

Supplemental Table S1. SNP marker name, GenBank dbSNP accession ID, polymorphism type, KASPar™ primer sequences (A1, A2 and Common Reverse) for all 96 SNP assays tested.

SNP Name	GenBank SS# ¹	SNP Type	A1 primer (5'→3') ²	A2 primer (5'→3') ²	Common Reverse (5'→3') ²	L ₃
AM18192	ss161142184	G/T	GAAGGTGACCAAGTTCATGCTTTAGA ACGTGAAACCAATCTGTGTTG	GAAGGTCGGAGTCAACGGATTATTTA GAACGTGAAACCAATCTGTGTTT	GTTGATCGACAGATG ATAAGGTCAGAAAT	1
AM18598	ss161142590	C/T	GAAGGTGACCAAGTTCATGCTAGTATT TAAAGGAACAAATATACTCTATTACG	GAAGGTCGGAGTCAACGGATTAGTAT TTAAAGGAACAAATATACTCTATTACA	GGTGGAAATTTAGC TTCGGTTGGGAA	1
AM18740	ss161142732	A/T	GAAGGTGACCAAGTTCATGCTATTCGA TTAATTTCAACTGCAACAAAGTAAAA	GAAGGTCGGAGTCAACGGATTGATT AATTTCAACTGCAACAAAGTAAAT	GATTGTGTTAGTTTC TGATTTCTGTTTATT	1
AM18741	ss161142733	C/T	GAAGGTGACCAAGTTCATGCTAAGGC GGCGAAAGAGGAAAGC	GAAGGTCGGAGTCAACGGATTGAAGG CGGCGAAAGAGGAAAGT	CGTCCAATATAAATT TTCTCTCCTCTA	1
AM18918	ss161142910	C/T	GAAGGTGACCAAGTTCATGCTATAGA AGTAAATTTGATATGACAAATTAAGAA G	GAAGGTCGGAGTCAACGGATTATAGA AGTAAATTTGATATGACAAATTAAGAA A	TCTCAATAACTCTTCT GCCCTACGAAATT	1
AM18919	ss161142911	A/G	GAAGGTGACCAAGTTCATGCTAAATTT GTTCTATTTATCTTTTTAATTTGTCA	GAAGGTCGGAGTCAACGGATTAAATT TGTTCTATTTATCTTTTTAATTTGTCTG	TTATGGTGTGTGGTA AAGTGAAAGA	1
AM19008	ss161143000	A/T	GAAGGTGACCAAGTTCATGCTGAGAA GTATAGGGCTGTCATCGTTA	GAAGGTCGGAGTCAACGGATTGAGAA GTATAGGGCTGTCATCGTTT	GTAATCCCTGCCTATG TCTAAGACAA	1
AM19009	ss161143001	C/T	GAAGGTGACCAAGTTCATGCTAATAAT GGGTAATTAATGAGTTAAGGGAC	GAAGGTCGGAGTCAACGGATTCTAAT AATGGGTAATTAATGAGTTAAGGGAT	CATCAGCAATTCTTCA AGCGAACCGAT	1
AM19010	ss161143002	C/T	GAAGGTGACCAAGTTCATGCTGCGAA CCGATTCCTGAGGGGAAAG	GAAGGTCGGAGTCAACGGATTAAAGCG AACCGATTCCTGAGGGGAA	GGAGTACTCAACCTA TAAGTCATGACTTT	1
AM19011	ss161143003	C/T	GAAGGTGACCAAGTTCATGCTTTCTCG GAAGCTAACATGTCTCG	GAAGGTCGGAGTCAACGGATTCTTCT CGGAAGCTAACATGTCTCA	GATTTGAACACTTAG TGCGCAAGATTGAA	1
AM19012	ss161143004	C/G	GAAGGTGACCAAGTTCATGCTCCAGT GGTATAAAAACCCGATCAAAG	GAAGGTCGGAGTCAACGGATTCCAGT GGTATAAAAACCCGATCAAAC	GAGACATGTTAGCTT CCGAGAAAGAAATA	1
AM19376	ss161143368	C/G	GAAGGTGACCAAGTTCATGCTCGTAC ATTCCTCACTCAC	GAAGGTCGGAGTCAACGGATTCTCGT CACATTCCTCACTCAG	CAATCCAATATCCACC TCAAAAACAAGGT	1
AM19378	ss161143370	G/T	GAAGGTGACCAAGTTCATGCTCATCAT CATCATCAATCCAATATCCC	GAAGGTCGGAGTCAACGGATTATATC ATCATCATCATCAATCCAATATCCA	GTACAGGTATGGATT GCTCGTCACAT	1
AM19379	ss161143371	C/G	GAAGGTGACCAAGTTCATGCTAGATA ACGGTCAAATGGATCACTTC	GAAGGTCGGAGTCAACGGATTAGATA ACGGTCAAATGGATCACTTG	ATGAATATTTCTTCTC ACAATTGAGCTCAA	1
AM19395	ss161143387	G/T	GAAGGTGACCAAGTTCATGCTAGTGC TAAGTATGTGTTACAGAGG	GAAGGTCGGAGTCAACGGATTAAAGTG CTAAGTATGTGTTACAGAGT	CAACATGTTCTTTCTG GGGACATATGTTT	1
AM19431	ss161143423	C/T	GAAGGTGACCAAGTTCATGCTGGCTA ATAAGTTAATATCATGTTATGGGG	GAAGGTCGGAGTCAACGGATTGGCTA ATAAGTTAATATCATGTTATGGGA	TAAGCTTTGAACTCC AACAAGATTGCGTA	1
AM19452	ss161143444	G/T	GAAGGTGACCAAGTTCATGCTCGCATT TTACGTGCCGATTAACAC	GAAGGTCGGAGTCAACGGATTCCGCA TTTTACGTGCCGATTAACAA	ATGATAGTAAGGTAA CGTCGAACCATGAA	1
AM19464	ss161143456	A/G	GAAGGTGACCAAGTTCATGCTGAAAT ATAAAAACAATATCTCACTTGATTTGAAT	GAAGGTCGGAGTCAACGGATTGAAAT ATAAAAACAATATCTCACTTGATTTGAAC	CTGAAATTCACCCAA AGACCTGAATGAA	1
AM1966	ss16114365	C/T	GAAGGTGACCAAGTTCATGCTCCGTTG ACATTAGGGATGCTTGG	GAAGGTCGGAGTCAACGGATTACCGT TGACATTAGGGATGCTTGA	GGATAATAACTAACA AGAAAAGAAAGGAA	1

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AM1 966 3	ss161 14365 5	C/ G	GAAGGTGACCAAGTTCATGCTGACTTT GATATAGCAAGTTACGATGAG	GAAGGTCGGAGTCAACGGATTGACTT TGATATAGCAAGTTACGATGAC	GGATAATAACTAACA AGAAAAGAAAGGAA A	1
AM1 966 4	ss161 14365 6	A/ G	GAAGGTGACCAAGTTCATGCTAATAA GAATACCAGTGTCCAGCTCT	GAAGGTCGGAGTCAACGGATTATAAG AATACCAGTGTCCAGCTCC	ACGGTGCATCGTAA CTTGCTATATCAAA	1
AM1 966 5	ss161 14365 7	G /T	GAAGGTGACCAAGTTCATGCTCAGAG TCAGAGCTGGAACACG	GAAGGTCGGAGTCAACGGATTCCAGA GTCAGAGCTGGAACACT	CACCCAATGGATAGC GACAGTGAAT	1
AM2 143 2	ss161 14542 4	A/ C	GAAGGTGACCAAGTTCATGCTGCATAT ACTCATTAAAGCCATTTATTGTAATGT	GAAGGTCGGAGTCAACGGATTATAT ACTCATTAAAGCCATTTATTGTAATGG	GTAAAAAGTCGAAGA ATCAAGGAGGGAT	1
AM2 154 6	ss161 14553 8	C/ T	GAAGGTGACCAAGTTCATGCTTTCAAG GATATTCATGCTTTAGTCG	GAAGGTCGGAGTCAACGGATTATTTT AAGGATATTCATGCTTTAGTCG	ACAGTAAACGGGAGT GATGTGGTTATTATA	1
AM2 190 1	ss161 14589 3	A/ G	GAAGGTGACCAAGTTCATGCTGAGTA TGTCGGCCAGAATTGGA	GAAGGTCGGAGTCAACGGATTAGTAT GTCGGCCAGAATTGGG	GGGATGAGGTATACC GCTGGAAAAT	1
AM2 190 5	ss161 14589 7	C/ T	GAAGGTGACCAAGTTCATGCTGATTAC TGAACCTGAAATCTTATTGAACATC	GAAGGTCGGAGTCAACGGATTATGAT TACTGAACTTGAATCTTATTGAACATT	GCTTATTCATAAGGC AACAAACAACATCAT	1
AM2 200 4	ss161 14599 6	A/ G	GAAGGTGACCAAGTTCATGCTAGCTTA GAGCCAAGGCACAACAA	GAAGGTCGGAGTCAACGGATTGCTTA GAGCCAAGGCACAACAG	TCCTTTCAGTCCAGA GCCTCCAAA	1
AM2 247 1	ss161 14646 3	A/ C	GAAGGTGACCAAGTTCATGCTCGGTG GTTTGAGTGTAGAGAAAAG	GAAGGTCGGAGTCAACGGATTGGTGG TTTGAGTGTAGAGAAAAGC	CCACTTGATCCAGCCT ACATTCCAT	1
AM2 248 7	ss161 14647 9	C/ G	GAAGGTGACCAAGTTCATGCTATTAGC TTGAATGCTAAGGATATGGC	GAAGGTCGGAGTCAACGGATTATTAG CTTGAATGCTAAGGATATGGG	GCTTTAGACACAAGA GAAATAAACTCCAAA	1
AM2 311 2	ss161 14710 4	C/ G	GAAGGTGACCAAGTTCATGCTATCAA GGAAAAATTTACTTTAAAGCTATGTTA C	GAAGGTCGGAGTCAACGGATTATCAA GGAAAAATTTACTTTAAAGCTATGTTA G	ACTCGAAGTGAATA CTTGTTACGTATT	1
AM2 315 8	ss161 14715 0	A/ G	GAAGGTGACCAAGTTCATGCTCTCCCA CGGATCATGTGCATAT	GAAGGTCGGAGTCAACGGATTCTCCC ACGGATCATGTGCATAC	CCTGAAAAGTGCCT AATCGTCAATGATA	1
AM2 319 6	ss161 14718 8	C/ T	GAAGGTGACCAAGTTCATGCTATATTC AGCAAATGATTCCTTCAATGATC	GAAGGTCGGAGTCAACGGATTATATT CAGCAAATGATTCCTTCAATGATT	CACAACAGTGGCTTA CTTTTTAATCAAGAT	1
AM2 385 7	ss161 14784 9	G /T	GAAGGTGACCAAGTTCATGCTAATTTT ATTATCAGTGATAATTTGTCTTTGCTG	GAAGGTCGGAGTCAACGGATTAATTTT ATTATCAGTGATAATTTGTCTTTGCTT	GTTGCTTTTGAGAA TCGAGCATAATGAT	1
AM2 389 1	ss161 14788 3	A/ T	GAAGGTGACCAAGTTCATGCTGACGC CTGCTGACCTGCATAAA	GAAGGTCGGAGTCAACGGATTGACGC CTGCTGACCTGCATAAT	TAGAGTCTCATTTAG GCGAGTTACCAT	1
AM2 417 7	ss161 14816 9	A/ G	GAAGGTGACCAAGTTCATGCTTATGGT CGTTAAAAAATATACGAACCGAT	GAAGGTCGGAGTCAACGGATTGGTCG TTAAAAAATATACGAACCGAC	AAAGTTTAGCACCTC TTTGGTTGCTTCTT	1
AM2 417 9	ss161 14817 1	C/ T	GAAGGTGACCAAGTTCATGCTTTTATG GTCGTTAAAAAATATACGAACCG	GAAGGTCGGAGTCAACGGATTTTAT GGTCGTTAAAAAATATACGAACCA	AAAGTTTAGCACCTC TTTGGTTGCTTCTT	1
AM2 445 7	ss161 14844 9	A/ G	GAAGGTGACCAAGTTCATGCTTATACA GTGTGGCTTTGGAGGCA	GAAGGTCGGAGTCAACGGATTATACA GTGTGGCTTTGGAGGCG	TAAATTGAGAGCACA ACGCAGTGCAA	1
AM2 466 1	ss161 14865 3	C/ T	GAAGGTGACCAAGTTCATGCTTGCACT TTGTGATTGTTAACGATAAATC	GAAGGTCGGAGTCAACGGATTCTTGC ACTTTGTGATTGTTAACGATAAAT	GCCAAACATATGTTA GAGGCAACTCAAT	1
AM2 498 3	ss161 14897 5	C/ T	GAAGGTGACCAAGTTCATGCTGTTGG AGTAGTTCATTACGATAAGAG	GAAGGTCGGAGTCAACGGATTGTTG GAGTAGTTCATTACGATAAGAA	GTTCAAATCTGGTTG GTGGATATGTTGAA	1
AM2 524 1	ss161 14923 3	C/ G	GAAGGTGACCAAGTTCATGCTCATTTT GAATATCAAATGTGATCATATGGC	GAAGGTCGGAGTCAACGGATTATTTT GAATATCAAATGTGATCATATGGG	CCTTTCTGACACAC CAAAAATAAATCAA	1
AM2	ss161	A/	GAAGGTGACCAAGTTCATGCTGTTGA	GAAGGTCGGAGTCAACGGATTGAAGC	TCCTTCTGACTGCC	1

526 1	14925 3	G	AGCCAAAGATTCAGGTCGT	CAAAGATTCAGGTCGC	GTGCTCA	
AM2 530 9	ss161 14930 1	A/ G	GAAGGTGACCAAGTTCATGCTAAAAC TATACTGAAAACCTACGCTATATAATTA	GAAGGTGGGAGTCAACGGATTA AAAAC TATACTGAAAACCTACGCTATATAATTG	CATGACTCTAAAAGG TTGTCATTGTAACAA	1
AM2 613 3	ss161 15012 5	A/ C	GAAGGTGACCAAGTTCATGCTCAGGC AATGTGGCTGGTGATGAT	GAAGGTGGGAGTCAACGGATTAGGCA ATGTGGCTGGTGATGAG	CTGCCTAAGTTTGCCCT ATCACACAGAT	1
AM2 643 8	ss161 15043 0	C/ T	GAAGGTGACCAAGTTCATGCTGAATA AATATTGAAGGTTGAACGTTGAAC	GAAGGTGGGAGTCAACGGATTGTTGA ATAAATATTGAAGGTTGAACGTTGAAT	AACCTTCAATCTTCAA CCATCTGCCAT	1
AM1 719 0	ss161 14118 2	C/ T	GAAGGTGACCAAGTTCATGCTGAGCC AACCTGACGAATATTCCC	GAAGGTGGGAGTCAACGGATTAGAGC CAACCTGACGAATATTCTT	GTGTAGATGCAACAC AGCTTCTCCTA	2
AM1 719 1	ss161 14118 3	A/ G	GAAGGTGACCAAGTTCATGCTGGATA GAAGTGTAGATGCAACACAGT	GAAGGTGGGAGTCAACGGATTGATAG AAGTGTAGATGCAACACAGC	AAGTAAAATAATTAG CGTCAGATAGGAGAA	2
AM1 808 1	ss161 14207 3	G /T	GAAGGTGACCAAGTTCATGCTAATCG ACGGCGTTATTAACCTCAC	GAAGGTGGGAGTCAACGGATTCTAAT CGACGGCGTTATTAACCTCAA	CTTAATGCATTTTAGA TATTTTATACATTA	2
AM1 808 2	ss161 14207 4	C/ G	GAAGGTGACCAAGTTCATGCTCATAA AAATAACTTTTTGGGCATGATGCG	GAAGGTGGGAGTCAACGGATTATAA AAATAACTTTTTGGGCATGATGCC	CGTCGATTAGCATGT GCACACAGT	2
AM1 809 2	ss161 14208 4	A/ G	GAAGGTGACCAAGTTCATGCTATAAAA CAGTACAATAATATTGTCTACAAAGCA T	GAAGGTGGGAGTCAACGGATTAAACAG TACAATAATATTGTCTACAAAGCAC	CAAGTTGGATTACAGC CCAGACTTCTA	2
AM1 896 0	ss161 14295 2	A/ T	GAAGGTGACCAAGTTCATGCTAATTAT GATTGGACACCATCAAGAAATAATATA	GAAGGTGGGAGTCAACGGATTAATTA TGATTGGACACCATCAAGAAATAATAT T	CCAATGGGTAATGGG TGATAGAGTATATT	2
AM1 896 1	ss161 14295 3	A/ C	GAAGGTGACCAAGTTCATGCTGATGTT GGGTTTTATAGAGGAAATTTTGTTAT	GAAGGTGGGAGTCAACGGATTGTTGG GTTTTATAGAGGAAATTTTGTTAG	ACCCATTGGCTATTAT TTTCATATTGAAAT	2
AM1 913 3	ss161 14312 5	A/ G	GAAGGTGACCAAGTTCATGCTATACTA TAATTCGCAAATAATCTTTATCAACT	GAAGGTGGGAGTCAACGGATTATACT ATAATTCGCAAATAATCTTTATCAACC	GGTGTGGGAAATAAC ACTATTCTCACTAA	2
AM1 952 7	ss161 14351 9	C/ G	GAAGGTGACCAAGTTCATGCTGATGA GAAGTATAAGTAGGAGACATC	GAAGGTGGGAGTCAACGGATTGATGA GAAGTATAAGTAGGAGACATG	CTTTAGGTTTCTCTTC ATGTCCTTCACTT	2
AM1 993 0	ss161 14392 2	A/ C	GAAGGTGACCAAGTTCATGCTATAGG AGTATAATAGTTGAAATGATTATGATT A	GAAGGTGGGAGTCAACGGATTATAGG AGTATAATAGTTGAAATGATTATGATT C	GAGGGAAATTGCATG TCACTCGGTT	2
AM1 993 1	ss161 14392 3	A/ G	GAAGGTGACCAAGTTCATGCTGATTCA GAATTAGTGTCAACCGAGTA	GAAGGTGGGAGTCAACGGATTAGAA TTAGTGTCAACCGAGTG	TTCTGCTTTTCTGACT GCTGAGTATTGTT	2
AM1 993 2	ss161 14392 4	C/ G	GAAGGTGACCAAGTTCATGCTACTAA AATAAAAAGTAATGTAGAATACTGTATA C	GAAGGTGGGAGTCAACGGATTACTAA AATAAAAAGTAATGTAGAATACTGTATA G	GCTGCTTTAGTTTGA AGCATATAAGCTT	2
AM2 051 2	ss161 14450 4	C/ T	GAAGGTGACCAAGTTCATGCTGTTAA AGCTCTACAGTTCTTTGAGC	GAAGGTGGGAGTCAACGGATTGTTGT TAAAGCTCTACAGTTCTTTGAGT	GCAACTTCACATAAAA TAAAGTGCACATGATT	2
AM2 053 6	ss161 14452 8	A/ G	GAAGGTGACCAAGTTCATGCTTAAAG TCTATAATTGTTAAATTAGATCGTAT	GAAGGTGGGAGTCAACGGATTAAAGT CTATAATTGTTAAATTAGATCGTAC	TGGCTTAATACTAAA TAGCACTATCAATAT	2
AM2 053 8	ss161 14453 0	C/ T	GAAGGTGACCAAGTTCATGCTGATAC ATCTTGCCAATTTAATACAAGTTC	GAAGGTGGGAGTCAACGGATTAATTG ATACATCTTGCAATTTAATACAAGTTT	CGAATTATGAATTGT ATCAATCTTATGAAA	2
AM2 088 6	ss161 14487 8	C/ T	GAAGGTGACCAAGTTCATGCTCCATCT AAAAATCAGGTTTGCTCTTTT	GAAGGTGGGAGTCAACGGATTCTCCAT CTAAAAATCAGGTTTGCTCTTTT	CAAAAGTTGGGCACA ACACAACAAACAA	2
AM2 112 0	ss161 14511 2	C/ T	GAAGGTGACCAAGTTCATGCTCCTCAA AATGATTTTATGAAAATCTACGATC	GAAGGTGGGAGTCAACGGATTACCTC AAAATGATTTTATGAAAATCTACGATT	GGGAGATGTTTTGTA CTTGATTAGGCTT	2
AM2 112 1	ss161 14511 3	C/ T	GAAGGTGACCAAGTTCATGCTAATAG ACCTTTGGGCTATCATCG	GAAGGTGGGAGTCAACGGATTGAATA GACCTTTGGGCTATCATCA	AAACATCTCCCGACT ACACTTATTGAGAT	2

AM2 112 2	ss161 14511 4	A/ G	GAAGGTGACCAAGTTCATGCTGATAG GCCAAAGGTCTATTCACA	GAAGGTCGGAGTCAACGGATTATAGG CCCAAAGGTCTATTCACG	GCAAGTTGATCAGTA TAATTACCAACCCAT	2
AM2 174 3	ss161 14573 5	A/ G	GAAGGTGACCAAGTTCATGCTCCTTGT TTATGTCACCTTATGATCAAGTCA	GAAGGTCGGAGTCAACGGATTCTTGT TATGTCACCTTATGATCAAGTCG	AAGAGAATTTGTACC AAAGCCGTGGAAA	2
AM2 177 3	ss161 14576 5	A/ G	GAAGGTGACCAAGTTCATGCTCAAATT TGGTTTCTAATATATTTTAAAGTGTT	GAAGGTCGGAGTCAACGGATTCAAAT TTGTTTCTAATATATTTTAAAGTGTC	GGCACGCACACTTCA CGCGAAT	2
AM2 184 2	ss161 14583 4	A/ G	GAAGGTGACCAAGTTCATGCTGGCGC CTCGATGCGCTTCAT	GAAGGTCGGAGTCAACGGATTGCGCC TCGATGCGCTTCAC	CAAGGATAAGTTAAT AACCAAAACCAACAA	2
AM2 209 9	ss161 14609 1	A/ G	GAAGGTGACCAAGTTCATGCTACAAA CTACTCCTGGATACTTTGAGAA	GAAGGTCGGAGTCAACGGATTCAAAC TACTCCTGGATACTTTGAGAG	ATGACCCCGACACGC ATCAATGATA	2
AM2 219 3	ss161 14618 5	A/ G	GAAGGTGACCAAGTTCATGCTCAAAG GGCATAACAGATTAGCTGAGA	GAAGGTCGGAGTCAACGGATTAAAGG GCATAACAGATTAGCTGAGG	GTCCAGCCAGCTGGC ATAACAAATT	2
AM2 239 3	ss161 14638 5	C/ T	GAAGGTGACCAAGTTCATGCTGTTTGA CTAACCAACAAGACAAAAACC	GAAGGTCGGAGTCAACGGATTGTTTG ACTAACCAACAAGACAAAAACT	CCACTCAACAAATAC AAATAAAAGACTCTT	2
AM2 242 6	ss161 14641 8	C/ T	GAAGGTGACCAAGTTCATGCTATATTT AATTC AAGTGAAAATGTTGATTGCAC	GAAGGTCGGAGTCAACGGATTATATT TAATTC AAGTGAAAATGTTGATTGCAT	TGCTCCCAGACAAGAA AGATCTTAATCTTA	2
AM2 255 8	ss161 14655 0	A/ G	GAAGGTGACCAAGTTCATGCTATTTGT AAAGGGTAAAATTTGAAATAGTGCATA	GAAGGTCGGAGTCAACGGATTGTAAA GGGTAAAATTTGAAATAGTGCATG	GCACAAGGCCCAAAA ATCAACAAAATTTT	2
AM2 278 1	ss161 14677 3	A/ G	GAAGGTGACCAAGTTCATGCTGGTAC TAACTACAATTCAAAACATCTTAATAA	GAAGGTCGGAGTCAACGGATTGGTAC TAACTACAATTCAAAACATCTTAATAG	CAGTACGACTATTCA TAGGCCTTAACATA	2
AM2 291 1	ss161 14690 3	A/ T	GAAGGTGACCAAGTTCATGCTAATCA AGTAGATTA AAAAGGGTTTTACTCTAA	GAAGGTCGGAGTCAACGGATTATCA AGTAGATTA AAAAGGGTTTTACTCTAT	AGTAACATGTTGTTC CTTTTGCAGGTCTA	2
AM2 300 6	ss161 14699 8	A/ C	GAAGGTGACCAAGTTCATGCTACTAAT AAGGTGACCCATATAGCTCT	GAAGGTCGGAGTCAACGGATTCTAAT AAGGTGACCCATATAGCTCG	CGCTAATATTTGATAT CAATGGGTCACTAA	2
AM2 335 4	ss161 14734 6	A/ G	GAAGGTGACCAAGTTCATGCTGTCCCG GGTGGGGAGAGAT	GAAGGTCGGAGTCAACGGATTCCCGG GTGGGGAGAGAC	CGATTAATTTGCTGC AGAAAACACTTCTT	2
AM2 380 8	ss161 14780 0	C/ T	GAAGGTGACCAAGTTCATGCTCATTGA GTTTACCACGCTGATAAGC	GAAGGTCGGAGTCAACGGATTATCATT GAGTTTACCACGCTGATAAGT	GCAAAGCGGCTTTTG CAGGTGTCT	2
AM2 389 5	ss161 14788 7	A/ G	GAAGGTGACCAAGTTCATGCTGTCCTT ACACGACTAAAAAACACCTTAT	GAAGGTCGGAGTCAACGGATTCTTAC ACGACTAAAAAACACCTTAC	AATGGAGTATAGCAT GTCAAGATCCAATAT	2
AM2 402 9	ss161 14802 1	A/ G	GAAGGTGACCAAGTTCATGCTATAAAT TTTTCAAAGTGAAGTACTGATTGCTA	GAAGGTCGGAGTCAACGGATTTTTTCA AACTGTAAGTACTGATTGCTG	GGTCGAACATGTTGA ACATGCTCAGAA	2
AM2 451 5	ss161 14850 7	A/ T	GAAGGTGACCAAGTTCATGCTAAGCC TAATTTGCTGCAGGAATAGATA	GAAGGTCGGAGTCAACGGATTAAGCC TAATTTGCTGCAGGAATAGATT	TCAAAGAATGTTCTTC TGGGGTGTCTTCTT	2
AM2 532 6	ss161 14931 8	C/ T	GAAGGTGACCAAGTTCATGCTGTAAA TAGTCCCATATGATATCTCG	GAAGGTCGGAGTCAACGGATTCTGTA AATAGTCCCATATGATATCTCA	CACCTCAAGTACTCAT GACAAATGTTCAA	2
AM2 549 7	ss161 14948 9	A/ G	GAAGGTGACCAAGTTCATGCTGTTAGT TTTGTAGAATCAAATGACAATGTCTT	GAAGGTCGGAGTCAACGGATTAGTTT TGTAGAATCAAATGACAATGTCTC	TCGACACTGATCTCT CGGTAACAT	2
AM2 591 9	ss161 14991 1	A/ G	GAAGGTGACCAAGTTCATGCTGTTATT GTTATGTATTGAGGTGTAATTGT	GAAGGTCGGAGTCAACGGATTATTGT TATGTATTGAGGTGTAATTGC	CACAATATCTCTTTCA GCCATACCATCAA	2
AM2 595 3	ss161 14994 5	C/ T	GAAGGTGACCAAGTTCATGCTTCATT AAATTACAAAAATTACATTACATGCG	GAAGGTCGGAGTCAACGGATTATTTA AATTACAAAAATTACATTACATGCA	ATGTGTATAAACACA TCACAATACTCTCTA	2
AM2 617	ss161 15016	C/ T	GAAGGTGACCAAGTTCATGCTAGGCT TTCCAGCAACACTCGTG	GAAGGTCGGAGTCAACGGATTAGGC TTCCAGCAACACTCGTA	TGAGCATAGCTGACT AAATAACACTAACAA	2

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AM1 950 1	ss161 14349 3	A/ G	GAAGGTGACCAAGTTCATG CTAGATTC CAGACACATATCATAACTTCTTT	GAAGGTCGGAGTCAACGGATT CCAGA CACATATCATAACTTCTTC	GTAAATCAACAAGTG AATGCTCTTCCTCAT	1 5	
AM1 950 2	ss161 14349 4	C/ T	GAAGGTGACCAAGTTCATG CTGCAAG CAGATTCCAGACACG	GAAGGTCGGAGTCAACGGATT ACTGC AAGCAGATTCCAGACACA	CTCATAGGACGAATC GTTTTGCCGAA	1 5	
AM1 950 3	ss161 14349 5	C/ T	GAAGGTGACCAAGTTCATG CTCATCAT GCAACATACGCACCTAC	GAAGGTCGGAGTCAACGGATT AGCAT CATGCAACATACGCACCTAT	GAAGAAGTGCATATG CTCTCCCAT	1 5	
AM2 033 3	ss161 14432 5	A/ C	GAAGGTGACCAAGTTCATG CTGGGTA ATATCATTATTCTTCAATTTTCAGTT	GAAGGTCGGAGTCAACGGATT GGGTA ATATCATTATTCTTCAATTTTCAGTG	CACGTACATCAGTAC AGTACACCTA	1 5	
AM2 053 3	ss161 14452 5	C/ T	GAAGGTGACCAAGTTCATG CTCGATA AAAGAAAAATATTCTCCGCCTTC	GAAGGTCGGAGTCAACGGATT CGATA AAAGAAAAATATTCTCCGCCTTT	CCAATCTTTAATGGG ACTGACCCAGAT	1 5	
AM2 156 8	ss161 14556 0	C/ T	GAAGGTGACCAAGTTCATG CTAAATG TTGTGACTTACGTTGTGTCG	GAAGGTCGGAGTCAACGGATT CAAAT GTTGTGACTTACGTTGTGTC	TACCTTCTCCATACTC CTCGGTCAT	1 5	
AM2 213 7	ss161 14612 9	A/ C	GAAGGTGACCAAGTTCATG CTGCATG CATACAAGCTTTAATTTGTCGAT	GAAGGTCGGAGTCAACGGATT CATGC ATACAAGCTTTAATTTGTCGAG	CATTGCCCCACCAAT TGTTCTTT	1 5	
AM2 422 4	ss161 14821 6	A/ G	GAAGGTGACCAAGTTCATG CTGGATG GGAACAAAGAAATGATGGCA	GAAGGTCGGAGTCAACGGATT GATGG GAACAAAGAAATGATGGCG	GGTTACATAACATGA TGAGCATGAACCAA	1 5	
AM2 446 0	ss161 14845 2	A/ G	GAAGGTGACCAAGTTCATG CTTAGATC AAGTCAGACACTGATTAACA	GAAGGTCGGAGTCAACGGATT AGATC AAGTCAGACACTGATTAACG	GATCTTGTCTTTTTT CCTACCATAGTTAT	1 5	
AM2 465 5	ss161 14864 7	A/ T	GAAGGTGACCAAGTTCATG CTGAATCT TCTCCAAATGAAAAGTTACTTCAAT	GAAGGTCGGAGTCAACGGATT GAATC TTCTCCAAATGAAAAGTTACTTCAA	CAATTGTTAGGAACC CTTCAGGGGAT	1 5	
AM2 500 2	ss161 14899 4	A/ T	GAAGGTGACCAAGTTCATG CTACTCAA TTTTGAACTTATAATCTTAATCAATA	GAAGGTCGGAGTCAACGGATT ACTCA ATTTTGAACTTATAATCTTAATCAATT	CAATTAACCTAATGC GTTGCAGTAACTCAA	1 5	
AM2 649 8	ss161 15049 0	A/ T	GAAGGTGACCAAGTTCATG CTGATTTG TTGCTGCTGGTTTGAGA	GAAGGTCGGAGTCAACGGATT CTGAT TTGTTGCTGCTGGTTTGAGT	CAAACAACCTCAGCAG AACCAGCACAA	1 5	

¹dbSNP in GenBank under the handle MAUGHAN in batch number 2009A, build B131.

²KASPar™ primers: A1 are A2 primers are SNP allele specific. Bolded portions of the primers identify the sequence tags used in the KASPar™ secondary PCR reaction.

³Linkage Groups are numbers as described by Maughan et al. [22].