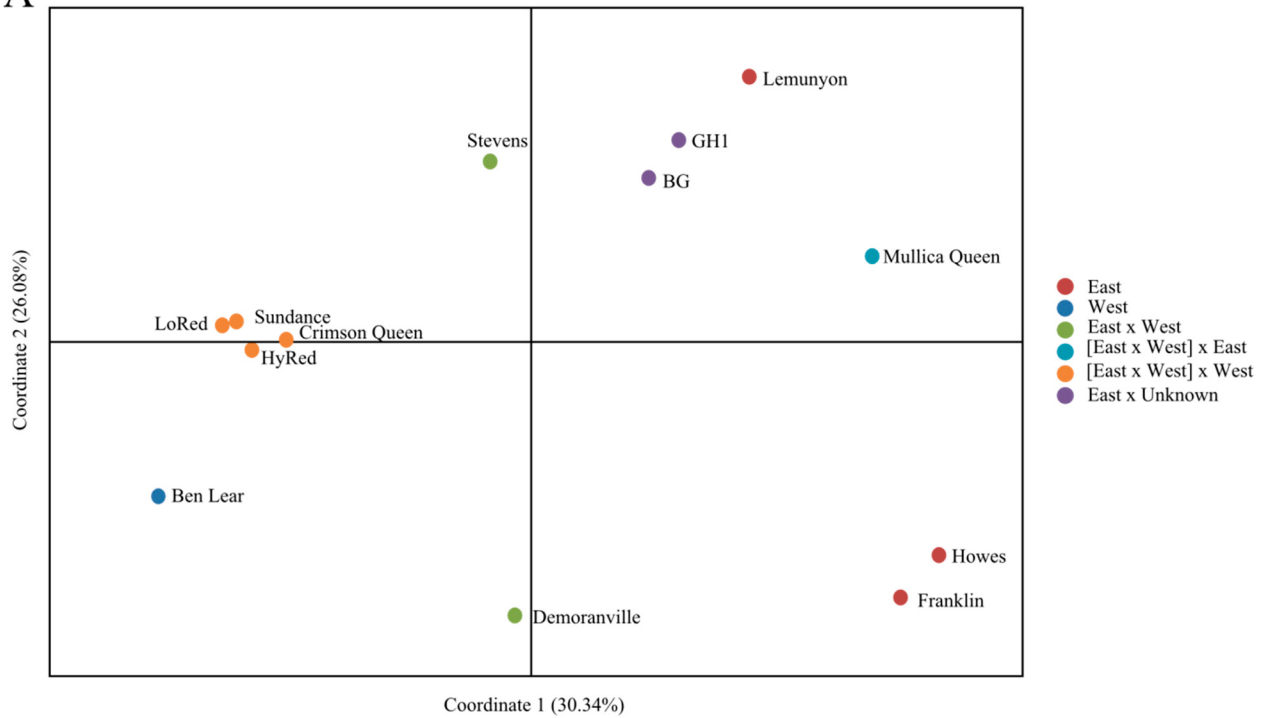
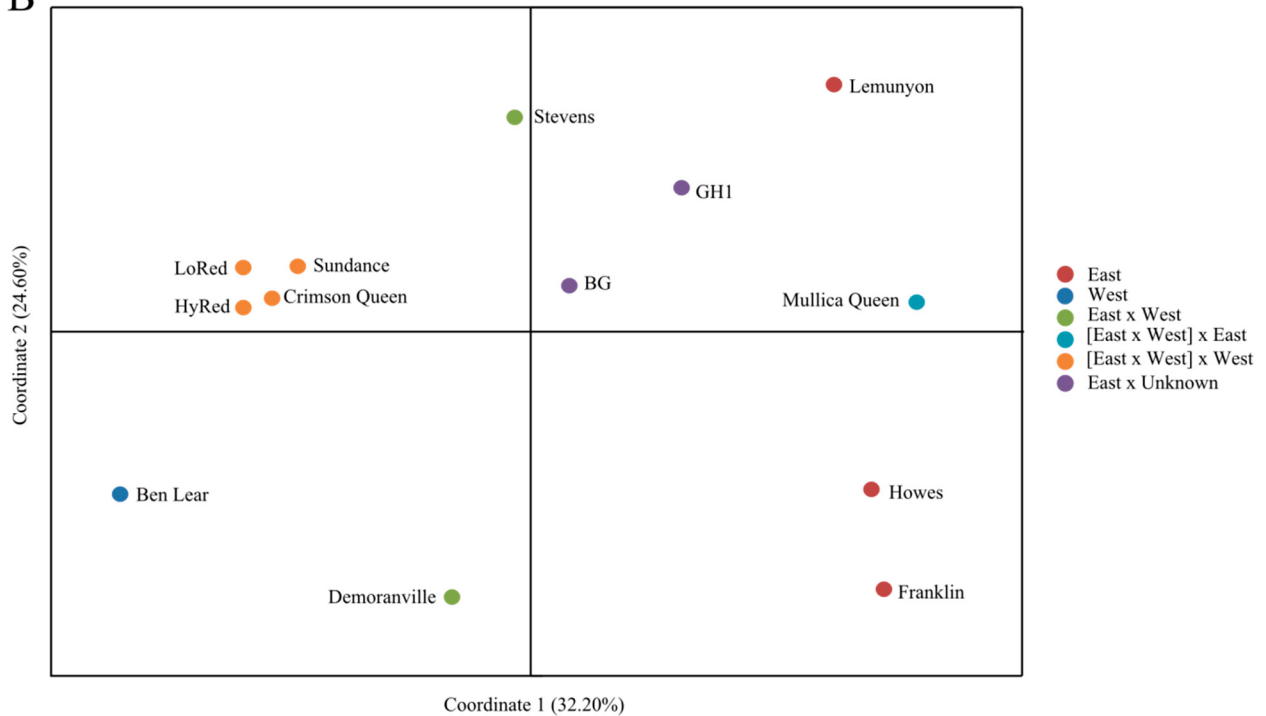


## Supplementary Materials

A



B



**Figure S1.** (A) Principle Coordinate Analysis (PCoA) based on 507 microsatellite markers and (B) 50 microsatellite markers tested and validated on a panel of 13 cranberry cultivars. Genotypes are color-coded based on the similarity of the geographic origins of their pedigrees (*i.e.*, geographic origins are specified as either east, west, or a combination of east and west of the Appalachian Mountains due to artificial selection).

**Supplementary Table 1.** Primer characteristics, diversity statistics, and segregation analysis statistics of 95 polymorphic EST-SSRs tested on a diversity panel of 13 cranberry cultivars and 16 progeny from a ‘Crimson Queen’ × ‘Mullica Queen’ cross.

| Primer ID           | Motif   | Primer Sequences (5'-3')                            | TM (°C)            | Allele Range | Description of Putative Function                     | GenBank Accession Number | Heterozygosity |                |                |                |      |
|---------------------|---------|-----------------------------------------------------|--------------------|--------------|------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|                     |         |                                                     |                    |              |                                                      |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 121633_K63          | (CT)18  | F:GCAGCTCTCTGTAAATTCCTT<br>R:ATGGTTGAAGATGTTGATGG   | F:55.53<br>R:55.77 | 288–333      | hypothetical protein POPTR_0004s16460g               | KP279163                 | 6              | 4.76           | 1              | 0.79           | 0.76 |
| 128239_K63          | (GA)19  | F:AAATAACGATGGCTACATCC<br>R:GTTTGTGTGATGACAATCCTG   | F:54.29<br>R:53.81 | 185–207      | dna-directed rna polymerases iv and v subunit 3-like | KP279164                 | 6              | 3.52           | 0.85           | 0.72           | 0.67 |
| 162108_K70          | (GA)15  | F:GAAGTCGAAACCCTAGCAG<br>R:GTCCCTCTCAGTCTCTCACTC    | F:55.1<br>R:55.49  | 285–318      |                                                      | KP279200                 | 7              | 4.57           | 0.92           | 0.78           | 0.75 |
| 16720_K63           | (TC)17  | F:CTACCTTCCCTCTCCTTGT<br>R:AGTTGAAGCTGAGAATTGTACC   | F:55.05<br>R:55.31 | 164–185      | cellulose synthase-like protein e1-like              | KP279159                 | 6              | 4.51           | 0.85           | 0.78           | 0.74 |
| 172672_K70          | (GA)16  | F:GATAGTTGTATGCGCTGTAAGA<br>R:GTTACCCGAATGAACAGGT   | F:54.97<br>R:54.87 | 325–356      |                                                      | KP279201                 | 8              | 5.83           | 1              | 0.83           | 0.81 |
| 187382_K70          | (TC)16  | F:CCTCCATTCTCTCTCTACTAA<br>R:CGTTTCTTTTCTCTCTCTCTC  | F:54.52<br>R:54.43 | 240–252      | probable receptor protein kinase tmk1-like           | KP279202                 | 7              | 5.83           | 1              | 0.83           | 0.81 |
| 198358_K70          | (AG)14  | F:AATCGTCTGTTGCTCAATGT<br>R:AACCATACTTACCACAACCAGT  | F:55.74<br>R:55.23 | 313–362      |                                                      | KP279203                 | 5              | 3.05           | 0.62           | 0.67           | 0.62 |
| 1trimcontig175770   | (CT)16  | F:GTGTAGCTTGAAAAATAGGAGT<br>R:ACTAGGGAGCGAGAGAGAGTA | F:54.48<br>R:55.13 | 327–346      | tonoplast monosaccharide transporter2 isoform 1      | KP279220                 | 6              | 4.83           | 1              | 0.79           | 0.76 |
| 1trimcontig176042   | (AGA)13 | F:CCGTTGTTGTTCTTCTGTAGT<br>R:TTCAACCTCTGAAGCCTCT    | F:54.55<br>R:55.04 | 226–234      |                                                      | KP279221                 | 3              | 2.18           | 0.62           | 0.54           | 0.46 |
| 1trimcontig176303   | (AG)14  | F:GCTGATTAGGTTCACTTTCTTC<br>R:TTTCTTCACCTCTTCTCTCTC | F:54.97<br>R:54.64 | 190–196      | shock protein src2                                   | KP279222                 | 4              | 2.99           | 0.85           | 0.67           | 0.6  |
| 1trimcontig176861   | (TC)16  | F:ATGGATGTATCTTGACAGGC<br>R:CTGCTGTTTCATTTCTCTGTG   | F:54.97<br>R:54.42 | 131–183      |                                                      | KP279223                 | 8              | 6.26           | 1              | 0.84           | 0.82 |
| 1trimcontig178358 * | (GA)15  | F:AATTGAACGATCCCTATTCC<br>R:GATTCATCACCCTTGAAC      | F:55.58<br>R:55.18 | 224–249      |                                                      | KP279224                 | 7              | 4.69           | 0.77           | 0.79           | 0.76 |
| 1trimcontig179737   | (CT)16  | F:CCTCCAACTTCTTCATCTTCT<br>R:ACTGGTAACTCCTCAGAAACAG | F:55.18<br>R:55.23 | 204–220      | PREDICTED: uncharacterized protein LOC102600962      | KP279225                 | 5              | 4.76           | 1              | 0.79           | 0.76 |

Table S1. *Cont.*

| Primer ID           | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | Description of Putative Function      | GenBank Accession Number | Heterozygosity |                |                |                |      |
|---------------------|---------|-------------------------------------------------------|--------------------|--------------|---------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|                     |         |                                                       |                    |              |                                       |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 1trimcontig182430 * | (AG)14  | F:GAAGATGGACCTGAGTAAGAAA<br>R:CTACCATTGTGTTCTCAAACCTG | F:55.21<br>R:55    | 184–194      |                                       | KP279226                 | 4              | 2.62           | 0.69           | 0.62           | 0.56 |
| 1trimcontig209220   | (TC)16  | F:GTATTTGTTACACTCACCAGA<br>R:ACAGTTGTCGAAGCCTCAT      | F:55.23<br>R:55.74 | 387–421      |                                       | KP279228                 | 7              | 4.36           | 0.92           | 0.77           | 0.74 |
| 1trimcontig217158   | (GAA)14 | F:GGAGTCGGTAAAAATCAAGAA<br>R:CCAAATTCAGTAGGAGTACACA   | F:54.44<br>R:54.53 | 154–169      |                                       | KP279229                 | 4              | 3.22           | 0.46           | 0.69           | 0.64 |
| 1trimcontig237406   | (GA)15  | F:TCTTAGGAAAAGACGAGAATC<br>R:GAAAGGAAGGTATGCTACAGTT   | F:55.36<br>R:54.48 | 314–342      |                                       | KP279230                 | 6              | 3.6            | 0.67           | 0.72           | 0.69 |
| 1trimcontig238080   | (AAG)13 | F:AGGGGTAATCTTCACACACTTA<br>R:ACAGGCTCTTCTAATCGTTTC   | F:55.44<br>R:55.37 | 403–423      |                                       | KP279231                 | 5              | 4.57           | 0.69           | 0.78           | 0.75 |
| 1trimcontig238343   | (TG)15  | F:GGTAATAGCTTTGTGATCTTGC<br>R:GATGGTGAATAAATTGCGAC    | F:55.81<br>R:55.58 | 291–329      |                                       | KP279232                 | 6              | 4.07           | 0.85           | 0.75           | 0.72 |
| 1trimcontig238795   | (AG)14  | F:AGAGGGAGAGAAGAGTATGGTC<br>R:CCGTCAAGATTTGTGAAGAT    | F:55.7<br>R:55.2   | 262–287      |                                       | KP279233                 | 4              | 2.79           | 0.85           | 0.64           | 0.58 |
| 1trimcontig239742 * | (GA)19  | F:AACAAGAACAATAAGACCACC<br>R:TACAAGTTTCAATCAGCCCT     | F:55.08<br>R:54.96 | 270–290      |                                       | KP279234                 | 7              | 4.39           | 0.85           | 0.77           | 0.74 |
| 1trimcontig326802   | (AG)14  | F:TTTTCAGAGCAAGAGGAAAG<br>R:CTGTCTGTATCATGGAATCAT     | F:54.97<br>R:54.21 | 201–221      | casp-like protein rcom_0464280-like   | KP279235                 | 7              | 5.93           | 1              | 0.83           | 0.81 |
| 1trimcontig328266   | (GA)15  | F:ACAGATCAAGCGAACACTAAAC<br>R:CCTGCTCCTGTATACTACCAA   | F:56.21<br>R:56.17 | 235–274      | pto-interacting protein 1             | KP279236                 | 6              | 4.17           | 0.85           | 0.76           | 0.73 |
| 1trimcontig332949   | (AG)15  | F:ACCCAAACACAAAAGAACAG<br>R:GACTGCAAGTGTCTAAATGCT     | F:55.2<br>R:54.78  | 306–349      |                                       | KP279237                 | 7              | 5.28           | 0.85           | 0.81           | 0.78 |
| 1trimcontig332960   | (GA)14  | F:GTCAACAGATTCAACACAACAC<br>R:CCTGCTTCTCTCTAATGAAGTC  | F:55.56<br>R:55.12 | 242–262      |                                       | KP279238                 | 5              | 2.78           | 0.73           | 0.64           | 0.6  |
| 1trimcontig337780   | (TC)14  | F:CTTGATCTTGTCGCTGTAGAC<br>R:TTCCTTATCGAAATCACGAG     | F:55.2<br>R:55.04  | 348–364      | udp-d-apirose udp-d-xylose synthase 2 | KP279239                 | 6              | 5.45           | 1              | 0.82           | 0.79 |

Table S1. *Cont.*

| Primer ID           | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | Description of Putative Function                     | GenBank Accession Number | Heterozygosity |                |                |                |      |
|---------------------|---------|-------------------------------------------------------|--------------------|--------------|------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|                     |         |                                                       |                    |              |                                                      |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 1trimcontig339726   | (GA)17  | F:TACTCATGTCGAAGCAATAGAG<br>R:CTTTAGCAGAGGAGAAACAAGT  | F:54.92<br>R:54.82 | 191–199      | low quality protein:<br>uncharacterized loc101228446 | KP279240                 | 5              | 2.14           | 0.54           | 0.53           | 0.5  |
| 1trimcontig344502   | (AG)16  | F:TGGAAATGGAAGTCTCTG<br>R:CACCGTCTACAGTTTAAGAACA      | F:55.35<br>R:54.77 | 145–165      |                                                      | KP279241                 | 4              | 2.91           | 0.67           | 0.66           | 0.6  |
| 1trimcontig351427   | (AG)17  | F:GACGGCTAAATTGTAAC TAACG<br>R:AGGGTCCTATCCTATCCTCTAA | F:55.91<br>R:55.22 | 220–245      |                                                      | KP279242                 | 7              | 5.28           | 0.92           | 0.81           | 0.79 |
| 1trimcontig352078   | (TC)14  | F:CGTGTTCCTGTTAGATAGCTTG<br>R:CTTGTAAGTGAAGATGCAAA    | F:54.63<br>R:54.95 | 223–229      |                                                      | KP279243                 | 4              | 3.65           | 1              | 0.73           | 0.68 |
| 1trimcontig435620   | (GA)17  | F:CAACCAGCCTTACAGTGAATA<br>R:GTCCGTTCAATTTCTTTTCC     | F:55.52<br>R:56.26 | 235–263      | dual specificity protein phosphatase dsp8            | KP279244                 | 8              | 5.54           | 0.92           | 0.82           | 0.8  |
| 1trimcontig436904   | (AAT)16 | F:TACCAACCACATCACACATC<br>R:CTTATGACGATCCAGTAGC       | F:54.95<br>R:54.91 | 237–255      | thaumatin-like protein                               | KP279245                 | 5              | 3.63           | 0.85           | 0.72           | 0.69 |
| 1trimcontig439466   | (TC)16  | F:CGAGTGGATAGTGATGATATTG<br>R:ACCAAGAGGAAC TACAGGTAAA | F:54.81<br>R:54.79 | 278–341      |                                                      | KP279246                 | 8              | 3.35           | 0.77           | 0.7            | 0.66 |
| 1trimcontig439861   | (TC)15  | F:CTCCTCTCTCGAATGACACTAC<br>R:TTCTTGTTGGCTGGAGATTA    | F:55.72<br>R:55.97 | 246–272      |                                                      | KP279247                 | 5              | 2.84           | 0.77           | 0.65           | 0.61 |
| 1trimcontig440008   | (AG)15  | F:GCAACAGGGACAGATATTTT<br>R:TACGGACTCATAGAAGGTTAGG    | F:54.3<br>R:55.3   | 179–195      |                                                      | KP279248                 | 6              | 3.38           | 0.69           | 0.7            | 0.66 |
| 1trimcontig440230   | (AGA)12 | F:ACACTTTGTAGGTGGTGGTTAT<br>R:ATTAGCAGTAGTCCAATCGGT   | F:55.23<br>R:55.53 | 235–243      |                                                      | KP279249                 | 4              | 3.56           | 0.77           | 0.72           | 0.67 |
| 1trimcontig440337 * | (TC)15  | F:CTTGGAGTTAGCCTTTTAGTCA<br>R:CTGGAAGAGTGAAGATGGAATA  | F:55.63<br>R:56.05 | 153–182      | alpha-galactosidase-like                             | KP279250                 | 6              | 4.23           | 0.85           | 0.76           | 0.73 |
| 1trimcontig443603   | (GA)15  | F:TGCACCTCCTCTCTCTCTAA<br>R:GGTTATGATGGTGGGAAAG       | F:55.24<br>R:55.24 | 147–151      | probable inactive receptor<br>kinase at1g48480       | KP279251                 | 3              | 2.21           | 0.62           | 0.55           | 0.49 |
| 1trimcontig444344   | (TC)18  | F:CTGCTAATGTTGTTGTTGTC<br>R:TATTATCTCCACCTAATGAGC     | F:54.52<br>R:55.15 | 253–270      |                                                      | KP279252                 | 6              | 4.83           | 1              | 0.79           | 0.76 |

Table S1. *Cont.*

| Primer ID         | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | Description of Putative Function                            | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------------|---------|------------------------------------------------------|--------------------|--------------|-------------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|                   |         |                                                      |                    |              |                                                             |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 1trimcontig450309 | (TCC)11 | F:AAAATCAGAGGGAAGAAAGC<br>R:TATTAGCCAGTCCTCCTTTGTA   | F:55.25<br>R:55.83 | 144–147      | ethylene-responsive transcription factor                    | KP279253                 | 2              | 1.99           | 0.58           | 0.5            | 0.37 |
| 214102_K63        | (TG)15  | F:GGTAATAGCTTTGTGATCTTGC<br>R:GATGGTGAATAAATTGCGAC   | F:55.81<br>R:55.48 | 219–256      |                                                             | KP279165                 | 5              | 3.63           | 0.69           | 0.72           | 0.69 |
| 242569_K70        | (AG)15  | F:GATATGAGAGACGAGGAATCAC<br>R:GTCAGTGGACGGTTTTAAGAT  | F:55.39<br>R:55.82 | 298–308      | octicosapeptide phox bem1p family                           | KP279204                 | 6              | 3.67           | 1              | 0.73           | 0.68 |
| 251788_K63        | (AG)18  | F:GATCTTTACCACTCCCCACT<br>R:GGATTCTCTGTCCATTGTTG     | F:55.57<br>R:55.46 | 190–208      | o-fucosyltransferase family                                 | KP279166                 | 6              | 4.69           | 0.92           | 0.79           | 0.76 |
| 252600_K70        | (AG)14  | F:CTAGTTTAGAGTCGTCCCAAAT<br>R:AAGCACCTGAAGATAGTAGGAA | F:54.5<br>R:55.01  | 204–212      | tetratricopeptide repeat protein 38                         | KP279205                 | 4              | 2.23           | 0.75           | 0.55           | 0.51 |
| 260167_K70 *      | (TC)15  | F:TCAACATCTTTGGGACTTCT<br>R:GCTTGCCTAATATACTTCCAAC   | F:54.73<br>R:54.99 | 274–287      |                                                             | KP279206                 | 5              | 3.45           | 0.77           | 0.71           | 0.66 |
| 281884_K70        | (AG)17  | F:TCCACTATCTTTAGAATCCCAC<br>R:AGAGGATGGAGTTCCTTGATA  | F:55.02<br>R:55.39 | 330–357      | probable u6 snrna-associated sm-like protein lsm1           | KP279207                 | 6              | 3.71           | 0.85           | 0.73           | 0.69 |
| 29080_K63         | (TC)14  | F:ATGAAAACAGGTAAGTGG<br>R:TCTCAACTCATAGAACTACGGA     | F:54.24<br>R:54.31 | 384–399      | probable gpi-anchored adhesin-like protein pga55 isoform x1 | KP279160                 | 6              | 3.45           | 0.92           | 0.71           | 0.66 |
| 297265_K63        | (CT)14  | F:GATCGTCATAACTAAGCTGGAT<br>R:GTCTCGAATCACAACAGGATA  | F:55.2<br>R:55.22  | 331–343      |                                                             | KP279167                 | 5              | 1.98           | 0.54           | 0.49           | 0.47 |
| 300409_K63        | (CT)16  | F:GGGGAATAGCAGGTAGTGAT<br>R:TATTTATCCACCCACTTCACAG   | F:55.69<br>R:56.67 | 218–235      |                                                             | KP279168                 | 5              | 4.39           | 0.77           | 0.77           | 0.74 |
| 305731_K63        | (CT)16  | F:GATTTCTTCGTGTTTCTCTCTC<br>R:TGCCTTTCTCTACTCTCTCTC  | F:54.91<br>R:54.84 | 379–391      |                                                             | KP279169                 | 7              | 3.93           | 0.85           | 0.75           | 0.72 |
| 307018_K70        | (AG)20  | F:TAAAACCTTACCTCCTCTCTG<br>R:TAACCTCGGATCTCCTTATCTA  | F:54.63<br>R:54.89 | 217–232      |                                                             | KP279208                 | 6              | 3.6            | 0.92           | 0.72           | 0.69 |
| 308539_K70        | (GA)14  | F:CTAAATTCTCAACATCTCTGGC<br>R:CCAAGAAGCATAAGGGATAGT  | F:55.79<br>R:55.2  | 304–313      | e3 ubiquitin-protein ligase sinat3-like                     | KP279209                 | 4              | 3.56           | 1              | 0.72           | 0.67 |

Table S1. *Cont.*

| Primer ID         | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | Description of Putative Function                                                              | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------------|---------|------------------------------------------------------|--------------------|--------------|-----------------------------------------------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|                   |         |                                                      |                    |              |                                                                                               |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 308812_K70        | (TC)15  | F:GAAAGGAAGGTATGCTACAGTT<br>R:TCTTAGGAAAGACGAGAACATC | F:54.48<br>R:55.36 | 316–344      |                                                                                               | KP279210                 | 7              | 5.28           | 0.92           | 0.81           | 0.79 |
| 308839_K70        | (TC)16  | F:ATAATGTGTCCAGTCCCTTTC<br>R:TTCCTTCCTCAATCCACTC     | F:55.58<br>R:55.05 | 292–313      |                                                                                               | KP279211                 | 5              | 3.48           | 0.85           | 0.71           | 0.66 |
| 309084_K70        | (AG)16  | F:CTTCTTTTCCTCTCCACTGATA<br>R:CTCTCCGTTGTCCATTCT     | F:55.37<br>R:55.18 | 389–400      |                                                                                               | KP279212                 | 5              | 2.91           | 0.54           | 0.66           | 0.61 |
| 309124_K70        | (GA)15  | F:AAAGGTCGTTAAGGCTATCAG<br>R:TGATGACTGCGATATGTACTCT  | F:55.42<br>R:55.02 | 157–177      | nucleic acid binding related                                                                  | KP279213                 | 8              | 6.15           | 1              | 0.84           | 0.82 |
| 311291_K70        | (TC)14  | F:CTTGATCTTGTCGCTGTAGAC<br>R:TTCCTTATCGAAATCACGAG    | F:55.2<br>R:55.47  | 287–303      | udp-d-apiose udp-d-xylose synthase 2                                                          | KP279214                 | 7              | 6.04           | 1              | 0.83           | 0.81 |
| 313711_K70        | (TC)16  | F:CGACTTAATCCCTCTCTTTCTA<br>R:CTTTACTTTTCCATCTCCCTC  | F:54.7<br>R:54.74  | 321–340      | beta-<br>-mannosyl-glycoprotein<br>4-beta-n-acetylglucosaminyltransferase-<br>like isoform x2 | KP279215                 | 5              | 3.98           | 0.77           | 0.75           | 0.71 |
| 313928_K70        | (GA)15  | F:CAATTATCAAGGAGGCAATC<br>R:TCACAAATGAGGATCTACACAC   | F:54.81<br>R:55.14 | 204–224      | photosystem ii 5 kda chloroplastic-like                                                       | KP279216                 | 6              | 3.22           | 0.85           | 0.69           | 0.66 |
| 314402_K70        | (GA)17  | F:TGGAAGAACTCGATACGAAC<br>R:GAGAAGTTGGATACTGGAAATG   | F:55.37<br>R:55.49 | 154–170      | 30s ribosomal protein chloroplastic-like                                                      | KP279217                 | 6              | 3.41           | 0.77           | 0.71           | 0.67 |
| 314761_K63 *      | (CT)14  | F:ATTGTTGGATACTTCATGGC<br>R:GTTGGTACTGGTAAACCCTAAT   | F:54.99<br>R:54.1  | 137–197      | hypothetical protein VITISV_008952                                                            | KP279170                 | 8              | 5.54           | 0.85           | 0.82           | 0.8  |
| 314797_K70        | (AC)14  | F:CTTGTTCTCCTCCTTTAGTCTG<br>R:CATCTTCATACTCCTATTGTCG | F:55.05<br>R:54.14 | 201–217      |                                                                                               | KP279218                 | 5              | 3.16           | 0.85           | 0.68           | 0.65 |
| 314831_K70        | (GA)14  | F:ATCTCTCGTGCCTGTCATAC<br>R:CTTTTCGATGTCGTACTTGTC    | F:55.21<br>R:55.05 | 159–169      | syntaxin-71-like                                                                              | KP279219                 | 4              | 2.89           | 0.85           | 0.65           | 0.6  |
| 1trimcontig191066 | (TCT)13 | F:GATATTAGTCCGGTTTACGAGA<br>R:GATACAGGAGTCGAGAATGAAT | F:55.22<br>R:54.99 | 290–309      |                                                                                               | KP279227                 | 5              | 4.39           | 0.85           | 0.77           | 0.56 |
| 319429_K63        | (GA)17  | F:GGAGATAGGAAGTGTGATGAAC<br>R:TTATTGTGCAAGCATACGAG   | F:55.31<br>R:55.09 | 180–194      |                                                                                               | KP279171                 | 6              | 2.86           | 0.69           | 0.65           | 0.62 |

Table S1. *Cont.*

| Primer ID  | Motif  | Primer Sequences (5'-3')                            | TM (°C)            | Allele Range | Description of Putative Function                              | GenBank Accession Number | Heterozygosity |                |                |                |      |
|------------|--------|-----------------------------------------------------|--------------------|--------------|---------------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|            |        |                                                     |                    |              |                                                               |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 354699_K63 | (TC)15 | F:GAAGCGATTTGGAAGAAAC<br>R:ACACAGAGAGATTACGAACACA   | F:54.98<br>R:54.97 | 172–191      |                                                               | KP279172                 | 7              | 5.12           | 1              | 0.8            | 0.78 |
| 364103_K63 | (TC)17 | F:TACAAACCCTAAGCTCTAAACC<br>R:CGACTTGAGTGATACCAAAGA | F:54.68<br>R:55.48 | 184–202      | nicastrin isoform x2                                          | KP279173                 | 3              | 2.3            | 0.85           | 0.57           | 0.47 |
| 372875_K63 | (TC)18 | F:CACACACAAATCCCAATTTC<br>R:GATGGTGTTTTCATAGTTCGAC  | F:56.29<br>R:56.23 | 198–228      | pentatricopeptide repeat-containing<br>protein at1g16830      | KP279174                 | 6              | 3.31           | 0.77           | 0.7            | 0.65 |
| 407841_K63 | (AG)17 | F:TTGAGTAGATACATGCTGGCT<br>R:CTCACCCCTTCTCTGTGATA   | F:55.17<br>R:54.52 | 274–294      | tyrosine-specific transport                                   | KP279175                 | 6              | 4.76           | 1              | 0.79           | 0.76 |
| 408825_K63 | (AG)16 | F:GTTCTCCTCTTTCATCATTCAG<br>R:AGTCTTGAACCTCTGTACTCG | F:55.61<br>R:55.39 | 262–286      | ankyrin repeat-containing                                     | KP279176                 | 6              | 3.93           | 0.92           | 0.75           | 0.71 |
| 409500_K63 | (CA)22 | F:GATTCTGGGTGTAGTTCTGT<br>R:CTTAGTCTTAAATGCTGGCTCA  | F:55.66<br>R:56.58 | 333–395      | pentatricopeptide repeat-containing<br>protein at1g08070-like | KP279177                 | 6              | 3.48           | 0.85           | 0.71           | 0.68 |
| 409618_K63 | (CT)14 | F:CTTCTCCTTCCCTTCACTTTA<br>R:TTAGTGTTAGTGTTGGTGTGG  | F:55.36<br>R:55.37 | 249–287      |                                                               | KP279178                 | 6              | 5.28           | 0.92           | 0.81           | 0.78 |
| 411145_K63 | (CT)16 | F:GGTAGGAATTAAGTGAAGACG<br>R:ACTAGGGAGCGAGAGAGAGTA  | F:54.88<br>R:55.13 | 370–389      | tonoplast monosaccharide<br>transporter2 isoform 1            | KP279179                 | 6              | 4.83           | 1              | 0.79           | 0.76 |
| 411348_K63 | (GA)18 | F:AATTACCAATGTTCACTCCG<br>R:GTTGATGTAGTTCTGTGGTTGA  | F:55.09<br>R:55.23 | 266–283      |                                                               | KP279180                 | 9              | 5.54           | 0.83           | 0.82           | 0.8  |
| 411475_K63 | (AG)15 | F:GCAACAGGGACAGATATTTT<br>R:TACGGACTCATAGAAGGTTAGG  | F:54.3<br>R:55.3   | 179–199      |                                                               | KP279181                 | 7              | 4.39           | 1              | 0.77           | 0.74 |
| 412234_K63 | (AG)17 | F:GTGCAAGCCGTTTCTTATG<br>R:ATCGGAGGTTCCATCATTTA     | F:56.95<br>R:56.94 | 147–155      |                                                               | KP279182                 | 4              | 3.41           | 0.92           | 0.71           | 0.65 |
| 414791_K63 | (GA)17 | F:ACGACTAGCAGCATTCAGTAA<br>R:CAGGAGATCAGAAAACACAATC | F:55.41<br>R:56.38 | 335–362      | PREDICTED: uncharacterized<br>protein LOC104588813            | KP279183                 | 8              | 5.73           | 0.92           | 0.83           | 0.81 |
| 416275_K63 | (TC)15 | F:GGTTATGATGGTGGGAAAG<br>R:TGCACCTCCTCTCTCTCTAA     | F:55.24<br>R:55.24 | 195–197      | probable inactive receptor<br>kinase at1g48480                | KP279184                 | 2              | 1.31           | 0.27           | 0.24           | 0.21 |

Table S1. *Cont.*

| Primer ID    | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | Description of Putative Function                                                | GenBank Accession Number | Heterozygosity |                |                |                |      |
|--------------|--------|------------------------------------------------------|--------------------|--------------|---------------------------------------------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|              |        |                                                      |                    |              |                                                                                 |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 416328_K63   | (AG)21 | F:GTATGCCCAAGATATCCATTAC<br>R:TAGTCACGAGGAAAGCTAAAGT | F:55.25<br>R:55.24 | 167–225      | chaperonin-like protein                                                         | KP279185                 | 7              | 4.33           | 0.77           | 0.77           | 0.74 |
| 416815_K63   | (GA)17 | F:CGTTTCTTTCTCTCTCTCTC<br>R:CCTCCATTCTCTCTCTCTACTAA  | F:54.43<br>R:54.52 | 240–252      | probable receptor protein kinase tmk1-like                                      | KP279186                 | 4              | 3.1            | 0.55           | 0.68           | 0.62 |
| 417587_K63   | (AG)19 | F:TGGGTAGATATTAGATGGCAGT<br>R:CTTCTTCTGGAAATCTGGTTAG | F:55.48<br>R:54.99 | 238–275      |                                                                                 | KP279187                 | 7              | 6.26           | 0.85           | 0.84           | 0.82 |
| 417854_K63   | (CT)17 | F:AAAAGGAGTCTTGGGAGTAAGT<br>R:TTGAGATGTAAGTATGCAGTCC | F:55.39<br>R:54.59 | 271–297      | 50s ribosomal protein chloroplastic-like                                        | KP279188                 | 7              | 3.48           | 0.85           | 0.71           | 0.68 |
| 418294_K63   | (AG)18 | F:CAAGAACAAGAAGAAGAGACC<br>R:AGAGACCACCCAAAAGATAAG   | F:55.01<br>R:55.07 | 336–348      |                                                                                 | KP279189                 | 6              | 4.76           | 1              | 0.79           | 0.76 |
| 418596_K63   | (CT)17 | F:CGTGAGTTTGAGTGAGTAATTG<br>R:AGGACATGGTGAGTTGAGAAT  | F:55.16<br>R:56.09 | 395–401      |                                                                                 | KP279190                 | 4              | 3.48           | 0.69           | 0.71           | 0.66 |
| 418931_1_K63 | (TC)15 | F:ATTAGCTCAGTTCCCAGTAACA<br>R:CTTCTTTCTCTTCTCTCTCTCT | F:55.74<br>R:55.33 | 165–177      | beta-galactosidase 3                                                            | KP279191                 | 5              | 3.28           | 0.85           | 0.7            | 0.64 |
| 419834_K63   | (TC)16 | F:GAAAAGAGAGGAGAAGATGGAT<br>R:TACCAGAACTGTGTGAGATTGT | F:55.75<br>R:54.8  | 183–208      | probably inactive leucine-rich repeat<br>receptor-like protein kinase at5g48380 | KP279192                 | 6              | 3.52           | 0.54           | 0.72           | 0.67 |
| 42710_K70    | (AG)16 | F:GTTACACACACACCCACAGA<br>R:GAGAGAGGACTAGGTCGTACAG   | F:55.12<br>R:54.9  | 181–203      | wd-40 repeat-containing protein msi2-like                                       | KP279194                 | 4              | 3.16           | 0.85           | 0.68           | 0.63 |
| 47166_K70    | (GA)15 | F:TATTGAGAGTGTGAGACCGTT<br>R:TGGTAAGTATCGTAGGTCCAAT  | F:54.87<br>R:55.4  | 310–315      |                                                                                 | KP279195                 | 3              | 1.91           | 0.69           | 0.48           | 0.39 |
| 482_K70      | (CT)15 | F:ACAGCGGCATAGTAAATGA<br>R:GTCACCGAAATCTCACTCAATA    | F:56.02<br>R:56.82 | 179–192      |                                                                                 | KP279193                 | 6              | 5.45           | 1              | 0.82           | 0.79 |
| 60699_K70    | (CT)19 | F:CTTCTCACTGTATTCTTCGAG<br>R:GGCTACTTTGTTAGGGTAGATT  | F:53.65<br>R:53.72 | 277–304      |                                                                                 | KP279196                 | 11             | 8.05           | 1              | 0.88           | 0.86 |
| 71002_K63    | (GA)16 | F:CTTCAATCCACGAATACCAC<br>R:CAATTATGCAAAGGAGGAAG     | F:55.5<br>R:55.07  | 235–248      |                                                                                 | KP279161                 | 8              | 4.63           | 0.85           | 0.78           | 0.76 |

Table S1. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3') | TM (°C) | Allele Range | Description of Putative Function          | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|--------------------------|---------|--------------|-------------------------------------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                          |         |              |                                           |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| 76126_K63 | (AG)16 | F:TTTATTGGAGCGAAAGAGAG   | F:54.94 | 231–242      |                                           | KP279162                 | 5              | 3.45           | 0.77           | 0.71           | 0.66 |
|           |        | R:AAAAGGGGAGGAGAGAGAT    | R:54.38 |              |                                           |                          |                |                |                |                |      |
| 76326_K70 | (GA)15 | F:AATGTCTTCCAAATCAGGTG   | F:55.03 | 279–294      |                                           | KP279197                 | 6              | 5.04           | 0.85           | 0.8            | 0.77 |
|           |        | R:CAAGAACGAACCCTCTATTTC  | R:55.63 |              |                                           |                          |                |                |                |                |      |
| 80734_K70 | (TC)15 | F:AGGGAGAACCAATTCCTTAC   | F:54.81 | 347–373      |                                           | KP279198                 | 7              | 5.12           | 0.92           | 0.8            | 0.78 |
|           |        | R:GACCTAACCCTAACCCAGTC   | R:55.16 |              |                                           |                          |                |                |                |                |      |
| 82171_K70 | (CT)14 | F:TAGTAGAGTTGAAGAGGAGGGA | F:54.97 | 168–185      | single-stranded dna-binding mitochondrial | KP279199                 | 6              | 3.52           | 0.77           | 0.72           | 0.68 |
|           |        | R:CTAGGGTTTAAGCAAGCATAGT | R:54.85 |              |                                           |                          |                |                |                |                |      |

Note: \* = marker displayed segregation distortion  $p < 0.05$ .

**Table 2.** Primer characteristics, diversity statistics, and segregation analysis statistics of 412 polymorphic genomic SSRs tested on a diversity panel of 13 cranberry cultivars and 16 progeny from a “Crimson Queen” × “Mullica Queen” cross.

| Primer ID | Motif    | Primer Sequences (5'-3')                             | TM (°C)              | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|----------|------------------------------------------------------|----------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |          |                                                      |                      |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| ct106280  | (AC)10   | F:GCCATAGCTATTTTGTAACGAG<br>R:TATCATGGACTAGGTCTCAACA | F:55.983<br>R:54.829 | 216–225      | KP279109                 | 3              | 2.43           | 0.69           | 0.59           | 0.50 |
| ct110752  | (TC)14   | F:ACACACACTAACGAAATCCTTC<br>R:CTAGCTCCGACATTGTTATCTC | F:55.903<br>R:55.823 | 126–141      | KP279110                 | 6              | 4.33           | 0.85           | 0.77           | 0.74 |
| ct115258  | (CT)13   | F:GTTTCGTTGTGGAAGTCACAT<br>R:CAAAATGAGTGCCAGATAGTG   | F:55.932<br>R:55.933 | 192–207      | KP279111                 | 6              | 4.57           | 1.00           | 0.78           | 0.75 |
| ct116900  | (GT)11   | F:CTCAAACATACCCTTTGAGC<br>R:GGTATAGCTTAACAACACACCA   | F:54.959<br>R:54.579 | 166–168      | KP279112                 | 4              | 1.91           | 0.62           | 0.48           | 0.43 |
| ct118602  | (TC)9    | F:TAGAATGCAGTCGTGAAGTGTA<br>R:ACTAAATGAGGGGTAGTACGTG | F:56.18<br>R:55.091  | 152–159      | KP279113                 | 3              | 2.66           | 0.77           | 0.62           | 0.55 |
| ct119523  | (AG)11   | F:GACTCATGGGAGTGAGGAC<br>R:TGAACCTGTGTAGTCTTTACCG    | F:55.238<br>R:54.77  | 234–279      | KP279114                 | 10             | 6.63           | 0.92           | 0.85           | 0.83 |
| ct119590  | (CT)9    | F:ACATGACATCAATTGCC<br>R:TATCCTACCTCAAAGAGCCTAA      | F:54.903<br>R:55.115 | 186–189      | KP279115                 | 4              | 2.50           | 0.67           | 0.60           | 0.52 |
| ct120091  | (CT)9    | F:GTTGAAAGCGACAAGTCTTC<br>R:TAATTTTGCCCTACCCACC      | F:55.143<br>R:57.415 | 181–183      | KP279116                 | 2              | 1.83           | 0.39           | 0.45           | 0.35 |
| ct121951  | (TTGGT)6 | F:CATGTAGCCGACTCCAATTA<br>R:TATCCCATTCGCTATAAGGTC    | F:56.296<br>R:55.632 | 178–193      | KP279117                 | 3              | 2.05           | 0.62           | 0.51           | 0.46 |
| ct124256  | (TC)9    | F:GCCGTTAGTTCGTGATATGT<br>R:CCTACATGCATACGTAAAACAG   | F:55.275<br>R:55.176 | 209–214      | KP279118                 | 2              | 1.95           | 0.69           | 0.49           | 0.37 |
| ct129169  | (AG)10   | F:TAAATCACCTTCTTCCTCCTC<br>R:GGTCCCAAACCTTACTACTCAAA | F:55.117<br>R:55.177 | 125–133      | KP279119                 | 4              | 3.22           | 0.77           | 0.69           | 0.64 |
| ct129202  | (CT)9    | F:CGACCTACACGAGATTGTTTAT<br>R:GTTCCAAATCTTCAGTAAGCTG | F:56.013<br>R:55.863 | 276–278      | KP279120                 | 2              | 1.99           | 0.92           | 0.50           | 0.37 |
| ct130570  | (TTC)6   | F:GTTCACAATCTGCATCTCCT<br>R:ACGTAATAGATCAAGAACAGGG   | F:55.176<br>R:55.133 | 197–200      | KP279121                 | 2              | 1.55           | 0.31           | 0.36           | 0.29 |

Table S2. *Cont.*

| Primer ID | Motif    | Primer Sequences (5'-3')                              | TM (°C)              | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|----------|-------------------------------------------------------|----------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |          |                                                       |                      |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| ct132010  | (TTTTA)4 | F:TACGTGAATTACCCATATCCAC<br>R:CTCACCCCTTTACTTCTCTTTGA | F:56.448<br>R:55.449 | 203–214      | KP279122                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| ct134336  | (TCC)6   | F:GAACACTCCTTCTCTAGCTCTG<br>R:CTTTTTAGTCTCCGACAATCTC  | F:55.183<br>R:54.98  | 195–201      | KP279123                 | 2              | 1.55           | 0.46           | 0.36           | 0.29 |
| ct135942  | (TC)12   | F:CTACTTGCCTTCCTCTTTGAC<br>R:TAAATAATCCGTCCACGAAC     | F:55.859<br>R:55.183 | 163–170      | KP279124                 | 4              | 3.43           | 0.17           | 0.71           | 0.66 |
| ct139553  | (CT)11   | F:GATCAAGCATTGTTCTCTTCC<br>R:AGCTATAGGGCTAGCGATG      | F:56.45<br>R:54.943  | 123–150      | KP279125                 | 5              | 3.35           | 0.77           | 0.70           | 0.66 |
| ct140233  | (GA)14   | F:TTACAGAAGGAAGAGAGAGGAA<br>R:ACTGGCTTCTATAGCTCATTTTC | F:55.096<br>R:54.707 | 224–249      | KP279126                 | 7              | 5.05           | 0.85           | 0.80           | 0.78 |
| ct144370  | (TC)11   | F:GTAGGAAAAGTTTGAACCGTC<br>R:TCAAAGGTTTCACGTTTCTC     | F:55.539<br>R:55.419 | 223–237      | KP279127                 | 4              | 3.31           | 0.77           | 0.70           | 0.65 |
| ct144558  | (AG)9    | F:TCATTACCCCTAACCTCTAAAC<br>R:ATTCGACTAGAGTGGAGAGAAA  | F:54.3<br>R:54.961   | 223–227      | KP279128                 | 3              | 2.18           | 0.69           | 0.54           | 0.46 |
| ct144936  | (AAACT)4 | F:AGGTGACTAAGGCAGTGTTTC<br>R:CGTGTCTGTTTGGTAGTAGGT    | F:54.398<br>R:56.015 | 181–191      | KP279129                 | 2              | 1.95           | 0.69           | 0.49           | 0.37 |
| ct145170  | (CTT)12  | F:GAATCCTAGCCTATTTTCCTTTG<br>R:GAAGCAAACACCACTCAATATC | F:56.31<br>R:56.383  | 208–223      | KP279130                 | 5              | 3.38           | 0.69           | 0.70           | 0.66 |
| ct145217  | (AT)10   | F:CCAGTACTAGATCCACTGCATA<br>R:TGTTCTAGAGAGGATGACATTG  | F:54.637<br>R:54.531 | 156–165      | KP279131                 | 5              | 3.16           | 0.77           | 0.68           | 0.65 |
| ct145906  | (AC)10   | F:TCTAGACTTGAGAAGCACTTTG<br>R:AGTTAGAGGAGGTTTCTGTTGA  | F:54.272<br>R:54.884 | 260–262      | KP279132                 | 2              | 1.55           | 0.46           | 0.36           | 0.29 |
| ct147864  | (ATT)6   | F:CTCTCTTTACCCCTCAATTTCTC<br>R:GGTCTAATATCAATCGATGACC | F:54.106<br>R:55.208 | 273–276      | KP279133                 | 2              | 1.26           | 0.23           | 0.20           | 0.18 |
| ct149097  | (TCT)6   | F:GAAGTACTGAGTCCACAAAAT<br>R:GAACAATAGTAACCCATGCAG    | F:55.879<br>R:54.865 | 257–263      | KP279134                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |

Table S2. *Cont.*

| Primer ID | Motif    | Primer Sequences (5'-3')                              | TM (°C)              | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|----------|-------------------------------------------------------|----------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |          |                                                       |                      |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| ct152567  | (TC)13   | F:GTGGCTTTTCTGATCTTGTT<br>R:AAAGTACTCTCAATTGGTACGG    | F:54.479<br>R:55.209 | 208–226      | KP279135                 | 6              | 4.23           | 0.85           | 0.76           | 0.73 |
| ct153008  | (CT)11   | F:CTTTCCAAGATCTTCATAGGC<br>R:CGACAGTATAATAGCATGGAGA   | F:55.707<br>R:54.741 | 257–266      | KP279136                 | 3              | 2.75           | 0.77           | 0.64           | 0.56 |
| ct154206  | (CT)14   | F:GAGAGCGTACGATACCTAATTC<br>R:CTGGTTAGGAAAACCACTAGAA  | F:54.976<br>R:55.337 | 198–204      | KP279137                 | 4              | 3.22           | 0.85           | 0.69           | 0.63 |
| ct154615  | (CT)9    | F:AAAATTGAGCACTGGCTAAG<br>R:CTCATACAAACAATAGGGGG      | F:54.889<br>R:54.62  | 131–135      | KP279138                 | 3              | 2.00           | 0.69           | 0.50           | 0.41 |
| ct154654  | (GA)10   | F:GATTTCTAGTGGGAAATGAAGG<br>R:GGTGTATGTGTGTGATTAAGGA  | F:56.876<br>R:55.03  | 167–171      | KP279139                 | 4              | 2.10           | 0.62           | 0.52           | 0.45 |
| ct155339  | (CCA)6   | F:AAGTTCCTCTGTTACAAGCTCT<br>R:ATGACGAACCTCTTCCTCCTTAT | F:54.254<br>R:56.116 | 219–228      | KP279140                 | 2              | 1.99           | 0.46           | 0.50           | 0.37 |
| ct155461  | (TG)10   | F:GGTTTCAAACTCGAACAAAG<br>R:ATCCTATAACTGGGGATAATGC    | F:55.007<br>R:56.239 | 258–277      | KP279141                 | 4              | 2.62           | 0.85           | 0.62           | 0.56 |
| ct159707  | (CA)9    | F:TGTTAGCTCCTTACTTTCCATC<br>R:GTGAAGAGGAAGATGAAGAATG  | F:55.403<br>R:55.606 | 185–188      | KP279142                 | 3              | 1.59           | 0.46           | 0.37           | 0.32 |
| ct160768  | (GTTTG)4 | F:GTGTGGTATGTTGGATGTAAAC<br>R:TAAGGGGATTTTCATTGGG     | F:54.46<br>R:55.759  | 139–144      | KP279143                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| ct161908  | (TATG)7  | F:CCTAGGAGATGGGTCAAGAT<br>R:ACCACTGTCTTCCATATTCACT    | F:55.666<br>R:55.263 | 156–173      | KP279144                 | 5              | 2.27           | 0.62           | 0.56           | 0.51 |
| ct165512  | (CT)9    | F:CTTCCTACTCTCTCCCTCTACA<br>R:GTTGGATCTTGATGGGTTTA    | F:54.567<br>R:54.967 | 128–139      | KP279145                 | 3              | 2.15           | 0.31           | 0.54           | 0.47 |
| ct171223  | (TG)9    | F:GCGTGTATTATTCTCTACCT<br>R:GGTACATTCTTTGACCGAGTAT    | F:54.47<br>R:54.968  | 152–154      | KP279146                 | 2              | 1.26           | 0.23           | 0.20           | 0.18 |
| ct174735  | (TC)14   | F:CTTATTTGTATGGCCTTCCT<br>R:GCAGCATATATTGTCCAGTTC     | F:53.652<br>R:54.93  | 171–194      | KP279147                 | 7              | 5.28           | 0.92           | 0.81           | 0.79 |

Table S2. *Cont.*

| Primer ID | Motif    | Primer Sequences (5'-3')                              | TM (°C)              | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|----------|-------------------------------------------------------|----------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |          |                                                       |                      |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| ct188529  | (GA)10   | F:TTGCAGAATCAATAGTACCTCC<br>R:CCTCATTAGCTATGGTGAAAC   | F:56.062<br>R:54.112 | 191–232      | KP279148                 | 7              | 2.91           | 0.85           | 0.66           | 0.63 |
| ct89348   | (CACCT)4 | F:GGCTCAATCTTGTGTAGGTATT<br>R:GAGAAAGTGGAAGATTGTGTG   | F:55.122<br>R:56.452 | 184–194      | KP279100                 | 3              | 1.70           | 0.39           | 0.41           | 0.35 |
| ct89379   | (TC)10   | F:ATGAAGAGCTTGAATGGCTA<br>R:ACACTTTACACCACAACTCGTA    | F:55.205<br>R:54.941 | 171–183      | KP279101                 | 5              | 4.63           | 0.85           | 0.78           | 0.75 |
| ct89711   | (CT)13   | F:CTCCACACCCACAATCTG<br>R:CGTCTTATTTTGTAGTCACCTGG     | F:55.585<br>R:55.749 | 137–149      | KP279102                 | 5              | 3.13           | 0.77           | 0.68           | 0.63 |
| ct92708   | (TC)10   | F:CCCTAGATATTTCTGGAACACT<br>R:AAGATAGAGAGAGACAAAGGAGG | F:54.261<br>R:55.22  | 144–152      | KP279103                 | 4              | 3.98           | 0.77           | 0.75           | 0.70 |
| ct93137   | (CT)11   | F:AAGATTTCCGCTACAGTACCT<br>R:GCTATGGGTGTCTCAAAAAG     | F:54.871<br>R:54.959 | 177–207      | KP279104                 | 5              | 3.41           | 0.92           | 0.71           | 0.67 |
| ct94504   | (AAACA)5 | F:CTCTAAAGCTCAAGAAAACGTC<br>R:AGCTGTGACTATAAGGGATTG   | F:55.359<br>R:55.284 | 258–268      | KP279105                 | 3              | 1.48           | 0.39           | 0.32           | 0.29 |
| ct95345   | (CT)9    | F:ACTCTACAAGGGCACGAAC<br>R:ATGGAAGTAAGAAAGTGAGTGG     | F:55.289<br>R:55.163 | 122–128      | KP279106                 | 3              | 2.09           | 0.46           | 0.52           | 0.44 |
| ct95842   | (GA)12   | F:GTGGAAAGAGATTGTTGATGTC<br>R:AAAATAATGGATGACGACG     | F:56.217<br>R:55.252 | 222–234      | KP279107                 | 5              | 3.22           | 0.77           | 0.69           | 0.64 |
| ct98042   | (AAAAT)5 | F:CCTTTTAAGTACTTTCCTTCC<br>R:CCCCTCATCTTTATGTGC       | F:55.482<br>R:53.806 | 266–272      | KP279108                 | 3              | 1.75           | 0.54           | 0.43           | 0.39 |
| SCF1001   | (ACA)7   | F:AAACTAGCATATCCCAAGGTAG<br>R:ATATAGCAACAGTGGGCAGT    | F:54.48<br>R:54.85   | 209–215      | KP278595                 | 2              | 1.90           | 0.46           | 0.47           | 0.36 |
| SCF100820 | (TG)10   | F:GTAATTCCACTTAACCCACTCA<br>R:GTTGAAGATAAACACCTTCC    | F:55.83<br>R:55.30   | 342–353      | KP278804                 | 4              | 2.97           | 0.62           | 0.66           | 0.60 |
| SCF101064 | (GT)9    | F:CATCAGACAGAAAGCAGTTAAG<br>R:CCCCAAGTATATTAGCAAACAC  | F:54.56<br>R:55.55   | 296–302      | KP278805                 | 3              | 2.27           | 0.69           | 0.56           | 0.49 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF101878 | (CAA)7 | F:GACTCATTGGATACGTGCT<br>R:TCTATGTAGCTTTGAAGTGAGG     | F:53.42<br>R:54.10 | 343–346      | KP278807                 | 2              | 2.00           | 0.54           | 0.50           | 0.38 |
| SCF101914 | (TC)10 | F:CTTTGGAGCACAACTCTA<br>R:GTGTAAAGACCAGGACCCTT        | F:55.72<br>R:55.65 | 150–165      | KP278806                 | 4              | 3.17           | 0.75           | 0.68           | 0.62 |
| SCF102347 | (AG)12 | F:GGTAGTGAGCAACGACATAAC<br>R:CCTGAAGGTAAAGAAAGTAGCA   | F:54.91<br>R:55.63 | 335–349      | KP278808                 | 7              | 4.94           | 1.00           | 0.80           | 0.77 |
| SCF10459  | (TC)11 | F:TCTTTGTTTCTGAGGTTGCT<br>R:ATTTGTAGGTACTATGGAAGCC    | F:55.15<br>R:54.32 | 253–257      | KP278631                 | 3              | 2.36           | 0.77           | 0.58           | 0.50 |
| SCF104688 | (GA)10 | F:ACAAAGAAATGTATGGCACC<br>R:CTTTTCGTCTCCTCTAATTCC     | F:55.7<br>R:54.89  | 194–207      | KP278809                 | 5              | 3.27           | 0.92           | 0.69           | 0.49 |
| SCF1047   | (AC)10 | F:GAGCTTTGGCCTCATATTACT<br>R:CGAATTACTCCAACCAACAT     | F:55.33<br>R:55.8  | 266–267      | KP278596                 | 3              | 2.27           | 0.85           | 0.56           | 0.49 |
| SCF105092 | (AT)11 | F:AGGAAGTAGGAAGTAGGAAGATG<br>R:GTGCTATACAGGCATACAAGTG | F:55.11<br>R:55.15 | 140–176      | KP278810                 | 5              | 3.89           | 0.31           | 0.74           | 0.70 |
| SCF10514  | (GA)11 | F:GTACTCTTTGTGCGGATGTTTTTC<br>R:GTTTCACTCCCACCTCTTAAT | F:55.55<br>R:54.90 | 240–252      | KP278632                 | 4              | 3.22           | 1.00           | 0.69           | 0.63 |
| SCF105151 | (GA)9  | F:CAGAATAAGATTGGGTAGAAGG<br>R:TTTGAGAATTACTTGGCACC    | F:54.81<br>R:55.38 | 284–286      | KP278811                 | 2              | 1.60           | 0.50           | 0.38           | 0.31 |
| SCF105925 | (TC)15 | F:CCGTGTCAAAAGATCAAGC<br>R:AGTTTGTGCCGTCGTACTC        | F:56.80<br>R:56.29 | 159–166      | KP278812                 | 4              | 2.70           | 0.62           | 0.63           | 0.57 |
| SCF106182 | (GT)11 | F:TACCCTTGTGTATCCCTACATT<br>R:GAACAATAGCAGCAACAGAAC   | F:55.25<br>R:55.20 | 151–153      | KP278813                 | 2              | 1.74           | 0.46           | 0.43           | 0.34 |
| SCF107429 | (CT)13 | F:ATGTGAGGTGGGATGATATTAG<br>R:ATATGGTGTGAGTGTGGTGTAG  | F:55.56<br>R:54.96 | 348–378      | KP278815                 | 9              | 7.51           | 0.92           | 0.87           | 0.85 |
| SCF107477 | (AG)10 | F:GTCTTATTTTCACTGTCGTGTG<br>R:CGGGCATTAACCTTATACCT    | F:54.98<br>R:55.87 | 190–200      | KP278814                 | 5              | 2.64           | 0.77           | 0.62           | 0.56 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF107715 | (AG)11 | F:AAAGCGAGTCAGAAACATAGAC<br>R:CCTATCAGTTCCTTTCCTATTG | F:55.46<br>R:54.81 | 244–302      | KP278816                 | 7              | 4.69           | 0.92           | 0.79           | 0.76 |
| SCF10785  | (TC)10 | F:ACATAAAGGAGAGGGAGTAGAG<br>R:ATACCACTTGATAGATTCCTCC | F:53.58<br>R:54.0  | 247–251      | KP278633                 | 3              | 1.49           | 0.39           | 0.33           | 0.30 |
| SCF108252 | (TC)10 | F:CCTATGTAATTGGATTCTACCC<br>R:GTGTATCAAGGTGGAGAAAGTC | F:54.48<br>R:55.38 | 204–208      | KP278817                 | 3              | 2.33           | 0.77           | 0.57           | 0.50 |
| SCF108294 | (TC)12 | F:GGTAAGATTGAGGTTCTGGTCT<br>R:GGTAGAAGCAAGAAGATGCAC  | F:56.44<br>R:56.70 | 240–260      | KP278818                 | 4              | 3.05           | 0.92           | 0.67           | 0.62 |
| SCF108454 | (TG)9  | F:CTAACTAAATGAAGTGTTCCCTT<br>R:ATGTCACGCTCTGAAGTTTG  | F:55.81<br>R:56.45 | 192–198      | KP278819                 | 4              | 2.50           | 0.62           | 0.60           | 0.52 |
| SCF109269 | (TC)11 | F:CACTCCTTCCTTATAGATCAGC<br>R:AAGTAGAAGAGCAGCACAAGAG | F:54.93<br>R:55.85 | 242–268      | KP278820                 | 5              | 2.27           | 0.69           | 0.56           | 0.51 |
| SCF109660 | (GA)9  | F:CCCCAACTGTCGTATAAAA<br>R:TAGAGTACAGGAAAAGCCCTAA    | F:55.27<br>R:55.18 | 289–291      | KP278821                 | 2              | 2.00           | 0.54           | 0.50           | 0.38 |
| SCF110168 | (GA)12 | F:AAAGGACTAGAGGGAAGTACAAC<br>R:CTTATTATCCAGAACTCGTGC | F:55.3<br>R:55.81  | 316–347      | KP278822                 | 7              | 4.39           | 0.92           | 0.77           | 0.74 |
| SCF110223 | (GA)11 | F:GATTCTGTTCCAATAGGCATAC<br>R:GGAGTAGTAGTGAAAGGACCAA | F:55.43<br>R:55.16 | 347–371      | KP278823                 | 6              | 5.04           | 1.00           | 0.80           | 0.78 |
| SCF110507 | (CT)14 | F:GTAGCTGAGGTGGAGGATAAC<br>R:GAGCTGGTGCTGAAATTAAC    | F:55.49<br>R:55.11 | 221–235      | KP278824                 | 5              | 3.89           | 0.92           | 0.74           | 0.70 |
| SCF11065  | (TC)11 | F:CTTTGTCCCAACACGTTAAT<br>R:AAGTCTATAAGCATCCTGCAAC   | F:55.17<br>R:55.42 | 191–193      | KP278634                 | 3              | 1.50           | 0.40           | 0.34           | 0.30 |
| SCF110757 | (GA)9  | F:TCATATCAACCTAACAATCGG<br>R:CACAAACAAGGAAATTAAGACC  | F:55.20<br>R:55.56 | 286–342      | KP278825                 | 6              | 1.82           | 0.46           | 0.45           | 0.43 |
| SCF11084  | (CT)9  | F:GTTGGCTGAGGTAGCTGATAG<br>R:CCTAAAAGGGCTCACAAGTTA   | F:56.74<br>R:56.27 | 312–316      | KP278635                 | 3              | 1.61           | 0.46           | 0.38           | 0.34 |

Table S2. *Cont.*

| Primer ID   | Motif   | Primer Sequences (5'-3')                                | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|---------|---------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |         |                                                         |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF110888   | (CA)9   | F:CTCCTACCCAAATTCAC TTGT<br>R:C AAAA ACTAA ACCATTTCTCAC | F:55.82<br>R:55.56 | 191–193      | KP278826                 | 2              | 1.35           | 0.31           | 0.26           | 0.23 |
| SCF111145   | (TA)9   | F:TTAGTCTGGCTGGTTTTAGTTT<br>R:TTGTACCTATTGTTGGATTGTG    | F:55.10<br>R:55.21 | 342–350      | KP278827                 | 5              | 4.08           | 0.60           | 0.76           | 0.72 |
| SCF111370   | (AC)14  | F:ACCACATCTTCATTTTGAGC<br>R:GTAAACAATACGGGTCCCTTAC      | F:55.19<br>R:54.63 | 273–284      | KP278828                 | 6              | 3.71           | 0.92           | 0.73           | 0.69 |
| SCF11186    | (TCC)9  | F:AGAAAGGCTAAAAGGGTATCTC<br>R:GCTCTCAACA ACTCGAAAGTA    | F:55.18<br>R:54.92 | 278–287      | KP278636                 | 2              | 2.00           | 0.54           | 0.50           | 0.38 |
| SCF112295 * | (AC)9   | F:AACATCTCTACCTCTCACGTTT<br>R:TAGTATTAGTTGATTTGGCGTG    | F:54.74<br>R:54.84 | 271–273      | KP278829                 | 2              | 1.08           | 0.08           | 0.07           | 0.69 |
| SCF112540   | (CT)9   | F:CAGTAGTGGTATTT CACAATCG<br>R:TTTAATGCTTTTGGAAGAGG     | F:54.97<br>R:54.80 | 224–226      | KP278830                 | 2              | 1.26           | 0.23           | 0.20           | 0.69 |
| SCF1128     | (AG)13  | F:GTTTGTTGTTGTGGTGGTTT<br>R:CCTTACTTGACGCTTACTTCAG      | F:55.83<br>R:56.12 | 304–322      | KP278597                 | 5              | 3.77           | 1.00           | 0.74           | 0.69 |
| SCF113389   | (AC)9   | F:GACATCACTCAAGCAAGATAAA<br>R:CCTCGATTCCCTCAAGATATG     | F:54.71<br>R:54.8  | 157–171      | KP278831                 | 5              | 2.70           | 0.77           | 0.63           | 0.58 |
| SCF113558   | (TTC)11 | F:GAGCTTGATCTGGGTATCTTT<br>R:CAAAATCAGAATCGACTGC        | F:55.13<br>R:54.24 | 200–206      | KP278832                 | 4              | 2.25           | 0.39           | 0.56           | 0.51 |
| SCF11431    | (TC)13  | F:GCTGCTGATTTGTTATGTAGAG<br>R:CACTTAGCCCCTTAAACTATTG    | F:54.53<br>R:55.8  | 306–318      | KP278637                 | 5              | 2.79           | 0.85           | 0.64           | 0.60 |
| SCF116329   | (AT)12  | F:GAATCCCACATTAGAAGTTGAT<br>R:TTGTATCTTCCCTATTCC TACTG  | F:54.85<br>R:54.47 | 191–199      | KP278833                 | 4              | 2.62           | 0.31           | 0.62           | 0.56 |
| SCF116485   | (CAT)7  | F:CAATATAAACGTCAGTCACCAG<br>R:ACTTTTGGTTATGCTGGAAG      | F:54.97<br>R:54.56 | 226–232      | KP278834                 | 2              | 1.95           | 0.69           | 0.49           | 0.37 |
| SCF116567   | (GAT)8  | F:GTTGGTCTACAATTCTGTTCCT<br>R:GCCCTTTTAGTTGAAATGC       | F:54.99<br>R:55.3  | 201–207      | KP278835                 | 3              | 2.75           | 0.85           | 0.64           | 0.56 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF116864 | (AC)9  | F:TGCCCCCTTGATTCTAATTTT<br>R:ATGCCTCAGATTGATTTACCT    | F:56.35<br>R:55.42 | 150–154      | KP278836                 | 3              | 2.60           | 0.77           | 0.62           | 0.54 |
| SCF117157 | (GA)15 | F:GGATAGAAACCTGATACGGAC<br>R:CGTTACCGTCCCAAATATAA     | F:55.26<br>R:55.24 | 194–204      | KP278837                 | 6              | 5.05           | 1.00           | 0.80           | 0.77 |
| SCF117385 | (GA)12 | F:TAAGAATCCTCGTCATAGGGT<br>R:CTGTCTTCTCAACTTTCCCTC    | F:55.43<br>R:55.67 | 145–153      | KP278838                 | 4              | 2.40           | 0.77           | 0.58           | 0.51 |
| SCF117422 | (TC)12 | F:TTCTGTTTCTTGGCTCTGTATC<br>R:TATTATGCTACATCGGTCGAG   | F:56.26<br>R:55.55 | 249–275      | KP278839                 | 7              | 3.76           | 0.77           | 0.73           | 0.69 |
| SCF11802  | (AAC)8 | F:CGAGGAACAAGTTTTATAGGAG<br>R:ACACTCACCTTTATTATGGGAC  | F:55.4<br>R:54.81  | 290–293      | KP278638                 | 2              | 1.99           | 0.62           | 0.50           | 0.37 |
| SCF118468 | (CT)15 | F:ATAAGCGGAGCACAGTTACA<br>R:GATAGGATGACCTGTTTTGGT     | F:56.10<br>R:55.58 | 242–260      | KP278840                 | 6              | 3.49           | 0.92           | 0.71           | 0.67 |
| SCF118608 | (TC)14 | F:AACTACTCGATCTTCACCCTTA<br>R:AGGAGACCAACACTTAACCTC   | F:54.86<br>R:54.96 | 239–256      | KP278841                 | 6              | 4.45           | 0.92           | 0.78           | 0.74 |
| SCF118999 | (AG)9  | F:CTAAACTCCAAAATGCCTAAAC<br>R:AAAGTGGATGGGTCTAAAAG    | F:55.4<br>R:55.8   | 272–313      | KP278842                 | 5              | 2.06           | 0.62           | 0.52           | 0.47 |
| SCF120352 | (GA)10 | F:AGTTCTATGACCCCTAACTGAA<br>R:GAAAGGAAAAGAAGCACTATCAC | F:54.70<br>R:54.96 | 272–295      | KP278843                 | 5              | 3.89           | 0.69           | 0.74           | 0.70 |
| SCF120937 | (GA)13 | F:TGTGCAAGAGTCATCTCCTAT<br>R:TATTCCCTTTTCATTCTCCTTC   | F:54.94<br>R:55.5  | 285–305      | KP278844                 | 6              | 4.76           | 0.92           | 0.79           | 0.76 |
| SCF121995 | (AC)14 | F:TAGTCGTGACCAAGAGTGATTA<br>R:GCCACCGAGTATATTTCTATGT  | F:55.7<br>R:55.9   | 169–179      | KP278845                 | 4              | 3.63           | 0.85           | 0.73           | 0.67 |
| SCF122746 | (TC)13 | F:ATTGTATGAAAACCCTAACCC<br>R:GAGACGATTCCAAATATAGCA    | F:54.74<br>R:54.59 | 191–218      | KP278846                 | 7              | 4.33           | 0.85           | 0.77           | 0.73 |
| SCF123189 | (TC)9  | F:CCTAGAAATGTTACTCTCCGAC<br>R:TTCACTTCCTTACTCCTTTTCAT | F:54.86<br>R:54.82 | 191–193      | KP278847                 | 2              | 1.74           | 0.62           | 0.43           | 0.34 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF124075 | (GA)13 | F:ATTTTCCCTCCAACCTCTAT<br>R:GGTGCAACCAACTAACATAA      | F:54.34<br>R:53.7  | 344–362      | KP278848                 | 6              | 4.69           | 0.85           | 0.79           | 0.76 |
| SCF124322 | (TC)9  | F:TAAAACTGTGAGGTTCAATGTG<br>R:CTTCGTGTCTCAAATTACAAAA  | F:55.41<br>R:54.83 | 214–235      | KP278849                 | 5              | 4.17           | 0.92           | 0.76           | 0.72 |
| SCF124927 | (TG)12 | F:CGAGTGTCATTAGCAACAGA<br>R:TATCACTTTAGATCGAGCAGAC    | F:54.92<br>R:53.99 | 230–236      | KP278850                 | 4              | 2.89           | 0.85           | 0.65           | 0.60 |
| SCF125251 | (GA)21 | F:TATACAGTCAGATCCAATCCAC<br>R:TGCAGATAAAGTACAAGAGTGC  | F:54.16<br>R:54.99 | 240–267      | KP278851                 | 7              | 5.28           | 1.00           | 0.81           | 0.79 |
| SCF125667 | (CA)10 | F:AAGGGAGACATTACACAACAA<br>R:TTCGAGATTGACCAAGTATGT    | F:54.72<br>R:54.80 | 171–188      | KP278852                 | 7              | 4.45           | 1.00           | 0.78           | 0.74 |
| SCF125889 | (GA)17 | F:TCTCGTGTATTTTGGAGTGA<br>R:GTTGTATCCTTTGTGCGATTCT    | F:54.19<br>R:53.47 | 175–195      | KP278853                 | 6              | 4.97           | 0.92           | 0.80           | 0.77 |
| SCF126708 | (CA)9  | F:CGACGAATAAAACAAATCAAGTA<br>R:GAGAAGAAGTGAAGGAGAGTTG | F:54.81<br>R:54.98 | 315–317      | KP278854                 | 2              | 1.95           | 0.54           | 0.49           | 0.37 |
| SCF127023 | (TC)14 | F:TATGCTAATCCACTTTGTAGGG<br>R:AATCTGGGTAATTGGGAACT    | F:56.8<br>R:55.9   | 200–212      | KP278855                 | 5              | 3.67           | 0.92           | 0.73           | 0.69 |
| SCF128015 | (TCT)7 | F:ACCCACTCTTTCTATTATCTTCC<br>R:GTGAGTTCCAAGTTCCACATA  | F:54.90<br>R:55.13 | 216–219      | KP278856                 | 2              | 1.90           | 0.62           | 0.47           | 0.36 |
| SCF128307 | (TG)14 | F:ACTCAGAAGTTGAAGCACAAA<br>R:GTATCAAGTACACCAACACCAG   | F:55.25<br>R:54.69 | 220–262      | KP278857                 | 11             | 6.15           | 1.00           | 0.84           | 0.82 |
| SCF128992 | (TC)11 | F:GAGTGTTGAGTTATAGGGGTTT<br>R:TCACAAGAATAGAAGGATGGA   | F:54.17<br>R:54.86 | 237–239      | KP278858                 | 2              | 1.90           | 0.31           | 0.47           | 0.36 |
| SCF13006  | (GCA)7 | F:AAAACATAAGAAAGAGCCCC<br>R:GGATGATGATGTATGGGAAT      | F:55.14<br>R:54.47 | 300–303      | KP278639                 | 3              | 1.81           | 0.46           | 0.45           | 0.38 |
| SCF131915 | (AT)9  | F:TTTTGTTTCCTTATTTTCGG<br>R:TGTAAGTGCATGAAATCGTAAT    | F:54.67<br>R:55.5  | 184–223      | KP278859                 | 6              | 4.65           | 0.83           | 0.79           | 0.75 |

Table S2. *Cont.*

| Primer ID   | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|---------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |         |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF132369 * | (TTC)14 | F:CTACTTTGGGATGGAGAGAGTA<br>R:AGGTTTAGGTAGTGTGGATTG   | F:55.25<br>R:55.5  | 261–292      | KP278860                 | 8              | 5.83           | 0.85           | 0.83           | 0.81 |
| SCF132506   | (TCA)10 | F:AATGTGCCAAGTTTGTAGAC<br>R:GTCCCCTATAAGTCATCTGAAA    | F:54.48<br>R:55.2  | 270–282      | KP278862                 | 3              | 2.30           | 0.85           | 0.57           | 0.47 |
| SCF132532   | (AG)12  | F:GACTGGATTTTCACGAATCTAC<br>R:CTTCATCTTCCTTGACACTTCT  | F:55.47<br>R:55.27 | 275–285      | KP278861                 | 4              | 2.30           | 0.77           | 0.57           | 0.50 |
| SCF132595   | (AC)13  | F:CAAACAAATCTCAACAACACC<br>R:ATTTCAAGATAAGCTCTCCACC   | F:55.64<br>R:56.64 | 222–277      | KP278863                 | 7              | 4.97           | 0.92           | 0.80           | 0.77 |
| SCF132922   | (AT)12  | F:TTAGACGCTTTATGTCCATTC<br>R:GAGTGTCTTGTCTTTGTTGTA    | F:54.68<br>R:54.52 | 199–256      | KP278864                 | 7              | 4.69           | 0.62           | 0.79           | 0.76 |
| SCF133376   | (AAG)9  | F:ATTAGCACCGAATTTAACACC<br>R:GATTATGGGTGAGTCTGTGAAT   | F:55.91<br>R:55.59 | 238–244      | KP278865                 | 3              | 1.62           | 0.46           | 0.38           | 0.35 |
| SCF136207   | (CT)9   | F:GTCTCTGTAGTCGGTGCTTT<br>R:GATTTTCGATTCCTTGACACT     | F:54.57<br>R:54.21 | 167–171      | KP278866                 | 3              | 2.50           | 0.77           | 0.60           | 0.53 |
| SCF136317   | (GA)10  | F:GAGAGTTCAAATTACCTGTACCA<br>R:GGAGATTAGGTTGTGGACTAGA | F:55.18<br>R:55.8  | 271–277      | KP278867                 | 3              | 1.49           | 0.39           | 0.33           | 0.30 |
| SCF136826   | (CA)9   | F:GATCTTGATTAGCTCCAACCTG<br>R:GCTTACACCAATTCTACAGTCA  | F:54.19<br>R:54.67 | 267–269      | KP278868                 | 2              | 1.99           | 0.31           | 0.50           | 0.37 |
| SCF13711    | (GAG)7  | F:GACTTCCTTGGTACTTGGTG<br>R:ACTTTGAGGGTAGGAGTAAACA    | F:54.68<br>R:54.78 | 348–354      | KP278640                 | 3              | 2.77           | 0.92           | 0.64           | 0.57 |
| SCF137494   | (CT)10  | F:CCAACATAAAGAGGACTAGAGG<br>R:GACCTAGACTCCAAATCACG    | F:54.87<br>R:54.76 | 336–397      | KP278869                 | 3              | 1.98           | 0.31           | 0.49           | 0.43 |
| SCF13753    | (CT)9   | F:AAGTCCTTTCCTTCTTTTGC<br>R:GCTATGTGATGTCGTTCTCTAA    | F:55.33<br>R:55.42 | 195–199      | KP278641                 | 3              | 1.81           | 0.54           | 0.45           | 0.38 |
| SCF13771    | (GA)11  | F:AGGATGATGAAATCTGCAAG<br>R:ATCAGTTAGGTGGGGTAAGG      | F:55.28<br>R:55.61 | 171–191      | KP278642                 | 6              | 3.60           | 0.92           | 0.72           | 0.68 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                               | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|--------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                        |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF138014 | (TC)11 | F:TTATTCTCTTCGCTTGGGTA<br>R:TCAGATCATGGATTACTGGTT      | F:55.22<br>R:54.54 | 243–245      | KP278870                 | 2              | 1.45           | 0.39           | 0.31           | 0.26 |
| SCF138394 | (GA)11 | F:AAGCCCAGAAGAAATAACCTA<br>R:TGCAAATGTTAGGAACTGTGT     | F:54.94<br>R:55.83 | 218–229      | KP278871                 | 4              | 3.31           | 0.83           | 0.70           | 0.37 |
| SCF138607 | (GA)17 | F:CATATAGAATACTGGACGGACA<br>R:TTCTGCCATCTCCTTTCTC      | F:54.42<br>R:55.40 | 203–215      | KP278872                 | 4              | 3.10           | 0.77           | 0.68           | 0.63 |
| SCF138992 | (GA)11 | F:ATACTTTACCCACAGAGCTTA<br>R:CCACTCATGCTCACATCAC       | F:54.91<br>R:55.78 | 227–229      | KP278873                 | 2              | 1.65           | 0.23           | 0.39           | 0.32 |
| SCF139334 | (GT)10 | F:GAGGGTCTAATATCTGGTTTCA<br>R:GAGAAAAGATGGAGCAAAAG     | F:55.2<br>R:54.31  | 203–205      | KP278874                 | 2              | 1.08           | 0.08           | 0.07           | 0.07 |
| SCF139660 | (GA)12 | F:ATAAATCTACGTCCATACAGCC<br>R:GAGTACATACAAATCCTCTTTTCG | F:55.9<br>R:54.89  | 333–379      | KP278875                 | 6              | 4.45           | 0.92           | 0.78           | 0.74 |
| SCF140628 | (GT)10 | F:GTGAAATTGGTCAGGTTGAT<br>R:GTCGTCATCATCATCTCCTC       | F:54.84<br>R:55.35 | 143–154      | KP278876                 | 3              | 2.70           | 0.77           | 0.63           | 0.56 |
| SCF14119  | (TC)9  | F:TAACAGTACAATGCCTAGTTCG<br>R:GGATTCTCTTGCTTTGGTATAG   | F:54.90<br>R:54.95 | 243–245      | KP278643                 | 2              | 1.26           | 0.23           | 0.20           | 0.18 |
| SCF141794 | (AAG)7 | F:CCATCTGCATCTATTGTTTTG<br>R:CATTGTGAGGTCTATCTTTTCGC   | F:55.84<br>R:55.81 | 149–164      | KP278877                 | 4              | 2.27           | 0.62           | 0.56           | 0.47 |
| SCF14189  | (TC)9  | F:GTCTAGGTGAGGATGGTTGAT<br>R:AAAACAGAGCCCAACAAGT       | F:55.58<br>R:54.82 | 263–280      | KP278644                 | 2              | 1.35           | 0.31           | 0.26           | 0.23 |
| SCF141985 | (AG)11 | F:GAATGGTCTTGAGGGATGTAT<br>R:ACTCTGGAAGAAATAAAACGG     | F:55.50<br>R:55.24 | 180–188      | KP278878                 | 5              | 4.12           | 0.85           | 0.76           | 0.72 |
| SCF142441 | (TC)10 | F:TTGCGTTTACTATCTAAGGAGG<br>R:CTCAGCCGTCCAAAAGTAT      | F:55.59<br>R:55.39 | 219–233      | KP278879                 | 5              | 3.63           | 0.92           | 0.73           | 0.68 |
| SCF142664 | (AG)9  | F:TACTGACGATGAGCTAGAGTTG<br>R:AATGACAAGTGGAATAGTAGGC   | F:54.98<br>R:55.12 | 247–249      | KP278880                 | 3              | 1.86           | 0.62           | 0.46           | 0.40 |

Table S2. *Cont.*

| Primer ID   | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF142767 * | (TC)10  | F:ATAGTTGGACGGGTGTAATG<br>R:CTCTCGCAAAGTAGAACAATCT   | F:54.95<br>R:55.62 | 257–293      | KP278881                 | 8              | 4.51           | 0.92           | 0.78           | 0.75 |
| SCF143035   | (AT)15  | F:TATTTATAGACGACCAACCTGC<br>R:GTGACCAATATACCAAACCAAG | F:56.7<br>R:56.10  | 166–208      | KP278882                 | 6              | 5.28           | 0.77           | 0.81           | 0.78 |
| SCF143318   | (GA)12  | F:CCGTGCTTAAATTCTGTAGTG<br>R:TCATCCATAGGAGAACATCC    | F:55.27<br>R:54.85 | 279–300      | KP278883                 | 5              | 3.63           | 0.92           | 0.73           | 0.68 |
| SCF144748   | (TC)10  | F:ATTTCCAATCCTTTCCTCTC<br>R:CTCTGACACCTTCTGACACATA   | F:54.85<br>R:55.39 | 151–153      | KP278884                 | 2              | 1.90           | 0.62           | 0.47           | 0.36 |
| SCF145689   | (TC)13  | F:GGCATAAGAGTAGACCATGAAC<br>R:GTACTATAAAATGCTTCCAGCG | F:55.50<br>R:55.98 | 260–277      | KP278885                 | 5              | 2.91           | 0.69           | 0.66           | 0.59 |
| SCF145739   | (CT)10  | F:AAATCCTCCTGTTTTAGACTCC<br>R:CCTCAAGTCATCATTCCT     | F:55.69<br>R:54.91 | 240–242      | KP278886                 | 2              | 1.99           | 0.46           | 0.50           | 0.37 |
| SCF146740   | (AC)15  | F:ATGGGACTGCTTATTGAACAC<br>R:CAAGTGGTGCAATTGTGAGA    | F:56.67<br>R:56.54 | 202–222      | KP278887                 | 6              | 3.52           | 0.85           | 0.72           | 0.68 |
| SCF147117   | (TC)9   | F:AGATATGGAGTGGATTAGGTTG<br>R:GTTAGAGTGAAATGAGCCCTAT | F:54.90<br>R:54.40 | 240–246      | KP278888                 | 3              | 1.49           | 0.23           | 0.33           | 0.30 |
| SCF147295 * | (GA)9   | F:ACTGAGGTAAAAGAGGAGTACG<br>R:CCATCAAGGTCTCAATCTGT   | F:54.54<br>R:55.1  | 199–207      | KP278889                 | 3              | 2.45           | 0.85           | 0.59           | 0.52 |
| SCF147358   | (AG)10  | F:GTACACTAAACACCTTGCGTTA<br>R:CTCACCTACATCCCTCTAGTTC | F:54.81<br>R:54.67 | 211–213      | KP278890                 | 2              | 1.74           | 0.62           | 0.43           | 0.34 |
| SCF149633   | (GA)14  | F:CCTTAATACCCATCCCATAATC<br>R:CTTCTTTTCATTGTTGTGGC   | F:56.46<br>R:55.87 | 289–310      | KP278891                 | 8              | 5.54           | 0.92           | 0.82           | 0.80 |
| SCF149976   | (TTC)19 | F:TATACCCATGTATGTACGCATC<br>R:ACTCTAAGCAGGACAATGCTAT | F:55.13<br>R:55.3  | 272–309      | KP278893                 | 8              | 6.26           | 0.92           | 0.84           | 0.82 |
| SCF149989   | (AG)11  | F:AGTAGGCATTGTTCACTCACTC<br>R:TTTCTCCTAAAGCTAAACTCCC | F:56.7<br>R:56.12  | 293–302      | KP278892                 | 5              | 1.98           | 0.62           | 0.49           | 0.47 |

Table S2. *Cont.*

| Primer ID   | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF150173   | (AG)12 | F:GTGTTGGGAAACAGCAGAT<br>R:TTATTCTCGTTGTCAGCCTT      | F:56.1<br>R:55.12  | 182–186      | KP278894                 | 3              | 2.07           | 0.77           | 0.52           | 0.42 |
| SCF150898 * | (AG)11 | F:AAGCTCCATGTATGCGTATC<br>R:ACACTGACTAGCGTTTGTGT     | F:55.35<br>R:55.6  | 311–317      | KP278895                 | 3              | 2.05           | 0.62           | 0.51           | 0.46 |
| SCF150919   | (AT)10 | F:TTGTTAGCACTTAGCATAACCC<br>R:GCTTCATCTCCACCAATACAT  | F:56.28<br>R:56.60 | 333–363      | KP278896                 | 5              | 4.23           | 0.85           | 0.76           | 0.72 |
| SCF1527     | (GA)9  | F:TCAAACGGTGACATCTATACAC<br>R:GTATCTACGCCTCTTACTCTCG | F:55.19<br>R:55.19 | 241–256      | KP278598                 | 4              | 2.44           | 1.00           | 0.59           | 0.50 |
| SCF153094   | (TC)9  | F:TGTCATTAGGGTTCCTCAAA<br>R:CACCTAGACAACATCGAAACTA   | F:55.64<br>R:54.68 | 210–235      | KP278897                 | 8              | 3.45           | 0.69           | 0.71           | 0.69 |
| SCF153636   | (TC)14 | F:GGTATCAAAGCAAGGTTGAG<br>R:CTCGTTAGAAGTATGTTGGTGA   | F:54.95<br>R:54.68 | 275–297      | KP278898                 | 6              | 4.57           | 0.85           | 0.78           | 0.75 |
| SCF153722   | (TC)11 | F:AGTTATGAGGCTTACGAGGAG<br>R:GATGGAACGATGAAACTGAT    | F:55.41<br>R:54.93 | 263–279      | KP278899                 | 4              | 3.89           | 0.92           | 0.74           | 0.70 |
| SCF154541   | (GA)12 | F:AGAAAGCACAGTAGGTATGGAG<br>R:CAAGAAACCCTAGAGACCAAT  | F:55.35<br>R:55.7  | 265–285      | KP278900                 | 7              | 5.12           | 1.00           | 0.81           | 0.78 |
| SCF155637   | (AT)13 | F:TGTTAGTGTTAGGACCCGTTA<br>R:AAAGTAGGAGTTAGGATGGGAT  | F:54.95<br>R:55.13 | 206–224      | KP278901                 | 6              | 5.12           | 0.85           | 0.81           | 0.78 |
| SCF155797   | (TC)9  | F:ATCATTAAGGCTCCCAAAG<br>R:GTACGTCTACTCTGACGGCTA     | F:54.37<br>R:54.83 | 187–188      | KP278902                 | 2              | 1.83           | 0.54           | 0.45           | 0.35 |
| SCF156807   | (CA)9  | F:AGGAGGTTTGGACTAGAAGTTT<br>R:CCTGGTTGTCTCGATTAGAT   | F:55.38<br>R:54.97 | 150–161      | KP278903                 | 4              | 2.33           | 0.31           | 0.57           | 0.48 |
| SCF157992   | (TTG)9 | F:TAGGTTTGTCTCTTATCCATCC<br>R:GAGTTTGTGATTTCTTAGGAGC | F:55.2<br>R:54.96  | 266–272      | KP278904                 | 3              | 2.27           | 0.62           | 0.56           | 0.49 |
| SCF158255   | (AG)15 | F:ATGCGTACACCTCAATCTTT<br>R:GTGGGTACTTGTTTTCAGTTC    | F:54.81<br>R:53.85 | 300–303      | KP278905                 | 4              | 3.45           | 0.11           | 0.71           | 0.66 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                            | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|-----------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                     |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF15845  | (AG)10  | F:AGGCTAATGAAGAAGAAGTCTG<br>R:GACCAAGACAAGATGAACAAG | F:54.74<br>R:54.82 | 312–328      | KP278645                 | 4              | 2.70           | 0.77           | 0.63           | 0.57 |
| SCF158633 | (GA)18  | F:AGATGCTGAAGTTTCCCTT<br>R:TATGTGGATTCTTTGCCTTG     | F:55.60<br>R:56.26 | 168–195      | KP278906                 | 8              | 4.72           | 1.00           | 0.79           | 0.76 |
| SCF158988 | (TC)10  | F:CTCTACCAAAAATCACCATTAG<br>R:CAAGTATCAAGTTTACGCGG  | F:56.39<br>R:55.74 | 228–264      | KP278907                 | 8              | 5.45           | 0.92           | 0.82           | 0.79 |
| SCF159195 | (CT)9   | F:AACAAAGACCTAATCAGACAC<br>R:ACAATCAAAACACCGTCAG    | F:54.99<br>R:54.35 | 309–315      | KP278908                 | 3              | 1.91           | 0.54           | 0.48           | 0.39 |
| SCF160647 | (GA)10  | F:TAACTCAAAGAACCTAACCCC<br>R:TAAAGTGACAGGTAATGTCGTC | F:55.8<br>R:54.51  | 162–178      | KP278909                 | 5              | 3.28           | 0.85           | 0.70           | 0.65 |
| SCF160663 | (TC)10  | F:TTACACCTATCTCCTGTTTTC<br>R:CAGTTCATCTTGCTAGTTATGC | F:55.1<br>R:54.53  | 149–155      | KP278910                 | 4              | 3.05           | 0.77           | 0.67           | 0.62 |
| SCF16166  | (AC)15  | F:CCTAGTCATTCTTCTACTCCCA<br>R:GGGTATCTCGTCCATATTGT  | F:55.25<br>R:55.54 | 307–322      | KP278646                 | 7              | 5.63           | 0.92           | 0.82           | 0.80 |
| SCF161998 | (GT)9   | F:ATATACCAAGTGCTCTTCCATC<br>R:AGACTTCTTCTCCAAAGGC   | F:55.4<br>R:55.32  | 273–275      | KP278911                 | 2              | 1.55           | 0.31           | 0.36           | 0.29 |
| SCF162175 | (TC)11  | F:ACACGTTGAGGTTCCAAAT<br>R:AGTTTCTGATTGACCTAGATGG   | F:55.38<br>R:55.8  | 175–179      | KP278912                 | 3              | 2.02           | 0.54           | 0.51           | 0.45 |
| SCF162565 | (GTA)10 | F:CTTCCGTGATTGTTCTTGTAG<br>R:ACACAGATGGGATGTTGTATC  | F:55.6<br>R:54.72  | 155–180      | KP278913                 | 5              | 4.23           | 0.85           | 0.76           | 0.73 |
| SCF163134 | (AG)12  | F:CAGTGCAATTAGTTTCCTATCC<br>R:TTCTTGGGTTGGTTATTCAG  | F:55.66<br>R:55.22 | 224–233      | KP278914                 | 5              | 2.58           | 0.62           | 0.61           | 0.57 |
| SCF16359  | (AG)12  | F:GAAGTGCTTTTCTTTCTAGAG<br>R:AGACAGATTAAGATCCACCTTG | F:55.35<br>R:55.8  | 316–328      | KP278647                 | 3              | 2.45           | 0.54           | 0.59           | 0.52 |
| SCF16407  | (TC)11  | F:GGCAGTGAATTAAAGGTCAAC<br>R:GATGAGAAAGAAGAGTAAGGCA | F:56.37<br>R:55.51 | 271–279      | KP278648                 | 3              | 2.09           | 0.62           | 0.52           | 0.35 |

Table S2. *Cont.*

| Primer ID   | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF1648     | (TG)10 | F:GTTGATCTGAAGGAAACCAA<br>R:TCGTATTAACCTCCCTATTGAC   | F:55.16<br>R:55.7  | 284–288      | KP278599                 | 2              | 1.83           | 0.54           | 0.45           | 0.35 |
| SCF164915   | (AC)12 | F:CTCAAAGTATCTCACTCACGC<br>R:ACTGTTGTCCCCTCTGACTAC   | F:55.20<br>R:55.74 | 191–211      | KP278915                 | 6              | 5.54           | 0.85           | 0.82           | 0.79 |
| SCF167793   | (GA)9  | F:GTGAAACGACAAGACCAAAT<br>R:AGGACATCCACCTTCAAAT      | F:55.10<br>R:54.29 | 180–184      | KP278916                 | 3              | 1.59           | 0.46           | 0.37           | 0.32 |
| SCF169090   | (TG)10 | F:GAGACAAAGTTCAAATAGGGAG<br>R:ATACTGCAACCGATACTGAGA  | F:54.82<br>R:55.0  | 249–258      | KP278917                 | 4              | 2.94           | 0.77           | 0.66           | 0.60 |
| SCF170213   | (TC)13 | F:GGGTTTGATGACTTGTTTGTA<br>R:CCTAGAAAATGCAGAAATCG    | F:55.14<br>R:55.22 | 158–166      | KP278918                 | 4              | 3.07           | 0.69           | 0.68           | 0.61 |
| SCF171621   | (CT)12 | F:CACCACTCCCCATTTTAAG<br>R:AAGGGACAGAGGAAGTATTTG     | F:55.50<br>R:55.7  | 196–209      | KP278919                 | 6              | 3.13           | 0.92           | 0.68           | 0.64 |
| SCF172019   | (GA)14 | F:TGTGAGTAGTTGTTGAAGGGA<br>R:CCTCGAAAATCCGGTAAAT     | F:55.82<br>R:56.64 | 244–279      | KP278920                 | 5              | 4.39           | 1.00           | 0.77           | 0.74 |
| SCF172027   | (CCA)9 | F:ACTCCTATTGCCATTCCAC<br>R:CAGTGACAGAGTTGTGGTTAAG    | F:54.95<br>R:55.6  | 161–173      | KP278921                 | 3              | 1.26           | 0.22           | 0.20           | 0.19 |
| SCF172149   | (CT)9  | F:GTTAAATGATGCTGTTAGGGAG<br>R:ATGTCCAGTCGTTATCTCTAGG | F:55.66<br>R:55.11 | 187–205      | KP278922                 | 5              | 3.41           | 0.77           | 0.71           | 0.67 |
| SCF172906   | (GA)10 | F:CTGTTCAAGGATTTGTACTGG<br>R:TATTGACATGAGAAGCACGA    | F:54.90<br>R:55.29 | 167–179      | KP278923                 | 3              | 2.31           | 0.44           | 0.57           | 0.49 |
| SCF173212 * | (TC)9  | F:TGTAGTGGGAGATGCTGATAC<br>R:AATTGGCGAACTAGAAAGTG    | F:55.25<br>R:54.72 | 198–206      | KP278924                 | 4              | 2.24           | 0.69           | 0.55           | 0.50 |
| SCF174394   | (CT)9  | F:GGTGGATGGAATGCTAAATA<br>R:CTTTATTGGTAGTGATTGGAC    | F:55.10<br>R:55.37 | 259–263      | KP278925                 | 2              | 1.95           | 0.54           | 0.49           | 0.37 |
| SCF174468   | (AG)13 | F:CAACATTCTTCGCTCACAA<br>R:CTAAGAGTTGACATGATTGGC     | F:55.81<br>R:54.97 | 174–178      | KP278926                 | 3              | 2.52           | 0.77           | 0.60           | 0.54 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                               | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|--------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                        |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF175823 | (CT)12  | F:AGGGGCAGTTTCTAGTCCTAGTAT<br>R:GCACGTCTTTTCTGTAGTTCAT | F:55.38<br>R:56.20 | 221–231      | KP278927                 | 3              | 2.25           | 0.85           | 0.56           | 0.47 |
| SCF177450 | (TC)10  | F:TCTAAAACTCTCCTCTCACCTC<br>R:GATAGCAGTGGACTCATGTCT    | F:54.51<br>R:54.31 | 268–271      | KP278928                 | 3              | 2.17           | 0.58           | 0.54           | 0.77 |
| SCF177451 | (AG)10  | F:GTACCATATAAGAAAGGGAGCC<br>R:CAATAGAAACCCAAGACAATC    | F:56.5<br>R:55.56  | 183–209      | KP278929                 | 8              | 4.76           | 0.92           | 0.79           | 0.77 |
| SCF17979  | (TC)17  | F:ATATCAGAACAAGGAGATGGTG<br>R:GATACCGAATGAACCAAGAA     | F:55.76<br>R:55.13 | 210–229      | KP278649                 | 6              | 3.76           | 0.85           | 0.73           | 0.70 |
| SCF180863 | (CT)11  | F:CCAGTTACAGATCCTTGAGTTG<br>R:GCAATGTTCCCTCGAATTA      | F:56.49<br>R:56.16 | 169–181      | KP278930                 | 4              | 3.35           | 0.85           | 0.70           | 0.65 |
| SCF181772 | (TTA)28 | F:AGCAACGTATGGTGGTATC<br>R:CATTGTGTTCCACAGCTTC         | F:53.36<br>R:54.16 | 129–179      | KP278931                 | 9              | 6.38           | 0.23           | 0.84           | 0.60 |
| SCF181909 | (CT)10  | F:CTCTCAATCTCTTGTCTTCTCC<br>R:TTCAAACCTCAGCAATCAG      | F:54.92<br>R:54.78 | 172–176      | KP278932                 | 3              | 2.38           | 0.75           | 0.58           | 0.50 |
| SCF183590 | (CT)11  | F:TTTGTAGTATGGGGACACTGAT<br>R:AAAGAGGCAGGTCAGAAAAT     | F:56.11<br>R:55.60 | 168–173      | KP278933                 | 3              | 1.89           | 0.54           | 0.47           | 0.42 |
| SCF18363  | (TC)10  | F:CAAAGACCGCTAGGTTTACA<br>R:ACTGCTCACTAGACAAGATCG      | F:55.66<br>R:54.77 | 170–176      | KP278650                 | 3              | 1.89           | 0.62           | 0.47           | 0.42 |
| SCF184873 | (TA)11  | F:AAGCGTAGAATATGTATGACCC<br>R:GGTAGTCCTCACGGAAGAG      | F:55.9<br>R:54.72  | 223–239      | KP278934                 | 4              | 2.94           | 0.70           | 0.66           | 0.61 |
| SCF18709  | (AC)12  | F:GTAATGGTAAGTGTCGAAATCC<br>R:CATAGATGTAACCACGCTTCT    | F:55.36<br>R:54.61 | 342–350      | KP278651                 | 4              | 3.63           | 0.85           | 0.73           | 0.67 |
| SCF187979 | (AG)10  | F:AGATAAGGCACCCGATAATAC<br>R:GATCAAGGAACGCAATCT        | F:55.0<br>R:55.26  | 201–269      | KP278935                 | 6              | 3.67           | 0.77           | 0.73           | 0.69 |
| SCF189612 | (AG)10  | F:GAGGATTGTTAATGGTTTCTTT<br>R:TACGCTTCATCTTGTTATTTTC   | F:54.25<br>R:54.9  | 148–154      | KP278936                 | 4              | 2.89           | 0.85           | 0.65           | 0.59 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                            | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|-----------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                     |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF189657 | (AG)10 | F:CATCCTTGAAAATAGACAGACC<br>R:CTTAGAAGACCGCACTTGAGA | F:55.48<br>R:55.79 | 238–240      | KP278937                 | 2              | 1.80           | 0.67           | 0.44           | 0.35 |
| SCF189827 | (AG)9  | F:TTCATTTTCCTTACACTTCCC<br>R:GTTAGCTTCTTCTCCTTCTTCA | F:54.27<br>R:54.86 | 184–187      | KP278938                 | 3              | 1.73           | 0.54           | 0.42           | 0.38 |
| SCF191642 | (CA)10 | F:CTACATCCACTAAATATCAAGGC<br>R:GATCAAGCCAAAGGAAGAA  | F:54.87<br>R:55.40 | 228–230      | KP278939                 | 2              | 1.17           | 0.15           | 0.14           | 0.13 |
| SCF192074 | (TA)9  | F:CCTTGGAAAACACCTTTTG<br>R:GCCAAACAATATGGGACAG      | F:55.71<br>R:56.39 | 187–189      | KP278940                 | 2              | 2.00           | 0.54           | 0.50           | 0.38 |
| SCF192219 | (GA)9  | F:GAATTTTGTCTGTTCCAGAGA<br>R:AAAAGAAGAAGAGGAATGGC   | F:55.33<br>R:55.25 | 150–158      | KP278941                 | 4              | 2.30           | 0.62           | 0.57           | 0.50 |
| SCF192715 | (AG)9  | F:CTCTGCCTTGTTCTGTCTCT<br>R:AACCAATCGAAGGTGACAA     | F:55.60<br>R:56.46 | 187–213      | KP278942                 | 5              | 3.45           | 0.77           | 0.71           | 0.67 |
| SCF193103 | (GA)11 | F:GAGGAGTTGAAACAATTAGTCC<br>R:TACCCACTTTAGTCGAAGGAT | F:54.65<br>R:55.50 | 150–168      | KP278943                 | 4              | 2.62           | 0.69           | 0.62           | 0.56 |
| SCF194552 | (CT)9  | F:CACAGGTGTAGGGTCTTGTT<br>R:AAAAGGAGGCAAGGATAGAG    | F:55.5<br>R:55.29  | 209–238      | KP278944                 | 7              | 4.23           | 0.69           | 0.76           | 0.73 |
| SCF19565  | (CT)13 | F:GGGTTTTATGAGTTAGAGTCCC<br>R:GTAGGTTTCTTCGATGGTCTT | F:55.95<br>R:55.6  | 287–317      | KP278652                 | 4              | 2.62           | 0.69           | 0.62           | 0.56 |
| SCF197903 | (GA)11 | F:TCTCGTGAGCGTTACAATATAC<br>R:ATGGAGTCAAGGTAAACCG   | F:54.81<br>R:55.5  | 147–155      | KP278945                 | 5              | 2.91           | 0.77           | 0.66           | 0.59 |
| SCF199831 | (TC)15 | F:GTAGGTATCATCGCTGTCTTC<br>R:GTGCATCACATACAAGCTCT   | F:54.4<br>R:53.73  | 182–201      | KP278946                 | 5              | 3.31           | 0.77           | 0.70           | 0.66 |
| SCF201915 | (AC)19 | F:ATGCACATCCTGAAGTACCA<br>R:CTGAACACATTGGACGGAT     | F:56.51<br>R:56.80 | 188–218      | KP278947                 | 8              | 6.26           | 0.92           | 0.84           | 0.82 |
| SCF204332 | (TC)9  | F:CGTGATCTCCCAGAGTTGT<br>R:CTTTTATTTCCCTATGTGTCCC   | F:56.3<br>R:56.72  | 169–182      | KP278948                 | 4              | 1.77           | 0.46           | 0.44           | 0.40 |

Table S2. *Cont.*

| Primer ID   | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-------------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|             |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF204979   | (CA)13 | F:GGAAAGAGGTAAGAAATGGG<br>R:TAAGAGTTCCCACAACCAAA     | F:55.38<br>R:55.72 | 149–153      | KP278949                 | 3              | 1.89           | 0.62           | 0.47           | 0.42 |
| SCF20681    | (GA)16 | F:AGCCTAAACCTCTGTTTGATG<br>R:TTACAATACCTCGCTCCTTAGA  | F:56.13<br>R:55.97 | 218–233      | KP278653                 | 3              | 1.48           | 0.39           | 0.32           | 0.29 |
| SCF208509 * | (GA)14 | F:GCTTCACACTTGATAGTAGGTTG<br>R:TACCGCCATTGTAGCAGAT   | F:55.82<br>R:56.75 | 146–165      | KP278950                 | 6              | 4.83           | 0.92           | 0.79           | 0.76 |
| SCF208875   | (CA)10 | F:AAGGAGTTCAGATAGTCAAAGG<br>R:AGGAATGAGATGGATATGGA   | F:54.42<br>R:54.35 | 172–182      | KP278951                 | 2              | 1.95           | 0.85           | 0.49           | 0.37 |
| SCF208883   | (GA)9  | F:GAGGAGTGAAGAGCCAGTAA<br>R:GACATTTCAAGTCCCACACT     | F:54.63<br>R:54.91 | 155–163      | KP278952                 | 3              | 2.00           | 0.54           | 0.50           | 0.41 |
| SCF21119    | (TA)9  | F:GGATTTGAGGACTATACCAAGA<br>R:TTAAAAGGCATACGCTGAC    | F:55.2<br>R:54.10  | 331–347      | KP278654                 | 6              | 3.84           | 0.92           | 0.74           | 0.70 |
| SCF213102   | (CAG)8 | F:GTGAAGATACAGTGGAGAGCA<br>R:ATGGTAGTTGTTGACCTGATG   | F:55.46<br>R:54.99 | 148–160      | KP278953                 | 4              | 2.25           | 0.62           | 0.56           | 0.51 |
| SCF21596    | (AC)11 | F:ATATACTGGCATAAACACCCTC<br>R:CCTTACTCTTATCATGGCTAGG | F:54.94<br>R:54.99 | 303–320      | KP278655                 | 8              | 5.20           | 0.92           | 0.81           | 0.78 |
| SCF22434    | (GA)9  | F:TATGTATAGTCCCACAACAAGG<br>R:TCCTGTCTATCACTCACATCAC | F:54.35<br>R:55.12 | 263–265      | KP278656                 | 2              | 1.74           | 0.46           | 0.43           | 0.34 |
| SCF22442    | (CT)11 | F:ACAAAGAAAGACACTCCATCTC<br>R:GTATTTGACTTCCATGACCAC  | F:55.10<br>R:54.45 | 338–348      | KP278657                 | 4              | 2.62           | 0.77           | 0.62           | 0.56 |
| SCF22477    | (CT)12 | F:CTCTCCCCTACTTTCTTCCTAT<br>R:GCCGCTAACACAATTAATAAC  | F:55.3<br>R:55.9   | 243–247      | KP278658                 | 3              | 1.77           | 0.42           | 0.43           | 0.37 |
| SCF2288     | (AGA)8 | F:CAATAGTAGTTTCGAGCTTTCC<br>R:GTTTCCAATTCAAGCCTCTA   | F:55.17<br>R:54.60 | 216–230      | KP278600                 | 4              | 3.22           | 0.85           | 0.69           | 0.64 |
| SCF22962    | (AC)9  | F:GTGCAACAGCTAACAGCATA<br>R:AGGACCAATACTCAGAACAAAC   | F:55.14<br>R:54.99 | 198–204      | KP278659                 | 2              | 1.95           | 0.54           | 0.49           | 0.37 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF23210  | (TC)11  | F:TTGATACTCTCGACCTCTTCTT<br>R:GTGGTGTTCGACATGATTTAC  | F:54.96<br>R:55.42 | 189–209      | KP278660                 | 5              | 4.28           | 1.00           | 0.77           | 0.73 |
| SCF23339  | (GA)15  | F:GCAAAACAGAGTTATAGTGGCT<br>R:TAGACAGAAGCACAGATTGGTA | F:55.49<br>R:55.24 | 253–270      | KP278661                 | 6              | 4.51           | 0.85           | 0.78           | 0.75 |
| SCF23691  | (TCT)13 | F:CGGCTTTGTTAGTTGATGTT<br>R:CGATGTTGTACTATTCATGTCC   | F:55.49<br>R:54.71 | 259–281      | KP278662                 | 7              | 5.12           | 0.92           | 0.81           | 0.78 |
| SCF24087  | (CTT)11 | F:GTCCCTTTCTCGTGTCTTTAT<br>R:GAGTAGTGACGATGCAACTAGA  | F:55.6<br>R:54.80  | 191–212      | KP278663                 | 4              | 2.47           | 0.54           | 0.60           | 0.52 |
| SCF2483   | (GTG)8  | F:TTTCCTTCATAGTGTTCCT<br>R:GTCTCCCTGTAAATCCACTC      | F:54.95<br>R:55.29 | 169–184      | KP278601                 | 2              | 1.74           | 0.31           | 0.43           | 0.34 |
| SCF25221  | (CT)10  | F:GTATCCCCACACTTACCACTAT<br>R:AGGATTGGACGGTAGCTTA    | F:54.69<br>R:54.89 | 317–331      | KP278664                 | 4              | 2.75           | 0.62           | 0.64           | 0.66 |
| SCF25446  | (CT)9   | F:TAGTGTGGACTTAACATGGAGA<br>R:ATCCAACCAAGTATCAGCAA   | F:54.91<br>R:55.67 | 159–161      | KP278665                 | 2              | 1.99           | 0.62           | 0.50           | 0.66 |
| SCF259    | (CT)10  | F:TGACAGTACCAATAGCAGGAC<br>R:AACACCCAGTCGTTATACATCT  | F:55.33<br>R:55.30 | 177–194      | KP278591                 | 5              | 3.49           | 0.69           | 0.71           | 0.66 |
| SCF25944  | (GA)10  | F:AACTATGCCAGAAGACTCAGAT<br>R:CTTCACAAATCACAACCACTAC | F:54.82<br>R:54.82 | 293–321      | KP278666                 | 7              | 4.69           | 1.00           | 0.79           | 0.76 |
| SCF26014  | (GA)9   | F:GGTCCCAGAATCAATGTCTA<br>R:GAAATCAGAGAAGAAACAGGTC   | F:54.94<br>R:54.75 | 166–170      | KP278667                 | 3              | 2.89           | 0.77           | 0.65           | 0.58 |
| SCF26049  | (TTC)13 | F:GTTTCAGGTCTGTTGTAAGGAAG<br>R:TTTCTTGTTAGGACGAAGTGG | F:55.63<br>R:55.46 | 168–187      | KP278668                 | 6              | 4.28           | 0.85           | 0.77           | 0.73 |
| SCF26697  | (CT)13  | F:TCGTAACCTATTCAGTGGGTGT<br>R:GGAGCAGTAGAGATTAAACGAC | F:54.76<br>R:55.0  | 272–282      | KP278669                 | 5              | 2.52           | 0.85           | 0.60           | 0.56 |
| SCF2714   | (AG)9   | F:ACAAGTCTCTGGAAGCTAACAT<br>R:GTTGATTGTTGGGTCTAAGTTC | F:54.90<br>R:55.39 | 202–208      | KP278602                 | 4              | 2.60           | 0.85           | 0.62           | 0.54 |

Table S2. *Cont.*

| Primer ID  | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|------------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|            |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF27510   | (GA)13  | F:CCTTCAGATTCAACGTATTCTC<br>R:GGTGTATCACATCCCCAAAC   | F:55.63<br>R:55.15 | 239–284      | KP278670                 | 8              | 5.73           | 1.00           | 0.83           | 0.80 |
| SCF27755   | (GA)11  | F:GAAGTGAGAGTAGGAATCGAAG<br>R:CCACAACACAAAACCTAAT    | F:54.96<br>R:55.0  | 335–357      | KP278671                 | 6              | 3.98           | 0.92           | 0.75           | 0.71 |
| SCF27811 * | (TC)10  | F:ATGTGACTAGCATGGGACTTA<br>R:TATTTACCTGGATAGGAGAAGG  | F:54.84<br>R:54.38 | 219–259      | KP278672                 | 4              | 2.97           | 0.77           | 0.66           | 0.61 |
| SCF27934   | (AC)9   | F:TCCAAATAGCCCAGAATAAG<br>R:GGTACTCCCATGTAATTGTTGT   | F:54.60<br>R:55.55 | 234–237      | KP278673                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| SCF28100   | (TCT)7  | F:TAGAACTAACATGGGAGGTGT<br>R:GCACGCTGTATTGATAGAAGAT  | F:55.43<br>R:56.23 | 239–295      | KP278674                 | 6              | 5.93           | 1.00           | 0.83           | 0.81 |
| SCF28279   | (TC)12  | F:GATACTTTACCTCCTCCTCAAG<br>R:TTGTCTCTATCTCTAACTCCC  | F:53.98<br>R:54.34 | 231–239      | KP278675                 | 4              | 1.63           | 0.46           | 0.39           | 0.36 |
| SCF28509   | (GA)9   | F:GCAAACACCACACTATATGAGA<br>R:ATAGAGAACCACAGAACAGGAC | F:55.35<br>R:54.97 | 212–221      | KP278676                 | 5              | 2.86           | 0.77           | 0.65           | 0.59 |
| SCF28613   | (CAA)16 | F:CATTCTTCACTCCAACCTCAG<br>R:CAAGTCCCATCATCATTTTC    | F:55.1<br>R:55.38  | 182–220      | KP278677                 | 5              | 2.94           | 0.92           | 0.66           | 0.60 |
| SCF28931   | (TC)13  | F:TCTCATAAGTCAGAACCTCACA<br>R:CTAAACTAAACCTCCTAACCGA | F:55.2<br>R:54.68  | 225–229      | KP278678                 | 5              | 4.07           | 0.69           | 0.75           | 0.71 |
| SCF28955   | (GT)9   | F:TATTCAAAGCCACTAGGCAC<br>R:CAAACCAAATTCTCCTTCTG     | F:55.57<br>R:54.93 | 235–246      | KP278679                 | 5              | 3.45           | 0.89           | 0.71           | 0.67 |
| SCF29560   | (GA)13  | F:GTGTGGTGTGGTCTCTACAAT<br>R:ACATCTCTTTGGCTGATACTTC  | F:54.87<br>R:55.22 | 248–258      | KP278680                 | 5              | 2.41           | 0.62           | 0.59           | 0.53 |
| SCF29735   | (TG)16  | F:CGTAAAATCTGTTGTCTCTGTG<br>R:TCTCTATGCTCCTTCCACTTAT | F:55.16<br>R:54.93 | 263–278      | KP278681                 | 5              | 3.84           | 0.85           | 0.74           | 0.70 |
| SCF30000   | (AGA)10 | F:GACTCTTCAACTTCCACGTTA<br>R:GAAATCTTAATCTTGCAGCC    | F:54.59<br>R:54.28 | 161–167      | KP278682                 | 3              | 1.98           | 0.69           | 0.49           | 0.43 |

Table S2. *Cont.*

| Primer ID  | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|------------|---------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|            |         |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF30010   | (CT)9   | F:CTCAAATCAACGATCAAGAC<br>R:GAAAGAGACAACAAAACCCCT     | F:53.16<br>R:53.45 | 302–337      | KP278683                 | 8              | 4.33           | 0.92           | 0.77           | 0.74 |
| SCF30734   | (TTA)8  | F:GTTGAAAACCCAACTGTGAG<br>R:AGATCCAGTCATGGTACTTTTG    | F:55.63<br>R:55.83 | 178–240      | KP278684                 | 6              | 2.89           | 0.69           | 0.65           | 0.62 |
| SCF30816 * | (TCG)8  | F:GTCCAAAATAGCATCGAAAG<br>R:CGCATTACTTCTTCACTATACG    | F:55.5<br>R:54.60  | 207–216      | KP278685                 | 3              | 1.89           | 0.62           | 0.47           | 0.42 |
| SCF31172   | (CT)11  | F:ACTGGATCTGGTGTTATTTACC<br>R:GGCTGGAAACAATTCAAAC     | F:54.81<br>R:55.61 | 161–167      | KP278686                 | 3              | 2.70           | 0.77           | 0.63           | 0.56 |
| SCF31208   | (CT)10  | F:AACAGCACCCTACAACACTT<br>R:AGAGAACAAATCGTCTAATCGTC   | F:54.89<br>R:55.22 | 306–359      | KP278687                 | 5              | 3.60           | 0.85           | 0.72           | 0.68 |
| SCF31394   | (TC)11  | F:GTAGCAAAAGAAGAGACACCAT<br>R:CGTTTTCCAGTTCCAGAGTA    | F:55.30<br>R:55.46 | 273–287      | KP278688                 | 5              | 3.80           | 0.85           | 0.74           | 0.69 |
| SCF3191    | (TCT)15 | F:GCACTATCAGGAAGAGGAATTA<br>R:GTAACACCAGAAAACAACCTGC  | F:55.32<br>R:54.96 | 238–260      | KP278603                 | 5              | 3.71           | 0.92           | 0.73           | 0.69 |
| SCF3261    | (TC)10  | F:GTTTACCATATTCACCTCCTTCC<br>R:TGAGACAGACCTAACATTTGAC | F:54.48<br>R:54.43 | 260–268      | KP278604                 | 3              | 2.77           | 0.77           | 0.64           | 0.57 |
| SCF32727   | (TC)18  | F:ATGTAACGGTCTCCACTTTCT<br>R:TAGTATCTTCGTGGTCAGAGGT   | F:55.41<br>R:55.59 | 192–210      | KP278689                 | 8              | 5.45           | 0.92           | 0.82           | 0.79 |
| SCF33047   | (GCT)8  | F:TAGGGAAGGAGTAGTTATCGAA<br>R:ATGCTGACCTCATCGTCTT     | F:54.96<br>R:55.65 | 161–173      | KP278690                 | 4              | 2.44           | 0.82           | 0.59           | 0.52 |
| SCF33185   | (CT)14  | F:AGCACACTACAGACAGGGTAAT<br>R:GTTTTGGCTCTGGCTAAGTAT   | F:55.53<br>R:55.41 | 198–202      | KP278691                 | 3              | 2.62           | 0.69           | 0.62           | 0.55 |
| SCF33471   | (TC)12  | F:TTTATTGCACACGAGAACAG<br>R:ATATTTTGTCCACGCTCACT      | F:54.94<br>R:54.81 | 288–329      | KP278692                 | 7              | 2.70           | 0.46           | 0.63           | 0.61 |
| SCF3362    | (TGC)9  | F:GTACAGCAAAATTCAGCACA<br>R:GGATTTATCTACAGCCCATTAC    | F:54.93<br>R:54.62 | 343–372      | KP278605                 | 3              | 2.25           | 0.46           | 0.56           | 0.47 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF34010  | (CA)10  | F:GAGAATATGTGATGTTGAGGTG<br>R:CAAGTGTTAGGCTCGTTTAGTT | F:54.64<br>R:55.57 | 285–287      | KP278693                 | 2              | 1.35           | 0.31           | 0.26           | 0.23 |
| SCF34071  | (TG)10  | F:CGTGTGCAGATTTACTTCAG<br>R:AATTCATAGATCCCCATGAC     | F:54.50<br>R:53.76 | 268–276      | KP278694                 | 3              | 2.94           | 0.85           | 0.66           | 0.59 |
| SCF3427   | (CT)11  | F:GCAAGACATCATCACAAACA<br>R:CTTATCCCAGTCCTTCAACTTA   | F:55.46<br>R:55.26 | 347–349      | KP278606                 | 2              | 1.35           | 0.31           | 0.26           | 0.23 |
| SCF34513  | (TG)10  | F:TACTAATCTTCTGGTTTGGGC<br>R:GTACACCACTCCTGATGGC     | F:56.5<br>R:56.34  | 228–232      | KP278695                 | 2              | 1.47           | 0.40           | 0.32           | 0.27 |
| SCF34584  | (AG)10  | F:GTCTGTTTGAAGAAGAAGGT<br>R:CTGTTTCGTCAATCCCTAGC     | F:55.9<br>R:55.82  | 199–213      | KP278696                 | 4              | 3.49           | 0.85           | 0.71           | 0.66 |
| SCF35507  | (GA)9   | F:GTCTAATCTAATGCAGAATGCC<br>R:AATGTGGACAACGAGTACATCT | F:55.73<br>R:56.19 | 238–240      | KP278697                 | 2              | 1.55           | 0.46           | 0.36           | 0.76 |
| SCF3551   | (AC)9   | F:CTTCGACGTTTCTGTGACTAT<br>R:AGTTGGTGATTGGAAGAGTAAG  | F:54.63<br>R:55.16 | 274–289      | KP278608                 | 6              | 4.76           | 0.92           | 0.79           | 0.76 |
| SCF3595   | (CA)10  | F:AGACTACAGTGAACAAAGACCA<br>R:CTGACTTGGTGTGATTAGTGAG | F:54.9<br>R:54.97  | 316–332      | KP278607                 | 6              | 4.90           | 1.00           | 0.80           | 0.77 |
| SCF36745  | (TC)14  | F:TCCTCATTAAGTATTGGACAGG<br>R:CTGGATTCTTGTTCTTAGCTTC | F:55.92<br>R:55.13 | 307–316      | KP278698                 | 4              | 2.94           | 0.69           | 0.66           | 0.60 |
| SCF37023  | (AAT)12 | F:GAATAGCCTTAACATACGCTGT<br>R:ATTGGAATGGTTTAGTGGTG   | F:55.46<br>R:54.92 | 332–351      | KP278699                 | 3              | 2.74           | 0.67           | 0.64           | 0.56 |
| SCF37628  | (GA)12  | F:ACCAGCTCAGATAACAATGC<br>R:GAGTAGGATACCTCCACACCTA   | F:55.39<br>R:54.96 | 255–263      | KP278700                 | 2              | 1.90           | 0.62           | 0.47           | 0.36 |
| SCF38340  | (TC)9   | F:CAAACCATTTTAACGGAGAG<br>R:AATCATCGTGCATACCTGTT     | F:54.99<br>R:55.52 | 336–339      | KP278701                 | 3              | 1.27           | 0.23           | 0.21           | 0.20 |
| SCF38430  | (GA)14  | F:CAATAGTTAGGAAGTTGGAACC<br>R:CTAAGAACCAAACAGAGCCTTA | F:54.73<br>R:55.63 | 156–176      | KP278702                 | 3              | 1.91           | 0.62           | 0.48           | 0.39 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF38553  | (GA)10  | F:CTTCTGTTTACTCACTTCCACC<br>R:ATGGTCCCAAGATACTTTAGC  | F:55.63<br>R:55.3  | 350–358      | KP278703                 | 4              | 2.09           | 0.46           | 0.52           | 0.48 |
| SCF38942  | (CT)11  | F:CTTGCTATTTGGTACTCGTCTT<br>R:CTTGACAGTTATTTCTCTTCGG | F:55.50<br>R:55.87 | 230–240      | KP278704                 | 3              | 2.86           | 0.69           | 0.65           | 0.58 |
| SCF3914   | (TAC)13 | F:TGTGGAGTTAGAGTGACATACC<br>R:GACAAGAATGATGAGTAGCGT  | F:54.30<br>R:54.52 | 345–372      | KP278609                 | 5              | 3.98           | 0.85           | 0.75           | 0.71 |
| SCF39242  | (TC)14  | F:ACTCCTGAAGAAGAAGAACAGA<br>R:AATGAATGCAGACCACAGAT   | F:54.98<br>R:55.48 | 246–276      | KP278705                 | 7              | 4.76           | 1.00           | 0.79           | 0.76 |
| SCF3932 * | (TC)10  | F:CAGAGTTTCAGTGGAGCATT<br>R:CTCAGCTTCTGTGTTTTGTGT    | F:55.44<br>R:55.62 | 311–319      | KP278610                 | 5              | 3.31           | 0.77           | 0.70           | 0.66 |
| SCF39705  | (AT)13  | F:GCAGGTAAATCCTATCTGGAAT<br>R:GTTGAAGACACCTAGTCCACTC | F:56.43<br>R:55.46 | 333–397      | KP278706                 | 7              | 3.08           | 0.70           | 0.68           | 0.64 |
| SCF40517  | (CT)12  | F:GTAGAATGGCAATAGGGTTT<br>R:GAAGAAGATGACGAAGATCAC    | F:53.47<br>R:53.91 | 245–259      | KP278707                 | 5              | 3.05           | 0.92           | 0.67           | 0.62 |
| SCF41361  | (CA)9   | F:AAAATTGCTTGGTCCTCAC<br>R:AAGTGTATAGTCTGGGGTGTTT    | F:55.17<br>R:54.87 | 231–233      | KP278708                 | 3              | 1.61           | 0.31           | 0.38           | 0.34 |
| SCF41971  | (GA)12  | F:ATACTTGACCTCTATGGCTTGA<br>R:GTACTTACGTGTTTGGTTCGTT | F:55.67<br>R:55.99 | 280–300      | KP278709                 | 7              | 4.83           | 0.92           | 0.79           | 0.77 |
| SCF42332  | (CT)10  | F:GATAGAATGACGAACTAACCC<br>R:AGTGGGGAGATAATTGAGAAG   | F:54.64<br>R:54.99 | 194–208      | KP278710                 | 4              | 2.60           | 0.92           | 0.62           | 0.54 |
| SCF4305   | (GA)13  | F:AATGAGTGGTTATGTAGGGAGA<br>R:AGATTGGTGAGATATGAGGAAG | F:55.36<br>R:55.0  | 179–191      | KP278611                 | 5              | 4.76           | 0.85           | 0.79           | 0.76 |
| SCF43145  | (TCT)7  | F:TGGTTTTGGATACACACTTG<br>R:AAGAACAAGATCACCCTCTG     | F:54.42<br>R:54.38 | 235–261      | KP278711                 | 7              | 6.76           | 0.69           | 0.85           | 0.83 |
| SCF43220  | (TC)14  | F:CTTGTCGAGCATCCTATATTTT<br>R:AAAAGTCATGGGAAGGTGTT   | F:55.74<br>R:56.6  | 154–159      | KP278712                 | 4              | 2.50           | 0.69           | 0.60           | 0.52 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF4386   | (TTC)9  | F:GTTACTCATTTCCTTTGCTGAGG<br>R:CCTCTTAGTGTTGGAGTTTCAT | F:55.86<br>R:55.16 | 200–203      | KP278612                 | 2              | 1.99           | 0.62           | 0.50           | 0.37 |
| SCF45712  | (CA)9   | F:GCAGTGTGCTTTTCTTTTCT<br>R:GTTACTAGGGTACTGGGTTTGA    | F:54.90<br>R:55.5  | 206–210      | KP278713                 | 2              | 1.35           | 0.31           | 0.26           | 0.23 |
| SCF46588  | (TG)11  | F:ACAAACCTTGAGCCTATTTG<br>R:GTCTGAGTTTCCACTATCGTCT    | F:54.56<br>R:55.13 | 350–356      | KP278714                 | 5              | 2.06           | 0.46           | 0.52           | 0.47 |
| SCF46739  | (TC)10  | F:ATGTTAGGTGATGCTGTTGTC<br>R:CAGGTGCTTATTTTCGTTTC     | F:55.15<br>R:55.13 | 247–249      | KP278716                 | 2              | 1.83           | 0.69           | 0.45           | 0.35 |
| SCF46751  | (AG)12  | F:ACCAGATGAAGAAGAAGAAGC<br>R:GCCTCTCATTACCATTACAAAC   | F:55.33<br>R:55.51 | 309–325      | KP278715                 | 5              | 3.07           | 0.85           | 0.68           | 0.63 |
| SCF46824  | (ATT)10 | F:GGAGATGCTGTAATAACGAAGT<br>R:TTAGTCAATATGCGTGCAAC    | F:55.27<br>R:54.90 | 193–209      | KP278717                 | 5              | 3.80           | 0.77           | 0.74           | 0.70 |
| SCF46833  | (AAC)7  | F:GGACCGCCGTATTTAGTTA<br>R:GCCCATACCCCTAGTTATTG       | F:55.36<br>R:56.12 | 208–211      | KP278718                 | 2              | 1.74           | 0.46           | 0.43           | 0.34 |
| SCF46912  | (AG)9   | F:GAACAATAAAGAGGCTAGAGGA<br>R:CATAGTTGTAGAGAAGATCGGG  | F:54.68<br>R:55.68 | 172–182      | KP278719                 | 4              | 2.50           | 0.69           | 0.60           | 0.55 |
| SCF47809  | (CAT)10 | F:CTTCTACCTTCCAAGATTTGTG<br>R:ATTACTATTTCCAGAGACGACC  | F:55.72<br>R:56.38 | 289–304      | KP278720                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| SCF48414  | (GA)12  | F:GTAGGGAAACAAGAATTGGAC<br>R:ACTGTGAGATTGGTGTGATATG   | F:55.30<br>R:55.1  | 284–286      | KP278721                 | 2              | 1.95           | 0.69           | 0.49           | 0.37 |
| SCF48645  | (CT)10  | F:AAAATAGGTCCCACATGAGTAG<br>R:GCTAGACGATGACACATTATTC  | F:54.98<br>R:54.10 | 310–312      | KP278722                 | 3              | 1.37           | 0.31           | 0.27           | 0.25 |
| SCF49598  | (TCT)8  | F:ATGAGGTTTTCCAACACAAC<br>R:TCAGAGGGAAGTACATGAGAAT    | F:54.93<br>R:55.48 | 258–261      | KP278723                 | 2              | 1.83           | 0.69           | 0.45           | 0.35 |
| SCF49656  | (TC)14  | F:ACTCTTACCCCTGAAACCAACT<br>R:TAGGTGCATGAGACTTTTAACC  | F:56.10<br>R:56.13 | 284–301      | KP278724                 | 5              | 3.71           | 0.85           | 0.73           | 0.69 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF51810  | (TGC)8  | F:TATTACTCTGTTGCTGCTGTTG<br>R:ACTAAACCCTAATGTCCCTTCT | F:55.91<br>R:55.21 | 189–204      | KP278725                 | 3              | 2.18           | 0.69           | 0.54           | 0.46 |
| SCF53282  | (GA)11  | F:GACAATCACATACCCATACAG<br>R:CCACTCTTCCCTCTATCG      | F:54.55<br>R:54.85 | 214–234      | KP278726                 | 3              | 1.61           | 0.46           | 0.38           | 0.34 |
| SCF53750  | (CA)10  | F:GTTTCATAGAGATGGGTTTCTG<br>R:CTTGTTCCCTAAGCTACATT   | F:55.48<br>R:55.27 | 316–353      | KP278727                 | 6              | 2.41           | 0.69           | 0.59           | 0.56 |
| SCF54155  | (GA)14  | F:TCGAAGAAAATGAAGGGAC<br>R:ACAAATGGAGAGGAAAAGTGTAG   | F:55.24<br>R:55.16 | 292–335      | KP278728                 | 8              | 5.54           | 0.77           | 0.82           | 0.80 |
| SCF55511  | (GA)9   | F:GAAGTGAAAATCTGAACCTCTC<br>R:ACTCTCGAATCTGTCTTCTTGT | F:54.75<br>R:54.84 | 178–183      | KP278729                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| SCF55751  | (CT)10  | F:ACTCACGTCCATTTTCTCAC<br>R:AGCGATATAACAATACCAGAGC   | F:55.9<br>R:55.38  | 227–239      | KP278730                 | 6              | 4.97           | 0.62           | 0.80           | 0.77 |
| SCF56032  | (GAT)11 | F:AGAAATGGCGCTCTGTATC<br>R:GAACAGTCTCATCTTCACGAC     | F:55.46<br>R:54.78 | 195–216      | KP278731                 | 3              | 2.25           | 0.85           | 0.56           | 0.47 |
| SCF56561  | (AG)13  | F:ATTAGCCATTCGTGATTAGG<br>R:TAAGGAGATACGACCAAGAAAC   | F:54.46<br>R:55.25 | 218–230      | KP278732                 | 4              | 2.84           | 1.00           | 0.65           | 0.58 |
| SCF56717  | (AGG)7  | F:GTGTTTGTGTTTGTGTCTGTG<br>R:GATGATTTACCTACATCGG     | F:54.91<br>R:55.42 | 199–211      | KP278733                 | 2              | 1.99           | 0.77           | 0.50           | 0.37 |
| SCF56747  | (GA)14  | F:TTAGAGAAAGGTCCCAACAG<br>R:GAAGAGGCTAAGAGGTCATGT    | F:54.50<br>R:55.20 | 256–280      | KP278734                 | 7              | 5.54           | 1.00           | 0.82           | 0.80 |
| SCF56816  | (AGC)9  | F:CGGATTGACTAATTTCTGTCTC<br>R:CTCTTATTCCACCAAACGAA   | F:55.63<br>R:55.39 | 210–219      | KP278735                 | 2              | 1.55           | 0.46           | 0.36           | 0.29 |
| SCF57479  | (CT)10  | F:AAGTGCAAGTGTGAGAGTGTAT<br>R:TGATGGGTGTAAGTGTAAGAG  | F:54.11<br>R:54.52 | 196–204      | KP278736                 | 4              | 2.50           | 0.62           | 0.60           | 0.52 |
| SCF57497  | (TC)10  | F:ATCTGTAGGTTGTGTTACCCC<br>R:ATCAACTGTATCTACCCACCAA  | F:55.53<br>R:56.11 | 239–240      | KP278737                 | 2              | 1.90           | 0.77           | 0.47           | 0.36 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF58861  | (TA)10 | F:GTTGACTAAAAGGCATTGGA<br>R:GACTACTATTTTCTGCACAGGG   | F:55.38<br>R:55.74 | 147–164      | KP278738                 | 7              | 6.15           | 1.00           | 0.84           | 0.82 |
| SCF59035  | (TC)16 | F:AGATTTTGAACGATGTCTGC<br>R:GATCTATCGCTTATCCAGTACG   | F:55.36<br>R:55.77 | 301–336      | KP278739                 | 5              | 3.28           | 0.92           | 0.70           | 0.65 |
| SCF59248  | (TTA)7 | F:TAGTTGAAAATGGAGAGAGAGC<br>R:TTAGATGCCCAACACTACATC  | F:55.51<br>R:55.26 | 194–204      | KP278740                 | 4              | 2.94           | 0.77           | 0.66           | 0.61 |
| SCF59739  | (CT)11 | F:GTATGACTGTACCAAACAAACC<br>R:CAGCTTTCCTTCTAAATGA    | F:53.79<br>R:54.78 | 334–350      | KP278741                 | 5              | 3.45           | 0.77           | 0.71           | 0.66 |
| SCF60761  | (GA)10 | F:ACTTAAACATCGGTCCATAGAG<br>R:AGAGTCGTGTCCTTTCTTTTC  | F:55.13<br>R:55.25 | 259–263      | KP278742                 | 3              | 2.12           | 0.55           | 0.53           | 0.47 |
| SCF61078  | (GAA)7 | F:GACTCTTCATATAACCCACAGC<br>R:AAAAGTGCTTGATCGTTAGC   | F:55.50<br>R:54.87 | 252–254      | KP278743                 | 2              | 1.17           | 0.15           | 0.14           | 0.13 |
| SCF61189  | (AG)9  | F:GCCATAACTCTCACTCAAATCT<br>R:ACCTATTCACCTACATCCAAAG | F:55.22<br>R:54.98 | 307–319      | KP278744                 | 5              | 3.49           | 0.69           | 0.71           | 0.66 |
| SCF6195   | (AG)14 | F:GACTATGAATCTGACGCTCAC<br>R:CCAGTAAATACGTGACTAATCG  | F:54.93<br>R:54.30 | 340–354      | KP278613                 | 5              | 3.52           | 0.85           | 0.72           | 0.67 |
| SCF64185  | (TG)9  | F:CACCTCATTTGGTTCATTCT<br>R:CAGATACTAAAGTTGCCGTA     | F:55.3<br>R:54.81  | 316–320      | KP278745                 | 3              | 2.43           | 0.77           | 0.59           | 0.50 |
| SCF64632  | (CT)12 | F:ACCTCCTAAAACACAACCCTA<br>R:CTGAGTAATCTTCGATGTGAGA  | F:55.42<br>R:54.69 | 149–175      | KP278746                 | 7              | 4.12           | 0.85           | 0.76           | 0.72 |
| SCF64758  | (TG)11 | F:TAAGAGGGTTTGAGCATTCA<br>R:TTGGGTCATAAACAACCTCA     | F:55.97<br>R:56.45 | 350–356      | KP278747                 | 3              | 1.90           | 0.46           | 0.47           | 0.43 |
| SCF6530   | (CT)9  | F:CCCCAAGTATAATGTGTAAAGG<br>R:AGTTCGCATAGAACTGTAGGA  | F:55.41<br>R:55.89 | 349–353      | KP278614                 | 2              | 1.95           | 0.54           | 0.49           | 0.37 |
| SCF65999  | (CT)11 | F:AGGTAGCATTAGACACGAGATT<br>R:GAGGTTTTACATGACCATTACC | F:54.88<br>R:55.20 | 288–300      | KP278748                 | 2              | 1.74           | 0.46           | 0.43           | 0.34 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                              | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|-------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                       |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF66692  | (CT)10  | F:AAAGTGTATTGGACGGCTG<br>R:TTGTTATGGCCCCTCATTA        | F:56.20<br>R:56.46 | 245–259      | KP278749                 | 7              | 4.02           | 0.92           | 0.75           | 0.72 |
| SCF68870  | (AG)11  | F:GTGAATTGTTGCAGAGTACCTA<br>R:TGAGTTGAGTTCATATAGCTGG  | F:54.67<br>R:54.76 | 166–168      | KP278750                 | 2              | 1.08           | 0.08           | 0.07           | 0.07 |
| SCF6926   | (CT)10  | F:ACATGCACTTCAAATAGTACCC<br>R:TTACAACCTTACACAGGAAGCAG | F:55.85<br>R:54.92 | 212–234      | KP278615                 | 4              | 2.09           | 0.46           | 0.52           | 0.48 |
| SCF69698  | (TC)9   | F:GAGGAGATAAAGGTTTGTGAG<br>R:CTTTGAGACTTTGAGTGAGACA   | F:54.82<br>R:54.80 | 297–303      | KP278751                 | 3              | 1.81           | 0.46           | 0.45           | 0.38 |
| SCF69981  | (CT)9   | F:AGCGTTACCACCGAATATAA<br>R:CGAGATATAGTTAAAAGGACGG    | F:54.98<br>R:55.1  | 226–244      | KP278752                 | 8              | 6.38           | 0.92           | 0.84           | 0.82 |
| SCF71136  | (CAA)7  | F:TCTGTTTTTCACAGCTATCACAC<br>R:GTTTCATCAAAGGCCAGAGT   | F:55.55<br>R:55.16 | 179–182      | KP278753                 | 2              | 1.26           | 0.23           | 0.20           | 0.18 |
| SCF71184  | (ATT)22 | F:TCTGTTTCAGTTGGGCTTTAT<br>R:GCTCACATTCACCTGTAATTC    | F:54.95<br>R:54.79 | 200–231      | KP278754                 | 7              | 4.97           | 0.92           | 0.80           | 0.77 |
| SCF7132   | (TC)10  | F:AAGGGGAAGGACAATAAGAA<br>R:AATTTGATGACTGTTGTGGC      | F:55.38<br>R:56.1  | 218–236      | KP278616                 | 3              | 1.98           | 0.54           | 0.49           | 0.43 |
| SCF7155   | (GT)11  | F:GGGATCTATGAGTTGTGGACTA<br>R:CCACGGAATAGTTGTAAGTTGT  | F:55.76<br>R:55.93 | 168–196      | KP278617                 | 4              | 1.91           | 0.54           | 0.48           | 0.43 |
| SCF72209  | (CT)12  | F:CTTTACCTTTTCCTTCAGTCGT<br>R:GAGGTTACCAAATCTTACCA    | F:56.77<br>R:56.65 | 206–210      | KP278755                 | 3              | 2.94           | 0.92           | 0.66           | 0.59 |
| SCF72229  | (CCA)7  | F:CAACTTCTACAACCACTCCAC<br>R:GATTTATTGTGCTACACTGGTC   | F:54.78<br>R:54.3  | 322–334      | KP278756                 | 3              | 2.27           | 0.60           | 0.56           | 0.50 |
| SCF72379  | (GA)12  | F:TAAGGAGATCGACTAGGGTTT<br>R:CATCAAGATTCAAGACCACAC    | F:54.76<br>R:55.56 | 202–217      | KP278757                 | 5              | 2.36           | 0.62           | 0.58           | 0.54 |
| SCF73288  | (TC)12  | F:CAGAGGAACAGCAGACTACAT<br>R:CCTAGTACGTCATTGGACATTA   | F:54.59<br>R:54.50 | 226–334      | KP278758                 | 5              | 3.89           | 0.77           | 0.74           | 0.70 |

Table S2. *Cont.*

| Primer ID  | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|------------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|            |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF7357    | (CT)9   | F:CAGCTTAATCATCAGTTCCAG<br>R:AGTGAGCATCGACTATTTACCT  | F:55.14<br>R:54.88 | 282–286      | KP278618                 | 2              | 1.65           | 0.39           | 0.39           | 0.32 |
| SCF74458   | (CT)10  | F:GCAGGAAGCTATGATTAAGGTA<br>R:TTGAATAGTGTCACTGGAGAAG | F:55.51<br>R:54.62 | 222–240      | KP278759                 | 4              | 2.43           | 0.62           | 0.59           | 0.53 |
| SCF74895   | (TC)9   | F:GTACTCCTCTCCGTCTAGCAT<br>R:GATTTTATGCGTTAGCTCCA    | F:55.24<br>R:55.65 | 153–219      | KP278760                 | 9              | 6.76           | 1.00           | 0.85           | 0.84 |
| SCF75572   | (TGA)7  | F:GACAAGTGGTTGGGGATAC<br>R:ACCCTCATCATCACTCCTT       | F:55.12<br>R:54.24 | 247–265      | KP278761                 | 3              | 2.05           | 0.46           | 0.51           | 0.46 |
| SCF7569    | (AC)10  | F:CCCAATAACGACTCATATACCT<br>R:ACCCAGTCAAAATCTCCTTT   | F:54.95<br>R:55.28 | 279–283      | KP278619                 | 3              | 2.25           | 0.62           | 0.56           | 0.47 |
| SCF76310   | (TC)11  | F:CTGTGTAGAACTGCATCAAAAC<br>R:TCCTAGAGACCAACCAATAC   | F:55.14<br>R:55.75 | 220–226      | KP278762                 | 4              | 2.50           | 0.77           | 0.60           | 0.55 |
| SCF77145 * | (TG)10  | F:TAGAATTAGCCTCCAAGAAGTG<br>R:AGAACTAGAAACACGAGAACGA | F:55.56<br>R:55.94 | 314–325      | KP278763                 | 3              | 1.86           | 0.54           | 0.46           | 0.40 |
| SCF77376   | (AAG)11 | F:CTCATCAAAAGAGAGGAGAACT<br>R:TGTAACCAATCTTCATGCTG   | F:54.51<br>R:54.68 | 256–273      | KP278764                 | 6              | 4.33           | 0.85           | 0.77           | 0.74 |
| SCF77645 * | (TC)10  | F:GGTTCTTTCTTCTGGGTTTT<br>R:TCAGACAATGAGCTACTACCCT   | F:55.1<br>R:55.74  | 298–343      | KP278765                 | 7              | 3.25           | 0.85           | 0.69           | 0.66 |
| SCF78184   | (CA)10  | F:CACATTTAAGAGCTACCACCTT<br>R:GGTGAAAGAGAAGACTGGATT  | F:55.35<br>R:55.0  | 260–276      | KP278766                 | 5              | 3.76           | 0.85           | 0.73           | 0.69 |
| SCF7845    | (CT)12  | F:GTTCTGACTATTGTGATGGGTT<br>R:TGCAATGAATACTGGAAGTG   | F:55.67<br>R:54.68 | 254–256      | KP278620                 | 2              | 1.90           | 0.62           | 0.47           | 0.36 |
| SCF79014   | (CT)10  | F:TCTCTGTCTCTGTCTCTGTCTG<br>R:CCAAATCAAGGTCTGTCTATCT | F:54.75<br>R:55.8  | 181–183      | KP278767                 | 2              | 1.94           | 0.46           | 0.48           | 0.37 |
| SCF79620   | (GA)15  | F:TAATAGCCCTTATACCTGCACT<br>R:GAGCATAGACAGCATACAAAAG | F:55.3<br>R:54.53  | 187–218      | KP278768                 | 8              | 4.97           | 0.85           | 0.80           | 0.77 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF804    | (GA)15  | F:CAGTCAACAGAGAATACACCAC<br>R:TTCCCTATGAAAATCCACAC   | F:54.79<br>R:54.96 | 221–231      | KP278592                 | 4              | 2.60           | 0.77           | 0.62           | 0.54 |
| SCF80520  | (TC)9   | F:TAAAGTGTTTTGGACGGCT<br>R:GCACAAATTATCGGAATCG       | F:55.9<br>R:56.62  | 172–178      | KP278769                 | 3              | 2.30           | 0.62           | 0.57           | 0.47 |
| SCF80703  | (AC)17  | F:GGTCTTTCTCCTAATCTCCAA<br>R:GGAACCCCTAAATAACATACAG  | F:55.11<br>R:54.56 | 196–220      | KP278770                 | 9              | 4.69           | 1.00           | 0.79           | 0.77 |
| SCF81294  | (CT)9   | F:CTATCGACGGCTGAGATTT<br>R:AAAAGGGGAAGATCCTAGAAG     | F:55.48<br>R:55.77 | 232–238      | KP278771                 | 3              | 2.07           | 0.69           | 0.52           | 0.42 |
| SCF8151   | (CTA)7  | F:CGTGCTAGAAGACGAGGTAT<br>R:TTAGGGAACAGTAGAAAGGAAG   | F:54.73<br>R:54.62 | 311–314      | KP278621                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| SCF81732  | (AG)9   | F:CGAGTATGTGGAGAGGCTTAC<br>R:GTGTATAAAATGGGCATCACAC  | F:56.58<br>R:56.92 | 295–315      | KP278772                 | 3              | 1.89           | 0.62           | 0.47           | 0.42 |
| SCF81909  | (GT)12  | F:TAGAGGAATCAGCAACTTCACT<br>R:TTCACACTCACACTCACACG   | F:55.87<br>R:56.57 | 311–322      | KP278773                 | 4              | 2.58           | 0.54           | 0.61           | 0.55 |
| SCF8223   | (AG)11  | F:CATTTAGCATCCATCCATTC<br>R:GACTGTGGGTATTCCTTGTAT    | F:55.51<br>R:54.81 | 341–355      | KP278622                 | 5              | 2.79           | 0.69           | 0.64           | 0.59 |
| SCF82535  | (AG)9   | F:TAGAAGAGGAAAAGTACGGA<br>R:TTGATGCAATCTGACAACG      | F:56.68<br>R:56.61 | 245–253      | KP278774                 | 4              | 2.52           | 0.69           | 0.60           | 0.56 |
| SCF82870  | (CTT)8  | F:GCTAAAGAACGAACAACAACAC<br>R:GTCCAACGAGTGAGTAGAGAAG | F:56.66<br>R:55.79 | 261–314      | KP278775                 | 7              | 4.51           | 0.92           | 0.78           | 0.75 |
| SCF83036  | (TC)14  | F:CAACAGTCCTCAAAAATCACTC<br>R:GTGAACAGAAGTAGAGATCGG  | F:54.82<br>R:54.6  | 313–323      | KP278776                 | 5              | 4.02           | 0.85           | 0.75           | 0.71 |
| SCF83615  | (TTC)11 | F:ATTAGTCGATCTCCTTTTCCTC<br>R:AAATTGTAGAGCCAACACTAGG | F:55.77<br>R:55.35 | 323–345      | KP278777                 | 5              | 3.76           | 0.62           | 0.73           | 0.69 |
| SCF83971  | (TTG)8  | F:ATTCTGGTACTGTTTGTTGCTC<br>R:GTTATGTTTCGTGTTCCACTCT | F:56.5<br>R:55.90  | 270–347      | KP278778                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                                  | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|-----------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                           |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF84804  | (CA)13 | F:CTAGTCTTCTTGTGACCTAGCC<br>R:TATTCTTTTAGTCCGAGCCA        | F:55.7<br>R:55.22  | 207–213      | KP278779                 | 3              | 1.62           | 0.46           | 0.38           | 0.35 |
| SCF85773  | (GA)12 | F:TCTTGAACACAGCACAACAT<br>R:ATAAGTTTGCCCTTTTGTC           | F:55.8<br>R:55.88  | 281–301      | KP278780                 | 8              | 6.26           | 0.77           | 0.84           | 0.82 |
| SCF85946  | (TC)10 | F:TGTGAACAGAACCTACCACTAA<br>R:AAAGAGCCCCGTAGATAGAT        | F:54.99<br>R:54.69 | 324–328      | KP278781                 | 3              | 2.20           | 0.62           | 0.54           | 0.48 |
| SCF86438  | (ATT)7 | F:CTATTGAAAACAAGGAACGG<br>R:CCTATACAACCTCTTCGGATAA        | F:54.99<br>R:55.23 | 336–340      | KP278782                 | 2              | 1.65           | 0.54           | 0.39           | 0.32 |
| SCF87990  | (TC)10 | F:GTGTAGGTGTAAATGTGCTTTG<br>R:GGCGTATAAAAGGATTCAAG        | F:55.3<br>R:54.21  | 260–262      | KP278783                 | 2              | 2.00           | 0.54           | 0.50           | 0.38 |
| SCF88396  | (GA)9  | F:ATAGAGGTTAATTGGTCCTCG<br>R:GACGAAGAACGACAGGTAGAT        | F:55.4<br>R:55.98  | 284–292      | KP278784                 | 3              | 2.30           | 0.62           | 0.57           | 0.47 |
| SCF8850   | (GA)10 | F:GTGTGATGTATTTAAGGAGTACCAC<br>R:ACAGATAGAGTAGTTACCAAGGGA | F:56.<br>R:55.45   | 344–356      | KP278623                 | 6              | 5.37           | 0.92           | 0.81           | 0.79 |
| SCF88902  | (TC)9  | F:GTGTTGTAGGATGAACCGAT<br>R:GATTTCCAGCATTTGATCTC          | F:54.88<br>R:54.73 | 315–368      | KP278785                 | 5              | 4.75           | 0.91           | 0.79           | 0.76 |
| SCF89247  | (GA)11 | F:TGGAGGAGGTGAAGAATACTAA<br>R:CCCTTTGGACAACAAAATAC        | F:55.64<br>R:54.65 | 198–218      | KP278786                 | 6              | 4.57           | 0.85           | 0.78           | 0.75 |
| SCF89447  | (TC)9  | F:TAAATAAGACCTTCTGCTGACC<br>R:AATATGCTCACCACCAGTAAAG      | F:55.40<br>R:56.1  | 192–196      | KP278787                 | 2              | 1.45           | 0.39           | 0.31           | 0.26 |
| SCF89672  | (GA)14 | F:CCACTATAATCTACCCCAAAGA<br>R:TACTACTGCCCCATCCTACTAC      | F:55.8<br>R:55.16  | 194–200      | KP278788                 | 3              | 2.43           | 0.31           | 0.59           | 0.50 |
| SCF89726  | (TC)9  | F:TTGCTGACTTGCTAACCT<br>R:ATTTACCGAACGCTACGAGT            | F:56.7<br>R:56.57  | 327–329      | KP278789                 | 2              | 1.65           | 0.23           | 0.39           | 0.32 |
| SCF89801  | (CT)14 | F:TAAACCTGTTCCGTCTCTTAGT<br>R:CTTTACTGTTGTGTTGTCTGCT      | F:54.93<br>R:54.81 | 323–338      | KP278790                 | 7              | 6.48           | 0.56           | 0.85           | 0.68 |

Table S2. *Cont.*

| Primer ID | Motif   | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|---------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |         |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF8987   | (CT)11  | F:AATCTTTGTCTGAGGTAAGTGG<br>R:AACCAGTGTAGTGCAGTTTATG | F:55.16<br>R:54.63 | 150–156      | KP278625                 | 4              | 3.71           | 0.85           | 0.73           | 0.68 |
| SCF90229  | (AG)10  | F:GTACTTTTGTGGAACCTAACGC<br>R:CTGTCCTTTCACCTCCTCTTTT | F:55.80<br>R:55.26 | 280–292      | KP278791                 | 5              | 2.79           | 0.69           | 0.64           | 0.59 |
| SCF9068   | (TC)14  | F:AAATCTAGGTAGGAGCAGGTCT<br>R:ATGGAGGAGGAGATATGTGAT  | F:55.49<br>R:55.0  | 174–186      | KP278624                 | 6              | 3.89           | 0.92           | 0.74           | 0.71 |
| SCF915    | (GA)9   | F:TTAGGGTTTGGAGTACCTGA<br>R:ACTACCGTCTTTCTTTATAGCC   | F:54.80<br>R:53.86 | 265–269      | KP278593                 | 3              | 2.54           | 0.77           | 0.61           | 0.68 |
| SCF9157   | (GA)9   | F:GGCTTAACAAATTAGCCCTT<br>R:GAGAGGATTTACCGACAAAAGTA  | F:55.33<br>R:55.25 | 301–330      | KP278626                 | 5              | 3.49           | 0.85           | 0.71           | 0.68 |
| SCF91821  | (TG)9   | F:TTCTGTGTCTGATTCCATCTC<br>R:ACTAGCCCAACAACCTTAGACTG | F:55.16<br>R:55.42 | 302–304      | KP278792                 | 2              | 1.55           | 0.31           | 0.36           | 0.29 |
| SCF92414  | (AG)12  | F:GTTATCCTCCCTTTGATATGTG<br>R:AAGAGCAACAAGATGGGTACT  | F:55.29<br>R:55.57 | 283–287      | KP278793                 | 3              | 2.15           | 0.54           | 0.54           | 0.47 |
| SCF92564  | (CTT)9  | F:TCATAACTCCCTCGTAATCAAG<br>R:AGGAAGAAGAGAATAAGGTTGG | F:56.7<br>R:55.85  | 181–194      | KP278794                 | 5              | 3.89           | 0.92           | 0.74           | 0.70 |
| SCF94237  | (TTA)14 | F:ATCGCATCAGGTAAGCTAGTAT<br>R:TCGAGTGTGATTGTAATAGGC  | F:55.0<br>R:55.42  | 330–363      | KP278795                 | 8              | 5.20           | 0.92           | 0.81           | 0.79 |
| SCF95754  | (TC)12  | F:CAGTGAGACTTCAGCTTGATAC<br>R:ATTGGTGACTTAGGAGTGAGAC | F:54.34<br>R:54.97 | 339–366      | KP278797                 | 6              | 3.49           | 0.85           | 0.71           | 0.68 |
| SCF95767  | (TA)9   | F:TGAGGAGAGGAGTATCCATAAG<br>R:CCTACAAGTCTCGCAATTCTA  | F:55.17<br>R:54.91 | 270–302      | KP278796                 | 5              | 4.12           | 0.62           | 0.76           | 0.72 |
| SCF95851  | (TG)9   | F:GACCTTGGAATTTGATGATG<br>R:TGTAGATGGATGTTGTTACCTG   | F:55.38<br>R:55.20 | 188–190      | KP278798                 | 2              | 2.00           | 1.00           | 0.50           | 0.38 |
| SCF96311  | (TC)9   | F:TGTATAATCTCAGGGGCATT<br>R:TTTCTCATTTCCCTCCCAC      | F:54.68<br>R:55.6  | 155–161      | KP278799                 | 4              | 2.18           | 0.62           | 0.54           | 0.79 |

Table S2. *Cont.*

| Primer ID | Motif  | Primer Sequences (5'-3')                             | TM (°C)            | Allele Range | GenBank Accession Number | Heterozygosity |                |                |                |      |
|-----------|--------|------------------------------------------------------|--------------------|--------------|--------------------------|----------------|----------------|----------------|----------------|------|
|           |        |                                                      |                    |              |                          | N <sub>A</sub> | N <sub>E</sub> | H <sub>O</sub> | H <sub>E</sub> | PIC  |
| SCF965    | (GA)14 | F:GTAAACTAACAAGCAACGATCC<br>R:GATTTAGCTGATGCAGAGTCAT | F:55.73<br>R:56.22 | 258–275      | KP278594                 | 6              | 5.37           | 0.85           | 0.81           | 0.79 |
| SCF96539  | (TG)9  | F:GTAGCATAACCACCTCTTATCC<br>R:ATCTTGATGACTGTGTAAGCTG | F:54.67<br>R:54.64 | 259–261      | KP278800                 | 2              | 1.08           | 0.08           | 0.07           | 0.07 |
| SCF9709   | (AT)9  | F:CCATTAGAAGAGTTTACCGTGT<br>R:TTATCAGTCCCTTACTCAATCC | F:55.20<br>R:55.2  | 270–272      | KP278627                 | 2              | 1.84           | 0.10           | 0.46           | 0.35 |
| SCF97378  | (CA)14 | F:GTAGAGATCGTTGTCGTCATTT<br>R:AACATCGTGGTGTATTGGAT   | F:55.98<br>R:55.19 | 233–248      | KP278801                 | 6              | 2.77           | 0.69           | 0.64           | 0.60 |
| SCF9815   | (GA)11 | F:CATAGGAAGATTGCCTTGAG<br>R:GCCTGTTACATAGATGGAG      | F:55.5<br>R:55.67  | 186–194      | KP278628                 | 2              | 1.99           | 0.62           | 0.50           | 0.37 |
| SCF98180  | (GA)10 | F:CTCCTCTGCTTATCTCTTCAAC<br>R:GGTTTTCCCTTCTCAAGATTAC | F:55.11<br>R:56.7  | 345–347      | KP278802                 | 2              | 1.45           | 0.39           | 0.31           | 0.26 |
| SCF98686  | (TC)11 | F:CGTAATTTACATCCTCGTT<br>R:CATAACCAGATAGCACCTCAAT    | F:55.25<br>R:55.94 | 236–253      | KP278803                 | 4              | 3.60           | 0.92           | 0.72           | 0.67 |
| SCF9872   | (TC)11 | F:ATGGGAGTGCATGAATAAAC<br>R:GGAGAATCGTATTTGTGAAGAG   | F:54.99<br>R:55.63 | 234–238      | KP278629                 | 2              | 1.26           | 0.23           | 0.20           | 0.18 |
| SCF9909   | (AG)11 | F:CGTAGGTGGATTTCTCTACAAT<br>R:GGCATCTTATTTATCGTCTCTG | F:55.13<br>R:55.74 | 134–173      | KP278630                 | 6              | 5.45           | 0.85           | 0.82           | 0.79 |

Note: \* = marker displayed segregation distortion  $p < 0.05$ .

**Table S3.** Primer characteristics for primer loci tested and validated on 4 cranberry cultivars, but not used in genetic diversity or allele segregation analyses.

| SSR ID            | Motif   | Sequence                                               | TM (°C)            | GenBank ID |
|-------------------|---------|--------------------------------------------------------|--------------------|------------|
| 119364_K70        | (CT)18  | F:ACCACAAAACCCTAGTTCTATC<br>R:TCCATAGTCTTAGCAACAACAG   | F:54.17<br>R:54.84 | KP279272   |
| 1trimcontig175833 | (TG)14  | F:CTCTTTCTGCCTGGTTCTAA<br>R:ACTACTATTGCGTATGGCTCTT     | F:54.84<br>R:55.08 | KP279278   |
| 1trimcontig178732 | (TC)15  | F:ATGGTCCCTGAGTCTAACTTC<br>R:GGATCTCTATTTTCAGTGTGTTG   | F:54.88<br>R:53.96 | KP279279   |
| 1trimcontig217288 | (AG)17  | F:ATAACAGAGGACAACGATCTG<br>R:TCACTCTACTTTTACCGAGACA    | F:54.37<br>R:54.39 | KP279280   |
| 1trimcontig240704 | (GA)16  | F:GAGAGAGGGAAGAGTAACAGG<br>R:AAGATGGTCTATTGAGTATGGC    | F:54.76<br>R:55.04 | KP279281   |
| 1trimcontig241039 | (GAA)11 | F:ATAATGGACTGCACGAACT<br>R:GTAGTAGGGATTTACAGGCTA       | F:54.81<br>R:55.28 | KP279282   |
| 1trimcontig336911 | (TC)14  | F:CATTTCCCTATTTTCATCCCCT<br>R:AACAGAGCGAGAGTAATTGAAG   | F:55.58<br>R:55.62 | KP279283   |
| 1trimcontig354570 | (TG)14  | F:ACCTGTTCTGTTGATTACGAGT<br>R:ACAGTATCGCACAAATGAGTTC   | F:55.50<br>R:55.32 | KP279284   |
| 1trimcontig439506 | (AG)18  | F:GATTTAGGTTAGGGTATGGGT<br>R:GCTTGTGTTAGGGTTTGTTA      | F:53.92<br>R:53.03 | KP279285   |
| 1trimcontig445838 | (CT)14  | F:GTTTTCTCTGAATCTCCACTA<br>R:GTCATACACAATACACAGTCGC    | F:55.20<br>R:55.71 | KP279286   |
| 1trimcontig448145 | (AC)15  | F:TGTGATTAGAGGGAGGATTTTC<br>R:AAATAAGGGAGTTTGAACCG     | F:55.80<br>R:55.88 | KP279287   |
| 204816_K70        | (AG)14  | F:CACTCTAATCACCCCTTTCACCTC<br>R:CAGAGAGGAATAATACAGGTGC | F:55.55<br>R:55.67 | KP279273   |
| 239628_K63        | (AG)16  | F:CTCTTTCTTGGATGTTGCTACT<br>R:CGAAACTCTCTAACTCTGGTGT   | F:55.47<br>R:55.38 | KP279257   |
| 247873_K63        | (TC)15  | F:GATCGGAGAGTTTTCTCTT<br>R:CAATTTCTTCCCCAACTAT         | F:55.07<br>R:55.66 | KP279258   |
| 24956_K70         | (GA)14  | F:AGAGAGAGGATTGTTATTGCTG<br>R:TGAACCAAGCCCATATAAGT     | F:55.39<br>R:54.77 | KP279270   |
| 281741_K70        | (GA)17  | F:GATTTGACTCGTAAAGCAGAC<br>R:GGAAATGGAGATGGATATGTAG    | F:54.26<br>R:55.21 | KP279274   |
| 284499_K63        | (AG)15  | F:ATTAGTTCTCCTATGTGGCTTG<br>R:TCAGAGCTTACCCTATTTTCAGT  | F:55.28<br>R:55.01 | KP279259   |
| 289194_K63        | (TC)14  | F:CTAGCACTGGCTCTTACCAC<br>R:TGTAGGATGTGTATATGGAGCA     | F:55.22<br>R:55.73 | KP279260   |
| 307461_K70        | (TC)17  | F:CAGACACTCCACTAACTCAGAA<br>R:GCATCAACAGTACAACAATACC   | F:54.67<br>R:54.78 | KP279275   |
| 307534_K70        | (AG)15  | F:ATCGTCTGCTATAAATACTCCG<br>R:GTGTCAACCTTCCTTACAAGAT   | F:55.39<br>R:54.99 | KP279276   |
| 310238_K70        | (AG)17  | F:GAGTAACAACAGTGGCAAAAC<br>R:AACTTCCTCATGTACTTTCCC     | F:54.96<br>R:54.90 | KP279277   |

Table S3. *Cont.*

| SSR ID     | Motif         | Sequence                                               | TM (°C)            | GenBank ID |
|------------|---------------|--------------------------------------------------------|--------------------|------------|
| 339139_K63 | (CT)18        | F:CTAATACTTTTCATCGTCAACCC<br>R:AGGAGAGAGAGAGGGTAGTTTGG | F:55.52<br>R:55.93 | KP279261   |
| 346445_K63 | (GA)16        | F:TAAGGGAAACCTGTAAAGACG<br>R:GATAGCAAAGTGGACGAGTATT    | F:56.12<br>R:55.27 | KP279262   |
| 35137_K63  | (CT)14        | F:GGAACATCAAAACTCCCATAC<br>R:GTTCTTCCCCATTTTCAGTAAGT   | F:55.99<br>R:56.41 | KP279254   |
| 36394_K70  | (AG)18        | F:CAGTGTTTGTGCTTGGTC<br>R:ATCTCACTCTCTGTTTCCCTC        | F:55.07<br>R:54.98 | KP279271   |
| 37487_K63  | (GA)15        | F:CTTTCATTAGAGGAGAGCTTGT<br>R:AGGAAACTAGCAATCAGTCAAC   | F:54.74<br>R:55.30 | KP279255   |
| 389746_K63 | (CT)17        | F:TTGTAAACCTCAAGACACACC<br>R:TATCACACAGTTTTGGAGAGAG    | F:55.21<br>R:54.62 | KP279263   |
| 413893_K63 | (TC)21        | F:TACTCCATTTTACAACACGA<br>R:ATCTCTGCTTCTTCTACCTCTG     | F:55.02<br>R:54.71 | KP279264   |
| 418138_K63 | (TC)16        | F:CCTCTTCTTCATATCATCCAGT<br>R:TTTAGCCCACTTTTATGCAC     | F:55.00<br>R:55.57 | KP279265   |
| 418192_K63 | (GA)18        | F:CAGGCAGAAGAAGAAAGAAA<br>R:TGAATTAAGAGAGGAGGAGAGA     | F:54.97<br>R:55.01 | KP279266   |
| 418730_K63 | (CT)17        | F:ACAGATCCAGTCTCTTCAAATC<br>R:ATACGGAGTGTAGATGTCTCCT   | F:55.02<br>R:54.53 | KP279267   |
| 419957_K63 | (GA)14        | F:AGACTCACCTCTCTTTCTTGTG<br>R:GACTATCTTTCGGTTGACACTT   | F:55.34<br>R:55.15 | KP279268   |
| 49132_K63  | (TC)18        | F:AACCCTAGAAATCAATGCAC<br>R:GTTTTCCGTTTTGTTCTGTC       | F:54.29<br>R:54.82 | KP279256   |
| 9053_K70   | (AG)15        | F:GCTGATTAGGTTCACTTTCTTC<br>R:TTTCTTCACCTCTTTCTCTCTC   | F:54.96<br>R:54.64 | KP279269   |
| ct117109   | (TC)9         | F:TTGacGTCTTCTCTCTCTTTCT<br>R:CTAGGGTTCATACTTCGAAAAG   | F:55.14<br>R:55.04 | KP279151   |
| ct118488   | (TC)9         | F:GTTCAGGACAAGTGATTtCTC<br>R:AGCTAAGTGtTTTcCtACTGGa    | F:55.51<br>R:55.09 | KP279152   |
| ct131127   | (AAT)6        | F:GAGTAGTCCcGtAtAtGGAaTg<br>R:GTTCaTTTCCCCATTCTGA      | F:55.32<br>R:55.81 | KP279153   |
| ct136900   | (AAAAGG)<br>4 | F:ACGATATGAGAGAAGAAGAGGA<br>R:CTCTAGTGCATACCAGCACTT    | F:54.87<br>R:54.83 | KP279154   |
| ct139597   | (GA)11        | F:CTTATAGGCAATGCACATAcAC<br>R:GTAACCTAATGGGGCTGAACTT   | F:55.08<br>R:55.11 | KP279155   |
| ct142970   | (ATATA)4      | F:AAACCTAAATaCCCGGAATG<br>R:TATAGAcgGCAtATGCAACA       | F:55.69<br>R:55.29 | KP279156   |
| ct146598   | (AC)13        | F:AATCTCATTTTTCTGggTC<br>R:CTTGATATgCtcTCTTAATGGC      | F:55.62<br>R:55.89 | KP279157   |
| ct170930   | (AAG)7        | F:ACCcGATTCCATAAAAGAAG<br>R:CAAGCTTCTCCTaCCTcca        | F:55.81<br>R:55.53 | KP279158   |
| ct89569    | (AC)9         | F:ACTAATCCCacgAAAACCTGA<br>R:aTCTaggCtTTCAAACtAGGGT    | F:54.79<br>R:55.49 | KP279149   |

Table S3. *Cont.*

| SSR ID    | Motif   | Sequence                                              | TM (°C)            | GenBank ID |
|-----------|---------|-------------------------------------------------------|--------------------|------------|
| ct97791   | (AC)10  | F:GACTTTGTGAGGATAGACCATT<br>R:ATGTAAGATGTGGaCaTaAgGG  | F:54.91<br>R:55.63 | KP279150   |
| SCF101363 | (TC)9   | F:CGATCTGTATCTAGTCGTGATT<br>R:GAGATGTACTATTGGAACCTGG  | F:53.70<br>R:53.15 | KP279053   |
| SCF102190 | (GA)11  | F:GAGGAAAGGGTGAGAGTTTT<br>R:GTTTGACGAAAAGGAGACTG      | F:54.99<br>R:54.98 | KP279054   |
| SCF102509 | (CT)10  | F:ATAGGATTTGTTAGACTTGGGG<br>R:GGAGCTGTTGAAGCTATTGTTA  | F:56.36<br>R:56.42 | KP279055   |
| SCF102538 | (GA)12  | F:TTACTGGGCAATAGAAGGACT<br>R:CACATAAGTTTGGCTACACAAC   | F:55.66<br>R:55.03 | KP279056   |
| SCF108101 | (TC)14  | F:AAATCTTCCATGAGCTTGTC<br>R:TACTGCGGTGTTGAATTAGA      | F:54.38<br>R:54.44 | KP279057   |
| SCF113304 | (ATA)24 | F:CCAGTCAACGAACAAATAGAG<br>R:CCTAAAGGGAAAGAGAAGTGA    | F:55.06<br>R:55.36 | KP279058   |
| SCF113895 | (AG)10  | F:GGAATCACTATGAACATGCAC<br>R:ATCAGAAACGAGTCCAAAGAC    | F:55.50<br>R:55.95 | KP279059   |
| SCF115821 | (CT)10  | F:TCACCACTTACAACATATCCAC<br>R:TTGACACTAGCAAATTCCATC   | F:55.03<br>R:55.39 | KP279060   |
| SCF117    | (CA)12  | F:ATAGCATCTGTCTTATTGGACG<br>R:GTGGGTTTCTGATCTTCATCT   | F:56.09<br>R:55.71 | KP278954   |
| SCF118209 | (GA)15  | F:AGGATTTAGGACGTTGGAA<br>R:GTAACAGAGAAAGCGAGAGC       | F:54.69<br>R:54.55 | KP279061   |
| SCF118536 | (GA)10  | F:GGGTACTATATGAAGGTGCCTA<br>R:CTACCATGTAAACCCTTGAAAGT | F:55.10<br>R:55.05 | KP279062   |
| SCF118603 | (TCT)13 | F:GGACAAACACTAAATAAGCCAC<br>R:CTGCTCACAGAATACCACTAAA  | F:55.58<br>R:54.84 | KP279063   |
| SCF119813 | (TG)10  | F:GTTAGTCGGCTCAAGTTAGTTC<br>R:ATGGACTTCCCATTCTTTTC    | F:55.07<br>R:55.62 | KP279064   |
| SCF119984 | (GA)10  | F:TTAGAATTGCGTTCCATACAG<br>R:GAAAATCAGTTCGATTCAGGT    | F:55.59<br>R:55.86 | KP279065   |
| SCF12084  | (TC)12  | F:CTCTTGTTGGACGGATCTATT<br>R:CCTAACATTTCTCCCACTCA     | F:55.90<br>R:55.21 | KP278974   |
| SCF122440 | (GA)12  | F:CTAATCTTCCTCCTCTTGTTGA<br>R:CGACAAACTAACATATCATCTCC | F:55.37<br>R:55.53 | KP279066   |
| SCF122552 | (AC)10  | F:TATATCGAGGTCATTGCGA<br>R:GAGTTGTCGTTAAGGTTTTGA      | F:55.15<br>R:54.62 | KP279067   |
| SCF123643 | (GA)9   | F:CAAGAATGAAGAGAAAGATTCC<br>R:CAGGTTTTATTAGCCTGTGTTT  | F:54.86<br>R:55.36 | KP279068   |
| SCF125768 | (AG)11  | F:CTCACTTCTCATAACAACATTGG<br>R:CACAACAGAACCATCAGTACAT | F:54.91<br>R:55.09 | KP279069   |
| SCF126993 | (AC)11  | F:TTATGGCTCTCATTAAGCAAG<br>R:CTTATTTGGGGTTGATGTGTA    | F:55.00<br>R:55.12 | KP279070   |
| SCF127382 | (TC)10  | F:GTCTTTAGTGCTGGGTTAAAAG<br>R:TGATTTCTAGTGTCTCCTCTCA  | F:55.10<br>R:54.23 | KP279071   |

Table S3. *Cont.*

| SSR ID    | Motif  | Sequence                                                 | TM (°C)            | GenBank ID |
|-----------|--------|----------------------------------------------------------|--------------------|------------|
| SCF12818  | (CT)9  | F:GTGAGGGAGAGTGTAGATAGC<br>R:ACAAGAGAAAGAACGACAAGAC      | F:54.82<br>R:55.34 | KP278975   |
| SCF128658 | (AG)9  | F:ATTATTGATGAGTAGTCCCCAC<br>R:TGGTTGATTTGTGTAGAAAGAA     | F:54.73<br>R:55.06 | KP279072   |
| SCF13045  | (CA)9  | F:TGTCCAGTGCTAATATCTGTGT<br>R:TCCTCCAAATCTATGCAAAC       | F:54.93<br>R:55.29 | KP278976   |
| SCF130555 | (ATT)8 | F:GGGTAAAATAAAAGGTTCTCC<br>R:TCCTTACTTGTCGATTAGGC        | F:53.82<br>R:54.64 | KP279073   |
| SCF130642 | (GA)9  | F:AGGCGGAAGATGAAAGTAAT<br>R:TGTCAACATAAAACGATAGCAG       | F:55.56<br>R:55.68 | KP279074   |
| SCF132006 | (GT)9  | F:ATTGAGGTCAGTACTAGGAGGTGTA<br>R:GAGGAGAGTGTTCATGTTCATGT | F:55.43<br>R:55.00 | KP279075   |
| SCF13231  | (CT)12 | F:GAAACAAAGAGGAGAAGACAAC<br>R:GTGAAAGGTAAGAGATGGGTAG     | F:54.83<br>R:54.70 | KP278977   |
| SCF132852 | (TC)13 | F:TGCTTGTGTTAGGGTTTGTTA<br>R:GTTAGAGATGATGGCTGAAGAT      | F:55.99<br>R:55.15 | KP279076   |
| SCF132868 | (TG)9  | F:CTGATTTGTGTTGATGGATAAG<br>R:CAGTTAGCACCACCTAGTTAGA     | F:54.85<br>R:54.06 | KP279077   |
| SCF133587 | (AG)10 | F:TTAAGCACCAACACTAAATCC<br>R:AGTTCATGTGACGTTGTATCA       | F:54.60<br>R:53.96 | KP279078   |
| SCF13393  | (AG)16 | F:ATATACACAATCGCACGAGAC<br>R:TCAGCTTACGATCTCACAAA        | F:55.28<br>R:54.54 | KP278978   |
| SCF134365 | (CTT)8 | F:GCCTTGTTATGTTACCTGTGA<br>R:ACAACATCTGGAAAAGGGTT        | F:55.34<br>R:54.52 | KP279079   |
| SCF134906 | (ATA)7 | F:GTATGATTGGTCTTGGTCTGAT<br>R:GCAACAGCTAGAGATGCTTAAC     | F:55.59<br>R:56.18 | KP279080   |
| SCF13628  | (CT)12 | F:AGAGGTCAATAGCTGAAGAAGA<br>R:AATTCCTGTAGTAAACAGTGGG     | F:55.11<br>R:55.05 | KP278979   |
| SCF13665  | (GT)9  | F:TTCTTTACTATACCCACAACCC<br>R:GTTTCCTAAGAGCATCAACAAC     | F:54.99<br>R:55.70 | KP278980   |
| SCF136684 | (CT)12 | F:TCTTATCCTGCTTTCTTACCC<br>R:ACAGGGTCATTACTGTCTTGTT      | F:55.31<br>R:55.34 | KP279081   |
| SCF14090  | (AC)13 | F:GTATTGTCTGGAGATTCCCTAA<br>R:GCTCTTTGCATCATACTCAA       | F:55.02<br>R:54.02 | KP278981   |
| SCF142636 | (AC)10 | F:GGTCATGGTGTCAATCAAG<br>R:CATGGACAGGTATTGGACA           | F:54.50<br>R:55.04 | KP279082   |
| SCF142785 | (AG)9  | F:AGGCTCACATTTCTAACTCAAG<br>R:ATATCTACCTCCCTAATTTCCTG    | F:55.47<br>R:55.62 | KP279083   |
| SCF14358  | (AG)10 | F:CCACTAAAACCCTATACTTGGA<br>R:GTCACCTTTCTATTGCTGGTG      | F:55.15<br>R:55.05 | KP278982   |
| SCF145195 | (GA)14 | F:CCACCTTCCATTATACAGCA<br>R:GAACAAGAGAAGAACCCAGATA       | F:56.13<br>R:55.20 | KP279084   |
| SCF14690  | (CT)9  | F:CCTTCCATCTTCTTCTTCAAC<br>R:AACAAGGTTAGGAACTAGGGT       | F:55.59<br>R:55.28 | KP278983   |

Table S3. *Cont.*

| SSR ID    | Motif   | Sequence                                             | TM (°C)            | GenBank ID |
|-----------|---------|------------------------------------------------------|--------------------|------------|
| SCF147678 | (CT)11  | F:ATTCATAGTTTACCCGTCCTC<br>R:GATTGCTGCTCTTTCAATGT    | F:54.96<br>R:55.52 | KP279085   |
| SCF14838  | (GA)9   | F:ATAATTTTGTCCCACACGG<br>R:TGAGAGTTCAAGGGCAATAA      | F:55.78<br>R:55.97 | KP278984   |
| SCF14877  | (TG)10  | F:CCCATGATCCTATGTATGCT<br>R:AGCTCTGATACCAAAGTGTCT    | F:54.95<br>R:55.58 | KP278985   |
| SCF148938 | (AT)10  | F:CTTCTGTCAATTTTAGTGTCTG<br>R:ACCTTTTGAACACATTGGAC   | F:54.23<br>R:54.93 | KP279086   |
| SCF149145 | (CT)12  | F:CTTCAACATATACCCACCCTAT<br>R:GACCAAACTAGAAAACCTCCCT | F:54.80<br>R:55.76 | KP279087   |
| SCF150395 | (TC)12  | F:CTCTGGTTCATCCCTCTGT<br>R:CAGACCCTGTCGTTACAAAT      | F:54.97<br>R:55.15 | KP279088   |
| SCF150410 | (TAC)7  | F:AACGTAGACACGAAAAGAAGAC<br>R:GCTAGACATGGTTGGAAGAC   | F:55.38<br>R:54.75 | KP279089   |
| SCF15112  | (GT)12  | F:GTATTGTGAGAGGATGACCTG<br>R:AAGGGCTTTAGTGTTGTTGT    | F:54.60<br>R:54.05 | KP278986   |
| SCF15143  | (AT)10  | F:AAAGCCTGCAAATACTCCTA<br>R:CAAAGTGGTACAAAGCACTTA    | F:54.42<br>R:54.92 | KP278987   |
| SCF152348 | (TC)9   | F:AGGAGCAAGAAGAGGTGTTT<br>R:CCATTGTTTTGCACTTCAG      | F:55.68<br>R:55.18 | KP279090   |
| SCF1524   | (GA)12  | F:TAACATACAGTCCTCGACAAGA<br>R:GATCTAGTTGTTCTTCCGCAT  | F:55.07<br>R:56.05 | KP278957   |
| SCF15729  | (GA)13  | F:GAAGTGGCTCACTAAAAGAAGT<br>R:GGTGCATAGCGATCTTACTATT | F:54.65<br>R:55.38 | KP278988   |
| SCF157301 | (AG)10  | F:CGTTACATACTCCACCCAAT<br>R:GATTTCAAGAAGGGTTTGTG     | F:54.95<br>R:54.75 | KP279091   |
| SCF157676 | (TC)10  | F:GTCCGCAGTGTCTATGTTT<br>R:CATACCTTAGATGGTGATTAGG    | F:53.53<br>R:53.18 | KP279092   |
| SCF16186  | (CT)10  | F:CTTGTATCAACTTCCATCGTCT<br>R:CCAAAACCTGAGAACTTAGAG  | F:55.99<br>R:55.06 | KP278989   |
| SCF164500 | (AG)10  | F:AAATCACCATTCTGGAACAC<br>R:GGTCGGAATACTAAAACAGAGA   | F:54.84<br>R:55.25 | KP279093   |
| SCF165    | (AG)9   | F:CCTCCTCAATCTTCTTCTCC<br>R:TATCTTAAACGGCTGATCTCTG   | F:55.50<br>R:56.36 | KP278955   |
| SCF171768 | (AG)13  | F:GTATCCCCTTATACAACCTGC<br>R:GGCTTCTATTATTCTATTGCCC  | F:55.30<br>R:56.25 | KP279094   |
| SCF18113  | (AG)11  | F:GAAGACATCAAAAGTGGGACT<br>R:TCAGATCAACACTGGACTAAGA  | F:55.79<br>R:55.02 | KP278990   |
| SCF186078 | (GAA)10 | F:TAGAAAGCAGTAGAGGAGGAAA<br>R:CTTTTCGGATCTGTTTGGT    | F:55.29<br>R:55.19 | KP279095   |
| SCF19055  | (CA)10  | F:AACTCTCACCAAAGGTATTGTC<br>R:GTGACGCTAGATGAGGACTTA  | F:54.99<br>R:54.71 | KP278991   |
| SCF195276 | (GA)9   | F:GTACACTCAAAAGGGAAGAAAC<br>R:TGGCGTATGAGAAGAAGATT   | F:54.74<br>R:55.04 | KP279096   |

Table S3. *Cont.*

| SSR ID    | Motif  | Sequence                                               | TM (°C)            | GenBank ID |
|-----------|--------|--------------------------------------------------------|--------------------|------------|
| SCF197012 | (CT)9  | F:GTACGATACAACATGGACACA<br>R:ATATAAACAGGGATGCGACT      | F:54.28<br>R:53.86 | KP279097   |
| SCF19788  | (TC)13 | F:TTCTCTGACTTGTCTCGACC<br>R:CATTCTGAAAACAACACTACTCC    | F:55.40<br>R:55.56 | KP278992   |
| SCF203038 | (TC)12 | F:CACTTCTGTACCCTCTTTTACC<br>R:GTCTCATACCTGAATTTTCTGC   | F:54.78<br>R:55.62 | KP279098   |
| SCF221037 | (TC)9  | F:ACACTACAAGCAACAGACAAGT<br>R:TAGTCGAGGTGTGCGTAAG      | F:54.21<br>R:54.95 | KP279099   |
| SCF22339  | (AG)11 | F:CCTCAATCTTATGGATCGAA<br>R:TTGTAGAAGAACCTGTAATGGG     | F:55.22<br>R:55.99 | KP278993   |
| SCF2270   | (AG)12 | F:TTGGTGTAAAGAAGGATAGGAG<br>R:GGCTCCAACTAATGCTATGA     | F:55.26<br>R:55.49 | KP278958   |
| SCF22993  | (CTT)7 | F:GACTGTGCGTAGACTTGATCT<br>R:AAGTATGTGTAGGCCGAAAA      | F:54.58<br>R:55.01 | KP278994   |
| SCF24570  | (TC)11 | F:GGATGCTGTCAAAGATATTG<br>R:TAAACAACCTGAGAAGTGTAGGC    | F:53.18<br>R:54.01 | KP278995   |
| SCF27509  | (AG)12 | F:ACCAGAAGAACCATGAAGT<br>R:CAAGAAGCCTGATATGTTGTC       | F:55.10<br>R:54.97 | KP278996   |
| SCF2942   | (GA)11 | F:ATAAGATCGGTGAAGGATAGG<br>R:AAGGAGATTAAGAAGGTCCAAG    | F:54.96<br>R:55.85 | KP278959   |
| SCF29521  | (AG)10 | F:CTCAATGCTTCGGAGTAGATA<br>R:CTCCTTGTTTTACAGGTATG      | F:54.82<br>R:54.90 | KP278998   |
| SCF29529  | (AG)12 | F:AACAGGGAGTTTTCTACTCTT<br>R:GTATGATGGGAATGGGATAGT     | F:55.38<br>R:55.30 | KP278997   |
| SCF30167  | (TC)11 | F:AGACATACGAAGTCCATGAAAC<br>R:CACCCATAACTCACCTCTAATC   | F:55.82<br>R:55.36 | KP278999   |
| SCF30716  | (TC)9  | F:ATCGGTGACAAAGGTAGATACA<br>R:TGTCTAGGTTGAAAACAAGGAG   | F:56.26<br>R:56.19 | KP279000   |
| SCF30747  | (AG)10 | F:AAGTCAACCAATAGGCATAGAC<br>R:TGTAGTAGCAAGCAAGCTGAT    | F:55.12<br>R:55.57 | KP279001   |
| SCF3187   | (GA)11 | F:CCAGAAAACCTACAGATACCCTC<br>R:GTACTTACCGGGACAACCTCTTA | F:54.70<br>R:55.20 | KP278960   |
| SCF32389  | (AG)10 | F:CACTATATCCTACCCCAAAGAG<br>R:TTTGCTGTGACTTGAAAGG      | F:54.69<br>R:54.87 | KP279002   |
| SCF32769  | (AG)13 | F:CTTACTGCCTTACATCCTCTTT<br>R:CTGGCAAATAGCTTACAGAAC    | F:54.64<br>R:54.52 | KP279003   |
| SCF33205  | (TC)9  | F:ATTCTGACTGTTTCATTGCC<br>R:AAATGTATTGGTGGGGAAGT       | F:55.19<br>R:55.85 | KP279004   |
| SCF33518  | (AG)9  | F:GTATTCGTACTCCACACCCTT<br>R:TACAGACAACCATAATTAGCG     | F:55.69<br>R:55.56 | KP279005   |
| SCF33654  | (CT)11 | F:CACAGCCTTAACACAGGATT<br>R:GTGGCTCCTTATCTGGGTA        | F:55.32<br>R:55.14 | KP279006   |
| SCF34663  | (CT)10 | F:GTTTAAAGTTCTAGCATAGCCGA<br>R:GTACACAAATACAGAGTGTGGC  | F:55.72<br>R:54.84 | KP279007   |

Table S3. *Cont.*

| SSR ID   | Motif   | Sequence                                              | TM (°C)            | GenBank ID |
|----------|---------|-------------------------------------------------------|--------------------|------------|
| SCF3507  | (CA)9   | F:GCTAATAAAGGTTGAAGTCTGG<br>R:CCATGTAGTAGTGAGAGCTGTG  | F:55.03<br>R:55.18 | KP278961   |
| SCF35370 | (TC)9   | F:AATCATGGTCTTCTCACGTT<br>R:GTATAATTGCGTAAGTGCTCG     | F:54.57<br>R:55.38 | KP279008   |
| SCF36355 | (CT)9   | F:GTGAAAGGACTGTTTTACCCTA<br>R:GAGGAGGGGTTTCTCTTTT     | F:55.17<br>R:54.90 | KP279009   |
| SCF36716 | (TG)9   | F:CTAGGCAATGATGACAAAGC<br>R:CCCAATAGTTACCACTAAGCAT    | F:55.99<br>R:55.17 | KP279010   |
| SCF36905 | (AG)9   | F:GATAAGCTGTGCTGAAACATC<br>R:CGATAGGGGATAGAATTAGTCA   | F:55.12<br>R:55.15 | KP279011   |
| SCF39229 | (TC)12  | F:AAAAGCTACGATACGAATGC<br>R:AGAAGGAGATAGTCAACGAATG    | F:54.85<br>R:55.24 | KP279012   |
| SCF39691 | (AG)9   | F:TAAACCATAGTCCTCTCCTCC<br>R:GTCCATAACTCCAAATAAGAGC   | F:54.99<br>R:54.79 | KP279013   |
| SCF40225 | (GT)11  | F:GCTTGACTGGATTAGAACAAC<br>R:CTGGGTATCAACATCAACAGTA   | F:55.30<br>R:55.20 | KP279014   |
| SCF41166 | (TAA)7  | F:TTCTAACTCAAGTAGTCCTCCTG<br>R:AGAAGAACAGCAGATTCCAC   | F:54.69<br>R:54.44 | KP279015   |
| SCF41759 | (GT)10  | F:TTGCCATCTTCTTGTCTTC<br>R:ACAACATGCTAATGTGGGTACT     | F:55.50<br>R:56.20 | KP279016   |
| SCF42256 | (GA)9   | F:ATACTGCTCAACTGATTTAGGG<br>R:CGGAGGAAAGTCTGCTATATT   | F:55.28<br>R:55.34 | KP279017   |
| SCF42549 | (CT)10  | F:CTCTTCAGCCCTAATCATATTC<br>R:CAGGACAAACATCTAGGTCAA   | F:54.87<br>R:55.31 | KP279018   |
| SCF4283  | (GAA)7  | F:CTTGACTTTGTAGTGGTGTGTTG<br>R:CTCCTCCCCTCTTTTAACTAAT | F:55.08<br>R:55.04 | KP278962   |
| SCF43996 | (ATT)10 | F:ATAGTGTATGTATCAGAGCGGG<br>R:TATTTACGGGAGGTGTGAACTA  | F:55.97<br>R:56.40 | KP279019   |
| SCF47689 | (CT)12  | F:TGTAGATGCCGTCAAAGAAT<br>R:ACTATAACTCCAAGCGCAGTAT    | F:55.83<br>R:55.08 | KP279020   |
| SCF48612 | (TTC)7  | F:GAACACGATTTGACATTTCC<br>R:CTCCTATGTTGTTTTCTGTCTGT   | F:55.45<br>R:56.06 | KP279021   |
| SCF50668 | (AC)11  | F:CTTAATATGTCCTAGCCCAAAC<br>R:GAGGTGTAGAATAGTGAAAGTGG | F:54.86<br>R:54.79 | KP279022   |
| SCF51607 | (AG)10  | F:TTATGTAACTGACGCTGATAGG<br>R:GTAGATTTGCGATGGTGTATG   | F:54.82<br>R:55.71 | KP279023   |
| SCF5230  | (CT)11  | F:TTCAAGATGCCTAAACCAGT<br>R:GTATAGTGGAGAAGAAGGGTGA    | F:54.95<br>R:55.08 | KP278963   |
| SCF53058 | (TC)11  | F:TACCACAGTCTCCTTAACAAAG<br>R:CATACTCTATAATCCACTTCCG  | F:53.86<br>R:53.34 | KP279024   |
| SCF54555 | (CT)10  | F:TTACCAAAGCACCCATTAAC<br>R:ACGACACATATCTCCAAAGTG     | F:55.26<br>R:55.16 | KP279025   |
| SCF55619 | (CT)9   | F:CAAAGAATCAGCAGGAGGT<br>R:GATGTCTAAGGTACAAGGAAGC     | F:55.35<br>R:54.84 | KP279026   |

Table S3. *Cont.*

| SSR ID   | Motif  | Sequence                                             | TM (°C)            | GenBank ID |
|----------|--------|------------------------------------------------------|--------------------|------------|
| SCF5899  | (GAA)8 | F:TAGCCTTGGGTATTAGAACACT<br>R:GGAAGACAAGACAAGAGGC    | F:54.91<br>R:54.84 | KP278964   |
| SCF5935  | (GA)9  | F:CTGAACTGAAACACCAAGAAC<br>R:AGAAATGAGACCTACACTGCAT  | F:54.91<br>R:55.58 | KP278965   |
| SCF6050  | (TC)9  | F:TAACAAAATAGAGACCTCCCTG<br>R:TTGACTGGTTGATGGTGTATAG | F:55.26<br>R:55.20 | KP278966   |
| SCF6053  | (CT)13 | F:GTTGAAGCATCCTACTCAAAAC<br>R:CCTAGTGAACAGTCATTTCTT  | F:55.70<br>R:55.16 | KP278967   |
| SCF61946 | (TG)9  | F:GGATAAAAGGGTACTCCATACA<br>R:GGTTCATAGTGGCGAAATTA   | F:54.92<br>R:55.34 | KP279028   |
| SCF61972 | (GA)9  | F:CAGATGAATTTAGACGAGTGG<br>R:TGCATAGCTCAAATATCCCT    | F:54.98<br>R:55.01 | KP279027   |
| SCF63953 | (GA)9  | F:GTTGGTGTGGTTCTCATTATC<br>R:GTGAGTGCTGATAGGGTAGAGT  | F:54.45<br>R:55.17 | KP279029   |
| SCF65004 | (TTC)9 | F:GAATCAATCCAGTCCATAGG<br>R:CTTACACCACTCTTCCCAAC     | F:54.44<br>R:54.68 | KP279030   |
| SCF65897 | (CT)10 | F:CTTATTTTGCTGAACCTTGG<br>R:CTCTAACTATTCTTGCAGCCTC   | F:55.15<br>R:55.31 | KP279031   |
| SCF662   | (GA)10 | F:TTGGACAATCTTACCCATAGAC<br>R:CTTGGCGTGCATAGAATAA    | F:55.76<br>R:54.99 | KP278956   |
| SCF66313 | (CT)10 | F:AATTTGACCCTCTTTCCCT<br>R:GTCCAAAATACACAACTAGCC     | F:55.19<br>R:55.58 | KP279032   |
| SCF68007 | (GAG)7 | F:CACCCACCACAACATAAAC<br>R:TCTTCTACTGAACAGCTTCTTG    | F:54.49<br>R:54.27 | KP279033   |
| SCF6819  | (CA)9  | F:TCATCATCACTCCAACACAGA<br>R:TGTAAATTCTGAGCCCTTGT    | F:55.75<br>R:54.95 | KP278968   |
| SCF74917 | (TA)11 | F:AAACATAAAGAGCAGCCAGTAG<br>R:CTGATAAATAGAGACAGACGGG | F:55.65<br>R:55.68 | KP279034   |
| SCF76055 | (GT)9  | F:GATCGAAATGAGGATTGTG<br>R:CTCTTCCACTGTCAACTTTTCT    | F:55.55<br>R:55.35 | KP279035   |
| SCF77055 | (CT)9  | F:GAACTGGTAAGGTTTGGAATA<br>R:CTTGGAAGGATTCTACTAGC    | F:55.17<br>R:54.95 | KP279036   |
| SCF77382 | (CA)9  | F:GTTTTCCACAAATCTAGTCGTC<br>R:TGTGAGACCAAAGTGACAAG   | F:55.55<br>R:54.58 | KP279037   |
| SCF7822  | (GA)9  | F:GTCACCTCATGGTAGTATTGTACG<br>R:AGTCTTACGTTTGGTGTCG  | F:54.02<br>R:53.66 | KP278969   |
| SCF80777 | (GA)10 | F:GAGGCAATGTTAGTCTTTGGT<br>R:GGATACAACAGCTAGAACCCT   | F:55.97<br>R:55.18 | KP279038   |
| SCF8189  | (GA)10 | F:GACAAGGAGGAAGAAATAGTGA<br>R:ACCAGCAGAAGCAGTTAAAG   | F:55.20<br>R:54.95 | KP278970   |
| SCF83079 | (AC)12 | F:GTATTCACCAAATCTACCCAGA<br>R:GTTAAGGATTGTGTCCCTCA   | F:55.76<br>R:55.03 | KP279039   |
| SCF83872 | (TC)10 | F:GGAGCTTGAAAACCTAAACA<br>R:GTTAGTGAGGAGGGGAGAG      | F:54.69<br>R:53.71 | KP279040   |

Table S3. *Cont.*

| SSR ID   | Motif   | Sequence                                             | TM (°C)            | GenBank ID |
|----------|---------|------------------------------------------------------|--------------------|------------|
| SCF84796 | (TC)10  | F:CTACTCTTAGGGCATCTCCA<br>R:CAACACTACTGACCTTCACAAT   | F:54.62<br>R:54.39 | KP279041   |
| SCF84921 | (TCT)7  | F:CTTCATCGTCTTATCAGGTTG<br>R:CCAAGTGAGTCTGTGATTGAT   | F:54.98<br>R:55.11 | KP279042   |
| SCF85469 | (AC)15  | F:CCAGATAAGTAACACAACACCA<br>R:GGGAGTGCTCATTTGTAGTC   | F:55.28<br>R:54.75 | KP279043   |
| SCF85776 | (AG)9   | F:CTAAGTTCCAAACAGAGCCTTA<br>R:AAGTTACCACCGCTAAGAAAC  | F:55.63<br>R:55.33 | KP279044   |
| SCF87305 | (CT)11  | F:AATGCTCTCCAGACTTTTCTAC<br>R:GTGCAGTATCAAATGTAAGACG | F:54.57<br>R:55.11 | KP279045   |
| SCF87786 | (CT)11  | F:AGGGAGATAGTTGTTCCCAT<br>R:GCCTAAACCTAGTAAACTCTGC   | F:55.07<br>R:54.43 | KP279046   |
| SCF9045  | (GA)10  | F:GCAAATGTCACTGTTAGGATAC<br>R:GAAAGGAAGAGAAGTTAAGCAG | F:54.03<br>R:54.49 | KP278971   |
| SCF9100  | (TAT)15 | F:TTAGTCCCCTCCTCAATTATC<br>R:GGGCTCACTATCACTACTCATT  | F:55.02<br>R:55.10 | KP278972   |
| SCF91560 | (AAT)10 | F:TATTAAACTCACTGCACCTCTG<br>R:TGACCATCTATGAGAAGCTATG | F:54.84<br>R:54.67 | KP279047   |
| SCF92986 | (AC)9   | F:AACTAACCCGGACACCTAGTAT<br>R:CGAGGGAGACAATATCAAAGTA | F:55.94<br>R:56.07 | KP279048   |
| SCF9350  | (TG)9   | F:GGATTTACCACACCATTCTG<br>R:AAGAAATTACCACATGCACC     | F:55.33<br>R:55.07 | KP278973   |
| SCF95879 | (AT)9   | F:TTTTACATGAAGTGGTAGAGGG<br>R:CCAGTTGTATAGATTTTGCTGG | F:55.99<br>R:56.54 | KP279049   |
| SCF96306 | (TC)9   | F:CCTGTAGTGAGTTACCTTCCAT<br>R:GCTGTCAACCATCCATTATT   | F:55.04<br>R:54.99 | KP279050   |
| SCF99113 | (GA)9   | F:CATGACTTGCTTGTATGGTG<br>R:CACAACCTCGCATAACTCTACTC  | F:55.06<br>R:54.42 | KP279051   |
| SCF99997 | (GA)9   | F:ATAGGTCATCTCCTTCTTGTTG<br>R:ACTACTACCGTTGATTGCCTT  | F:55.08<br>R:55.60 | KP279052   |