

Table S1. List of the primers used in this study. For each of the 24 SNPs, we specified the amplicon sequences as well as its two alleles and the contig where the SNP is located (see Rubinstein et al., 2020). For each SNP - Specific Target Amplification primers (STAs), Locus Specific primers (LSPs) and Allele Specific primers (ASPs) are provided.

SNP	Name	Contig	Position	Allele1	Allele2	STRAND	STA_primer	LSP_primer	ASP1_primer	ASP2_primer	AMPLICON_SEQ
1	AV 003 301_10	g30150t 00001	810	C	T	forward	CATTCAAAACAACCA GTGAATAGATTAG	TCTCAGACTGCTTTGG CTTCTCC	TGGGGCACAATAAAGG GATGCC	TGGGGCACAATAAAGG GATGCT	CATTCAAAACAACCAAGTGAATAGATTAGGAGCTGGGCGAAGAG GGTGGGGCACAATAAAGGGATGC[T/C]AGGGATGGAGGAGTC AGTGAGGGAGAAGCCAAAGCAGTCTGAGA
2	AV 005 099_40	g09915t 00001	540	A	G	forward	CCAGTCAAAATGCCCT GAAGAAA	TGACTCTGATAGTTG GAGTGATTCTTG	CTAAGATCTACCATGAT ACTTCCGACATA	CTAAGATCTACCATGAT ACTTCCGACATG	CCAGTCAAAATGCCCTGAAGAACTCGAGCAGCAGGATGGCTA AGATCTACCATGATACTTCCGACAT[G/A]CTTTAAACATGGCAGT TCAAGAATCACTCCAATATCAGAGTCA
3	AV 011 221_46	g22101t 00001	1346	C	G	reverse	AATGATATGGCTTGTT AAAACGCTT	GTCCTGAATCCGATC GAAGTAAGTAC	TCTTGTCAGGTCCTTAG CCTCCTG	TCTTGTCAGGTCCTTAG CCTCCTC	AATGATATGGCTTGTTAAACGCTTCTTGTCAGGTCCTAGCCTC CT[G/C]TTTCCATGTGAGTACTTCTCGATCGGATTCAGGAC
4	AV 012 267_37	g26796t 00001	137	C	T	reverse	GCATGGCCACTCTAG CCCA	AGGTCCACTTTGAGC CCCTATTAT	CGGAGAGGCCCTTTCAT AACC	CGGAGAGGCCCTTTCAT AACC	GCATGGCCACTCTAGCCACGGAGAGGCCCTTTCATAACC[A/G] AGACTGATAAATAGGGGCTCAAAGTGGACCT
5	AV 024 157_50	g15753t 00001	550	C	G	reverse	GAAATCCCCAAAACCTC ATCAAATAA	GTGAAGAGAAGGAA GATAACTGGAGAG	CCCTCTCTTTGCCTTTCA ACTCG	CCCTCTCTTTGCCTTTCA ACTCC	GAAATCCCCAAAACCTCATCAAATAACCTTTTTATGAATTCCTC CCCTCTCTTTGCCTTTCAACTC[G/C]TCTTTCTATCTATTAGATGA AGATCTCTCCAGTTATCTTCTCTCTTCTAC
6	AV 038 262_46	g26200t 00001	546	A	T	reverse	TGTACTCACTCACCTT CTTCTTTTC	AGATCCCATGGCACG TTGATCG	CCACCACCTTCGTCGTG CCT	CCACCACCTTCGTCGTG CCA	TGTACTCACTCACCTTCTTCTTTTCCAATTTTGGGCCAATGCCAC CACCTTCGTGTCGCC[T/A]GCTGAGATCTTCCCTGCGAGGCTGC GATCAACGTGCCATGGGATCT
7	AV 054 048_97	g04881t 00001	897	A	C	reverse	CCAAGCTCACTAATAA GCACGC	TTGACATAATTGGAG GGAATGCTCG	GAAAGATGCCAAAGTAC TTCACGCT	GAAAGATGCCAAAGTACT TCACGCG	CCAAGCTCACTAATAAGCACGCGTACTTCAGAAAGATGCCAAAG TACTTCACGC[T/G]CAGGAGCATTCCCTCCAATTATGTCAA
8	AV 057 210_87	g21033t 00001	1087	A	G	reverse	GTCATGACTACTAGCC TCAACTTAG	CATACCTGATGGGTG CCTTGAACC	AAAAGTATATGCCTAT GAAGCCTTCT	AAAGTATATGCCTATG AAGCCTTCC	GTCATGACTACTAGCCTCAACTTAGCTAAGGCTGTGCAGAAAC TGATATGCCTATGAAGCCTT[C/T]ATGCCGCTTCAACCAAGTCA GGTTCAAGGCACCATCAAGTATG
9	AV 058 213_34	g21382t 00001	834	C	T	forward	GCAATCATGGTGCAA ATAACACAA	GTGGGAGATGAGGTA TAGGATCGC	GCCCCTCGCAGCCTCCA AC	GCCCCTCGCAGCCTCCA AT	GCAATCATGGTGCAAATAACACAAGCCCTCGCAGCCTCAA[T/ C]GCGATCCTATACCTCATCTCCAC
10	AV 078 076_17	g07659t 00002	517	A	T	reverse	ATTAATACCTGTGTT AGGTTGAGAA	CGCCACATCAGGAA AAGATTCATA	AAATGGAAGGTTCTTT CACTGCCT	AAATGGAAGGTTCTTT CACTGCCA	ATTAATACCTGTGTTGAGGTTGAGAAATGGAAGGTTCTTTC ACTGCC[A/T]GGTTATGAATCTTTCTGATGTGGGCG
11	AV 081 109_35	g10924t 00001	235	A	C	forward	CATGGAGTAGGAATA GTAGTTTTAAAC	TCCTACATATGTATGT ATGAGGGAGGG	AAAGATATGGCCATTAA CGGGTTGA	AAAGATATGGCCATTAA CGGGTTGC	CATGGAGTAGGAATAGTAGTTTTAAACACTAGATAATCAAAGTT GACAAAGATATGGCCATTAAACGGGTTG[C/A]TACAAATCTCAA CCCCCTCCCTCATACATACATATGTAGGA
12	AV 087 055_34	g05557t 00001					GCTCCTTCTGTGCTC ACTTT	TCAGAATGTTCACAAT TCAGGCGG	GAAGAGTTCTAGGGATT AAGCTATTGTTA	GAAGAGTTCTAGGGATT AAGCTATTGTT	GCTCCTTCTGTGCTCACTTTCAAGTAGTCAAGAAGAAGAGTT CTAGGGATTAAGCTATTGTT[C/A]GTGGGTTGTAATTCTGCCG CCTGAATTGTGAACATTCTGA
13	AV 088 277_95	g27701t 00001					CTCCTTCCCTACACCT ATTACACA	GGGGTTCAATCATCA AACTTCACATG	AAATCCATACATGATG GCTGAGTACA	AAATCCATACATGATG CTGAGTACG	CTCCTTCCCTACACCTATTACACACTACCATCTAGATCGTATAAA AATCCATACATGATGGCTGAGTAC[A/G]TTAAGGACGTCAAAGC ATGTGAAGTTTGATGATTGAACCC
14	AV 101 088_32	g08815t 00002					ATCCCTTGATATCAAT TCATTGGAGA	CTGCGCGATATTCTG GCTAAAAAAG	GTAAGCCCCGGCATCAA ACCT	GTAAGCCCCGGCATCAA ACCG	ATCCCTTGATATCAATTCATTGGAGAATGTAAGCCCCGGCATCA AACC[T/G]CGCTTTTTAGCCAGAATATCGCGCAG

15	AV 103 131_12	g13103t 00001	TCATCATAACCCAATG ACACACTG	AATGGTCCCCACTTTG AGTCTGG	TCATCGTCGTCGTTGTTATCATCGTCGTCGTTGTTA GACACA GACACT	TCATCATAACCCAATGACACACTGCCATGCGTCCCCTGATCATCA TCGTCGTCGTTGTTAGACAC[A/T]GTGGATGAAACATCAATGGC ATCCCCAGACTCAAAGTGGGGACCATT
16	AV 107 214_11	g21486t 00001	TCTGGGAAACAGGTT TTCTGAGA	TCGATGTCATCCATGA TTCGTAGAAC	ATGTCCTTGAAAGAAGC AGCTGAAG AGCTGAAT	TCTGGGAAACAGGTTTTCTGAGAAGGAATGGCGTAGGTTTTTA TGTCCTTGAAAGAAGCAGCTGAA[T/G]TGACGGTTCCAGGTTTT TTGAAGGTTCTACGAATCATGGATGACATCGA
17	AV 108 249_68	g24900t 00001	TGTTTGTACCATGTGAGAGATTTTCTGGCGCTTCTCTCAGATTTTAAAAATTCCTCAGATTTTAAAAAT CCCCAA	GATGGTG	GACAACAGCTA GACAACAGCTC	TGTTTGTACCATGTGACCCCAAAATAATAGTACAGACAGTCCTC AGATTTTAAAAATGACAACAGCT[C/A]CAATGGGTCCAGTCAAG ACACCATCAGCGCCAGAAAATCTC
18	AV 114 003_23	g00342t 00001	TGGGAAAACCTAAA CAAGTTCG	GATCTCCGGCGTTTAC TGAGC	GCAGCGCACATCTTGCA GGT GGA	TGGGAAAACCTAAACAAGTTCGAGCGCACATCTTGCAAGG[A/ T]CGCGCGCATCACC GGCTCAGTGAACGCCGGAGATC
19	AV 121 031_57	g03109t 00001	AGACTGTAGAACTG AGACTGGC	TGAGGGTTTCTCTCAG GTTACGTTT	CCGGAAGAATCCTATTT TAAGTATTCA TAAGTATTCT	AGACTGTAGAACTGAGACTGGCCGGTGAAGCGTAGCGTCCG GAAGAATCCTATTTTAACTGATTC[T/A]GGGTCAATTTGAAAAGCC CAAACGTAACCTGAGGAAACCTCA
20	AV 146 072_75	g07246t 00001	GGATAGCATCACAAT CTCATCAAAA	TGGGCTTCATTTAGAC TTCCTGTTTT	AACTTTGTTAGAATAAG CGAAATATACAGTAC CGAAATATACAGTAT	GGATAGCATCACAATCTCATCAAAAACCTTTTAAAGCAACTTTG TTAGAATAAGCGAAATATACAGTA[C/T]AAGAGATGTATTTTG AAAAACAGGAAGTCTAAATGAAGCCCA
21	AV 166 149_06	g14937t 00001	TGACAAAGCTTTCTTA TTTATATATGTGAA	AGTCTATATAGGTTGT ATGAAGTCAGGAC	ATGATCAAAGACCTAAC AACCTTCTGT AACCTTCTGA	TGACAAAGCTTTCTTATTTATATATGTGAAAAAAGAAGTCAATG AGAATGATCAAAGACCTAACACCTTCTG[A/T]GCCAAAAGTGG TCCTGACTTCATACAACCTATATAGACT
22	AV 167 054_69	g05485t 00002	CAAAAGCAAACTTTTATTCTCTGTAGAAAGTA TTGAGTGCC	AGTAACAAAACAAAAT GGCGGGT ATTCTTCATGCCG ATTCTTCATGCCT	AGTAACAAAACAAAAT ATTCTTCATGCCG ATTCTTCATGCCT	CAAAAGCAAACTTTTATTGAGTGGCTAACAGTACAAGTAACAAA ACAAAAATATTCTTCATGCC[G/T]ATCTATAGCAGAGGGCTCAC GCCACCCGCTACTTCTACAGAGGAA
23	AV 169 254_87	g25456t 00001	GAGAAGACTACAAGA AGTTGAGAGG	AATTGAAGGTACGTC CAAACAGGC	AAGTTCTGAAGGTATTT CTTATGTGTG CTTATGTGTG	GAGAAGACTACAAGAAGTTGAGAGGTCTTTGCTAACAGTTCT GAAGGTATTTCTTATGTGTG[C/T]GGTTGTCAATCTCAGGGCCT GTTTGGACGTACCTTCAATT
24	AV 188 021_32	g02123t 00003	CTCTTTGAATAATTCT TCCCTCAACC	GTGCAAAATTCCTACC TACCAATTGG	TCTTGGAATTTGGATCC AGATAACTTTA AGATAACTTTC	CTCTTTGAATAATTCTTCCCTCAACCAGAAATCTTAGAATAGCTC TTGGAATTTGGATCCAGATAACTTT[A/C]TCAAGTATACCATGAC GTGCTGGCCAATTGGTAGGTAGGAATTTGCAC