

Supplemental Table 1. A list of primers used for the SNP genotyping in this study

Chr.	Position (bp)	SNP_marker_name ^a	Forward-primer_seq	Reverse-primer_seq	SNP_primer_seq ^b
1	590339	SP-1177Ct	GTAGGTGCAAAGTGTGCC	CAGCATGGTGTACCAGGA	CTCTTTAGGGTGTACCATG
1	1946270	SP-155Tg	TCTCCTTCCAGTCGATGC	TCCCAAATCGCCCTCTTTGC	AGCGACATGGTTGCTCTA
1	6522242	SP-2077Tc	CCTAATGGGCGAATTTATAACG	GCGAAAGGCGAGGTTGATG	CAAAGTAATTTGGGATCTTTAC
1	8896815	SP-185Tc	GATGTACGTCGGACTATTCATC	CGACGTGCATGCTCATTAGC	TTAAACATATGTCCAAAGTCAA
1	11026011	SP-192Tg	TCCCTGCTGCTAGGATCTTG	ATCCATCAAGTCAGCAGGTG	GCTGTGAATGGATGCCAA
1	14312329	SP-5191Tc	GCTATCATTGGCTAGAACACAC	ACGGAGTTCCAGCGAATGAG	GATCGATCTTCATTAACCTCAATCT
1	17803741	SP-1208Tg	GAGGCCATTCTCGCAAC	ATCGACCGAGCATTCTAGC	TCACTCTCTCACCGATC
1	20366961	SP-2016Tc	GCTAGAACTAATTCGCAGTAGAG	CAATCTCGGCCACAATTACATAG	CACCGCCACTCAATTTAC
1	24412981	SP-1217Ct	CTCCAGTGATGTTTATTTTCGTCC	CTAAACAGGTTGCATTTTGGTGC	TAAGTGTGGACTTATTTTATCA
1	25979477	SP-2478Ag	GTTCCAGATACACCATACGG	GCCTTAATATGGAGGAAAGCG	TAACCTCGGTTCCAGGAATC
1	27840561	SP-242Ga	AGCACGGCTATGTAAGACTAAC	AGAACGTCATCGACAGCATG	TGGACCAAACTTCACTTAGTA
1	31371175	SP-262Ga	GCAGCAGGACAAAGGCTAAC	ACCCTTCTTCAAGCTCCATC	TCACAACCGGACCAGATGAC
1	35598472	SP-1244Tc	CCTCCATTGATGTCGGTCA	AGCAGCCCAATTATCTTTGGAC	GGATATATTCACTCTTTTCACT
1	39677014	SP-2056Gt	TGCTGGTGAAATGTGGGTAG	CTCTGCAACCAACATTGCAC	CAACAAGCACACAAGATGAAA
1	42000585	SP-2079Ta	AACTCACCGCTGGTAGGAG	GGCCAAGCCCACTTAATCC	CACACCAATGGAGGATTGT
2	151976	SP-3541Gt	GAGATGGCGTGAGTACTAAG	GTGTAAGGTGGCTTATAGC	TAAATCGGGCACTCTTTGTT
2	1758809	SP-3547Ag	TAGTTGCCTAACCAAGTAGGC	CAATCCAGATTCATAGCCAGAG	GATTGACTACTTCCTCAATTTTC
2	3922571	SP-1387At	CCAAACCAACCGCTTCCAC	CCGCTTTATACACCCGCATC	ATGCGCGCTTTTCTTTCTTT
2	7030897	SP-1398Gt	CAACAGCTGTGCAGCAGTTG	ACTTTCTGAAGGCGCCTGC	GGTTTGGTTGATGAACTAGCT
2	9256584	SP-29Gc	GGACAGGAACAAGAGAATGTG	AAGATGGTGAGACAGGGAGA	GTAACAGTTGTCTGGCTA
2	12146325	SP-33Gt	GCATGTGTCACATGGTTCTAAC	GGATGTCATGAACCCATCAC	TTGATTTTGAGGTAGCTTTG
2	14655638	SP-1413Tc	CCTCATTGGACGGTAAACGC	GATCTGCTGTTGGTGAAGCTC	ATCCACCACCTGGATG
2	18881343	SP-3783Gt	GTCCAGATCAGTGTGAGTGC	ACCTTTGAACCACTGCAACC	TTCTGCATTTTCGTTGTGATG
2	22086348	SP-954Tg	GCAGCAAAAGGTTAACGACC	GCCTGCTGCATTCTCTAG	CACATATATAGGTAATTTTATGGA
2	25263253	SP-2941Ct	GTACCATGGTTGCTAAGTTGG	CACTACACCAACCTTCTGAC	GGCTACCAACCTCATTTTTC
2	27919903	SP-1444Ag	ACCACACAACAAGACTCAGG	GTACGGCGTCATGAATGATC	AATTTGTCTGCTCTGCTCT
2	29345357	SP-1450Ga	GGAACAACAGTCCAGGCTGA	TGAAGCATGGACATGTACGG	ATTGCTGGAGGCTCACAT
2	31272546	SP-1461Ca	CTGACTGCATTTGCTTTGAAGC	GGATGGTTCATCATCTGGTC	GAAGGAAAAGTTAAAGGATGAT
2	33189264	SP-1471Ta	TGGTGAGGGATGATTCATCC	GTATGGCAGTATGCTGGTTC	GCAAAGCAGTTACATATACT
2	35267219	SP-3571Ta	GAAGGCAGCCAGATGAGC	CACTCGCTCTGTATCAATTGG	CTCATCTCCTGGCTAATATC
3	577726	SP-111Ag	GCGTCGTGGATGATGACG	GCCTCCTCTTCGGCTTCG	GTAGACCTCGTCGTAGGA
3	3979349	SP-1289Cg	CATGCAAGAATTGACCTGGC	GCTTAACACTGACGATCGGATC	GGTCTCGGAATTCACCT
3	6660541	SP-1302Ct	GTAGAGCCGGTAGATAGTC	TCAAACCGAGCGGTGAAC	GATGCCTCACTTTTTACAGA
3	8780254	SP-1311Ga	TAGGTAATGCTCCGCAAGTTC	CTTGACCTGCCTTAATGTGC	AGAGCATGGAACAGGACA
3	11073623	SP-1323Ta	CTATGGAAGAAGCTGCATCG	CATTGATGCATTGATTGGGAGAC	GATTGTTGAGCGATTTTCGAG
3	13984287	SP-1331Ga	CAATTGTTTCATCGGCCTCAG	TGCTGCAAATGGTGAAGTGC	CAGTATGTGATCTAGAGAAAAAC
3	15737302	SP-294Ct	GGCACGGATCTGATACAAG	TGCAGTTCCTGTGCCATCG	GAGCTACCCAGAAATTTAGC
3	19071470	SP-3143Ag	GATCTGCTTAACTCCAGTGC	GACATTGGCTCGGTTTAGAG	GTGGTTTCTTTGTCTTTATTTCTT
3	22287129	SP-306Tg	CATATTCTACAGCGTTCTCGTC	AACACCAAGGGCGATCGAG	ATACCGAGCCCAGCAAT

Chr.	Position (bp)	SNP_marker_name ^a	Forward-primer_seq	Reverse-primer_seq	SNP_primer_seq ^b
3	24488442	SP-3148Ac	GTCTGATCGATCGAGCAATC	TGCACAGTGGATTACGCTAC	TGTCCAATGCAACATCTCC
3	26352992	SP-3135Ag	TAGCAACTAGGACAGATGGC	CTCAGTTCATCATCAGGTTAC	GATGTAATCCGCAAACACTGCATA
3	30021442	SP-1355Cg	CCTAGCAGCAAGATATGAACTG	GCCTGAATTCTGCAATACATTGC	CTATGGATGGATCCAGACA
3	31580078	SP-334Ct	GCGTGACATATAGCAATTCCG	GGTGTTCATCGCCATTAATGG	GCAATTACGACTCACGAATTCT
3	33640115	SP-348Ga	CCAGAGAACCCTTTTATGTACAG	CCGAGACATGATATAGTAACAGC	ATTGGATTTTCGCATTTTTCG
3	35945011	SP-362Tc	CTGTGGTTAGCTCCTAAGGC	AGTCAGGACTCAACTCAAGC	TCTACAGCGCAGATTTCGG
4	218809	SP-2590At	CTACACATTAGCTCGCTGGA	CACTGCACAACAATCAAGATCAG	CCATTACTTCTATACGTGATA
4	2471151	SP-2595Ga	GCCAAAACACTAGTGAGTGAG	CACCACAATGAGGTATCCATC	CATGTTTTTGTGCATCCTAGTT
4	6456488	SP-372Ct	CTGACAATTGATGCAGACGC	CTGCAGACTCCTTCTAAGC	CGTGACCTCATTCTCTGAAA
4	8285219	SP-3233Ag	CAAATGATTGGAGACCAGGAC	GATGGCATATCTCGTAGGATG	GTTATTTAGCTCATAATTTGCC
4	11949079	SP-375Tc	GCTTATTCTGACAGGTTGCC	CATATGACTGATTGGATGGAGC	TCCAGGTCTAGCTTATTGC
4	19650008	SP-386Tc	AGTGCCTGTCAGGATCAG	GGATTCAACTGACGAGTATTGC	GTAATCTATCTTGATGGAGTATTA
4	23043128	SP-3269Tc	CCTTAAATTAGCAGGACCTGTG	GAAAACCGCTAATTGACCTCAG	AATAGTCAGTAGTCACCTGC
4	25877141	SP-402Ga	CTTGGTTCATTTCTCCAGAAG	CATAACTGAGCACCTTGGTG	CTCTTAAACAACACTTTTGGCA
4	28349285	SP-409Ac	CAGAGCAAATTGGCTGCC	GTATGGCACCATGCTTATCC	CCATTTCCACAACCTTTAGTTTG
4	32342809	SP-423Ga	AAGGAGAGCTTTGAGCACG	GGATCAACTTGCTTCAGCTC	CTGGAGGGTGTGCCTTC
4	34498729	SP-436Ct	CTCAGTAAGAAGGCACTCG	CTTGTAGCTAGCGCTTGTC	CTCTGAATGTATCAACCAACATA
5	40031	SP-487Ag	CCTTGATCGAGTTTGAGCTG	CCCATCAACCATGATTCCAC	ACATACCGTCCCTCCTAC
5	1047930	SP-495Tc	CCAGTCAAAGCCTCAGACC	CTCTCAATGCAAGGTCTGAC	AGGATGACAAGGGCGATTA
5	3173133	SP-505Ct	ACAAGATCCTCAAGCATGGC	CATTCATGAACACCGCGTTC	CAATGTACTTGAAGTTCGCTCAT
5	5073404	SP-516Tg	CTTGGTATAAAGCCGGTGTTT	CCAACGTCGAGGTCTGAAG	AATTGCAGTAGCCCTGCT
5	7305956	SP-1526Ga	GGTGATGCATGACCTAGG	CCACCTTGCTGGTGATCA	GCTCAGCTGAGACTTGT
5	12908872	SP-526Gc	CCGACCGTCATTGTGTAGTG	GTTCTGGCCAATATGGCTTG	AGTCATCTTGGCCAACAGTT
5	15459785	SP-1537Ac	CAATGATGCCAGGTCTGACAT	TATGCAGGACACTCTCCATG	TGTACAGTCAATAATGCACTTG
5	18878114	SP-1546Tc	CTGCTTGAATGATTCAAGTGGTT	GTACCGTAGTTGAGCATTGATG	TGACCAGCAAATCTGGGA
5	21331373	SP-548Tc	CTGTTAGGTGGTAGTATTAGCC	AACCGAAGACATGGATTTCC	CGGAAAGCGGCGGAGA
5	24581478	SP-563Ct	ACTTGAGAGCCATGGACTTG	AGCTCACTGAGAGTAAGTGC	CAAGAAGTTAGCTTGTCTGGA
5	26499154	SP-1573Ag	CATGTTACGTAAGAGCACATG	TCAGTCACTCCGGTATCG	CCACAACACAAAATAGCATTAGTTTC
5	28699770	SP-3325At	CTCTGGCTGCAAGTCATCAC	CTTCTGAGGATGATTCCAGC	ACACATACCTTCTTGGGAGT
6	372258	SP-590Ag	CAAGTTCATGTCAAGCTCGG	GATGGAGCTTACAGCCAG	TGCCGCCAGGTACATG
6	2584447	SP-2505Ag	TCGTGGAGCTATGTCTGGAG	GTGGATGGCACACATTAATACAC	TACCACTAAACCATGCCTAG
6	4185220	SP-600Ct	GGACTGTCACTATCATAGGC	CGTCTGAAACTGTGCAATGTAC	CACTATCATAGGCACGTTTC
6	6290821	SP-2510Ct	GCCATGTAACACAAACAGTGG	TGGTGCTGGTACAGAATAACC	ACAATTTTCCGACATATCT
6	7554759	SP-611Tc	CTGAAGTATCCTGCTGACC	CTCCCTGAAGATATGCAACTTG	GTGTTGCCATTGAAACTGTG
6	10671175	SP-1603Tc	CCTAGTCCCTAAAGATCTCATG	GATAGACTGACGAGAGAAGTG	GGTGGTGTATCTCTAGT
6	13689109	SP-3005Ct	CTTCTGAGTGAATCGACGAC	ATTTGCTCTGGTGGAGATGG	GGTATTAGCTAAGCAATCACA
6	16525923	SP-2270Ta	CCTAAACAGAAGTGCCAC	GGTGCACGATTGAACTCTATG	CCAGAGGAGGCTTCAGA
6	20235922	SP-3022Cg	GGGTGGATAAGTCAACTACTG	GGCCTAATATGTATGTTCTTGC	TTTACGGCAAACAGATCTT
6	22907151	SP-1613Ga	GAAATCACATCCGATGACTGG	CACTCATATGTGGATGTGTCAG	CAATGGCCATAAGGAAATGC
6	25711515	SP-3026Tc	GGACACTTATCTCAAGGTTTAGG	GCACCAAGTTCACTCATGGC	CAAAGGGCAACAATCTCT

Chr.	Position (bp)	SNP_marker_name ^a	Forward-primer_seq	Reverse-primer_seq	SNP_primer_seq ^b
6	28329768	SP-1629Ac	TCCTTCTGTGTACTGGCATC	ACAACCGTGTGGATGCACTG	CCTAAGGGAGCTGAAACT
6	29975546	SP-673Ca	AATCGTGGGTGATGGGTCG	CATGCGGCGTAGAGTAGG	AAGGCCTGGAGGAAGG
7	260864	SP-676Ta	GTTATAACCCTGCACACATGAC	GTCGTTTCGTCGTCATTTCTG	CTGGATTTGTTTTACAAAAACCAA
7	1743980	SP-4168Ag	ACATGGTTGTCATCGATGTCC	ATCTTCGCTATGCTTCACACG	GTCTTCCTGCTGAAGATGAC
7	3898132	SP-683Ga	GGGATCTTCAGTAGTAGCAAC	GCCACTATAGTTGGGAATCATG	CAAAGGTATGGAACATAATACA
7	6843696	SP-1648Ta	CACGGGAACATCATACTGC	GTTAGGTGTCTTCGGCAAG	TGTAATGATACCTCACTCCA
7	10130032	SP-3066Ag	GCAGGGCCATCTTGATG	CAGCTTCACTCTCACATTCAG	TATGGAACAAAGGCGCCAT
7	13302019	SP-1657Ag	TCAGCCAGAGCGATCTCTG	CTATGCGGAATCATACTAGC	CTCTTTCACCAGCAATAGCT
7	17327528	SP-2345Ga	ATGCTCGACATGGCATTGC	GCGATATCTACAACACCAAATCAG	TGCTTATGTGTGCCAGCA
7	18571959	SP-1662Ct	CGCAGCAGTAAGTAGGTTAC	CGCCAAATGGATGTAGAAATGC	ACTGACAGTCTGACACCAA
7	21942076	SP-3095Gt	CATTTGGATGGATCGTGAGTG	GGAAACATGAGGCCGTA	TACTACGAGTCAACGGATTA
7	25490053	SP-741Tc	CAGAGCTGGCAACTTATGTAC	AGCTTCCTTAACTGGACCAC	TGAAGAAGCTGAAGGACTTG
7	27473590	SP-749At	GTCACAAGACACTACAACATGC	TGAAACCGCGGATTTAACGG	GAAACAACACAAGGAAATCC
7	29361700	SP-2356Ag	GTTCTGGAAGTAGAATGTGACTG	GAACAAGTTTGGGCAGTGAG	TTGGCACTGCCTGTAG
8	195223	SP-761Tc	TGAAGATGTACACTGCGTCC	AGTTCTGCAGTTTCCACACG	CTTGCTAGTTGTACCCAA
8	1669653	SP-976Ct	CAGAGATCAACACACCAATGC	CACCAAGACATGTCGGTTC	GCAATTA
8	3553188	SP-2551Tg	GGATAGCCTTGCCTTGGAG	CAGCAACAATGGCTAATTGCG	CTTTCAGTCAATCATTGGACA
8	5278855	SP-3598Ag	CCATACCTGAAGAACTGTCC	GGATGTTAACTGAACACTGG	TCAGAGTTGAAGTGCATCCT
8	8094582	SP-795Ct	CATTGCATGTGGAGGCTTG	GCGGTAACAACGAGCATG	CTTTGGCTGGCTGAAGAAA
8	10572009	SP-1707Tc	ACGTGCAAGGTGTATGCC	CTTGTCTACTGCTACCCGA	CAGCCTGTGTTACTCTGTT
8	14520452	SP-3608Cg	CGTGAATGAATGGCGATCTG	TGGGATTAGTGTGGCTCTTG	CCTCTTCAAGATAATAATGCTA
8	18114324	SP-809Tc	GCTTACATCATGATGCACGC	CAGACTCCATTCTCAAGACC	GCTTTGAAGAAAAGGCATC
8	19903905	SP-3199Tc	GAGGCCCTATAAGTTTGATTGG	CATGCGCACTTTCTTAAACGC	ACAAACGCAGACCCTCATAA
8	23167567	SP-2408Gc	CTCTTGTGGGAAAGTAGGAG	CAGTGGAGTAGCTAGCACAG	CTGAGTCCCCTTTGCT
8	25921712	SP-1734Ac	CTACTGTGCCGAGATTGC	AAGGAGAATACTTGGAGGCG	GTCACCAACAAGCTTGC
8	27758654	SP-844Tc	GTTTGCTTCCTAGCTACAAGC	ACAGTAACACGGCGAGTG	CAAATGTCTGAAACAGTTTGTA
9	1	SP-3968Tg	TCGAGGTGACACCAAATGGC	GCATTGCAACTTGGAAGTTGTG	AACTTAGTTCACTATACTTGAA
9	452497	SP-2183Ag	CAATGTACGATGTAAACGACAGC	GCTCCTCTGGAAGGTAAG	CCGTAAAATTTCTCAATCCAAA
9	3066192	SP-866Ta	CAACATCAAACACAGAGAACGAG	GTTTGAAGAGTTCTTTCTAGCC	CGGAGCCATACATTATCATC
9	5167966	SP-2129Tc	AGTGCTTCACGCGATAGTCT	GTTTCACCAACCTAGTTACGG	GTATTGAACGTTGGGTCCAT
9	6999573	SP-2144Ag	GACATCTGCCATTGTGTCC	GCGGTTGCAAACTTGGTATTC	CAACTCCATGTAATGTGGATAC
9	10483155	SP-875Tc	GCGATTGAAAGAAGCTAAC	GTTGCGAAGAGTACAAAGGC	CTAACAACTATGAGGTTCAATATA
9	13253953	SP-2180Tc	CTAGGGAGTCAAATTACACCG	TACATTCTGGGCACCGTTCA	CATACCCCTTAAACAAGAAAAC
9	15063825	SP-1747Ga	CAACAGCAAGATTGGGAAGC	GCAACTGCAATCAGTATACGG	CGGCTTTGTATTGCCAATTT
9	17880593	SP-909Tc	TGCAGTGCAGTACTACATCG	CAGCTACAGATGTACACCATAC	ATACCAATTTCTCTGACATG
9	19336407	SP-1761Ct	ACAGCCATGCTCGACTTCAG	GCAGCAGAGGAGATGTTCTC	AAATGAAATGAGCACCTCCT
9	20652100	SP-2125Tc	GGATGAACATGTAGGGTTCCG	GCTATTCCATTTTGGTAAGCGC	CCA
10	94506	SP-924Gc	GTAAGTAAGTGTGTAGTATAGG	GCTCGACAGATGGACCTCTC	CCATAACGGACATATATACG
10	2541199	SP-932Ag	AACGACAAAATTCTGCAGCAAC	CTACTAGTTTGTGGAGAACC	GACAGCTTCTGCTTGTGTTGT
10	7069227	SP-948Tg	AGCAATCTCATCAGCCAGATC	GATTTATGCTGCAGCTTGGC	GTTGACACTTCTAAAGCTG

Chr.	Position (bp)	SNP_marker_name ^a	Forward-primer_seq	Reverse-primer_seq	SNP_primer_seq ^b
10	9791595	SP-956Tc	GGCGAAAGAATTGGTGTTTCAG	GGTGCTTAAAGATGAAAGGCCGA	CCATATCATGAAATTCTGATGCAT
10	11824766	SP-3358Cg	GCCTTTCTCATGCTAACAGCA	GGCATAACATCAGGACCTAG	AAGCGTTGGTGTGACTAT
10	14502855	SP-1774Ag	CGATAAGCCAGGCATCCT	AAGGCATAAGCATGCTCGTCA	GTCAGAAAAATGAGGGAATAC
10	17555159	SP-981Tc	ATGGGCTGGTGCCTACTG	CCTTGGTCTGTTACATAGCG	CTTTGATATCCGGGAAGG
10	19468326	SP-992Gc	CCCTTGTAACCTGTTCTTCGTG	GCTTATCCTCCAAACGACAAC	CACATGAGCTAGATGATGAT
10	21171786	SP-1794Tg	CTCTTGTTACTCGATTCCGCA	GAACGTGTAAGCTATATGGCAG	CCAAGTGATTCAAGAATTTTACA
10	22686557	SP-1013Ag	AATGGTCTTCCCTCCGTTTGC	GATTACCAGCTTGAGTACTCG	GTTTTTGTCTCCTTTTCTCAA
11	827222	SP-2650Ga	GCTAATACCTTCTATGAAAGCTC	CGCTCTGCAAAAGGCAAG	GTGTGTAATTGGAGACAAAGCA
11	2489967	SP-2816Tc	GCCATGGCGTATTATTAGCAC	GCATGGAATGGATCTGAACTG	CGCATTCTTTCAGTTTTTCATCT
11	4005384	SP-2656Ta	GATGAAGCTCATCGAGCCT	GAGCTTGATATGGAGGAAACC	GTATCAAATATACCTCACGGAC
11	5687240	SP-1034Ga	GAATGTAGATTGACAGATTGCAC	CCTATATATGCTGGCTCCAC	CACATTACATTAGAGAGAGCA
11	7481468	SP-3417Ag	CGAGAAGAAGTATTCGACACC	CTCTGCATAAGTGAAAGTGAGC	CGTCTTTGTTTCCGTCGTAT
11	11922302	SP-3385Tc	CCACCCAATCCTTGCATGG	GAATTGGAGCTAGTAGTGAGC	TACATGCAAACTGAACAGC
11	17424916	SP-2672Ag	GTGTTGGTCAATTGTGCCATC	GAAGTGTCCGTTAACTTTGAGG	CAACAGCCTGGCTTTTGT
11	19050305	SP-1062At	TGCGCTTCTACATGACCTG	AAGTGACCTGCTGGAGC	CTGTGTAAGTGAAGGTACAAA
11	21896773	SP-1073Tc	ACATACGGCGAGTGCAC	GAGAAGGTTGGAACCGTG	ATCTTGCGATGCAACCATA
11	24002145	SP-3403Ct	TGAGAGGTGTAGAGAAGAGC	AGCCTGTAGACCCTCACAG	CTGAAGAAGCATGCAACTCTT
11	25561274	SP-1085Tc	GGTTGGATATCATCTGAACTGC	CTCGATCACACTGAACTGC	GGGCGGATATATATCCAAT
11	27656337	SP-5095Ga	GCAGTACCTTTGTCCTTAACG	TTTGGTGCTCCTTCTCTGC	GTCATCTTGCTTCTCTGGG
12	322928	SP-2831Gc	TGTGGTTGGTTGATGTGGAG	CACAACTCCACCAACCAAG	CACTATTCCTTCCCGGATT
12	2225082	SP-1106Ac	CAATGTTTCAAGTGTGGGAGCT	CTCAGCTACCTAGCTTATGAG	TTGCTTCAGTAAGAGAGGAC
12	3849039	SP-1115Ac	AAGCATTGGCGCCTCATCG	TAGTGCCTAGGAGCTCTCTG	TTTCTGCCTGGAGAAACACA
12	5510849	SP-3499Ta	TCACAGAGGCCACTGTTCTG	CAGATGCCATGTTAGTCCTTC	ATCGATGAAATGCTGGGAGA
12	10041580	SP-1828Tc	AACGTTAGGCAGGTGCAG	GACGATGAACAACTGGGAAC	CGTCATCGTCATATATAGCCT
12	12334210	SP-3455Ag	CTCACTTTGAGCATACTCCTC	CGTTGGTCCACAATCTGAC	ACTTGACTCCTCACTCAC
12	14689883	SP-2687At	ACTACAGTGATGCTTCTGGC	GTATTTGGCAGTGCGTTCC	GACGTAGTAGCCATATTGGA
12	17499935	SP-3747Cg	CTATTGACCTTGTGCTGGTAC	CTCAAGCTTAAGTGTGTTGC	CAGTGTTTAAGCTTAACAAAGCTT
12	21257971	SP-2697Ct	ATGATTTGACTCCCGTAGTCC	GGATGAGAGCCTAAGCTTAC	GTAATCCTTGCTTAGTTAGTATTA
12	23828918	SP-1160Tc	ACGTCATGCACCCTGATCG	GGGCTTCCATGGTTCATGC	AACTCGTCGTTTCTAGGATC
12	27011209	SP-2705Ag	CTTCAGCGGGAAGTCTGTC	GTTAAGGTATGATCCGTTGCC	TCTTAGGCATATCCCTTTC

^a Each SNP position is located at 1bp-downstream of the corresponding SNP_primer_seq.

^b A capital letter and a small letter following each SNP_primer_name indicates a Koshihikari-allele and a rufipogon-allele of the corresponding SNP.