## **Table S1.** *ERMAP* primers

| Name | Sequence (5’→3’) | Orientation | Use | | |
|---|---|---|---|---|---|
| | | | Primary amplicon | Nested PCR allele-specific | Sequencing |
| ScF3 | GTGCTCCATGAGTCAAGCGATTAC | Sense | Yes | No | Yes |
| SCSEQ_1 | CCGCCTGTCTTGCTTTCATA | Anti-sense | No | No | Yes |
| SCSEQ_2 | TTCTCGCTGTCCCTGTAAA | Anti-sense | No | No | Yes |
| SCSEQ_3 | CAGGGTGTAGCTGGAGATAAAG | Sense | No | No | Yes |
| SCSEQ_4 | CCATCACCAAGGATAGCAGATAA | Anti-sense | No | No | Yes |
| SCSEQ_5 | CAGAGCAAGACCCTGTCTTAAA | Anti-sense | No | No | Yes |
| SCSEQ_6 | GCAAATGACCACCACACTTTAC | Anti-sense | No | No | Yes |
| SCSEQ_7 | TGCACCAGATGCTGGAAATAA | Anti-sense | No | No | Yes |
| SCSEQ_8 | GGTACCCTGAAGTGTGTATGAT | Sense | No | No | Yes |
| SCSEQ_9 | GGAGACTGGGAAACTGAAGATG | Anti-sense | No | No | Yes |
| SCSEQ_10 | GTCCCTAGGAAGGTTGCATAAC | Anti-sense | No | No | Yes |
| SCSEQ_11 | CAATCCCAGCTCTGCTACTTAC | Anti-sense | No | No | Yes |
| SCSEQ_12 | GGAAGGGATGAGGAAGAGGATA | Anti-sense | No | No | Yes |
| SCSEQ_13 | AATGGACATGGCTGGGTAAG | Anti-sense | No | No | Yes |
| SCSEQ_14 | TGCCCAAGAGGGAAGTGTC | Sense | No | No | Yes |
| SCSEQ_15 | CCCAAACCATGTCTTTGCATTT | Sense | No | No | Yes |
| SCSEQ_16 | GTTGTGGTGAGCCCAGATAG | Anti-sense | No | No | Yes |
| SCSEQ_17 | CTTGTCCTCTCTCCACTCTCT | Anti-sense | No | No | Yes |
| SCSEQ_18 | CCTCCCGAGTAGCTGGATTA | Sense | No | No | Yes |
| SCSEQ_19 | AGGACCATACCCTGGCAGAG | Sense | No | No | Yes |
| SCSEQ_20 | CTTTGCCCATGTCCCTAAGTAA | Sense | No | No | Yes |
| SCSEQ_21 | CGGCTACTTAGGAGACTGAATG | Sense | No | No | Yes |
| SCSEQ_22 | AGGACCATCCAAACCATTCC | Sense | No | No | Yes |
| SCSEQ_23 | TTAGACATCTCCCTGAGGT | Sense | No | No | Yes |
| SCSEQ_24 | TCCAACACTCCTGCCCTTAT | Sense | No | No | Yes |
| SCSEQ_25 | GGAGTCGAGTAGCTTGAACAT | Sense | No | No | Yes |
| SCSEQ_26 | GCAGTGGTAAAGCAAGGAATG | Sense | No | No | Yes |
| SCSEQ_27 | GGAAAGGCTAATGAAGGGAGTT | Anti-sense | No | No | Yes |
| SCSEQ_28 | GGAGGTGGAGGTGAAGATAGA | Sense | No | No | Yes |
| SCSEQ_29 | GTCAGTGACACCTCAGATCATT | Sense | No | No | Yes |
| SCSEQ_30 | GAGAGGATTCAGTGCCTACTTC | Sense | No | No | Yes |
| SCSEQ_31 | GCCGACAGCAGAAATGAAAC | Sense | No | No | Yes |
| SCSEQ_32 | ACGTTTCACCAGGAAGAGATAG | Sense | No | No | Yes |
| SCSEQ_33 | GTGAGCCGAGATTGCACTATT | Sense | No | No | Yes |
| SCSEQ_34 | CTTCCGTACCAACTTATCTCCTG | Sense | No | No | Yes |
| SCSEQ_35 | GTGACTTGTCTGTTCCTGTTCTA | Sense | No | No | Yes |
| SCSEQ_36 | CCTTCAGGCAGAGTACAACAA | Sense | No | No | Yes |
| SCSEQ_37 | GTTCATCAAGTCTGCACAATAGC | Sense | No | No | Yes |
| SCSEQ_38 | ACTTCCCACTAAGCCCTACCT | Sense | No | No | Yes |
| SCSEQ_39 | GCAGTGGCAGTGACCCTGGAC | Sense | No | No | Yes |
| SCSEQ_40 | GGAGGAAGTGCTCTGAGATATG | Anti-sense | No | No | Yes |
| SCSEQ_41 | CCAGTCCCTGACTTCTTACTTATC | Sense | No | No | Yes |

| | | | | | |
|---|---|---|---|---|---|
| SCSEQ_42 | CTAGCTGGACCTCTCTGAATCT | Anti-sense | No | No | Yes |
| SCSEQ_43 | CTGCTCACTGACTCACTACATAC | Anti-sense | No | No | Yes |
| SCSEQ_44 | GAGATAGGGCCTTGCTCT | Sense | No | No | Yes |
| SCSEQ_45 | GAGACAGAGTCTCGCTCCGT | Anti-sense | No | No | Yes |
| SCSEQ_46 | GAGACAGAGTTTCACTCTGC | Anti-sense | No | No | Yes |
| ScR3 | TACCTTCCCCACAACTCCTCATTC | Anti-sense | Yes | No | Yes |
| SCAS_1 | GGGCGGATCACAAGGTCA | Sense | No | Yes | No |
| SCAS_2 | GGGCGGATCACAAGGTCG | Sense | No | Yes | No |
| SCAS_3 | CCAAATGTGGGCGGGCCTT | Anti-sense | No | Yes | No |
| SCAS_4 | CCAAATGTGGGCGGGCCTC | Anti-sense | No | Yes | No |
| SCAS_5 | ACCAAAACACAAATACCAAACTTTC | Anti-sense | No | Yes | No |
| SCAS_6 | ACCAAAACACAAATACCAAACTTTT | Anti-sense | No | Yes | No |
| SCAS_7 | AATGCACATAATGTAGCACTTGGTG | Sense | No | Yes | No |
| SCAS_8 | AATGCACATAATGTAGCACTTGGTA | Sense | No | Yes | No |
| SCAS_9 | GGTGTTAGCTTTGGTGAACTT | Sense | No | Yes | No |
| SCAS_10 | GGTGTTAGCTTTGGTGAACTC | Sense | No | Yes | No |

**Table S2.** Genetic variations detected in the *ERMAP* gene

| Location | Nucleotide Change * | dbSNP reference no. | Protein residue change † | Donor observations (N=50) | | | HWE *p* value | Global VAF‡ | Observed in the present study | Position in Table 1 and Table S4 |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Homozygous | Heterozygous | VAF | | | | |
| Intron 1 | -121-1490A>G | rs7538928 | NA | 1 | 10 | 0.12 | 0.707 | 0.131 | Yes | 1 |
| | -121-1257T>C | rs12126596 | NA | 10 | 22 | 0.42 | 0.493 | 0.382 | Yes | 2 |
| | -121-795T>C | rs6600425 | NA | 50 | 0 | 1.00 | NA | 0.989 | No | NA |
| | -121-522T>C | rs6691307 | NA | 0 | 2 | 0.02 | 0.885 | 0.020 | Yes | 3 |
| | -121-452G>A | Novel | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 4 |
| Intron 2 | -6+634G>T | Novel | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 5 |
| | -6+798C>T | rs190962346 | NA | 0 | 1 | 0.01 | 0.943 | 0.002 | Yes | 6 |
| | -6+1397G>A | rs6658001 | NA | 5 | 19 | 0.29 | 0.585 | 0.286 | Yes | 7 |
| | -6+1466C>T | Novel | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 8 |
| | -6+1835C>A | rs1471747 | NA | 50 | 0 | 1.00 | NA | 0.989 | No | NA |
| | -6+1993C>T | rs183580459 | NA | 0 | 1 | 0.01 | 0.943 | 0.001 | Yes | 9 |
| | -6+2239A>G | rs35531445 | NA | 0 | 1 | 0.01 | 0.943 | 0.029 | Yes | 10 |
| | -5-1676G>A | rs35245962 | NA | 1 | 11 | 0.13 | 0.846 | 0.132 | Yes | 11 |
| | -5-1479G>A | rs114193579 | NA | 0 | 2 | 0.02 | 0.885 | 0.008 | Yes | 12 |
| | -5-1374C>G | rs6703396 | NA | 0 | 2 | 0.02 | 0.885 | 0.017 | Yes | 13 |
| | -5-1072C>T | rs529383471 | NA | 0 | 1 | 0.01 | 0.943 | 0.001 | Yes | 14 |
| | -5-477G>C | rs551984772 | NA | 0 | 1 | 0.01 | 0.943 | 0.001 | Yes | 15 |
| | -5-297C>T | rs35568889 | NA | 0 | 1 | 0.01 | 0.943 | 0.010 | Yes | 16 |
| Exon 3 | -3C>T | rs543001910 | NA | 0 | 1 | 0.01 | 0.943 | 0.000 | Yes | 17 |
| | -2G>A | rs12124733 | NA | 7 | 28 | 0.42 | 0.290 | 0.335 | Yes | 18 |
| | 11C>T | rs35757049 | Ala4Val | 0 | 2 | 0.02 | 0.885 | 0.017 | Yes | 19 |
| | 54C>T | rs33950227 | Leu18Leu | 1 | 11 | 0.13 | 0.846 | 0.146 | Yes | 20 |
| | 76C>T | rs33953680 | His26Tyr | 2 | 11 | 0.15 | 0.331 | 0.142 | Yes | 21 |
| Intron 3 | 86-85G>T | rs12727498 | NA | 4 | 19 | 0.27 | 0.798 | NA | Yes | 22 |
| | 86-79G>A | Novel | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 23 |
| | 86-60C>A | rs138466210 | NA | 0 | 1 | 0.01 | 0.943 | 0.000 | Yes | 24 |
| Exon 4 | 103G>A | rs146429994 | Gly35 Ser | 0 | 0 | 0.00 | NA | 0.002 | No | NA |
| | 139G>A | rs56047316 | Glu47Lys | 0 | 0 | 0.00 | NA | 0.001 | No | NA |
| | 169G>A | rs56025238 | Gly57Arg | 0 | 0 | 0.00 | NA | 0.001 | No | NA |
| | 178C>G | rs56136737 | Pro60Ala | 0 | 0 | 0.00 | NA | NA | No | NA |
| | 242G>A | rs368064875 | Arg81Gln | 0 | 0 | 0.00 | NA | NA | No | NA |
| | 307_308delGA | rs387906265 | Asp103Cysfs | 0 | 0 | 0.00 | NA | NA | No | NA |
| Intron 4 | 433+296T>G | rs17386017 | NA | 2 | 11 | 0.15 | 0.331 | 0.158 | Yes | 25 |
| | 433+436T>G | rs115186448 | NA | 0 | 9 | 0.09 | 0.484 | 0.03 | Yes | 26 |
| | 433+792A>T | rs12123271 | NA | 6 | 18 | 0.30 | 0.312 | 0.266 | Yes | 27 |
| | 433+1097A>G | rs12028144 | NA | 2 | 10 | 0.14 | 0.230 | 0.158 | Yes | 28 |
| | 433+1162G>A | rs34052572 | NA | 0 | 4 | 0.04 | 0.768 | 0.007 | Yes | 29 |
| | 433+1225C>T | rs191545157 | NA | 0 | 1 | 0.01 | 0.943 | 0.002 | Yes | 30 |
| | 433+1239A>G | rs11210725 | NA | 50 | 0 | 1.00 | NA | 0.989 | No | NA |
| | 433+1281T>C | rs11580112 | NA | 6 | 29 | 0.41 | 0.159 | 0.445 | Yes | 31 |
| | 433+1345C>G | rs34496324 | NA | 0 | 4 | 0.04 | 0.768 | 0.035 | Yes | 32 |
| | 433+1492T>C | rs11802698 | NA | 0 | 4 | 0.04 | 0.768 | 0.044 | Yes | 33 |
| | 433+1548A>G | rs10789427 | NA | 50 | 0 | 1.00 | NA | 0.988 | No | NA |
| | 433+1577G>A | rs35837615 | NA | 0 | 1 | 0.01 | 0.943 | 0.002 | Yes | 34 |
| | 433+1763A>G | rs56161641 | NA | 17 | 29 | 0.63 | 0.084 | 0.679 | Yes | 35 |
| | 434-1838C>T | rs4660671 | NA | 0 | 12 | 0.12 | 0.334 | 0.157 | Yes | 36 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | 434-1588A>G | rs11210726 | NA | 16 | 28 | 0.60 | 0.238 | 0.662 | Yes | 37 |
| | 434-1479T>C | rs747148476 | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 38 |
| | 434-1474G>A | rs12073215 | NA | 0 | 4 | 0.04 | 0.768 | 0.044 | Yes | 39 |
| | 434-1409G>A | rs58724795 | NA | 0 | 2 | 0.02 | 0.885 | 0.027 | Yes | 40 |
| | 434-1173T>C | rs7540312 | NA | 4 | 24 | 0.32 | 0.466 | 0.276 | Yes | 41 |
| | 434-1061G>A | rs7548186 | NA | 44 | 5 | 0.93 | 0.100 | 0.877 | Yes | 42 |
| | 434-874T>C | rs7540604 | NA | 20 | 24 | 0.64 | 0.768 | 0.660 | Yes | 43 |
| | 434-456T>C | rs35805842 | NA | 0 | 8 | 0.08 | 0.538 | 0.140 | Yes | 44 |
| | 434-46T>C | rs4660672 | NA | 16 | 20 | 0.52 | 0.159 | 0.418 | Yes | 45 |
| Intron 5 | 550+96C>G | rs4660673 | NA | 22 | 23 | 0.67 | 0.775 | 0.748 | Yes | 46 |
| | 551-12T>C | rs149950197 | NA | 0 | 1 | 0.01 | 0.943 | 0.018 | Yes | 47 |
| Intron 6 | 583+253C>T | Novel | NA | 0 | 2 | 0.02 | 0.885 | NA | Yes | 48 |
| | 584-314A>T | rs11581978 | NA | 1 | 8 | 0.10 | 0.432 | 0.114 | Yes | 49 |
| Intron 7 | 616+110C>G | rs1466548 | NA | 17 | 21 | 0.55 | 0.284 | 0.446 | Yes | 50 |
| | 616+504G>C | rs17386162 | NA | 1 | 8 | 0.10 | 0.432 | 0.114 | Yes | 51 |
| | 616+675G>A | rs11210727 | NA | 2 | 18 | 0.22 | 0.729 | 0.186 | Yes | 52 |
| | 616+719C>T | rs7522285 | NA | 47 | 3 | 0.97 | 0.826 | 0.971 | Yes | 53 |
| | 617-498C>T | rs35932223 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 54 |
| | 617-485C>T | rs35828903 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 55 |
| | 617-398C>A | rs11210728 | NA | 50 | 0 | 1.00 | NA | 0.976 | No | NA |
| | 617-336G>C | rs34391768 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 56 |
| | 617-204C>A | rs35761132 | NA | 1 | 8 | 0.10 | 0.432 | 0.114 | Yes | 57 |
| Intron 8 | c.637+33C>G | rs34228099 | NA | 0 | 1 | 0.01 | 0.943 | 0.009 | Yes | 58 |
| Intron 9 | 658+29G>A | rs12034000 | NA | 7 | 25 | 0.39 | 0.719 | 0.260 | Yes | 59 |
| Intron 11 | 712+161G>A | rs11210729 | NA | 3 | 17 | 0.23 | 0.776 | 0.186 | Yes | 60 |
| | 712+250G>A | rs1466549 | NA | 50 | 0 | 1.00 | NA | 0.996 | No | NA |
| | 713-1097G>A | Novel | NA | 0 | 1 | 0.01 | 0.943 | NA | Yes | 61 |
| | 713-606A>G | rs11210730 | NA | 50 | 0 | 1.00 | NA | 0.004 | No | NA |
| | 713-556G>A | rs12078281 | NA | 3 | 26 | 0.32 | 0.168 | 0.267 | Yes | 62 |
| | 713-364C>G | rs35303774 | NA | 0 | 1 | 0.01 | 0.943 | 0.017 | Yes | 63 |
| | 713-34C>G | rs34993626 | NA | 0 | 3 | 0.03 | 0.826 | 0.018 | Yes | 64 |
| Exon 12 | 888G>A | rs35972628 | Glu296Glu | 0 | 1 | 0.01 | 0.943 | 0.001 | Yes | 65 |
| | 936G>A | rs140414272 | Glu312Glu | 0 | 1 | 0.01 | 0.943 | 0.000 | Yes | 66 |
| | 994C>T | NA | Arg332Ter | 0 | 0 | 0.00 | NA | NA | No | NA |
| Exon 12 (3' UTR) | c.*484_*485insT | rs55986603 | NA | 0 | 0 | 0.00 | NA | NA | No | NA |
| | *645G>A | rs1484324 | NA | 47 | 3 | 0.97 | 0.826 | 0.0940 | Yes | 67 |
| | *939G>C | rs10789428 | NA | 50 | 0 | 1.00 | NA | 0.989 | No | NA |
| | *1122T>C | rs36098574 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 68 |
| | *1129T>C | rs148274743 | NA | 0 | 1 | 0.01 | 0.943 | 0.001 | Yes | 69 |
| | *1424A>G | rs34137903 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 70 |
| | *1526A>G | rs34423918 | NA | 0 | 3 | 0.03 | 0.826 | 0.012 | Yes | 71 |
| | *1736A>G | rs12406279 | NA | 1 | 8 | 0.10 | 0.432 | 0.115 | Yes | 72 |

* relative to NCBI Reference Sequence NM_001017922.1

† relative to NCBI Reference Sequence NP_001017922.1

‡ global VAF from 1000Genome phase 1 genotype data from 1094 worldwide individuals

VAF-variant allele frequency

NA- Not available

## **Table S3.** *ERMAP* genotypes observed in the 50 individuals

| Genotype number | Genotype | Total |
|---|---|---|
| 1 | A/A T/C C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/T G/G C/C T/T T/T A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 2 |
| 2 | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C A/A C/C C/C C/C G/G G/G C/C T/T T/T T/T A/A<br>G/G C/C G/G T/T C/C T/T G/G G/G A/A C/C A/A T/T G/G G/G C/C<br>A/A T/T T/T T/T C/C T/T C/C A/A G/C G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/G G/A A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 3 | A/A T/T C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/G C/C C/C C/C G/T G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G C/C C/C T/T G/G G/G G/G C/T G/G T/T G/G G/G T/T<br>A/A C/C T/T C/C G/G T/T C/C A/A C/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/G G/G A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 4 | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C A/A C/C C/C C/C G/G G/G C/C T/T T/T T/T A/A<br>G/G C/C G/G T/T C/C T/T G/G G/G A/A C/C A/A T/T G/G G/G C/C<br>A/A T/T T/T T/T C/C T/T C/C A/A G/G G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C A/A G/G A/A G/G G/G A/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 5 | A/A T/C C/C T/T G/A G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/T G/G C/C T/T T/T T/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/C C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 6 | A/A T/C C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/T G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/T<br>A/A C/C T/C C/T G/G T/T C/C A/A G/C G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/G C/C C/C G/G G/G G/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 7 | A/A T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/T A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/A G/C G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/G G/A A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 8 | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C A/A C/C C/C C/C G/G G/G C/C T/T T/T T/T A/A<br>G/G C/C G/G T/T C/C T/T G/G G/G A/A C/C A/A T/T G/G G/G C/C<br>A/A T/T T/T T/T C/C T/T C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 9 | A/A T/C C/C T/T G/G G/T C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/T G/G G/G C/C T/G T/T T/T A/G<br>G/G C/C G/G T/T C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G C/C<br>A/A C/T T/T C/T G/C T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
|  |  |  |

| | | | |
|---|---|---|---|
| 10 | | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/G A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A C/T T/C T/T G/C T/T C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 11 | | A/G T/T C/C T/T G/G G/G C/C G/A C/C A/A C/T A/A G/A G/G C/C<br>C/C G/G C/C C/C G/G C/C C/T C/T G/T G/G C/C T/G T/T A/A A/G<br>G/G C/C G/G T/C C/C T/T G/G G/G G/G C/C G/G T/T G/G G/G T/T<br>A/A C/C T/T C/C G/G T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 12 | | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/G A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A C/T T/C T/T G/C T/T C/C A/A G/G G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/G C/C<br>T/T T/T A/A A/A A/A | 1 |
| 13 | | A/G T/T C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/C G/G C/C C/T C/T G/T G/G C/C T/G T/T A/A A/G<br>G/G C/C G/G T/C C/C T/T G/G G/G G/G C/C G/G T/T G/G G/G T/T<br>A/A C/C T/T C/C G/G T/T C/C A/T G/C G/C G/A T/T C/C C/C A/A<br>G/G C/A C/C G/G G/A A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/G | 1 |
| 14 | | A/G T/T C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/T G/G C/C C/T T/T G/G G/G C/C G/G T/T A/A G/G<br>G/G C/C G/G T/T C/C T/T G/G G/G G/G C/C G/G T/T G/G G/G T/C<br>A/A C/C T/T C/C G/G T/T C/T A/A C/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/G G/G A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 15 | | A/A T/T C/C T/T G/G G/G C/C A/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/G C/C C/C C/C T/T G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G C/C C/C T/T G/G G/G G/G C/C G/G T/T G/G G/G T/T<br>A/A C/C T/T C/C G/G T/T C/C A/A G/C G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/G G/A A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 16 | | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/G C/T G/A T/T G/G G/G T/C<br>A/A C/C T/C T/T G/G T/T C/C A/A G/G G/G A/A T/T C/C C/C A/A<br>G/G C/C C/C G/G A/A A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 17 | | A/G T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/C G/A C/C C/T C/T G/G G/G C/C T/G T/G A/A A/G<br>G/G C/C G/G T/T C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/T G/C G/C G/G T/T C/C C/C A/A<br>G/G C/A C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/G | 1 |
| 18 | | A/A T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/T A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A T/T T/T C/T G/C T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 19 | | A/A T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/C G/A C/C C/T C/T G/G G/G C/C T/G T/T A/T A/A<br>G/G C/C G/G T/T C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/C G/A G/A A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 20 | G/G | T/T | C/C | T/T | G/G | G/G | C/C | G/G | C/C | A/A | C/C | A/A | A/A | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | T/T | T/T | G/G | G/G | C/C | G/G | T/T | A/A | G/G | |
| | G/G | C/T | G/G | T/T | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/T | C/C | G/C | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/A | C/C | G/G | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/G | | | | | | | | | | | |
| 21 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/T | A/A | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/A | C/C | G/A | T/T | G/G | G/G | T/C | |
| | A/A | C/T | T/T | C/T | G/C | T/T | C/C | A/A | G/G | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | A/A | G/G | A/A | G/G | G/G | A/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 22 | A/G | T/T | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/A | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/T | C/T | G/T | G/G | C/C | T/G | T/T | A/A | A/G | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/T | C/C | G/C | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/A | C/C | A/A | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/G | | | | | | | | | | | |
| 23 | A/A | C/C | C/C | T/T | G/G | G/G | C/C | G/G | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 2 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/G | G/G | C/C | T/T | T/G | A/T | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/A | C/T | G/A | T/T | G/G | G/G | T/T | |
| | A/A | C/T | T/C | T/T | G/C | T/T | C/C | A/A | G/G | G/G | G/A | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/A | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 24 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/G | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | A/A | C/C | C/C | C/C | G/G | G/G | C/C | T/T | T/T | T/T | A/A | |
| | G/G | C/C | G/G | T/T | C/C | T/T | G/G | G/G | G/A | C/C | G/A | T/T | G/G | G/G | T/C | |
| | A/G | T/T | T/T | T/T | G/C | T/T | C/C | A/A | C/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/G | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/G | C/C | |
| | T/T | T/C | A/A | A/A | A/A | | | | | | | | | | | |
| 25 | A/G | T/T | C/C | T/T | G/G | G/G | C/C | G/G | C/C | A/A | C/C | A/A | G/A | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/T | C/T | G/G | G/G | C/C | T/G | T/T | A/A | A/G | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/A | G/G | G/G | G/A | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/A | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 26 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/G | A/T | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/A | C/C | G/A | T/T | G/G | G/G | T/T | |
| | A/A | C/T | T/T | C/T | G/C | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/G | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 27 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/T | A/T | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/A | C/C | G/A | T/T | G/G | G/G | T/C | |
| | A/A | C/T | T/T | C/T | G/C | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/G | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 28 | A/A | T/T | C/C | T/T | G/G | G/G | C/C | A/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/C | C/C | T/T | G/G | C/C | T/T | T/T | A/A | A/A | |
| | G/G | C/C | G/G | C/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/A | G/G | G/G | A/A | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/G | A/A | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 29 | A/A | T/C | C/C | T/T | G/G | G/G | C/T | G/G | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/T | G/C | C/C | C/C | G/A | C/C | C/C | C/C | G/G | G/G | C/C | T/T | T/T | A/T | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/G | C/T | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/T | T/C | C/C | G/G | T/T | C/C | A/A | G/G | G/G | G/A | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/A | A/A | G/A | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |

| | | |
|---|---|---|
| 30 | A/G T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/A G/A C/C<br>C/C G/G C/C C/C G/A C/C C/T C/T G/G G/G C/C T/G T/T A/T A/G<br>G/G C/C G/G T/T C/C T/T G/G G/A G/A C/C G/A T/C G/G G/G T/C<br>A/A C/T T/T T/T G/C T/T C/T A/T G/C G/C G/G T/T C/C C/C A/A<br>G/G C/A C/C A/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/G | 1 |
| 31 | A/A T/T C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/G A/A A/A<br>G/G C/C G/G T/T C/C T/C G/G G/G G/A C/C G/A T/T G/A G/A T/T<br>G/G T/T T/T C/T G/G T/T C/C A/A G/G G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C A/A G/G A/A G/G G/G A/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 32 | A/A T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/T A/T A/A<br>G/G C/C G/G T/C C/C T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 33 | A/A T/C C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/T G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/C C/G T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/C T/T C/T G/C T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 2 |
| 34 | A/A T/C C/C T/C G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/G<br>C/C G/G C/T C/C A/A C/T C/C C/C G/G G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/T C/G T/T G/G G/G G/A C/C A/A T/T G/G G/G T/C<br>A/G C/C T/C T/T C/C T/T C/C A/A G/G G/G G/A T/T C/C C/C A/A<br>G/G C/C C/G G/A G/A A/A G/G G/G G/A C/G C/C G/G G/A A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 35 | A/A T/T C/C T/T G/G G/G C/C G/A C/C A/A C/C A/G G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/T G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/C C/C T/C G/G G/G G/G C/C G/A T/T A/A G/G T/T<br>A/G C/T T/T C/T G/G T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 36 | A/A C/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/A C/C C/C C/C G/G G/G C/C T/T T/T A/A A/A<br>G/G C/C G/G T/C C/G T/T G/G G/G G/A C/T G/A T/T G/G G/G T/C<br>A/A C/C T/T C/T G/C T/T C/C A/A G/C G/G G/G T/T C/C C/C A/A<br>G/G C/C C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/A | 1 |
| 37 | A/A T/T C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/G G/G C/C<br>C/C G/G C/C C/C G/G C/C C/C C/C G/T G/G C/C T/T T/T A/A A/A<br>G/A C/C G/G T/C C/C T/T G/G G/G G/G C/C G/G T/T G/G G/A T/T<br>G/G C/T T/T C/C G/G T/T C/C A/A C/C G/G G/G T/C C/T C/T A/A<br>G/C C/C C/C G/G G/G A/A G/G G/G G/G C/C C/G G/G G/G A/A C/C<br>T/C T/T A/G A/G A/A | 1 |
| 38 | A/G T/C C/C T/T G/G G/G C/C G/G C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/C G/A C/C C/T C/T G/G G/G C/C T/G T/G A/A A/G<br>G/G C/C G/G T/T C/C T/T G/G G/G G/A C/C G/A T/T G/G G/G T/C<br>A/A C/T T/T C/T G/C T/T C/C A/T G/C G/C G/G T/T C/C C/C A/A<br>G/G C/A C/C G/A G/G A/A G/G G/G G/A C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/G | 1 |
| 39 | A/G T/T C/C T/T G/G G/G C/C G/A C/C A/A C/C A/A G/A G/G C/C<br>C/C G/G C/C C/C G/G C/C C/T C/T G/T G/G C/C T/G T/T A/A A/G<br>G/G C/C G/G T/C C/C T/T G/G G/G G/G C/C G/G T/T G/G G/G T/T<br>A/A C/C T/T C/C G/G T/T C/C A/T C/C G/C G/G T/T C/C C/C A/A<br>G/G C/A C/C G/G G/G A/A G/G G/G G/G C/C C/C G/G G/G A/A C/C<br>T/T T/T A/A A/A A/G | 1 |
| | | |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 40 | A/A | T/T | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/G | A/A | A/A | |
| | G/A | C/C | G/G | T/C | C/C | T/C | G/G | G/G | G/A | C/C | G/A | T/T | A/A | G/G | T/T | |
| | A/G | C/T | T/T | C/T | G/G | T/T | C/C | T/T | C/C | C/C | G/G | T/T | C/C | C/C | A/A | |
| | G/G | A/A | C/C | G/G | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/A | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | G/G | | | | | | | | | | | |
| 41 | A/G | T/T | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/A | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/T | C/T | G/T | G/A | C/A | T/G | T/T | A/A | A/G | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/A | C/C | G/G | G/A | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/G | G/A | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 42 | A/A | C/C | C/C | T/C | G/G | G/G | C/C | G/G | C/C | A/A | C/C | A/A | G/G | G/G | C/G | 1 |
| | C/C | G/G | C/C | C/C | A/A | C/T | C/C | C/C | G/G | G/G | C/C | T/T | T/T | A/T | A/A | |
| | G/G | C/C | G/G | T/T | C/C | T/T | G/G | G/G | G/G | C/T | A/A | T/T | G/G | G/G | T/C | |
| | A/A | C/T | T/C | T/T | C/C | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/G | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 43 | A/A | T/T | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/T | A/A | A/A | |
| | G/G | C/C | G/G | C/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/G | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 44 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/A | C/C | A/A | C/C | A/A | G/G | G/A | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/T | G/G | C/C | T/T | T/T | A/T | A/A | |
| | G/G | C/C | G/G | T/C | C/C | T/T | G/G | G/G | G/A | C/C | G/A | T/T | G/G | G/G | T/C | |
| | A/A | C/T | T/T | C/T | G/C | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | A/A | G/G | A/A | G/G | G/G | G/A | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 45 | A/A | T/C | C/C | T/T | G/G | G/G | C/C | G/G | C/T | A/A | C/C | A/A | G/G | G/G | C/C | 1 |
| | C/C | G/G | C/C | C/C | G/A | C/C | C/C | C/C | G/G | G/G | C/C | T/T | T/T | A/A | A/A | |
| | G/G | C/C | G/G | T/T | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/T | T/T | T/T | G/G | T/T | C/C | A/A | G/C | G/G | G/G | T/T | C/C | C/C | A/A | |
| | G/G | C/C | C/C | G/A | G/G | A/A | G/G | G/G | G/G | C/C | C/C | G/G | G/G | A/A | C/C | |
| | T/T | T/T | A/A | A/A | A/A | | | | | | | | | | | |
| 46 | A/A | T/T | C/C | T/T | G/G | G/G | C/C | A/A | C/C | A/A | C/C | A/A | G/G | G/G | C/C | 2 |
| | C/C | G/G | C/C | C/C | G/G | C/C | C/C | C/C | T/T | G/G | C/C | T/T | T/T | A/A | A/A | |
| | G/A | C/C | G/G | C/C | C/C | T/T | G/G | G/G | G/G | C/C | G/G | T/T | G/G | G/G | T/T | |
| | A/A | C/C | T/T | C/C | G/G | T/T | C/C | A/A | C/C | G/G | G/G | T/C | C/T | C/T | A/A | |
| | G/C | C/C | C/C | G/G | G/G | A/A | G/G | G/G | G/G | C/C | C/G | G/G | G/G | A/A | C/C | |
| | T/C | T/T | A/G | A/G | A/A | | | | | | | | | | | |

**Table S4.** Comparison of alleles predicted by MaCH and confirmed by allele-specific PCR

| Allele number | GenBank number | Allele (confirmed haplotype) | Frequency Predicted by MaCH | Frequency Confirmed by sequencing |
|---|---|---|---|---|
| 1 | KX265235 | ATTGGCACCAGGCCGCCGCCCTGCTTAAGCCCTGGCGTGGTACTCGTCACGGTCCGCCGGGGCCGGATTAAA | 7 | 8 |
| 2 | KX265236 | -C----G----------A---G----T---T---A-A---C-T-TC---G--------A--A---------- | 11 | 12 |
| 3 | KX265189 | -------------------------------------------------G-A-------A------------ | 7 | 7 |
| 4 | KX265190 | G-----G---A--------TTG--G--G--T-----------------T-C--------------------G | 5 | 5 |
| 5 | KX265191 | -C----G--------------G-------------T-------CT----G-A-------A------------ | 4 | 5 |
| 6 | KX265192 | -C----G----------A---G--------TG--A-A---C---TC---G--------A--A---------- | 3 | 4 |
| 7 | KX265193 | ----------------------------A-----------------------C----------G---C-GG- | 3 | 3 |
| 8 | KX265194 | ------G--------------G-------------T------------------------------------ | 3 | 3 |
| 9 | KX265195 | -C----G----------A---G---GT---T---A-A---C-T-TC---G--------A--A---------- | 3 | 3 |
| 10 | KX265196 | -C----G----------A---G---GT---T---A-A-----T-TC---G--------A--A---------- | 3 | 3 |
| 11 | KX265197 | -C----G----------A---G----T---T---A-A---C-T-TC---G-A-------A------------ | 3 | 3 |
| 12 | KX265198 | ---------------------G-------------------------------------------------- | 2 | 2 |
| 13 | KX265199 | -----------------------------------------------------TTC---------------- | 2 | 2 |
| 14 | KX265200 | ----------------------------------------------------------A------------- | 1 | 2 |
| 15 | KX265201 | -C----G----------A---G--------T---A-A---C-T-TC---G--------A--A---------- | 1 | 2 |
| 16 | KX265202 | -C----G----------A---G--------T-----A---C---T----G-A-------A------------ | 2 | 2 |
| 17 | KX265203 | -C----G----------A---G----T---T---A-A---C-T-TC-------------------------- | 2 | 2 |
| 18 | KX265204 | G-----G---A--------TTG--G--G--T----------------------------------------- | 2 | 2 |
| 19 | KX265205 | -C----G--------------G-------------T------------------------------------ | 1 | 1 |
| 20 | KX265206 | -----------A----------------------------------------------A------------- | 1 | 1 |
| 21 | KX265207 | --------------------------------------A---------T-C-------------A------G | 1 | 1 |
| 22 | KX265208 | ------G--------------G--------T--------A-GT------G--------A--A---------- | 1 | 1 |
| 23 | KX265209 | ------G--------------G--------T--------A-GT----------TTC---------------- | 1 | 1 |
| 24 | KX265210 | G-----G---A--------TTGAAG-----T--------------------A-------A------------ | 0 | 1 |
| 25 | KX265211 | ------GT---------A---G--------T-C-A-A-A--GT-T--------------------------- | 1 | 1 |
| 26 | KX265212 | -CC---G-----G----AT--G----T---T---ATA-----T-TC-------------------------- | 0 | 1 |
| 27 | KX265213 | -----TG------TC--A---G----T---T-----------T-T----G--------A-AA---------- | 0 | 1 |
| 28 | KX265214 | ------G----------A---G---G----T-C-A-A----GT-T---T-C--------------------G | 1 | 1 |
| 29 | KX265215 | ------G----------A---G---G----T-C-A-A-A--GT-T----G--------A--A---------- | 1 | 1 |
| 30 | KX265216 | ------G--G-------A---G--------T-C-A-A-A--GT-T---TGC--------------------G | 0 | 1 |
| 31 | KX265217 | -------------------------------------------------G--------A--A---------- | 1 | 1 |
| 32 | KX265218 | --C---G-----G--T-AT--G----T---------A------CTC---G-A-----G-A--G--A------ | 0 | 1 |
| 33 | KX265219 | ------G--------------G---------------------------G-A-------A------------ | 1 | 1 |
| 34 | KX265220 | G-----G---AA-------TTG--G--G--T--A---C------T--TT-C-----A-A------------G | 1 | 1 |
| 35 | KX265221 | ------G----------A---G--------T----------GT-T---------------------G-C--- | 1 | 1 |
| 36 | KX265222 | G-----G---A--------TTG--G--G-TT----------------------------------------- | 1 | 1 |
| 37 | KX265223 | G-----G---A--------TTG--G--G--T------------------G--------A--A---------- | 1 | 1 |
| 38 | KX265224 | G-----G---AA-------TTG--G--G--T--A---C------T--TT-C-----A-A------------G | 1 | 1 |
| 39 | KX265225 | ----T-G-------------TG--G-TG--T---------C------------------------------- | 1 | 1 |
| 40 | KX265226 | ---A----------------------T-------------------C--G-A-------A------------ | 0 | 1 |
| 41 | KX265227 | -C----G----------A---G--------T---A-A------CT-------------A-------G----- | 1 | 1 |
| 42 | KX265228 | -C----G--------------G-------------T-------CT----G----------------G----- | 1 | 1 |
| 43 | KX265229 | --------T----------------------------------------G--------A--A---------- | 1 | 1 |
| 44 | KX265230 | ------G---------T---TG--G--G--T---------C------T------------------------ | 1 | 1 |
| 45 | KX265231 | ------G--------------G-------------T------T----------------------------- | 1 | 1 |
| 46 | KX265232 | ------G---A--------TTG--G-----T------------------G-A-------A------------ | 1 | 1 |
| 47 | KX265233 | -C----G----------A---G---G----T---A-A---C-T-TC---G------A-A--A---------- | 1 | 1 |
| 48 | KX265234 | -C----G----------A---G----T---T---A-A---C-T-TC---G--------AA-A---------- | 1 | 1 |
| 49 | NA | ------------------------G-----T----------------------------------------- | 1 | 0 |
| 50 | NA | --------------------------T----------------------G--------A--A---------- | 1 | 0 |
| 51 | NA | --------------------------------------A---------T-C-----A--------------G | 1 | 0 |
| 52 | NA | G-----G---A--------TTGAA---------------------------A-------A------------ | 1 | 0 |
| 53 | NA | ------G--------------G-------------T------T-T----G-A-------A------------ | 1 | 0 |
| 54 | NA | -CC---G-----G----AT--G----T---T-----A------CTC---G-A-----G-A--G--------- | 1 | 0 |
| 55 | NA | -C----G------TC--A---G----T---T------------CT----G--------A-AA---------- | 1 | 0 |
| 56 | NA | ------G--G-------A---G--------T-C-A-A-A--GT-T----G--------A------------- | 1 | 0 |
| 57 | NA | ------G--------T-A---G--------TG--A-A---C---TC---G--------A--A---A------ | 1 | 0 |
| 58 | NA | -C----G----------A---G--------T---A-A-----T-TC-------------------------- | 1 | 0 |
| 59 | NA | -CC---G-----G----AT--G----T---T---ATA---C-T-TC---G--------A--A---------- | 1 | 0 |
| 60 | NA | -C-A--G----------A---G----T---T---A-A---C-T-TCC--G-A-------AG----G------ | 1 | 0 |
|  |  | Total | 100 | 100 |

NA- Not available