGTAATTGCATTCAT	60.0	612	INTERGENIC				
CaPOPI_6603	scaffold1731	39857	AATATATATATATATATAT/AAATATATATATATATAT	ATGTTTTGGATTTTGGCTCG	GCACCGTGAGTAAATTCGGT	59.9	704	INTERGENIC				
CaPOPI_6604	scaffold1731	49034	CATATATATATATATATATA/CATATATATATATATATA	ATGGGAAGCAACAACGATTTC	CCGTACCGTTTCTGGGATAA	59.9	784	DRR	Ca_27041	IR		ABC transporter-like
CaPOPI_6605	scaffold1731	53952	AATATATATATATAT/AAATATATATATATATAT	TTTGGATATTGGTTCGGAGG	AGGAGGTTTGTGTTGACGG	59.8	514	INTERGENIC				
CaPOPI_6606	scaffold1731	65474	TTTATTATTATTATTATT/TTTATTATTATTATTATTATTAT	TAATCGGGGACTCAACATCC	CCCTTTGGATGCGAAATAAA	59.8	279	INTERGENIC				
CaPOPI_6607	scaffold1731	85329	CATATATATATATATATA/CATATATATATATATATATA	TCTCCGCATAAGCTTTCGAT	GCTTCGACACTGTAGCACCTC	59.9	478	DRR	Ca_27043			
CaPOPI_6608	scaffold1731	86422	AATATATATATATATATAT/AAATATATATATATATATATAT	TTTTGGGAATTCCTGCTCTG	GTGACACCCTAAACCCAAA	60.2	299	DRR	Ca_27043			
CaPOPI_6609	scaffold1736	8297	TG/T	GTGAGATGAACGGGAATGCT	ACAACGAGGGGTGAGTATCG	60.1	935	INTERGENIC				
CaPOPI_6610	scaffold1736	8593	GTA/GTATA	TGGCATAGTATCAGGCCATCC	ACAACGAGGGGTGAGTATCG	60.1	237	INTERGENIC				

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CaPOPI_6611	scaffold1736	21426	GTTTTTTTTT/GTTTTTTTTT	CTTTTGCAGGGTGTGGTTT	TCTCGAGGCATCACATT CAG	60.0	790	INTERGENIC				
CaPOPI_6612	scaffold174	19539	GAAAAAAAAA/GAAAAAAAAA	CGATGATGGTTGAAGTGTG	GGGTGGCTGTGAACTTT TGT	60.0	225	INTERGENIC				
CaPOPI_6613	scaffold174	82773	AAGAG/AAG	AACCGTCAAGGGTGTGA AAG	ACTCTTGTTGAAGCATG GGG	60.0	506	INTRON	Ca_21709			PDZ/DHR/GLGF
CaPOPI_6614	scaffold174	111558	TAAA/TAAA	CCAATCAACATCATTCA TGC	ATTGGTGGTTGCCTAAG TGG	58.8	556	INTERGENIC				
CaPOPI_6615	scaffold174	111791	TGGGG/TGGG	CCGGATATAACCGCCA CAC	ATTGGTGGTTGCCTAAG TGG	60.2	289	INTERGENIC				
CaPOPI_6616	scaffold174	136798	TG/T	GAAGGTAGACGTTGGG GACA	CTGTGGACGACCTTTTG GAT	60.0	585	INTERGENIC				
CaPOPI_6617	scaffold174	140361	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	CGGGTGAATGTGGCTTT ATT	TTTCTGTTTTGGACCC CTG	59.8	395	INTERGENIC				
CaPOPI_6618	scaffold174	159321	ATTTTTTT/ATTTTTTTTT	CTAACGAGTCTGCAACG CAA	TGAAAGGTAATAATCGG TGCG	60.2	319	INTERGENIC				
CaPOPI_6619	scaffold174	169758	CG/C	GTCAATCACAAGGAAGG GGA	TCGAAAGTTGGTGTGAA AAGC	59.9	326	INTERGENIC				
CaPOPI_6620	scaffold174	192838	GATA/GATAAAACATCTTTTCATA	GCGCCGTTTATATAGCC AGT	AAATCCACACTAACATTG AAAACTT	59.3	355	INTERGENIC				
CaPOPI_6621	scaffold174	206548	GCTCTCTCTCT/GCTCTCTCT	ACCAAAGCAAAGCTCC TCA	TTATTCACGAGGTCCTT GGC	60.0	455	INTERGENIC				
CaPOPI_6622	scaffold174	225469	CAAAAAA/CAAAAAA	GTGATTTGCACCTTCAAG CGA	CCGAGGATGATGGTCAA TTT	60.0	653	INTERGENIC				
CaPOPI_6623	scaffold174	279541	ATTTTTTT/ATTTTTTT	AATGTAGCAGCAAACCA CCC	TTGATGCATTGTCTTCTC GC	60.0	602	INTERGENIC				
CaPOPI_6624	scaffold174	327909	ATTTTTTTTT/ATTTTTTTTT	TGGCAACCACAAGGAGT GTA	TCAAAAGGGAAAAACAAT TGACA	60.2	661	INTERGENIC				
CaPOPI_6625	scaffold174	351626	GAAAAAAAAA/GAAAAAAAAA	CCTCGATCACTTCGTCT ACCA	AGAGCAAGGCCTCACAA AAA	60.3	478	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_6626	scaffold174	359071	GAAAAAAAAA/GAAAAAAAAA	TCTGTCAATTGAGCTGC GAC	CGTCCATGAAAAGAGGG AAA	60.1	446	INTERGENIC				
CaPOPI_6627	scaffold174	373713	TAAAAAAAAA/TAAAAAAAAA	AGTTGATTCGCTCATGG GTT	TCCACAAAGCACACATA CATCA	59.6	307	INTERGENIC				
CaPOPI_6628	scaffold174	376719	ATTTTTTTTT/ATTTTTTTTT	TCGAGTCCCAACACATG GTA	GCAGAGGTCATGGGATT CAT	60.0	503	INTERGENIC				
CaPOPI_6629	scaffold174	490723	ATTTTT/ATTTTT	GCCGTTGCCTTATTTTG TGT	TTTTTCTTCAGCTTGATG TTGAT	60.0	574	INTERGENIC				
CaPOPI_6630	scaffold1740	2698	TAA/TA	CGATTTGGCCATACAGG AAT	CCCATCTACATACCCAT CCG	59.8	498	INTERGENIC				
CaPOPI_6631	scaffold1750	124578	A/AGTGCGAAAT	TTACGATCACCAGCCAT GAA	TCCAAAGAGACCACTCT TCTCA	60.1	730	INTERGENIC				
CaPOPI_6632	scaffold1756	5242	CGGT/A/C	GGTGAGGCTTTTGCCT CAA	TTGGATGAAGGCCATAA AGG	60.2	665	INTERGENIC				
CaPOPI_6633	scaffold1756	43727	CATATATATATATATATATATAT/C ATATATATATATATATATATATATA TATAT	GTTGGTTCCTAGCACCC GTA	GGCTGTTAGCCCAGTTT TTG	60.0	658	INTERGENIC				
CaPOPI_6634	scaffold1757	1167	CTT/CTTATT	AAGCGTACCTGTGGGAA TTG	TTAATGAGGGGCTGAAT TGG	60.0	259	INTERGENIC				
CaPOPI_6635	scaffold1757	47237	ATTTTTTTTT/ATTTTTTTTT	ATGCTACTGGACAACCC GAC	TGTCAGCTTAAATGTATT TTTGTTTT	60.0	594	INTERGENIC				
CaPOPI_6636	scaffold1761	69178	CTT/CTTAGTT	GAGATTGGCGTGGTTT TGT	GAGGGAAAAGCCAGAT TTC	60.0	951	INTERGENIC				
CaPOPI_6637	scaffold1768	12788	T/TC	GGTCCTCGATTTCATCT GGA	GTACGAAAATCGCCCAA AAA	60.0	320	INTERGENIC				
CaPOPI_6638	scaffold1777	47085	T/TAAAACTTG	CTCAACAGGGGCAACTC ATT	AGAGGCGAAACAAAGTG CAT	60.1	698	INTERGENIC				
CaPOPI_6639	scaffold1777	282839	CCAGATGCA/CCA	TGCATCAGTATCTGCCT TCG	TTCTTTCAAGAGGTCGC AGC	60.0	329	DRR	Ca_23266	L	ERF	SNF2-related
CaPOPI_6640	scaffold1777	347891	ATTTTT/ATTTTT	CCCAAACTCACGGGAT AAA	ATTTGGGCCCATCATAA ACA	59.8	729	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6641	scaffold1777	513940	C/CT	ATGCTGTCTTGTGCTGG ATG	CGCTTTTATTTTCAATTG CTG	59.9	205	DRR	Ca_23271	BK	MYB_related	SET domain
CaPOPI_6642	scaffold1778	1269	C/CG	ACTTCCGCGCTAGATT CAA	TCCTGGTCCTCGATTTC ATC	60.0	282	INTERGENIC				
CaPOPI_6643	scaffold1779	131414	CAAAAAAAAA/CAAAAAAAAA	TTGTTTCTCCCAGTTTT GG	TTCCATATCACACGGAA CCA	59.9	275	INTERGENIC				
CaPOPI_6644	scaffold1779	131497	ATTTTTTT/ATTTTTTT	TTGTTTCTCCCAGTTTT GG	TTCCATATCACACGGAA CCA	59.9	275	INTERGENIC				
CaPOPI_6645	scaffold1779	132071	ATTGTGTGTTGTT/AT	ATGGAAAAGTGCTGCAA AAA	TTTCGCCCTCAATTCAA AC	58.4	688	INTERGENIC				
CaPOPI_6646	scaffold178	605	AACACAC/AACAC	CAATAGGCCAAGGAAGG ACA	ACATTGAGGCCATTTTC GTC	60.1	236	INTERGENIC				
CaPOPI_6647	scaffold1802	20448	CG/C	ATTTTCTCCGTTCCGAT TT	AAGGAAGCGCACTAGCA GAG	60.0	816	INTERGENIC				
CaPOPI_6648	scaffold1810	98576	GGTTGT/GGTTGTGT	TGACGATACGAAACGAT GGA	AGCGATGCATGTCTCAA GTG	60.1	430	URR	Ca_26004			
CaPOPI_6649	scaffold1810	103255	GC/GCC	TTGCTAGTTGCTGATGT GGC	GGTGTCACTCGGAGTCT GTT	60.0	300	INTERGENIC				
CaPOPI_6650	scaffold1810	103852	GAAAA/GAAAAA	AACAGACTCCCGATGAC ACC	AACATTTATGACGATATT TATGAGTGA	60.0	438	INTERGENIC				
CaPOPI_6651	scaffold1815	5752	A/ATAC	TGTCCATCACAGGCTAC ATGA	TGTGGGCAAAATCTTGT GGT	60.1	434	INTERGENIC				
CaPOPI_6652	scaffold1816	53607	ATATATAATTTATATAATTTATATAATTT/ ATATATAATTTATATAATTT	TGGTGAGGAAATGAGCA ACA	ACAAATGAAGGTGCGG AAG	60.2	679	INTERGENIC				
CaPOPI_6653	scaffold1822	17416	GTT/GTTT	AAGACCAATTACCGAG GTG	TTGTATTTGGCGTGTCC GTA	60.0	720	INTERGENIC				
CaPOPI_6654	scaffold1825	148166	ATTTTTTTTT/ATTTTTTTTT	GTTTTGGCGTTGGTTTC ACT	TACGTGTATATTCGCGC ACC	60.0	904	INTERGENIC				
CaPOPI_6655	scaffold1830	4465	CTATA/CTA	CCAAGGGAAGACGAAAA TGA	TGCATCCAACAGGTGTG TTT	60.0	665	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6656	scaffold1835	8173	CAA/CA	TCATTGCTCCTTTGAGTTGC	ATTTGCCACAGATACCGCTC	59.0	453	INTERGENIC				
CaPOPI_6657	scaffold1835	8463	TAAAAAAAA/TAAAAAAAAA	GAGCGGTATCTGTGGCA AAT	CGGTTTGTGGCTTTCCT AAA	60.1	486	INTERGENIC				
CaPOPI_6658	scaffold1835	10086	GCC/GCCC	TGGTTAACCTTGACCA CAA	GGATGCTTGAATTATGC CGT	60.0	672	INTERGENIC				
CaPOPI_6659	scaffold1835	11243	GAACAACAAC/GAACAAC	AAACGCATCCCGTAAAT CAG	CGATTGCCCTAGAAAAT GGA	60.0	610	INTERGENIC				
CaPOPI_6660	scaffold1844	2095	AAA/AAAATAA	AACATGGGACGAGCTGT TTC	GGGATATTCAATAAGTG AAATTCAA	60.1	923	INTERGENIC				
CaPOPI_6661	scaffold1844	2214	T/TC	TGCAATTATGATCATGCT TTATATG	GGGATATTCAATAAGTG AAATTCAA	58.2	732	INTERGENIC				
CaPOPI_6662	scaffold1844	2526	CA/CAA	GACCTTTGAATTTATCTC TCTTTGAA	TTACAACATGTCAGGCC GAA	58.5	373	INTERGENIC				
CaPOPI_6663	scaffold1844	40976	TAAAA/TAAAA	CACTCGCATTTCATAG TTCA	ATTTGGTGTCTTTGTGG AGG	59.9	578	DRR	Ca_24135			Epsin domain, N-terminal
CaPOPI_6664	scaffold1844	101225	CTTTTTTTTT/CTTTTTTTTTTT	CCTTCGCGAACTCACT GAT	TTGGAATTTCTTCGCAG CTT	60.4	116	INTERGENIC				
CaPOPI_6665	scaffold1844	123387	GTT/GTTT	TCGCGTAGTGGTAGCCT TCT	TCACAAGGGAGGCTCTA TGG	60.0	181	INTERGENIC				
CaPOPI_6666	scaffold1844	136314	CTTTTTTT/CTTTTTTTTTTT	CCACCATTGAATCAAGT CCA	GACTCCATACAGGGCCG TC	59.3	354	INTERGENIC				
CaPOPI_6667	scaffold1844	146939	TT/TTAGACTTGT	CAATCAAAATTGGTCTA GCCG	TCAAAATGGGCCAGTGT TTT	59.6	274	INTERGENIC				
CaPOPI_6668	scaffold1844	155952	GAAAAAAAA/GAAAAAAAA	TCAATCGGTTCTCTCA CAA	TTAAATGCGTTCGACAG ATCA	59.2	857	DRR	Ca_24144		MYB_rela ted	Glycoside hydrolase, family 16
CaPOPI_6669	scaffold1844	165772	TATATCTC/TATATCTCTTAATATCTC	CCCCCTCTTAGCGTAC TTC	CTTGTTGCGGTACCTCG TGT	60.1	340	INTERGENIC				
CaPOPI_6670	scaffold1844	166678	TC/T	GGCTAGACGAGTTCGAC GAC	CTAGATGGTCGCATTCT GGG	60.0	418	DRR	Ca_24145			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6671	scaffold1844	167253	CAAAAA/CAAAA	CCCCAATTTGCGATCAATAA	TCAAAACTAAGAACTCGCCAA	60.6	694	DRR	Ca_24145			
CaPOPI_6672	scaffold1844	167398	GTATATAT/GTATATATAT	CCCCAATTTGCGATCAATAA	TCAAAACTAAGAACTCGCCAA	60.6	694	DRR	Ca_24145			
CaPOPI_6673	scaffold1845	47422	GA/G	GACCCAACGATTTGCGTA	TTAGGTTAGCATGGCCAAAC	59.8	505	INTERGENIC				
CaPOPI_6674	scaffold1845	71268	AATGTA/AA	CAAAGCGATGATCGAACAATAA	TGGATTAAAAGTTCGGGTCG	59.8	285	INTERGENIC				
CaPOPI_6675	scaffold1852	76175	ATTTTTTT/ATTTTTTTTT	GGTTGGTCTTCCAACGCTAA	GGTGTGTTTGTACAACTTTTGG	60.1	358	INTERGENIC				
CaPOPI_6676	scaffold1852	94390	AT/ATGCTCAACCATT	GGTCCAACATCGACGCTAAT	CGAGCACAATCCATGGTATC	60.0	234	INTERGENIC				
CaPOPI_6677	scaffold1852	94526	ATTTTT/ATTTTT	GGTCCAACATCGACGCTAAT	TCGGATGTTACACACCTCACA	60.0	515	INTERGENIC				
CaPOPI_6678	scaffold1852	94771	GGTGTGT/GGTGT	GGTCCAACATCGACGCTAAT	TTTCAGTCATTGATTTCGGA	60.0	531	INTERGENIC				
CaPOPI_6679	scaffold1852	94935	ATTGTT/ATT	TACCATGGAGTGTGCTCGAA	TTTCAGAACACAATCTGCATGT	60.3	765	INTERGENIC				
CaPOPI_6680	scaffold1852	103209	ATTTTTTTTT/ATTTTTTTTTTTTT	TTGAGGACCAATGAGTGTCTG	GTAAATTCGGGGTCGAGGT	59.7	553	INTERGENIC				
CaPOPI_6681	scaffold1864	5989	ATAGT/AT	TTGCCCATTTCTCCAAGTTTC	CGGATATAAGCATGGCAATCA	60.1	659	INTERGENIC				
CaPOPI_6682	scaffold1864	14836	TAAAAAA/TAAAAAA	CGCTCTGTTAAGTCGGTTCA	CATCCACGGAGCAAAAATT	59.1	251	INTERGENIC				
CaPOPI_6683	scaffold1866	62792	AAATAAA/AAATAAATAGAATAAA	TTGCTCCTACGTATCTCCG	TTAAGTTGGTTTGGGCTTGG	60.2	855	INTRON	Ca_26041	R		Uncharacterised protein family, ATP binding
CaPOPI_6684	scaffold1866	113475	AAATTATTTTACAATTATTT/AAATTATTT	TTAAACAGACCTCGCCACC	GAGGAGAAGTCCACGTACAGC	60.1	595	INTERGENIC				
CaPOPI_6685	scaffold1866	116123	GAA/GAAA	TTCCACTTATGGTGAGTAATGATG	GCGAGCATGAGAAGTTGTTG	58.1	632	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6686	scaffold1867	226694	ATTT/ATTTT	ATCGATTTTGTCCGTTTGC	GGAGGGTTTTGGTTGGAAT	59.9	473	INTERGENIC				
CaPOPI_6687	scaffold1867	228749	CGGGG/CGGGGG	TTGGAAGGAGCCCTTACCTT	TTCCCAACTCCTTCCTCCTT	60.1	255	INTERGENIC				
CaPOPI_6688	scaffold1869	19075	AG/A	CTCGATTTTCATCTGGCCATT	CGAAAGTCGCTCCAAAAGTC	60.0	524	INTERGENIC				
CaPOPI_6689	scaffold1869	20055	CAA/CAAA	TTTCAGGCGATTTTCGTACC	ATTGTGTTTCGGGTTTCGAG	60.1	825	INTERGENIC				
CaPOPI_6690	scaffold1870	21211	TAAAA/TAAA	ATGGACTGAAATCGAGTGGC	CATATACAAAAATTGAGTTGCAAAA	60.1	333	INTERGENIC				
CaPOPI_6691	scaffold1878	7439	T/TTA	TGGCCTTCGATCTTTGAAGT	CATTGGTTTGACCAACCTTGT	59.8	693	INTERGENIC				
CaPOPI_6692	scaffold1878	40480	CTCA/CTCAAGGATTTTGATTCA	GCTTGGAACAGCCTCAGAC	ACATTCAAGCGCAGGTCCT	60.0	612	INTERGENIC				
CaPOPI_6693	scaffold1878	45211	TAAAAAAAA/TAAAAAAAAA	GCCCTCAGATGAGAGTCAGG	GGAGGGTAGGCTTATTTGGC	59.9	780	INTERGENIC				
CaPOPI_6694	scaffold1878	56174	TCTTCAAATC/TCTTCAAATCTACTTCAAATC	CCTTGACCCTACAAGCCAAG	TCATACCTGGCTGATGTGTG	59.7	896	INTERGENIC				
CaPOPI_6695	scaffold1878	73171	ATTTTTTT/ATTTTTTTT	GGTTGGGTCCTGGTTTGTTA	CCTCTGGATCCAACACAGGT	59.7	626	INTERGENIC				
CaPOPI_6696	scaffold1878	77007	TAAAAAAAAA/TAAAAAAAAA	TTGCGAGAGCGGTCTTAAT	CCTCAAGATCTCGTGTGCAA	60.0	358	INTERGENIC				
CaPOPI_6697	scaffold1885	40622	TAACC/T	CCATTGTGGTCGTTTAGGCT	CCCAATGACATCAAAAGCCC	60.0	572	INTERGENIC				
CaPOPI_6698	scaffold1885	47510	A/AG	GTAGCTTCGGCTACACCGAC	ATTCGGTTGTGCACTTGATG	59.9	664	INTERGENIC				
CaPOPI_6699	scaffold1886	17788	TTAT/TT	GAGAGAGGCATTGCACAACA	CGAAATTTCTTTAACGAGGGG	60.0	537	INTERGENIC				
CaPOPI_6700	scaffold1886	17993	TA/TAA	GAGAGAGGCATTGCACAACA	CGAAATTTCTTTAACGAGGGG	60.0	537	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6701	scaffold1899	8615	TTTATTATTATTATTA/TTTATTATTATTA	CCCCACTCCCCGTACTT ATT	TGGTGGATGTGAACGAC ACT	60.1	484	INTERGENIC				
CaPOPI_6702	scaffold1905	1617	CTG/CTCTGATG	ACTGATGTCAAGAGGGC CAG	AGAGGGTGGCAATGGTA ATG	60.3	251	INTERGENIC				
CaPOPI_6703	scaffold1911	12969	CAGAAGA/CAGA	GTGCCAGTCGATTGCCT AAT	TGCAATTCAAGCTCACTT GG	60.1	993	INTERGENIC				
CaPOPI_6704	scaffold1918	17379	TAAAAAAA/TAAAAAAA	GCGGATGCTATTTAACC GAG	TAATCGGTTGCACCGAA AAG	59.7	107	INTERGENIC				
CaPOPI_6705	scaffold1918	23098	GATATAT/GAT	TGTTGTTCAAAATGGGC TTG	GCAGCCAACAAAAGAAC AGA	59.6	712	INTERGENIC				
CaPOPI_6706	scaffold1918	31828	GTTT/GTT	TTCACTTGCTTTTTTCGG GG	TGTGCGTATTGGTGCGT ATT	60.1	584	INTERGENIC				
CaPOPI_6707	scaffold1918	78141	AGCGCGCGCGC/AGCGCGCGCGCGC	TATTTGCGCCACATCGT TTA	TCACGGTTGTGTGAGAT GCT	60.1	482	INTERGENIC				
CaPOPI_6708	scaffold1918	187805	TAAAAAAA/TAAAAAAA	GTTTCGAGTTTCTCCGTC TGC	AAAAGTTGAGTGTGGGG ACG	60.0	309	INTERGENIC				
CaPOPI_6709	scaffold1918	244709	TCACATACA/TCA	GCATGATTGGTCGATGT GAG	CAAAGGAAAGTGGCAGG AAA	60.1	498	INTERGENIC				
CaPOPI_6710	scaffold1923	10722	ATTTTTTTTT/ATTTTTTTTT	GGCCCCCAATATTTTGG TAA	ATTATTGGCCCCAACTC ACA	60.7	383	INTERGENIC				
CaPOPI_6711	scaffold1928	13480	ATATATATATGTATATAT/ATATATAT	ACCAGGGAGGAAGGAAA TGT	TTGAGTTGCAACGAGAG TGG	59.8	307	INTERGENIC				
CaPOPI_6712	scaffold1928	14034	TCC/TC	GGGTTCCAAATCACCTT GAA	CTTATCGGATTGCATTG CCT	59.8	222	INTERGENIC				
CaPOPI_6713	scaffold193	64250	GTT/GT	AACCAACACCAATTCA GCC	TGCAAGGGTGTGTTTCA TGT	59.8	628	INTERGENIC				
CaPOPI_6714	scaffold193	79630	TAAAAAAA/TAAAAAAA	AAAATAATGCGCCGTA TGC	AGATCATGTGCAAAAAG GGG	60.0	477	INTERGENIC				
CaPOPI_6715	scaffold193	79687	TAATAA/TAATAATAAAATAA	AAAATAATGCGCCGTA TGC	AGATCATGTGCAAAAAG GGG	60.0	477	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6731	scaffold1946	1221	TTATATATATATATAT/TTATATATATATATATATAT	ACATTAAATTTCGGGGGAGG	CACACTCTCACCCGGCTAAT	60.0	388	INTERGENIC				
CaPOPI_6732	scaffold1946	40975	TGAAAATTTAAG/TGAAAATTTAAGAAAA TTTAAG	AATATACGGTTGTCGCAAGGC	GCGGAGAATTCAAATTGGTTG	60.0	582	INTERGENIC				
CaPOPI_6733	scaffold1954	1371	TA/TAGTAA	TCCTATATTCGCCCCAC TTG	GTGGCATGGGAGTCTGT TTT	59.9	433	INTERGENIC				
CaPOPI_6734	scaffold1956	63720	GTAAACCATAAAACCATAAAACCATAA AACCATAAAC/GTAAACCATAAAACC ATAAAACCATAAAAC	TTCGTTATGCAGTCAAAT TTCTAA	TCTGACGAAGAACCCGA AAC	58.1	667	INTERGENIC				
CaPOPI_6735	scaffold1956	63893	ATATTATTATTATTATTATTATT/ATA TTATTATTATTATTATTATTATTATT	TTCGTTATGCAGTCAAAT TTCTAA	AAAATGGACCAACGTCC GTA	58.1	719	INTERGENIC				
CaPOPI_6736	scaffold1956	85954	GGTTTAG/GGTTTAGGGTTTAGTGT TTAG	TAGGCGATTTTCGTACCA ACC	ATAACCCGAACCTCAAA CCC	60.0	282	INTERGENIC				
CaPOPI_6737	scaffold1959	47247	GC/GCC	TCCTCCTCAAGTTGGAG CAT	ATATTGCATTGCAGTGG TGG	59.8	458	DRR	Ca_26462	K	G2-like	Signal transduction response regulator, receiver domain
CaPOPI_6738	scaffold1959	67541	GT/G	CCTACGGATGACCTCTC TCG	TAACGGTGAGTTGACGA CGA	59.8	400	INTERGENIC				
CaPOPI_6739	scaffold1959	95637	CAAAAAAAAA/CAAAAAAAAAAAAA	AAATCCAACAATGTCC CGA	CGGATCAAATTAGTGCC GTT	60.2	354	DRR	Ca_26466			
CaPOPI_6740	scaffold1962	124223	T/TATTATTATA	TTATCACGATTTTGGTG GCA	TCCCCCAAACCAAAATAT CA	59.9	498	INTERGENIC				
CaPOPI_6741	scaffold1962	159146	AAATATAAGCAGAAAATTAA/AAATATAA GCAGAAAATTAATATAAGCAGAAAATTA A	CTTTTTACAGCGCTTGT GGG	AAGCCGTGTAATCTGAA CCG	60.8	557	INTERGENIC				
CaPOPI_6742	scaffold1962	170714	GTTTTTTTT/GTTTTTTTT	TCAAGGACCCAAAGCAC ATT	TACTCCCCCTTTGAGCT TGA	60.5	423	INTERGENIC				
CaPOPI_6743	scaffold1964	11011	A/ACTC	ATGTTCTCGCCAATCA TTC	TTCCAAAAGAGGAATGG TGC	59.9	771	DRR	Ca_25209	G		Histidine phosphatase superfamily, clade-1
CaPOPI_6744	scaffold1964	11658	AACACA/AACA	GCACCATTCCTCTTTTG GAA	GATGGACCACCTTCTCT CCA	60.1	553	CDS (FRAME SHIFT)	Ca_25209	G		Histidine phosphatase superfamily, clade-1
CaPOPI_6745	scaffold1964	11803	TAGAATTATGCAG/TAGAATTATGCAGA ATTATGCAG	GCACCATTCCTCTTTTG GAA	GATGGACCACCTTCTCT CCA	60.1	553	CDS (FRAME SHIFT)	Ca_25209	G		Histidine phosphatase superfamily, clade-1

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CaPOPI_6746	scaffold1964	20327	TTTCTT/TTT	TGTTGTTTCCAACCACT CCA	TTGGATCGAAATTTGGG TGT	60.0	861	INTERGENIC				
CaPOPI_6747	scaffold1964	21448	CAAAATAAAATAA/CAAAATAA	GGGTCAGTTCATCCCAT GAC	TATGCATCTTTGTTGAC GCC	60.2	292	INTERGENIC				
CaPOPI_6748	scaffold1964	172119	ATTGG/A	TTGTTTTGTTAGAAACG CG	ACCCACATAGCGCAAGA TTC	58.9	313	INTERGENIC				
CaPOPI_6749	scaffold198	70179	ATTTTTTTTTTT/ATTTTTTTTTT	TCAAAATCCCCCAATAAC CA	GCTGTGAGTTCCTCAAC AAT	60.0	302	INTERGENIC				
CaPOPI_6750	scaffold198	267630	A/AG	TCCTAGAACATGCATCA CGC	AGCCACATCCAAGCAA AAC	59.8	473	DRR	Ca_20909			
CaPOPI_6751	scaffold198	274491	ATTTTTTTTTTT/ATTTTTTTTTT	TGGATTGTTATCCCTT TTT	TGTGTGTTTCGTTCAAC GGT	59.2	293	INTERGENIC				
CaPOPI_6752	scaffold198	501505	CA/CAA	TTGGCCAAGTCCCTGTT TAC	CGTTCCTGAGGGAATTG TGT	60.0	498	INTERGENIC				
CaPOPI_6753	scaffold198	626672	TAAAAAAAA/TAAAAAAAA	TGGACACCTTCAATTAT GCG	CGCAATTCTTGAGTTTCG ACA	59.5	404	INTERGENIC				
CaPOPI_6754	scaffold198	637595	TTATTTTATATATTTTATATATTTT/TTAT TTTATATATTTT	TGACCGCAACCAGTTCA ATA	CCAACTCACAAATACATC GCC	60.1	386	INTERGENIC				
CaPOPI_6755	scaffold1981	100589	AAATTATAATTTATAA/AAATTATAA	ATTTCCACATCACCCA AAA	TCATTACTCACACCATAA GTGGAA	60.0	436	INTERGENIC				
CaPOPI_6756	scaffold1981	117409	TTTATTATTATTATTATTA/TTTATTATTA TTATTATTATTA	TTCTTAATTGTCCAATT GCTAAGT	AGGTGCGATCACGTAAA ACC	58.3	534	INTERGENIC				
CaPOPI_6757	scaffold1981	118118	ACTCTCTC/ACTCTC	GGTTTTACGTATCGCA CCT	ATCGGAATTTTGTGCC TTG	60.0	783	INTERGENIC				
CaPOPI_6758	scaffold1981	183798	TACTTATAAACTTATAAAA/TACTTATA AAA	AACAACCTCTCATGTTTCG CAA	CACTTATCCGCTCCA TTT	58.4	746	INTERGENIC				
CaPOPI_6759	scaffold1981	239519	AATATATATATATATATATATATATATAT A/AATATATATATATATATATATATATATA TATATATA	AAATTTGCGTTTAAATAA CGGG	TGGATCCTCCCTTTTGT ACG	59.3	779	INTERGENIC				
CaPOPI_6760	scaffold1981	287943	TTTATTATTATTATTATTATTATTATTAT TATTATTATTA/TTTATTATTATTATTATT ATTATTATTATTATTATTATTATTATTAT TA	CTTTCAAATAAAACCCG CCA	TTTAGGCATTGTTGCTG CTG	59.9	179	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_6761	scaffold1981	317439	TAAA/TAAAA	TCTCATTGCTCCCGACTCT	TTGTCTCAACAATCTCCCAC	60.0	501	DRR	Ca_21265			
CaPOPI_6762	scaffold1981	345037	ATTTTTTTTT/ATTTTTTTTT	ACACTTCCAATGCCAAGGTC	TGGCTTGTGGTTGTGAATC	60.0	655	INTRON	Ca_21268			Polyketide cyclase/dehydrase
CaPOPI_6763	scaffold1981	355117	TCCC/TCCCC	AAACCTCGAATTTTGTGAATC	GGGGCCTTTCAAATATCGT	57.3	502	INTERGENIC				
CaPOPI_6764	scaffold1981	355366	A/AC	ACGATATTTTGAAAGGCCCC	CGCGGATCCAATATCTCACT	60.2	426	INTERGENIC				
CaPOPI_6765	scaffold1981	357850	GTTTT/GTTTT	TCAAGTGTCTATTTTGTGGCA	CCTTTTGCAATTGGTTGGT	59.7	559	INTERGENIC				
CaPOPI_6766	scaffold1981	358146	TAAAAAA/TAAAAAA	ACCAACCAATTGCAAAAAGG	TAAACTTGTGTCCGGAAGC	59.8	553	INTERGENIC				
CaPOPI_6767	scaffold1981	366756	GTTTTTAAATTTTTTAAATTTTT/GTTTTTAAATTTTT	TCGGACTACCTGGCTATTCAA	GCACCATGAACACCCCTACT	59.7	784	INTERGENIC				
CaPOPI_6768	scaffold1981	370536	AAATAATAATAATAATAATA/AAATAATAATAATA	GGTGTTTGCTTTTAATAGGCTCA	TCACCCACTCTACTCTTTTGTTT	59.7	934	INTERGENIC				
CaPOPI_6769	scaffold1981	371440	TAAAAAA/TATAAAAAAA	TTTCGTGGTCCTAAATGCC	AAAAGGGACATGGAACAACAA	59.9	698	INTERGENIC				
CaPOPI_6770	scaffold1981	421474	A/AT	GCGCGAGTATGGGCTTATTA	ATTGATTGGATGAGGGACCA	60.2	714	INTERGENIC				
CaPOPI_6771	scaffold1981	421693	TAG/T	TCATTGGATCAATAAGCCTCA	ATTGATTGGATGAGGGACCA	58.2	206	INTERGENIC				
CaPOPI_6772	scaffold1983	23052	GTT/GTTT	AGCAGGTCTGTCCAATCAGG	CATCAGCCCCTCTAAACCAA	60.3	852	INTERGENIC				
CaPOPI_6773	scaffold1983	63035	TAAA/TA	GCGGGTGTAAGTGACATGTTG	TGTGGCCGTAAACATTCAAA	60.0	415	INTERGENIC				
CaPOPI_6774	scaffold1984	106927	ATG/ATGTTG	GCAAGGAATCCCCCATAT	TGTGACCGATTTTGTGACTGA	60.0	825	INTERGENIC				
CaPOPI_6775	scaffold1984	284025	CAAAA/CAAA	GCTCTCATCTGAGGGCAAG	ATTTGGGAAGTTACAGGGGC	60.1	562	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6776	scaffold1984	323626	T/TCCG	GCTTGTCCGCGTAAC TTC	ACGATTTAGAAGAGGC GCA	60.0	601	INTERGENIC				
CaPOPI_6777	scaffold1984	386637	GTT/GT	CGGTAAAAAGTGTGCGG ATT	TGAATGGAAGTGGGACA ACA	60.0	491	INTERGENIC				
CaPOPI_6778	scaffold1985	19601	TCTTTTCCTTTTCCTTTTCCTT/TCTTTT CCTTTTCCTTTTCCTTTTCCTT	AGGAAGAGTGGAGTTGC GAA	TATTTTGGATTTTGCTC GG	60.0	511	INTERGENIC				
CaPOPI_6779	scaffold1988	7769	TACACACAATCAAA/TACACACACAATC AAA	ACCATACAAGTCCCCGC ATC	GAAGGAGCAGTAAGCCA TCG	59.8	725	INTERGENIC				
CaPOPI_6780	scaffold1990	8359	TTGAAATGAAAT/TTGAAAT	ACGTCTTCTTTGTGGG TCG	TTAAGCAACAGGCCAA TTC	60.1	196	INTERGENIC				
CaPOPI_6781	scaffold1996	1333	TG/TGG	CGGATGAATCATTGGGA AAT	AGTGAAACCAACGCCAA AAC	59.6	325	INTERGENIC				
CaPOPI_6782	scaffold1996	5730	GAAAAAAAA/GAAAAAAAAA	TGTTAGGAGGATCTCAC GGG	ATTGTTGGAATTTGCG TGC	60.1	823	INTERGENIC				
CaPOPI_6783	scaffold1999	8100	GAAAA/GAAAAA	TGGATGCACGAGATTGG TTA	TGCATCCAATAGGCGTT TTT	60.1	938	INTERGENIC				
CaPOPI_6784	scaffold1999	24246	TAAAA/TAAAA	GCCTAGGGAGGACGAAA ATC	AACCAATGTTGTGCATC CAA	60.0	375	INTERGENIC				
CaPOPI_6785	scaffold1999	27916	CAAA/CAAAA	AGGGAGGACGAAAATGA CCT	CTTGGGCATCCAATAGG TGT	59.9	763	INTERGENIC				
CaPOPI_6786	scaffold1999	29603	GACA/GACACA	AGGGAGGACGAAAATGA CCT	AACCAATCTTGTGCATC CAA	59.9	670	INTERGENIC				
CaPOPI_6787	scaffold1999	29835	TAAAAA/TAAAAA	AATCCAACGACAACGGA ACT	CCGATGTTGTGCATCCA ATA	59.5	541	INTERGENIC				
CaPOPI_6788	scaffold1999	30095	AT/A	ATCCAACGACAACGGAA CTT	AACCAATGTTGTGCATC CAA	59.5	939	INTERGENIC				
CaPOPI_6789	scaffold2	18928	A/AT	GTCAGGCATTCCCTCT ACA	TTGCGTTGGTGACCCTT TAC	60.1	118	INTERGENIC				
CaPOPI_6790	scaffold2	69919	GC/G	TTGCGAACTCCACTCTT CCT	CAACGCAACATAACACC CAG	60.0	477	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6791	scaffold2	515747	TTATATATATATATATATATAT/TTATATA TATATATATATATATAT	TGGACTGGCATGATTGG ATA	ACCACTCAAAGTGTTTG GGC	59.9	833	INTERGENIC				
CaPOPI_6792	scaffold2000	1544	GAAAAAAA/GAAAAAAA	GCCTAGGGATGACGAAA ATG	TGTGTTTGCCTCATTGG ATT	59.5	566	INTERGENIC				
CaPOPI_6793	scaffold2000	14213	CA/C	AAGCCTAGGGAGGACGA AAA	TGCCACTGTGACTTATC CAATC	60.2	509	INTERGENIC				
CaPOPI_6794	scaffold2000	22359	AATTGGCCT/A	GCTGTGCACCTTGATGCT GAT	TGTGTCGTTCCGGTGAAC ATT	60.0	465	INTERGENIC				
CaPOPI_6795	scaffold2003	11976	T/TG	TCATTGGCTTATTCTTGC CC	TAGGGACGACGAAAATG ACC	60.0	504	INTERGENIC				
CaPOPI_6796	scaffold2003	13286	ATT/AT	CAATCTTGTGCATCCAAT CG	AGGGAGGACGAAAATGA CCT	60.1	567	INTERGENIC				
CaPOPI_6797	scaffold2003	32381	ATTTTTT/ATTTTTTT	CTGTGGAGTTCTAGGGG CTG	TGGCATAAGAGAGTGGC TCA	59.9	479	INTERGENIC				
CaPOPI_6798	scaffold2003	33197	GTT/GTTT	AATTGCGTTTCAACCTT CG	AAACTGGCCAACAGAGG ATG	60.1	344	INTERGENIC				
CaPOPI_6799	scaffold2005	14756	TAAAAAAA/TAAAAAAA	AAATCCAACAATCTCCC CC	CGGTCTCAACCTCTCCC ATA	60.0	515	DRR	Ca_28003			
CaPOPI_6800	scaffold2005	32399	ATTTTTTTTT/ATTTTTTTTTT	CCAGACCAGACTTCGAA AGG	GACTGTCTGTCAGGGGC CTA	59.8	549	INTERGENIC				
CaPOPI_6801	scaffold2010	3634	AT/ATT	AATCGATTGATTCAGCC CAG	TGATTTCCAACGGTCAT CAA	60.0	869	DRR	Ca_27976			
CaPOPI_6802	scaffold2010	6749	T/TC	TTCCCTTTCGTTGTGTAT CG	GGGCACCGATGTTACAT AAA	58.6	857	URR	Ca_27976			
CaPOPI_6803	scaffold2010	7925	ATTTTTTTTT/ATTTTTTTTTT	AAAGTGCCTTCTTCTTG GCA	ATGTTTCTTTTGGGTTG CG	60.0	564	URR	Ca_27976			
CaPOPI_6804	scaffold2018	4354	TGGAG/TG	CATGGTTTGTGTTGTCG TGC	TGTTTGCTTTAAGCGAT GTCA	60.0	462	INTERGENIC				
CaPOPI_6805	scaffold2018	16998	CAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT/CA ATAATAATAATAATAATAATAATAAT AATAATAATAATAATAATAATAATAA	AAGGCTCACTTGCAAAG ACG	GGTATTGCTGCAGTTTT TGG	60.6	445	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6806	scaffold202	17670	ATTTTT/ATTTTTTT	TCACAAGGGTAGTTTTG GGTTT	CTGCCAGCTCACCTCCT ATC	59.8	685	INTERGENIC				
CaPOPI_6807	scaffold202	17816	AAA/AAATAA	TCACAAGGGTAGTTTTG GGTTT	CTGCCAGCTCACCTCCT ATC	59.8	685	INTERGENIC				
CaPOPI_6808	scaffold202	19978	GT/G	GGAATTTTCAGAAAAC GGA	CTGTCCGCCTAATTTTC GAG	60.1	778	INTERGENIC				
CaPOPI_6809	scaffold202	20536	CTA/C	TGCATCCAACTTTGGTG TGT	ACACCGTTGTTTATGCA CGA	60.0	373	INTERGENIC				
CaPOPI_6810	scaffold202	22635	CG/C	GGATTACATTCGTTCT CCG	GCAAAACAATGCGAAACA GAA	59.7	804	INTERGENIC				
CaPOPI_6811	scaffold202	22768	AT/A	TTGCAATCATGAGGCAA GTC	GCAAAACAATGCGAAACA GAA	59.8	235	INTERGENIC				
CaPOPI_6812	scaffold202	36674	TAAA/TAA	AAATCGGTGTCAACGGT CTC	TTCACCTGTCAATTGGG TTG	60.0	559	INTERGENIC				
CaPOPI_6813	scaffold202	37860	TAAA/TAA	ATTGGAGGCTGGTTTTG TTG	ATCGTGGGGATGAATTT GAA	60.0	539	INTERGENIC				
CaPOPI_6814	scaffold202	37967	T/TC	ATTGGAGGCTGGTTTTG TTG	ATCGTGGGGATGAATTT GAA	60.0	539	INTERGENIC				
CaPOPI_6815	scaffold202	39185	TATG/TATGATG	GCACCGGAAAATACGTA GGA	ATTATCTTGTCGCGGCC TAA	60.0	359	INTERGENIC				
CaPOPI_6816	scaffold202	39293	CTTTT/CTTTTT	GCACCGGAAAATACGTA GGA	ATTATCTTGTCGCGGCC TAA	60.0	359	INTERGENIC				
CaPOPI_6817	scaffold202	61873	GTAAGTTTATATTTTAAAGTTTATATTT AAATAAAATGAAATAAAATGA	CAGCCCTTGAATTCGAT CAT	GCTGTTTGGCTCAACCA TTT	60.0	331	INTRON	Ca_27125			
CaPOPI_6818	scaffold202	93888	A/ACAAGATC	GTGCAGTGAAAGGGTTC CAT	AATTTGATATCGTGCGC GAG	60.0	881	INTRON	Ca_27126	U		Vacuolar protein sorting-associated protein
CaPOPI_6819	scaffold202	99484	TAAAGTTTATATTTTAAAGTTTATATTT TAA/TAAAGTTTATATTTTAA	CCTCTTTCTCAATTGCA GCC	ATGTTTGGGAGAGCCAT TTG	60.0	792	DRR	Ca_27127	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_6820	scaffold202	100589	A/AG	CATCAAATCACGAATGG CAG	GTTAGGGGAGATGGGG TGAT	60.1	543	DRR	Ca_27126	U		Vacuolar protein sorting-associated protein

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6821		scaffold202	103994	ATTTTTTTTT/ATTTTTTTTTTT	AAATTGCTTATTAGTAG TGTCATCG	AACTCAGCAAAACCCAA AACA	58.5	409	URR	Ca_27127	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_6822		scaffold202	104373	TAAAAAAAAA/TAAAAAAAAA	TGTTTTGGGTTTTGCTG AGTT	TGGATGGATTGGATGAA TGA	59.6	180	URR	Ca_27127	A		Like-Sm ribonucleoprotein (LSM) domain
CaPOPI_6823		scaffold202	104727	TTA/T	TCATTCAATCAATCCATC CA	TCGAGTGTCTGATCTCAA GGA	59.7	489	INTERGENIC				
CaPOPI_6824		scaffold2020	7500	AATA/AA	CTTGCTAGAGCTTGGCG ATT	ACATTTCTTTGGCGGTT TTG	59.8	569	INTERGENIC				
CaPOPI_6825		scaffold2024	1945	CAAA/CAAAA	GAATGTTAGGGTTTCCG GGT	GATGAAATCGAGGACTG GGA	60.1	338	INTERGENIC				
CaPOPI_6826		scaffold2027	955	GAAAAAAAA/GAAAAAAAA	AGAAAGGCTCAAACGAC CAA	ACAGAGGAAGCTGCCAC CTA	59.9	672	INTERGENIC				
CaPOPI_6827		scaffold2030	4596	ATT/ATTTT	AGGGTTTAGGATTTCG GTT	CATATCAAAACCCAAAT GACC	60.0	243	INTERGENIC				
CaPOPI_6828		scaffold2033	183883	CGAAGAAGAAG/CGAAGAAGAAGAAG	CTTGGGGTGGCAAGTAC AGT	TCGAATACATGAATTAAC AAAAGGA	60.0	371	DRR	Ca_26143		bHLH	Lipase, GDSL
CaPOPI_6829		scaffold2036	83593	TAATAATAATAATAATAATAATAATA AATAATAATAATAA/TAATAATAATAA ATAAATAATAATAATAATAATAATAA TAAA	TGAATTGGAGGTCATGG TGA	TCCAACGAATTGATGTC CAA	59.9	551	INTERGENIC				
CaPOPI_6830		scaffold2036	151113	AATATATATATATATATATA/AATATATAT ATATATATATATA	TATTTTGATTTTGCTC GG	AGGAAGAGTGGAGTTGC GAA	59.9	394	INTERGENIC				
CaPOPI_6831		scaffold2036	238131	TGTAGTA/TGTA	TTCAAAAAGCGCGGTAA ATC	AGAATCCACCCACACAA AGC	60.2	821	DRR	Ca_26067		ARF	Transferase
CaPOPI_6832		scaffold2039	15621	C/CTAGTT	GCAAGAGGAAAAGACGA ACG	CGTTTTGCTTTTTGTTGG GT	60.0	516	INTERGENIC				
CaPOPI_6833		scaffold2039	52513	A/ACTTTCTCT	TGCAAAAACCAATGTGG AAA	AGGCCAAACTCGTGCTT AGA	59.9	575	INTERGENIC				
CaPOPI_6834		scaffold2039	83114	TAAAAAAAA/TAAAAAAAAA	CCACTCACTCGAATCTC GAAC	GACTCAAAAGCTGGGCA CTC	59.9	661	INTERGENIC				
CaPOPI_6835		scaffold2039	128633	ATTTTTTTTTTT/ATTTTTTTTTTT	TTGTCCCTGAATGATT CGT	TTGTGGCTGTCAAAG CAG	60.3	613	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6836	scaffold2040	102148	A/AC	TGGTCCTCAACGAACAA CAA	TTGCAAAAGTGAGTGCC TTG	60.1	386	INTERGENIC				
CaPOPI_6837	scaffold2040	154810	AATATATATATATATATATAT/AATATATA TATATATATAT	ATTTTGGTTCGGAGGCT TTT	TCTCTCACGCCGTTTT CTT	59.9	539	INTERGENIC				
CaPOPI_6838	scaffold2040	159577	CA/CAGGTA	TGAAGAGGGGAATCCAT CTG	TTAACAACCTCTGGTTC GGG	60.0	372	INTERGENIC				
CaPOPI_6839	scaffold205	40693	C/CAAG	CTACTCTCAATTTCCGC CG	GCACAATCAGAAGCGCA TTA	59.8	761	DRR	Ca_25491			
CaPOPI_6840	scaffold205	46882	GAGGA/GAGGAAGGA	GAGAGGATTGTGTTCC CGA	GGAATGCTCAAAGGTG CAT	60.1	235	INTERGENIC				
CaPOPI_6841	scaffold205	75804	G/GA	TGAAGAGGGGAATCCAT CTG	ACTCCAAACGGCATAAC CAG	60.0	745	INTERGENIC				
CaPOPI_6842	scaffold2051	10215	ATTTTT/ATTTT	CCTTTCCATTCTTTGAG GG	GGCACCCAACTAGGTTT GAA	58.6	818	DRR	Ca_25399	R		Sugar/inositol transporter
CaPOPI_6843	scaffold206	162025	GTTTT/GTTTT	CTTGGATTCATTGATCC GCT	GTTTGGTTTTCTTTGGG GGT	60.0	423	INTERGENIC				
CaPOPI_6844	scaffold206	176077	T/TATAG	CTCTCGCTATGAAAAAC GGG	TGGGTTCAATTGGCATT TTT	59.8	759	INTERGENIC				
CaPOPI_6845	scaffold206	190834	CATATATATATATATAT/CATATATAT ATATATATATAT	ATCCCTAACGCCGTTTT TCT	ATATTGGCTCGGAGGCT TTT	60.0	480	INTERGENIC				
CaPOPI_6846	scaffold207	6894	AC/A	GCAAACTCGACAGGAAA AGC	TTGGTGAAGATGTCAGC CAG	60.0	370	INTERGENIC				
CaPOPI_6847	scaffold208	95031	ATATTATTATTATTATTACTATTATT ATTAT/ATATTATTATTATTATTATTAT TTACTATTATTATTAT	CATTGGATGCACCATTT CAG	TCAATCACCACAAACATC CC	59.9	720	INTERGENIC				
CaPOPI_6848	scaffold208	131475	GTT/GT	TGCAAAAACCACTTTCAA GG	TTTGGACCAATTTGTG GCT	58.8	620	INTERGENIC				
CaPOPI_6849	scaffold208	174233	GAAAA/GAAA	CCTTGGAGTATTCTCGG CAG	TGCTGATCCGTGAGAGA TTG	59.8	894	INTERGENIC				
CaPOPI_6850	scaffold210	31686	CAA/CAA	TTTCTCGCAAAACATGC AG	TTGCAACTCCACTCTT CCT	60.0	712	INTERGENIC				

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CaPOPI_6851	scaffold210	32630	TAAAA/TAAAAA	AGGAAGAGTGGAGTTGC GAA	TATTTTGGATTTTGGCTC GG	60.0	512	INTERGENIC				
CaPOPI_6852	scaffold210	411319	GTTTTTTT/GTTTTTTTTT	CCACAACCTCTCACATC CCT	TCACAGTTGGTAGTGGC ACC	60.0	239	INTERGENIC				
CaPOPI_6853	scaffold210	532061	CATATATAT/CATATAT	AAGCGCTGTAATATGCC CAC	CTGGGCAAGGGATCTGA ATA	60.1	639	DRR	Ca_21912		Trihelix	Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_6854	scaffold210	577121	AGAAATCGATTGG/AGAAATCGATTG GAAATCGATTGG	TTGCCAAGTGTGGATGT TGT	GGGTACGAACCGGTAG GATT	60.0	947	INTERGENIC				
CaPOPI_6855	scaffold2103	124174	GTTTTC/GTTTTCATTTTC	AACCCAATCACTGGAGA TGC	AGGAAGAGTGGAGTTGC GAA	59.9	540	INTERGENIC				
CaPOPI_6856	scaffold2103	145039	GTATATATATATATATATAT/GTATAT ATATATATATATAT	GCCAGAACACCGACCAT ACT	CCAAGTGGTACAACCTGG TGCTCT	60.0	581	INTERGENIC				
CaPOPI_6857	scaffold212	125792	TA/TTCA	TGTCCAATCTTAGGGGT CAAA	AATTTGCCAATTCAAGG CAG	59.4	641	INTERGENIC				
CaPOPI_6858	scaffold212	180804	T/TA	CGAAGATTCGAAGGCAA AAG	CCGTTCTTGGTTTTCAC ACA	60.0	722	INTERGENIC				
CaPOPI_6859	scaffold2126	3526	GATATATATATA/GATATATATATATA TA	CCATGAAAAGAAGAAGG GCA	GCCTTTTACTGCACTTT GGC	60.2	472	INTERGENIC				
CaPOPI_6860	scaffold2134	5442	TTA/T	GAAAAAGGAACGAAGGG AGG	AACGGAACGAGCGAGTC TTA	60.0	566	INTERGENIC				
CaPOPI_6861	scaffold2152	34103	CTTTTT/CTTTT	GGGGTGCTCAACTTGTT TGT	TGATCAAATCCCCCAC ACT	60.0	589	INTERGENIC				
CaPOPI_6862	scaffold2152	76304	AATTATTATTATTATTATTATTATTA TTATTATTGTTATTATTATTAT/AATTATT ATTATTATTATTATTATTATTATTAT TATTGTTATTATTATTAT	TTCATGGGAACACAAGC AAG	GAAGGAAAGGGTCAAGG CTC	59.7	258	INTERGENIC				
CaPOPI_6863	scaffold2152	76522	AATTATTATTATTATTATTATTATTA T/AATTATTATTATTATTATTATTATT ATTAT	GAGCCTTGACCTTTTCC TTC	TGGGGGTATAAACCATC AAAA	60.2	596	INTERGENIC				
CaPOPI_6864	scaffold2152	108576	CT/CTATATTTCATATCTT	TTTCAGCTTCATCGCATT CA	GAGATTGCCAAGAACA GGC	60.5	448	INTERGENIC				
CaPOPI_6865	scaffold2153	19763	CTATTTATTTATTTATTT/CTATTTATTTA TTTATTTATTT	TGGAAAACACAAGAAAG GGG	TGGGGATACGTAGGAGC AAG	59.9	606	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6866	scaffold2158	81348	AATATATATATATATATATATATATAT TTATATATATAT/AATATATATATATATAT ATATATATTTATATATATAT	GGATTTTGCTAGGAGG CTT	AAATGGAGGAGAAGGAG GGA	59.7	438	INTERGENIC				
CaPOPI_6867	scaffold2158	133975	ACCCCCCCCCCCC/ACCCCCCCCCC	GTAGCAAGAATCCAGG GTG	AATGGCCACTTCGAGTC AAC	59.6	317	DRR	Ca_24818			
CaPOPI_6868	scaffold2158	178374	TTACTAC/TTACTACTAC	TATCTCAACCCCCACC ATA	ATCAACAGCCAGACCCA TTC	60.0	829	INTERGENIC				
CaPOPI_6869	scaffold2161	5214	GGGGT/GGGGTGGGT	TACCCTTCTGGGTTGCT TCA	AAGCCTCCAATGCTTCT TCA	60.6	154	INTRON	Ca_26956	H		Folylpolyglutamate synthetase
CaPOPI_6870	scaffold2161	14357	TAAAAAAA/TAAAAA	TTTCAGTATCGTTGCGT GGA	ACGCACCAAACACATTG AGA	60.3	575	INTERGENIC				
CaPOPI_6871	scaffold2161	32357	GAAAAAAAAA/GAAAAAAAAA	GAGGGATGAGAAGGTG ACGA	TTTTGTGCCGTAGTCC CTC	60.2	744	INTERGENIC				
CaPOPI_6872	scaffold2161	184512	CATTATTATTATTATTATTATTATTA TTATTATTGTTATTATTATTATTATT ATTATAATTATTATTATT/CATTATTATTA TTATTATTATTATTATTATTATTATT	TGCATTGGTATATGGAG GCT	GGCCTGCCAGCTTATCA TAG	58.1	841	INTERGENIC				
CaPOPI_6873	scaffold2164	67799	TTGTG/TTG	TAAACCCCATACAACC CGA	TCCTAGAACATGCATCA CGC	60.0	109	INTERGENIC				
CaPOPI_6874	scaffold2166	41038	AG/AGG	GCTCGAAACTGGTGGCT ACT	TCCACAACAACCTACGT CCA	59.5	245	INTERGENIC				
CaPOPI_6875	scaffold2166	49190	CTTTTTTTTT/CTTTTTTTTT	TGTTGGTTCAAATGGG GTT	TCCATGGTGCCTTTGTA TCA	60.1	872	INTERGENIC				
CaPOPI_6876	scaffold2166	85838	AATATATATATATATATATATAT/AATATA TATATATATATATATATAT	TTTCAAAGGATTCAGT CCC	GCACCATAATGCCCTG TAT	60.1	536	INTERGENIC				
CaPOPI_6877	scaffold2170	4201	ATTTGGCTTCGTGGTCTTTTGGCT/ATT TGGCT	GCTATCGGTCACTGGTT GGT	CGAGGACCAGCTTTGGT AAG	60.0	372	INTERGENIC				
CaPOPI_6878	scaffold2170	5002	AACCTTACCTTACCTTACCT/AACCTTA CCTTACCT	GCAAAATCAAGGTTGCAG TCA	ACACTCTAATGGGGACA GCG	59.8	222	INTRON	Ca_26928	YU		
CaPOPI_6879	scaffold2170	5357	C/CTATTGGG	CGCTGTCCCCATTAGAG TGT	GTTTGCCAATTAGGGA CAT	60.1	387	INTRON	Ca_26928	YU		
CaPOPI_6880	scaffold2170	12258	CTTTTT/CTTTT	TGCTTTGTCAATTGCTT GC	GGAGTCCCGGAAATTT CAT	60.0	531	INTRON	Ca_26929	O		

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6881	scaffold2170	12676	ATATGTAT/ATATGTATGTAT	GAAATTTTCGGGACTCAT	AGCTCTTTCACCTCAA GCA	60.1	618	INTRON	Ca_26929	O		
CaPOPI_6882	scaffold2170	14347	AC/ACC	GCTCATTCTGTCCCCA AAA	GCCTCTGCTAATTGGTCTCG	60.1	583	INTRON	Ca_26929	O		
CaPOPI_6883	scaffold2173	19315	TAAAAAAAA/TAAAAAAAA	GGACAAAAATGACCCAA ACG	TTTTGTCTCCTTGGC TTA	60.2	513	INTERGENIC				
CaPOPI_6884	scaffold2173	19619	TAAAAA/TAAAAA	GGATGACACAAACGCAC CTA	ATTTTGTCTCCTCCCTTG GCT	59.6	385	INTERGENIC				
CaPOPI_6885	scaffold2173	19824	A/AG	CCAAGGGAGGACAAAA TGA	TTTTCGTCTTCACAG CTT	59.9	515	INTERGENIC				
CaPOPI_6886	scaffold2173	56248	ATT/AT	CCTTGGGAAGACGAAAA TGA	CCATCCAATACGTGTGC TTG	60.0	363	INTERGENIC				
CaPOPI_6887	scaffold2173	56515	GACACCAACACACCAA/GACACCA	CCTTGGGAAGACGAAAA TGA	TCCAATCTGGTCCATCC AAT	60.0	673	INTERGENIC				
CaPOPI_6888	scaffold2177	10444	CATTAAAT/CATT	CCGTGGAATTGATGGAA CTT	CTGCCACTTCGAGAACA ACA	59.8	331	INTRON	Ca_27883			Glycoside hydrolase, family 28
CaPOPI_6889	scaffold2179	20401	CTTTT/CTTT	GGGACACGTGTTGCCT TTT	AATGTCAAGGATGGCCT CAC	59.9	601	INTERGENIC				
CaPOPI_6890	scaffold2179	20793	TCCCCC/TCCCC	ATCAGCGAGGATGCAGA ACT	CATCGCTCAGTTTGGAC TCA	60.0	789	INTERGENIC				
CaPOPI_6891	scaffold2179	35934	TG/TGCG	GAATTTGAACCTCCAAG CCA	ATAGCGGAGAAGCCCAT ACA	60.1	404	INTERGENIC				
CaPOPI_6892	scaffold2179	35973	TC/TCC	GAATTTGAACCTCCAAG CCA	ATAGCGGAGAAGCCCAT ACA	60.1	404	INTERGENIC				
CaPOPI_6893	scaffold2179	36066	ATAG/A	GAATTTGAACCTCCAAG CCA	TGCATTCCACATACAAG GGA	60.1	582	INTERGENIC				
CaPOPI_6894	scaffold2183	19955	TATTAATTAATT/TATTAATT	TAGGGCGATTTTCGTAC CAC	TTTTCGCATATTTATTG ACAACCTC	60.0	468	INTERGENIC				
CaPOPI_6895	scaffold2183	67523	GT/G	AGTCGCTCGAAAAGTCC AAA	TCCTGGTCTCGATTTC ATC	60.0	528	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6896	scaffold2183	69871	ATTTTT/ATTTTT	GATGAAATCGAGGACTG GGA	TGAAATCTAGCGCAGAC CCT	60.0	245	INTERGENIC				
CaPOPI_6897	scaffold2183	70044	AGGGG/AGGGGG	AGGGTCTGCGCTAGATT TCA	AGGGTTTCTCGGTCCTT GAT	60.0	127	INTERGENIC				
CaPOPI_6898	scaffold2192	2178	GA/GAGAA	CATGGAGTTGAAATGGC AAA	CGTTGTAAAAATCGGG GTG	59.5	589	INTERGENIC				
CaPOPI_6899	scaffold2193	31576	AA/ACAAACACA	GCCAAATAGAGGATGGAA GCA	TATGCCAAAGCCATGTT TCA	60.2	437	INTERGENIC				
CaPOPI_6900	scaffold2193	161568	ATTTTTTTTT/ATTTTTTTTT	CCGTTTCGAGTCTCAAG GAG	GCTTCCATGTTGCTCCT CTC	60.0	679	INTERGENIC				
CaPOPI_6901	scaffold22	24507	AAT/A	ATGAGGCTCAAAATGCC ATC	GCCAACTTTTCCAATGC CTA	60.0	727	INTERGENIC				
CaPOPI_6902	scaffold22	34524	GTTTTT/GTTTTTTT	GCAGCATCGCAGATCAT AGA	CGAATTGGGTTTTCTGT CTC	60.1	181	INTERGENIC				
CaPOPI_6903	scaffold2205	49159	ATT/ATTT	TTTTTAACCAATCTTCGG CG	AGGGAGGACGAAAATGA CCT	60.1	272	INTERGENIC				
CaPOPI_6904	scaffold2208	20005	CA/CATA	CAAACACACCTGTTGGA TGC	CCCTAGGCTTATTCTTG CCC	60.0	362	INTERGENIC				
CaPOPI_6905	scaffold221	61534	CT/CTAAGTGTTATGT	CCCGTGATAGGCAGTAC GTT	CGATTTCCTGCATGTT TTT	60.0	352	INTERGENIC				
CaPOPI_6906	scaffold2210	15184	CG/CGGATTTG	TCCAGATGAAATCGAGG ACC	AAATCCGACACGTAAC CGG	60.0	531	INTERGENIC				
CaPOPI_6907	scaffold2210	36171	AATTATATTA/AATTA	TCTTCGTTATGCAGTCA AACCT	TGCAAGAAAAACACCAT GAATTG	58.9	612	INTERGENIC				
CaPOPI_6908	scaffold2216	16725	AATATATATATATATAT/AATATATATA TATATAT	CTATCGGCTCGACCAAT GAT	TTTTGGCTGGGTATAGG CAC	60.1	451	INTERGENIC				
CaPOPI_6909	scaffold222	40304	CTTTTTTTTT/CTTTTTTTTT	GTTTGTTCCTAACA GCA	GGTATCTGGGAACAGA TTTCTC	60.0	279	INTERGENIC				
CaPOPI_6910	scaffold2222	1209	G/GGATGCACAA	TGGATGCACAAGGTTGG TTA	AGGTCATTTTCGTCTC CCT	60.0	559	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6911	scaffold2227	7998	TAAAAAAAAA/TAAAAAAAAA	TTTGACCAAACTCATTTGCAC	GGTCTCGATTTCATCTGGA	60.0	418	INTERGENIC				
CaPOPI_6912	scaffold2227	27932	CCCCAATCGATTG/CCCCAATCGATTGCCAATCGATTG	TCAGCCCAGGATTTTGTTC	CCCGTGAGATCCTCCTACAA	60.1	537	INTERGENIC				
CaPOPI_6913	scaffold2227	31662	AATATATATATATATATATA/AATATATATATATATATA	CTTGGAAGTGGAGAGGAAG	AATGGAGGAAGGAGGAGAA	60.0	541	INTERGENIC				
CaPOPI_6914	scaffold223	82674	GTTTTT/GTTTTTTT	AATCTTCCCATGGATGTTCA	TCAGCAAAGTCAAGAAGGCA	59.2	541	INTERGENIC				
CaPOPI_6915	scaffold223	95879	AGCGACTACT/A	TTGGTCTCCTTGTTGTGTC	TGGAGACCCCTTGATGAAC	59.7	502	INTERGENIC				
CaPOPI_6916	scaffold223	177357	TACT/TACTAACAACT	GACCAGCAGCAAACCTCTCC	AGATGTAAGCTCCGATGCGT	60.0	971	INTERGENIC				
CaPOPI_6917	scaffold2235	878	GTTTT/GTTTTT	AGGTCATTTTCGCCTCCCT	TTGGATGCACAAGATTGGTT	59.9	267	INTERGENIC				
CaPOPI_6918	scaffold2249	1002	CT/CTT	TATTCACCCACGATCATT	CAACCAAGCATTTTCCATT	60.0	871	INTERGENIC				
CaPOPI_6919	scaffold2249	12435	CCAA/CCAACAA	CAGCTGAATACCAAGCGTGA	TGTCACCAAAATCTCGTCCA	60.0	772	INTERGENIC				
CaPOPI_6920	scaffold2269	43256	A/ACGATTC	TCATCCCAAGGGAATGA	CTTTATTGGTCCCCACCTT	60.2	308	INTERGENIC				
CaPOPI_6921	scaffold2269	45593	T/TAA	CTTTGAGAAGCAGGCCATTCT	CGGTTGCGTGAGGTTTTTAT	60.0	562	DRR	Ca_27076			
CaPOPI_6922	scaffold2269	121644	TAAAAAAAAA/TAAAAAAAAA	TTTGATGAAGTTGATGCCA	TGACTTGTTCTTCACGGC	60.0	645	DRR	Ca_27079	R	G2-like	RNA recognition motif domain
CaPOPI_6923	scaffold227	135497	TCC/TCCC	CTTGGATGTGGTAGCCGTTT	GGTCTTGTTGGTGGCTTTTGT	60.0	651	INTRON	Ca_25190			
CaPOPI_6924	scaffold227	140947	TTA/TTAAAGTA	ACCCTTTTGTTCACACGAG	TACGGATGTTGACGCAATGT	60.0	511	INTRON	Ca_25190			
CaPOPI_6925	scaffold227	144419	C/CACAATAG	CCTCAAACCTCCATGGCTA	CAACTGGAATTTTCGGGAGA	60.1	641	DRR	Ca_25191			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6926	scaffold227	194790	TAAAAAAAA/TAAAAAAAA	GCCGAACTCAATCACA CCT	TGCCAGTTTGTCTGGATA AGTT	60.1	429	INTERGENIC				
CaPOPI_6927	scaffold227	195682	CAA/CAAA	AGACACAAACCCCGCAA TAG	GGATGCCACCATTCAG TTT	60.0	338	INTERGENIC				
CaPOPI_6928	scaffold227	196111	TAAAAAAAA/TAAAAAAAA	AAACTTGAATGGTGGCA TCC	AGTAATGAATGGGCGAG TGG	59.8	595	INTERGENIC				
CaPOPI_6929	scaffold227	196280	TAAAA/TAAAA	AAACTTGAATGGTGGCA TCC	AGTAATGAATGGGCGAG TGG	59.8	595	INTERGENIC				
CaPOPI_6930	scaffold227	197474	TAAAAAAAA/TAAAAAAAAA	CCTAATGCGGAAATTG TGT	TAATCAGACCGTGTGGG TGA	59.8	626	INTERGENIC				
CaPOPI_6931	scaffold227	325938	CTATATATATATATATATATAT/CTAT ATATATATATATATATATATATAT	CAATTCTTGATTGGCAT GCTT	GCTAATTTTCGCGTCTT CG	60.1	327	INTERGENIC				
CaPOPI_6932	scaffold2273	24986	GAAAA/GAAAA	AAAATCCAACATCTCCC CC	CCCTGCTACTCCTGCTT TTG	60.0	590	DRR	Ca_28242			
CaPOPI_6933	scaffold2275	15734	AATATATATATATATATATATAT/AATA TATATATATATATATAT	AGTGATAACCCGTGGG TCG	TTGGAGTCATGCTTTTC ATCA	61.0	229	INTERGENIC				
CaPOPI_6934	scaffold228	136549	A/AC	GATGAAATCGAGGACAG GGA	TGCGTCTTTCTCAAGTG CAT	60.0	445	INTERGENIC				
CaPOPI_6935	scaffold228	176693	ATATTATTATTATTAT/ATATTATTATTAT	GGTTTCGAGGAACTGG ACA	TTGTTTATTGACAACTC AATTGTTCT	60.1	794	INTERGENIC				
CaPOPI_6936	scaffold2289	12871	ATTT/ATTTT	TGTGTTTGTGCCATTGG ATT	AGGGAGGATGAAAACGA CCT	59.8	475	INTERGENIC				
CaPOPI_6937	scaffold229	13642	A/AG	TTGGATGCCTAAGACTG CCT	AGGTCATTTTCGTCCTC CCT	59.8	168	INTERGENIC				
CaPOPI_6938	scaffold229	81575	AAGG/AAGGAGG	TAGGGAGGACGAAAATG ACG	AACCATTTCATGTGCATC CAA	60.1	865	INTERGENIC				
CaPOPI_6939	scaffold2301	3312	C/CT	CCTAGGGTGACGAAAA TCA	ATCCTCCCGTGGCTTAT TCT	59.9	232	INTERGENIC				
CaPOPI_6940	scaffold2301	22791	CTT/CT	CAAACACACCTGTTGGA TGC	CCTCGCTTGGCTTATTC TTG	60.0	466	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPl_6941	scaffold2301	53889	CAAATGAAC TTATTGGAT/C	ACACA AATGCACCTGTT GGA	TCATTTTCGT CCTCTT GG	60.0	554	INTERGENIC				
CaPOPl_6942	scaffold2301	54382	ATG/ATGTG	CCAAAGGAGGACGAAAA TGA	GCGTGTTTGTGACATTG GAG	60.0	349	INTERGENIC				
CaPOPl_6943	scaffold2301	54476	C/CA	TGGATGCACATGATTGG TTT	AGGTCATTTTCGT CCTC CT	59.8	316	INTERGENIC				
CaPOPl_6944	scaffold2301	56350	TT/TTTAT	GAGGATACC GGGAATAA GGG	TGACAAAACTAAGGGA GGT TG	59.6	351	INTERGENIC				
CaPOPl_6945	scaffold2325	58485	TAA/TA	AGGTCGTTTTCGTCCTC CTT	GCATGCCCAAGATTGGT AAA	60.1	268	INTERGENIC				
CaPOPl_6946	scaffold2328	13583	GTTTT/GTTTTT	TGTGTTTGTGCCATTGG AGT	AGGGAGGACGAAAATGA CCT	60.0	245	INTERGENIC				
CaPOPl_6947	scaffold2345	549	C/CA	CCCCAAAAGTCCAGATG AAA	TTCGGACTAGACGAGGG CTA	60.0	453	INTERGENIC				
CaPOPl_6948	scaffold2346	28393	GA/GAA	TGGGCGATTTTGTACT TCC	CCCGAAAAGTCCAGATG AAA	59.9	395	INTERGENIC				
CaPOPl_6949	scaffold235	57295	TAAAAAA/TAAAAAAA	GCCAAAACGACCACAAA GTT	GGGAGTAGAGCTGATCA GAGGA	60.0	779	INTERGENIC				
CaPOPl_6950	scaffold235	178169	CATATATATATATATATATATATAT/C ATATATATATATATATATATATATATA TATAT	TGGAAGTTGCACCAGAC AAA	AAAGGACCAAATCAGGA AAAA	60.3	930	INTERGENIC				
CaPOPl_6951	scaffold2356	103676	AATTATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTAT/A ATTATTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTATTA	GGAACTCACATGAATTA GCAGAA	GTTTTTCACCTTTTGCTTG GC	58.4	299	INTERGENIC				
CaPOPl_6952	scaffold2356	138194	TT/TTCT	CCTTGAAGCTGTTGTCTG GCA	CCAACAACATCAAATTCA TCG	59.9	687	INTRON	Ca_24344	Q		Alcohol dehydrogenase superfamily, zinc-containing
CaPOPl_6953	scaffold2356	138866	TG/TGAG	ACCCAATTCCTTCATGTC CA	AGATCCACCAAAGGCAA CAG	60.2	213	INTRON	Ca_24344	Q		Alcohol dehydrogenase superfamily, zinc-containing
CaPOPl_6954	scaffold2356	144020	CAAAAAAAAA/CAAAAAAAAAA	GGATAACAGCGATGGGA AGA	ATCCCTCATTTGCAATCC AC	60.0	590	DRR	Ca_24345	A		Ribonuclease T2
CaPOPl_6955	scaffold2358	1353	ATTTTT/ATTTT	GATGAAATCGAGGACTG GGA	CTTTTCGGGCGATTTTC ATA	60.0	479	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6956	scaffold236	45554	GTT/GTTT	TGGACTTTTCGAGCGAC TTT	CTTCGTTTTGTGTTTCG GGT	60.0	511	INTERGENIC				
CaPOPI_6957	scaffold236	60071	TCC/TC	GGTCCGCGTTAGATT CAA	GCGGAACCTGAAACACA TTT	60.1	820	INTERGENIC				
CaPOPI_6958	scaffold2368	53512	TGGG/TGGGG	AACCCTGGAGATGGGAA AGT	CTAGCCATTAGCTTCGA CCG	59.8	607	DRR	Ca_26720	P		Zinc/iron permease
CaPOPI_6959	scaffold2368	54204	GTT/GTTT	CATCGGTCAAACACCAT CTG	GCTTTGCAGAACATGCG TAA	60.0	490	DRR	Ca_26720	P		Zinc/iron permease
CaPOPI_6960	scaffold2368	54372	CAGATA/CAGATAGATA	CATCGGTCAAACACCAT CTG	TTTGGCGTACATGATGC AAT	60.0	800	CDS (FRAME SHIFT)	Ca_26720	P		Zinc/iron permease
CaPOPI_6961	scaffold2368	59799	TC/TCTCC	CTCCAAATCCCAATCTC CAA	CTCACTGTCAAGGTGCC GTA	59.9	725	URR	Ca_26721		MYB	
CaPOPI_6962	scaffold2371	73153	TAAAAAAAAA/TAAAAAAAAA	TGTGTGCGGAGAATCTTC CCT	ATCGACGATAAGTCATC GGG	59.7	950	INTERGENIC				
CaPOPI_6963	scaffold2371	73366	ATTTTATTTT/ATTTTATTTTATTTT TATTTT	CAAGAAAAAGTTTGACT TCCGA	ATCCACGCCACATAAAC CAT	59.8	919	INTERGENIC				
CaPOPI_6964	scaffold2371	73819	GTT/GT	ATGGTTTATGTGGCGTG GAT	TGAATGAAGCGAAATG TGC	60.1	321	INTERGENIC				
CaPOPI_6965	scaffold2371	150056	TGGG/TGG	GCATTGCGGGGTATGTT TTA	CATCTTCCTTCCACAATT TCITT	59.7	970	INTERGENIC				
CaPOPI_6966	scaffold2371	287452	CTTTTTTTTT/CTTTTTTTTT	CGACTCGTGTCTAAAA CTCAA	TTTCATGCCATAAGTCAT TGTG	59.4	884	INTERGENIC				
CaPOPI_6967	scaffold2371	323810	CAGAGAGAGAGAGAGAGAGAGAGA GAGAGAGA/CAGAGAGAGAGAGAGAGA GAGAGAGAGAGAGAGAGA	GAAAACACCAAGAAGGG CAA	ACGAAACTCATCGGAAA ACG	60.1	672	INTERGENIC				
CaPOPI_6968	scaffold2373	4581	TGGTGAGGGTGAGGGTGAGGG/TGGT GAGGGTGAGGGTGAGGGTGAGGG	AGGATGTGGGTGAGGTT GAG	TCACCAGCAGCAGAAAC ATC	60.0	463	INTERGENIC				
CaPOPI_6969	scaffold2373	39709	TG/T	GGCAGTGGAGGAGAAC ACAT	TCAAACAGATGCTAAAT GCAAA	60.1	269	INTERGENIC				
CaPOPI_6970	scaffold2373	40568	CATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTA/CATTA TTATTATTATTATTATTATTATTATT ATTATTATTATTA	TGCATATTTAGAAACGTC AACGA	TTCAGGTCAAACGGTTT TCA	59.7	339	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6971	scaffold2373	53283	TTATATATATATATATATAT/TTATATA TATATATATATATATAT	GTCGCACGGAAATAACG ATT	AAGGCATGGTATTGGAG TCA	60.0	234	INTERGENIC				
CaPOPI_6972	scaffold2373	69117	TCA/TCACA	GCGAAGCTCCATCCTT TCTT	AAAAATGCGCACGACAG ATT	59.8	254	INTRON	Ca_27075			Transposase, PttA/En/Spm, plant
CaPOPI_6973	scaffold2373	88920	TT/TTTTGTATAAT	TGTGGATCTGTTTGAT CGC	TCCACACAAGCCAACTG AAA	59.7	110	INTRON	Ca_27075			Transposase, PttA/En/Spm, plant
CaPOPI_6974	scaffold2373	97344	TAAAAAAAAA/TAAAAAAAAA	AATTGTTGGATCTGCC TTG	GAGATTGAACACGCCAC TTCT	59.9	888	DRR	Ca_27075			Transposase, PttA/En/Spm, plant
CaPOPI_6975	scaffold2378	17251	AGGTGAATGGTGAATGGTGAA/AGGTG AATGGTGAATGGTGAATGGTGAA	CATCACGTGTGTGATT ACTTTATTTG	AAAACTTTTCCGCTGCTT GA	59.0	357	INTERGENIC				
CaPOPI_6976	scaffold2385	5093	TCC/TC	GAGTGAATTGTACAGC CCAAA	GGACTTGCGGTGAAGAA GAA	59.1	720	INTERGENIC				
CaPOPI_6977	scaffold2385	5335	TT/TTTCAAT	GAGTGAATTGTACAGC CCAAA	TCATTTCGACGCTTTCA CAC	59.1	968	INTERGENIC				
CaPOPI_6978	scaffold239	109266	CA/C	GGTTTCAACCCC AATGC TTA	TCGACTTGTAATCGCT TTG	59.8	808	INTERGENIC				
CaPOPI_6979	scaffold2392	10820	TTTCTTCTTCTTCTCT/TTTCTTCTTCT TCTTCTTCT	GGTAGCCCTTGGGCTA GTGT	TTGGAAGGAGCCCTTAC CTT	60.5	729	INTERGENIC				
CaPOPI_6980	scaffold2392	18107	AT/A	TTGCTCCACGAACATCT CTG	CTGAGTTGCATTGATCT CGC	60.0	870	INTERGENIC				
CaPOPI_6981	scaffold2392	20138	CATATAT/CATAT	CGCATCGAGACGAGAAA ACT	GCGCGACCCCTTATATT ACA	60.5	871	INTERGENIC				
CaPOPI_6982	scaffold2392	61104	AAGAGAGAGAGAGAGAGAGAGAGA GAGAGAGAGA/AAGAGAGAGAGAGAGA GAGAGAGAGAGAGAGAGAGAGA	CATCTCGGTTTTTCTTC ACA	CCGTTACACGGTTTTGT TCA	59.8	180	INTERGENIC				
CaPOPI_6983	scaffold2392	321808	ATTT/ATT	GGAAACTAGGCCAAA CCC	CATGCACACCCCATGTT AAA	59.8	692	INTERGENIC				
CaPOPI_6984	scaffold2392	326211	AATATTT/A	TCATCCCCACCTACAC AAG	GTGCATGTGGCTGAAAA ACA	58.4	552	INTERGENIC				
CaPOPI_6985	scaffold2392	354336	AAACAA/AAA	TGTTGCGTTTTTCA TTC TCA	TACCAAATATCCCAGGC CAA	59.3	859	DRR	Ca_25138	KL		Xeroderma pigmentosum group D protein

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_6986	scaffold2392	355121	GTTTTTTTTTTT/GTTTTTTTTTTT	TGCACCCAATCTGCAAA TAA	TGGGCTAGTTAGCTTTT GCC	60.1	433	INTERGENIC				
CaPOPI_6987	scaffold2392	355152	ATTT/ATTTT	TGCACCCAATCTGCAAA TAA	TGGGCTAGTTAGCTTTT GCC	60.1	433	INTERGENIC				
CaPOPI_6988	scaffold2392	355244	AAATTATATT/AAATTATATTTTAATTATA TT	TGCACCCAATCTGCAAA TAA	TGGGCTAGTTAGCTTTT GCC	60.1	433	INTERGENIC				
CaPOPI_6989	scaffold240	38776	TTATATATATATATATATAT/TTATATA TATATATATATATATAT	TATTTTGGATTTTGGCTC GG	TAGGAGAAACGGAGGG GTTT	59.9	575	INTERGENIC				
CaPOPI_6990	scaffold240	73293	TA/TAA	CAAGGTGTCGATGTTGG TTG	CTGGTGGCTACTTTCTT GGG	60.0	472	INTERGENIC				
CaPOPI_6991	scaffold240	150038	GTATATATATATATATATATAT/GTAT ATATATATATATATATAT	GGAGGCTTTGAAATTAG GGC	CTCCAGCGCACAAACATC TAA	60.0	783	INTERGENIC				
CaPOPI_6992	scaffold240	151385	TAAAAAAA/TAAAAAAA	AGATGCATGTGATGAAA CCAA	TACTCCCATTTCTCCC CTT	59.0	727	INTERGENIC				
CaPOPI_6993	scaffold240	156860	AAACAACA/AAACA	GACAATCGCAGGAAGTG GTT	GCATTGCACCAAAACAC AAC	60.1	699	INTERGENIC				
CaPOPI_6994	scaffold2408	4043	TTC/T	TGTTCTCATGAGGCAAT ATGCT	CAAAGAATTCACTTGATA CATGGC	59.7	594	INTERGENIC				
CaPOPI_6995	scaffold2415	126110	AGG/AG	CGTTTTTCAAAGCGAGG GTA	TGGAGAACTCTTCCGC TGT	60.2	128	INTERGENIC				
CaPOPI_6996	scaffold2415	137080	AATATATATATATATATATATATA/A ATATATATATATATATATATA	ATCGTTGGAAGTAGGGA CCA	CCACCAACAACAATTC CCT	59.4	484	INTERGENIC				
CaPOPI_6997	scaffold242	53694	TC/TCAC	TGCTTTGCGAGAAGATG TTG	ATATGCCAAATGGGAGG TCA	60.1	459	DRR	Ca_22259	R	C2H2	
CaPOPI_6998	scaffold242	123686	TTCAGAAAACTCAGAAAACTC/TTCA GAAAACTC	GCATCATGAGTTTGTG CCA	CAATGAAGGTGACACGG TTG	59.5	367	INTERGENIC				
CaPOPI_6999	scaffold242	225770	CAAAAAA/CAAAAAA	TGTGTCAGAAGGATCTT GCG	CCTCTTGATTGAGGAC CCA	60.0	667	INTERGENIC				
CaPOPI_7000	scaffold242	238083	TATGCA/TA	TGCCAAATGAAGTTGGA CAC	CTCCAATATTTGACCGC CAC	59.5	391	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7001	scaffold242	260122	T/TTG	TTCACCAACTTTGCACTCA	AAAGAAAGCCGCTTAGAGGG	60.3	620	INTERGENIC				
CaPOPI_7002	scaffold242	316249	TAAAAAAAA/TAAAAAAAAA	CAGATGGCTGCTGTTCTCAA	GAAGGACATCGTGAAGGAA	60.1	614	INTERGENIC				
CaPOPI_7003	scaffold242	393693	CAAAA/CAAAA	TTAGAGGGGCTAGGAGGGAA	TCGCCTTTGCAAAACACATAC	60.2	487	INTERGENIC				
CaPOPI_7004	scaffold242	393744	ATTTTTTTTT/ATTTTTTTTT	TTAGAGGGGCTAGGAGGGAA	TCGCCTTTGCAAAACACATAC	60.2	487	INTERGENIC				
CaPOPI_7005	scaffold242	416343	GAAAA/GAAAA	CCAGGAGATGAGAGGTCCAA	TGGCTTTCAACCATTTTTCC	60.2	435	INTERGENIC				
CaPOPI_7006	scaffold242	430857	CAAAAAAAAA/CAAAAAAAAA	CCATACCACTACTTGTTTCCCA	GCTATCCCACTTTTGGGGTT	60.1	802	INTERGENIC				
CaPOPI_7007	scaffold242	458674	TAAAAAAAA/TAAAAAAAAA	GGCAACAAGCATATTGCTCA	TTGGATTCATCATTGCCTCA	59.8	294	INTERGENIC				
CaPOPI_7008	scaffold242	494583	ATTTTTTT/ATTTTTTTT	GTTGGACACCCAACACCTC	AATTAGGGGGCATAGGGATG	60.3	794	INTERGENIC				
CaPOPI_7009	scaffold242	494657	TAAAA/TAAA	GTTGGACACCCAACACCTC	AATTAGGGGGCATAGGGATG	60.3	794	INTERGENIC				
CaPOPI_7010	scaffold242	509048	TAA/TAAA	AAAGGCCTGAAAGGGGAAA	TGGGCTAACAGAAAATCGCT	60.0	679	INTERGENIC				
CaPOPI_7011	scaffold242	509072	GTATTATTATTATTATT/ATTATTATTATTATTATTATTATT	AAAGGCCTGAAAGGGGAAA	TGGGCTAACAGAAAATCGCT	60.0	679	INTERGENIC				
CaPOPI_7012	scaffold242	523949	TC/TCC	CAAGGTGTGAGATCAACCGA	TCATGACTTTTGACCGACGA	59.7	417	INTERGENIC				
CaPOPI_7013	scaffold242	593752	ACCC/ACC	GGTTGTTTGAGCAAACCTGCAT	TTTGATTGTGTTGATGAGCCA	60.2	634	INTERGENIC				
CaPOPI_7014	scaffold242	643894	ATTTTT/ATTTTTT	TGAAATGGTTCCTTGCAATTC	ATGCCTTCCTTGTTGATGG	58.5	318	INTERGENIC				
CaPOPI_7015	scaffold242	692807	GAAA/GAAAA	TTGTCTTGCTTGCATCCTTG	TGTGTAAAGATTGGCGGTTG	60.0	399	DRR	Ca_22275	F		Guanylate kinase

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7016	scaffold242	696950	TTATATATATATAT/TTATATATATATATATATAT	CTGGCCATGAGGAATGAGTT	AACTACGCCTTGGTGGA TTG	60.1	412	INTERGENIC				
CaPOPI_7017	scaffold242	710240	TTTATTATTA/TTTATTA	ACTTGTTCACCCATGCCA	CTTCACGTGAGCCAAAC TCA	60.0	510	INTERGENIC				
CaPOPI_7018	scaffold242	721932	ATT/ATTGTT	TGGTGACTCGTTCATATACCCA	AAAGACGGTGCCAAAAA TGT	60.2	882	INTERGENIC				
CaPOPI_7019	scaffold242	722081	GAAAAA/GAAAA	CACAAGATCTTTAAGTTCATATTTTCA	TTTCTCCATCCAAATTCC CA	57.3	951	INTERGENIC				
CaPOPI_7020	scaffold242	735562	A/AC	CGAACTTGAGAATTCACCGC	GTGGAAGGGGATTGG ATT	60.8	371	INTERGENIC				
CaPOPI_7021	scaffold242	771258	TAAAAAAAA/TAAAAAAAAA	CGAGATGGTGACGTGATA	CACACGAATACGATTCC ACG	60.0	984	INTERGENIC				
CaPOPI_7022	scaffold242	771316	TAAAAAAAA/TAAAAAAAAA	TGTGCTTCATGGGTCAA GTC	CACACGAATACGATTCC ACG	59.7	469	INTERGENIC				
CaPOPI_7023	scaffold242	804134	CTTT/CTTTT	TGAAATGGAAATGCTACCATCA	TGGTCAGAAACAACGCA AGA	60.3	710	INTERGENIC				
CaPOPI_7024	scaffold242	804233	CTTTTTTTTT/CTTTTTTTTTT	TGAAATGGAAATGCTACCATCA	TGGTCAGAAACAACGCA AGA	60.3	710	INTERGENIC				
CaPOPI_7025	scaffold2433	2492	ATT/AT	TATGATCCCGCTTGACACAA	TTTGGGAAAATCCACAA ACA	60.1	369	URR	Ca_27860			
CaPOPI_7026	scaffold2434	76263	TGG/TG	TTCTTCGTTTTGTAGTTGTACTCAATG	GGCAACAAGAACCGGAAAC	60.0	638	INTERGENIC				
CaPOPI_7027	scaffold2434	76563	TAAAA/TAAAAA	TTCGGTCTTGTTGCC TCT	CCTTTATCTTCTTGTTGG CCG	59.9	382	INTERGENIC				
CaPOPI_7028	scaffold2446	7253	A/AC	TTCTCTGCGAAAATAAACCTC	TGCCCTTGTTTCAGTTCAA	59.7	394	INTERGENIC				
CaPOPI_7029	scaffold249	73354	AA/AATTGA	CAGCCCAAAATACTGCAT	CTTTGTTGGTGC GTGTG TTC	60.0	422	INTERGENIC				
CaPOPI_7030	scaffold25	35858	ATTTT/ATTT	AGGTCAATTTTCGTCCTCCT	TGGATGCACAAGATCGG TTA	59.9	168	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7031	scaffold25	51854	AC/A	TCCGTCCTCCCTAGGCTAT	GGACCAAAATGACCCAAATG	60.1	388	INTERGENIC				
CaPOPI_7032	scaffold25	72914	ATTTT/ATTTT	TGAACCAATCTTGTGCACTCC	AGGGAGGACGAAAATGACCT	59.5	672	INTERGENIC				
CaPOPI_7033	scaffold2501	7458	TG/T	AACCGATCTTGTGATCAA	AGGGAGGACGAAAATGACCT	60.5	373	INTERGENIC				
CaPOPI_7034	scaffold2505	1462	TCCC/TCCCC	ATTCCAAACCAAAACCCTCC	TTGCTCACTACCACGCTACG	60.0	884	INTERGENIC				
CaPOPI_7035	scaffold2505	1793	TG/TGGAAGG	CGTTTCCACACAACCACAAA	TTGCTCACTACCACGCTACG	60.4	112	INTERGENIC				
CaPOPI_7036	scaffold2511	1442	TTGTG/TTGTGTG	AAGCTTCAATGGCCAAAAGA	CCTGACAAGTTTCCTTGGA	59.8	246	INTERGENIC				
CaPOPI_7037	scaffold2511	7402	CT/C	TGTTGAAGAAGGTTTGTGG	CCAATAACGATCAAGCATCG	59.9	359	INTERGENIC				
CaPOPI_7038	scaffold2522	24043	ATTT/ATTTT	AGGTGTGTTTGTGCATTGGA	AGGGAGGACGAAAATGACCT	60.0	248	INTERGENIC				
CaPOPI_7039	scaffold2528	19502	GTTTTT/GTTTT	GTCTCCGTTGGCTTATCA	GGACGAAAATGACCAAAAGG	60.1	488	INTERGENIC				
CaPOPI_7040	scaffold2542	2207	TAGGAG/TAG	TCATTTGGACTTTTCGGGAG	TCAATTTGGGTTTCAGGTGT	60.0	816	INTERGENIC				
CaPOPI_7041	scaffold2557	49964	AA/AATTA	CTTGGGCAAAACACCTCCTAA	TGCATTGGTATATGGAGGCT	60.1	907	INTERGENIC				
CaPOPI_7042	scaffold2557	101354	CATATATATATA/CATATATATATA	TCCCTCCAACAAACACACA	CGGTGAATCCTTTACGGAGA	60.0	130	INTERGENIC				
CaPOPI_7043	scaffold2557	102326	CT/CGCTCTTTTTGT	ATGGCGAACAATCACACAA	TTGTAGCAATCATGTGGGA	60.0	644	INTERGENIC				
CaPOPI_7044	scaffold2557	112937	CGG/CGGTTGG	TTTTAGCTTTCCATCGCCGTG	CTCAGAGGGTCCAATTCCA	60.3	717	INTERGENIC				
CaPOPI_7045	scaffold2560	60629	T/TA	GGAGAACATTATCCGTTTCCA	TCAAATTTTCATCCTCACCCA	60.2	536	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7046	scaffold2560	61168	ACACGCACGCAC/ACACGCACGCACGCACGCAC	GGGTGAGGATGAAATTTGAAGA	ATTCGGTAGCACATTCGTCC	60.3	864	INTERGENIC				
CaPOPI_7047	scaffold2560	61734	TC/T	GGACGAATGTGCTACCGAAT	GCACCCGCAAGAATAACAT	60.0	121	INTERGENIC				
CaPOPI_7048	scaffold2569	65788	GATATATATATATATATATATAT/GATATATATATATATATATATATAT	GCCGCGGTCTATTTGTGTAT	CCCTGTCCAGATTGAGTGGT	60.0	646	INTERGENIC				
CaPOPI_7049	scaffold2575	196132	C/CA	ACTTTTCACCACATCCCTCG	ATCCATTCCTCCACATTGAAA	60.0	347	INTERGENIC				
CaPOPI_7050	scaffold2575	245742	ATTTTTTTT/ATTTTTTTTT	CGCAATAAATTTTTTGACGCC	TACCCATCAGGGCAGAACTC	60.4	535	INTERGENIC				
CaPOPI_7051	scaffold2575	278772	TGAAGAAG/TGAAG	TGGTGGCAAATGATGAAGAA	CAGGGACTACATCCAACAAAA	60.0	769	INTERGENIC				
CaPOPI_7052	scaffold2575	279175	CTAT/CTATTAT	TTTGATTGACTTAGCACACAG	TAAAAGATGATGTGTGTGTGT	58.8	557	INTERGENIC				
CaPOPI_7053	scaffold2575	279306	TAA/TA	TTTTTGTGGATGTAGTCCCTG	CATGAACATTTAAGAGTTTGCAATT	59.0	583	INTERGENIC				
CaPOPI_7054	scaffold2575	280082	C/CATTGATA	TCCCAAGGTATCATTGTTCTCTTT	TCGGAGTTTTGTGTGAGTGTG	59.0	316	INTERGENIC				
CaPOPI_7055	scaffold2575	280195	TTA/T	CACCTTTGTCCCTGAGCTGT	TCGGAGTTTTGTGTGAGTGTG	60.3	178	INTERGENIC				
CaPOPI_7056	scaffold2575	282023	CGAGAG/CGAG	GAACCCGCCTAACATTTCATCA	TTCAATTGTCCATAAGCATGCA	59.9	401	INTERGENIC				
CaPOPI_7057	scaffold26	145340	CAAAACAAAACAAA/CAAAACAAA	GAGGAGAAGGGAGAAATGGG	GGCTCGGAGGTATTTTAGCC	60.0	287	INTERGENIC				
CaPOPI_7058	scaffold26	506230	GTT/GTTT	ATTGGCGTGAACACCGTTAG	TGACGGGTCTGCACAATTATTA	60.0	538	INTERGENIC				
CaPOPI_7059	scaffold260	287454	AATATATATATATATATATATAT/AAATATATATATATATATATATATAT	CGTGAGACAGGGAGAGGAAG	CGGTGAATCCTTTACGGAGA	60.0	281	INTERGENIC				
CaPOPI_7060	scaffold260	341696	AT/ATGT	AGGAAGAGTGGAGTTGCGAA	GCATTCAGCAGCAAAAACAA	60.0	670	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7061	scaffold260	356606	GTTT/GTTTT	ATCGATTGATTCAGCC CAG	TTCTCATCTCCATTCCC GTC	60.0	154	INTERGENIC				
CaPOPI_7062	scaffold260	413792	A/AG	TATTTTGGA TTTTGGGCT GG	AAATCTCTGCTCGCGA TGT	59.9	668	INTERGENIC				
CaPOPI_7063	scaffold2603	6501	CCA/CCACA	AGCAGCTTCAAGCAAAG CTC	TGAACCA GTCCAATTCA ACAGT	60.0	485	INTERGENIC				
CaPOPI_7064	scaffold2603	9101	TA/TAA	GGCCAACCAAAAAGTTT GAA	ATTGAGTGAGTTTGCC CAC	60.0	552	INTERGENIC				
CaPOPI_7065	scaffold2603	19509	ATTTTTTTTT/ATTTTTTTTTT	TTGCGTGTGATCATG TGA	TCACCTTAGGGTTGAAA TGA	60.1	884	INTERGENIC				
CaPOPI_7066	scaffold2603	67369	GTT/G	AATCCGCAACGGAGTTT ATG	TGAACGAGCTGAGAGAA GCA	60.0	617	INTERGENIC				
CaPOPI_7067	scaffold2617	66007	AATATATATATATATATATATATAT ATATAT/AATATATATATATATATATAT ATATATATATAT	GACCCAACCATGTGGAG TTT	GGTGAGTGATCGCATCC TTT	59.7	594	INTERGENIC				
CaPOPI_7068	scaffold2617	195587	GAATATATTAAATA/GAATATATTAAATA TATTAATA	GACCGCGTAGATGTGGA ACT	GAATGCCCTACTTTTTG GCA	60.1	634	DRR	Ca_21875			Aminotransferase-like, plant mobile domain
CaPOPI_7069	scaffold2617	234200	AATATATATATATATATATATATAT/AA TATATATATATATATATATATAT	TTTGGGAAACTGAACCA ACA	AAAAATTGAAATTATCAAG AAAGTTGTG	59.0	322	DRR	Ca_21877			
CaPOPI_7070	scaffold2617	320997	TAAAA/TAAA	TGGGGTATT CCTTTACG TCCT	TGAAAGAGGGGAAAAGG AGC	57.6	296	DRR	Ca_21883		WRKY	DNA-binding WRKY
CaPOPI_7071	scaffold2617	321825	TAAAA/TAAAAAAAAA	TTGGTCATGCGCACATA ATA	GATGGCTGTGTCGGAGA CTT	58.6	529	DRR	Ca_21883		WRKY	DNA-binding WRKY
CaPOPI_7072	scaffold2617	324497	TGTG/T	AAACAAGTTGGTGGTGG AGC	AAAGTTAATTCAAATGCA CTGTCA	60.0	290	INTERGENIC				
CaPOPI_7073	scaffold2617	402483	GAA/GAAA	GTTGCAAGGGTGGAGT GATT	AACAATTGTGAAACGTC TCCG	60.0	640	INTERGENIC				
CaPOPI_7074	scaffold2617	402519	TG/T	GTTGCAAGGGTGGAGT GATT	AACAATTGTGAAACGTC TCCG	60.0	640	INTERGENIC				
CaPOPI_7075	scaffold263	177694	A/AC	TCTGATGCAGTGT TTGG CTC	TTTTCTGGTCTGCCTTG GTC	60.0	329	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7076	scaffold2651	4275	TT/TTGT	CTTGTGCATCCAATAGG GGT	TCTTCATCCAATGCCAC AAA	59.8	640	INTERGENIC				
CaPOPI_7077	scaffold2660	12451	TAAAA/TAAAAA	CCTAGGGACGACGAAAA TGA	TGCATCCAACAGGTGTG TTT	60.1	462	INTERGENIC				
CaPOPI_7078	scaffold2662	1313	T/TC	TGCACCTTGCAACACATC TCA	TGGCTATTGATTATCCC ATTTTG	60.0	866	INTERGENIC				
CaPOPI_7079	scaffold2662	10211	AAATAATAATAATAATAATAATA AT/AAATAATAATAATAATAATA ATAATAAT	TTGCTCCTACGTATCTC CCG	TTCTTTTCGCTATTTTAT TTTCGTG	60.2	699	INTERGENIC				
CaPOPI_7080	scaffold2662	26227	TT/TTCT	AACACCATGAAACGCTC CTC	CGAAGCCGAGAAAATGA CTC	60.1	589	INTERGENIC				
CaPOPI_7081	scaffold2662	31062	TAA/TA	AGAGGATGCGGATCAAT GTC	GGACAACCTGGGAAAAG TGA	60.0	898	INTERGENIC				
CaPOPI_7082	scaffold2669	16328	AATATTGATATTGAT/AATATTGAT	TTTTAGGCGATTCTACG TGC	TTGAGGGGTGGCAAGTT TAG	58.1	641	INTERGENIC				
CaPOPI_7083	scaffold2692	13450	GGTTAAGTT/GGTT	TTGAGAAAACCGCCAT ACC	CCCTCTAAGCCCCAGG TTA	59.9	730	INTERGENIC				
CaPOPI_7084	scaffold2692	14114	TATAATAATAATAATAATAATAA TAATAATAATAATAATAATA/TA TAATAATAATAATAATAATAATA ATAATAATAATAA	TAACCTGGGGCTTTAGA GGG	TTTGACAGGTCAATTTCA AACC	60.4	654	INTERGENIC				
CaPOPI_7085	scaffold2692	14565	ATTTTTTT/ATTTTTTT	ACCTGTCAAAGTTTTC AGCA	TCCTTCACCAACCAAC AAA	58.9	420	INTERGENIC				
CaPOPI_7086	scaffold2692	14759	ATTTTTTT/ATTTTTTT	ACCTGTCAAAGTTTTC AGCA	TTTCCTTCACCAACCAAA CA	58.9	422	INTERGENIC				
CaPOPI_7087	scaffold271	179145	ATTTTTTT/ATTTTTTT	GAGGTGCAGAAAATGC AGC	TTGCTCCTACGTATCTC CCG	60.9	592	INTERGENIC				
CaPOPI_7088	scaffold271	196964	ATTTTTTTTT/ATTTTTTTTT	TATCATTTAGGGTGAGG GCG	AGAAGTGGAAGGGGTG CCT	59.9	605	INTERGENIC				
CaPOPI_7089	scaffold271	205973	GAA/GA	GCACCTGAGTAAATTC GGT	TATTTTGATTTTGCTC GG	60.0	692	DRR	Ca_25334			
CaPOPI_7090	scaffold271	244115	TTATATATATATATATATATATAT T/TTATATATATATATATATATAT ATAT	GAGAAAGGAGGGAAATT GGC	CATCGCCACCGTAGTA AGT	60.0	577	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7091	scaffold2722	70279	TAAAAAAAA/TAAAAAAAA	TTTGTACCAATCCATCAG TTTTT	TGCAGTTGAGTAGATAT GCCAAA	59.7	883	INTERGENIC				
CaPOPI_7092	scaffold2722	77542	ATTTTTTTTT/ATTTTTTTTT	GGAAGGAGAACGCCTAA GGT	AAAAATGGATCTCACGG TGC	59.7	946	URR	Ca_27216		C2H2	Glycoside hydrolase, family 28
CaPOPI_7093	scaffold2726	4506	G/GA	CAACACCCCTATTGGA TGC	AGGTCATTTTCGTCTC CCT	60.2	380	INTERGENIC				
CaPOPI_7094	scaffold2729	5336	AAAA/AAACAAA	CAAATGCCACACATTTAA CGA	AATTGTGTTTCGAGTTC CGC	59.5	787	INTERGENIC				
CaPOPI_7095	scaffold273	49066	TAAAAAAAA/TAAAAAAAA	TTTCAGGCGAAATCGT ACC	ATAACCCGAACCTCAA CCC	60.1	547	INTERGENIC				
CaPOPI_7096	scaffold273	190574	CAAAAAAAAA/CAAAAAAAAA	GAGAAGGTCCCAAGGG TTC	CGCTCTTCCCCTTCTC TTT	59.9	757	DRR	Ca_26226			
CaPOPI_7097	scaffold2734	606	TGCAAG/TGCAAGCAAG	TTTCTTTTTCCCTCCAAG CA	GGGGGAGAGAACAATC CAT	59.8	550	INTERGENIC				
CaPOPI_7098	scaffold2736	3361	ATTTTTTT/ATTTTTTTTT	TGGACAAAAGCGTTGT AAA	GA CTGGGCATTTCTCT GAA	59.2	340	INTERGENIC				
CaPOPI_7099	scaffold2736	3536	GAAAAA/GAAAAA	TTCAAGGAAATGCCCA GTC	TGTTTGCGACAACACAA CAA	60.1	385	INTERGENIC				
CaPOPI_7100	scaffold2737	9370	AAATAATAATAA/AAATAATAATAA AATAA	TCTTCGTTTTACGGTTTT ATTCA	AACATATAACAAATTGA GTTGTCAA	59.2	419	INTERGENIC				
CaPOPI_7101	scaffold2738	4048	ATTT/ATTTT	GAGAGCTTTCGTTTCGA TGG	GAGCCACGAGGCATGAT ATT	60.0	775	INTERGENIC				
CaPOPI_7102	scaffold2738	27122	GTTTTT/GTTTTTTTTT	TACCCTGTGGATGGGAA TGT	CAAAAGATGTGTAACGG CCC	60.1	441	INTERGENIC				
CaPOPI_7103	scaffold2738	27897	ATATGAACTTAATGTTATGAACTTA/ ATATGAACTTAA	GGAGAAGGCATGGATGT TGT	TTGCATCGTACCACTTT GGA	59.9	519	INTERGENIC				
CaPOPI_7104	scaffold2744	48855	T/TCG	ACCCAAATGCATCAGAC TCC	TGTGTGTTTGTGGAG GGA	59.9	565	INTERGENIC				
CaPOPI_7105	scaffold2748	27802	TCA/TCACA	TCTCGTTTAGATCGTCC GCT	TGGAATTCTTCTCCAAT GCC	60.0	551	INTRON	Ca_28188			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7106	scaffold275	67453	AG/A	CGTACTTGCATCCATGAACA	CATCGCCGTAGTCAAAC TCA	59.6	563	INTERGENIC				
CaPOPI_7107	scaffold275	162362	TG/TGG	CGAAGCACAAAGGAGATGACA	GGTTTGGGCAATCTGCT TTA	60.0	762	INTERGENIC				
CaPOPI_7108	scaffold275	187416	CTT/C	CAGCAGCAGGAAAACATCAA	TCTTATCCTTGCGGGAA TTG	60.0	393	INTERGENIC				
CaPOPI_7109	scaffold275	377072	AATATATATATATATATATATAT/AATATATATATATATATATATATATATATAT	TCAAGATACCCAGTGCA CCA	AGCGACATGTGAACAAC AGC	60.1	551	INTERGENIC				
CaPOPI_7110	scaffold2763	9760	C/CCTCACG	ATGCCAGTCGTTATTCC CAG	GAGATGCCATTGAAGCC ATT	60.0	400	CDS (large-effect mutations)	Ca_24393	R		
CaPOPI_7111	scaffold2763	81370	T/TG	AACCAACTGGTCCTGAC TGG	GAATGGAGAAGGTCGTG CAT	60.0	536	DRR	Ca_24399			
CaPOPI_7112	scaffold2766	1362	GTATATATATATATATATATATATA T/GTGATATATATATATATATATATA TATATATAT	TTTGGAATTGTGATTATG TGTGTG	CAAACCCATCGGCTCTCC TTA	59.7	421	INTERGENIC				
CaPOPI_7113	scaffold2766	6783	AATATATATATATATATATATATAT ATATATATATAT/AATATATATATATAT ATATATATATATATATATATATATAT	CGGCAGTAGGGATAACC AAA	TGTTGAAGATGAAATCTT GGCA	60.0	652	INTERGENIC				
CaPOPI_7114	scaffold277	4447	TACTGA/TA	TAAAGGAGCATCCGTGG AAT	TGCATGTATCATAGACC GCC	59.5	472	INTERGENIC				
CaPOPI_7115	scaffold277	4542	AATATATATATATATATATA/AATATATAT ATATATATA	TAAAGGAGCATCCGTGG AAT	TGCATGTATCATAGACC GCC	59.5	472	INTERGENIC				
CaPOPI_7116	scaffold277	4861	AATATATAT/AATATAT	TGGAGAAACCTTGTGAA CCA	GAAACGGAAGGGGAAC AAT	59.1	316	INTERGENIC				
CaPOPI_7117	scaffold277	205504	TTATATATATATATATATATAT/TGATAT ATATATATATATATAT	GGTTTAGGTGTGGGAGT GGA	TGATACAAGGTTC AACCGCA	59.8	444	DRR	Ca_25752			
CaPOPI_7118	scaffold277	252454	CTCTT/CT	CCCATTGCATTGCCTTC TAT	TAAAGGACCATGTCGGG AAG	59.9	329	INTERGENIC				
CaPOPI_7119	scaffold2770	650	AT/ATT	AATCGATTGATTCAGCC CAG	TTTACAGGCAGCGGAAA AGT	60.0	682	INTERGENIC				
CaPOPI_7120	scaffold2777	4052	GTTAAC/G	CATTGATTAAGAACGCA AATGG	AGTTGGTCCCAAAAGTG CAA	59.5	199	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7121	scaffold2782	6224	AGG/AGGG	CTTTTCGGGCGATTTTCATA	GATGAAATCGAGGACTGGGA	60.0	483	INTERGENIC				
CaPOPI_7122	scaffold2782	27408	GAAAAAAAA/GAAAAAAAAA	CTCGAAACCCGAAACACAAAT	CGAATTTTCGTTGTCAACTCAT	60.0	574	INTERGENIC				
CaPOPI_7123	scaffold2792	14181	GTTTTT/GTTTT	AGGTTTCATTTGGGTCATTGG	AACCTTGGGAGGACGAAAT	59.6	973	INTERGENIC				
CaPOPI_7124	scaffold280	15504	ACTAAACCTAAACCTAAA/ACTAAACCTAAACCTAAACCTAAA	AAACCTGAACCGCAAAACAC	TCGTCCAATAAGAACAAGTCAA	60.0	150	INTERGENIC				
CaPOPI_7125	scaffold280	52649	CTCAAT/CTCAATTGATTTATCAAT	TGGTCATGCAGAAACTAGC	ACTCTCATCTGAGGCGAAG	60.0	330	INTERGENIC				
CaPOPI_7126	scaffold280	83786	CAAAACCTAAACCTAAACCTAAAC/CAAAACCTAAACCTAAACCTAAACCTAAAC	CCAAAAACCAAAACCAAAAA	TCAAGCTATTAGTGCAAAAGAGTCA	58.9	532	INTERGENIC				
CaPOPI_7127	scaffold280	114213	AG/AGCTTTGG	AAGGCTACTCACTCGCGGTA	ATGAGTTCTTTGCATTGGGC	60.0	575	INTERGENIC				
CaPOPI_7128	scaffold280	128741	CAA/CAAA	ATTCCAAACCAAAACCTCC	TGATTTTGGGGGAAAAATGAA	60.0	943	INTERGENIC				
CaPOPI_7129	scaffold280	266426	TAAC/T	TCTTCGTTATGCAGTCAAACT	CGGAACCCGAAACAAGTTA	58.9	598	INTERGENIC				
CaPOPI_7130	scaffold281	1263	CAA/CAATTAA	TGTTCGACACTCAGTCTACGG	TGCATGCCCTTTGATTTACA	60.3	287	INTERGENIC				
CaPOPI_7131	scaffold281	1388	GAAAAAAAA/GAAAAAAAA	TGTTCGACACTCAGTCTACGG	TGCATGCCCTTTGATTTACA	60.3	287	INTERGENIC				
CaPOPI_7132	scaffold281	1467	GGCATGCATG/GGCATG	TGTTCGACACTCAGTCTACGG	ATCGGAAAAGTGACATTGGG	60.3	515	INTERGENIC				
CaPOPI_7133	scaffold281	2224	CT/C	TGGGCAGATTTGTAACACGA	GCGAAACCCGATTCTATTGT	60.1	593	INTERGENIC				
CaPOPI_7134	scaffold281	3002	TAAAA/TAAAAA	ACAATAGAATCGGGTTTCGC	AGGACTATTTTGGTCTCCCA	59.0	623	INTERGENIC				
CaPOPI_7135	scaffold281	3090	AATATATATATATAT/AATATATATAT	ACAATAGAATCGGGTTTCGC	AGGACTATTTTGGTCTCCCA	59.0	623	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7136	scaffold281	3414	GAAAAGAAA/GAAAAGAAAAGAAA	TGGGAGACCAAAATAG TCCT	CGTTGACCATTTTAAGC TTGG	57.7	534	INTERGENIC				
CaPOPI_7137	scaffold281	3735	A/AATT	TGGGAGACCAAAATAG TCCT	CAAGAGGGGTGCAAGT GTT	57.7	648	INTERGENIC				
CaPOPI_7138	scaffold281	4125	TGG/TG	AACACTTGCAACCCCTC TTG	ATGATGATTTTCTCCCC GTG	60.1	595	INTERGENIC				
CaPOPI_7139	scaffold281	4227	AG/AGGAATTATG	AACACTTGCAACCCCTC TTG	ATGATGATTTTCTCCCC GTG	60.1	595	INTERGENIC				
CaPOPI_7140	scaffold2812	19841	CT/C	GACGCTTCTCCTCCTG CTA	TGAAGATAAAGCAATCC CCG	59.7	761	INTRON	Ca_26641		TALE	Serine/threonine-protein kinase domain
CaPOPI_7141	scaffold2815	71444	T/TGCG	CGGTGCTAGTGGACCA TTT	CCCGCTGACAGTTAAT CAT	60.0	788	INTERGENIC				
CaPOPI_7142	scaffold284	4461	CTC/CTCCTCCTCCTCATC	TACGATGATGAACAGTC GGC	TTGGTTTCAAGACCTGC ATCT	59.7	424	INTERGENIC				
CaPOPI_7143	scaffold284	14484	ATTTT/ATTTT	TTTGCCTCATTGCTTTT CC	CCCCTTTCTCCTAGAAT CGC	60.2	294	INTERGENIC				
CaPOPI_7144	scaffold284	15317	ATTTTTTTTCTGCGTTTTTTTTC/ATT TTTTTTC	CCAGAATCGGACTTGT TCG	TTCTTGTGTGGAGTGT GGC	60.6	515	INTERGENIC				
CaPOPI_7145	scaffold284	40796	TA/T	TCCTGCACTTGAATGGA CAG	TTGGGTTTTTCTTTCAAC GG	59.8	693	INTERGENIC				
CaPOPI_7146	scaffold284	205698	AATATATATATATAT/AATATATATATA TATATAT	GGTCATGAGAAGGGGA GTGA	AAATTGGTCCACTAGCA CCG	60.0	480	INTERGENIC				
CaPOPI_7147	scaffold284	428305	CTATTATTATTATT/CTATTATTATTA TTATTATT	TGTTGTTTACACACTTTA AGATGAAGA	GTCGCGTCTTCCATTCA TTT	58.5	361	INTERGENIC				
CaPOPI_7148	scaffold284	483743	ATTTTTTTTTT/ATTTTTTTTTT	CAATCCGAAAGTCCTCC AAA	GCTTGAGGCACAAATTG ACA	60.0	847	INTERGENIC				
CaPOPI_7149	scaffold284	516497	AATATATATATATATATATATATATAT ATATATATAT/AATATATATATATATAT ATATATATAT	CCTCCAATAGCCCCAA AAT	GTTCCCTTGGCAAGTCA GGA	60.1	720	DRR	Ca_20600	C	C3H	Oxidoreductase, molybdopterin-binding domain
CaPOPI_7150	scaffold284	680277	CATATATATATATATATATATA/CATA TATATATATATATATA	CCCACATGAAAACTCC ACC	TAAGGGCTGAACCAAAA TCG	60.2	779	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7151	scaffold2845	27323	CA/CAA	CCCTGATGGAAAATCAA TGC	TCCAGTCCCCTAGTCA GAA	60.3	858	INTERGENIC				
CaPOPI_7152	scaffold2848	2441	GCTCCTCT/GCTCCT	AAGGCAGCAGACCTCAA AAA	GCACACGACCTTCTCGT ACA	60.0	449	CDS (large-effect mutations)	Ca_27862			Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_7153	scaffold2871	30418	AGT/AGTGT	GGTTTGGATTGGGCT ACA	GGGTATGGCTTTGATC ATGT	59.8	521	INTERGENIC				
CaPOPI_7154	scaffold2871	32080	TG/TGG	CCCTGACCAAAACCGTA AAA	GTGCCATTTATCCTTG CTT	59.8	916	INTERGENIC				
CaPOPI_7155	scaffold2871	33759	GTTTTATTTATTTTAT/GTTTTATTTAT	TACCAATTGCGTTAGCG ATG	TCGTTCTCCTTCGTCGT CTT	59.7	487	INTERGENIC				
CaPOPI_7156	scaffold2893	10683	AGG/AGGG	GCCAGATCTTTCGATTC AGC	CCTTCAATGGAACCGCA TAC	59.9	255	INTERGENIC				
CaPOPI_7157	scaffold2896	30850	GAAAAAAAAA/GAAAAAAAAA	CTGGCACACAAGCACA ACT	AGAGACAGAGGTGGGAA GCA	59.9	521	INTERGENIC				
CaPOPI_7158	scaffold29	101084	AGG/AGGG	CGCGGAACCTGAAATAC AAT	TCCAGATGAAATCGAGG ACC	60.0	401	INTERGENIC				
CaPOPI_7159	scaffold290	112115	A/ACTAAC	CATGGGAAAATCGTTGA GGT	TTGGGTCCTAGCTTTCT CCA	59.8	839	INTERGENIC				
CaPOPI_7160	scaffold290	122806	AG/AAGCTTTGCGGG	ACATTTGTGGCGGTCTT AGG	ACAAAGGAGACGTTTG TGG	60.0	243	INTERGENIC				
CaPOPI_7161	scaffold290	124623	CTTTTTTTTT/CTTTTTTTTTT	AATTTTGGTTGACTTTGC CG	GAGGCTTTTGCATGGA GAG	60.0	526	INTERGENIC				
CaPOPI_7162	scaffold290	178205	TAAAAAAAAA/TAAAAAAAAA	CACATCGAAGCAATCGT CAT	TCAGAACTGAACTTTGC CCA	59.7	767	INTRON	Ca_19830	F		Xanthine/uracil/vitamin C permease
CaPOPI_7163	scaffold290	189028	TAAAAAAAAA/TAAAAAAAAA	TCAGGAGGATGACGGGT TAC	TTGATCATGGGGTGAT TTT	59.9	624	INTRON	Ca_19830	F		Xanthine/uracil/vitamin C permease
CaPOPI_7164	scaffold290	204899	GTACACAATAT/GT	ACCTTGGTCCGATGACA AAC	TTTCCCAATTGAAAGGAT TGA	59.8	656	INTRON	Ca_19830	F		Xanthine/uracil/vitamin C permease
CaPOPI_7165	scaffold290	206705	GAT/GATCAATTAAAT	TCCCTCTTTCAAGTCAA CTCA	TCGCTCTAGGCTAATCC AACT	59.0	318	INTRON	Ca_19830	F		Xanthine/uracil/vitamin C permease

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7166	scaffold290	231729	AATATATATATATATATA/AATATATATATATATATATA	TTTCACACCTCAATGCGAAG	ACCGAATGGCAGATTCAAAC	59.8	789	INTERGENIC				
CaPOPI_7167	scaffold290	233617	A/AC	GGACGACCTAGCCTATCCC	TGATCCGTTACAAAATGCCA	59.9	430	INTERGENIC				
CaPOPI_7168	scaffold290	280894	TAATTATTG/TAATTATTGAATTATTG	GGTTCGCATATTTGCCTTGT	TTGGCACATCTACTTCACTGC	60.0	222	INTERGENIC				
CaPOPI_7169	scaffold290	285456	AG/AGG	TTGGTCGTTTGAGCCTTCT	GGGGCTTCAGTAAGGGTAGG	59.9	436	INTERGENIC				
CaPOPI_7170	scaffold290	293241	ATTATTTATTTATTTATTTATTTATT/ATTATTTATTTATTTATTTATTTATT	TTGCTCTTAATTTTCTCCGA	GTGAGTCTGCGACCACTTGA	58.2	602	INTERGENIC				
CaPOPI_7171	scaffold290	377065	ATT/AT	TGCTTCAAGCTGCAATCTCT	CGCCTTGGTTACCTTCAT	58.9	789	INTERGENIC				
CaPOPI_7172	scaffold290	400824	TAAAAAAAA/TAAAAAAAA	TTGTGTTGCATTGTGGATTCT	CACAGCCCTCTAAACCAAC	59.0	650	INTERGENIC				
CaPOPI_7173	scaffold290	418174	GT/GTT	GAAGAGGCTAAACGGGGAAG	ATGCAAAGGTTGGTCATTCC	60.2	409	INTERGENIC				
CaPOPI_7174	scaffold290	429778	ATTTTTTTTT/ATTTTTTTTT	ACTCCGATGCACTGTGATCCC	TAATGTGTCGTGCTTCAGCC	60.0	751	INTERGENIC				
CaPOPI_7175	scaffold290	434027	CTTTTTTT/CTTTTTTTTT	GGGACCATGCTTTTTGCTAT	ACAAGGCAAATATGCGAACC	59.0	243	INTERGENIC				
CaPOPI_7176	scaffold290	434453	ATTATTTTATTTTATT/ATTATTTTATTITTTATTTTATT	GGTTCGCATATTTGCCTTGT	TGCGGTAGAGTAAATGTGACAAA	60.0	570	INTERGENIC				
CaPOPI_7177	scaffold290	452067	GAAA/GAA	GAAAAATTCACCACCGATTAGG	TACAATCAGGATGCGTCAACAA	59.7	632	INTERGENIC				
CaPOPI_7178	scaffold290	533287	TAAAAAAA/TAAAAAAA	CGATGATCATTCACCTTACCA	ACATTGGGTTTGGTTATGCC	58.4	839	INTERGENIC				
CaPOPI_7179	scaffold290	571667	ATTTTT/ATTTTT	ATTCCTCCATTCTTAATGCC	GGTAAGGGCTCCTTCCAAC	60.0	529	INTERGENIC				
CaPOPI_7180	scaffold290	572854	AATATATATATATATATAT/AATATATATATATATATATAT	TCACCAAGCAAACCCACATA	CATGCAACCAAATCGACAAC	60.0	554	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7196	scaffold2932	2304	GTTTT/GTTTTT	ATTGTCGTCCTCCCTAG GCT	ACACCTATTGGATGCC AAG	60.1	670	INTERGENIC				
CaPOPI_7197	scaffold2950	515	CA/CATTA	TGGAATAATCCACCGGG TAA	ACAACGACAACGACAAC GTG	60.0	782	INTERGENIC				
CaPOPI_7198	scaffold2950	671	CTTTTTTTTT/CTTTTTTTT	TACGGTCTCCAAATCC CTG	TTTGTTGGTTTGCCTT ACC	59.9	846	INTERGENIC				
CaPOPI_7199	scaffold2950	1436	ATTTT/ATTTT	GTCCTCTGAAACCTCCC ACA	TTTTGGGTCGTGACACT TGA	60.1	337	INTERGENIC				
CaPOPI_7200	scaffold2950	6843	A/AG	CCAAATTACAACCGACC CAC	AAAGGCGCTCCTCTATC ACA	60.1	650	INTERGENIC				
CaPOPI_7201	scaffold2950	6903	AAA/AAATAA	CCAAATTACAACCGACC CAC	AAAGGCGCTCCTCTATC ACA	60.1	650	INTERGENIC				
CaPOPI_7202	scaffold2950	7749	ATTTT/ATTTT	CACGTTTTAAAGGGTT TGC	GGTAAAGCCATTCTGA CCA	59.5	845	INTRON	Ca_27517	L	FAR1	BRCT
CaPOPI_7203	scaffold2950	8204	T/TG	TGGTCAGATGGGCTTT ACC	TTCAGAAGGCCAGAAG AAA	59.9	506	INTRON	Ca_27517	L	FAR1	BRCT
CaPOPI_7204	scaffold2950	10165	AGG/AGGG	AGTTGTTGGATACACC GGC	AGTGCTGTGGCTGGACC TAT	59.9	662	INTRON	Ca_27517	L	FAR1	BRCT
CaPOPI_7205	scaffold2950	10696	G/GT	TGATGATATCAGGCAAC GGA	TGTCCCACAGGTAGCT TTC	60.0	588	INTRON	Ca_27517	L	FAR1	BRCT
CaPOPI_7206	scaffold2955	6116	TTTTGAGAAA/TTTTGAGAAATTTGAGA AA	ACAAGTTGATGGGACTT GGC	GTCATCTGACCCCAACG ACT	60.0	572	INTERGENIC				
CaPOPI_7207	scaffold2955	9708	T/TCTAC	ACTATGCAAAGGTGCAA GGC	CACCATTTCCGTCCAC TCT	60.3	374	INTERGENIC				
CaPOPI_7208	scaffold2955	10080	CT/CTT	AGAGTGGACGGAAAATG GTG	AAACTTGGTGCCCTGAC TTG	60.0	621	INTERGENIC				
CaPOPI_7209	scaffold2955	11390	ATTTT/ATTTT	TAGAATAAGGCTCGACC GGA	TCCAAGCCCTTTCTCTT CA	59.8	402	INTERGENIC				
CaPOPI_7210	scaffold2955	11713	GTTTT/GTT	TGAAAGAGAAAGGGCTT GGA	AACTCGTTTGTTCAATG GTGA	59.9	649	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7211	scaffold296	11327	TCC/TCCC	TGGACGTAGTCCGAGTTGGT	CTTGTCCTTCGGTTACAGCA	60.6	517	INTERGENIC				
CaPOPI_7212	scaffold296	16183	TAAAAA/TAAAAAA	GCAGGGATCCAAAAGTTCAA	GTTTGGCAGTGAGAAAAAGGC	60.1	456	INTERGENIC				
CaPOPI_7213	scaffold296	78708	TTATA/TTA	TATGGACCGGAAATGGA TGT	GACATTGCATTTTGACACG	60.0	606	INTERGENIC				
CaPOPI_7214	scaffold296	84993	TAAAAAAAA/TAAAAAA	TCTCCGCATAAGCTTTC GAT	TGATTGCAAAATAGACC CAA	59.9	241	INTRON	Ca_20533			
CaPOPI_7215	scaffold296	257003	ATTTTTTT/ATTTTTTTT	CAATGTCTGCCAAAAA GCA	CTCAATAGGAGTTCGCA GGC	59.7	433	INTERGENIC				
CaPOPI_7216	scaffold296	259048	A/ATT	AAGGTCAAGCAGTGGCA GAT	CATCTTCAAAGGGGCAT GAT	59.9	741	INTERGENIC				
CaPOPI_7217	scaffold296	261410	AAGAGAGAG/AAGAGAGAGAG	CATTGTGGGAGCGTAAG ACA	TCGCAACTCTCATGTGT ATGG	59.7	388	INTERGENIC				
CaPOPI_7218	scaffold296	261628	TACACACACAC/TACACACACACAC	CATTGTGGGAGCGTAAG ACA	TCGCAACTCTCATGTGT ATGG	59.7	388	INTERGENIC				
CaPOPI_7219	scaffold296	261904	CAAAAA/CAAAA	CCATACACATGAGAGTT GCGA	TTGACTCAGCCTTAAATT TTTATTGA	59.7	534	DRR	Ca_20542			
CaPOPI_7220	scaffold296	262823	ATATTATTATTATTATTATTA/ATATTATT ATTATTATTA	CAC TTTT TAACCGGAGG AATG	GCAGTGGATAAGGCCGA TAA	58.6	140	DRR	Ca_20542			
CaPOPI_7221	scaffold296	265325	AACTACTA/AACTA	TCAAGCCATAAATGATG CCA	ATCTGCCACTGCTTGAC CTT	60.0	257	INTERGENIC				
CaPOPI_7222	scaffold296	335726	TTATATATATATATATATATAT/TTATA TATATATATATATATAT	TGATCTTCGGGGCACTA CTC	ATCGTTCCCCAAAGTGA CAG	60.2	445	INTERGENIC				
CaPOPI_7223	scaffold296	406805	GTTATTATTATTATTATTATTATTAT TATTATTATTATTATTAATATTATTATTA T/GTTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATIT	AGTTATTTACGACGCAC GGG	GGCACGACATCATCATC ATC	60.0	547	INTERGENIC				
CaPOPI_7224	scaffold298	2633	AAT/ATAT	CATCCACCCCTCTAAAC CAA	TCGATTGATAGACCTTG CATTT	59.8	416	INTERGENIC				
CaPOPI_7225	scaffold298	8123	TGA/T	AAATGAAAAGTGCGAG GAC	AGTTACCCATTGTGGC AGC	59.2	740	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7226	scaffold298	76407	ATTTTTTTTT/ATTTTTTTTT	GTTCAAACAACACGCTC ACG	GATTGGACTTGTGGCTT GCT	60.3	569	INTERGENIC				
CaPOPI_7227	scaffold298	208119	GTTTTTTTT/GTTTTTTTT	AGTCGGAGGTTCTAGC ACA	ATTGTTGGGCTTGTCTAG TCC	59.9	471	INTERGENIC				
CaPOPI_7228	scaffold2981	12753	ATTTTTTT/ATTTTTTTTT	TGTTATAGGTTTCGCC CAG	CTTTTCGGGCGATTTTC ATA	60.0	840	INTERGENIC				
CaPOPI_7229	scaffold299	27346	GATAATAATAATAATAATAATAATA TAA/GATAATAATAATAATAATAATA ATAA	CTACCGCGATCAAATAC GGT	CCCTTTTGTCTTCTTGTG GC	60.0	977	INTERGENIC				
CaPOPI_7230	scaffold299	63392	AATATATATATATATATATATATAT ATA/AATATATATATATATATATATATA TATA	AAATATCTTCTCTCGCC GCA	CTGAGATGCAGCGTTTT TCA	59.9	528	INTERGENIC				
CaPOPI_7231	scaffold299	213491	AGG/AGGG	ACGGGAGCAAAAGTCTC TGA	CCAAAAGAAAATGCCCA AGA	60.0	705	INTERGENIC				
CaPOPI_7232	scaffold3015	68656	A/AACCGGCACAGCC	TTCGCAGACAAAACCTCA TGC	AGCATTATGGGCCATCT GAG	60.0	283	CDS (large-effect mutations)	Ca_27318			
CaPOPI_7233	scaffold3015	69170	AG/A	GGCCATAATGCTCAAG TGT	TCATAGGCATGGGATTT GAA	60.0	472	DRR	Ca_27318			
CaPOPI_7234	scaffold3015	73264	TGGCATAG/TG	TTTGTGTTTGCATGAC GAT	TAAGAGCGGAGTTTCTC CCA	60.1	792	INTERGENIC				
CaPOPI_7235	scaffold3015	73454	TTTTGACTTTGACTTT/TTTTGACTTTGA CTTGACTTT	GCTCGCGTTGAGTTAA GGG	TAAGAGCGGAGTTTCTC CCA	59.9	489	INTERGENIC				
CaPOPI_7236	scaffold3015	73940	TG/T	TGGGAGAACTCCGCTC TTA	TGATGGCTCCAAGGTGT ATG	59.9	538	INTERGENIC				
CaPOPI_7237	scaffold3015	74020	AAAATCATA/AA	TGGGAGAACTCCGCTC TTA	TGATGGCTCCAAGGTGT ATG	59.9	538	INTERGENIC				
CaPOPI_7238	scaffold3015	74169	TTT/TTTCTT	TTTGAATTTAGGGTGT CACG	TGATGGCTCCAAGGTGT ATG	59.0	221	INTERGENIC				
CaPOPI_7239	scaffold3019	18112	CAAA/CA	ACCCGCAACTGGTAGAC ATC	AATTGTTTGGCCTCAAAT GG	60.0	597	INTRON	Ca_28069			XS domain
CaPOPI_7240	scaffold3019	18761	GAAAAAAAAAAAAA/GAAAAAAAAAA	ACCCCAACCAACAAAGA CAG	CAAGCCTGGAGCTATTG AGG	59.9	369	INTRON	Ca_28069			XS domain

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7241	scaffold3019	20892	AT/AATGGTT	TGCATGAGTTGTTAAGGCGA	TATGCAAAACGGGACTTCCT	60.4	582	URR	Ca_28069			
CaPOPI_7242	scaffold303	16790	ATTTTTTTTT/ATTTTTTTTTT	TTTTTCTCTGCCCAAGGCTA	ACCATGCAAAGACATCCACA	60.0	467	INTERGENIC				
CaPOPI_7243	scaffold303	162542	AAGCGCTGT/AAGCGCTGTGGAAACGAGCGCTGT	GCCATTTCACAGCGCTTTTTC	TGAAATTATGGGTGGGCTATT	59.9	357	DRR	Ca_26661		Trihelix	
CaPOPI_7244	scaffold3032	11288	GCCCCC/GCCCCCC	AGGTCATTTTCGTCCTCCCT	TATCCAATGACCAAAACGCA	59.9	487	INTERGENIC				
CaPOPI_7245	scaffold3038	10393	TG/T	TGTGCATCCAAGAGGTGTGT	GGCGAGAATGACCAAAATGT	60.2	756	INTERGENIC				
CaPOPI_7246	scaffold3038	17812	C/CTTAAGT	AGGTCATTTTCGTCCTCCCT	TCGACTTGCAATCGCTTTG	59.9	645	INTERGENIC				
CaPOPI_7247	scaffold3046	14446	AGGG/AGG	TTGGATGAACATTTCCGTCA	AAGCCTAGGGAGGACGAAA	59.9	240	INTERGENIC				
CaPOPI_7248	scaffold305	168595	TTAATAATAATAATAATAATAATAATAAT AAT/TTAATAATAATAATAATAATAATAAT	AAGACACAAGGCAATGCAAA	GGTGGTGGAGGGTTACTTTT	59.3	540	INTRON	Ca_25903			Phospholipid/glycerol acyltransferase
CaPOPI_7249	scaffold3051	4826	AATA/AA	GGAGGAACCCCTCCTTGAAA	ACAAACAAGTTGAGCACCCC	60.4	648	INTERGENIC				
CaPOPI_7250	scaffold306	128535	TA/T	ACCGAAAGGAGAACACATGG	TGCAAAATGAAAGTTTAAAGACCA	60.0	240	INTERGENIC				
CaPOPI_7251	scaffold306	128902	AACA/AA	AAGGAGAACACATGGACTTGC	TGAGGCTTCAAGGAATTGG	59.2	961	INTERGENIC				
CaPOPI_7252	scaffold306	130271	GAAAAAAAAA/GAAAAAAAAA	TGCAAAATTCATCAAATCCA	CGTAGCCTTTGTTGTGCTG	57.5	415	INTERGENIC				
CaPOPI_7253	scaffold306	166393	TAAATCGATTG/TAAATCGATTGGGAAATCGATTG	TGCACAAGTCAGTAGCACCC	GCCAATCGATTACCCCTCAAA	59.9	138	INTERGENIC				
CaPOPI_7254	scaffold306	196935	T/TA	CAAGCGTTGGAGTTTGTGT	TTTATTTGTGGGGGTTCTCG	60.1	859	INTERGENIC				
CaPOPI_7255	scaffold306	477894	TAAAAAAAAA/TAAAAAAAAA	CGTCATTTGCTTCTTCCCAT	TGGGACTTAAAAGCGTCGTT	60.1	880	INTRON	Ca_22723	C	NAC	Cytochrome b561, eukaryote

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7256	scaffold3092	1124	TAAAAAAAA/TAAAAAAAAA	GAGGTATTTTACAGCGCTCTTC	TTGGGCTGAAGAATGGCTC	58.7	117	INTERGENIC				
CaPOPI_7257	scaffold3093	19732	GATATATATATATAT/GATATATATATATATAT	GAACCCTCACAATCACACGA	GAGCGCTGTAAACACCCTC	59.5	863	INTERGENIC				
CaPOPI_7258	scaffold311	26152	TA/TAA	TCAACCAAAGTGCATCCA AAA	GGAGGCCGAAAATGACATAA	60.1	564	INTERGENIC				
CaPOPI_7259	scaffold311	91768	CAAAAA/CAAAA	TGGGCAAGAAAAAGCCTATG	AGGTCATTTTCGTCTCCCTCCT	60.2	836	INTERGENIC				
CaPOPI_7260	scaffold311	131360	A/ACAT	GAAGCTCAGATGGCACACAA	CAATCTCCCCCTTGAGTTGA	60.0	716	DRR	Ca_26332			
CaPOPI_7261	scaffold3115	46887	TC/T	TGCTACATTCTCTTTTCATCTTGA	TTTCTAAAATCGTTTCTGTCCC	59.7	600	INTERGENIC				
CaPOPI_7262	scaffold3115	55767	TATACATACATACATACATACATA/TATACATACATACATACATACATA	TGCATGTCCCTCAAAGGTAA	TCATTGTCTTACAAAGCC	59.1	830	INTERGENIC				
CaPOPI_7263	scaffold3115	62578	ATTTTTTTTTTT/ATTTTTTTTTTTTTTT	CTTGGTGGTCCACTATGTGC	GGAGGTCAAAATACTAACTGCGA	59.0	594	INTERGENIC				
CaPOPI_7264	scaffold3115	62639	CTTTTTTT/CTTTTTTTT	CTTGGTGGTCCACTATGTGC	TTCATAGGAGGCTGCCATTTC	59.0	632	INTERGENIC				
CaPOPI_7265	scaffold3115	62933	TTTATTATTATTATTATTATTATTATT TTTTATTATTATTATTATAATTATTA TTATTA/TTTATTATTATTATTATTAT TATTTTATTATTATTATTATAATTA	CTTGGTGGTCCACTATGTGC	TTCATAGGAGGCTGCCATTTC	59.0	632	INTERGENIC				
CaPOPI_7266	scaffold3115	63986	AATATATATATATATATATATATATAT A/AATATATATATATATATATATATATA TATATA	TGAAGCATATGCCGTGAG	GCGTCAATGAACCTTACATGC	60.0	559	INTERGENIC				
CaPOPI_7267	scaffold3115	87750	T/TAAGA	GGGGACTTGAATTTCTGCAA	ATGCCTGCATTTTGTAGGTC	60.1	220	INTERGENIC				
CaPOPI_7268	scaffold3127	8863	A/AT	AATCCAATGGCACAAACACA	GGACATTTTCGTCTGCTACTA	59.8	488	INTERGENIC				
CaPOPI_7269	scaffold3134	12154	ACATC/A	TAAACGAGGTAAACCGGTGC	GAAAGTCGCATGTGC AAC	60.0	437	DRR	Ca_27104	O	C2H2	Peptidase A1
CaPOPI_7270	scaffold3134	13610	A/AAG	TTGATTCGTGCAAAATCAGGA	CCAAGAGAAAGGCAGCTGAG	60.2	289	DRR	Ca_27104	O	C2H2	Peptidase A1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7271	scaffold3134	15211	TAAA/TAAAAA	CCTGGTTGAGTCTGGATAGCA	GCATTGGCGTATCTGT TCA	60.3	874	INTRON	Ca_27104	O	C2H2	Peptidase A1
CaPOPI_7272	scaffold3134	109334	AATATATATATATATATATAT/AATATATATATATAT	AGGAAGAGTGGAGTTGCGAA	TTAATGTGTTGCGGGTGAAA	60.0	342	INTERGENIC				
CaPOPI_7273	scaffold3135	4161	TCC/TC	TCCAGATGAAATCGAGGACC	CCCGAAAAGTCCAGATGAAA	60.0	882	INTERGENIC				
CaPOPI_7274	scaffold314	79817	GAA/GA	GAAGGCCCTCAAATCATCA	CACAGCACCAGGTTATCCCT	60.0	615	INTERGENIC				
CaPOPI_7275	scaffold314	451895	TTTCCACCATT/TTTCCACCATTCTTCCACCATT	CAAAAGGCTTCAGCACACAAA	CGAGGAGGGTCTGTTGGATA	60.0	678	INTERGENIC				
CaPOPI_7276	scaffold314	543872	C/CTA	AACCAAGGGAGGACGAA AAT	CTTGGGCATCCAATAGGTGT	59.8	268	INTERGENIC				
CaPOPI_7277	scaffold3149	9644	TAG/TAGGAG	TTTCATCTGGACTTTTCGGG	ATCGTCGATGGGTACGA AAG	60.0	452	INTERGENIC				
CaPOPI_7278	scaffold3155	24057	GAAAAAAA/GAAAAAAA	TGCATATTTTGAAACGAA TGACA	TGCAACCATCGGTTAAATG	60.4	505	INTRON	Ca_27114	R	NF-YB	
CaPOPI_7279	scaffold3160	9833	TGG/TG	AACCAGTCACTCAAGCGTCC	TGGCTGGTGATTTGTGTGAT	60.3	165	INTERGENIC				
CaPOPI_7280	scaffold3160	10499	AG/AGG	TGGCTTTTAGTTAGAGCACCA	GCAAAACAAAGGAAACGGAAA	59.1	629	INTERGENIC				
CaPOPI_7281	scaffold3164	2274	ACC/AC	CGTATTTCCGGGAAGAGTCA	TCGAGATTGTGTGCAAGGAG	60.1	614	INTERGENIC				
CaPOPI_7282	scaffold317	8959	TTATATATATATATATATATATAT/TATATATATATATATATATATATATATATATAT	AATGGAGGAAGGAGGGAGAA	GACCAAGTCCAACCTTG CAT	60.0	492	INTERGENIC				
CaPOPI_7283	scaffold317	30584	CAAAAAATAAAAAAAA/CAAAAAATAAAAAATAAAAAATAAAAAAAA	CTCGCTCGGTTACCTCTCATA	AGTTTCGATTCAAAGACCCCA	60.2	682	DRR	Ca_25635	D		Cyclin
CaPOPI_7284	scaffold317	203820	AATATATATATATATATATA/AATATATATATATATATATATA	GAAATTTTGACGGAACGGA	AACGACTGTAACACGCCAAA	59.9	974	INTERGENIC				
CaPOPI_7285	scaffold3170	61619	TTATATATATATAT/TTATATATATATATATAT	AGCATTAGCAATCCTCCGAA	ACGAGAAAGCTGGACAGGAA	59.8	484	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPl_7286	scaffold3170	205155	T/TTTG	TATGTCGCATGATTGAG GGA	TCTTCAACTCCACAACC CC	60.0	443	INTERGENIC				
CaPOPl_7287	scaffold3170	216441	CA/CAA	CGGGTACGTATGCAGG TCT	TTGCTTCATTCTCATTTGG CA	60.0	515	INTERGENIC				
CaPOPl_7288	scaffold3171	2398	C/CTA	TGATGGAGGATTGAGGA AGG	GTTGACAAATGCCAAAAT GCG	60.0	431	INTERGENIC				
CaPOPl_7289	scaffold3171	2647	ATTTTTT/ATTTT	TGATGGAGGATTGAGGA AGG	GTTGACAAATGCCAAAAT GCG	60.0	431	INTERGENIC				
CaPOPl_7290	scaffold3175	11875	CT/C	CGAAAAATCGCTCGAAAA GTC	GGTCCTCGATTTCATCT GGA	60.0	613	INTERGENIC				
CaPOPl_7291	scaffold319	3243	AATATATATATATATATATATATAT ATAT/AATATATATATATATATATATAT ATATATATATATATAT	GAGAATTCCGGGAAGGA GAC	GTTGGTCCCTAGCACCC GTA	60.0	790	INTERGENIC				
CaPOPl_7292	scaffold3191	26393	ATTTTTT/ATTTTT	TTCGTAATGGACGGGAT GAT	GGGTTTTGCATGTTGAG CTT	60.2	492	DRR	Ca_27210		M-type	
CaPOPl_7293	scaffold3209	943	TC/TTTTTCC	GGTCCTCGATTTCATCT GGA	TTTGTCGAGGGGTACGA AAC	60.0	620	INTERGENIC				
CaPOPl_7294	scaffold321	38512	A/AT	CCAAGGAGGACGAAAAT GAC	ACCAATCTTGTGCATCC CAT	59.5	768	INTERGENIC				
CaPOPl_7295	scaffold3212	725	CTT/CTTTT	CGAGTCGTGTCTTGATA ATGGA	CCCATTAGTGGTGATGC TTC	60.1	125	INTERGENIC				
CaPOPl_7296	scaffold3212	1519	GAAAAAAAA/GAAAAAAAAA	AATGACATTTGCCCCG TAGA	ATCGGTGGCATGT CCTT ACT	59.3	741	INTERGENIC				
CaPOPl_7297	scaffold3212	1828	TAATCTAA/TA	GCAGAAATTAAATAG TG GTGTG	TGGAAGGTGGAGGTTC A GAG	59.9	715	INTERGENIC				
CaPOPl_7298	scaffold3212	2564	A/AC	TGAACCTCCACCTTCCA TTC	CAAACAAATGAGTGGCG ATG	59.9	439	INTERGENIC				
CaPOPl_7299	scaffold3212	6334	ATTTTTTTT/ATTTTTTT	GAGCACATGATCTCGCA GAA	CACTGCTGAAGCGGAAT ACA	60.1	213	INTERGENIC				
CaPOPl_7300	scaffold3217	4699	TTA/TTACTATA	CGCTTTGCCCTTAGTTT GAG	ATTCCCCATCAATTTGGA CA	60.0	298	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7301	scaffold322	4062	CT/CCTGTAGAAGACTGGT	TGCAAGAGCATATGGCA AAG	AATAAGCGACCATTGTT CCG	60.0	227	INTERGENIC				
CaPOPI_7302	scaffold322	32031	ATT/AT	AGGTCAATTCCTTCGTG CCT	GGACGAAAACGACCTAA ACG	59.9	216	INTERGENIC				
CaPOPI_7303	scaffold322	55500	TCTACT/TCT	AAGTGCATATCAGCAGC GTG	ACCAGGTATTGAATGCA GCC	60.0	163	INTERGENIC				
CaPOPI_7304	scaffold322	77924	GTTGATATTTTG/GTTGATATTTTGATAT TTTG	TTAGGAATCGAACCCTG GTC	TCCTTGAAGACAAGCAA CCA	59.9	346	INTERGENIC				
CaPOPI_7305	scaffold3225	20595	AT/AGT	TTTGATGCCCGATTAA AAA	GGTACCGCGAGTAATTC CAA	60.3	646	INTERGENIC				
CaPOPI_7306	scaffold3228	1705	GAA/GAAA	TTGGTGAAGGAGGAGGA TTG	CTCACCTTGAATGCCA CTT	60.0	149	INTERGENIC				
CaPOPI_7307	scaffold3228	1858	CATA/CATATA	TCAGCTTTTGGCTGAT GTG	CTTGTGGATTGGGTCTT GTG	60.0	247	INTERGENIC				
CaPOPI_7308	scaffold3228	47967	C/CAA	TGACAAAAGGGGGAGAT TGA	TGCGTCTTTCTCAAGTG CAT	60.4	414	DRR	Ca_27761			
CaPOPI_7309	scaffold3228	48150	GAATCGATTGATAAATCGATTG/GAATC GATTG	ACCAAAGTTGGAGGATG CAC	TTTCCATCAATCGATTTG CC	60.0	596	DRR	Ca_27761			
CaPOPI_7310	scaffold3229	5378	TA/TATTGCA	AGCTGAAATCCACAAG GCA	GATAATGGCCGCATGAA AAG	60.8	366	INTERGENIC				
CaPOPI_7311	scaffold3229	6703	GAAAAAAAA/GAAAAAAAAA	CAACGATTTAGCCATTG TTGA	TTGATGCCTCTTGGCTC TTT	58.7	398	INTERGENIC				
CaPOPI_7312	scaffold3229	8934	GATATATATATATATATATATATATATAT AT/GATATATATATATATATATATATA TATATAT	TGAAGCACAATGTTGGT TTTG	TGTAAAGTGAACACCC GTC	59.6	692	INTERGENIC				
CaPOPI_7313	scaffold3234	4828	A/AATCC	TCACGGGTCAACACGAT TTA	CCACGAGATGATTCCAT GTG	60.0	285	INTERGENIC				
CaPOPI_7314	scaffold324	86326	TTATATATATATATAT/TTATATATATA TATATATAT	ATCCCAATAAAGTGCCA TCG	ATGCCCAACCATAAATTT CA	59.8	826	DRR	Ca_24915		NAC	Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_7315	scaffold324	147338	GGGT/G	TCCAGATGAAATCGAGG ACC	TTTTCGGGCGATTTTTG TAG	60.0	488	INTERGENIC				

[illegible]

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7331	scaffold330	10729	AC/A	TTCCCTCATTCACTATG GC	GTGCTCGAAATTTTGTG TCG	59.9	561	INTERGENIC				
CaPOPI_7332	scaffold331	202046	C/CGA	ATTCCAAACCAAAACCT CC	GTGATTGGTGCGAATT GTG	60.0	581	INTERGENIC				
CaPOPI_7333	scaffold331	207791	CC/CCTCTTCTCCAGATCAC	GCTGTCATGATTGCGTT CAA	GAACAACGCTGCAAAAG TCA	60.0	273	CDS (large-effect mutations)	Ca_25648			
CaPOPI_7334	scaffold3314	5786	TTTTTTCTTTTTCTTTTT/TTTTTCT TTTTTCTTTTTCTTTTT	AAGGTGAATCGTTCGAG AGAA	GCAAATCAATTTTCTGG GG	58.9	587	INTERGENIC				
CaPOPI_7335	scaffold3317	732	TA/TAA	TACCACTGCGGATGCA TAA	TTTCGCTACCCATCATAC CC	60.1	717	INTERGENIC				
CaPOPI_7336	scaffold3317	3339	TGACGAC/TGAC	GCATCTGTGTAGCCATC CAA	TAGGTCAATTTTCGTCCT CCG	59.7	738	INTERGENIC				
CaPOPI_7337	scaffold3321	35578	TGG/TG	GGAAGGGGATCATCAGC AAA	TGTGCAGATCCACACAC TCA	60.0	410	DRR	Ca_25707	U	FAR1	Zinc finger, RING-type
CaPOPI_7338	scaffold3321	59785	GAAGCA/GAAGCAAGCA	GATTGTGAAAGGGTGG AGA	AACCTCTGCAATACCA GCG	60.1	586	DRR	Ca_25712	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_7339	scaffold3321	61130	C/CTTT	AAAATGTCACGCCACCA AAT	GGACCGCATATGTAATT TAGCC	60.2	507	DRR	Ca_25712	GC	HSF	UDP-glucuronosyl/UDP-glucosyltransferase
CaPOPI_7340	scaffold3321	69689	TAA/TA	TCTTGCAAGGCTTGGA TTT	TGTGCCGACAATTAACC AAA	60.0	681	INTERGENIC				
CaPOPI_7341	scaffold3321	69753	AAAAAGAGAAAAGAGA/AAAAAGAGA	TCTTGCAAGGCTTGGA TTT	TGTGCCGACAATTAACC AAA	60.0	681	INTERGENIC				
CaPOPI_7342	scaffold3322	4199	TAAAAAA/TAAAAAAA	GCCACAAAATTGGTCCA AAA	CGTGAGGCTGTTGGGAT ATT	60.7	544	INTERGENIC				
CaPOPI_7343	scaffold333	8945	TCC/TC	GATGAAATCGAGGACCA GGA	GACTTTTCGAGCGATTT TCG	60.0	299	INTERGENIC				
CaPOPI_7344	scaffold333	91813	GAACAACAAC/GAACAAC	GATGAAATCGAGGACCA GGA	GTGCCAGTCGATTGCCT AAT	60.0	519	INTERGENIC				
CaPOPI_7345	scaffold3336	8274	GATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT/ GATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT	CGGCCGTTTCTAACATC ATT	TTGCTTTTGAAACCAATT TAGGA	60.0	569	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7346	scaffold3336	39173	TAAAAAAAA/TAAAAAAA	TGAGATTGAATTGATATTGTGTTGA	TCTCTTCTCCTGCCTTCA	59.8	502	INTERGENIC				
CaPOPI_7347	scaffold335	45267	GATATATATATATATATA/GATATATATATATATATATA	ACAAACCACGTACTCCCTCG	GCCCATTCCTATGTCTAAT	60.0	553	INTERGENIC				
CaPOPI_7348	scaffold335	88156	GTTATTATTATTATTATTATTATTATTATT/GTTATTATTATTATTATTATTATTATTATTATT	TTGTCTTCTGTGGCCGACT	TTTTACAGGCGATTGGAGC	60.8	785	INTERGENIC				
CaPOPI_7349	scaffold335	208290	AATATATATATAT/AATATATATATATATATATATAT	CGAAACAGGGAGGTTTGT	TATTCTGGATTTGGCTCGG	60.0	576	INTERGENIC				
CaPOPI_7350	scaffold335	233856	GTTTTTTTTT/GTTTTTTTTT	ATGCCGTGTATATTTCCGC	CCATTCTCATGTGTGTGC	59.8	409	INTERGENIC				
CaPOPI_7351	scaffold3354	665	T/TA	CAACACAATTGAGCTGTCAAA	TTCGTAAGTACAACCTCAAAACGAA	57.4	585	INTERGENIC				
CaPOPI_7352	scaffold336	292805	A/AT	TTCATCTTTATCTTCATTCGGC	GCGCTGTTGTATCCTCCATT	59.6	640	INTERGENIC				
CaPOPI_7353	scaffold336	360914	A/ATTATGG	TGCACATTTTACAGCGCTTC	CTGGGCAAGGATCTGATA	60.0	666	INTERGENIC				
CaPOPI_7354	scaffold336	441916	T/TC	TCCCTAGTTCGAATCTGCGT	CCTCCATCGAATTTCTCCAA	59.8	663	INTERGENIC				
CaPOPI_7355	scaffold336	546259	A/AG	TTTCGCCGATAAATTTCTG	GGGCATCACTCAAGTCCGT	60.0	642	INTERGENIC				
CaPOPI_7356	scaffold336	624730	AG/AGTCACTCTCATGTTCTCTG	TTAACCCAAGATTTACGGC	CCCACAAAGGGTAGTTGAA	59.9	617	DRR	Ca_21292			
CaPOPI_7357	scaffold336	633921	A/AC	GAGAAAGGCAAGACCAGTGC	TTGCAATTCAACTGATGGGA	60.0	365	INTERGENIC				
CaPOPI_7358	scaffold336	825176	TAAAAAAAAA/TAAAAAAAAA	TTCTTATCCTCAACGTCCCG	TCCTTTAGGACGCAAGTTGTGA	60.1	714	INTERGENIC				
CaPOPI_7359	scaffold3364	43644	T/TG	AGCCAAGGGAGGATGAATAAT	CGTCCACCTTTGATTATCC	59.9	214	INTERGENIC				
CaPOPI_7360	scaffold3369	18856	T/TA	TTCAACGTGACCTGCTCATC	ATGGGTCCAGGTCACTCAG	59.8	671	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7361	scaffold3369	22053	TATAATAATAATAATAATAATAATAA TAATA/TATAATAATAATAATAATAA TAATAATAATAATA	TCGCCACCGATTTTATTT TT	AATTAATGGTTGTCGCT GCC	59.4	674	INTERGENIC				
CaPOPI_7362	scaffold3371	7999	AAAAATAATAATAATAATAATAAAT A/AAAAATAATAATAATAATAATAA ATAATAATAATA	CCTGGGGATATGTAGGA GCA	CATTATTGTTGTTGCGT CCG	59.9	348	INTERGENIC				
CaPOPI_7363	scaffold3371	33866	AC/A	CGAGCCAAAATCCAAA ATA	ATGGTTGATTGGTTGCG AAT	59.9	256	INTERGENIC				
CaPOPI_7364	scaffold338	76520	GTATATATATATATATAT/GTATATATAT ATATATATAT	CTTGCCCATAAAATCGG AAA	AGGATGCATGGGATGAA AAG	59.9	661	INTERGENIC				
CaPOPI_7365	scaffold3397	17802	TATTGCAAAATTGCA/TATTGCA	GATCAGATCTGGCAGCA ACA	GAGGATGGAATTGCTG CAT	60.0	366	DRR	Ca_26271			
CaPOPI_7366	scaffold340	51387	A/ACT	TCCATCAATTCATCCAC CA	CCTTTGCCTCTAGCGAT TTG	59.7	587	INTRON	Ca_24956	DL		ATPase, AAA+ type, core
CaPOPI_7367	scaffold340	66713	ATTTTTTT/ATTTTTTTTT	AACACACGCACCAACAA AGA	TGAATATGCGTCGACTG AGC	60.2	559	INTERGENIC				
CaPOPI_7368	scaffold340	100873	TTCTC/TTC	AACGTGGGTTACGTCCA GTC	AAATGCAGAGCACCTCC AAC	59.9	530	INTRON	Ca_24959	U		Longin
CaPOPI_7369	scaffold340	119249	GAAAAAA/GAAAAAAA	GGTTGCGTAGTGGTAGC CAT	CTCCGAGCCAATATCCA AAA	60.0	623	INTERGENIC				
CaPOPI_7370	scaffold340	135811	ATTTTTTT/ATTTTTTTTT	TTTGACGCTTTAACTATC CCG	AACTTTGTCCATTTATT GGCTT	59.3	530	INTERGENIC				
CaPOPI_7371	scaffold340	161360	ATTTTTTT/ATTTTTTTTT	GCGGATATCGTAGGGTG CTA	TACATCCAGAAGGCTAC CGC	60.1	539	INTERGENIC				
CaPOPI_7372	scaffold340	205523	TAA/TA	CCCCAAAAGTTGGAGA ACA	TTCTAACCTTGCAACCG GAG	59.9	398	INTERGENIC				
CaPOPI_7373	scaffold340	210507	GA/GAA	AACGGAGAATGTTCAAC AGG	TGCAGAAATCGTGGAGAT TGA	60.0	383	INTERGENIC				
CaPOPI_7374	scaffold340	225242	TAAAAAAA/TAAAAAAA	TCACCTTGAAAAGTCT GCC	TATCCCCCAAGATTGG TCA	60.2	683	INTERGENIC				
CaPOPI_7375	scaffold340	261525	GTTTTTTTT/GTTTTTTTTTT	TTTCCAAGAGTTTCAACC CG	TGTTTAGGCTGCTGATG GTG	60.1	387	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7376	scaffold340	261564	ATTTTT/ATTTTTT	TTTCCAAGAGTTTCAACCG	TGTTTAGGCTGCTGATG GTG	60.1	387	INTERGENIC				
CaPOPI_7377	scaffold340	287997	ATTATTTATTTATTTATTT/ATTATTATTTATTTATTT	GTCACAGAGGGAACGGATGT	TTGGAAGAGCCACCTACAC	60.0	524	INTERGENIC				
CaPOPI_7378	scaffold340	318031	CAAAAAAAAAAAAA/CAAAAAAAAAA	ATGTACCTCCGCCTCATTTG	CTTTACAGCGCTCGAT TCC	60.0	175	INTERGENIC				
CaPOPI_7379	scaffold341	135211	TATATATAGAAA/TA	AATGGAGTTGCGACGAGAGT	TCTCCGTAAAGGATTCA CCG	59.9	540	INTERGENIC				
CaPOPI_7380	scaffold341	135303	GAAAA/GAAAAA	AATGGAGTTGCGACGAGAGT	TCTCCGTAAAGGATTCA CCG	59.9	540	INTERGENIC				
CaPOPI_7381	scaffold342	164779	TTATATATATATATATAT/TTATATATATATATAT	TTCCAACATGCTTGAACCTCA	GGCCGAAATTCATTCA ACA	59.3	703	INTERGENIC				
CaPOPI_7382	scaffold342	249187	ATTTTTTTTT/ATTTTTTTT	CAACGGTGAAGCCATAACT	TGGGTGTTAAATTCTC CTCTTG	60.0	841	INTERGENIC				
CaPOPI_7383	scaffold342	310549	CATATATAT/CATAT	TTGTGACATTCATCAAA CACA	CAACCGACGTTGAAGAA CAA	57.5	933	INTERGENIC				
CaPOPI_7384	scaffold342	340574	TC/T	TGTTCCAGCATACCAAA TGC	AGCAAAATCCGAGGAGG AAT	59.5	557	INTERGENIC				
CaPOPI_7385	scaffold342	370625	TTATCAT/TT	TGGGGTCCTTTCTCTTC TCC	TATGCCATTGAGTTGG ACA	60.6	387	INTERGENIC				
CaPOPI_7386	scaffold3432	23969	CAATAAT/CAAT	CCTGAATCCGAGACAAGACG	TCATGGGTTGTATGGAA GCA	60.8	487	INTERGENIC				
CaPOPI_7387	scaffold3434	7567	GAAAAA/GAAAAAA	CGACATTCGTCATGGTT TTG	CATAGCAATCCAACAAC AAGAAA	60.0	876	INTERGENIC				
CaPOPI_7388	scaffold3434	11167	AGGGG/AGGG	CTTTCTCCATTTCCACCC AA	TCACTCAAAGGGCTACT GCC	59.9	532	INTERGENIC				
CaPOPI_7389	scaffold3436	9281	GAGACTTAT/G	GGCCATGAATTCACAACAA	TTGCCAAATACAAAAAGA AATGAA	59.4	570	INTERGENIC				
CaPOPI_7390	scaffold3436	9959	TAATA/TTAATAATATACAAATA	TGGAGTTGGGGCTAAGTACAG	CGTGCTTGCAGAAAAAC AAA	59.4	309	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7391	scaffold3453	1173	CA/CAAA	ATATGCCTCTACCGTGC AGC	TCGTGAAAGCAAACAAA GGA	60.3	507	INTERGENIC				
CaPOPI_7392	scaffold3472	6763	GTATATATATATATATATATATATATA TA/GTATATATATATATATATATATAT ATA	CAAGCATGATCCAGGGA GAT	CTCGGCGAGTTTGTGTG TAA	60.0	471	INTERGENIC				
CaPOPI_7393	scaffold3472	7148	TATTAATAATT/TATTAATAATTAATAA ATT	CAGGCTAGCTAAATGCC TCG	ACCATGGTTGTTGCAAG TGA	60.1	720	INTERGENIC				
CaPOPI_7394	scaffold3472	7670	CA/C	AAACCCAAAAATAGTCC GCC	CCGTAACACATGCTTTC CCT	60.2	361	INTERGENIC				
CaPOPI_7395	scaffold3472	9063	CAA/CAAA	GCTCCATGTGCTTCCACA CAC	GTGACACGTGACAATCC CAC	60.3	107	INTERGENIC				
CaPOPI_7396	scaffold3472	9396	TC/TCC	TTTTGACAGAGAAACCC GCT	CTGTGAGAGGCGAAGAT GGT	59.9	223	INTERGENIC				
CaPOPI_7397	scaffold3472	71251	CTACAGCGCTT/CTACAGCGCTTGTTTT ACAGCGCTT	GAAAGCGCTTCCGTTTA CAG	GACATTTAACAGCGCCC ATT	60.0	159	INTERGENIC				
CaPOPI_7398	scaffold3475	6139	AG/A	GGCCTGGAGACCCTTAT AGC	ACCACTCGACGAAAATG GAC	60.1	616	INTERGENIC				
CaPOPI_7399	scaffold3475	6197	AT/ATT	GGCCTGGAGACCCTTAT AGC	ACCACTCGACGAAAATG GAC	60.1	616	INTERGENIC				
CaPOPI_7400	scaffold3475	31282	TG/TGG	GCTATTTTCGTACCACC CGA	GCCCAAAAGTCCAGAT GAA	60.0	326	INTERGENIC				
CaPOPI_7401	scaffold3489	2052	TAATAAAAAATAAAAAATAAAAAATAAAA AA/TAATAAAAAATAAAAAATAAAAAA	TCGTTCTGTTGGACCTT TTC	AGTGGAATAATGCCGT TGC	60.1	521	INTERGENIC				
CaPOPI_7402	scaffold3489	2940	ATTTTTTTTT/ATTTTTTTTT	GCACATTCCTAAGGGGC ATA	AGTGCAAATGAGTTTGT GTCA	59.9	373	INTERGENIC				
CaPOPI_7403	scaffold349	70134	GTATATATATATATATATATATATAT/GT ATATATATATATATATATATATATAT	TTCGGAAGTCCATCGGT ATC	AATGCATGCTCCCCTAA TTG	59.9	643	INTERGENIC				
CaPOPI_7404	scaffold349	177787	GTTATTGAATT/GTTATTGAATTCCTTTA TTGAATT	GCGATAATCCCCGTAAG GAT	TAGGTGCAGGTCATGAA ACC	60.1	652	INTERGENIC				
CaPOPI_7405	scaffold349	335267	ATT/ATTT	TTGGTCAATGTGGCTTC TCA	CTGAGCTTGTGACCAAA TCG	60.2	531	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7421	scaffold3539	5454	TAAAA/TAAAA	GGAGGGCGAAAATGATG TAA	CTTGCGCATCCAACAAG TTA	59.9	861	INTERGENIC				
CaPOPI_7422	scaffold3542	507	AGGGGGGG/AGGGGGG	GAAGAGTTACGCGGACA AGC	CCGAGCCAAAATCCAAA ATA	60.0	566	INTERGENIC				
CaPOPI_7423	scaffold3542	22091	G/GAT	ATTGCAACTGCCGGAAA TAC	GGGCTCACAGCTAGTTT TCG	60.0	874	INTERGENIC				
CaPOPI_7424	scaffold3542	24843	TTAG/TGATTAGCTGGGTAG	GGTGGGTTCATCGTTT CTA	CAAGACAGCCAATCCGA AAT	59.8	530	INTERGENIC				
CaPOPI_7425	scaffold355	1384	GTTTT/GTTTT	GGGGCGTTACATGTGGT ATC	CAGATTACGAAGGTCA CACA	60.1	314	INTERGENIC				
CaPOPI_7426	scaffold3562	1038	ATTT/ATT	AGGGAGGACGAAAATGA CCT	CCAATTGGTGTGTTTGC ATC	59.9	556	INTERGENIC				
CaPOPI_7427	scaffold3594	965	GAGCTAAAAAGCTAAAAAGCT/GAGCTA AAAAGCT	CGTTCAAAACGAGATCG TCA	TACAATGCCGAGCAAAT CAA	59.8	575	INTERGENIC				
CaPOPI_7428	scaffold36	138770	GAAAA/GAAAA	CCAATCATTGTCCAAGA GAGC	TTGGGCTGATGCAATAA ACA	59.7	607	INTERGENIC				
CaPOPI_7429	scaffold36	294954	AATATATATATATA/AATATATATATAT A	CTTGGGCTTTACCCATG AAA	TGTCGTGTGCTTCAAAA AGG	59.9	598	INTERGENIC				
CaPOPI_7430	scaffold3604	961	AAATCGATT/AAATCGATTAAGTAATCG ATT	AATTGCACAAGTCAGTG GCA	TATCGCGGGTCTTGTTT TTC	60.3	591	INTERGENIC				
CaPOPI_7431	scaffold362	29056	A/AATTCGT	AAATAATTTTGGGGCGA AGC	TCCAATGGCAAATGATT CAA	60.3	625	INTERGENIC				
CaPOPI_7432	scaffold362	148917	T/TG	ATTTCTCCATGCTCAATC CG	TTGTTGGTTATCCAGGC ACA	60.0	255	INTERGENIC				
CaPOPI_7433	scaffold362	166434	TGA/T	CCCGGTATTGTTTGTGC TCT	CACATCAGCCACATTTG ACC	60.0	774	DRR	Ca_24991	C		Aldehyde dehydrogenase NAD(P)-dependent
CaPOPI_7434	scaffold362	246595	AATATATATATATATATATATA/AATAT ATATATATATATATATATA	CGACTGCCGGTATCAAT TTT	TCATATTTCTTGTGTGT TTGGTT	60.0	648	INTERGENIC				
CaPOPI_7435	scaffold362	267543	A/AC	TATCTTGTCCGACCCA ACC	CTTGAATTCATGCGTC CTT	59.8	698	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7436	scaffold363	83340	CTGT/CT	AGGTTCTCTACGCCGTCT	CTATCCATTGTGACGGCT	60.3	502	INTERGENIC				
CaPOPI_7437	scaffold3643	22491	AG/A	AGCCTAGGGTGGACGAAT	CCATCCAATACGTGTGCTTG	60.0	164	INTERGENIC				
CaPOPI_7438	scaffold3643	22623	TAAAAAAAA/TAAAAAAAAA	CAAGCACACGTATTGGATG	TTTGTGCGTGACATTGGATT	60.0	111	INTERGENIC				
CaPOPI_7439	scaffold3659	2503	AT/ATT	GCCATTAATTATGTTAACGTTTGG	CAGAACATTTAACGTGAGCAAGA	58.8	665	INTERGENIC				
CaPOPI_7440	scaffold3663	4120	T/TG	TTTTATTGTTTTACTACAATACGACGA	AAGTTTGACTGCATAACAATGACA	57.7	631	INTERGENIC				
CaPOPI_7441	scaffold3663	4430	TAAA/TAAAA	TGTCATTGTTATGCAGTCAAACCTT	TCTTCGTTTTATGGTTTTATTCA	58.7	280	INTERGENIC				
CaPOPI_7442	scaffold3666	3244	GATATATATATATAT/GATATATATATAT	ACAAATGATGCTTGCTCTGTG	TCAAATTGGTCCTGTCCCTCA	59.9	534	INTERGENIC				
CaPOPI_7443	scaffold3666	3853	TTATATATATAT/TTATATATATATAT	CCAATTTGAATTGTCCGTCC	TATCGATCACCAGTGCCAAA	60.2	909	INTERGENIC				
CaPOPI_7444	scaffold367	6329	AGGGG/AGGG	GACACCCTAGGCCAAATGAA	TAGATTGGGTGGATTCTCTC	59.9	556	INTERGENIC				
CaPOPI_7445	scaffold367	15516	GTTCTTCTT/GTTCTT	CCTCATCATGTATGCCATCG	TTGGAGAAACTTTTCCGCTG	59.9	449	DRR	Ca_27355			
CaPOPI_7446	scaffold3673	1634	ATTTT/AT	TATTTTGGATTTTGGCTCGG	AAATGGAGGAAGGAGGGAGA	59.9	431	INTERGENIC				
CaPOPI_7447	scaffold3689	16240	AATT/AATTATT	GACATGCCAACACCAGACAC	TAAATCATGGGGTTCTCTCA	60.0	201	INTERGENIC				
CaPOPI_7448	scaffold369	73666	GTATATATATATATATATATATATAT/ GTATATATATATATATATATATAT	CGGTGAATCCTTTACGGAGA	AATGGAGGAAGGAGGGAGAA	60.1	297	INTERGENIC				
CaPOPI_7449	scaffold370	37851	GAA/GA	TTATTTAGTACCACTACAACGAAGA	AGTCCAGATGAAAGCGAGGA	57.0	395	INTERGENIC				
CaPOPI_7450	scaffold370	75163	AC/A	GATTTTCGTACCCCTCTGTCA	AGTCGCTCGAAAAGTCCAAA	59.9	533	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7451	scaffold370	89771	GAAA/GAAAA	GGTTCGAAAATTGCCTGAAA	CCCGAAACGCAGTTACA AAT	60.1	416	INTERGENIC				
CaPOPI_7452	scaffold370	101037	CAA/CA	TCCTGGTCCTCGATTTCATC	CGGGTTCAAACACTAGC CAT	60.0	434	INTERGENIC				
CaPOPI_7453	scaffold3705	4075	T/TGGGCGAAAACC	CAATAACCCTTCAATGGCTCA	GCTTTGCTCCCTTTCC TCT	59.9	393	INTERGENIC				
CaPOPI_7454	scaffold3724	53525	TAAAA/TAAA	AAGCACTTGCTCCCAATGAC	ACGAGTTGCTGGTTGAC CTT	60.3	372	DRR	Ca_27522	A	HD-ZIP	Queuine/other tRNA-ribosyltransferase
CaPOPI_7455	scaffold373	20809	TAAAA/TAAAAA	TCCAACGACACAAATGACG	AGGTCATTTTCGTCTCCCT	60.6	290	INTERGENIC				
CaPOPI_7456	scaffold373	25857	ACTTC/ACTTCTTC	AGCCACGAATTTAAGCTCCA	AGGGACAAAGGGCAAGA AAT	59.8	559	INTERGENIC				
CaPOPI_7457	scaffold374	13002	AC/ACC	CAAATTCAACGAGGTCA CACA	ATTGGAGCGTTACATT GGG	59.6	184	INTERGENIC				
CaPOPI_7458	scaffold374	14684	CAA/CA	AGTCACTCATACCAACGGGG	TTTTGGGGAATTGGTA AAA	59.8	633	INTERGENIC				
CaPOPI_7459	scaffold374	142006	TAAA/TAA	AATTCCTTCCCACACAA CCA	AGCGGAGATTTTACCGG AAT	60.2	128	INTERGENIC				
CaPOPI_7460	scaffold374	149528	CTT/CTTTT	AAGGGTGGAAGAGGAGGAAA	TGATGTTTGAGATGCAA AAGC	60.0	473	INTERGENIC				
CaPOPI_7461	scaffold374	154680	TAAAAAAAAAAAAA/TAAAAAAAAA	GATTTGATGTTGGGACCGTT	TCAAATGCTTCAACTTGT GCTT	59.7	477	INTERGENIC				
CaPOPI_7462	scaffold374	158468	ACACGATCAGCACGA/ACACGA	CCTATCACAGGTCAGCA CGA	GGTGTGGATGGAATTTG GAG	59.9	531	INTERGENIC				
CaPOPI_7463	scaffold374	205813	CAT/CATCCTGAT	AGCTGTTTCTGCTAGGCTGG	TTTATTTACGCGAATGCCCT	59.8	941	DRR	Ca_26214	O		K Homology
CaPOPI_7464	scaffold374	205921	ATTTTTTTTT/ATTTTTTTTTTT	CAAAAGTTGCGATTCTTCTGG	TTTATTTACGCGAATGCCCT	59.9	483	DRR	Ca_26214	O		K Homology
CaPOPI_7465	scaffold3742	3802	TTAT/TTATAT	CGATAGACTCAAGTTGGACCTG	GTGTCTGCTTGTTTGCC TGA	58.9	632	INTERGENIC				

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CaPOPI_7466	scaffold3742	11903	ACC/AC	TTATAGCCGTTGGAAGTGGG	TTCAGCCTCGAATCCAGAGT	60.0	804	CDS (FRAME SHIFT)	Ca_27449			
CaPOPI_7467	scaffold377	75306	C/CAT	TCACGGGTCGACACAATT	AACTGGACGTTGAGAATGGG	60.0	403	INTERGENIC				
CaPOPI_7468	scaffold3784	2352	AATATATATATATATATATA/AATATATATATATATA	TAAACGAGGGAGGACGAAA	GAAACGAACACCGGAGAAA	59.8	764	INTERGENIC				
CaPOPI_7469	scaffold3789	5837	CAAAAAAAAA/CAAAAAAAAAAAAA	TGCTCCATCAATCAATCA	TTACGTGGTGGTGAAGGTGA	60.0	280	INTERGENIC				
CaPOPI_7470	scaffold379	131210	GAAAAAAAA/GAAAAAAAA	TTATTGTGGGCATTGGGATT	GTGCCATTGAATTGGGAAT	60.0	590	INTERGENIC				
CaPOPI_7471	scaffold379	132536	TAAAAAA/TAAAAAA	GTAATGAAGTGGCTGCGCA	GTTTTGTTCATGGCGGTC	59.9	407	INTERGENIC				
CaPOPI_7472	scaffold379	194523	AATATATATATATATATATA/AATATATATATATATATA	CCGAACTTTACTGGGCCATA	ACCGTTTTGGTGTTCCTTGC	59.2	602	INTERGENIC				
CaPOPI_7473	scaffold3794	17881	ATTTTTTTTT/ATTTTTTTTT	ATTGATCAGGTGCGATCTCC	GCAACGAAAGAAAGAGTGGC	60.0	508	INTERGENIC				
CaPOPI_7474	scaffold3794	37384	CAAAAA/CAAAAA	TGTCGACGAGTAAAGTGCAA	TTTTGACCCACATGTTTCA	59.5	391	DRR	Ca_26695	GMW		
CaPOPI_7475	scaffold3794	59832	GAAAAAAAA/GAAAAAAAA	TCGATTATGCGTAGGGAGG	TTTTCTGAGTTGTTAGGCCACA	60.1	605	INTERGENIC				
CaPOPI_7476	scaffold3794	61760	TTTAAATT/TTTAAATTAAATT	GTTTAGGCCGCCACAAATA	GGGACTTCTGTTGTCGGGTA	60.0	703	INTERGENIC				
CaPOPI_7477	scaffold3794	71924	A/AT	TTGATCAAAGGTGTGTCCCA	CCCCATTGACCAAAATCATC	59.9	440	URR	Ca_26696	GMW	NAC	Exostosin-like
CaPOPI_7478	scaffold3794	79952	TAAAAAA/TAAAAAA	AAGTTTGCAAGAACCTTCCAT	CATATATGGTGGGATTGGC	57.9	616	INTERGENIC				
CaPOPI_7479	scaffold3794	82476	CCAC/CC	CAAAGGACCACACCTCTTT	TTGGCCCTTTAGTGATTCG	59.0	554	INTERGENIC				
CaPOPI_7480	scaffold38	25353	TAAAAAA/TAAAAAA	TGGATGTGTTGCATTGCTT	CAAACCTGGTTTAAATGTTGGC	57.5	568	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7481	scaffold38	135300	GTTTTT/GTTTTTTT	TGGTTGAAATTAAGCC AAGG	TCACATCAGGAAAAATG GCA	59.1	565	INTERGENIC				
CaPOPI_7482	scaffold38	138674	TA/TAGCAAA	CGTCGCAACTCAATTGA CAG	TTTTTCTCGGTGTGTAG GGG	60.4	950	INTERGENIC				
CaPOPI_7483	scaffold38	281889	TAAAAAAAAA/TAAAAAAAAA	ATCACCATTGTGGCATT GAC	TTGCAATAATGCGAACC AAA	59.2	464	INTERGENIC				
CaPOPI_7484	scaffold38	285083	CTTTTTTT/CTTTTTTTT	TTCAATAATTTCTTGTT GAGCCA	TCTGTGTCCACGTCAT TTG	60.0	399	INTERGENIC				
CaPOPI_7485	scaffold38	334106	CACTCAAGACATACTCA/CACTCAAGA CATACTCAAGACATACTCAA	GAAACTATTCTGCCTT CCG	CACACACCGAATCAATT TGC	59.8	699	INTERGENIC				
CaPOPI_7486	scaffold38	350628	GTTTTTTT/GTTTTTTT	ACCAAGACAACCTCTCC CCT	TGGGTACCCTTCTCCTT CCT	60.0	199	INTERGENIC				
CaPOPI_7487	scaffold38	350706	C/CAT	ACCAAGACAACCTCTCC CCT	TGGGTACCCTTCTCCTT CCT	60.0	199	INTERGENIC				
CaPOPI_7488	scaffold38	412147	ATTT/ATT	GGGAGTGGAGCGATTG ATTA	ATTTGTGAGGGTCAAGG ACG	60.0	567	INTERGENIC				
CaPOPI_7489	scaffold38	413791	ATTTT/ATTTTT	CTTCGCTGCAAAATTC CTC	TTGATGTCGGGTAGTGT CTGA	60.0	755	INTERGENIC				
CaPOPI_7490	scaffold38	474073	TAAAAAAAAAAAAA/TAAAAAAAAA	TGTGTCAGAAGGATCTT GCG	TGAGATTCGCCAGTTAA CCC	60.0	652	INTERGENIC				
CaPOPI_7491	scaffold381	6830	AAG/A	TGCAAAAGGGTCACTTG ATTT	CCCCAAACCCTAAACCC TAA	59.6	355	INTERGENIC				
CaPOPI_7492	scaffold3811	19567	GAAAAAAAAA/GAAAAAAAAA	GCACATCCATGCCATGT TTA	TGGATGCGTCCATCATT GTA	60.4	754	INTERGENIC				
CaPOPI_7493	scaffold3811	24750	CTATATATATATATATATATATAT/CT ATATATATATATATATATAT	TACTATGCAACCATCCC GGT	TGAAACAAGAAACCCGA ACC	60.2	663	INTERGENIC				
CaPOPI_7494	scaffold3823	3884	CAACAATAA/CAA	TGGCAAATCGATTGACA GAA	GTCCTGAAATCCAAC GGA	60.2	780	DRR	Ca_27909			
CaPOPI_7495	scaffold3824	21914	TACACAC/TACAC	ACGGTTGAGAATTGAGT GGC	ACAAAAACCACATTCGC ACA	60.1	572	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7496	scaffold3837	2371	ATTTTTTTTTTT/ATTTTTTTTTTT	CTTCTTGGTGGCATGTTT	TACCCTGTGGATGGGAA TGT	60.0	591	INTERGENIC				
CaPOPI_7497	scaffold3837	5661	AT/ATT	GCCTCCGAGTCAATACC AAA	ATTGAGGGTAGGGGAG CAGT	60.1	415	INTERGENIC				
CaPOPI_7498	scaffold3837	5910	ACCC/ACC	ACCTCGATCTGGAATC ACG	ATTGAGGGTAGGGGAG CAGT	60.1	467	CDS (FRAME SHIFT)	Ca_27570			
CaPOPI_7499	scaffold387	16023	CAT/C	CACACCCCTTGCAACA CTG	TTAAGCTGAGAGCCTTC CCA	60.0	439	INTERGENIC				
CaPOPI_7500	scaffold387	16971	TT/TTGT	CTCAACAAGGACGCCAA TTT	GGATTGATTACGCTTGT TGGA	60.1	299	INTERGENIC				
CaPOPI_7501	scaffold387	19261	TATAATAGAT/TAT	CCTTGAGGAACAACAAA ACCA	TTTTGGGGTTTAGGGTG TCA	60.0	757	INTERGENIC				
CaPOPI_7502	scaffold387	22975	AATC/AATCATC	CGCAATCTGAACAAATG ACAA	TCCACTAACCACCTTGA CCC	59.7	338	INTERGENIC				
CaPOPI_7503	scaffold387	23485	ATTTTT/ATTTTTTT	GGGTCAAGGTGGTTAGT GGA	TCCTCTGCCTTTCATGT GTG	59.8	496	INTERGENIC				
CaPOPI_7504	scaffold387	23589	ATGTGTGTG/ATGTGTGTGTG	GGGTCAAGGTGGTTAGT GGA	TCCTCTGCCTTTCATGT GTG	59.8	496	INTERGENIC				
CaPOPI_7505	scaffold387	160969	TTA/TTACTA	AGCTCCAAATCCAGAGC AAA	GGGATATGATCTTCTAC CCCA	60.0	835	INTERGENIC				
CaPOPI_7506	scaffold39	39921	TTATATATATATATATAT/TTATATATA TATATATATATAT	CGGCCATCTACGTTGTC TTT	AACAACTCCTTCGCTC CAA	60.1	316	INTERGENIC				
CaPOPI_7507	scaffold3917	4350	ATTT/ATTTT	TGAGGCGTATCATGTGT TGA	CAACTTTGGTGAGGCCA TTT	58.6	662	INTERGENIC				
CaPOPI_7508	scaffold3918	4292	TAAAAAAAA/TAAAAAAAAA	ATGCCTTCGTCCTCTCC TTT	ACATTGAAACTGCCCAT TCC	60.2	612	INTERGENIC				
CaPOPI_7509	scaffold3918	4537	CTTAATT/CTT	ATGCCTTCGTCCTCTCC TTT	CGAGTGAAGGCATGGGT ATT	60.2	914	INTERGENIC				
CaPOPI_7510	scaffold3923	3230	GA/GAA	TGCTGCAACTTCTACAT CCG	AGAAAGCGTGAAAACTC CGA	60.0	695	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7511	scaffold3927	1574	ATTTTT/ATTTTTTT	GAATCCTGGGCTGAAATCAA	CGTGGAATCGCGTAGGAAT	60.0	342	INTERGENIC				
CaPOPI_7512	scaffold3939	3327	GATAATAATAATAATAATAA/GATAATAATAATAATAATAATAA	TCCAGATCAAAATCGAGGACC	AGAGGCCAACCAAGAACCGAA	60.0	450	INTERGENIC				
CaPOPI_7513	scaffold395	7068	T/TCTGA	TTTACAGCGCTTCTCCC AAT	TCCCAACCCAATAAACCAA	59.8	667	INTERGENIC				
CaPOPI_7514	scaffold395	42393	TA/TATTTTGAA	TGACACTGTAAACCCCCA	ATGGCAAATAATTGGTGGGA	59.8	537	INTERGENIC				
CaPOPI_7515	scaffold395	101675	ATATTATTATTATTATTATTATTATTATTATT/ATATTATTATTATTATTATTATTATTATTATTA	ACGCGACAATCGAGGTA AAC	TACGTACGGCAGTAGCCCTT	60.1	787	INTRON	Ca_24514	K	G2-like	Signal transduction response regulator, receiver domain
CaPOPI_7516	scaffold3950	7394	GTATATATATATATA/GTATATATATATA TATA	CCAGATGTCGTTTCTCC GAT	TTGTATGACATCTCGCC ACC	60.1	665	INTERGENIC				
CaPOPI_7517	scaffold3950	7697	C/CTT	TTTCTCTTTGGTGGTTGCC	TCCACCAATATGCAAAA GCA	60.1	854	INTERGENIC				
CaPOPI_7518	scaffold3950	7767	TAAAAA/TAAAA	GGTGCGAGATGTCATACAA	TCCACCAATATGCAAAA GCA	59.5	366	INTERGENIC				
CaPOPI_7519	scaffold3950	8174	TAAAAAAAA/TAAAAAAAAA	TGCTTTTGCATATTGGTGGA	AAACATGGCCTTCAAC TGG	60.1	475	INTERGENIC				
CaPOPI_7520	scaffold3950	8477	TAAAAAAAAA/TAAAAAAAAA	TGCTTTTGCATATTGGTGGA	AAACATGGCCTTCAAC TGG	60.1	475	INTERGENIC				
CaPOPI_7521	scaffold3950	8667	AAATAATAATAATA/AAATAATAATAA	CCAGTTGAAGCCATGT TTT	TTTTATGGAAGCATGTG GCA	60.0	528	INTERGENIC				
CaPOPI_7522	scaffold3950	12638	T/TTACGCA	CAAGAGCCTAAGGATGCTGC	AGCATGAAACGGTGGAG AAT	60.1	919	INTERGENIC				
CaPOPI_7523	scaffold3951	1843	CAA/CA	GAGTCACAGTGGCACTCAG	TCGACTTGTCaatcgct TTG	59.4	226	INTERGENIC				
CaPOPI_7524	scaffold396	371269	TAAAAAAAA/TAAAAAAAA	GTTTTGACTGGCCAAAGAG	GAGCGCTGTAAAGACC ACC	59.7	588	INTERGENIC				
CaPOPI_7525	scaffold396	372299	CATATATATATATATATATATATA/CA TATATATATATATATATATA	TGTATTTCTGCGcatttCG	TTGTTAGTTTGACGAGG GCA	60.0	357	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7526		scaffold396	577559	GAA/GA	TCCCAACCCAAATAAAC CAA	AAGCTCAACATGCAAAA CCC	60.0	538	INTERGENIC				
CaPOPI_7527		scaffold396	577641	ACCC/ACCCC	TCCCAACCCAAATAAAC CAA	AAGCTCAACATGCAAAA CCC	60.0	538	INTERGENIC				
CaPOPI_7528		scaffold396	588477	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAA/AAATAATAA TAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAA	AGGCGATTTTCATCCTC CTT	AGAGGCAAACAAGAACC GAA	60.0	513	INTERGENIC				
CaPOPI_7529		scaffold397	23446	A/AT	TGGAGGCGGCTACTAGT GTT	ATTGAATTCGCCATAAAC GG	59.9	411	INTERGENIC				
CaPOPI_7530		scaffold397	167388	AATATATATATATATATATAT/AAATA TATATATATATATATATATATAT	GATTTGCTTTCGTGAC AGA	CGGTGAATCCTTTACGG AGA	60.0	279	INTERGENIC				
CaPOPI_7531		scaffold398	17888	CTTTTTTTTT/CTTTTTTTTT	AAACGCAATCCTTGAGT TCG	AAATGTTGCAATCCTC CCA	60.2	362	INTERGENIC				
CaPOPI_7532		scaffold398	17995	ATAATCAACTAA/ATAA	AAACGCAATCCTTGAGT TCG	TCGATCAATTGAAAATCC ATCA	60.2	601	INTERGENIC				
CaPOPI_7533		scaffold398	33224	CTTTTTTTTT/CTTTTTTTTT	AGTGATCCAACCCAAC ATCG	TCGAATAAATCAATCCAA AATCAA	60.0	561	INTERGENIC				
CaPOPI_7534		scaffold398	33315	AG/AGG	AGTGATCCAACCCAAC ATCG	TCGAATAAATCAATCCAA AATCAA	60.0	561	INTERGENIC				
CaPOPI_7535		scaffold398	33778	AATAT/AATATAT	TTTGATTTTGGATTGATT TATTCG	CATGGGCACTCAAAGCA CTA	59.3	494	INTERGENIC				
CaPOPI_7536		scaffold398	33851	A/ATTTTT	TTTGATTTTGGATTGATT TATTCG	CATGGGCACTCAAAGCA CTA	59.3	494	INTERGENIC				
CaPOPI_7537		scaffold398	45043	T/TGTA	CCCTACGACGTCCGTTA AAA	TCGCTCGTTGCACCATA TTA	60.0	554	INTERGENIC				
CaPOPI_7538		scaffold398	133623	AAAATAAATAAATAAATAA/AAAATAAA TAAATAAATAAATAAATAA	TTGACCTATGTCCCCTC TCG	CGCACACTTAGCAAATG CAG	60.1	269	INTERGENIC				
CaPOPI_7539		scaffold398	160107	CAAA/CAA	CAACTTCCGAAACTCT GGG	TTTCGCAAGATGTGAT TGA	59.7	250	DRR	Ca_22283		C2H2	Zinc finger, TRAF- type
CaPOPI_7540		scaffold398	213400	TAAAAAAAAAAAA/TAAAAAAAAAA	CATGCCTCTAAAGCCCT TGT	TGAAGGAAACGACACAT GGA	59.3	729	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7541	scaffold398	252607	CAAAAAAAAA/CAAAAAAAAA	TGCTCAGACCACCAATGAA	CAACTTCAAACGACAAACG	60.2	299	INTERGENIC				
CaPOPI_7542	scaffold398	260710	AC/ACC	TTGTCCTTCAACCACGTCA	CACAAAGCAATTCCAAACCA	60.1	379	DRR	Ca_22288	I		Male sterility
CaPOPI_7543	scaffold398	261122	CTATATATATATATATATATATA/CTATATATATATATATATATA	ATGGACTCTCCCTCTCAGCA	TCTGCATGTCAGCCTACAG	59.8	589	DRR	Ca_22288	I		Male sterility
CaPOPI_7544	scaffold398	269493	GTTTTTTTTT/GTTTTTTTTT	TACTGGAGTGATGCAGGCAA	CAAAAGTCCAATAAAATGAGCA	60.4	330	INTERGENIC				
CaPOPI_7545	scaffold398	270063	CAAAAAAAAA/CAAAAAAAAA	TGCTCCATTTTATTGGACTTTTG	TGTTGCAAAGATCGAACGTC	60.3	579	INTERGENIC				
CaPOPI_7546	scaffold398	270743	TAAAAAAAAA/TAAAAAAAAA	GTAGTGGTTGAAGTGGCGGT	CTACTCCATCGGGTCTCCAA	60.0	462	INTERGENIC				
CaPOPI_7547	scaffold398	288064	AGGG/AGG	AATTCTCAGGCCAGCTCAAA	TGAAGCTTACCAATTCCCA	60.0	444	INTERGENIC				
CaPOPI_7548	scaffold398	289050	CAAAAA/CAAAAA	TGATGAGCTAGGAACCTCCG	GCAGTTTAAGTCTGCTCCG	60.4	592	INTERGENIC				
CaPOPI_7549	scaffold398	290361	ATTTTT/ATTTTT	AAAACGGATTTTACGGTCCC	AGAGCACCCCATACCTAT	60.1	598	INTERGENIC				
CaPOPI_7550	scaffold398	290707	CAAAAA/CAAAAA	AAAACGGATTTTACGGTCCC	GTTGGTCCTTTTGACCTCA	60.1	990	INTERGENIC				
CaPOPI_7551	scaffold398	319085	TG/T	TTGCATGAAACATGGCAGT	GTTGTTGATGTGGAGGGCTT	60.1	337	INTERGENIC				
CaPOPI_7552	scaffold398	339301	TAAA/TAA	GGATGCTGGAATTTGAAGG	GCAGTAATATGTGATGGTTT	59.5	713	DRR	Ca_22294	K	C3H	Endonuclease/exonuclease/phosphatase
CaPOPI_7553	scaffold398	339502	T/TG	GGATGCTGGAATTTGAAGG	TTTTACTTCCGCCAGCTTGT	59.5	810	DRR	Ca_22294	K	C3H	Endonuclease/exonuclease/phosphatase
CaPOPI_7554	scaffold398	344928	CCAATTGCAATTGCAATTT/CCAATTTGCAATTT	CGAACTCCTAAAAACGCGAG	TGTTTTCCAGTGGTGTTCTTGT	60.0	434	INTRON	Ca_22294	K	C3H	Endonuclease/exonuclease/phosphatase
CaPOPI_7555	scaffold398	348013	TAAAAAAAAA/TAAAAAAAAA	AAATTATGAGGCGCAGTTGG	TCCGGTTGGAATTGCTCTTA	60.1	348	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7556	scaffold398	372482	TTGTGTG/TTGTGTGTG	TGGGAGTTTGTGAGGTA TTTC	GCCAAAGAAGAAGTGAA CCG	60.2	772	DRR	Ca_22296	J		Protein synthesis factor, GTP-binding
CaPOPI_7557	scaffold398	379143	AGAA/AGAAATTGAA	TCTGAGGAAGAGGAGGA CGA	AGCGTGGCAGATTTTGA AAG	60.1	778	INTERGENIC				
CaPOPI_7558	scaffold398	443064	ATTTTTTTTT/ATTTTTTTTT	TTCCGATGGAGCTATTC TGG	TTTTCTTGGGTAGCAAT CGG	60.2	609	INTERGENIC				
CaPOPI_7559	scaffold398	454951	GTTTTTTTT/GTTTTTTTT	GGTGGAGAATGAAACGG AGA	GATCTCTTTGGGCCAAT CAA	60.1	775	INTERGENIC				
CaPOPI_7560	scaffold398	459574	CAAAAAAAAA/CAAAAAAAAA	TCGGGTTGTATGGGTT TTA	TTGTCGTTTGAGCCTT TCT	60.0	477	INTERGENIC				
CaPOPI_7561	scaffold398	466018	ACCCCC/ACCCC	TGCATGCAGACAAGAGT CAA	TTGGAAAAGCCACCTA CAC	59.1	468	INTERGENIC				
CaPOPI_7562	scaffold398	479794	CTTTTTTT/CTTTTTTT	GCTGGCCTTATCCATT GAA	TGAAATCAGTGCAGGGA GTG	60.0	580	INTERGENIC				
CaPOPI_7563	scaffold398	485833	ATTTTTTTTT/ATTTTTTTTT	TGGTTGTGCACCTCAAA CAT	TCTCTCCTCCTACCCT TCC	60.0	870	INTERGENIC				
CaPOPI_7564	scaffold398	492512	ATTTTTTTTTTT/ATTTTTTTTTTT	AGCTTCTTGAATAGCTG CGG	CCATTGATTCGACCATT GTG	59.8	740	INTERGENIC				
CaPOPI_7565	scaffold398	495732	ATTTTTTTTTTT/ATTTTTTTTTTT	TCAACAAACCAAGAACG ATGA	GGGAAGGACTGGATGTA GCA	59.2	636	INTERGENIC				
CaPOPI_7566	scaffold40	41230	CTTT/CTTTT	TGGGAGTCATGGATGAG TGA	CCGAGCCAAAATCCAAA ATA	60.0	341	INTERGENIC				
CaPOPI_7567	scaffold40	41514	GATATATATATATATATA/GATATATA TATATATA	TATTTTGGATTTTGGCTC GG	GAGGAAAGAGGGAGAAT GGG	59.9	432	INTERGENIC				
CaPOPI_7568	scaffold40	56808	CATA/CATATA	ATTGACGGAAGTCA TCC	CCTCCACCTCCTCCTCC TAC	59.9	810	INTERGENIC				
CaPOPI_7569	scaffold40	123508	TA/T	TTTGGTCCCCAAACACC TTA	TTAGTTCACGTGTCCCC CTC	60.2	959	INTERGENIC				
CaPOPI_7570	scaffold40	466805	ATTTTT/ATTTT	GCCTGAAATATGCCGAG GTA	TCGGCTCTCATGTCAG ATA	60.1	420	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7571	scaffold40	922923	TAAAAAAAAA/TAAAAAAAAA	GATTTCATTAGATATT GTGGTGA	CATTACATGGTCGTTTT GG	59.3	851	INTERGENIC				
CaPOPI_7572	scaffold40	973137	TTGTGTAACAAATCAT/TTGTGTAACAA ATCATGTGTAACAAATCAT	GCCAAGAAGGGTGATT TCA	CATATGGGTTTGGCACC TCT	60.1	314	DRR	Ca_18995	S		
CaPOPI_7573	scaffold400	44195	GTTTTTTTT/GTTTTTTTT	CGATGACAAGCAATCAA TGG	CCAAAGATCTCTACCCC TACCA	60.1	123	INTERGENIC				
CaPOPI_7574	scaffold4011	17091	CAAAAAA/CAAAAAA	TTTCTTCCACAGGGGA TTG	TGCGGTTTATCAGCTC TCT	59.9	269	INTERGENIC				
CaPOPI_7575	scaffold4011	114159	AAATAACACACAATAAC/AAATAACACA CAATAACACACAATAAC	TCTGTGTCCATCTCTC GAC	TAGCTCGGCCAAACTTT GTT	60.0	481	INTERGENIC				
CaPOPI_7576	scaffold4011	143675	GAAGGTTGTAAGGTTGT/GAAGGTTGT	TCTGGTGGTGGTCAGT GTA	TAATTTGGTGTGTGCGC AGC	60.0	612	INTERGENIC				
CaPOPI_7577	scaffold4028	27326	T/TG	GGTTTGACTGCATAACG GAGA	TTGAATACACCTACAAA CGAAGA	60.1	552	INTERGENIC				
CaPOPI_7578	scaffold4038	835	AATATA/AATATATA	GCCCTCAGATGAGAGTC AGG	AGGGTTACAGTCTACCC GCA	59.9	780	INTERGENIC				
CaPOPI_7579	scaffold4038	1082	TG/T	TTGGAGAACTTTTCCG CTG	CGAACTGGGCTCAGAGA AAC	60.4	632	INTERGENIC				
CaPOPI_7580	scaffold404	161683	T/TC	CGTGAGATCCCCCTATC GTA	TTGATTTAGCCCAGGA TTC	59.9	334	INTERGENIC				
CaPOPI_7581	scaffold404	180224	CAA/CA	AGTTGGACACTTGCCT TCT	TCGCATCATTTTACCGC ATA	60.1	856	INTERGENIC				
CaPOPI_7582	scaffold404	202624	AATATATATATATATATATATATATAT ATATATATATATAAATATATATATATATA TATATATATATATATA	TATTTTGATTTTGGCTC GG	AAATGGAGGAGAAGGAG GGA	59.9	417	INTERGENIC				
CaPOPI_7583	scaffold404	237330	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATTATTATT TATTATTATTATTATTATTATT	AGAGGCAAAACAAGAAC CAA	GCAACCAAAATTGAAACA CCA	59.9	581	INTERGENIC				
CaPOPI_7584	scaffold4041	994	CT/CTTT	TCATTCTAATTCTGCCT GATG	GTCCAAACCCAGCACAA TCT	59.2	494	INTERGENIC				
CaPOPI_7585	scaffold4041	15702	T/TG	AGGAATTGGATCGGGAG ATT	AAGGAAATGAGGAAAT GGGGA	59.7	626	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7586	scaffold4041	15753	TAAAAAAAA/TAAAAAAAAAAAA	AGGAATTGGATCGGGAG ATT	AAGGAAATGAGGAAAT GGA	59.7	626	INTERGENIC				
CaPOPI_7587	scaffold4041	15867	AT/ATT	GGGTTGGGATATGTTAG CAAA	GAATGCGAAAGCCACAA TTT	60.1	851	INTERGENIC				
CaPOPI_7588	scaffold4041	15956	TAAAAAAAA/TAAAAAA	TCCCATTTTCTCATTTCTT	GAATGCGAAAGCCACAA TTT	59.8	493	INTERGENIC				
CaPOPI_7589	scaffold4041	16171	AAA/AAATTAA	GGCAGTCCCTATTTTT GAA	GAATGCGAAAGCCACAA TTT	59.9	345	INTERGENIC				
CaPOPI_7590	scaffold4045	1604	GTTT/GTTTT	CACAACGCCAAGATGCT AGA	CCCCCTTTTGCATAAG TGA	60.0	779	INTERGENIC				
CaPOPI_7591	scaffold4064	835	AT/ATTAGT	ATGCTCTGCACTTGCACTA	TGACTTGACTCTTGCC GCA	59.9	581	INTERGENIC				
CaPOPI_7592	scaffold4064	1366	TTAT/TT	AAAAGCATGCAGTGCAACAC	TCCCGTCTGAAAATTAT GGC	59.9	367	INTERGENIC				
CaPOPI_7593	scaffold4069	1182	AATATATATATATATATA/AATATATATATATATATA	AACCGACACTCAACCACTC	TTTGAAGGAACCTGCT TTG	60.0	260	INTERGENIC				
CaPOPI_7594	scaffold408	3361	T/TGTTGA	CAAGGAGGAGCAAGATCAGG	GGGAAAGCGGACGTGT ATTA	59.9	631	INTERGENIC				
CaPOPI_7595	scaffold408	3569	TCCCC/TCCCCC	TAATACAGTCCGCTTT CCC	CGAACCTGCTGTCCAAA AAT	60.0	394	INTERGENIC				
CaPOPI_7596	scaffold408	130988	T/TG	GTGGTGATATTTGGGAAGCC	TCGTGGTTTTGGTGTTG GTA	59.2	662	INTERGENIC				
CaPOPI_7597	scaffold408	131029	AT/AAGT	GTGGTGATATTTGGGAAGCC	TCGTGGTTTTGGTGTTG GTA	59.2	662	INTERGENIC				
CaPOPI_7598	scaffold4088	5270	AT/A	ATCAACTTGCAAGGCAGCTT	TACCATTCAATTGGCGA ACA	60.0	454	INTERGENIC				
CaPOPI_7599	scaffold4088	17489	TTCT/TT	TAGGTGATGGAGATCTCGGC	TTGTCAGTGTGCGATC ATA	60.2	592	INTERGENIC				
CaPOPI_7600	scaffold41	114200	ATTTTTTTTT/ATTTTTTTTTTTT	ACCAGTCCCCTAAACCAACA	TTGATTGAAACATTGATT TCCG	59.3	660	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7601	scaffold41	122306	ATT/ATTT	TCGCTACGGCTCTAGTGTT	AAGTCCTGTAGCCGAAAGCA	60.0	294	INTERGENIC				
CaPOPI_7602	scaffold41	122382	C/CG	TCGCTACGGCTCTAGTGTT	AAGTCCTGTAGCCGAAAGCA	60.0	294	INTERGENIC				
CaPOPI_7603	scaffold41	122436	GC/G	TGCTTTCGGCTACAGGACTT	CGGGGAGTTGAAATAAGCA	60.0	282	INTERGENIC				
CaPOPI_7604	scaffold4107	9634	CT/CTAAATT	CCTAAACCTAAACCAAAACC	TCGTCCAATAAGAACAAAGTCAA	57.4	127	INTERGENIC				
CaPOPI_7605	scaffold4108	8749	CTT/CT	CAAAACCGAAACGCTTAAC	TTTTGGGCTTCGAGTTAGG	59.6	294	INTERGENIC				
CaPOPI_7606	scaffold411	193597	CAATAATAATAATAATAATAATAATAATA/CAATAATAATAATAATAATAATAATAATA	TGTTCCGGCTTATTGCAGTTG	AGAGGAGGTGATGGTGATGG	59.9	482	INTERGENIC				
CaPOPI_7607	scaffold411	251051	TTTATTATTATTATTATTATTATTATTAT/TTTATTATTATTATTATTATTATTATTATTATTA	CCCTTCTCCTTCCGTAGAGC	TTGACACGGTCTGCGTAGTT	60.3	371	INTERGENIC				
CaPOPI_7608	scaffold411	298521	A/AGATTG	CTTGCATGGCAATTATCAACAA	TTGGGCTGATGCAATAAACAA	59.5	469	INTERGENIC				
CaPOPI_7609	scaffold411	334354	GAA/GA	GAGGTTTCACAGTGCAAGCAA	TTCTTAGCCATGCTGGTGTG	60.0	649	INTERGENIC				
CaPOPI_7610	scaffold411	339806	T/TA	GACAATGTCCCACCTTGAGAA	CACGGTTGTGATGACTGGAC	60.0	671	INTERGENIC				
CaPOPI_7611	scaffold411	340187	TAAAAA/TAAAA	ATTGGTGTGTGCAGGTGAAGAA	CACGGTTGTGATGACTGGAC	60.0	109	INTERGENIC				
CaPOPI_7612	scaffold411	343473	A/AGTG	TCATTTTCATGAAGACCAACA	TCATTTGACCATCAATCA	58.1	462	INTERGENIC				
CaPOPI_7613	scaffold411	436040	CATA/CATATA	ACCCGAATACCTCAAGGGTC	TCGTTTATTCGGATTCTGCTC	60.2	922	INTERGENIC				
CaPOPI_7614	scaffold414	21975	GAAAAA/GAAAA	TTCCTATTGCTCACCCCTTG	GAAAAACAAGACCCGCGATA	60.1	516	DRR	Ca_27849			
CaPOPI_7615	scaffold4155	7060	AATATATAT/AATATATATAT	CGGTTCAACGTAACCGACTT	TTGGGCAACAATCGATGTAA	60.0	402	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7616	scaffold418	8392	T/TC	TAATCTTCAGCAGTGGT GGC	TTTTCTTTTCGATTTGAT CCG	58.9	680	INTERGENIC				
CaPOPI_7617	scaffold418	154196	AA/AATA	ACTCCTCAAAACTCGGC AAA	TTGAAC TTGCATTCGTTC CA	59.9	719	DRR	Ca_24681			
CaPOPI_7618	scaffold418	157125	TCC/TC	TCGGTTCTCAATCTAAC CATTTG	TTTTATGGGTTTTGGTTG AAAA	60.4	660	INTERGENIC				
CaPOPI_7619	scaffold419	148627	CA/CAA	AACAAGCAAGCCATTCA AGC	GGTGAGGATCTGGTGTG GTT	60.4	657	INTERGENIC				
CaPOPI_7620	scaffold419	335182	TAAAAAAAAAAAA/TAAAAAAAAAAAA	GGGCATTTTTCAACAAG GTG	ATGTTCCAACAATCTCC CCA	60.3	457	INTERGENIC				
CaPOPI_7621	scaffold4192	3302	C/CGATTGGTAAATCGA	AGGGAGGACGAAAATGA CCT	CGATTGCCTCAAAC TTG GAT	59.9	724	INTERGENIC				
CaPOPI_7622	scaffold4192	3668	T/TC	ATCCAAGTTTGAGGCCAA TCG	CGATTTTCGCAGGTCTT GTT	60.1	484	INTERGENIC				
CaPOPI_7623	scaffold4197	16348	GAAA/GAA	AATGCCCACGAATCTGA AAG	GTGCGGAAGCCATGAGT AAT	60.1	483	INTERGENIC				
CaPOPI_7624	scaffold4197	38400	AATATA/AATA	GGCCTGGGTTATGGGTT AAT	AAATTGAGTTTCAAAACC ACCAA	59.9	830	DRR	Ca_27296			
CaPOPI_7625	scaffold4197	56545	GAAA/GAAAA	TCCAGATGAAATCGAGG ACC	TATTTTCGACCAGACG AGG	60.0	606	INTERGENIC				
CaPOPI_7626	scaffold420	69655	CAA/CAA	ATGGCGAAGAATTATGG TGC	CATGTACCGCCCATCTC TTT	59.9	265	INTERGENIC				
CaPOPI_7627	scaffold420	86760	GATCAT/GAT	TGTTGCTAGGCAGAGTG TGG	AGAAAGGTCCAACCGGC TAT	60.0	415	DRR	Ca_22197			
CaPOPI_7628	scaffold420	109389	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT/TTTA TTATTATTATTATTATTATTATTATT ATTATTATTATTATT	CCCAAAATCCCTAACATG TGG	GTTGTCCATTGTTTTGC GTG	60.0	520	INTERGENIC				
CaPOPI_7629	scaffold420	156465	TTATATATATATATAT/TTATATATATATA TATAT	TATGTCCCATTACACTC GG	CTGGATTTTGCACTCTG CCT	59.4	411	INTERGENIC				
CaPOPI_7630	scaffold420	265273	GAAAAAAAA/GAAAAAAAA	CGTGATCGTGTTTGGTT GTC	GGGAATGGCAGCAAAATA GAA	60.0	587	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7631	scaffold4221	569	AAAGAA/AAA	ATTGATTTTGAATCGCCCA	CAGTTTCCTGCCAGCCTTAG	60.3	441	INTERGENIC				
CaPOPI_7632	scaffold4221	691	A/AG	CTAAGGCTGGCAGGAACTG	CGCTTCTTTGGTCATGCA	60.0	443	INTERGENIC				
CaPOPI_7633	scaffold4221	7762	TAAAAA/TAAAA	TGCCAGAACTGATTTCTGCT	GAGCGCTGTAAACACCTCC	60.0	540	INTERGENIC				
CaPOPI_7634	scaffold4221	54414	GTTTTTTTTTTTT/GTTTTTTTTTT	GAGCCCGAATCGTTATTG	TTGTGGTATACCCGACAAGAA	59.5	695	INTERGENIC				
CaPOPI_7635	scaffold4221	54516	A/ATTAGGG	GAGCCCGAATCGTTATTG	TTGTGGTATACCCGACAAGAA	59.5	695	INTERGENIC				
CaPOPI_7636	scaffold424	29738	T/TA	ACTCGACAAAAATGGAACTGG	CTTTTGGCCTATTAGCGTCG	60.0	496	DRR	Ca_27938	L	bHLH	RNA-binding, CRM domain
CaPOPI_7637	scaffold4243	1042	CGG/CG	GGTACGGAAATTGCCTGAAA	GGTCCTCGATTTCACTGGA	59.9	204	INTERGENIC				
CaPOPI_7638	scaffold4243	14917	CT/CTT	TGCTTGATTGCTTGAGTTCC	GATGAAATCGAGGACTGGGA	59.0	537	INTERGENIC				
CaPOPI_7639	scaffold4243	16781	CTTTTT/CTTTTT	TTTCATCTGGACTTTTCGGG	TCGAGGATAGGGAGACCTT	60.0	964	INTERGENIC				
CaPOPI_7640	scaffold4244	559	TAA/TAAA	CCCAGTTCCCAAGAGTCAAA	GGAACGCATTTCTCGTGTTT	60.1	122	INTERGENIC				
CaPOPI_7641	scaffold429	33115	TAAAAAA/TAAAAAAA	AATTAGCGTGTTGATTCGGG	AATCCTGGTGCACGATTTC	60.0	720	INTERGENIC				
CaPOPI_7642	scaffold4319	1139	ATTT/AT	CGATTTCCCTCACGACAAT	TTTTGGACAGCTACAAGTGTT	59.9	582	INTERGENIC				
CaPOPI_7643	scaffold4319	1245	TAAAAA/TAAAA	CGATTTCCCTCACGACAAT	TTTTGGACAGCTACAAGTGTT	59.9	582	INTERGENIC				
CaPOPI_7644	scaffold433	8383	GAAAAAAAA/GAAAAAAAAA	ACATGTAAGGCAAGGCCAAC	GCCAGTCACCCCACTTTA	60.0	377	INTERGENIC				
CaPOPI_7645	scaffold433	18841	TAAAAAAAAA/TAAAAAAAAA	CGGCGATAGAAAGCCTACTG	ATGCAAGGTGGGTGCTAAAG	60.0	371	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7646	scaffold433	47351	AAAAA/AAAAACAAA	GAGGCGTCAAGCTAATG ACC	AAGCTCAAATGGGCTAG CAA	59.8	530	INTERGENIC				
CaPOPI_7647	scaffold433	74147	TTATATATATATA/TTATATATATATATA	GCAGCCGTTCTCTTTTGTTC	ACGTGTGTCGGACATTCA TCA	60.0	709	INTERGENIC				
CaPOPI_7648	scaffold433	86247	GTTT/GTT	GCCCTCAGATGAGAGTC AGG	AGAATTACGAGCAGCG GAA	59.9	287	INTERGENIC				
CaPOPI_7649	scaffold433	98245	CTAACTTAACCTTA/CTAACTTA	CAAGATCCAGTTTGTCCTCGT	CGCATGGAGGAGAAAG GATA	60.0	266	INTERGENIC				
CaPOPI_7650	scaffold433	144718	GCC/GCCC	TGGCTAATCGCCAGTTT TCT	AATGATCGTCTTCGGAT TGC	59.8	854	INTERGENIC				
CaPOPI_7651	scaffold433	146170	TAAAAAAAA/TAAAAAAAA	GTTGCCAAAGCAGGGTA AAA	TGAAACGGATTTTCAAC CAA	60.1	434	INTERGENIC				
CaPOPI_7652	scaffold433	146841	AATTATTATTATTATTATTATTATT/ATTATTATTATTATTATTATT	TGGTGACAATTGATGG TTCT	CAGTGCGATGGAGAAAT CAA	57.9	523	INTERGENIC				
CaPOPI_7653	scaffold433	147086	ATTTTTTTTT/ATTTTTTTTT	TGGTGACAATTGATGG TTCT	TCGATTATGCGTAGGGA AGG	57.9	770	INTERGENIC				
CaPOPI_7654	scaffold433	147750	TTTTTATTTAT/TTTTTATTTATTTTAT	TTTTAGCGGATGTCGTA GGG	TCACAAGGGAGGCTTTA TGG	60.1	717	INTERGENIC				
CaPOPI_7655	scaffold433	157672	GATATATA/GATATA	GCAATTCAGATGGGCA GTT	AATGATCGTCTTCGGAT TGG	60.1	714	INTERGENIC				
CaPOPI_7656	scaffold433	165941	A/AG	AAAATTGAAACATCCGA CGC	ACTTGTGCTGGACGAA TCT	59.9	512	DRR	Ca_26821			
CaPOPI_7657	scaffold4331	1786	ATT/AAATCTCCTT	CCTTGTGTGCTTGGGT TGA	AGAAGCAATGGCTCGAA GAA	59.6	528	INTERGENIC				
CaPOPI_7658	scaffold4349	1831	GTTTT/GTTT	AGGTCATTTTCGTCCTC CCT	CAAACACACCTGTTGGA TGC	59.9	182	INTERGENIC				
CaPOPI_7659	scaffold436	67143	A/AC	CAAACACCTGTTGGA TGC	AGGTCATTTTCGTCCTC CCT	60.0	478	INTERGENIC				
CaPOPI_7660	scaffold436	68438	A/AT	GGCCGGATGAAATGAA CTA	ATTTTCGTCCTCCAAAG GCT	59.9	513	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7661	scaffold4366	635	A/AG	ATGCACACGATTGGTGA AAA	TCATTTTCGTCTCCTCAAA GG	60.0	757	INTERGENIC				
CaPOPI_7662	scaffold4366	1890	G/GC	GGACATGAATAGGGCAA TGG	GGTCATTTTGTCCACG CTT	60.2	532	INTERGENIC				
CaPOPI_7663	scaffold4367	11881	CTAAAAATTAAAAATTAA/CTAAAAATTA A	TGGATGCACAAGATGGG TTA	ATTTTCATCCTCCCAAG GCT	59.9	351	INTERGENIC				
CaPOPI_7664	scaffold437	2817	ACCC/ACC	CCTGCTTTTCCAACCAT GT	TGGCACAGTTCCAAGAT CAA	60.0	507	INTERGENIC				
CaPOPI_7665	scaffold437	11434	TATGG/TATGGGTGAAATGG	ACAATCCCCCAATGTG AAA	GTTGGTTCCTAGCACC GTA	60.0	841	INTERGENIC				
CaPOPI_7666	scaffold437	45718	CAATATTAAAAATATTAAA/CAATATTA AAAAATATTAAATATTAAAAATATTAA A	TCGAAGAGGACCATTCA TCA	AGGTCGCACTCCAAATA TCG	59.2	777	INTERGENIC				
CaPOPI_7667	scaffold4374	728	GCCTAAACCCTAAACCCTAA/GCCTAA CCCTAA	ATAAACCCGAACCGCAA AAC	AGGGTTTAGGGTTTAGG CCA	61.1	848	INTERGENIC				
CaPOPI_7668	scaffold4374	1159	CTAAACC/CTAAACCATAAACC	TAAACCCCAATGACCG AAA	AGGGGTTAGGGGTTAG GGTT	60.2	444	INTERGENIC				
CaPOPI_7669	scaffold4377	6572	AA/AAGA	TCCAGATGAAATCGAGG ACC	AGGCGATTTTCGTACCA CAC	60.0	319	INTERGENIC				
CaPOPI_7670	scaffold4387	5507	ATAGTATA/ATAGTATAGCTAGTATA	GCACAAAAACCTTATCC CCA	AAATGCTCGCCTCTTTTT GA	59.8	311	INTERGENIC				
CaPOPI_7671	scaffold4397	932	TAAAAAA/TAAAAAA	GTCAAGGCAGACCAGAA AGC	GAACGACGGTGATGCCT ACT	60.0	168	INTERGENIC				
CaPOPI_7672	scaffold44	290551	TTTA/TTTACAATTA	AACCAAGAGGCTTTCG TCA	GGAGCAGTTTCTTGGCG TAG	59.9	705	DRR	Ca_25417			
CaPOPI_7673	scaffold440	30262	CAAAA/CAAA	ACCAAAATAAGCCAGG GAG	TTGCCATTGCATGAACA TTT	60.3	354	INTERGENIC				
CaPOPI_7674	scaffold442	20594	TGGGGGGG/TGGGGGGG	TGGACGCACAAGATTGG TTA	AGGTCATTTTCGTCTC CCT	60.1	370	INTERGENIC				
CaPOPI_7675	scaffold446	219694	GGT/GGTGT	TCCAGTCCTCGATTTC ATC	CGGGTTATGCGTCAGAT TTT	60.0	699	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7676	scaffold446	224556	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATA/AAATAAT AATAATAATAATAATAATAATAATAAA TAATAATAATAATAATAATAATA	TTCATCTGGTCTTTTG GC	CATTGAGTACAAC TACA AACG GACG	60.1	771	INTERGENIC				
CaPOPI_7677	scaffold446	235656	TAA/T A	TCTGACA ACTCAATTTG CTCT ATG	GTTGTACTTCATAACGA CACAA TACT	59.8	521	INTERGENIC				
CaPOPI_7678	scaffold450	9894	CTTTTTTTTT/CTTTTTTTTT	TCATTGCTTTGGGTGAT TGA	TGGTAACGTGGACGATT TGA	60.0	597	INTERGENIC				
CaPOPI_7679	scaffold450	255127	GAAAAAAAA/GAAAAAAAAAAAA	ACGACC CATATTGAGCA AGG	AGTTACGTGGCATGACC CTC	60.0	528	INTRON	Ca_23798			
CaPOPI_7680	scaffold450	299447	ATTTTTTTTT/ATTTTTTTTT	TGCCACTACTAGGCACT AGCC	TCGCATTTGATTATTTCA CACA	59.6	659	INTERGENIC				
CaPOPI_7681	scaffold450	322861	TA/T	ACACGTAACATGCAGGT CCA	TTGTTCTCATTAAGTGTT GGATTGA	60.0	283	INTERGENIC				
CaPOPI_7682	scaffold4508	4751	TAAAAAAAA/TAAAAAAAAAAAA	CCGGAAA ACTTCATCCC AAA	AGAAA ACCGAATTGGCC CTT	59.9	810	INTERGENIC				
CaPOPI_7683	scaffold4508	36727	TAA/TA	TTGTGTTTGT CACAGCG CAT	TCAGGAACAACA ACTCA ACCC	60.0	371	INTERGENIC				
CaPOPI_7684	scaffold451	10137	ATATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTAT TATTATTATTATT/ATATTATTATTATTAT TATTATTATTATTATTATTATTATTATTA	TGTTTCAACGCTCTTTT CTTTTT	TGGTGTCTGTGGCAACA CTT	59.3	574	INTERGENIC				
CaPOPI_7685	scaffold451	17388	AAGTA/AA	TGCTCAAGGATGCACTC AAC	GCCATTGATGAGTACGC TGA	60.0	671	CDS (large-effect mutations)	Ca_22599		C3H	
CaPOPI_7686	scaffold451	30168	TA/TAA	GCAGCCACAATAAGTG GGT	AACCAAAGCCTGAGCTT GAA	60.0	810	INTERGENIC				
CaPOPI_7687	scaffold451	37858	TTATATATATATATATAT/TTATATATATA TATAT	ACAGCGAACAACCACAT CAA	TAAATGCCGATTTCCCA AAG	60.2	569	INTERGENIC				
CaPOPI_7688	scaffold451	324149	G/GAAAAAC CCTTATCT	TGAATTCAACGCAAATG ATCT	TCAACAAAACCTAGCC ACC	58.2	162	INTERGENIC				
CaPOPI_7689	scaffold4511	11167	CATATA/CATA	TGAGTGGTAGGAAAATC GCC	TTTCATTTGGACTTTTCG GG	60.1	844	INTERGENIC				
CaPOPI_7690	scaffold4511	22911	CAAAAA/CAAAA	CTCCCCCTGAGTTTTGG AAT	GACGACAATCACCCGAA GAT	60.3	753	DRR	Ca_28219		Trihelix	Peptidase C48, SUMO/Sentrin/Ubl1

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7691	scaffold4511	22953	TAAAA/TAAAAA	CTCCCCCTGAGTTTGG AAT	GACGACAATCACCCGAA GAT	60.3	753	DRR	Ca_28219		Trihelix	Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_7692	scaffold4511	38356	GTTTTTTTTT/GTTTTTTTTTTT	AATGCCACCCATAATT CA	CTGGGCAAGGGATCTGA ATA	60.0	642	INTRON	Ca_28219		Trihelix	Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_7693	scaffold4515	721	TG/T	GTGTTTGTGTCGTTGGA TGC	ACCTATTGGATGCACAA GCC	60.0	677	INTERGENIC				
CaPOPI_7694	scaffold453	76859	GAAAAAAAA/GAAAAAAAAA	TTCATTGATGTGTCTTT GGA	CGGCAATGCAAGTTTGA CTA	60.1	478	INTRON	Ca_21728		MYB_rela ted	Toll-Interleukin receptor
CaPOPI_7695	scaffold453	80166	T/TCATG	AATTTAAACCGCCAAA ACC	TCACTCATAAATATCCTC ATGGACA	60.1	578	INTRON	Ca_21728		MYB_rela ted	Toll-Interleukin receptor
CaPOPI_7696	scaffold453	281880	CATATATATATATAT/CATATATATAT ATATATAT	GTTGGTTCCCTAGCACG GTA	AACGTGGTATCAGCCCT TTG	60.0	777	INTERGENIC				
CaPOPI_7697	scaffold453	497792	CAATAATAATAATA/CAATAATAATA ATAATAATA	GCCGTGATTTGGAAAAA GAA	TGTCAGTTTTGAGCCCA ATG	60.1	479	URR	Ca_21748			SAC3/GANP/Nin1/mts 3/eIF-3 p25
CaPOPI_7698	scaffold453	498751	GATAT/GATATAT	GCCCCTCAAAGATAACCC AT	GACCATGATTTCTTACTA GCCGTT	60.2	838	URR	Ca_21748			SAC3/GANP/Nin1/mts 3/eIF-3 p25
CaPOPI_7699	scaffold453	503657	TAAA/TAA	GAACATTGCAGAAACGC AGA	CTATTGACGCCTTGCGT GTA	60.0	728	INTERGENIC				
CaPOPI_7700	scaffold4580	704	CATATA/CATATATATA	TTGGTTTATTGGGTTG GGA	CCATGAAAAGAAGAAGG GCA	60.0	717	INTERGENIC				
CaPOPI_7701	scaffold4582	7612	A/AG	TCCAGATGAAATCGAGG ACC	CGAAATTTGACACGGAA CCT	60.0	258	INTERGENIC				
CaPOPI_7702	scaffold46	6079	CTTTT/CTTTT	GGGCCGAGAGTCCCTTA TAG	GGTCCTCGATTTTCTCT GGA	60.1	304	INTERGENIC				
CaPOPI_7703	scaffold461	26285	CAAAAA/CAAAAAAA	CGATTCCCACATCGATT CTT	TGCTCAAGACACGTGAA AGG	59.9	207	INTERGENIC				
CaPOPI_7704	scaffold4643	53525	CAAA/CAAAA	ATGCAATGCGTATATGC CAA	GCCTGTGATAGGCGGTA CAT	59.9	185	INTERGENIC				
CaPOPI_7705	scaffold466	12138	AATATATA/AATATATATA	ATTCAGTTCCTTGCA GAT	TCTCCGCATAAGCTTTC GAT	59.7	661	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7706	scaffold466	168483	TTATTAAAAATATTTAAAAATATTTAA A/TTATTAAAAATATTTAAAAATATTTAA AAAAATTTAAAAA	AGCAAAAAGTGTCGAG AGC	AGTCACCAGTCACCAGT CCC	59.6	655	INTRON	Ca_25699			
CaPOPI_7707	scaffold466	169717	A/ATGCAAAAGATTCTA	CTTTCGTGCCCTTGATT TGT	CGTGGCCTATCGATCCT TTA	60.1	740	INTRON	Ca_25699			
CaPOPI_7708	scaffold466	170442	CA/CACGGA	ACCCTTTTGTTCCACAC GAG	AAGCTGACTTCGGTTGG CTA	60.0	270	INTRON	Ca_25699			
CaPOPI_7709	scaffold466	254290	TCTTCTCCACTT/TCTT	GGATTCCGCGTAAGATT TCA	ACTAGGTTTTGGGTTCC GCT	60.0	465	INTERGENIC				
CaPOPI_7710	scaffold4696	3564	T/TA	CAAAACACCTGTTGGA TGC	AGGTCATTTTCGTCTCTC CCT	60.0	180	INTERGENIC				
CaPOPI_7711	scaffold470	169493	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TCAAGAGGAAGCGAAAG GAA	GCCCCCTATTTTGCAG TTT	60.1	277	INTERGENIC				
CaPOPI_7712	scaffold470	318535	TTATATATATATATATATATAT/TTA TATATATATATATATATATATAT	AATTAGGGGATCGAGGG AAA	AGGTGGCAACCTTCTCA TTG	59.7	472	INTERGENIC				
CaPOPI_7713	scaffold470	336358	TTATGTAT/TTAT	GTCATCCTAGCCATCGT CGT	GTGTCCCAAACTCAAG GGA	60.1	876	INTERGENIC				
CaPOPI_7714	scaffold470	365605	CTTTTTTTTTTT/CTTTTTTTTTTT	AGAAGCAAGCTAGCTCG TGG	ATTGGAGCACATTGAGG CTT	59.9	815	INTERGENIC				
CaPOPI_7715	scaffold470	370786	TAAAAAA/TAAAAAA	CATGCCAGTTGCTACAT GCT	GCTTGGACTCAGTGGCT AGG	59.9	949	INTERGENIC				
CaPOPI_7716	scaffold470	372719	GAAA/GAAA	ATTTTATGCTGCGACAT CCC	GCAATCCACACTTGG AGT	59.9	265	INTERGENIC				
CaPOPI_7717	scaffold470	375954	AATATATATATATATATATATATAT ATATATATATAT/ATATATATATATATA TATATATATATATATATATATAT	AGGGAATCGAGGGAAAA ATG	AGGTGGCAACCTTCTCA TTG	60.3	463	INTERGENIC				
CaPOPI_7718	scaffold4708	20906	CTTT/CTTTT	TGTTTGAAATCAGATGC GGA	AATTGTGTTTCGGGTTT TGC	60.2	526	INTERGENIC				
CaPOPI_7719	scaffold4711	5708	GTTTTTTT/GTTTTTTT	AGGTCATTTTCGTCCTC CCT	TTGGATGCACAAGATTG GTT	59.9	271	INTERGENIC				
CaPOPI_7720	scaffold4711	6211	GTTTTTTT/GTTTTTTT	TTTTCGTCCTCCCTAGG CTT	AGGAACTTATTGGATGC CCA	60.2	470	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7721	scaffold4711	9037	CA/CAA	AACCAATCTTGTGCATC CAA	AAGACGAGGGACGACAA AAA	59.0	379	INTERGENIC				
CaPOPI_7722	scaffold4713	1946	TG/TGG	TCATCCAATGACACAAA CGC	AGGTCATTTTCGTCCTC CCT	60.5	193	INTERGENIC				
CaPOPI_7723	scaffold4733	507	AT/ATT	ACAGTGAACGTGCACCG ATA	CTGGTTATGCCGTTTGG AGT	60.0	697	INTERGENIC				
CaPOPI_7724	scaffold475	141188	A/AAATGGGG	GAGGAGCGACCAAGTTGT TTC	GAAACTAATGCGACCGG TGT	59.9	884	INTERGENIC				
CaPOPI_7725	scaffold475	163127	C/CCT	TTCAGGCAATCCAATCTT CC	TGGGTCCAAGGACAGG TAG	60.0	503	INTERGENIC				
CaPOPI_7726	scaffold475	174713	GTTTTTTT/GTTTTTTT	AAGGTTGACTGCATAAC GAAGA	CAACACCATTTGACAAC ACCA	58.9	730	INTERGENIC				
CaPOPI_7727	scaffold477	10236	CAAAAAAAAA/CAAAAAAAAA	TTGGAAAAGCCCACCTA CAC	TGCAGTGCAATGTCCAT TTT	60.0	208	INTERGENIC				
CaPOPI_7728	scaffold477	11283	C/CA	TGTCATCTTGTTTGCCTT GG	TGATGAACTCTGAACT CGTGG	59.7	114	INTERGENIC				
CaPOPI_7729	scaffold477	20714	TA/TGA	CCCCCTAATGCTCAATTT CA	TGCAACAAGAGGCAAAA CAC	59.9	288	INTERGENIC				
CaPOPI_7730	scaffold477	28410	TAAAAA/TAAA	GTAGGAGGATCTCAAGG GGC	CCAAAATTAGGAAGCAC CCA	60.0	567	INTERGENIC				
CaPOPI_7731	scaffold477	46653	GAAAAA/GAAAAAA	ATGCAACTGTCGTTTTA GCA	TTAGAGCGCCTTCTGAT GGT	57.0	405	INTERGENIC				
CaPOPI_7732	scaffold477	49382	GCTCTCACTCTCACTCTC/GCTCTCACTCTCACTCTCACTCTC	CCCGCAATAACTCCAA TAA	TACCCACCACTGACC AGA	59.9	583	INTERGENIC				
CaPOPI_7733	scaffold4773	12822	ATCT/AT	CTTGTA AAAACGCGCT GTA	TAGCTTGTCGCGTTGAT TTG	60.1	612	INTERGENIC				
CaPOPI_7734	scaffold4773	12850	TA/T	CTTGTA AAAACGCGCT GTA	TAGCTTGTCGCGTTGAT TTG	60.1	612	INTERGENIC				
CaPOPI_7735	scaffold4773	13699	TTTTATTATTTATTTATTTATTTATTT/TTTATTTATTTATTTATTT	TATGCCACATGCCAAC TAC	TAGGCCGACTGCTCTTA TGG	59.4	247	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7736	scaffold4773	14894	CAAAA/CAAAA	CCGCAGTCCCTTTGTTT TTA	CTCCACGGTTCTGTCA CAG	60.1	684	INTERGENIC				
CaPOPI_7737	scaffold4773	16885	TNNNNNNNNNN/TNNNNNNNNN	TGCGGCTATTCAACA TGG	GCATATCTGAGGCTGCC AAT	59.5	600	INTERGENIC				
CaPOPI_7738	scaffold4773	18351	GAAA/GAAA	TGGGGGATTGTTGAAA ATA	GGGACAGAAAGAAAGG GGAG	60.0	313	INTERGENIC				
CaPOPI_7739	scaffold4773	19083	A/ATTCACAGCATTGT	TTTAAGCGCCATATTGA GGG	GTGGTGTGGCTGCAAC TTA	60.1	448	INTERGENIC				
CaPOPI_7740	scaffold4773	19668	TAAA/TAA	TAA GTTGACCCAACAC CAC	GGGTTTTCCCATTTAG CAT	59.8	700	INTERGENIC				
CaPOPI_7741	scaffold4773	19970	ATT/ATTT	ATGCTAAATGGGAAAA CCC	CACGAAAGTTAGGAGC AAGA	60.0	106	INTERGENIC				
CaPOPI_7742	scaffold4773	29645	CAAAAAAAAAAAAA/CAAAAAAAAAA	GGCATGCTGCGATTAAT TTT	TTGTTACTCGGTGGACG ACA	60.1	282	INTERGENIC				
CaPOPI_7743	scaffold4773	30145	AATATATATATATATATATATATAT ATATATATATATAT/ATATATATATATAT ATATATATATATATATATATATAT	GCGTTTACATGCAATCG TGT	TGATTTTGGTTTGTTC TTGTT	59.6	910	INTERGENIC				
CaPOPI_7744	scaffold4773	33470	GAAAA/GAAAA	TGAATAGTGGTGGTGAG TTTTCA	TGTGGAGAAGAGGGAG CAAT	59.5	405	INTERGENIC				
CaPOPI_7745	scaffold4773	36112	T/TCCTGC	CGCAATGGGTAAACCC CTA	AGCCTTCGAGATACGGT TGA	59.8	663	INTERGENIC				
CaPOPI_7746	scaffold4773	36184	GATATATATATATAT/GATATATATAT ATATATATAT	CGCAATGGGTAAACCC CTA	AGCCTTCGAGATACGGT TGA	59.8	663	INTERGENIC				
CaPOPI_7747	scaffold4773	52490	ACTTCTTTGG/ACTTCTTTGGCTTCTTT GG	CCAAGTAGGCGTTGGA TAA	CACGTGATGTTTGGGCA TAG	60.0	408	INTERGENIC				
CaPOPI_7748	scaffold4773	55151	CCTTCTT/CCTT	GCTGCTGTTTCGTTTT TTC	CTGTTGGCTTCCACTTC CAT	60.0	307	INTERGENIC				
CaPOPI_7749	scaffold4777	29741	CAAAAAAAAA/CAAAAAAAAAA	TGGCTTGTGTTTCTCTC CCT	TGTTGTTCTACATGCGC TGA	59.8	663	INTERGENIC				
CaPOPI_7750	scaffold4777	118728	CTTTTTTT/CTTTTTTTTT	AACGGTTTGGTTTGATC TGC	ACGTCGTCAAACAGATG CAC	60.0	231	INTRON	Ca_26711	R		WD40 repeat

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7751	scaffold4784	684	TG/TGATGGCTAG	TCTGTGCCTCGATTTC ATC	GGGCCGAGAGACCCTTA TAG	60.0	339	INTERGENIC				
CaPOPI_7752	scaffold479	7594	TTA/TTAGGCATA	TGTGTTTGTTGGCATTGG ATT	AGGGAGGACGAAAATGA CCT	59.8	329	INTERGENIC				
CaPOPI_7753	scaffold479	125417	CTTTT/CTTTTT	ACAAACCAATCGATTTC CCA	CGGAGGACGAAAATGAC CTA	60.2	180	INTERGENIC				
CaPOPI_7754	scaffold48	11811	AAATAATAATAATAATAATA/AAATA ATAATAATAATAATAATAATAATA	GCTAACTGACTTGCATT GCG	ATTCATCAGTTGCGCAA AAA	59.6	758	INTERGENIC				
CaPOPI_7755	scaffold48	15048	AAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT AATAATAA/AAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT C/CTTTCTTCCCT	TCGGTTCATCATGTTGG AAAT	TCTTTTGATGTGGGTTA GTGAGAA	60.2	677	INTERGENIC				
CaPOPI_7756	scaffold48	140670	C/CTTTCTTCCCT	TTTGCCCTTTTGTATTGG TC	GCAAATTGGACAGCAGA TGA	59.9	467	INTERGENIC				
CaPOPI_7757	scaffold480	43150	TCCC/TCCCC	AACGTACTGCCTATCAC GGG	TGTTTCATCGTATTTGGC GTG	60.0	836	INTERGENIC				
CaPOPI_7758	scaffold480	69498	TTTTATTATTTATTTATTT/TTTTATTTA TTTATTTATTTATTT	AGAGGTGCGCACTATGG ACT	CTGGAAGTGGCAGTGAA TGA	59.9	695	INTERGENIC				
CaPOPI_7759	scaffold4804	893	TAAAAAAAA/TAAAAAAAA	AGCCTAGGGGTGACGAA AAT	GTCCTCCCCAGGCTTAA TTC	60.0	516	INTERGENIC				
CaPOPI_7760	scaffold4804	1921	TAAG/TAAGCCAAG	TTGGATGCACAACATTG GTT	AGGTCATTTTCGTCCTC CCT	59.8	561	INTERGENIC				
CaPOPI_7761	scaffold4804	8867	CTT/CT	TGGATGCACCAGATTGG TTA	AGGTCATTTTCGTCCTC CCT	59.9	570	INTERGENIC				
CaPOPI_7762	scaffold4822	847	A/AGAATACT	CAGCGGATCCCCAGATA TAC	AGGTCATTTTCGTCCTC CCT	59.4	545	INTERGENIC				
CaPOPI_7763	scaffold4829	6279	TCCC/TCCCC	GACCCGCATTTTCCTCA TTA	GGAGAACGTTAAGGCAG CAG	59.9	507	INTERGENIC				
CaPOPI_7764	scaffold4829	6512	AGGGG/AGGG	CTGCTGCCTTAACGTTT TCC	CCAAAAATCAGCCCGAT CTA	60.0	262	INTERGENIC				
CaPOPI_7765	scaffold4829	8205	TAAAA/TAAA	CAATAGCATGCAGTTGG AGG	GGGACTCCCATACATT GGC	59.3	500	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7766	scaffold4833	740	TTTTTGTTTTT/TTTTT	TGGGAATGTAGTGGATG AACC	TCCCGAACACCTATGCT TTT	59.7	529	INTERGENIC				
CaPOPI_7767	scaffold4833	3774	T/TA	CCAAGCCAGTCAAACAC AAA	GGGCTCGCTATGTACAG CA	59.7	839	INTERGENIC				
CaPOPI_7768	scaffold4833	3926	CATATATATAT/CATATATATAT	CAATTCAAATTGGCCCT GTC	GGGCTCGCTATGTACAG CA	60.3	477	INTERGENIC				
CaPOPI_7769	scaffold484	11805	CAATATCAAATATCAAATATCAAATATCAAATATCAAATA/CAATATCAAATATCAAATATCAAATA	CGAATACCTCCAAGGTC CAA	TCGTTTATTCGGATTTCG CTC	59.9	814	INTERGENIC				
CaPOPI_7770	scaffold484	136302	TCCCC/TCCC	ACCGAGGTGCCACTTAT CAC	ATAGTGGTGA CTGGATG GGC	60.0	229	INTERGENIC				
CaPOPI_7771	scaffold484	435397	CATATATATATAT/CATATATATAT	TTGCTATGAAGGGACCA AGG	TCAAGTGGGGAGTGGA GAAC	60.1	252	INTERGENIC				
CaPOPI_7772	scaffold484	575607	AGA/AGATTGA	TCCGATGACTTTGTGAA GCA	AAGATGATGGGAGGCAA ACA	60.4	559	INTERGENIC				
CaPOPI_7773	scaffold484	656687	AC/A	TATCACCTATCAGAGCG GGG	TGATTCCGGGGAAGTAC AAC	60.1	472	INTERGENIC				
CaPOPI_7774	scaffold484	793859	CACACTA/CACACTAACACTA	GGAAGGTGTGTGGGAA GTGT	ATATTGCCTCCTCCCC TGT	59.9	631	INTERGENIC				
CaPOPI_7775	scaffold485	131454	TCC/TC	TCAATCCACCACTGG GTA	TGTTGGTTTATGGGGGA AGA	59.8	475	INTERGENIC				
CaPOPI_7776	scaffold4851	2996	G/GCGATTTTC	GGTCCTCGATTTCATCT GGA	GGGCCGAGAGACCCTTA TAG	60.0	130	INTERGENIC				
CaPOPI_7777	scaffold4851	3617	TAAAAAA/TAAAAAAA	CGCGGAACCTGAAACAC TAT	CCGATGCTAAAAATGGC AGT	60.1	616	INTERGENIC				
CaPOPI_7778	scaffold487	87751	T/TC	ACATTGAGGTCATTTTC GCC	AGCCTAGGGAGGATGCA AAT	59.9	229	INTERGENIC				
CaPOPI_7779	scaffold4872	661	G/GTTCTATCA	TGGGCACATGCTTCTCA GTA	TACTGGAACGACCACA CAA	60.4	498	INTERGENIC				
CaPOPI_7780	scaffold4902	30200	AAATTCCAAAA/AAATTCCAAAAATTAAT TCCAAAA	TCACCATGTGCTACTTC ATTCA	GTGACGGTGTTCGTTGC TAA	59.2	503	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7781	scaffold4902	30281	ATTTTT/ATTTTTTT	TCACCATGTGCTACTTCATTCA	GACACCCAAATCTCAGGGA	59.2	779	INTERGENIC				
CaPOPI_7782	scaffold4902	65969	ATTTTTTTTT/ATTTTTTTTTT	TGAAAAACGCAACGAAGATG	CTTTTGCCAATTAACCCGAA	59.8	746	INTERGENIC				
CaPOPI_7783	scaffold4902	72921	CTT/CT	GGGGTTACATTAACGGGGTT	CACCTCATAACGTGTTGGC	59.8	613	INTERGENIC				
CaPOPI_7784	scaffold4902	73019	AA/AACTGAAATTTA	GGGGTTACATTAACGGGGTT	CACCTCATAACGTGTTGGC	59.8	613	INTERGENIC				
CaPOPI_7785	scaffold4902	73796	CTTTTTTTTT/CTTTTTTTTT	GTCGGCCCAACACGTTAT	AGCGGCCTCTCTATCAACA	59.4	532	INTERGENIC				
CaPOPI_7786	scaffold4902	73891	CGG/CGGGG	TTTGATAGAGAGCCGCTTG	ACTAAGCGTGGAACG GTG	60.5	372	INTERGENIC				
CaPOPI_7787	scaffold4902	75211	ATTTTTTTTT/ATTTTTTTTT	GGTTGTGGCGTTTCTTCAT	AAAAC TTGTTTACATGGA CAATGC	60.0	458	INTERGENIC				
CaPOPI_7788	scaffold4902	82598	TAA/TAAA	TTGTCACACTACAAGGTG CAT	CCAATCCATTTCCATCAAGC	58.2	635	INTERGENIC				
CaPOPI_7789	scaffold4902	83305	CTTT/CTTTTT	GCTTGATGGAAATGGATTGG	AAAAACGCAACCAACATCAA	60.3	609	INTERGENIC				
CaPOPI_7790	scaffold4920	19062	CA/C	CAGAAAATCGATTGCCAGT	AGTCCAAGTAGCAAATGCCG	60.1	497	INTERGENIC				
CaPOPI_7791	scaffold4923	11425	AATATATATATATATATATA/AATATATATATATATATATA	TTGGATTTTGGCTCATAGGC	CGCGTTAACAGAGGAAGAGG	60.0	392	INTERGENIC				
CaPOPI_7792	scaffold493	25789	GT/GTCATAGGTCTTCCCTATT	ACAATCGTGCCTAAATGCC	TTGGACTGCAATGAAAGGA	60.0	495	INTERGENIC				
CaPOPI_7793	scaffold493	149227	CTTTTTTT/CTTTTTTTTT	AAGCCTATTACAGCGCTCTTTG	GGTCTTTTAAAGCGCTTGTTG	60.1	930	INTERGENIC				
CaPOPI_7794	scaffold493	297027	AT/ATATATATATGTGT	ATGTTTTGGATTTGGCTCG	AAATTGGTCCACTAGCACCG	59.9	643	INTERGENIC				
CaPOPI_7795	scaffold4943	1324	A/AC	GAAGTCGGGTGGTACGA AAA	CGCGGAACCAAAAACATAGT	60.0	731	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7796	scaffold495	33497	TAAAAAAAAAAAAAAAAA	AACTCTTTGGCTTTCTG CCA	GGGGAAATTCGCTTTGA TTT	60.0	480	INTERGENIC				
CaPOPI_7797	scaffold495	126369	GAAAAAAAAA/GAAAAAAAAA	TACATTGCGGTCCTT AAC	AGCCAAATTTAGGGAG GCA	60.0	859	INTERGENIC				
CaPOPI_7798	scaffold496	54994	CAAA/CAAAAGTTGAAAA	GGAATAAGGAAAAGTCG CCC	TCAAGTTGCCACTGACT TGC	59.9	637	INTERGENIC				
CaPOPI_7799	scaffold496	121429	CT/C	TCCTGGTCCTCGATTT C ATC	AATCGCTGAAAAGACG AGA	60.0	379	INTERGENIC				
CaPOPI_7800	scaffold496	211993	GTATATATATATAT/GTATATATATAT	CCTTATGAACCGCAAT ACA	TCTCCGCATAAGCTTTC GAT	59.5	651	INTRON	Ca_27203			
CaPOPI_7801	scaffold497	69293	ATTTATTTT/ATTTATTTTATTTT	GGTAGTCAAGCCTGAGG CAG	TCTTGATGTTTGATTAA TGTTAGGTG	60.0	585	INTERGENIC				
CaPOPI_7802	scaffold497	69995	GTTTTTTTTT/GTTTTTTTTT	TGGTGCTTTTGAAAAA GTG	ATTTGGTTTGGTTGCATT CG	58.8	446	INTERGENIC				
CaPOPI_7803	scaffold497	70043	CAATAAATAATAATAAAT/CAATAAAT AAAT	TGGTGCTTTTGAAAAA GTG	ATTTGGTTTGGTTGCATT CG	58.8	446	INTERGENIC				
CaPOPI_7804	scaffold4978	33825	AGG/AG	CACAATTGGGGGAACAA GAG	CGAACCACGTCGCTAA TAA	60.3	399	INTERGENIC				
CaPOPI_7805	scaffold498	206145	GTTTTTTTT/GTTTTTTTT	CACCGCCTCTGTTCCAT ATT	GAGATTTAGAACCATCA AATTGTCA	60.0	829	INTERGENIC				
CaPOPI_7806	scaffold498	214228	CATAATAAACTAATAATAAACTAATA AT/CATAATAAACTAATAATAAACTAA TAATAAACTAATAAT	TTTCATGGTCATGTTTTG GC	GAAAGGCCAATGTCCAG AAA	59.4	781	INTERGENIC				
CaPOPI_7807	scaffold498	214273	TACACACACACAC/TACACACACACA C	TTTCATGGTCATGTTTTG GC	GAAAGGCCAATGTCCAG AAA	59.4	781	INTERGENIC				
CaPOPI_7808	scaffold498	214558	CTTTT/CTTTTTT	CACACACACGTAAGAAG GCTG	TTGGACAGAATCAAGGC TCC	59.4	544	INTERGENIC				
CaPOPI_7809	scaffold4983	27276	ATTT/ATT	AAGGTGGTACGAAAATC CCC	GCACGTGGGAAAATGAG ATT	60.1	893	INTERGENIC				
CaPOPI_7810	scaffold50	6994	AGGG/AGG	ACCTGTGTAGCCGACAA ACC	AATCCCGAACCTCCTCA AGT	60.0	769	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7811	scaffold50	86754	TTTATTATTATTATTATTATTATTAT TATTATTATT/TTTATTATTATTATTATTA TTATTATTATTATTATTATTATTATT	CTTCGGGCTCCGATTTT TA	TCTGAAATCCCAAACC AGG	60.2	857	INTERGENIC				
CaPOPI_7812	scaffold50	191851	GAAAAAAAAA/GAAAAAAAAA	GTTCTTCCGCAGAAGTC AGG	GAGATCTCGGTGCTACT GCC	60.0	325	INTERGENIC				
CaPOPI_7813	scaffold50	192238	A/AGTGATAGAAATT	CTGCCCATTAGCCCTTC ATA	CTGAATGCAAGAGAGAG GGG	60.1	291	INTERGENIC				
CaPOPI_7814	scaffold501	66521	TCC/TCCC	ATTTTGGACTCCCTTG GCT	AATCCAATGCCACAAAC ACA	59.9	686	INTERGENIC				
CaPOPI_7815	scaffold501	87430	CATATATATATATATAT/CATATATATAT ATATATAT	TGGGTGTGCCTATATAC ACGTAA	TTCTTTGCCACACACCAT GT	59.3	519	INTERGENIC				
CaPOPI_7816	scaffold5030	906	AAATAATAAT/AAATAAT	TGGGGATACGTAGGAGC AAG	TGTTGGTCCATTTTGA CGA	60.1	432	INTERGENIC				
CaPOPI_7817	scaffold506	18074	TAAA/TAAAA	CTATGGTAGAGCGGTTT CGC	TTCTCCCGAGTTTGGT CTC	59.9	487	INTERGENIC				
CaPOPI_7818	scaffold506	18975	TA/TAA	TCTCGATACCATCGTGG ACA	TCCCATTTGATTGCTGA ACA	60.1	489	INTERGENIC				
CaPOPI_7819	scaffold506	33758	TTCT/TT	TGACCAACTCTTTTGTG CCA	AGCCAACCTCTGTCTCA TGG	60.3	667	INTERGENIC				
CaPOPI_7820	scaffold506	39512	GAA/GA	AAACCTTTGAGAAATGC CCA	AATGGAGTTCGGAGATT GGA	59.5	563	INTERGENIC				
CaPOPI_7821	scaffold5083	2034	AG/A	AACCCAAAACGCTAAAC CCT	TCCGTCCAATAAGAGCA AATG	59.9	559	INTERGENIC				
CaPOPI_7822	scaffold5086	3516	ACC/AC	TAGGGAGGACGAAATG ACG	CCAATCGTGTGCATCCA ATA	60.1	469	INTERGENIC				
CaPOPI_7823	scaffold5089	3720	TAAAA/TAAAAA	AGCCTAGGGAGGACGAA AAA	AAACAATCGTGTGCATC CAA	60.2	541	INTERGENIC				
CaPOPI_7824	scaffold509	266782	AG/A	GGTGGTAGCTGGTAGG GTGA	TGCACTTGACCTTTCTTC CC	60.0	935	INTERGENIC				
CaPOPI_7825	scaffold5094	2305	TAA/TA	TGGCACATGAATAGTTC CACA	GCCACCTCATTCAAATAT TGC	60.0	669	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7826	scaffold510	85609	TAACA/TA	TTGTCAAATAAGTAACA ACAAAACG	TTGCAACAATTGTACCC GAA	58.7	995	INTERGENIC				
CaPOPI_7827	scaffold510	86131	TAAA/TAAAA	TTTTGGTCCCCAAACA TAA	AAAAGTCTCTCCGCTC CTC	60.0	514	INTERGENIC				
CaPOPI_7828	scaffold511	101350	AATATATATATATATATATAT/AA TATATATATATATATATATATAT AT	CGGTGAATCCTTTACGG AGA	GGAGGAGAAGGAGGGA TTTG	60.1	306	INTERGENIC				
CaPOPI_7829	scaffold511	101474	GAAAAAAAA/GAAAAAAAA	CGGTGAATCCTTTACGG AGA	GGAGGAGAAGGAGGGA TTTG	60.1	306	INTERGENIC				
CaPOPI_7830	scaffold511	193038	AATATATATATATATATATA/AATAT ATATATATATATATATA	TTTCAGGTTATCGACTG GGG	AACAAGAAAGCGCAAGC AAT	59.9	729	INTERGENIC				
CaPOPI_7831	scaffold511	194529	AAA/AAACAA	AATCTGCTTCGTTAGC TGC	TGCACAATAACCTGCT TGC	59.6	667	INTERGENIC				
CaPOPI_7832	scaffold512	111039	GAAAAAAAA/GAAAAAAAA	GGTCCTCGATTTCATCT GGA	GACCGGGAGACCCTTAT AGC	60.0	168	INTERGENIC				
CaPOPI_7833	scaffold5120	14840	TTATATATATATATATATATATAT/T TATATATATATATATATATATATAT	TATCGTGCCTGTTGAGA ACG	CTAATTAGCGTCGGAGT CGG	59.9	527	INTERGENIC				
CaPOPI_7834	scaffold5120	15547	TAGAGTACGAGA/TAGA	CCGAAGTAATAGTGGGG CAA	GGACCAGGTTCTGCATC AAT	60.0	214	INTERGENIC				
CaPOPI_7835	scaffold515	42759	C/CT	GGTCCTCGATTTCATCT GGA	TTTCATCTGGACTTTTCG GG	60.0	652	INTERGENIC				
CaPOPI_7836	scaffold515	43016	GAAAA/GAAAA	CAAGAGTCTCCTGGTCC TCG	CTCCCCAAAAGTCCAAA TGA	60.0	912	INTERGENIC				
CaPOPI_7837	scaffold515	216518	ATTTTTTTTT/ATTTTTTTTT	TAATAAATGAGGCGGT GGC	TTAGCATCGTCATTTCT TCAA	59.9	902	INTERGENIC				
CaPOPI_7838	scaffold515	235422	CTATATATA/CTATATATATA	TTGCTCCAAATTGATCAC GA	AACCGATGCTAATCCGA CAC	60.2	818	INTERGENIC				
CaPOPI_7839	scaffold515	266354	TAG/TAGAG	CCACCAACAAAATGG AAC	CATAGAACAAAATTGAG TTGTGAGA	60.1	635	INTERGENIC				
CaPOPI_7840	scaffold5152	20235	CTTTTTTTTT/CTTTTTTTTT	CCAAGGGGAGCAATTAT GAA	TGATGCAATTGTGTGAG TCATT	59.9	366	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7856	scaffold528	215682	CAA/CAATAA	TTTCAATTATGTCAATC GATTTT	TGCGAGAATGAGAAATT GTTG	58.2	572	INTERGENIC				
CaPOPI_7857	scaffold528	241367	ATTTT/ATTTT	TGAGGCGTTACAAGAGG TGA	ATGTGCTCCCTCCAACA ATC	59.4	443	INTERGENIC				
CaPOPI_7858	scaffold528	312579	A/AAAT	TTGAGGGAAGGCATAAT TGC	TGGAATAGTGTGGGGA AAA	60.0	294	INTERGENIC				
CaPOPI_7859	scaffold53	1354	T/TG	ACCACAATGTAACACCC CGT	CGATTGAATTAAGCCCA GGA	60.0	788	INTERGENIC				
CaPOPI_7860	scaffold53	137170	CTT/CTTT	GGACTGGTGGCTCAAG GTA	TCGACCGGGAGTTTTGA TTA	60.1	671	INTERGENIC				
CaPOPI_7861	scaffold530	10667	CG/C	ACCAAATTTGTCGAACC AGC	TTGAGTGTGAGTGCCA GGG	60.0	342	INTRON	Ca_27188	J		Ribosomal protein L14b/L23e
CaPOPI_7862	scaffold5306	9364	GAAAAAAAA/GAAAAAAAAA	TAGATGGGTGTGACGGT GAA	TGAGGGAGCACTATTGG GAG	60.0	590	INTERGENIC				
CaPOPI_7863	scaffold531	11911	A/AT	ATTCCATTTGGCATGCTT TC	TTTGGGTACAAAATCAG AAAATTG	59.9	892	INTRON	Ca_22388			Domain of unknown function DUF231, plant
CaPOPI_7864	scaffold531	83931	CCGG/CCGGCCGGTTCGG	GAGAACGCAAGCTAACG GAC	ACCTTGTGGATGGCAGT TTC	60.0	180	DRR	Ca_22395			
CaPOPI_7865	scaffold535	94648	GATATATATAT/GATATATATAT	AATGGAGGAGAAGGGA GGAA	TGAAAAGGGTAGGCAA CAC	60.0	563	INTERGENIC				
CaPOPI_7866	scaffold5420	685	ACC/ACCC	AAGGGAGGATGGAAATG ACC	ATTTTGTCTCCTTGG GCT	60.1	613	INTERGENIC				
CaPOPI_7867	scaffold543	69059	TGGGG/TGGGGG	TCGCTACTGAAGATGGG CTT	TTGATAACTGAAAACGA AATGAAA	60.0	363	CDS (FRAME SHIFT)	Ca_24780			
CaPOPI_7868	scaffold543	229568	ATTTTT/ATTTT	TTTGCCCCCAACTCTAC ATC	ATGGGCACATGCTATCA TCA	59.9	755	DRR	Ca_24786			
CaPOPI_7869	scaffold544	41662	CT/CTT	GTACCTGTGGATGGGA ATG	TGGATGCACTCGATTGG TAA	60.1	606	INTERGENIC				
CaPOPI_7870	scaffold544	58853	ATTT/ATTTT	GCAATCGATTGGTAAAA CCC	AGGTCATTTTCGTCTC CCT	59.3	261	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7871	scaffold544	82660	AGGG/AGG	AATCCAATGACCCCAAT GAA	TCATTCTCATCTCCCAA GG	60.0	190	INTERGENIC				
CaPOPI_7872	scaffold544	147706	CAAAAA/CAAAA	CCCCCTTTTGCATAAG TGA	GAGGAGACATCTGCTGA GGG	59.9	582	DRR	Ca_26540			
CaPOPI_7873	scaffold544	342056	GTTTTTTTT/GTTTTTTTTT	CGGGGTGTTACTCAT CCT	CGACATCCGTCAAAC AAC	59.8	846	INTERGENIC				
CaPOPI_7874	scaffold545	116816	ATATTATTATTATTATTATTATT ATTATTATTATT/ATATTATTATTATT ATTATTATTATTATTATTATTATTAT T	TTCGGGCTACATTCTT AGG	TCACATTCAITTCCAAAG CG	60.2	775	INTERGENIC				
CaPOPI_7875	scaffold545	193109	CAAAAA/CAAAAAA	AATCTCCCCCTGAGTTT TGG	ATCTTTGGACACCGTCG TTC	60.3	643	INTERGENIC				
CaPOPI_7876	scaffold546	67935	AG/A	TTTGACC AATTTTGTG GCT	TGCAAAAACCACTTTCAA GG	60.3	652	INTERGENIC				
CaPOPI_7877	scaffold547	96984	CAAAA/CAAAAA	CACGATGGCTAGTGCTT GAA	CGATCGGTATGAACATT GACC	60.0	276	INTERGENIC				
CaPOPI_7878	scaffold547	155914	ATCAAA/ATCAAAAGTTCAAA	TCGATCTGTACGAACAT TGACC	CGGAACCCGAAACACTT TTA	60.0	295	INTERGENIC				
CaPOPI_7879	scaffold547	156143	CAAA/CAAAA	TTCGGTCTATTTTGTGCG GG	CGGAACCCGAAACACTT TTA	59.9	219	INTERGENIC				
CaPOPI_7880	scaffold548	114800	ACCCC/ACCCCC	AATCGACATTCGACCCA CTC	CCCCGCTCTGATAGGTG ATA	59.9	384	INTERGENIC				
CaPOPI_7881	scaffold548	212010	G/GA	GGAACACTTCGGTGTGG ACT	CATGTCCCGAAAGAGC AAT	60.0	563	DRR	Ca_21489			
CaPOPI_7882	scaffold548	238316	AATATATATATATATATATATAT ATATATA/AATATATATATATATATATA TATATATATATATATA	AACAAACTCCTCGCTC CAA	GTGCTTGCTAAACACAA GCG	59.9	470	INTERGENIC				
CaPOPI_7883	scaffold548	523039	GTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATTATT/G TTATTATTATTATTATTATTATTATT ATTATTATTATTATTATTATTATTATTAT	ATTTTTGCCTAGTTGTC CCT	CTAAATGAAGAGCCGCA AGG	60.0	170	INTERGENIC				
CaPOPI_7884	scaffold548	593356	CATATATATATATATATATATATAT ATA/CATATATATATATATATATATAT ATATATATATATATATA	CTAGCACCTTAGCGTGG AGG	AAAACGTGGTTTGGGAA GTG	60.0	481	INTERGENIC				
CaPOPI_7885	scaffold548	612534	A/AT	TATTTTGATTTTGCTC GG	AGGAAGAGTGGAGTTGC GAA	59.9	416	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7886	scaffold549	19237	ATTTTTTTT/ATTTTTTT	AATTGGCCACGTCAAAG AAC	TGACGAAATCATTGTTTT GG	60.0	531	INTERGENIC				
CaPOPI_7887	scaffold549	41362	CTATATATATATATATATATATATAT/CTATATATATATATATATATATATATA T	TGTCGTGCCATAAATAT CCG	CAAGCATGATCCAGGGA GAT	59.4	522	INTERGENIC				
CaPOPI_7888	scaffold549	44384	CATATATATAT/CATATATATATATATAT AT	TCAATGCAGAAAAC TCA ACCT	AGGTGGTGTTGGTGAAG GAG	57.5	518	INTERGENIC				
CaPOPI_7889	scaffold549	61007	GTATATATATATATA/GTATATATATA TATA	TGCCAATTCGAAGATCA AAA	CACCCCTTACCTCGACT GAA	59.2	570	INTERGENIC				
CaPOPI_7890	scaffold5504	1323	T/TTA	ACCAATCAAGTGCATCC CAT	TAAGCCTAAGGAGGACG CAA	60.2	175	INTERGENIC				
CaPOPI_7891	scaffold5514	3914	TG/TGG	AGGAAGAGTGGAGTTGC GAA	CTTGGGAGTTGGAGAGC AAG	60.0	489	INTERGENIC				
CaPOPI_7892	scaffold553	2669	CTT/CT	TTGGTTCACTCCCTGGA TTC	AACATCAGTCAAGCGCA CAA	59.9	484	INTERGENIC				
CaPOPI_7893	scaffold553	2745	TAAAAAA/TAAAAAAA	TTGGTTCACTCCCTGGA TTC	AACATCAGTCAAGCGCA CAA	59.9	484	INTERGENIC				
CaPOPI_7894	scaffold553	325514	CT/CTAT	ATCGGAAGTTGGACAGG TTG	TGGCAATCAGCAGAGA CAC	60.0	317	INTRON	Ca_19934	L		
CaPOPI_7895	scaffold553	871030	TTATATATATATATATATATATATATA TATATATAT/TTATATATATATATATATAT ATATATATATATATAT	TGCTCACTCTTAAACCG CCT	AACCCATCGCAAAAGAG AAA	59.9	652	INTERGENIC				
CaPOPI_7896	scaffold5551	550	CTTTTTTT/CTTTTTTTT	GATACGTTGGAGCATCG ACA	CACGAAACACCCTCTTC CAT	59.7	230	INTERGENIC				
CaPOPI_7897	scaffold556	1805	G/GC	TCATTTTCGTTCTCCCAA GG	TGGATGCACAAGATGGG TTA	60.0	664	INTERGENIC				
CaPOPI_7898	scaffold5580	1246	GAAAAA/GAAAAA	CGAGGATCGATTGTCCC TTA	GGTCCTCGATTTTCATCT GGA	60.0	824	INTERGENIC				
CaPOPI_7899	scaffold5598	9627	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA AAAA	TTTCCAACAAGTGAGGG GTC	AAAAACCCATCCAACA ACA	59.9	472	INTERGENIC				
CaPOPI_7900	scaffold5598	13569	ATTTTTTTTTTTTT/ATTTTTTTTTTTT	CGGCATTGGATCATGGT TAG	TTTCGACTGCCTAGCGA TTT	61.2	549	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7901	scaffold560	30079	TATAATAAAATAAAATAA/TATAATAA TAATAAAATAAAATAA	GCATTCTCGTTCATCTC ACG	CGAATCTTGATTTCGGT AACCT	59.4	906	INTERGENIC				
CaPOPI_7902	scaffold560	156538	ATTTTTTT/ATTTTTTTTTTT	AGGTGGTGTGGTGAAG GAG	TCAATGCAGAAAACCTCA ACCT	60.0	522	INTERGENIC				
CaPOPI_7903	scaffold560	160741	ATT/AT	TGTTTCATCATGAGGAGA GGG	TGGTCCAAATGAATGAG TCTTG	58.6	360	INTERGENIC				
CaPOPI_7904	scaffold5602	4886	TG/TGG	ACAAAGGAATGAGTGGC ACC	TCAAGTCTCGCACACA ACC	60.0	347	INTERGENIC				
CaPOPI_7905	scaffold561	25431	CTCTTTCT/CTCT	TTGATTCATCAACACCC GGA	AAATTGGGTTCTGCCAA TCA	59.9	399	DRR	Ca_26215		MYB_rela ted	
CaPOPI_7906	scaffold564	2634	ATTTTT/ATTTT	TCGAATGCTCGACTTTA CCC	GCGGAATAACATGGTTG CTT	60.2	641	INTERGENIC				
CaPOPI_7907	scaffold564	5212	G/GAAC	TGGGATGCAAAACATTC TCA	TTGTCAATTTGGGAGTG CAA	60.0	560	INTERGENIC				
CaPOPI_7908	scaffold564	8317	TAAAAA/TAAAAAA	CAACATCCAATTTTGTT ATAGAGC	CGACATGCATGCCTTAT TTG	58.3	143	INTERGENIC				
CaPOPI_7909	scaffold564	13897	T/TG	GAGCACATTGGAGGACA CTG	CGGAGATAAAAACAATT GGCA	59.3	659	INTERGENIC				
CaPOPI_7910	scaffold564	15097	TTAT/TTATAT	TGGAGAAATGCTAAATC CCG	GATGGCAGGTAAAGCG AAA	60.0	599	INTERGENIC				
CaPOPI_7911	scaffold564	15227	ATATCTATTATCTATTAT/ATATCTATTA T	TGGAGAAATGCTAAATC CCG	AGATGGCAGGTAAAAGC GAA	60.0	600	INTERGENIC				
CaPOPI_7912	scaffold564	25971	TA/TAGTTTATTAATAGTTAA	GTATCTGAGCCTCTGCC AGC	AATTGGTGTGTCTGCGT CAA	60.1	555	INTERGENIC				
CaPOPI_7913	scaffold564	26112	A/AG	GTATCTGAGCCTCTGCC AGC	AATTGGTGTGTCTGCGT CAA	60.1	555	INTERGENIC				
CaPOPI_7914	scaffold571	18167	TTACATCTCATA/TTA	CCTCACGGTTTCAATTG CTT	CTTAATGCACAGCCTAC CCC	60.1	670	INTRON	Ca_27520	T	NAC	Serine- threonine/tyrosine- protein kinase
CaPOPI_7915	scaffold571	41234	GAAAA/GAAA	GAGGGCAAAGATGACCT GAA	AGGTTGTTTTCTGCTCTC CCT	60.2	693	INTERGENIC				

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CaPOPI_7916	scaffold5730	659	ATTTTTTTTTTTTTTTT/ATTTTTTTTT	ACAAAGGCAACCTTTTG TGG	CTGCCACCGTTGTATTCT	60.0	866	INTERGENIC				
CaPOPI_7917	scaffold575	65125	G/GT	TTGAAGTTAAGGGGTGCTGC	TCCATCCAACCTTGTGGATT	60.2	531	DRR	Ca_27003			
CaPOPI_7918	scaffold575	66804	CTTTTTTT/CTTTTTTT	AACCGGATGTTGGGATGTAA	CCCATTCACTCCCACTCTGT	60.1	348	INTERGENIC				
CaPOPI_7919	scaffold575	67025	ATTTAGGGTA/ATTTAGGGTATGGTTTGGGTA	ACAGAGTGGGAGTGAATGGG	CCTAAGCCTGACCCTACCCT	60.0	397	INTERGENIC				
CaPOPI_7920	scaffold575	67830	TGGTTTAGGGTTTAGGGTT/TGGTTTAGGGTT	GGGTTAGGGTAGGGTCAGGA	AGGCTGGAATCGTAAGTGA	60.2	357	INTERGENIC				
CaPOPI_7921	scaffold575	82549	TAAAAA/TAAAAAAA	GCAATAACGAAATGGCTGTG	CCCTAACTCCCTAAACCCA	59.2	101	INTERGENIC				
CaPOPI_7922	scaffold575	89948	TAAAAAA/TAAAAAAA	GGATTGGCCCCAATAGAAT	CCCTTGTCATTGCTGCTGTA	60.0	722	INTERGENIC				
CaPOPI_7923	scaffold575	90216	G/GA	CCCAAAATGCAATAACCAAGG	TACCGTTTCCCACTCACACA	60.2	637	INTERGENIC				
CaPOPI_7924	scaffold575	91034	AATATATATATATATATATATAT/AATATATATATATATATATAT	TGTGAGTGTGGGAAACGGTA	GGCAATGTCATAAACA AAAA	60.0	426	INTERGENIC				
CaPOPI_7925	scaffold575	98810	TC/T	TAGCCAGGGCTTTCTTTCA	CCTCCACTCCAAACCTACCA	60.0	404	INTERGENIC				
CaPOPI_7926	scaffold575	99188	CT/CTGT	TGGTAGGTTTGGAGTGGAGG	GGCTAAGTCTGAAAGTGGCG	60.0	263	INTERGENIC				
CaPOPI_7927	scaffold575	103253	AGGGG/AGGGGG	AAACAACGAGTATGGGCGAC	AGCTTGCTTTGAAAGGGACA	60.0	113	INTERGENIC				
CaPOPI_7928	scaffold575	103640	ACCCCC/ACCCC	AAACAACGAGTATGGGCGAC	CGCAATTAGCCTCTTTCTGTC	60.0	707	INTERGENIC				
CaPOPI_7929	scaffold575	103819	AT/ATGCCTTATT	TCTTCTCGCTGACTTGGGAT	CGCAATTAGCCTCTTTCTGTC	60.0	205	INTERGENIC				
CaPOPI_7930	scaffold575	110510	GT/GCTT	CTTTCTGGTCAAGGCCTCAG	CTAGACCTGCGGAAGACAGG	60.0	446	INTERGENIC				

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CaPOPI_7931	scaffold575	111632	TA/TAAACAAATAA	GTTCTCTGCTGCTATC GAC	TTTAACAACCGTGGGCT AGG	60.0	229	INTERGENIC				
CaPOPI_7932	scaffold575	113273	ATT/AT	TTCGGCAACATTCCGTA TTT	GCCTGACCTATGGCCTA TCA	60.3	283	INTERGENIC				
CaPOPI_7933	scaffold575	113513	ATCTC/ATCTCTC	TGATAGGCCATAGGTCA GGC	GCTAAGTGGTCTTTCCG CTG	60.1	440	INTERGENIC				
CaPOPI_7934	scaffold575	113710	GAAAAA/GAAAAAA	TGATAGGCCATAGGTCA GGC	GCTAAGTGGTCTTTCCG CTG	60.1	440	INTERGENIC				
CaPOPI_7935	scaffold5761	842	CTTTT/CTTTTT	GGTCTCGATTTCATCT GGA	AACGCCTTAAAGCCCA AAT	60.0	684	INTERGENIC				
CaPOPI_7936	scaffold5761	1101	C/CG	TCTGGTCTCGATTTC ATC	AACGCCTTAAAGCCCA AAT	60.0	362	INTERGENIC				
CaPOPI_7937	scaffold5777	16517	CTT/CTTT	TTGCAATTGGCACACAA AAT	TGAGTTGCTTCAAAGTG ATGTG	60.0	742	INTERGENIC				
CaPOPI_7938	scaffold5777	16560	TAATAAATAAATAAATA/TAATAAATAAA TAAATAAATA	TTGCAATTGGCACACAA AAT	TGAGTTGCTTCAAAGTG ATGTG	60.0	742	INTERGENIC				
CaPOPI_7939	scaffold578	11617	CTTTTTTT/CTTTTTT	TTCAATTGATCTTTTCGG GG	CCTCGAGAAAAATGGAC CAA	59.9	513	INTERGENIC				
CaPOPI_7940	scaffold578	38009	C/CGGTCTT	GACTTTTCGAGCGATTTC TCG	ATCGAGGATGAGGAGAC CCT	60.0	312	INTERGENIC				
CaPOPI_7941	scaffold5780	2877	AC/A	GGAATCCGGTTTCTTTTC CAT	GACCATTATTCACACGG TGG	60.1	765	INTERGENIC				
CaPOPI_7942	scaffold5780	5394	CAAAAAA/CAAAAAA	CGTGTCTCTCCCGTGTA TTT	ATGTGACACCCTAAACC CCA	59.9	488	INTERGENIC				
CaPOPI_7943	scaffold5780	5464	ATT/AT	CGTGTCTCTCCCGTGTA TTT	ATGTGACACCCTAAACC CCA	59.9	488	INTERGENIC				
CaPOPI_7944	scaffold5780	5895	ATT/ATTT	TGGGGTTTAGGGTGTCA CAT	AGGCTTTTCAGGCCCTA TCT	60.1	659	INTERGENIC				
CaPOPI_7945	scaffold5780	8742	CTTTTT/CTTTTT	AAGTTCGCGATTAGGCC TTT	GTTTGGGTCAAGGCTAT GGA	60.1	444	INTERGENIC				

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CaPOPI_7946	scaffold5780	9297	GAAAC/GAAACGTCAATAAAAC	TCCATAGCCTTGACCCA AAC	CCCAGTCTTGCAATAA TGA	59.9	404	INTERGENIC				
CaPOPI_7947	scaffold5781	12542	A/AT	CAAGGCTGTTTCAGCAT TCA	TTGTCCGTGAGAGACTG CAC	60.0	574	INTERGENIC				
CaPOPI_7948	scaffold5792	19474	TTATATATATATATATATATATATAT/TATATATATATATATATATATATAT	CCCTTTTCTCACCATCG AAA	AAAATCTCCTTGACACC CCC	60.0	424	INTERGENIC				
CaPOPI_7949	scaffold5812	30560	G/GC	GTGCTCCATGTTTTCCC AGT	CCGGGATCCTTAGGGTA TGT	60.0	515	INTRON	Ca_27755			
CaPOPI_7950	scaffold5823	938	GAA/GA	ACACACCTATTGGACGC ACA	AGGTCATTTTCGTCCTC CT	60.0	278	INTERGENIC				
CaPOPI_7951	scaffold583	4145	CTTTTTTT/CTTTTTT	TGAATGAAACCAATGCC AAA	TGATTGCAAATAGCACC CAA	59.9	152	INTERGENIC				
CaPOPI_7952	scaffold583	129627	TAAAA/TAAAA	GCTTACGGTGAAGGAGA ACG	CAACACATATTTTAAACA CATGCAA	59.9	770	INTERGENIC				
CaPOPI_7953	scaffold583	164184	G/GA	CTCTCATCTGAGGCCAA AGC	ATTAAGTCAGGGGCTCC GTT	60.1	389	INTERGENIC				
CaPOPI_7954	scaffold584	233927	AGCCGAGG/AG	ATTGGATGCATACGGTT GGT	AGGTCATTTTCGTCCTC CCT	60.1	271	INTERGENIC				
CaPOPI_7955	scaffold5867	874	TA/T	TCCAGATGAATTCGAGG ACC	CTGAACGTTTTGGGCAA TTT	60.0	431	INTERGENIC				
CaPOPI_7956	scaffold587	18087	T/TCA	GTCCTTGCGCTTATGCT TGT	TGCTTGATTGCTTGAGA TCC	60.4	347	DRR	Ca_27621			
CaPOPI_7957	scaffold587	23045	AC/A	CCCCAAAAGTCCAGATG AAA	GCGATTTCCGTACCACC TAA	60.0	329	INTERGENIC				
CaPOPI_7958	scaffold587	50853	TAAAA/TAAAAA	AGGGGAATTTTCGTACC ACC	ATCGAAGACCAGGAGAC CCT	60.1	638	INTERGENIC				
CaPOPI_7959	scaffold587	51041	CAAAAAAAAA/CAAAAAAAAA	AGGGGAATTTTCGTACC ACC	ATCGAAGACCAGGAGAC CCT	60.1	638	INTERGENIC				
CaPOPI_7960	scaffold587	53018	CAAAA/CAAAA	TACACGAAACCCGAAC ACA	CGAGGACCAGGAGACC ATTA	60.0	749	INTERGENIC				

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CaPOPI_7961	scaffold587	54888	AATATATATATATATA/AATATATATATATATA	CAAGACATGCCAAAGTCGAA	TCCAGCTTCTCAAAGCCTA	60.0	484	INTERGENIC				
CaPOPI_7962	scaffold587	56115	GAA/GAAA	AAC TGCCAAAGAGATGTGGG	TGCAGTTC CATCTCATGCTC	60.1	338	INTERGENIC				
CaPOPI_7963	scaffold587	70502	CAAA/CAAAA	GATGAAATCCAGGACCGAGA	TTCGAACGATTTTCGTACCC	60.0	732	INTERGENIC				
CaPOPI_7964	scaffold589	178513	ACCCC/ACCC	TCAGAAGGCTTCACTCGGAT	GTTTGGGGTTACCAATGCAC	60.0	693	INTERGENIC				
CaPOPI_7965	scaffold589	309093	TTAAAAA/T	TTTGAAAAACGGGGTGCTAC	GTTTGGCGTTGGTTTCTACT	60.0	886	INTERGENIC				
CaPOPI_7966	scaffold5891	5025	TTATATAT/TTATAT	GCCCAATCGATTATCGCAAGT	CCCTGTGACAAACACAACTCG	60.1	481	DRR	Ca_27904			
CaPOPI_7967	scaffold590	3079	AT/ATT	AATAAAAGACCAAATCGGAAAA	TGACAACCATTTATATTTGCCAC	58.2	393	INTERGENIC				
CaPOPI_7968	scaffold590	3166	TTATATATATATATA/TTATATATATATATA	AATAAAAGACCAAATCGGAAAA	TCAACCAAAGTTGGAGGATG	58.2	578	INTERGENIC				
CaPOPI_7969	scaffold590	19258	TT/TTACCATAGT	TCCTAAGAAAGCTACCC CACC	TGGCAAAGCACAAAGACACTC	59.6	398	INTERGENIC				
CaPOPI_7970	scaffold590	19474	AG/AGG	CTATCCATGCATGTGCAACAC	TGGCAAAGCACAAAGACACTC	60.0	175	INTERGENIC				
CaPOPI_7971	scaffold590	96189	TTATATATATATAT/TTATATATATATATATAT	AGGAAGAGTGGAGTTGCGAA	TATTTTGGATTTTGGCTCGG	60.0	385	INTERGENIC				
CaPOPI_7972	scaffold5901	5039	CAT/CATATAT	AATCGTGGCACTTTTGTCT	TTCAGGATTGTTGGGGAATC	59.9	493	INTERGENIC				
CaPOPI_7973	scaffold5904	17347	TG/T	TCCGTCGAATAACTTGTGGA	ACACCTTCTTTTGCCCTTGA	59.1	958	INTERGENIC				
CaPOPI_7974	scaffold5904	23362	CTATATATATATAT/CTATATATATATATATAT	AATGGAAGGAACCGAGTCAG	GGTCCAAGATCCATCCATGT	59.1	854	INTERGENIC				
CaPOPI_7975	scaffold5916	1178	CAAAA/CAAAA	TGACACCATCTCTAGGCC	AGGGAGGACGAAAATGACCT	60.1	310	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7976	scaffold592	18365	GTTTTTTT/GTTTTTTT	TAACCAATCTTGTCGTCCA	AGGGAGGACGAAAATGCCCT	60.1	873	INTERGENIC				
CaPOPI_7977	scaffold592	21132	TT/TTAT	TTTTGGTCCTCCCTAGGCTT	GGCGAAAAATGACCTAATG	60.1	807	INTERGENIC				
CaPOPI_7978	scaffold5920	7700	AATATATATATATATATATATATAT/AATATATATATATATATATATATATATAT	CAAACCGACTAATCACTCCTAAA	CAGTTGATCAAAAGACC GGA	57.5	514	INTERGENIC				
CaPOPI_7979	scaffold5928	4085	CTATATATATATA/CTATATATATATA TATA	AGCAAAAGGAAGCAACG AAA	ACACACCTATCGGATGC ACA	60.0	598	INTERGENIC				
CaPOPI_7980	scaffold593	86436	ATTTTTTT/ATTTTTT	TTGTTGGGTTATCGTTGTCG	GTGCAATGTTGCATGAGCTT	59.4	575	INTERGENIC				
CaPOPI_7981	scaffold593	181350	AATATATATATATATATATAT/AATATATA TATATATATAT	GCCCCAACCTGAATTAGTGA	ATTTGTGGGGCACAGA CTC	59.9	871	INTERGENIC				
CaPOPI_7982	scaffold593	191195	CTTTT/CTTTTT	AGCCAAGTCGATTGACG AAT	CAGACTTTCAGCGTCA CAA	59.7	738	INTERGENIC				
CaPOPI_7983	scaffold593	209468	TC/T	GCAAACCTTTGCAAAAA GAAA	GGAATAAAATATGCATC CGAGC	59.4	153	DRR	Ca_26412		C2H2	Glycoside hydrolase, family 28
CaPOPI_7984	scaffold593	209698	CT/CTTT	GCAAACCTTTGCAAAAA GAAA	GGAATGGAATAATTGA AAAGTTTG	59.4	847	DRR	Ca_26412		C2H2	Glycoside hydrolase, family 28
CaPOPI_7985	scaffold593	211628	TT/TTGTGAT	TACGTACGGCAGTAGCCCTT	ATTTCCCCGGAATCATTA GG	59.8	673	URR	Ca_26412		C2H2	Glycoside hydrolase, family 28
CaPOPI_7986	scaffold5954	1414	A/AG	TGGATGCACAAGGTTGG TTA	AGGTCATTTTCGTCCTC CT	60.0	367	INTERGENIC				
CaPOPI_7987	scaffold5977	4624	GAA/GAATTTTTTGAAA	CGTGGTAATCGCGTAGG AAT	GGACTTCTGCTGAGCCA ATC	60.0	166	INTERGENIC				
CaPOPI_7988	scaffold5977	7940	GTTTT/GTTTTT	CCGCAATGAGACCAAGT TTT	TTTGCAATCCAACAACC AGA	60.1	555	INTERGENIC				
CaPOPI_7989	scaffold5977	14707	GTTTTTTTTT/GTTTTTTTTT	TGAGAATGATGCAAAATG GGA	TGGTCAACCTTTTGTTG ATG	60.0	640	INTERGENIC				
CaPOPI_7990	scaffold598	126131	GAT/GATCAT	CCATCATCGATATTCATG CG	TTCCAAACTGAAGCAAA GAACA	59.9	170	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_7991	scaffold598	131012	GA/GAA	GAGGCTCCTCTCTATC GGT	TCCTTAATGACACCCCA AAA	59.8	727	INTERGENIC				
CaPOPI_7992	scaffold598	165238	ATTTTTTTTT/ATTTTTTTTT	TGAAGGAGGAGGATCCT GAA	TGAGAGGGGTCAAGAG GTG	59.7	696	DRR	Ca_21754			
CaPOPI_7993	scaffold598	232941	CAAA/CAA	ACATCCATTCCGGTCC ATA	GCCCTCAGATGAGAGTC AGG	60.0	582	INTERGENIC				
CaPOPI_7994	scaffold598	311554	GTTTTTTTTT/GTTTTTTTTT	ACGAATGCCACACTAA AGG	TTCATTGTGTGCTTTTCA CCA	60.0	408	INTERGENIC				
CaPOPI_7995	scaffold598	318052	GAAAA/GAAAA	TCGGGAAAAAGATACG TGG	AGATTGTGGCGCAGAAG ACT	59.9	116	INTERGENIC				
CaPOPI_7996	scaffold598	392260	CATATATATATATATAT/CATATATATATATATAT	ATTCCCCCTCATCTTG GAC	TTGTTTGCAATGCATG CTC	60.1	345	INTERGENIC				
CaPOPI_7997	scaffold598	478255	AATATATATATATATA/AATATATATATATATA	GTTGGTTCCTAGCACC GTA	TTTGGCATGAAGTGAA ACA	60.0	753	INTERGENIC				
CaPOPI_7998	scaffold598	563403	CAAAAA/CAAAAA	TTTTGCAATGTGACACA CGA	AACGCATCAATCCTACG ACC	59.7	897	INTERGENIC				
CaPOPI_7999	scaffold598	568507	CTCAAAATCAAAATCAAAATCAAAATCA AAATC/CTCAAAATCAAAATCAAAATCAA AATCAAAATCAAAATC	CAGCCACTACATTGGCC TTT	AGGATTCTCCAAGTTGG CCT	60.1	499	INTERGENIC				
CaPOPI_8000	scaffold599	91366	GTATATATATATAT/GTATATATATATATATATATAT	TAAAGAGATTCGCAGCG GTT	ACTTGCAGAGCGCAGT TAT	60.0	372	INTERGENIC				
CaPOPI_8001	scaffold599	123496	GAAAAA/GAAAAAA	AACTCGCCAAGCGAAAA TAA	CTCGCAAGTCACAGTCG AAA	59.9	952	INTERGENIC				
CaPOPI_8002	scaffold599	187793	CCT/C	TTGGTATTGAACTCGGA GGC	TTCTTTCCACACAACCA CA	60.1	690	INTERGENIC				
CaPOPI_8003	scaffold599	282543	CTTTTTTTTT/CTTTTTTTTT	AATTTTGGCGTCATGG TTC	TCCATTGTGCCACATCA ACT	59.8	392	INTERGENIC				
CaPOPI_8004	scaffold599	284681	GAAAAAAA/GAAAAAA	AACGAACCTACCGGGC TTT	GGCCTGAAAGCATACCA AAA	60.1	634	INTERGENIC				
CaPOPI_8005	scaffold599	286707	AT/A	TTGAAATTACCGCTGGA GATG	CACTTGC GTATCACTGC GTT	60.1	485	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8006	scaffold599	291369	GACTT/GACTTACTT	TTGTTTGTTCGCAATCC TCC	TTTCCAACCGGTGAGTT TTC	60.0	597	INTERGENIC				
CaPOPI_8007	scaffold599	307088	CTTATTATTATTATTATTATTATTAT T/CTTATTATTATTATTATTATTATTA TTATTATTATTATTATTATT	TCTTCCCATTCTTGCTC GG	GGCGTAGCCCAATATT CAA	60.0	120	INTERGENIC				
CaPOPI_8008	scaffold599	307530	AATATATATATATATATATATATATAT ATAT/AATATATATATATATATATATAT	TCTTCCCATTCTTGCTC GG	TGTGTGCTTCCTATGAT GTTCT	60.0	855	INTERGENIC				
CaPOPI_8009	scaffold599	307947	AT/A	AGAACATCATAGGAAGC ACACA	CAACATTAAGAAGACGG CGA	57.4	317	INTERGENIC				
CaPOPI_8010	scaffold599	312899	CTTTTTTTTT/CTTTTTTTTTTTTT	CGTTGTCGTCGGTAGGA TTT	TTCAAAAGTTATTCGGT GGAAA	60.0	521	INTERGENIC				
CaPOPI_8011	scaffold599	322634	GTTTTTTTTT/GTTTTTTTTTTTT	TTGATAAACGCCATGA CAA	TTTTGCTTGCCTATTT TT	59.9	563	INTERGENIC				
CaPOPI_8012	scaffold599	323301	TTATATATATATATATATATATATA/TT ATATATATATATATATATATA	AAAAATACGGCAAAGCA AAA	TTGAGGTTGAGAGTCTT TTCCA	57.5	732	INTERGENIC				
CaPOPI_8013	scaffold599	329422	CAAAAAAAAA/CAAAAAAAAA	CACGTAAAAATCGCTAA AATCT	CCGATAGTAAACGACA TCCTG	57.6	562	INTERGENIC				
CaPOPI_8014	scaffold599	330437	AAATATTCAAATT/AAATATTCAAATT AATATTCAAATT	AAAATTCTGTTGGGGG ACC	TTGAGTATTGCTTGCC TTG	60.0	599	INTERGENIC				
CaPOPI_8015	scaffold599	335351	CTTTTTTTTT/CTTTTTTTTTTTTT	GCCAACCATGTAATCG CAT	TCAATCATCAATTTTGT GTGTTTC	60.7	327	INTERGENIC				
CaPOPI_8016	scaffold599	338561	CTATATATATATATATATATATATA/C TATATATATATATATATATATA	ATTGGGTGGGATACAA TGA	GATCTTGAAAAATTGATG GTGC	59.9	307	INTERGENIC				
CaPOPI_8017	scaffold599	347393	CTTTTTTT/CTTTTTT	CCTCTTTCTTCGATTT CG	AACAACAGCCCAATGT AGC	60.0	504	INTERGENIC				
CaPOPI_8018	scaffold599	358992	CAAAAAAAAA/CAAAAAAAAAAAAA	GGGGTTTTAGAAAATC CGTCA	TTTTGCCTTGCCATATCT TTTT	59.5	349	INTERGENIC				
CaPOPI_8019	scaffold599	366068	ATTTTTTTTT/ATTTTTTTTTT	AGAGCGCAATCATTTCA GGT	CTTTTGAAAGAAGCCC TCC	59.8	613	INTERGENIC				
CaPOPI_8020	scaffold599	369580	T/TCA	AGGGCACTTTGGAAAAC CTT	TCATTTAAAGCCTCAAT ACGAT	60.0	492	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8021	scaffold599	371527	TAAAAAA/TAAAAA	CAGCGTTGTTGTTGTTGTTTT	TTTCGAATGAACATGGATGA	60.1	531	INTERGENIC				
CaPOPI_8022	scaffold599	373801	TAAAAAAAAA/TAAAAAAAAAAAAAA	CCCCCTAAGTTCATTCCACA	GGCTTGTCCGTCGGTAAATA	59.8	567	DRR	Ca_25347			Transposase, Pta/En/Spm, plant
CaPOPI_8023	scaffold599	391375	GTTTTTTTTT/GTTTTTTTTTT	TGCGGTGAAGAAGACAGTG	CACATCAAAGAGGAAATGCC	60.0	666	INTERGENIC				
CaPOPI_8024	scaffold599	410067	GTTT/GTTT	ATCGATTCCCAATCGGTTA	TATACCTATAGCCACGGCG	59.2	609	INTERGENIC				
CaPOPI_8025	scaffold5992	921	TTCTCTCTCTCTCC/TTCTCTCTCTCTCTCTCC	TTGAGAAACTTTTCCGCTG	TCATCTCACCCCTTACCTCG	60.4	686	INTERGENIC				
CaPOPI_8026	scaffold5992	1551	G/GA	CGAGGTAAGGGGTGAGATGA	TCCCCGAATCACTAGGTTTG	60.1	544	INTERGENIC				
CaPOPI_8027	scaffold5993	18562	GTTTTTT/GTTTTTT	TTGATGTACGAAAAGTTTAGCAAG	GGGGGCACCTATTATCCTT	59.0	267	INTERGENIC				
CaPOPI_8028	scaffold5993	18598	CTTATATTTTATATTTTATATTT/CTTATATTTTATAITTT	TTGATGTACGAAAAGTTTAGCAAG	GGGGGCACCTATTATCCTT	59.0	267	INTERGENIC				
CaPOPI_8029	scaffold601	49572	CTTTTT/CTTTTT	GGGGACATTCGAGAGTCAA	TCACAAGGGAGGCTCTATGG	60.1	519	INTERGENIC				
CaPOPI_8030	scaffold604	14590	TAATAAATAAATAAATAAATAA/ATAAATAAATAAATAA	TGGGCTTCACTTTTGGAC	CGATTTTGATTGCATGCTT	60.1	536	INTERGENIC				
CaPOPI_8031	scaffold604	40273	CTTTTT/CTTTTT	CCAACTCGCTGAGTAGGAGG	ACCGAATTGGATTGGTGAAA	60.0	575	DRR	Ca_27531			
CaPOPI_8032	scaffold604	70429	CTTTTT/CTTTTT	ACGCATTTATTGGATGCAACA	TGAAACGTTTGGAGAGTGGA	60.0	776	INTERGENIC				
CaPOPI_8033	scaffold6066	2831	CCT/C	CTGCAAAGCAACCATCTCAA	CCTCAGATGAGAGCCAGGAC	60.0	797	INTERGENIC				
CaPOPI_8034	scaffold6113	1438	GAAAA/GAAAA	ACAAGCCTATCGTTTGGCAC	GATGCAACATTGGAGCATGA	60.1	589	INTERGENIC				
CaPOPI_8035	scaffold612	28576	GAAAAA/GAAAAA	AAAAAGGGAGGGTCACATGAT	TCACCAATATCTTAACCAACAAAA	59.7	701	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8036	scaffold612	30300	TAAA/TAA	TGCCACAAATTCGAGGACT	ACACGTTAAATCGCATAAAATCT	60.6	321	INTERGENIC				
CaPOPI_8037	scaffold6120	2075	CTTTTT/CTTTTT	AATCAAAGTCGGTCTGGTGG	AGCAAGCTCTGCTTGACACA	60.0	797	INTERGENIC				
CaPOPI_8038	scaffold6120	3713	GAGATA/GA	TCTGAAAGCCGTGAAAGACC	CGTGACAACCACCAACTCTTT	60.4	929	INTERGENIC				
CaPOPI_8039	scaffold6125	1553	TAAAGA/TA	ATGCGATCCTCTCGGTTCTA	GAGACCGAAGAGTATTGGAGA	59.8	838	INTERGENIC				
CaPOPI_8040	scaffold613	78619	CNNNNNNNNN/CNNNNNNN	ATTCGAAATTCGTTTGTGC	TAAAAGACGACGGAGTTGGC	59.9	763	INTERGENIC				
CaPOPI_8041	scaffold6154	548	CCGCCTCA/CCGCCTCAGGCGCCTCA	AACCGCTCCAATGGTGTAG	GAAGATGATGTGCGCTTGAA	60.0	221	INTERGENIC				
CaPOPI_8042	scaffold6177	3708	AG/A	TTTTGTGTCATCGGACCA	AAATCCGTTTGATTTGCAG	59.9	613	INTERGENIC				
CaPOPI_8043	scaffold6179	967	TAAAAAAA/TAAAAAAA	TGGGTGCACAAGATTGGTTA	AGGTCATTTTCGTCCTCCCT	60.0	468	INTERGENIC				
CaPOPI_8044	scaffold618	24350	TA/TAA	GAACACGTTTGTGTTGGTCG	TTCAAATTGATGATGTTCCCA	60.0	299	INTERGENIC				
CaPOPI_8045	scaffold618	197211	AATATATATATATATATA/AATATATATATATATATATA	TGTTGAGCACCTAGGGAATT	AACATCAGTCAAGCGCACAC	59.6	758	INTERGENIC				
CaPOPI_8046	scaffold6185	2912	GA/G	GCAAAGTCGCATTATGGTATGA	AGCCCTCACATTAATTCGCA	60.0	740	DRR	Ca_27924			Lipase, GDSL
CaPOPI_8047	scaffold6185	6573	CAAAAAAAAA/CAAAAAAAAAAAAAA	TGCACATTTACAGCGCTTC	AATCTTTTAACTCCATGTGAAA	60.0	785	URR	Ca_27924			Lipase, GDSL
CaPOPI_8048	scaffold62	150253	AGTTGTCCAAT/A	AACATTTAAGAAAATTGAGTTGTCAA	GTGTGTTGGGCTGTTTGGG	58.7	405	INTERGENIC				
CaPOPI_8049	scaffold62	338714	ATT/ATTT	CCATCGTCAAGTCGGAAT	CCAAAACGAAACCCAAA	59.9	565	INTERGENIC				
CaPOPI_8050	scaffold622	10235	TAAAAA/TAAAAAA	ATAGGCCTAGGGAGGACGAA	TTTAGCCAACCTGTGCACTCG	60.1	381	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8051	scaffold622	30884	A/AC	TGGGTGCACAAGATTGTTA	AGGGGTGTTTGAGTCATTGG	60.0	832	INTERGENIC				
CaPOPI_8052	scaffold622	46025	A/AC	CACTCCTATGGGATGCAAA	AGGTCATTTTCGTCTCCCT	59.5	373	INTERGENIC				
CaPOPI_8053	scaffold622	61725	GACACACACACACAC/GACACACACAC	CAAAACCCACCTATTGGATGCTG	GGTCATTTTCGTCTCGCTA	60.2	310	INTERGENIC				
CaPOPI_8054	scaffold626	94461	CATATATATATAT/CATATATATAT	AGTGTGTCAATGTTACTTTATTTCAA	GGGTTTGAGGTTCCGGTTAT	57.6	695	INTERGENIC				
CaPOPI_8055	scaffold626	172733	C/CAATTA	GTGAGCAAAATGCTGGGAAT	GTTGTTGAGTTGTTGGGCT	60.1	393	INTERGENIC				
CaPOPI_8056	scaffold626	219233	CAAA/CAAAA	GGATTAGGGTTTTGGCCTT	GATGAAATCGAGGACTGGGA	59.3	654	INTERGENIC				
CaPOPI_8057	scaffold626	225194	T/TG	TACAGATGTTCCAGCCCTCC	GAACCTGTACCTCCAGCCAA	60.1	501	INTERGENIC				
CaPOPI_8058	scaffold626	236880	AGGG/AGG	CCCATCCACAAAATATGCC	GATGAAATCGAGGACCAAGA	60.0	302	INTERGENIC				
CaPOPI_8059	scaffold626	242253	A/AAAAATGATCGTTTTTC	CCGATGCGTAGATTGACAGA	GGTAACCAATCCGAAGACGA	59.8	177	INTERGENIC				
CaPOPI_8060	scaffold626	258123	ATTTTT/ATTTTTT	AACTGTGTTTCGGGTTCTGG	CTTTTCGGGCGATTTTCTATA	60.0	432	INTERGENIC				
CaPOPI_8061	scaffold626	268228	CAA/CAAA	TAACCCAAACCTCAAACCCA	TTCATCTGGACTTTTTTGGGC	60.2	760	INTERGENIC				
CaPOPI_8062	scaffold626	334424	C/CGCT	TGCATAGGCCTCTTGCTCTT	AACCTGTGTTTCAGGTTCCG	59.8	728	INTERGENIC				
CaPOPI_8063	scaffold626	452443	CAAA/CAAAA	GGTCCTCGATTTCATCTGGA	CGAAATCGCTCGAAAGTCTC	60.0	336	INTERGENIC				
CaPOPI_8064	scaffold626	464649	GT/G	CAGTGTTCGATTCTGGGT	TTCAACTGGACGTTTAGGGC	60.0	769	INTERGENIC				
CaPOPI_8065	scaffold626	504911	AG/A	CTATGTTTTTGGTTCCGCGT	GTTTCGTACCCCTCGACAAA	60.0	930	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8066	scaffold626	512589	ATTTA/ATTTAGGGTTTA	CCCGACAAAACGGACTAAA	ATAACCGAACCTCAAA CCC	60.0	359	INTERGENIC				
CaPOPI_8067	scaffold626	515112	TTAT/TTATAT	CGTTATAAGTAAACTA CATTGCGAA	AAATTTAGGAGACGAAT GCTTTTT	59.2	848	INTERGENIC				
CaPOPI_8068	scaffold626	520360	CTTT/CTTTT	AAGGTCTCCTGGTCCTT GGT	CACGAAACCGAAACAA AGT	60.0	515	INTERGENIC				
CaPOPI_8069	scaffold626	522371	CTTT/CTT	TTTGTGAGGGGTACGA AAC	GGTCTCGATTTCTCT GGA	60.0	691	INTERGENIC				
CaPOPI_8070	scaffold626	524724	ATTTTTTTTTT/ATTTTTTTT	AAATCCCCGAAAATAC CAG	TCCAGATCAAATCGAGG ACC	60.0	670	INTERGENIC				
CaPOPI_8071	scaffold626	553162	AT/A	TCCAGATGAAATCGAGG ACC	TTTCATTTGGGCTTTTCA GG	60.0	325	INTERGENIC				
CaPOPI_8072	scaffold626	554690	TAAGAAGAAGAA/TAAGAAGAA	GGTCCTCGATTTCATCT GGA	CCATCGTCTGGTTCGAA AAT	60.0	415	INTERGENIC				
CaPOPI_8073	scaffold626	631432	ATAT/A	TTGATTTGACCACCCATT TTT	CAGCCCAACACACTAAA CCC	59.2	242	INTERGENIC				
CaPOPI_8074	scaffold63	6585	GTT/GTTT	CCCCAGCTTTGTTGTTT CAT	CCAATTTGAATGAAGG CGT	60.0	600	INTERGENIC				
CaPOPI_8075	scaffold63	8644	TAAA/TAA	ACCCCATCCTTGTTGTTT CA	TATGTTTCGAGCCGGCT ATC	60.2	425	INTERGENIC				
CaPOPI_8076	scaffold63	59319	TAA/TAATAAA	CGAGGTAAGGGGTGAG ATGA	AGGTTTGTGAGACCCTC CCT	60.1	481	INTERGENIC				
CaPOPI_8077	scaffold637	107635	ATT/ATTT	GCCTTGAGGAATCGGTA TCA	GTGTGAATGCAACCTTC CCT	60.0	313	INTERGENIC				
CaPOPI_8078	scaffold6382	1419	CTCCCTATGCTT/CT	AGGTCATTTTCGTCCTC CCT	CAAACACACGTTTTGGA TGC	59.9	181	INTERGENIC				
CaPOPI_8079	scaffold639	11325	T/TC	TGGTGCAATTACTTTCT CGG	TTCGGTTCTTGTTTGGC TTT	60.1	783	INTERGENIC				
CaPOPI_8080	scaffold639	103317	AATATATATATATAT/AATATATATATATATATAT	TTCGACTCCCTTCCCTTT TT	CATTCTTTTATGCGTTTG GC	60.0	551	INTERGENIC				

INDEL IDs	marker	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
									Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8081		scaffold642	60062	AATATATATATATATATATATATATAA ATATATATATATATATATA	TATTTTGGGACTCTGGC TCG	CGTAGCGTGGTAGTGAG CAA	60.0	619	INTERGENIC				
CaPOPI_8082		scaffold642	78334	TTATATATATATATATATATA/TTATATAT ATATATATATATATA	CTGAGATGCAACGTTTT CCA	AGCAAAAGGAAGCAAAC GAA	59.8	334	INTERGENIC				
CaPOPI_8083		scaffold642	79362	CGTC/CGTCGTGTAGGTC	TTGGTGTGGTTTTTGTG GAA	CACATATCACGGGCAG CAC	59.8	375	INTERGENIC				
CaPOPI_8084		scaffold642	171116	CC/CCGCTCTTCCAAGTTTTTC	GGCTCTGTTGGTCAGCT TTC	AAAATTGGGCTCGCTAG GTT	60.0	157	INTERGENIC				
CaPOPI_8085		scaffold642	287766	TTTTATTATTTATTTATTATT/TTTTAT TTATTATTTATTTATTATT	AAAAATGGGAGAAGGGG TTG	ATTTGGAAC TTGGGCTT CCT	60.2	366	INTERGENIC				
CaPOPI_8086		scaffold642	500946	GTTTTTTTTTT/GTTTTTTTTTTTT	TGCAACAACCCGATAA CAA	CGAAGACATGCTCGTCT TAAA	60.0	432	INTERGENIC				
CaPOPI_8087		scaffold6429	4894	CCTA/C	GGGTGGACGAAAATGAG CTA	TGTGTCATTGGATTGCG ATT	60.1	537	INTERGENIC				
CaPOPI_8088		scaffold645	73896	AGGGG/AGGGGG	ACATCTTGCTTGGGTTT TGG	CCCCCTCAGAAATGCT TCA	60.0	229	INTERGENIC				
CaPOPI_8089		scaffold645	254689	AATATATATATATATATATATATATAT ATATAT/AATATATATATATATATATAT ATATATATATATATAT	CACCGTAGTGTGGTGGT GAG	ATTTTGGCTCGGAGGTT TTT	60.1	659	INTRON	Ca_25158	I	Trihelix	Phospholipid/glycerol acyltransferase
CaPOPI_8090		scaffold6458	24160	T/TAATAAACAGA	AAGAGGCCACACCGCT ACA	AGATGTTTGCTCTGCTG CAA	59.9	530	INTRON	Ca_27555	T	C3H	NUDIX hydrolase domain
CaPOPI_8091		scaffold647	200535	AJAT	CAAGCTGTGCGTTGAAG ACA	AACAATCTCCCCTTTTT GG	60.0	603	DRR	Ca_27495			
CaPOPI_8092		scaffold6480	530	ATTTT/ATTT	TAATCGATCATCCGAGA CCC	TACAATTGGGCTCCTTC ACC	59.7	900	INTERGENIC				
CaPOPI_8093		scaffold6480	672	CTTTTTTTTTTT/CTTTTTTTT	AGAAACATTTGCACGGT CCT	TACAATTGGGCTCCTTC ACC	59.6	612	INTERGENIC				
CaPOPI_8094		scaffold6568	659	TAAATTA AAAAAAAAAATTA AAAAAA/TAAA TTAAAAAAA	CACGCACGGGTTACACA CTA	ACAAC TTCATCCGTTTTG GC	60.6	270	INTERGENIC				
CaPOPI_8095		scaffold661	266987	GAAAAAAA/GAAAAAAA	TTTTTCTTTCGATTCCGT CG	TCCATTCATATGATTCCA TCCA	60.2	749	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8111	scaffold674	394555	A/AT	CGGCTACGTCACCTTCAT	TGCAAAAATTCATACG GTG	60.3	410	INTERGENIC				
CaPOPI_8112	scaffold674	394638	ATTTTTTTTT/ATTTTTTTTTT	CGGCTACGTCACCTTCAT	TGCAAAAATTCATACG GTG	60.3	410	INTERGENIC				
CaPOPI_8113	scaffold674	401473	TAAAA/TAAA	TGCATTAGTCGATGTCC CAA	AATCGATTTGCGTTTG TTC	60.1	134	INTERGENIC				
CaPOPI_8114	scaffold674	437989	TAACAACAACAACAACAACAA/TAACAA CAACAACAACAACAACAA	GCATAATCGTGCTCGA CAA	CAGATTCAACCAAAGCA GCA	59.8	333	INTERGENIC				
CaPOPI_8115	scaffold674	439330	A/AG	AAGACCTTGCCTGTCTC GAA	TGCATCTGTTACCACCA TCG	60.0	284	INTERGENIC				
CaPOPI_8116	scaffold674	441706	GATATATATATATATATA/GATATATA TATATATATATATA	ATGTGAATCCCACCAGG AAA	GAAAGAGCGCTGCAAAA GAC	60.2	533	INTERGENIC				
CaPOPI_8117	scaffold674	468778	ATT/ATTT	GCTAAGAGCATCTCCAA CGG	TTTAGAGCATCTCCAAC GGG	60.0	590	INTERGENIC				
CaPOPI_8118	scaffold674	468848	TAAAAAAAA/TAAAAAAAAA	GCTAAGAGCATCTCCAA CGG	TTTAGAGCATCTCCAAC GGG	60.0	590	INTERGENIC				
CaPOPI_8119	scaffold674	518331	ATTTTTTTTT/ATTTTTTTTTT	TTTTGACAAACCTGCGA AAC	TTTTAAAGAGGACTGA CCACAA	58.8	386	INTERGENIC				
CaPOPI_8120	scaffold674	570233	TATATATA/TATATATAATATATA	CGGGGTGTTACACAAC T GAG	CGCATCGTCACAATTCA TTT	59.1	601	INTERGENIC				
CaPOPI_8121	scaffold674	617218	C/CTCATTGTGTTT	GACAGCTCAACCTTTT CAA	CACCCAATCCAAGCTAC GTT	60.2	534	INTERGENIC				
CaPOPI_8122	scaffold674	705834	CT/CTT	TTGAGCTCCCTTTTCT GA	GTCAAAGGTGACCCTTC TGC	59.9	718	INTERGENIC				
CaPOPI_8123	scaffold674	711627	CAAAAAAAAA/CAAAAAAAAA	TCCACCCTTTGATGCTTT TC	TGCTTTCGGTGTCAC TTG	60.1	669	INTERGENIC				
CaPOPI_8124	scaffold674	833729	ATTTTTTT/ATTTTTTTTT	GCTTCAGGTAGGAGAAG GCA	TGCATATCCAAGTGAC TTTTGTG	59.6	665	INTERGENIC				
CaPOPI_8125	scaffold674	868010	GA/GACCTAAATATTAA	CCAAGGGAAGTCCAAAA TGA	CATTTTCGTCACCCCTC AAC	59.9	589	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8126	scaffold675	81863	CTTTTT/CTTTTTT	TATCAGAGTTCTCCCA CCG	AAACATGACGAGGGCAT TTA	60.1	895	INTERGENIC				
CaPOPI_8127	scaffold675	81930	TT/TTGAAAAT	TATCAGAGTTCTCCCA CCG	AAACATGACGAGGGCAT TTA	60.1	895	INTERGENIC				
CaPOPI_8128	scaffold675	82372	T/TC	TAAATGCCCTCGTCATG TTT	CCCCTTTCACGGCTAT TAT	58.1	444	INTERGENIC				
CaPOPI_8129	scaffold676	84081	CTTTT/CTTT	CACGAAACCCGAAACAC TTT	GCCATCGTCTAATCCGA AAA	60.0	146	INTERGENIC				
CaPOPI_8130	scaffold676	84534	GCAC/GCACAAAACAC	TTTTCGATTAGACGAT GGC	GATGAAATCGAGGACCA GGA	60.0	796	INTERGENIC				
CaPOPI_8131	scaffold676	104156	GAAAAAAA/GAAAAAAA	TTTCATCTAGGCATTTCG GG	TCCAGATGAAATCGAGG ACC	60.0	475	INTERGENIC				
CaPOPI_8132	scaffold676	104639	ACC/ACCC	GGTCCTCGATTTCATCT GGA	GACACTCGCTCGAAAAG TCC	60.0	686	INTERGENIC				
CaPOPI_8133	scaffold6760	618	TC/T	TGTTTTCAAAGGGGGT CAG	GGGCTGAGATGGACACA TTT	59.9	621	INTERGENIC				
CaPOPI_8134	scaffold6760	921	TT/TTCT	TGTTTTCAAAGGGGGT CAG	GGGCTGAGATGGACACA TTT	59.9	621	INTERGENIC				
CaPOPI_8135	scaffold6760	1141	ATTTTTT/ATTTTT	AAATGTGTCCATCTCAG CCC	TCAAAAACCTCAAGGGGC AAT	59.9	545	INTERGENIC				
CaPOPI_8136	scaffold678	12833	TTAT/TT	CGCCGCCCAATAAAGTA TTA	TTTGGTGGAGAATTCCA AGG	59.9	276	INTERGENIC				
CaPOPI_8137	scaffold678	14639	CG/C	GCTACCATGGGCTTGAA AAA	GTGGTACATGAGCGGAG GAT	60.1	772	DRR	Ca_26300			
CaPOPI_8138	scaffold678	39763	TAGTTATTAAGTTATT/TAGTTATT	AGGAGTTTGAGCATCGC ATT	ATCCCACCCCTAAAACC AAG	59.8	470	INTERGENIC				
CaPOPI_8139	scaffold678	40865	CTATTATTATTATTATTATTATTAT/C TATTATTATTATTATTATTATTATTA TTAT	GAACAGCTTTGAGGGCA ATC	TTTGAATTTGGTCTTTTG AAAGTG	59.8	647	INTERGENIC				
CaPOPI_8140	scaffold678	40998	TAAAAAAA/TAAAAAAA	GAACAGCTTTGAGGGCA ATC	CGATCACCACGTGACAC TTC	59.8	849	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8141	scaffold678	41072	T/TG	TCATTTTGGCTTTTGTGAAA	CGATCACACGTGACACTTC	58.3	753	INTERGENIC				
CaPOPI_8142	scaffold678	42464	TAAAAA/TAAAAAA	GCGCACAATAGATGGGT TTA	TTTTCCAACGAGTCCAC CTC	58.7	816	INTERGENIC				
CaPOPI_8143	scaffold678	73978	A/AG	TGGTTGATGAAGACGCGATA	CCGGAACCAACCCTTATTT	60.2	549	INTERGENIC				
CaPOPI_8144	scaffold6782	544	AC/A	ACTCACCCACATCCAA CAT	ATGGTACCGCAAAGAAC GTC	60.1	337	INTERGENIC				
CaPOPI_8145	scaffold6782	758	ATTTTTTT/ATTTTTTTT	GACGTTCTTTGCGGTAC CAT	TCAAACGCTCACACACA CAA	60.0	292	INTERGENIC				
CaPOPI_8146	scaffold6782	1068	GA/GAGAAA	GACGTTCTTTGCGGTAC CAT	CAAATGTCAACCACACA TTTTG	60.0	428	INTERGENIC				
CaPOPI_8147	scaffold6782	1165	C/CA	GACGTTCTTTGCGGTAC CAT	TTTAAATTGCTGCTAAGA TTGGT	60.0	469	INTERGENIC				
CaPOPI_8148	scaffold6790	910	TATAATAATAATAATAATAATAATAA TAATAATAATAATAATAATAATAATA ATAATAATAATAATAATAATAATAAT AATAATAATAATAATAATAATAATAA	TAGTTATGCTGAGGGGA CCG	TGCAAGTACATTCCCGA TCA	60.1	714	INTERGENIC				
CaPOPI_8149	scaffold6790	1414	C/CA	TCCTTGACCCCAATTCTG TAG	TTTTGGGGTTTAGGGTG TCA	59.9	356	INTERGENIC				
CaPOPI_8150	scaffold6790	2258	ACC/ACCC	TTCAAATTGGCCTTGTC CTC	CATAGACCAACGAGGGG AGA	60.1	317	INTERGENIC				
CaPOPI_8151	scaffold682	196858	TTTTATTTATTTATTTATTTT/TTTTA TTTATTTATTTATTTATTTT	TCTTTTAAGTGGACATC CCGT	GCGTTACAGTTGGTCAT GGA	58.6	840	INTERGENIC				
CaPOPI_8152	scaffold682	239323	AGATGATG/AGATG	CAACTCCCCCTGCAAACTTA	TGCGTGACAGGAACAAG AAG	60.1	417	DRR	Ca_23188	R	ERF	Integrase, catalytic core
CaPOPI_8153	scaffold682	302365	A/AGAGAGAT	GCTGCAAAAGTCAACGT CAA	CACCTTGAACTTTGGA GGA	60.0	177	INTERGENIC				
CaPOPI_8154	scaffold682	375189	ATTT/ATTTT	GTGTTGCCTACCCCTT TCA	GGTTTGATGTAGCTGTG CGA	60.0	430	INTERGENIC				
CaPOPI_8155	scaffold682	506392	GATATATATATATATATATATATATAT ATATAT/GATATATATATATATATATA TATATATATATATATATAT	AGGGAGGTTTGTGTTTG ACG	TTTAATGTGTTGCGGGT GAA	60.0	408	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8156	scaffold682	539867	CT/CTTT	TCGCCATTGTACTTGCT CTG	CCATGCCTCCAATCAA AGT	60.0	886	INTERGENIC				
CaPOPI_8157	scaffold682	540419	TGAG/TGAGAG	ACTTTTGATTGGAGGCA TGG	TAATATGGGGAGAGGGG AGG	59.9	665	INTERGENIC				
CaPOPI_8158	scaffold682	540642	T/TC	ACTTTTGATTGGAGGCA TGG	GAAGCAAAACCAGGGAA TGA	59.9	886	INTERGENIC				
CaPOPI_8159	scaffold682	540845	A/AT	AAGGACTGGTTCACCA GAG	GAAGCAAAACCAGGGAA TGA	60.3	437	INTERGENIC				
CaPOPI_8160	scaffold682	579426	GTTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTATT/GTTATTA TTATTATTATTATTATTATTATTATT ATTATTATTATT	CGGAACAATGACGTCTC AAA	GGAGGAGTGGAGGGGT TTAG	59.7	352	URR	Ca_23199	I	G2-like	AMP-dependent synthetase/ligase
CaPOPI_8161	scaffold683	20681	TAA/TAAA	GAAGGATGAAAATGGGG GTT	TTGGAAAGGCTGAAATC TGG	60.0	670	INTERGENIC				
CaPOPI_8162	scaffold683	25444	T/TC AAGA	TGGCAAATCGATTGACA AAG	TGTTGCTCCTCACGAAT CTG	59.7	533	INTERGENIC				
CaPOPI_8163	scaffold6846	522	T/TC	TGCATTGGTATATGGGG GTT	CGATCGACAGGAAGAGG AAG	59.9	538	INTERGENIC				
CaPOPI_8164	scaffold686	108971	GATATATATATATATATATATA/GATA TATATATATATATATATATA	GGGAGAAGGAGGAAGA ATGG	CTTGGGAAC TGAGAGC AAG	60.0	564	INTERGENIC				
CaPOPI_8165	scaffold686	134728	ATATTATTATTATTATTATTATTATT ATT/ATATTATTATTATTATTATTATT	TGAGAAATGCACTCTTC CCAAT	CATCCGCCTCTAAAGTG AGC	59.7	506	INTERGENIC				
CaPOPI_8166	scaffold686	140005	TT/TTAT	AGGCTTATGATCCCCA ACA	TCGACCAACCATGTCTT TCA	59.4	262	INTERGENIC				
CaPOPI_8167	scaffold686	162105	ATTTTTTTTTTTT/ATTTTTTTTTTTTT	AGCTTAACAAAGCGCG ATA	CCCTTTACATGTGCATC ATCA	60.0	563	INTERGENIC				
CaPOPI_8168	scaffold686	182712	CTA/CTAATA	ATGGGGTTCAAACCATG CTA	GCAAGGACTTTTGCTTT TGC	60.2	696	INTERGENIC				
CaPOPI_8169	scaffold686	183469	AT/ATT	TGGATTAATCATTCCCC CA	ATCCCTGTTGATTTGCTT CG	60.0	617	INTERGENIC				
CaPOPI_8170	scaffold686	184091	ACCC/ACC	AGGCCACGATACTATGC CAC	TAGGCCAACGAGAGGAG AAA	60.0	259	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8171	scaffold6873	1457	T/TA	TACCCAATCTTGTGCAACCA	CCTAGGGTCGACGAAATGA	60.0	575	INTERGENIC				
CaPOPI_8172	scaffold688	2385	GAAT/GAT	AGGTCAATTCGCTCCTCCT	GACACGAACACACCTCATGG	59.9	388	INTERGENIC				
CaPOPI_8173	scaffold6903	5314	A/AT	GCACACCACAACAAATGGA	GCATCCTCTGATTGTTTGGG	60.4	458	INTRON	Ca_28223			Domain of unknown function DUF239, plant
CaPOPI_8174	scaffold6903	17324	CT/CTTCGATGT	CCCACATTATAAATCGCTCA	TCCGATATGCATCACTCTGC	59.8	470	CDS (FRAME SHIFT)	Ca_28223			
CaPOPI_8175	scaffold692	50884	GTATATATATATATA/GTATATATATATATA	TCAAGTATGGACACGCCAAA	TTAGCTGCGGTGAATCCTTT	60.1	605	INTERGENIC				
CaPOPI_8176	scaffold696	39655	T/TC	TCGTATGAAAAGTCAATGCCTC	TGTTCTGGTGCCACATCATT	59.2	133	INTERGENIC				
CaPOPI_8177	scaffold696	43108	C/CT	GATGTGGCATCACAAAATGC	GCGTGAAGATCACCAAGGTT	59.9	840	INTERGENIC				
CaPOPI_8178	scaffold696	52341	CATATAT/CATATATAT	AACGGAAGTCAAAGAGGCA	TGACTGAGGCAAGATGGTTG	59.9	692	INTRON	Ca_25809		bHLH	Terpene synthase-like
CaPOPI_8179	scaffold6980	22077	AATATATATATA/AATATATATATATA	GCCAATTCTATCCCTCACCTC	CCGATGTTTGAGGGGTTT	59.9	859	INTERGENIC				
CaPOPI_8180	scaffold7	215103	A/AC	TTGATCCTTGCAGTCACTCG	TGGCACTCCGATTAACTGA	60.0	805	INTERGENIC				
CaPOPI_8181	scaffold702	49940	ATATTATTA/ATATTA	GTTTTCGAATCAACGAGGGA	TTTGGCTCGAAGGCTTTTAA	60.1	452	INTERGENIC				
CaPOPI_8182	scaffold702	55303	CAAAAAAAAA/CAAAAAAAAAA	GCATCTGCACATGAAAAACAA	CAACCCAATTTGATCCGAC	59.7	865	INTERGENIC				
CaPOPI_8183	scaffold702	99680	ATTTTGCATAGTTTTTGCATAGT/ATTTTGCATAGT	CGCTCGATAACCCCAATA	ATTACCGACATTGCAGAGGG	59.9	577	INTERGENIC				
CaPOPI_8184	scaffold702	114373	AGGGG/AGGGGG	TACATTTGGAAGTGGGGACG	GATGGTTGAAAAAGCTTGGC	60.7	596	DRR	Ca_25203			
CaPOPI_8185	scaffold702	156460	TAAAAAAAA/TAAAAAAAAA	TGGACAAAATTGGAATCTACA	GTGACACGTCGGAAGGAAT	59.3	525	INTERGENIC				

[illegible]

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8201	scaffold7081	2451	A/AC	TTAATGAGGGGCTGAAT TGG	AAGCGTACCTGTGGAA TTG	59.9	259	INTERGENIC				
CaPOPI_8202	scaffold7081	2734	ATTTT/ATTTT	CAATCCCACAGGTACG CTT	TGGGGGTAAAGGGATT AGG	60.0	465	INTERGENIC				
CaPOPI_8203	scaffold709	4010	GTTTT/GTTTTTT	ACTCAAATGATTTGGC GCT	CATGAGGAAACAATTGT GCAG	60.7	788	INTERGENIC				
CaPOPI_8204	scaffold71	29022	AATTATTATTATTATTATTATTATTA TTATTATTATTATTATTATTAT/AATT ATTATTATTATTATTATTATTATTAT TATTATTATTATTATTATTAT	GGTCGCATCCTAGACTT GTGA	TCAAGGGTTTGCTACTT GGG	60.3	555	INTRON	Ca_27236			Domain of unknown function DUF239, plant
CaPOPI_8205	scaffold7107	12825	AA/AAAGA	GGGGACTAAAATTGGGG AGA	TGCAGGCAATCAATGAA AGA	60.1	459	INTERGENIC				
CaPOPI_8206	scaffold7107	14640	AA/AATTA	TAATAGAAGGTGCGATC CCG	TGTGTCAAACGAAATGA TGTG	60.1	368	INTERGENIC				
CaPOPI_8207	scaffold7107	15792	CAAAATCATCTAAAAATCATC/CAAAAT CATC	TCACTCGGTTGCATCAC ATT	GGAGGTTCTAGCCCTA TAGCTT	60.1	323	INTERGENIC				
CaPOPI_8208	scaffold7107	16409	CTATATATATATATATA/CTATATATA TATATATA	GGGGCTAGAACCTCCTA CAA	CCATTTCATGATTCCA CAC	58.3	946	INTERGENIC				
CaPOPI_8209	scaffold7107	16449	TTTCAT/TTTCATCTTCAT	TCCAATGCTTACAATCCT CTCTC	CCATTTCATGATTCCA CAC	59.7	508	INTERGENIC				
CaPOPI_8210	scaffold711	184195	TTA/T	TCCCAAGCAGAATTTTG GAC	TAAGGGGTCAGTTCATC CCA	60.1	477	INTERGENIC				
CaPOPI_8211	scaffold711	198349	AATATATATATATATATATA/AATATAT ATATATATATATA	CAAAAGATGGGTCGTGT CTTG	TTGATCTGACATGTGAC ACAACTT	60.5	711	INTERGENIC				
CaPOPI_8212	scaffold711	204653	GATATATATATATATA/GATATATATA TATATA	AATGTGAATCCCACCAG GAA	TTTACAGCGCTTGTCTC CAA	60.2	796	INTERGENIC				
CaPOPI_8213	scaffold716	112534	GTTTT/GTTTT	CCTCTTGACTCTACAGC CCG	GTTGCCAAGTCCGCAAT AAT	60.0	277	INTERGENIC				
CaPOPI_8214	scaffold716	135403	AATTATTATTATTATTATTATTATTA TTATTATTATTATTATTAT/AATTATTATT ATTATTATTATTATTATTATTATTAT TATTAT	TGATCATATAAAAAACAA TGCTCACA	TGTGCAAGATTCTCTGT CCA	59.8	410	INTRON	Ca_24965		bHLH	Protein kinase, catalytic domain
CaPOPI_8215	scaffold716	163516	C/CA	TCCCAACCCAAATAAAC CAA	TTTACAGCGCTTCTCCC AAT	60.0	744	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
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CaPOPI_8216	scaffold716	189823	TAAA/TAAA	AAGCTTGTGCAAAGGGA AAA	TGGTTTTGATGGGACCA AAT	59.9	113	INTERGENIC				
CaPOPI_8217	scaffold719	123762	TAAAA/TAAA	AGGTCATTTTCGTCTC CCT	TTCATCCAATGGCACAA AGA	59.9	695	INTERGENIC				
CaPOPI_8218	scaffold72	23400	AATATATATATATATATATATA/AATAT ATATATATATATATA	TCAAATGTTTACCGCAA CGA	CCGCCACAAATGTTTC TTT	60.1	686	DRR	Ca_27654			Transposase, PttA/En/Spm, plant
CaPOPI_8219	scaffold720	372071	T/TTA	ACCAACATTTCAGGCTC ACC	TAGAGCGCCAAACCCTA ATG	60.0	486	INTERGENIC				
CaPOPI_8220	scaffold721	191166	GA/GAA	CGGAGGACGAAATGAC CTA	TGTGCATCCCATAGGTG TGT	60.1	473	INTERGENIC				
CaPOPI_8221	scaffold7210	7073	GA/G	TTTTCGTCCTCCCTAGG CTT	TTGGATGCACATGATTG GTT	60.2	364	INTERGENIC				
CaPOPI_8222	scaffold724	100088	ATTTTTTT/ATTTTTTTTTT	ACAGGAGGGTGATCGA GAGA	TGCATACTTGTGTGCCA TTTT	59.8	727	DRR	Ca_25051	Q	NAC	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_8223	scaffold724	100193	TAAAAAAA/TAAAAAAA	CTGTAAGCGGAGAAAA TGG	TTGCATACTTGTGTGCC ATTT	57.5	319	DRR	Ca_25051	Q	NAC	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_8224	scaffold724	100328	TAAAAAAA/TAAAAAAA	CTGTAAGCGGAGAAAA TGG	AATGGTAGTCCCTCTGG CCT	57.5	690	DRR	Ca_25051	Q	NAC	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_8225	scaffold724	100591	AATTTAACATAT/A	AAATGCCACACAAGTAT GCAA	AATGGTAGTCCCTCTGG CCT	59.1	392	DRR	Ca_25051	Q	NAC	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_8226	scaffold724	126741	CTTTTT/CTTTT	TCGCACCTCAATATGCTT CG	AAAGGCCATGCAAGAAG AGA	60.0	851	URR	Ca_25052	Q	NAC	Short-chain dehydrogenase/reduct ase SDR
CaPOPI_8227	scaffold7279	558	AA/AAAGGGTGTGGTCGA	GGAATCGAGAGCTCCAA GTG	TCTCAACGCCAGTTAG CTT	60.0	523	INTERGENIC				
CaPOPI_8228	scaffold7280	1708	AC/ACC	GTTTCGTACCCCTCGAC AAA	TCCAGATGAAATCGAGG ACC	60.0	311	INTERGENIC				
CaPOPI_8229	scaffold7293	13170	AG/A	TGCCTCTGGATTGGTTG AAT	AATCTATCCACCCGGAA ACC	60.5	471	INTERGENIC				
CaPOPI_8230	scaffold7293	15472	TT/TTAGAAAAGTGATAGT	TTTCATGCCAGCAACTCT TTG	TGCTTTGCTATGCACCA GTC	60.0	626	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8231	scaffold7293	20198	TC/T	TTGCTGCCTTCTCCTGT TTT	ATGATGCACTTTGGGCC TAC	60.0	661	INTERGENIC				
CaPOPI_8232	scaffold7299	551	AATATATATATATATAAATATATATAT A/AATATATATATATATATATAAATAT ATATATA	CACCAAACTTAATTCC CCTTT	TGATTCCTATGCATCGT ATTTTG	59.7	459	INTERGENIC				
CaPOPI_8233	scaffold731	94332	ATTTTTTTTT/ATTTTTTTT	GAGCGCTGTAAAGACC TCC	TGAAGATGGTTTGCAAT GGA	59.1	188	DRR	Ca_23810		B3	
CaPOPI_8234	scaffold731	315903	GATGA/GATGAATGA	AACTCGAAGTGCCATGC TTT	CAATACGCAATGGTGGT GAG	59.9	660	DRR	Ca_23814	J		Ribosomal protein S11
CaPOPI_8235	scaffold731	322781	T/TCAAATTCATTAAAA	ATCCCCGATTCTCTCA AGT	AATTCCTACTGGATGCA CGC	59.9	479	INTERGENIC				
CaPOPI_8236	scaffold731	323192	ATT/AT	GCAGGAATCCTCGTACC TCA	CTGCGAATTGCGTGAAA GTA	60.2	296	INTERGENIC				
CaPOPI_8237	scaffold731	324478	AT/AAATAGT	TGTTTGGAAGACCGAAA ACC	CAACCATCCCGTTTGGT ATC	59.9	257	INTERGENIC				
CaPOPI_8238	scaffold731	342154	CAAAAAAA/CAAAAA	AAATGGAGGAGAAGGAG GGA	ACCCAATTACTGGAGAT GCG	60.0	574	INTERGENIC				
CaPOPI_8239	scaffold731	354972	T/TATAATCATAC	ATAACCTTAGCGCATTC CCA	CCTCCCGTAAGATCCAA CAA	59.6	308	INTERGENIC				
CaPOPI_8240	scaffold731	359790	T/TAGCAAGTGC	ATTTCTGGGAGGCAACT CCT	AAGACGCGTAAGCGGAT CTA	60.1	298	DRR	Ca_23818			Cytochrome f
CaPOPI_8241	scaffold731	361613	TGG/TGGG	TGTGCTATTGCTCAAA CCG	AGCAGTCGTTTCCAGCT GTT	59.8	640	DRR	Ca_23818			Cytochrome f
CaPOPI_8242	scaffold731	366076	GAA/GAAA	TCTCGCGGATTTTCATA ACC	CCATCCATTCCGTATT GCT	60.0	100	INTERGENIC				
CaPOPI_8243	scaffold731	374028	AA/AAGGGAGATAGTGCA	TCCTTGGGGTGATCTCG TAG	ATGGACGGTAGTTGGAG TCG	60.1	222	INTRON	Ca_23820			
CaPOPI_8244	scaffold731	390482	C/CAA	TATCATAGGCCGTAGGC CAG	TTATTCGTCCAATTCCT CG	60.1	482	INTRON	Ca_23820			
CaPOPI_8245	scaffold731	392660	TT/TTTTTGCTAATCTAAT	GAACGACGGAACCTGTG AAT	AGGAAGCCCAAGTTCCA AAT	60.0	665	INTRON	Ca_23820			

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8246	scaffold731	392845	TTATATATATATATATATATATATATATATATAT/TTATATATATATATATATATAT	GAACGACGGAACCTGTGAAT	AGGAAGCCCAAGTTCCAAT	60.0	665	INTRON	Ca_23820			
CaPOPI_8247	scaffold7330	2275	AG/A	TTGGTCGACAAGCAACTGAG	AAAATCCAACAATCTCCC	60.0	699	DRR	Ca_28207			
CaPOPI_8248	scaffold735	3461	CTTTTTTTTT/CTTTTTTTTT	TTCTGAAATATGCCCTTCG	AAGTGATGGCGAGGAAC	60.0	563	INTERGENIC				
CaPOPI_8249	scaffold735	192011	CTTTTTTTTT/CTTTTTTTTT	AACTCAACCCAACATTGAACA	TGGTGATGTGGCAATCATTT	58.0	824	INTERGENIC				
CaPOPI_8250	scaffold7364	2154	CAT/C	TCAATTTGGGTTTAGGGTGC	TGTAGTGGCATGTTTGGCAT	59.8	497	INTERGENIC				
CaPOPI_8251	scaffold7364	2278	GTTTTTTTTTT/GTTTTTTTTT	ATGCCAAACATGCCACTACA	TGCCACCTTGACTAATGCAC	60.0	378	INTERGENIC				
CaPOPI_8252	scaffold7377	545	CT/CTT	TTTCTTCCCAACCTTCATCG	GCCGTTGGAACCTTCATCATT	60.0	816	INTERGENIC				
CaPOPI_8253	scaffold738	2137	T/TC	TGAATATCGCCCGAAAAATC	TTTCATAGCAGACGAGGGCT	60.0	292	INTERGENIC				
CaPOPI_8254	scaffold738	5098	ATTTTT/ATTTTT	TCGGGTGGTACTTAAATCGC	ATCTGACGTGAAACCGAAC	60.0	274	INTERGENIC				
CaPOPI_8255	scaffold738	10670	GAAAA/GAAAAA	GTACCACCCACAAAAATGG	CATCAGGACTTTTGGGGCTA	59.9	637	INTERGENIC				
CaPOPI_8256	scaffold743	14244	AACACACA/AACACA	TGCTTGATTGCTTGAGTTCC	GTACCCTGATTGCCCTCTGA	59.0	321	INTERGENIC				
CaPOPI_8257	scaffold7448	21480	GAAA/GAAAA	AGGATCTCCCGATTCTCGAT	TTCCGGGTCAGATTTCACAA	60.0	287	INTERGENIC				
CaPOPI_8258	scaffold7477	2293	TAAA/TAA	TTGGTGGATTGAGACCAACA	ACTTCCCTTGCACATTTGG	59.9	652	INTERGENIC				
CaPOPI_8259	scaffold7477	6564	TTTG/TTGTG	CCTGCAAGAAAGCAAAACAACA	ACCTTGGAAGGAGGAGAA	60.0	590	INTERGENIC				
CaPOPI_8260	scaffold749	1624	CTATATATATATATATATATATATAT/CTATATATATATATATATATAT	CTTGGAAGCTGGAGAGCAAG	GAGGAGGGAGGGATTTTGGAG	60.0	536	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8261	scaffold750	31851	GAAAAAAAA/GAAAAAA	TGAGTTTCTATGCAAGG GCA	TTCATGAAGACACCGGA ACA	59.4	273	INTERGENIC				
CaPOPI_8262	scaffold750	32434	AGG/AG	GCTTGTCCCCAAACAAC AAT	TTGGGATGGTGATTCTC ACA	59.8	627	INTERGENIC				
CaPOPI_8263	scaffold750	38979	AT/A	CACTGATAACGCGACTA ATTTGA	ACCGCCACAATGATAA AGC	59.3	748	INTERGENIC				
CaPOPI_8264	scaffold750	58677	TAA/TAAA	CGTAGCATCAGCAACCT TCA	TGCTTTTGGGTGTAACC ATTT	60.0	634	INTERGENIC				
CaPOPI_8265	scaffold750	59023	ATTGTTGTTGTT/ATTGTTGTTGTTGTT	CGTAGCATCAGCAACCT TCA	TCCCTCTTTGTTTTTCC CA	60.0	989	INTERGENIC				
CaPOPI_8266	scaffold750	59256	TATGTTCTGCTAATGT/TATGT	TGGTTACACCCAAAAGC AAA	TCCCTCTTTGTTTTTCC CA	59.1	373	INTERGENIC				
CaPOPI_8267	scaffold750	248395	CAAAA/CAAA	AGCTCGTCCACGAAAG AAA	TCGACTTGCAATCGCT TTG	60.0	645	INTERGENIC				
CaPOPI_8268	scaffold750	318580	ATATAACTTAACTTATAACTTAACTTATA ACTTAA/ATATAACTTAACTTATAACTTA ACTTATAACTTAACTTATAACTTAA	AAGCGCTGTAAAGGTG CAT	AGCATCTTGCAAGGGAT CTG	59.9	436	DRR	Ca_25943			
CaPOPI_8269	scaffold750	360259	GA/G	TGTTTGCTTGCTGCTTT GC	AAAATCCAACATCTCCC CC	60.2	626	DRR	Ca_25944			
CaPOPI_8270	scaffold7502	560	TTATATATATATATATATATATATATATA T/TTATATATATATATATATATAT	GTTGGTCCCTAGCAC GTA	TATCCAATCTTGTCGT CCA	60.0	806	INTERGENIC				
CaPOPI_8271	scaffold752	3867	CAAAAAAAAA/CAAAAAAAAA	TGGATGACAATGGGTAG GGT	TATAGTACCCATTCCGC CCC	60.1	645	INTERGENIC				
CaPOPI_8272	scaffold752	41940	ATTTTTTTTT/ATTTTTTTTTT	AGCACACATGACACAA GCA	TGAATTGTGAGGGTGT GGA	58.9	569	INTERGENIC				
CaPOPI_8273	scaffold752	131814	GTATATATATATATATAT/GTATATATAT ATATATATAT	GTTGGTCCCTAGCAC GTA	ATTGCCAGAGGTGTTGG AGT	60.0	754	INTERGENIC				
CaPOPI_8274	scaffold752	505163	TTTTTTTTTATTTTAT/TTTTATTTT ATTTATTTTATTTATTTTAT	AGCCATTGCAGTCTCG TCT	TCGTGTCTCAAACTCA AGGAA	60.0	854	INTERGENIC				
CaPOPI_8275	scaffold758	13400	AATATATATATATATATATATA/AATAT ATATATATATATATATA	CTCGTCCAATCCCCTT TTT	CGATTTTACGTGAATATA CGAACAC	60.3	603	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8276	scaffold758	26328	TTATATATATATATATATATATATATA TA/TTATATATATATATATATATATATA TATATATATATATATATA	TTTGCTCGAAGGCTTT TTA	GTTGGTCCCTAGCAC GTA	60.0	600	INTERGENIC				
CaPOPI_8277	scaffold7650	9735	T/TG	TATGGCATTGTGGTCA CTT	GGATTA AAAATTGGAAT GTTCAAGA	60.0	482	URR	Ca_27809	O		SKP1 component
CaPOPI_8278	scaffold7650	9922	CA/CATA	CCGCAATTATATCTGCG ACA	AGTTCAA AATACGCG GTG	59.7	857	URR	Ca_27809	O		SKP1 component
CaPOPI_8279	scaffold7657	660	CACAACAA/CACAA	AGGGAGGACGAAAATGA CCT	GGTGTGTTTGTGTCGT GGA	59.9	412	INTERGENIC				
CaPOPI_8280	scaffold766	179582	GTTTTTT/GTTTTT	TGGGTGGATTTTTCTGA AGC	TTTTATGGGGCCAACAA CTC	60.1	426	DRR	Ca_24688			Zinc finger, GRF-type
CaPOPI_8281	scaffold766	183062	TAAAAAAAAA/TAAAAAAAAA	AAAAGAAACGGAGGAG GGA	GCAACCTTTATTGATTG CTATGC	60.0	592	INTERGENIC				
CaPOPI_8282	scaffold768	560	T/TG	CCATGAGAGTCGAAATC GGT	TCCCACAGATCCACATT CAA	60.1	188	INTERGENIC				
CaPOPI_8283	scaffold769	1084	TTT/TTTCAATT	AAATGAACCAATTTAATG AGCTACC	CCCTCCCCAACACCCT TAT	59.0	479	INTERGENIC				
CaPOPI_8284	scaffold769	2786	TGGCAGCAG/TG	ACGTACACGTCAGCGTT TTG	CCCAATTCTCAATCCCA CTT	59.8	147	INTERGENIC				
CaPOPI_8285	scaffold769	3178	ACTCTCT/ACTCT	ACGTACACGTCAGCGTT TTG	AGCTGGATGATCACCAT GATA	59.8	975	INTERGENIC				
CaPOPI_8286	scaffold769	3493	CTAA/CTAATAA	TCCAAGAAAACAGTTTC CGA	TGAATGGTTTTATTGAG CTGGA	58.3	588	INTERGENIC				
CaPOPI_8287	scaffold769	5414	AATATATATATATATATATATATAT ATAT/AATATATATATATATATATAT	TCACTCGCGTTAATTTG ATG	GCGAGTGAATACATGTG CCA	58.8	518	INTERGENIC				
CaPOPI_8288	scaffold769	5924	AATATATATATATAT/AATATATATATA TATATAT	TGGCACATGTATTCACT CGC	TGTTGTTATTTGTGCG GAA	60.7	489	INTERGENIC				
CaPOPI_8289	scaffold769	17748	AATATATATATATATATATATAT/AA TATATATATATATATATATATATAT	TTGCTCCTTTTGC AAT AAA	TTGTGTGGCAGCTTCTA ACG	57.7	545	INTERGENIC				
CaPOPI_8290	scaffold769	27694	T/TAA	CTGGGCAAGGGATCTGA ATA	TCACAATCAGTG CACAC AACA	60.0	311	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8291	scaffold769	29353	AGC/AGCCCACTAATATGC	GCACTCTATTATCCCACA	CCACATGTCATTTAACCTGTC	59.6	370	INTERGENIC				
CaPOPI_8292	scaffold7697	589	G/GA	CTAGCCCTCGTCTGTTCAG	AATCCGTATTTTCGCACAG	60.0	521	INTERGENIC				
CaPOPI_8293	scaffold7698	946	AAA/AAATAA	CCGGTGGATATGATGAGCTT	GGCTTTTGAATCACCGAAA	59.9	650	INTERGENIC				
CaPOPI_8294	scaffold772	11892	TAAA/TA	GGCACACTCCCGTAAATTC	TTTTTCGCACACCAATGAGA	59.4	539	INTERGENIC				
CaPOPI_8295	scaffold772	64471	CAAAAAAAAA/CAAAAAAAAAA	TTTCTCAACCACTCCT	AGGGAGAGAGTGACACGCAT	59.5	734	INTERGENIC				
CaPOPI_8296	scaffold772	213642	AGG/AGGG	ACTTGAGGGCGAAGAACAAA	TTGGATGACCTACGACTCCC	59.9	573	INTERGENIC				
CaPOPI_8297	scaffold772	251341	CATATATATATATATATATAT/CATATATATATATATATATATAT	GCTCCACCATGAAGACATT	TGTTCCCTAACACCGTAGC	59.9	768	INTERGENIC				
CaPOPI_8298	scaffold774	3829	GAAATGACC/GAAATGACCAAAATGACC	TGGATGCACAAGATTGGCTA	AGGTCATTTTCGTCCTCCCT	60.2	468	INTERGENIC				
CaPOPI_8299	scaffold775	110824	TAAA/TAA	GCCGAATCGATTTTGTGAGT	GGAGGGTTTGGTTTGGAAAT	60.1	521	INTERGENIC				
CaPOPI_8300	scaffold775	388602	CATATATATATATATAT/CATATATATATATATATAT	CTTCGCGAAATAAAGCTTGG	TTGGTATTGAACTCGGAGGC	60.0	567	INTERGENIC				
CaPOPI_8301	scaffold775	446063	TTATATATATATAT/TTATATATATATATAT	TTTTGCAAGATCTGCCACTG	TGGAAGGATCCGGAACATG	60.0	867	INTERGENIC				
CaPOPI_8302	scaffold775	449733	CTTATCAATTGTGTTT/CTTATCAATTGTGTTTATCAATTGTGTTT	CTCTCTTCTGCGCATCACT	TTGACCATGACACATGCCTT	58.3	459	DRR	Ca_23414		NAC	Pectinesterase, catalytic
CaPOPI_8303	scaffold775	450377	TG/TGG	AAGGCATGTGTCATGGTCAA	TTTACGGGAACGAGGAGAGA	60.0	738	DRR	Ca_23414		NAC	Pectinesterase, catalytic
CaPOPI_8304	scaffold776	224423	T/TTCCCTA	TGGGATACGTAGGAGCAAGG	TGTCCGTGAAAAATGAGTCG	60.1	310	INTERGENIC				
CaPOPI_8305	scaffold7765	977	ATTTTTTTTTT/ATTTTTTTTTTTTTT	AGATGGCTGCAGCTCAAGT	TTTCCAAGAGGTTTGGGTC	60.2	464	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8306	scaffold787	91954	C/CA	AGGTCATTTTCGACCTCCT	TAGAACAAAGCCTCGGGAAGA	59.9	331	INTERGENIC				
CaPOPI_8307	scaffold787	149556	ATTTT/ATTTT	CGGGATGGTGGCATAATATC	AGCAGGGTTTCTCCCAAATC	60.0	343	INTERGENIC				
CaPOPI_8308	scaffold787	154027	TAAAAAAAA/TAAAAAAAAAAAA	AATCCAATGACACAACGCA	TCAGTCAAGCGCACATAAAA	60.0	415	INTERGENIC				
CaPOPI_8309	scaffold787	289233	TAAAAAAAA/TAAAAAAAAAAAA	CAAGCTATTCTTTGCCGACAT	CGCATTCAACATGACCCTT	59.4	621	INTERGENIC				
CaPOPI_8310	scaffold787	334329	ATTTTTTTT/ATTTTTTTTT	CTTCTCTGTGCCACATCCT	TTCATTCGTGTCTGCTTTGG	60.3	598	INTERGENIC				
CaPOPI_8311	scaffold787	348087	TTATATATATAT/TTATATATATAT	GAGGGGATGGTGAGAGTGAA	GCAGACATCACATGGAAAGA	60.0	595	INTERGENIC				
CaPOPI_8312	scaffold787	429004	G/GGA	TCATTTCAATGCCCTCTTCC	TCTTTGAGGGATTCTGTTGG	60.0	316	INTRON	Ca_25848	R	NAC	RNA recognition motif domain
CaPOPI_8313	scaffold787	437054	CAAAAAAAAA/CAAAAAAAAAAAAAA	TCAATGGCTCATCAAAACCAA	TTTTGTGCATCGATTGTGGT	60.0	397	INTERGENIC				
CaPOPI_8314	scaffold787	460684	CAT/CATAT	TATGGGAAGGAAATGTGGGA	TCACTCGCAACGAGAAGTTG	60.1	601	INTERGENIC				
CaPOPI_8315	scaffold787	472975	T/TTA	ACGCTGTTGGTCCATGTAAA	TGAACAAATCTAAAGCGTAAAGG	59.1	428	INTERGENIC				
CaPOPI_8316	scaffold7890	680	TG/TGG	TTTCTCCCTTTCTTTCCGT	GAAGGGACTGCGGCATAATA	60.0	162	INTERGENIC				
CaPOPI_8317	scaffold7891	3768	CAAA/CAAAA	TCTGGACTTTTCGAGCGATT	AGTGCATTTTAGTCGGGTGG	60.0	379	INTERGENIC				
CaPOPI_8318	scaffold7902	684	CTT/CTTT	GGGTAGCATGGCAAGTTGTT	CGAGTAAAGCGTTTTGACTAACG	60.0	363	INTERGENIC				
CaPOPI_8319	scaffold7923	2123	AAGCTCA/AA	TCGGGGTCTTTAGTCGTCAT	GCGAGGAAGCAAAAGCTAGA	59.6	796	DRR	Ca_27506	O		
CaPOPI_8320	scaffold7923	22242	CAAAAAAAAA/CAAAAAAAAAAAAA	TTTCCCGACTTGGTCCTTTA	TTTGC GTTACGAATTTGATGA	59.5	177	DRR	Ca_27507	QI	bHLH	Cytochrome P450

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8321	scaffold7923	22388	GAGAGAA/GAGAA	TTTCCCGACTTGGTCCTTGA	GGAGGGAGAACATCTGTGG	59.5	741	DRR	Ca_27507	QI	bHLH	Cytochrome P450
CaPOPI_8322	scaffold7923	25395	ATC/A	AAAATATGCCATTCGATCAAGA	AAATGGCTTGTTATGGCTG	58.6	200	URR	Ca_27507	QI	bHLH	Cytochrome P450
CaPOPI_8323	scaffold793	49023	CATAATAATAATAATAATAATAA/CATAATAATAATAATAATAATAATAA	TGTATGAGCAACGGATGTTGA	GCAAGGCGCGAGTTAGTATC	60.1	351	INTERGENIC				
CaPOPI_8324	scaffold793	127009	T/TA	TGGTGTCAATCAAGAAATGA	TTCCAGCATAATCCGAGTCC	59.0	577	INTERGENIC				
CaPOPI_8325	scaffold793	135694	TG/TGGG	CCAAACACACCATTTATGCG	CACTAGTGAATGGAAGGGC	59.8	254	INTERGENIC				
CaPOPI_8326	scaffold793	248408	T/TA	TGCTCATGCATTTTCATGCT	GAGTCCCTGTGTTGCCAAT	60.4	410	INTERGENIC				
CaPOPI_8327	scaffold794	138143	GA/G	CTGTCAAACCGGTTCTGTT	TGCTTGCACTGCTTCATCTT	60.0	378	INTERGENIC				
CaPOPI_8328	scaffold796	7462	GTTTTTTT/GTTTTTTT	TCTCCCTTGCTTATCTT	GGAGGACGAAAATGACCTGA	60.0	607	INTERGENIC				
CaPOPI_8329	scaffold796	26479	GTT/GTTT	TCATTTTCGTCTCTCTTGG	GCCTATTGGATGCACAGGAT	60.0	470	INTERGENIC				
CaPOPI_8330	scaffold797	15287	CAAAAA/CAAAAAA	GGTGATTTTTATGATGTGCTAGTTTT	CCCTTTCAATCCCGTTT	59.0	689	INTERGENIC				
CaPOPI_8331	scaffold798	16927	T/TC	ATGCAATGCGTATATGCCAA	TAAATCGTGTGACCCGTGA	59.9	233	INTERGENIC				
CaPOPI_8332	scaffold80	25932	TAAAAAAAA/TAAAAAAAAA	AATGTAGTCCCAACCCGATG	CGATACTACCCCTCGTTGT	59.7	210	INTERGENIC				
CaPOPI_8333	scaffold80	56806	GCC/GC	ATGCCTCCTCTCTCTCCCTT	GGAAATTCATGGTTTCA	59.3	544	INTERGENIC				
CaPOPI_8334	scaffold80	301960	GATATATATATATATATATA/GATATATATATATATATA	GCTTTGTGGAGGAAATGAA	TTGTCTCTCGACGAACGATG	60.1	745	INTERGENIC				
CaPOPI_8335	scaffold801	4383	CCTC/CC	ATGGTGGTGAGCAACTTCC	TATTTTGATTTTGCTCGG	60.0	626	INTERGENIC				

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CaPOPI_8336	scaffold801	106576	AGG/AG	CCGTGTTCTGTGAATCA ATG	GGTGAGTTGGGCATGCT TAT	60.0	348	INTRON	Ca_26177			WD40 repeat
CaPOPI_8337	scaffold801	118356	TG/TGAGTCGTGTAG	ATGGGCCACCGTGTTAG TAG	CAATTCTCGCACGACTC AAA	59.9	507	INTERGENIC				
CaPOPI_8338	scaffold801	152306	ATTTTTTTTTTT/ATTTTTTTTTT	TCCCCATTCTCTTCTCA CC	TGGTGGTCTTGTGGTT TCA	59.1	778	INTERGENIC				
CaPOPI_8339	scaffold801	161086	TAAAAAAAAA/TAAAAAAAAA	CAGGATGCGACCATGTA GTG	TTTGTGTTCCGACATCT CCA	60.1	244	INTERGENIC				
CaPOPI_8340	scaffold801	189547	CTAAATTGATA/CTAAATTGATAATTGA TA	CAGGAAAAAGAAGGAAC CGA	TGCAAACACTTTCCAAT GTCA	59.3	637	INTERGENIC				
CaPOPI_8341	scaffold801	192338	ATTTTTTTTTT/ATTTTTTTTTT	TGTGCAGATAAATGGCC AAA	GAGCTGTGTCCTTGGCAA TCA	60.1	792	INTERGENIC				
CaPOPI_8342	scaffold801	202304	TAAAAAAAAA/TAAAAAAAAA	TGCTTCTTTTGCACGTTT TG	AGACGCTTTTCTTTTGC GGA	60.0	837	INTERGENIC				
CaPOPI_8343	scaffold801	260992	CATAT/CAT	TCGTCCGTAAAAGATAC CGC	GGAGGACCAAAATTGA GCA	60.1	661	INTERGENIC				
CaPOPI_8344	scaffold806	37447	AATATATATATATATATATA/AATATATAT ATATATATATATA	TTGGTATTGAACTCGGA GGC	CGAGGCAGAGGAAGAAA ATG	60.1	359	INTERGENIC				
CaPOPI_8345	scaffold81	91419	A/AC	TGAGGAGAAACAAATG GGG	ATGGAAGGGTCGTTGAC ATT	59.9	458	INTERGENIC				
CaPOPI_8346	scaffold811	56559	GATATATATATATATATATAT/GAT ATATATATATATATATATATAT	TTTAACGTGTGCGCTCT TTG	GAATAAAATGCACCGGC ACT	59.9	748	INTERGENIC				
CaPOPI_8347	scaffold811	159571	TTATATATATATATATATATATATAT/T TATATATATATATATATATATATAT	TTGCAACATGCTATTTCC CA	TGGGTGCTATTTGCAAT CAA	60.1	613	INTRON	Ca_27462			
CaPOPI_8348	scaffold811	234762	GTAATAATAATAATAATAAAAAAT AATAATAATAATAATA/GTAATAATA ATAATAATAATAATAATAAAAAATAT AATAATAATAATAATA	GGTGTGCTGTGTGTTT GCC	GGTCCTCGATTTCACTC GGA	60.1	683	INTERGENIC				
CaPOPI_8349	scaffold811	238697	CTATATATATATATATATATA/CTATA TATATATATATATATATA	GGTGTGCTGTGTGTTT GCC	CCGTGCTAATCTCTGCT TCC	60.1	447	INTERGENIC				
CaPOPI_8350	scaffold812	215247	TGG/TG	AGAAGGAACAACGAGAA CGC	TGTCCTTCTCATTGGGA ACC	59.5	178	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8351	scaffold812	216839	TAAAAAAAA/TAAAAAAAA	GCATTGATCGTCCCTC ACT	GGACAAAGCACACCAGG AAT	60.1	447	INTERGENIC				
CaPOPI_8352	scaffold812	228611	TAAAAAAAA/TAAAAAAAA	CAAGTGCATTCCCCAA GAT	CGCATGAATATTGTCAA CGG	59.9	529	INTERGENIC				
CaPOPI_8353	scaffold812	245558	GAAAAAAAA/GAAAAAAAA	CAAAGTCTTCACACACC GACA	TGTTGACTCCAGTCACC GAG	59.8	736	INTERGENIC				
CaPOPI_8354	scaffold812	285596	TAAAAAAAA/TAAAAAAAA	GATGTTCTCGGCAGTTG ACA	CCGGTACTTAATATGCG ACTCA	59.8	365	INTERGENIC				
CaPOPI_8355	scaffold812	311738	AATTATTATTATTATTATTATTATT TTATT/AATTATTATTATTATTATTAT TATTATTATTATTATTATT	TTGTTTGTGGGCAGC TTA	GGATGCGACCATCTACT GCT	60.0	460	INTERGENIC				
CaPOPI_8356	scaffold812	320576	ATTTTTTTTTT/ATTTTTTTTTTTTT	AAAACGTTGGAGCATTT TGC	AGGGAAATGGAACCAA CCC	60.1	442	INTERGENIC				
CaPOPI_8357	scaffold812	350314	GAAAAAAAA/GAAAAAAAA	ACACCACGACGACGTAC AAA	AATGGTTCTCACTATCG CCG	60.1	239	INTERGENIC				
CaPOPI_8358	scaffold812	354262	TTTCTTCTTCTTCTTCTTCTTCTTCT /TTTCTTCTTCTTCTTCTTCTTCTTCT TTCTTCT	GCTACGGCTAGTGCCTT CAC	GTCAAAGCAACGATCA GCA	60.0	514	INTERGENIC				
CaPOPI_8359	scaffold812	378934	TAAAAAAAA/TAAAAAAAA	TTGGAAGGAGCCCTTAC CTT	TGAATTGGTTTCGAG CTT	60.1	716	INTERGENIC				
CaPOPI_8360	scaffold812	407862	ATTTATCATTTATGTTTTAT/ATTTATCA TTTATGTTTTATCATTTATGTTTTAT	TTGTGCAAAGACATGGG AAA	TCAACTGTTGCACCTTC GAG	60.1	527	INTERGENIC				
CaPOPI_8361	scaffold812	487308	GAACAAATAACAACA/GAACA	CTTACCATGCTCAGTC CAA	CCCAAATCAGTCGGTTC TGT	59.8	840	INTERGENIC				
CaPOPI_8362	scaffold812	526031	TGG/TG	TCGACTTGCAATCGCT TTG	CACTCCAGTGCTGAGGG AAT	60.0	215	INTERGENIC				
CaPOPI_8363	scaffold820	15078	A/AG	TCATCATGGGCTTACGA CCT	GGCCAAACCCATTAAAA CCT	60.5	343	INTERGENIC				
CaPOPI_8364	scaffold823	52739	TATAATAACATATAATA/TATAATAACA TATAATAATAACATATAATA	CCTTTTAAAGTTTGACTG CATAACAA	TGAAATAAAACCATAAAA CGAAGA	60.0	830	INTERGENIC				
CaPOPI_8365	scaffold824	6128	CA/C	CACCCAGTTTTGAGGG TAA	CGATTGTGTTGTGACA GGG	59.8	191	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8366	scaffold829	10973	T/TA	TTTATTTGACAACTCGTT TTTGT	GAGCGAATTGAGAAACG AGG	57.1	799	INTERGENIC				
CaPOPI_8367	scaffold829	12450	GT/G	AATCGAATTCACAAGCG ACC	GAACCAAGGGCCAAAA TCT	60.1	153	INTERGENIC				
CaPOPI_8368	scaffold8301	5927	AGTTAGTTTTTTATTGTTAGTTTTT/A GTTAGTTTTT	ATGTCGCGTCTTCATCA ACC	ACAATTTATCCGTGTCG CGT	61.1	546	INTERGENIC				
CaPOPI_8369	scaffold831	50051	A/AAG	TGACCAAAATGCTCATC CAA	AGGTCATTTTCGTCTCT CCT	60.0	285	INTERGENIC				
CaPOPI_8370	scaffold8314	868	CAAAAAAAAA/CAAAAAAAAA	TGAATGGTTGCATGGTT ATCA	GTGGGAAGTGGTAGAGT GCG	59.8	415	INTERGENIC				
CaPOPI_8371	scaffold8314	1258	CTTTTTTT/CTTTTTTT	AATTTAGCTCATTGCTG CCG	TACCTCCTTGGAAGCA TGG	60.4	353	INTERGENIC				
CaPOPI_8372	scaffold8314	2052	G/GC	TCAATTAGGCCCTTCAC CAC	GTCCTCTGAAACCTCCC ACA	59.9	915	INTERGENIC				
CaPOPI_8373	scaffold8315	17783	GTATATATATATATATAT/ATATATAT ATATATATATATATATAT	AGGGTCTCCAAGTCCTC GAT	TTTTAGGGCTAGTTGTA CACATGAA	60.1	377	INTERGENIC				
CaPOPI_8374	scaffold8315	18988	T/TTTA	AAAAATTTATATTGCGTC AATTGG	GTGCTGGCCATAGGAAA TGT	59.6	565	INTERGENIC				
CaPOPI_8375	scaffold8315	20409	ATT/AGTTTTT	TTTCCAACTCGGGAGTA ATTG	TGGAAGAATGTTTAAG GTTTTGA	59.1	777	INTERGENIC				
CaPOPI_8376	scaffold8315	20462	GTTT/GTT	AAAAGGATATTCAACTCT CCAAAA	CGATTTTGCTACAAAA TTTCC	58.7	759	INTERGENIC				
CaPOPI_8377	scaffold8393	1553	ATTTT/ATTTTTT	CCGGTTGCACAACATTC TTA	TCTTTCTTATGGTTCTGT AAGCTGA	59.6	378	INTERGENIC				
CaPOPI_8378	scaffold8412	961	TAAAAAAAA/TAAAAAAAA	TTTTCACATTCAAAAGC ATGA	TCACATCTTCCTTATGTC CGC	58.3	342	INTERGENIC				
CaPOPI_8379	scaffold842	20647	TA/TAA	TGATTCCTGTAACACCC CAA	AACCAACACACAAGGA AATATGA	58.8	332	INTERGENIC				
CaPOPI_8380	scaffold842	30005	CAAAA/CAAAAAAAAA	GATACTATGCCACCATC CCG	TGGTCATGCAGAACTC AGC	60.2	848	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8381	scaffold8442	1501	CA/C	AACCAAACTGGTGATCACA	AGCCTAGGGTGGACGAAAT	60.0	676	INTERGENIC				
CaPOPI_8382	scaffold845	2172	TTA/TTCTTTAGTA	CAACATTTTGGGTGCATTTG	TGGTTATTTTGCATGTAGCGA	59.8	657	INTERGENIC				
CaPOPI_8383	scaffold845	2505	ATTTTT/ATTTTTTT	TCGCTACATGCAAAATAACCA	TCACGTCACTTTTTCAATGG	59.2	388	INTERGENIC				
CaPOPI_8384	scaffold845	3348	TAAAAA/TAAAAA	ACAAATGAATGTGGGTGGT	TGATCATCTTTTGTGGAGTTTC	60.0	701	INTERGENIC				
CaPOPI_8385	scaffold845	3378	TAAA/TAA	ACAAATGAATGTGGGTGGT	TGATCATCTTTTGTGGAGTTTC	60.0	701	INTERGENIC				
CaPOPI_8386	scaffold845	23562	CT/C	TCGATCAACCTAGATTGGCA	TCTGAACACTATCGTATCATGTTTCTT	59.2	655	INTERGENIC				
CaPOPI_8387	scaffold845	31907	CTATAACAA/C	TGTGGTTTGGTTGGATGATG	AGAGAATGTGGCCTTCAACA	60.2	653	INTERGENIC				
CaPOPI_8388	scaffold845	33752	CATCAAATCAAAT/CATCAAAT	AAAAACCTATCATGCTGCC	ACGCCCATTCGTAGATGTC	59.0	299	INTERGENIC				
CaPOPI_8389	scaffold845	39704	GAAAAA/GAAAAAA	TGAAACGTTGAAATGGCAC	TTGTTATCGCAGGGGAAATC	59.6	251	INTERGENIC				
CaPOPI_8390	scaffold845	61188	CTGTT/CT	TTCGAAAGTTTTCATTTTCG	TGGAGAAGACCATATTGCC	58.9	405	INTERGENIC				
CaPOPI_8391	scaffold845	69832	A/AT	TTGTTTTTCAGGTTGGGTTTC	CCTACGGACTTGTCGTGGAT	59.8	511	DRR	Ca_22414	R		RNA recognition motif domain
CaPOPI_8392	scaffold845	81876	GAAAAAAA/GAAAAAA	GGTTTTTGGTTGGAATGTGG	AAAAGGGAGGGGCAATCTAA	60.1	382	INTERGENIC				
CaPOPI_8393	scaffold845	102274	TTAAGTAAG/TTAAG	ACTCTAAGTGCCTCTCCGTT	TTGACGGTCAGGTGAGACAG	60.1	233	DRR	Ca_22415	R		
CaPOPI_8394	scaffold845	102446	CAA/CAAA	CTGACCGTCAAAAGCACAGA	ACGCATAATACCTGAACGGC	60.0	480	DRR	Ca_22415	R		
CaPOPI_8395	scaffold845	111245	ACGAAT/A	GGCTCGGTAGGTATCCGTAA	TTATATTAGTCGGGCGTGG	59.1	166	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8396	scaffold845	132751	CAAAATAAT/CAAAATAATAAAT	AGTGTGTTTGGGTTGG GAG	TCGATTGACATTTGCG TGT	59.9	526	INTERGENIC				
CaPOPI_8397	scaffold845	132810	GA/GAAATTCTAA	AGTGTGTTTGGGTTGG GAG	TCGATTGACATTTGCG TGT	59.9	526	INTERGENIC				
CaPOPI_8398	scaffold845	133191	CAAA/CAA	CCACCAAAAACCAACCA ACT	GGCCTAACCTGGAAGCC TAT	59.7	730	INTERGENIC				
CaPOPI_8399	scaffold845	134750	CAA/CAAAA	CCGTTTGGGCCCTTAGT TAT	TCGTGTCCATTGCTATTT TCA	60.2	546	DRR	Ca_22417	U		Zinc finger, RING-type
CaPOPI_8400	scaffold845	141061	TAA/TAAA	CCGGCATAATCTGACAA CCT	GTGCTTTGTGGGGATGA TCT	60.0	453	INTRON	Ca_22417	U		Zinc finger, RING-type
CaPOPI_8401	scaffold845	152531	GTACTTAC/GTACTTACTTAC	CACGTGCAAGTAAAGC CAA	TGCTGCACCATAATTCC AAA	59.9	537	INTERGENIC				
CaPOPI_8402	scaffold845	170625	ATTT/ATTTT	ATTTGGTGCGCATGATA AGA	AAAAATGAGGTGGGTTA GAAATTA	59.1	777	INTERGENIC				
CaPOPI_8403	scaffold845	171362	ACA/ACAATGTCA	TCAATCACACCCGTTCA AAT	TGATTGCCGACAATACC AAG	58.8	159	INTERGENIC				
CaPOPI_8404	scaffold845	174410	CA/C	GCATAGATGCAGTGGA GCA	ATTACCTGCAGGAGCCC TTT	60.0	848	INTERGENIC				
CaPOPI_8405	scaffold845	194654	GGTGTGATTTTCTGT/GGTGTGATTTTC TGTGTGATTTTCTGT	TGAATTTGAATGCCCAT GA	CATTGCGCACACGTCAA TAC	59.9	318	INTERGENIC				
CaPOPI_8406	scaffold845	331956	TG/TGG	TTGCTTGAAAGGAAAA TCG	GGGGCCAAATAATGTTG CTA	60.2	802	INTERGENIC				
CaPOPI_8407	scaffold845	357903	GTTTTTTTTTT/GTTTTTTTTTT	TGGAATTCATACCCCC AAA	CCCGGCCAATTTTATTT CTA	60.0	304	DRR	Ca_22428	R	G2-like	RNA recognition motif domain
CaPOPI_8408	scaffold847	117106	TCAATCGATTGGGCAATCGATTG/TCAA TCGATTG	CCCGTGAGATCCTCCTA ACA	CTCGTGTCGTTCTGTGA GAA	60.1	642	INTERGENIC				
CaPOPI_8409	scaffold848	72755	ATTT/ATT	ACAACATGCACTCGTGG GTA	CGTTTGTGCGATATTG AAA	60.0	608	INTERGENIC				
CaPOPI_8410	scaffold848	226354	GTCT/GT	TTTTGGCGTAGTGTGTG CTC	CAGCAAACGTTCTCCGT TTT	59.9	678	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8411	scaffold8493	9496	A/AT	CGACCATGATTTAACGA CCA	GTTTCAAGAGGTGGCC TTG	59.4	360	INTERGENIC				
CaPOPI_8412	scaffold855	8963	AATATATATATATATATATA/AATATAT ATATATATATA	TGGAAGTCACTACGTACG GCA	TTTTCTCTATCCCCAT GTTATTC	60.3	521	INTERGENIC				
CaPOPI_8413	scaffold855	30812	TTATATATATATATATATATA/TTATAT ATATATATATATATATA	AGGCCGTGATGTTTTG AAC	GCATCATATGTGTGGC AAG	60.0	268	INTERGENIC				
CaPOPI_8414	scaffold855	31194	ACCC/ACC	CTCGTACGCTTTTGGTG TGA	GTAGGGGGTAGAAAACC CCA	59.9	556	INTERGENIC				
CaPOPI_8415	scaffold855	31470	TTAATATCC/T	AATTGGATACCCCTTTT GGC	GTAGGGGGTAGAAAACC CCA	60.0	384	INTERGENIC				
CaPOPI_8416	scaffold855	31510	TTAT/TTATATAT	AATTGGATACCCCTTTT GGC	GTAGGGGGTAGAAAACC CCA	60.0	384	INTERGENIC				
CaPOPI_8417	scaffold8565	6875	GTTTTTTTT/GTTTTTTTTT	TGACCAAAATCCATCCC TTC	TTTACAGCGCTTGTTCC AAA	59.7	517	INTERGENIC				
CaPOPI_8418	scaffold864	221220	GGAGAGAGAGAGAGAGAGAGAGAG AGA/GGAGAGAGAGAGAGAGAGAG AGAGAGAGA	TAACCAAAATCCCA CCA	GGGTCACGTCCTTGCT ACC	60.0	377	INTERGENIC				
CaPOPI_8419	scaffold864	247808	TGGGG/TGGGGG	TTCTGCCCTCATGGATT TTC	CATGGCTCGAGTGAAC AGA	60.0	349	CDS (FRAME SHIFT)	Ca_24213			
CaPOPI_8420	scaffold864	319669	CAA/CA	TTCACTTGTTGACCAATC GC	TGCGTGAAACAAGACGA AAC	59.7	727	INTERGENIC				
CaPOPI_8421	scaffold8646	2745	TAAAAA/TAAAAAA	AGTCTACGACGAAGCGT TCC	TCCATAGGAGGTCGATG GTC	59.5	532	INTERGENIC				
CaPOPI_8422	scaffold866	36146	CA/CAGA	GAACAACAAGTGGGATG CCT	TGTGAAAAATGAACACC CCA	60.0	360	INTERGENIC				
CaPOPI_8423	scaffold866	36277	ACCC/ACC	GAACAACAAGTGGGATG CCT	TGTGAAAAATGAACACC CCA	60.0	360	INTERGENIC				
CaPOPI_8424	scaffold866	142956	CTT/CT	GGATCCCCAATCGATAA CCT	CTGTTGAGCCTTAGGGC AAG	60.0	450	INTERGENIC				
CaPOPI_8425	scaffold868	30710	TGG/TG	AGGGAGGACGAAATGA CCT	AGGGTTTTTGCCCAATC TTT	59.9	180	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8426	scaffold869	6196	TAAAAATAAAATA/TAAAAATA	CACCCATGGCAAAAGA AAT	TTGCTGAACCTTTTCT CC	59.8	389	INTERGENIC				
CaPOPI_8427	scaffold869	39678	TTATATATATATATATAT/TTATATATATA TATAT	GTAATAAGCGCTT CGC	GCATTCTTCACTGCAAA CTCA	60.0	658	INTERGENIC				
CaPOPI_8428	scaffold869	135112	ATTTT/ATTTT	TTAGTCATGGTCGCTCC GAT	TAACGGGATTTAAGGTG GGG	60.6	360	INTERGENIC				
CaPOPI_8429	scaffold87	361359	GAAAAAAAAA/GAAAAAAAAA	GTTCCAGAACGAGAGAT GGG	AGGACTGAGCCTGGCTT ACA	59.7	803	INTERGENIC				
CaPOPI_8430	scaffold87	468940	TT/TTCGGAT	GAGAATGGCAGCCCAAA ATA	TCGGTATTTGCCATGAG ACA	60.0	533	INTERGENIC				
CaPOPI_8431	scaffold87	585278	TTTTTTTATTTT/TTTTTT	TATGCATGCAGGCAAGA GTC	TTGGAAAAGCCACCTA CAC	60.0	570	INTERGENIC				
CaPOPI_8432	scaffold87	594427	CAGATA/CA	TGACCGATTTGGTGACT GAA	TTGGTGATCATGATGCT GGT	60.1	555	INTERGENIC				
CaPOPI_8433	scaffold87	597245	TAAAAAAAAA/TAAAAAAAAA	TAGCCAAATAACCCGC TCC	TCTCCCATCCTCTCAT CAC	60.1	573	INTERGENIC				
CaPOPI_8434	scaffold870	39934	TTTATTATTATTATTATTATTATTAT TATTATTATTATTATTAT/TTTATTATTAT TATTATTATTATTATTATTATTATTA TTATTATTAT	AGAGGCAACAAGAACC GAA	GGTGAGCCACCTTCATT TGT	59.9	517	INTERGENIC				
CaPOPI_8435	scaffold870	82369	GTTTTTT/GTTTTTTT	TGGTGGTGCAATTCACA TCT	TTTCACCGTCATGCTTTT TG	60.0	540	INTERGENIC				
CaPOPI_8436	scaffold870	82445	GT/GTT	TGGTGGTGCAATTCACA TCT	TTTCACCGTCATGCTTTT TG	60.0	540	INTERGENIC				
CaPOPI_8437	scaffold873	18311	GAAAAAA/GAAAAAA	TGTTGGGTCCACAAAGA GAG	TGTTGTTCTCCTCTGAC ACAATG	58.7	402	INTERGENIC				
CaPOPI_8438	scaffold873	199356	CTTATTATTATTATTATTATT/CTTAT TATTATTATTATTATT	CCCTTACTTGGACCAAA GTTACC	CTGCGAACTGGACAAAT GAA	60.1	585	DRR	Ca_23485			Clp, N-terminal
CaPOPI_8439	scaffold873	269556	GATATATATATATATATATATATATAT ATATATATATAT/GATATATATATATATA TATATATATATATATATATATATATAT	TTTTGCAATGAAACCCAT CA	TGTGGCAAGCGTTTATT CTG	59.9	614	INTERGENIC				
CaPOPI_8440	scaffold873	309839	TAAAAAA/TAAAAAA	TTTCATGGTGTCTTCTTG GCA	ATGGGGAAAAATCGCTTA CCT	60.1	691	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8441	scaffold8734	801	TAA/TAAA	TTGGGCGAAAATGGATA AAG	CCCCGCTCTGATAGGTG ATA	59.9	802	INTERGENIC				
CaPOPI_8442	scaffold8734	1079	TAAA/TAAAA	CTGTGACACCCTAAATC CCA	GATCTATGAGGACAGGG CCA	58.4	798	INTERGENIC				
CaPOPI_8443	scaffold876	3909	CCTGTCGCG/C	CACGAGTGCCGATATGT GTC	TAGTGCGGATTCTTTT TCG	60.1	531	INTERGENIC				
CaPOPI_8444	scaffold876	4050	TACGACGACG/TACGACG	AAATCCAACATTGCTCT GCC	CTATTGCACCTGGGGAT ACG	60.1	388	INTERGENIC				
CaPOPI_8445	scaffold876	34017	AC/A	ACGATCCACACCAAAAC ACA	TACGGTGCTAGGGAACC AAC	59.9	449	INTERGENIC				
CaPOPI_8446	scaffold876	63698	CAA/CAAA	GCTCGTCGAACTTTTTC AGG	TCATCAGTATCGTGGGT GGA	60.0	602	INTERGENIC				
CaPOPI_8447	scaffold876	163249	ATTTTTTTTTTT/ATTTTTTTTTT	AAATAGGCCGACCTCTC GTT	TGAGGGAGAAAAACAAG CGT	60.1	479	DRR	Ca_24591	K	ARR-B	Signal transduction response regulator, receiver domain
CaPOPI_8448	scaffold876	622726	TAA/TAAA	TCAGGAACAACAATCCA ATCC	TTACCCTCAAACTGGG GTG	59.8	331	INTERGENIC				
CaPOPI_8449	scaffold877	10844	TAAAAA/TAAAA	GCAGCAGTTGCAGCAGT TTA	TGATTTAGCGTCGGTGT CAG	60.3	601	DRR	Ca_28083	F		Orotidine 5'-phosphate decarboxylase domain
CaPOPI_8450	scaffold88	20403	ATTTTTTTTTTT/ATTTTTTTTTT	AATGGATTGCTCTGTTT GGC	TCCCTCTATGCTTTGTC CCT	60.1	728	INTERGENIC				
CaPOPI_8451	scaffold88	63256	TAAAAAAAAA/TAAAAAAAAA	AAATCCTTTTGGGGTGA AGC	TTTTTGAAACTGCCAG GTG	60.3	655	INTERGENIC				
CaPOPI_8452	scaffold882	70530	CAAAAA/CAAAAA	CACATCAACAGCAGCCT TGT	TGATGTTGCCTCTGTTT GC	59.9	385	INTERGENIC				
CaPOPI_8453	scaffold882	314543	CTTTTTTTTTTT/CTTTTTTTTTT	TCTGGAATTGCTTTGAC GTG	TGCATTGTCACGTGTTT TTTG	59.8	813	INTERGENIC				
CaPOPI_8454	scaffold882	326048	GTATTATTATTATTAT/GTATTATTA TTATTATTAT	TTTCGAAGAAAGCGATA ACAA	GAGGAAAAACAAATGGA CAAGC	57.7	757	INTERGENIC				
CaPOPI_8455	scaffold882	344839	GAAAAAAAAA/GAAAAAAAAA	TTTGTGTTTGACTGGCT TGG	GACACCCTAAACCCGA AAT	59.7	416	DRR	Ca_23984		Trihelix	

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8456	scaffold882	436721	GAAAA/GAAA	CGTACCAAGGGCAATG AAT	GCTCTGCATCCCATCAA AAT	59.8	323	INTERGENIC				
CaPOPI_8457	scaffold882	446893	GTTT/GTTTT	TGGTTGGTTTTGTGGT GAA	TCACGGGCAACACAAT TTA	59.8	644	INTERGENIC				
CaPOPI_8458	scaffold882	513030	AATATATATATATATATATATATAT A/AATATATATATATATATATA	ATTCTTGATTCGCCTCC CTT	CACCGTAGTGTGGTGGT GAG	60.0	680	URR	Ca_23986			
CaPOPI_8459	scaffold882	639280	CTTTTTTTTT/CTTTTTTTTT	AGGAATGACCAAAACGT TCG	CACTTGTATTATTGAAAC ACAAGGT	60.0	881	INTERGENIC				
CaPOPI_8460	scaffold8825	968	TAAAA/TAAAAA	AATCGATTGGCATCAAC ACA	CCAGTCAAGCATTCCCA TCT	59.9	475	INTERGENIC				
CaPOPI_8461	scaffold8836	981	GAAATAAAA/GAAA	CAACACAACAAGAACGA GCAA	TCCAAGTAGGTCTGCCC AAT	59.9	288	INTERGENIC				
CaPOPI_8462	scaffold886	151276	AG/AGCTG	AGGGATGCTGTAGTGG TTGA	TTTGACGTGCATCCAAT GTT	59.6	162	DRR	Ca_26671			
CaPOPI_8463	scaffold886	151448	TA/T	GACAACATTGGATGCAC GTC	TCGTGGTATGCTTGACC TGT	60.0	259	DRR	Ca_26671			
CaPOPI_8464	scaffold886	164957	AGG/AG	GCTAATTGGCGGCAC TTCTA	CGAGTTAGTGAATCATC CCCTC	60.4	614	INTERGENIC				
CaPOPI_8465	scaffold886	172563	AATATATATATATATATATATAT/AATA TATATATATATATATATATAT	AAGCCGACAATTTGTTTT TCT	TCATTCTGATTTGGGG GTA	57.9	382	INTERGENIC				
CaPOPI_8466	scaffold8866	2222	CTAAATTAAT/CTAAAT	TCTGATACGCCTCATAG CCC	AGGGCAAAAGTCTCAAA GGA	60.2	519	INTERGENIC				
CaPOPI_8467	scaffold89	23867	ACAT/ACATCAT	CATGGTAGTCCCGACA TTT	ATTTCCAACGATTCATC CG	60.0	712	INTERGENIC				
CaPOPI_8468	scaffold89	30029	AATATATATATATATATATA/AATATAT ATATATATATA	GGATTGAACCTCCTATG CGA	TTCCGAGTTGTTTGAGA GGA	60.0	716	INTERGENIC				
CaPOPI_8469	scaffold890	1120	ATATTATTATTATTCTTATTATT/ ATATTATTATTATTATTATTCTTATT ATTATT	TTCGGGCAATCATTAC ACA	TGGCTGAAATACGCCAC ATA	59.9	359	INTERGENIC				
CaPOPI_8470	scaffold8913	2269	TG/T	CAATGGATGGGTAGGA TTG	AGCGACAGTGAACGATG TTG	60.0	366	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8471	scaffold8913	2342	ATTTTT/ATTTT	CAATGGATGGGGTAGGATTTG	GCAGGAGATTTAGATGGAGGG	60.0	878	INTERGENIC				
CaPOPI_8472	scaffold892	26717	ATT/ATTT	TCAAGCTTCCTCTCCACACA	AATTAATATCCACGCAACGC	59.5	255	INTERGENIC				
CaPOPI_8473	scaffold892	29801	CAAAAA/CAAAA	GAGCCATGAAACCTTCCA	ATGCAACATTTCCACCTC	60.1	392	INTERGENIC				
CaPOPI_8474	scaffold892	33546	TTTCTT/TTTCTTCTT	TCCCAATTTGGTTTGGTGT	TGGAATCTTCACCTGACAA	60.1	713	DRR	Ca_27455	R		Sugar/inositol transporter
CaPOPI_8475	scaffold892	33776	TC/T	TCAAAAGACACCAATGGAAAA	TGGAATCTTCACCTGACAA	59.5	251	DRR	Ca_27455	R		Sugar/inositol transporter
CaPOPI_8476	scaffold892	38411	AATATATATATATATAT/AATATATATATATATATATAT	GTAATGGCAGGTAGAGGCG	ACCACTAACTCGGTGCCAAC	59.7	826	INTERGENIC				
CaPOPI_8477	scaffold892	42751	TGGGG/TGGGGG	GACGATGAAAAATATGCGG	TGTTGATTGGCGAACACAA	60.3	387	DRR	Ca_27456			
CaPOPI_8478	scaffold892	44352	TAAAAAAA/TAAAAAAA	CTGAGTTGCGACGAGAGTTG	TTGGAAGGAGCCCTTACCTT	59.8	465	INTERGENIC				
CaPOPI_8479	scaffold892	56842	TAAAAAAA/TAAAAAAA	CCCCCTTTAGTGGAAGTTG	TTGGTATAGGCGATTTTGGG	58.6	471	INTERGENIC				
CaPOPI_8480	scaffold8920	817	A/AAT	CATCAGGGTGCTTTGGTCCT	GGTACGAAATCGCCTGAAA	60.0	699	INTERGENIC				
CaPOPI_8481	scaffold893	6971	CATATATATATATATAT/CATATATATATATATAT	CTTTAACATGCGTTTCCGGT	TCAAGTCGACAAGCCTTCCT	60.0	819	DRR	Ca_27923		B3	
CaPOPI_8482	scaffold893	10885	A/AG	GAGATTGTGGCCAATTCGAT	CTCTACCCAAGAAGATCGC	59.9	395	INTERGENIC				
CaPOPI_8483	scaffold895	103999	TTTATTATTATTATTATTATTATTATTT/TTTATTATTATTATTATTATTATTATTATT	AGAGGCAACAAGAACCAGAA	GAAGGCTATGGTTGATGGGA	59.9	479	INTERGENIC				
CaPOPI_8484	scaffold896	47144	TAAA/TAAAA	AGGGAGGACGAAATGACCT	TGTGCATCAATAGGCGTGT	59.9	259	INTERGENIC				
CaPOPI_8485	scaffold898	27647	TA/T	TGTAATTGTATTCAATGGCAAAGA	CGTTATTAAGTACAACAAATAAACGAA	58.6	469	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8486	scaffold9	34748	CACAACAA/CACAA	GGACAACTACCCCTCC TTTTC	TCTTCCCCATAAACCA ACA	60.2	317	INTRON	Ca_27384		WOX	
CaPOPI_8487	scaffold900	12737	GCAC/GCACTAGTACAC	CCATTTTGTCTCTGCT CAT	AAGGCCAATGCCACATA AAG	59.9	604	INTERGENIC				
CaPOPI_8488	scaffold901	229595	TTATATATATATATATA/TTATATATATAT ATATATA	CCATTTTCAGCCGTGAT TTT	ACCTTGCTCCCTTACCC ACT	59.9	703	INTERGENIC				
CaPOPI_8489	scaffold9059	539	ATT/ATTT	TTAGGGCTCATACGATT CCG	GGAAATTAGCCACGGA TCA	60.1	443	INTERGENIC				
CaPOPI_8490	scaffold909	6733	AATATA/AATA	TTTCATCTGAACCTTTCG GG	TAGGGTGGTACGAAAT CGC	60.0	365	INTERGENIC				
CaPOPI_8491	scaffold909	21317	T/TA	CCCGACAAAATAGACC GAA	TGCTTGATTGCTTGAGA TCC	59.9	429	INTERGENIC				
CaPOPI_8492	scaffold913	140774	CAT/CATAT	TTGAGTTATGGCTAATG AAGGTCA	AGCGAGCCGCTCAATTA GTA	60.0	269	INTERGENIC				
CaPOPI_8493	scaffold913	161492	GTCTATCTAT/GTCTAT	ATGTGAAACGATGGTGG AAA	ATAAGCCAAGGGCCAAC TCT	59.0	464	DRR	Ca_23205		HD-ZIP	Homeobox
CaPOPI_8494	scaffold913	251896	C/CA	AGCGTGAAAGGCAAGTG AGT	CCCATGCAAGGTATGCT TTT	60.1	441	INTERGENIC				
CaPOPI_8495	scaffold913	252010	AGTGTG/AGTG	CCAAAAGTAGCGTGAAA GGC	ATGGGATTGACTTGCTC TGG	59.9	947	INTERGENIC				
CaPOPI_8496	scaffold913	252195	T/TG	ATGCGTGCCCAAGATTCT GTT	ATGGGATTGACTTGCTC TGG	59.6	668	INTERGENIC				
CaPOPI_8497	scaffold913	282492	ATTTT/ATT	TTGGATTTTCATCCACACA CATC	AAAATCCGTTGGAAATTT TGG	59.6	466	INTERGENIC				
CaPOPI_8498	scaffold916	3519	AATATATATATATATATATAT/AATATATA TATATATATAT	ACATCTCATGCCATTGT GGA	GAGACAGTCAGAAGGCC ACC	59.9	520	DRR	Ca_21034	G	E2F/DP	Major facilitator superfamily MFS-1
CaPOPI_8499	scaffold916	4344	GAAAAA/GAAAAA	TGTTGACGAATGTCCAT GAAA	CCTCCAAAACCACTA CCA	60.0	181	INTERGENIC				
CaPOPI_8500	scaffold916	4805	T/TACAATA	TGGTAGTTGGGTTTTGG AGG	TTCATGACATGCATCCAT CC	59.8	907	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8501	scaffold916	4868	GTTTTTTTT/GTTTTTTTTT	TGGTAGTTGGTTTTGGAGG	TTGATGACATGCATCCATCC	59.8	907	INTERGENIC				
CaPOPI_8502	scaffold916	5303	A/AT	TGTCTCTTTTACGCCGAAT	CTAGGCATTGCAACAGGAT	60.8	738	INTERGENIC				
CaPOPI_8503	scaffold916	7772	AG/A	TGTCCTTCTGTTCAATCAATAACC	TGGTGGTGCATAGTTGGTGT	59.4	636	INTERGENIC				
CaPOPI_8504	scaffold916	8185	TT/TTCGATTAAT	ACACCAACTATGCACCACCA	ATAGGCCCAATTAACCCAC	59.9	376	INTERGENIC				
CaPOPI_8505	scaffold916	8308	ATT/AT	ACACCAACTATGCACCACCA	ATAGGCCCAATTAACCCAC	59.9	376	INTERGENIC				
CaPOPI_8506	scaffold916	9278	CTTT/CTTTT	TCACATAGGGATTGCCACA	TCCCACCACATTCAATCCTT	59.9	769	INTERGENIC				
CaPOPI_8507	scaffold916	9496	TACTA/T	CCCATATGGTTGGGAATCA	TCCCACCACATTCAATCCTT	60.4	257	INTERGENIC				
CaPOPI_8508	scaffold916	9949	AAG/A	AGGATTGAATGTGGTGGAAT	GCAGAAAAATAAGGGCGATG	60.2	354	INTERGENIC				
CaPOPI_8509	scaffold916	10023	ACC/ACCC	AGGATTGAATGTGGTGGAAT	GCAGAAAAATAAGGGCGATG	60.2	354	INTERGENIC				
CaPOPI_8510	scaffold916	10051	CCCT/C	AGGATTGAATGTGGTGGAAT	TAAACAATTTGGGGGTCCTG	60.2	443	INTERGENIC				
CaPOPI_8511	scaffold916	10102	CTTTT/CTTT	CATGATAGACCATCGCCCTT	TAAACAATTTGGGGGTCCTG	59.9	119	INTERGENIC				
CaPOPI_8512	scaffold916	134889	TTT/TTATT	AAATGTGGTCTCGGTTTGC	TTGTTTTGTGAGTTTGAAATGATGTT	60.0	770	INTERGENIC				
CaPOPI_8513	scaffold916	363659	TAAAAATAAAAATTAAAAATAAAA/TA AAATTAAAAATAAAAATAAAAATTA AA	CCACCCTCTACCATGCAACT	TGTTTTCCATGTGTGCCACT	60.0	569	INTERGENIC				
CaPOPI_8514	scaffold916	429531	ATTTTTTTTT/ATTTTTTTT	TGCGTTCAATTTAAAGGTGTTG	TCGCCTCAAAACATCAAGAA	60.0	321	INTERGENIC				
CaPOPI_8515	scaffold918	49291	CAAA/CAAAA	TAGCGAGGACGAAAAATGACC	CGTCCTCCCTGGGTTTATTC	60.2	820	INTERGENIC				

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								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8516	scaffold919	73303	GCTTCTTCTTCTTC/GCTTCTTCTTCTTCTTC	CACCCCTCGCTTAGAAAAACG	TTTGGAGACCAATGGTGACA	59.9	878	INTERGENIC				
CaPOPI_8517	scaffold919	83832	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAA	GTTTGAAGTTGTCCGCTCT	GACACTTGCGCCCTATAAA	60.3	479	INTERGENIC				
CaPOPI_8518	scaffold92	45246	ATATTATTATTATTATT/ATATTATTATTATTATTATTATTATT	TGCAATAAACCATATAA CGAAGA	TGTTTGAATGCATAACGAAGA	57.9	438	INTERGENIC				
CaPOPI_8519	scaffold922	47157	ATTGTT/ATT	AGAGGAGGTGATGGTGTGG	TTTTGGTAATTGTTGGTTTATTCAA	59.9	357	INTERGENIC				
CaPOPI_8520	scaffold924	202228	TTATATATATATATAT/TTATATATATATAT	AGGAAGAGTGGAGTTGCGAA	CAGGTTTGATGCAACCATTG	60.0	689	INTERGENIC				
CaPOPI_8521	scaffold9240	617	ATTTT/ATTTT	TTTAGGTTCATTTTCGTGCC	CCTTTGGACGCACAAGATT	60.1	476	INTERGENIC				
CaPOPI_8522	scaffold9247	528	GATATATATATATATATATATAT/GATATATATATATATATAT	CAACCATTGAGCCTTGGTTT	CGTTTGTGAATATCTGCTCA	60.0	562	INTERGENIC				
CaPOPI_8523	scaffold9281	4465	CAAAA/CAAAA	TGATCAAAGCAACAAGCTCA	ATGTGCAGTCTGAGCTACCG	59.6	316	INTERGENIC				
CaPOPI_8524	scaffold929	17042	TA/TAA	GCAGGAGCAACAACAGATGA	AGGCTTAATTGCACTTTTGG	60.0	444	INTERGENIC				
CaPOPI_8525	scaffold929	20949	AA/AAACA	GATGAAATCGAGGACCA GGA	GATGAAATCGAGGACCA GGA	60.0	133	INTERGENIC				
CaPOPI_8526	scaffold93	6623	TAAA/TAAAGGAAAA	GGATCGTAATCCGTGGGTAA	GAGAGAGCGATCATCAAGGC	59.6	415	INTERGENIC				
CaPOPI_8527	scaffold93	116733	CATATATATATATATAT/CATATATATATATATATAT	AGGAAGAGTGGAGTTGCGAA	TTATGATTTGGCTCGGAGG	60.0	505	INTERGENIC				
CaPOPI_8528	scaffold93	141155	CAA/CAAA	TCGATTGGCTTAAACCAAGG	AGAATTTACGAGCAGCGGAA	60.1	617	INTERGENIC				
CaPOPI_8529	scaffold93	338023	TCCCC/TCCC	AAACTTGCAAGCCATTC CAG	TTTGAGAAATATGCTGGGC	60.2	876	INTRON	Ca_23073	L	GRAS	
CaPOPI_8530	scaffold9303	1186	CT/CTT	AAGACCACATCATTGTGTCACC	TGTTTGTTCGCTCTTAATTTT	59.8	439	INTERGENIC				

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CaPOPI_8531	scaffold9303	1378	TAAAAA/TAAAAA	AAGACCACATCATTGTG TCACC	CAATGGAGGTTTTCTTG TGA	59.8	713	INTERGENIC				
CaPOPI_8532	scaffold931	100930	A/AC	TTTGAGCCCCCTTCAAT ATG	GATTCTCCTTGGGGATG GAT	59.9	616	INTERGENIC				
CaPOPI_8533	scaffold931	116282	GTTTTTTTTTTTTT/GTTTTTTTTTTTT	TCAGTTGCAATTTCTTC CC	TAAACCGATTGGGAG TCG	60.1	519	INTERGENIC				
CaPOPI_8534	scaffold931	116416	ATTT/ATTTCCCTAGATGCTCTTT	CGACTCCCAATCGGTT TTA	TTGGGCTGATGCAATAA ACA	59.9	260	INTERGENIC				
CaPOPI_8535	scaffold931	116537	ATT/ATT	CGACTCCCAATCGGTT TTA	TTGGGCTGATGCAATAA ACA	59.9	260	INTERGENIC				
CaPOPI_8536	scaffold931	117076	CAA/CAA	TGCCACAACCAATCTTC ATC	AGACAGTGGGTGTTCCA AGC	59.5	391	INTERGENIC				
CaPOPI_8537	scaffold931	118275	GAAAA/GAAAA	TGCTCTGACTCATTCAA CCG	CACCAACAATTGGCATC AAG	60.0	725	INTERGENIC				
CaPOPI_8538	scaffold931	180349	GATATATATATATATA/GATATATATA TATATA	TCGTCCCATGTAATTG TCA	TGGATACCCAAAAACCA TTCA	59.8	281	INTERGENIC				
CaPOPI_8539	scaffold931	181299	G/GTT	GTAGAGTGCCAACGACA CCA	TGAACTATTGATTGGAT CGTGC	59.8	665	INTERGENIC				
CaPOPI_8540	scaffold931	246666	TTATATATATATATATATAT/TTATA TATATATATATATAT	GGGTGTCACATCACCC TTT	GCGGAAGACTTTATAGT GAAAGGA	59.7	191	INTERGENIC				
CaPOPI_8541	scaffold931	250258	CATATATATATATA/CATATATATATATA TA	GCCACCAATTCCAGACA CTT	TTGATTGGATCGTGCAG AGA	60.0	791	INTERGENIC				
CaPOPI_8542	scaffold931	251946	GAAAAA/GAAAAA	TTGACACCCTAAACCC AAA	AATGGGCGCTGTTAAAT GTC	60.2	177	INTERGENIC				
CaPOPI_8543	scaffold9314	650	C/CATTAT	TAAGTTGTCTGGGGAG GTG	GTTTGGGATCGGAATTG AAA	60.0	463	INTERGENIC				
CaPOPI_8544	scaffold933	3249	TA/TAA	TTGTCTCTTGACATTC CCC	TTTTCCAGTGCACCTG TGA	59.9	548	INTERGENIC				
CaPOPI_8545	scaffold933	4208	GTTTTTTTTT/GTTTTTTTTTT	TCAAACCCAGTGGTCTC CTT	AGTCCGATGAAGGGTCA CAG	59.5	654	INTERGENIC				

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CaPOPI_8546	scaffold9371	631	TTTTT/TTTTGT	GCGGCTGAAAGAGAGAGA GAGA	AAAGATTTCCGGTACAC ACCA	60.0	687	INTERGENIC				
CaPOPI_8547	scaffold939	1093	ATTT/ATT	GTGACGTTGGGGGAGTT AAA	TCGAGCCTTATGGCAAG ATT	59.8	317	INTERGENIC				
CaPOPI_8548	scaffold9411	2770	A/AG	TCAATAGACCGATATGG GGAA	GAAGCATCTCCAACAGC TCA	59.2	838	INTERGENIC				
CaPOPI_8549	scaffold9411	2893	TAAC/T	GGATATGTCAGAAAAGG AACGG	GAAGCATCTCCAACAGC TCA	59.8	393	INTERGENIC				
CaPOPI_8550	scaffold943	141649	AATATATATATATATATATAT/AATA TATATATATATATATATAT	AAACCGGTTAAATCTCC GCT	TATTTGGATTTTGGCTC GG	60.0	703	INTERGENIC				
CaPOPI_8551	scaffold943	163051	ATTT/ATT	TGGCAAATCGATTGAAA CAA	GTGCCAGTCGATTGCCT AAT	60.1	516	INTERGENIC				
CaPOPI_8552	scaffold943	267949	CAC/CACGGAATGAATTAATGAAC	AATCACGTTTGTGGAA AGC	CGTCCAGTCCCGAAAT AAA	60.0	544	INTERGENIC				
CaPOPI_8553	scaffold944	672	ATTTT/ATTT	TTGTAAGTTGAGTTGCG ACGA	TGTGGTCGCAGGTTTTA TGA	59.5	308	INTERGENIC				
CaPOPI_8554	scaffold944	2389	CAAAAAA/CAAAAAA	GAACGGAAATATTCAC GTCAT	TCGGACCACACTCCTAA TCC	60.1	495	INTERGENIC				
CaPOPI_8555	scaffold944	2557	TG/T	GGATTAGGAGTGTGGTC CGA	CAACTGGGTACCACTAA GCCA	59.9	450	INTERGENIC				
CaPOPI_8556	scaffold944	3122	GAAAAAAA/GAAAAAAA	TGGCTTAGTGGTACCCA GTTG	TGGCGCTTATATTCAAA GCA	60.0	643	INTERGENIC				
CaPOPI_8557	scaffold944	3226	GTTTTTTT/GTTTTTTT	TGGCTTAGTGGTACCCA GTTG	TGGCGCTTATATTCAAA GCA	60.0	643	INTERGENIC				
CaPOPI_8558	scaffold9444	2167	AAGTTAACTGAATGAGTTAACTGAAT GA/AAGTTAACTGAATGA	TTTAAGTCAAGGTTTAGA AAGAAACA	TTGAGTAAGAGAAGGAA AGCAAAAA	57.1	572	INTERGENIC				
CaPOPI_8559	scaffold945	2482	CATATTCTGTAATAAGTAATTT/CATAT T	AAATCCGTTTGATTG CAG	TCCAGAAAAATCGTTT AGG	59.9	428	INTERGENIC				
CaPOPI_8560	scaffold948	113626	ATT/ATTT	TTTGTGGCTTGAATTGG ATG	CATGCTCACTCCCACTG CTA	59.5	174	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8561	scaffold948	136923	TAAAAAAAAAAAAA/TAAAAAAAAAAAAA	TGCTCAATAGGAATGG CATC	GGCATGCACGTTTACAA CAC	60.1	484	INTERGENIC				
CaPOPI_8562	scaffold949	3822	CAAAAA/CAAAAAA	AAGAGGGGCGTGAACCT TTT	GCTTCATACCTGTTTT GGG	60.1	646	CDS (FRAME SHIFT)	Ca_25481			Photosystem antenna protein-like
CaPOPI_8563	scaffold949	12574	GTTTTTTTT/GTTTTTTTTTTT	TTGGGCCATTGGATAA TGT	ATGCACACGATTGGTTG AAA	60.0	589	INTERGENIC				
CaPOPI_8564	scaffold949	26559	GTT/GT	AGGTCATTTTCGTCCTC CCT	TCCAATGACACCAACAC ACC	59.9	692	INTERGENIC				
CaPOPI_8565	scaffold953	17853	T/TG	AAGGATAGGTACGGGTT GGG	AAATTGAAATACATGCG CCC	60.1	381	INTERGENIC				
CaPOPI_8566	scaffold953	37096	TAA/TAA	TGCAAGAACCCTCCTC TAT	GCGTGTGGATGCAAAAT ATG	60.0	305	INTERGENIC				
CaPOPI_8567	scaffold953	39457	CTTTTTTT/CTTTTTTTT	CATGTTGTGACAATTG GTGG	CGTGAGTTGGTGTGAT TCG	59.7	812	INTERGENIC				
CaPOPI_8568	scaffold953	44175	ATTTTTTT/ATTTTTTTT	GCATGCATGTTGAGGTC ATT	TGGATGGGTAGATGTG TGTT	59.5	494	INTERGENIC				
CaPOPI_8569	scaffold953	44845	CTTTTT/CTTTTTT	CAGGGGAGACTACAAC TGC	GGCGGATCTTGACATGT TTT	59.7	272	INTERGENIC				
CaPOPI_8570	scaffold953	69667	GA/GATA	TGGATAAGGTTTCCAC GAG	TCGTTGAGAGCGTGT GTC	59.9	650	INTERGENIC				
CaPOPI_8571	scaffold953	75360	GAAAAAAAAA/GAAAAAAAAA	TCAATGGGATTCCTTCT ATGC	CACCCTCGCTTAGAAAA ACG	59.0	762	INTERGENIC				
CaPOPI_8572	scaffold953	135204	CAGAAGAAG/CAGAAG	TTGCAAAATACCCCC AAT	TGGCGTCATGTCAAGAG AAG	60.0	403	INTRON	Ca_26911		MYB	Protein of unknown function DUF3741
CaPOPI_8573	scaffold953	142447	ATTTTTTT/ATTTTTT	GCACGTGCACCAGAAAA ATA	GCCTCCGAGTTCAATAC CAA	59.7	505	INTERGENIC				
CaPOPI_8574	scaffold954	3708	GA/G	AGGTCATTTTCGTCCTC CCT	TGGATGCACGAGATTGG TTA	59.9	568	INTERGENIC				
CaPOPI_8575	scaffold956	19709	G/GCTTCTT	TCCAGATGAAATCGAGG ACC	GGATTAGCCTTTTCGAGT CCC	60.0	381	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8576	scaffold959	57749	GAAAAAAAAA/GAAAAAAAAA	AAGGCGTGCATATCCCA TAC	TGTTCTGCAAAATGTCC CAA	59.8	553	INTRON	Ca_27234		Trihelix	Peptidase C48, SUMO/Sentrin/Ubl1
CaPOPI_8577	scaffold96	192974	ATTATTTATTTATTTATTTATTTAT TTATTTATTTATTTATTTATTTATTTA TTTATTTATTTATTTATTTATTTATTT TATTTATTTATTTATTTATTTATTT	CTAGTGGGTACCCGCAA AAA	AGTCGGGAAGACAATGA TCG	60.0	388	INTERGENIC				
CaPOPI_8578	scaffold960	20793	ATTTT/ATTT	TACGGTGCTAGGGAAC AAC	CAAGGCTGTTTCAGCAT TCA	60.0	845	INTERGENIC				
CaPOPI_8579	scaffold962	157050	AATATATATATATATATATATATATAT ATATATATATA/AATATATATATATATATA TATATATATATATATATATATATATA	AATCGATTGGCTGAAAT CCA	TAAACACATGCGCTTCC AAA	60.4	564	INTERGENIC				
CaPOPI_8580	scaffold962	214783	TT/TTCAT	GGATGCTTCAATGTG TGC	ATACGCGTTTTAATTG CG	59.1	687	INTERGENIC				
CaPOPI_8581	scaffold963	17319	AATATATATATATATATATATATATAT ATATATATATAT/AATATATATATATATAT ATATATATATATAT	CCGGGGATAATGGCTTA AAT	GGGGTATGCATTTGTG GAC	60.0	429	INTERGENIC				
CaPOPI_8582	scaffold964	79837	TATTAATAA/TATTAATAATAAATTAATA A	TTGAAGGTGCAATGCCT TTA	GCATGAACAGCAACGTC AAC	59.3	469	INTERGENIC				
CaPOPI_8583	scaffold9757	838	TAAAA/TAAAA	TGTTAATCCAACGGCAC AAA	TCCCCTGGCTTATTGTT GTC	60.0	279	INTERGENIC				
CaPOPI_8584	scaffold977	6872	GTGATGATG/GTGATGATGATGATG	CGTATTTCCAACGATC CAT	ACGAGGTCGTACCAACC AAC	59.6	637	INTERGENIC				
CaPOPI_8585	scaffold98	168374	CAAAAAAAAA/CAAAAAAAAA	CGTCAAAGAGGATTGA TACCAC	CGTCTTGTTATGCCATT GTTG	59.9	436	INTERGENIC				
CaPOPI_8586	scaffold98	241916	AATATATATATATATATATATATAT/AA TATATATATATATATATATATATATAT	ATTTGGGGTTTAAGGGT TGG	AACAAACAAAGAAAAGC AAGGC	59.9	663	INTERGENIC				
CaPOPI_8587	scaffold98	379604	AAGTTTTA/AA	TTGCGATGGTAAGAAGG GTT	ATTCTTGAGCCGATCA ATG	59.6	349	DRR	Ca_21386	OE	WRKY	Peptidase S10, serine carboxypeptidase
CaPOPI_8588	scaffold98	474976	TAA/TA	GAGGAAGGGATTTGGT GGT	GCAAAACCCACGTAAGT GCT	60.2	400	INTERGENIC				
CaPOPI_8589	scaffold981	9701	GAAA/GAAATCCTAAA	TCCCAAATCACTTAACC CGT	TGGGGTTTAGGGTTTCA CAA	59.3	555	INTERGENIC				
CaPOPI_8590	scaffold981	10301	GA/GAAA	ACCCGAAACCTAAACCT CTT	GGTTTAGGCGTTAGGGT TGA	58.9	300	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8591	scaffold981	10911	CGAAACCTGAAACCTGAAACCTGAAACCT/CGAAACCTGAAACCTGAAACCT	AACCCGAGAACCAAAATCCT	GTTTCGGGTTTACGGTTCA	59.8	326	INTERGENIC				
CaPOPI_8592	scaffold981	84130	AT/ATCTTTTCCTT	GATGGAGAAGCACCGGATTA	CTTGCTAACCCACAAAAGCC	60.0	110	INTRON	Ca_27591	U		Endonuclease/exonuclease/phosphatase
CaPOPI_8593	scaffold981	84325	AATATATATATA/AATATATATA	GAAGCAGTCCCATGTGGTTT	TCACCTTTCACCATTCACCA	60.0	981	INTRON	Ca_27591	U		Endonuclease/exonuclease/phosphatase
CaPOPI_8594	scaffold9813	1199	GAAA/GAAAA	AAAATCGCGCGAAAAGTCTA	TCCTGGTCTCTCGATTTCA	60.0	772	INTERGENIC				
CaPOPI_8595	scaffold982	874	ATT/ATTT	TTGGATGGAGTGCCACAATA	AACTTGGGTTGAAGATGAAGA	59.9	164	INTERGENIC				
CaPOPI_8596	scaffold982	1298	CTTTTTTT/CTTTTTTT	TTGGATGGAGTGCCACAATA	TTTCCCGACTTGGTCCTTTA	59.9	727	INTERGENIC				
CaPOPI_8597	scaffold982	1547	GAAAAAAAAA/GAAAAAAAAA	TTGGAGAGGAAGATGAAAAACC	GGCTAATATATCCGTGGTCCC	59.6	461	INTERGENIC				
CaPOPI_8598	scaffold982	14935	CT/CTAACTCTCGTAACAGT	GTCCATAGTCTTGCCGGTGT	GCGATGAGTTGGATGGAAGT	60.0	632	URR	Ca_28025		G2-like	Peptidase S8/S53, subtilisin/kexin/sedolisin
CaPOPI_8599	scaffold983	71344	ATT/ATTT	TATGATGGATCCTCCTTCGC	TCAACCCTAAGGCGAATGTC	60.0	377	INTERGENIC				
CaPOPI_8600	scaffold983	88220	T/TG	CACCCACAAGGAGGAAGAAC	CATGGATCAAACAGGCTTCA	59.5	517	INTERGENIC				
CaPOPI_8601	scaffold983	88456	AGTG/AG	TTTATTCGCATGTTGTTGCC	CATGGATCAAACAGGCTTCA	59.6	274	INTERGENIC				
CaPOPI_8602	scaffold983	88622	A/ATTGTTG	TTGGTCCTACCAGACCAAGG	TCCGACAATTTGTGCACATTC	60.0	458	INTERGENIC				
CaPOPI_8603	scaffold983	142002	AG/ACATAAAGG	GGTTGTTACAAAGCCAAATTGAA	ACGGGTCTGCACGATTTACT	59.0	905	INTERGENIC				
CaPOPI_8604	scaffold983	169332	GTTT/GTT	AAATCCGTTTGATTTCAG	TTTCAACAGCGTCAAGGATG	59.9	535	INTERGENIC				
CaPOPI_8605	scaffold983	255175	GTTTT/GTTT	TTACCGGATTACTCACGGC	ACCCGTCAAATACGACGAAC	60.0	319	INTERGENIC				

INDEL marker IDs	Chromosomes/unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDCC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (°C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8606	scaffold983	267429	GTTTTTTTTT/GTTTTTTTTT	CGGTTTTGTCCATAAGC GAT	ACATTGCCAAGTTCGTA GGG	60.0	371	INTERGENIC				
CaPOPI_8607	scaffold984	143777	CTTAATAATGTAATTAATAATGTAAT/CT TAATAATGTAATTAATAATGTAATTAATA ATGTAAT	AGCGATTTTGAACCAC CTG	AACAATCTCCCCCTTTT GG	60.1	539	INTERGENIC				
CaPOPI_8608	scaffold99	78741	GATATATATATA/GATATATATATATATA TATATATA	TATTTGGATTTTGGCTC GG	AAATGGAGGAAGGAGG GAGA	59.9	611	INTERGENIC				
CaPOPI_8609	scaffold992	36461	CATATATATATATAT/CATATATATAT ATATATAT	AAATTGGTCCACTAGCA CCG	TGCGTTACGTGTGAAAT GGT	60.0	475	INTERGENIC				
CaPOPI_8610	scaffold992	36900	ATT/AT	ACCATTTCACACGTAAC GCA	GCCAGGTGCACTAAGGT TGT	60.0	598	INTERGENIC				
CaPOPI_8611	scaffold992	37820	ACTC/ACTCTTTCTCTC	GCACCTCATAAACGAC GGT	AAAGAGCCAAGAGGCAT CAA	60.0	349	INTERGENIC				
CaPOPI_8612	scaffold992	40484	CA/CACCGA	TCAATGCCAAACATGC AAT	TTCGGATGTCCCTTAA ACA	59.9	513	INTERGENIC				
CaPOPI_8613	scaffold992	42011	CT/C	CAACCTTAACGCACCGT ACC	TTTGTTCAATTCATGCT CCC	60.4	563	INTERGENIC				
CaPOPI_8614	scaffold992	42112	GAAAAA/GAAAAAA	TCGATAAAAGCAACGGA TTG	AGGGAGAAAGACAGATG AGTGC	58.8	676	INTERGENIC				
CaPOPI_8615	scaffold992	42301	CTCT/CTTTCT	GGGAGCATGAAATTGAA CAAA	TCCTTTGCGTCTGAATTT GG	59.9	708	INTERGENIC				
CaPOPI_8616	scaffold992	46266	GTTTTTT/GTTTTTTT	GCTTGGGGACAAGCAAT AGA	CCCAGTTCCAAGAGTC AAA	60.2	393	INTERGENIC				
CaPOPI_8617	scaffold996	37798	GTATATATATATATAT/GTATATATAT ATATAT	CGCTGTTGAATCAATG GTG	GAATCAAGTGGGGAGG GAAT	60.1	323	INTERGENIC				
CaPOPI_8618	scaffold996	44276	TAAGAAGA/TAAGA	CGGTCTTCCGTGAGTA ATGA	TGAATAAACTGCGCGTA TGTG	60.1	561	INTERGENIC				
CaPOPI_8619	scaffold996	87555	GTTTTTT/GTTTTTTTTTTT	TGGCGTACTGAGAGCTG CTA	TGTGCACCGGAAACTT GTA	59.9	435	DRR	Ca_25583			
CaPOPI_8620	scaffold996	113638	AAATAATAATAATAATAATAATAATA ATAATAAT/AAATAATAATAATAATAATA ATAATAATAATAATAATAAT	CAGTTAACGCTTTGAG TGCG	GGGGATGCGACCATCTA CTA	58.6	689	INTERGENIC				

INDEL marker IDs	Chromosomes/ unanchored scaffolds	Physical positions (bp)	InDels (<i>Kabuli</i> reference genome-CDC Frontier/PI)	Forward primers (5'-3')	Reverse primers (5'-3')	Annealing temperature (0C)	Expected amplified product size (bp)	Structural annotation		Functional annotation		
								Sequence components of <i>kabuli</i> genome	<i>Kabuli</i> gene accession IDs	NCBI-KOG	TFs	NCBI-nr database
CaPOPI_8621	scaffold996	203068	TTATATATATATATATATATATATATATATATATATA/TTATATATATATATATATATATATATATATATATATATATATATATATATA	TGGTGC GTTAAGCATGA AAC	TGTGTCCTGTTGGGAA CAA	59.7	398	INTERGENIC				
CaPOPI_8622	scaffold999	77364	A/AT	AGGAAGAGTGGAGTTGC GAA	GGATCAAGGCAGTGGAT TGT	60.0	854	DRR	Ca_28108			Photosynthetic reaction centre, L/M
CaPOPI_8623	scaffold999	123867	CT/C	CCAAATGTTATGATCACT ATGCC	TGCGAAGAAGCTCACTT GAA	58.4	734	INTERGENIC				
CaPOPI_8624	scaffold999	130386	TG/TGG	TGTAACCTGCTTGCAC ACC	CTGCACAACAATCCAC AAC	59.8	160	INTERGENIC				