# Microsatellite primers for red drum (*Sciaenops ocellatus*)

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In this note, we document polymerase-chain-reaction (PCR) primer pairs for 101 nuclear-encoded microsatellites designed and developed from a genomic library for red drum (*Sciaenops ocellatus*). Details of the genomic library construction, the sequencing of positive clones, primer design, and PCR protocols may be found in Karlsson et al. (2008). The 101 microsatellites (GENBANK Accession Numbers EU015882-EU015982) were amplified successfully and used to genotype 24 red drum obtained from Galveston Bay, Texas (Table 1). A total of 69 of the microsatellites had an uninterrupted (perfect) dinucleotide motif, and 30 had an imperfect dinucleotide motif; one microsatellite had an imperfect tetranucleotide motif, and one had an imperfect and compound motif (Table 1 ). Sizes of the cloned alleles ranged from 84 to 252 base pairs. A 'blast' search of the GENBANK database indicated that all of the primers and the cloned alleles were unique (i.e., not duplicated).

Summary genotypic data, based on 22–24 assayed red drum, also are given in Table 1 and include number (and size range) of alleles detected, observed and expected heterozygosity, and probability values from tests for conformity to Hardy-Weinberg equilibrium expectations. One microsatellite (*Soc*734) was monomorphic; the number of alleles detected at the remaining 100 (polymorphic) microsatellites ranged from 2 to 26. Estimates of observed and expected heterozygosity and tests for conformity to Hardy-Weinberg and genotypic equilibrium expectations were performed with GENEPOP (Raymond and Rousset, 1995). Observed heterozygosity (polymorphic microsatellites) ranged from 0.042 (*Soc*706) to 1.000 (11 microsatellites, Table 1) and averaged (±standard deviation [SD]) 0.775 ±0.211; expected heterozygosity ranged from 0.042 (*Soc*706) to 0.971 (*Soc*636) and averaged 0.806 ±0.201. After Bonferroni correction (Rice, 1989), genotypes at 99 of the polymorphic microsatellites did not differ significantly from Hardy-Weinberg equilibrium expectations. At one locus, *Soc*706, there were only two alleles, one of which was observed only in a heterozygote; this microsatellite was not tested for Hardy-Weinberg equilibrium. Analysis with MICRO-CHECKER (Van Oosterhout et al., 2004) indicated the possible occurrence of null alleles at nine of the microsatellites, and single base-pair shifts (i.e., alleles differing by only a single base pair) were observed at five of the microsatellites (Table 1). Tests of genotypic disequilibrium were nonsignificant after Bonferroni correction. Given that red drum possess 24 haploid chromosomes (Gold et al., 1988), several of the microsatellites undoubtedly are linked; determination of linkage will await formal mapping studies.

Along with PCR primers for red drum microsatellites developed previously by O'Malley et al. (2003), Saillant et al. (2004), and Karlsson et al. (2008), the primers developed here will be useful in a variety of applications (Liu and Cordes, 2004), including analysis of stock structure, monitoring and assessment of red drum stock enhancement, parentage analysis as employed in aquaculture, and the generation of a genetic map for red drum. A table of the 269 PCR primers developed for red drum may be found at <http://wfsc.tamu.edu/doc> under the file name "PCR primers for red drum (*Sciaenops ocellatus*) microsatellites."

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**Table 1**

Summary data for 101 microsatellites developed for red drum (*Sciaenops ocellatus*). Primer sequences are forward (top) and reverse (bottom) primers used in PCR amplification of both DNA strands. Repeat sequence indicates repeat motif; subscript indicates number of replicates in the cloned allele. Cloned allele is size (in base pairs) of the sequence in GenBank. $N$ is the number of individuals assayed; $N_A$ is the number of alleles detected. Size range refers to size (in base pairs) of alleles thus far detected and size includes the 21 base pair 5′ tail-sequence primer used for PCR amplification. $H_O/H_E$ is observed and expected heterozygosities, respectively. $P_{HW}$ represents the probability of deviation from Hardy-Weinberg expectations.

| Micro-satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*628 | GCACTGCTGCTACCTGACAC<br>TCCAACTCACTCGTTGTTTACAG | $(GA)_{29}$ | 181 | 24 | 18 | 174–220 | 0.917/0.932 | 0.783 |
| *Soc*630 | CGCTGCTTCTCACGCTCTG<br>GGTGTCATGTATGGATACTGCTCTT | $(CA)_{16}$ | 144 | 24 | 10 | 155–175 | 0.833/0.841 | 0.357 |
| *Soc*631 | TGGGTCCTCCAGCTCTGATA<br>TCTGTTTCCATTGCTGTGTCA | $(CA)_{10}(N)_{22}(CA)_{14}$ | 222 | 24 | 22 | 189–241 | 1.000/0.965 | 1.000 |
| *Soc*632 | TCTTTTCTCTGCGTTTGATAG<br>TCTCTGTGTTTTCGCTTCCA | $(CA)_{12}$ | 242 | 24 | 2 | 262–264 | 0.083/0.082 | 1.000 |
| *Soc*633 | CAAATGACAAGGAAGACAAGAGC<br>CCGCCTCAGTTACAGGAAATG | $(GA)_{18}(N)_2(GA)_5$ | 188 | 24 | 8 | 191–217 | 0.875/0.830 | 0.277 |
| *Soc*635 | CATCAGCACGGTTATTTTCTTG<br>CCTCTCTCTTTTCTTCCCTCG | $(CA)_{23}$ | 245 | 24 | 10 | 249–269 | 0.708/0.781 | 0.609 |
| *Soc*636 | AACACGTAACAACATCCATG<br>GATCAAATTAGCATCAGTAATGT | $(CA)_{35}$ | 150 | 23 | 25 | 131–217 | 0.957/0.971 | 0.134 |
| *Soc*637[1] | AGAGGGTTAGAAGGGGAGAA<br>AGTATCAAAACTTGGCATCC | $(CA)_{31}$ | 194 | 22 | 20 | 178–230 | 0.818/0.940 | 0.007 |
| *Soc*638 | CTTTCATTTGGACTGGCTTTG<br>TGGTCTGCTCTGCTTTTGATT | $(GA)_{14}$ | 220 | 24 | 5 | 236–250 | 0.792/0.755 | 0.323 |
| *Soc*639 | ATCTTCTCTCACAAACACTCAC<br>CCAAACTGTCAAGGATGTCA | $(CA)_{13}$ | 138 | 24 | 7 | 148–168 | 0.792/0.740 | 0.989 |
| *Soc*640 | AGGACATTTGGAGTGGAAGAGTA<br>ATGGGGACAGGAGGTTTTCTA | $(CA)_{14}$ | 159 | 24 | 13 | 179–209 | 0.875/0.898 | 0.225 |
| *Soc*641 | ATGCGGAGTAGAGAGAGGAGG<br>TGACCTGAATGAAGATGTATGGA | $(CA)_{17}(N)_2(CA)_6$ | 136 | 23 | 20 | 142–202 | 0.913/0.958 | 0.117 |
| *Soc*642 | CAGAGAAGGTTACAGGAGGTG<br>ATGTGCTGGGACAGGTTG | $(CA)_{22}$ | 200 | 23 | 9 | 210–228 | 0.870/0.881 | 0.539 |
| *Soc*644 | GCTACGGTCGGGAATCAGA<br>GCTGCCCTTCAGTGGTTTT | $(CA)_{32}$ | 167 | 23 | 18 | 155–205 | 0.913/0.952 | 0.319 |
| *Soc*645[1] | GAGTTGGTCAATAGCCACAGG<br>ATCTGAAGGGCAGGTGTTTG | $(CA)_{20}$ | 150 | 24 | 10 | 157–181 | 0.708/0.891 | 0.025 |
| *Soc*646 | GGGAAAGTAGATAGGGGCACA<br>AGAGGTCAGGGTTGAGCAGAGT | $(CA)_{16}$ | 132 | 22 | 4 | 130–156 | 0.273/0.318 | 0.559 |
| Soc647 | GCACAGATTCGTCCCAGATT<br>TGTTCAGTTGCTCACAAACCA | $(CA)_{51}$ | 247 | 23 | 26 | 203–283 | 0.957/0.967 | 0.463 |

*continued*

**Table 1 (continued)**

| Micro–satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*648 | GCTTCCAGATGCGATGTAAAC<br>GCTACTGCCACCACAAACAC | $(CA)_5(N)_2(CA)_{22}$ | 181 | 24 | 14 | 179–225 | 0.833/0.888 | 0.266 |
| *Soc*649[1] | GTACTTGTAGTAATCAGGGTATTTT<br>AAACGCACTTCTTTGAGACTA | $(TG)_{20}$ | 154 | 24 | 11 | 152–182 | 0.708/0.878 | 0.040 |
| *Soc*650[1] | CCGTGTTTGCTTGGCTTT<br>CAATGTGTATGGGTATGGGTAGG | $(CA)_{22}$ | 125 | 24 | 14 | 127–175 | 0.583/0.893 | 0.002 |
| *Soc*651 | TGAAAGACGAAATTCAGCAAAA<br>AGGAAGGCAGGTGGATAGTAAA | $(CA)_{23}$ | 187 | 24 | 20 | 193–263 | 1.000/0.931 | 1.000 |
| *Soc*652 | TCGCCATCATTCATAAAACT<br>GTTCTCAAAAGAGTCTACCTGTC | $(CA)_{19}$ | 196 | 24 | 10 | 204–232 | 0.833/0.785 | 0.821 |
| *Soc*653[1, 2] | GAAACAGCCTCCCACACAG<br>TCCTCCTCTTCGCTCATCA | $(CA)_{26}$ | 252 | 24 | 17 | 138–274 | 0.792/0.931 | 0.157 |
| *Soc*654[2] | CTCCGCTGCCAAACTGAC<br>TGTGCTCTACATCCTCCTCCT | $(CA)_{13}$ | 164 | 23 | 5 | 173–186 | 0.565/0.575 | 0.191 |
| *Soc*655 | CTGAAAGGGCCGTTGGTTT<br>GAGGATGCAGAGTCAAGCAAGA | $(CA)_{18}(N)_2(CA)_3(N)_2(CA)_8$ | 166 | 24 | 10 | 172–192 | 0.792/0.836 | 0.642 |
| *Soc*656 | CGTGCTGAGACAGGTGGTAGT<br>GTAGGCGTGGAGACGGAGT | $(CA)_{24}$ | 213 | 24 | 23 | 221–279 | 1/0.955 | 0.442 |
| *Soc*657 | GGAAAGCAAAGCAAAAGAAACT<br>AGCCGAATGAGACAGAGGAAA | $(CA)_{34}$ | 232 | 22 | 17 | 210–268 | 0.955/0.946 | 0.757 |
| *Soc*658 | AATCTCCCAGTGCCTTTGA<br>CTGCTTTTTCCCTCTATTTCTC | $(GA)_{14}$ | 149 | 24 | 7 | 162–176 | 0.542/0.558 | 0.789 |
| *Soc*659 | GCATCCCTCCCCTCTCTCC<br>GCCTGGCAAACATCCAACTT | $(CA)_{17}$<br>$(CA)_{12}(N)_2(CA)_2(N)_2(CA)_5$ | 189 | 23 | 10 | 200–228 | 0.870/0.854 | 0.462 |
| *Soc*660[2] | TTGCCAATGTTCTTTCTCTCT<br>ATTCCTACTCCTGCCAAGAT | $(N)_2(CA)_2(N)_2(CA)_7$ | 123 | 24 | 11 | 130–184 | 0.833/0.847 | 0.783 |
| *Soc*661[1] | ACCGCCTCAAAACAACACA<br>AGGAGATTGGGAGTGGAGATA | $(CA)_{13}$ | 145 | 24 | 11 | 154–176 | 0.667/0.859 | 0.004 |
| *Soc*662 | CGTCTTTAGGAAGGTGTGGC<br>CCTGTCTGGAGGGGAAAAC | $(CA)_{20}(N)_2(CA)6(N)_2(CA)_3$ | 108 | 22 | 13 | 90–144 | 0.818/0.910 | 0.385 |
| *Soc*663 | TCAGGGTATGTACGCAGATG<br>CAAGCACTTCACGAGGAAC | $(CA)_{14}$ | 172 | 24 | 21 | 190–274 | 0.917/0.930 | 0.753 |
| *Soc*664 | GAGGTTCAGTTTGGCTGCTG<br>CGTGTGTGTTTTCGCTCAGTT | $(CA)_{23}$ | 136 | 24 | 15 | 137–169 | 0.875/0.907 | 0.268 |
| *Soc*665 | TCACAGTGGCTCTCCAGGTAA<br>TTGCCCTCTTGTCGTTCATCT | $(GA)_{33}$ | 132 | 24 | 22 | 115–189 | 0.833/0.944 | 0.268 |
| *Soc*666[1] | TAATCTCTGTGTGTGTCCAGGTG<br>GACGCAAGGCTGAGGCATA | $(CA)_4(N)_2(CA)_{21}$ | 201 | 24 | 18 | 207–263 | 0.750/0.921 | 0.020 |

*continued*

**Table 1 (continued)**

| Micro–satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*667 | TAACGCTCTGTCCATCACTG<br>CATCTACGAATGCCCAACA | $(CA)_{14}(N)_4(CA)_5$ | 232 | 23 | 6 | 245–261 | 0.652/0.699 | 0.198 |
| *Soc*668 | TGATGAGGACCAAGTGACAAC<br>ATCAGTGTTTTTCCATTAGCC | $(CA)_{18}$ | 96 | 23 | 15 | 107–163 | 0.870/0.901 | 0.095 |
| *Soc*669 | GAAGGAGGCAGGCACACATA<br>GAGAGCGAGCGAGAGAAAGA | $(CA)_4(N)_2(CA)_{21}$ | 117 | 23 | 17 | 115–167 | 0.957/0.889 | 0.996 |
| *Soc*670 | TTCGTCCCGTCACAGCACA<br>CAAAGAGAGATGAATAAACCCAAAG | $(CA)_{30}$ | 245 | 23 | 12 | 225–273 | 0.826/0.852 | 0.296 |
| *Soc*671 | CGCCTCTCTTCCTCAGATGT<br>ACAGTGGGCAAATCCATACA | $(CA)_{30}(N)_4(CA)_4$ | 228 | 23 | 14 | 233–271 | 0.826/0.910 | 0.152 |
| *Soc*672 | CGTATGGTGAGTGTTGGCA<br>TGTCGTCTCTGAATGTGTCCT | $(CA)_{22}$ | 199 | 24 | 19 | 199–243 | 0.875/0.946 | 0.056 |
| *Soc*673 | AAAGACTGACACAAGGCTGACA<br>AATCTCTGCTCATTTCCTCATCT | $(CA)_{24}$<br>$(CAGA)_4(N)_4(CAGA)_2(N)$ | 194 | 22 | 10 | 193–227 | 0.773/0.819 | 0.807 |
| *Soc*675[1] | TGTCCCCATAAAGAACAAGG<br>ACACAACGTCTACAGGAAGGC | $(CAGA)_2$ | 96 | 24 | 6 | 108–234 | 0.417/0.608 | 0.037 |
| *Soc*676 | TGAACTGTCACGTCCGTCAT<br>CCTTGTTCTTTATGGGGACA | $(CA)_{20}$ | 166 | 24 | 15 | 173–211 | 0.875/0.919 | 0.320 |
| *Soc*678 | CTGGCTGGTTGATGTAAGTC<br>AGACAGTGGGGCGTTAGAT | $(CA)_{19}$ | 128 | 24 | 12 | 132–158 | 0.875/0.898 | 0.577 |
| *Soc*679 | ACACCTTCCACTGACTGACCAC<br>GAATGTGTGCGTGTCTGCGT | $(CA)_{27}$ | 146 | 24 | 14 | 162–194 | 0.792/0.889 | 0.013 |
| *Soc*680 | GCTGCCTCCTCTGTCACTCT<br>TCACGCACCTTCTCCTCTTT | $(CA)_{12}$ | 93 | 22 | 19 | 106–152 | 0.955/0.949 | 0.632 |
| *Soc*681 | TATGGCTCCGACACACTCCT<br>CCACCCCAGTAGACACTCAGA | $(GACA)4(CA)_{12}$ | 111 | 24 | 9 | 123–151 | 0.875/0.849 | 0.671 |
| *Soc*682 | TCCACTGTAGGTGTTGTTTCA<br>ACTTTTAGGCGGGAGAGTC | $(CA)_{15}$ | 200 | 24 | 11 | 202–236 | 0.750/0.880 | 0.171 |
| *Soc*683 | TTCGCACACATACATAACTAAACT<br>AGCGTCATAATCCAACTGTCA | $(CA)_6(N)_2(CA)_7$<br>$(GA)_5(N)_8(GA)_4(N)_2(GA)_2$ | 185 | 23 | 7 | 190–230 | 0.565/0.647 | 0.312 |
| *Soc*684 | CAGCCATACAGACGGACAC<br>TTTGAATAGAAGTCAGAAGTGC | $(N)_2(GA)_6(N)_2(GA)_9$ | 198 | 24 | 13 | 185–233 | 0.917/0.833 | 0.860 |
| *Soc*685 | TCAAACAGGGTCATTGGTGA<br>AGGAGAAACGCAGGGAAGA | $(CA)_{14}$ | 215 | 23 | 2 | 233–235 | 0.261/0.232 | 1.000 |
| *Soc686* | AAAGTGACCCTGAGTTCCTCTG<br>GCAAAAACAATGAAACCCTCT | $(CA)_{19}$ | 226 | 23 | 12 | 233–265 | 0.826/0.881 | 0.564 |
| *Soc*687 | GCTGGAAGGGGAGTCTTATGA<br>AAGGCTCTCTCAAGCAGTGTT | $(CA)_{12}$ | 157 | 23 | 16 | 172–206 | 0.870/0.928 | 0.351 |

*continued*

**Table 1 (continued)**

| Micro–satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*688 | GCTCTCTTGTCCTCCATACCTG<br>GGGAAACCTGCTGTGACCA | $(CA)_{18}$ | 192 | 24 | 15 | 198–242 | 0.875/0.854 | 0.901 |
| *Soc*689 | GACTCTTCAATCCTACTCACCA<br>ACATTTCTTTTGTCCGTTCA | $(CA)_{25}$ | 182 | 23 | 20 | 204–246 | 1.000/0.937 | 0.951 |
| *Soc*690 | CGTCTTCTGTGTTTGTGGGA<br>TGATTCATCTGCGTCGTGTT | $(GA)_{21}$ | 101 | 22 | 11 | 109–139 | 0.909/0.862 | 0.100 |
| *Soc*691 | CAGTGAGAGACGCAAACCAG<br>GTCAAGTAGGTAAATAAAGCCTGA | $(CA)_{31}$ | 129 | 22 | 15 | 112–158 | 0.909/0.926 | 0.832 |
| *Soc*692 | TGCTGCCATTGAGAAGAGA<br>TTTGTATGTTAGGGGTTGTGT | $(CA)_{10}$ | 117 | 23 | 6 | 126–140 | 0.652/0.647 | 0.650 |
| *Soc*693 | AAGTTGTTTCTTTTGTTCCAGTA<br>TAGATGAAGGCTTGTTTTTCTCT | $(GA)_{18}(N)_1(GA)_7$ | 192 | 24 | 22 | 279–337 | 1.000/0.950 | 0.022 |
| *Soc*694 | CTCGCTCCCATCGTGACT<br>TCCTGAAAGTTGTGCTTGTCC | $(CA)_{11}$ | 168 | 21 | 9 | 185–207 | 0.810/0.846 | 0.424 |
| *Soc*695 | TCTGGAGGGATGATGTGTTT<br>CCTGTTTCACTGCTACTCGC | $(CA)_{21}(N)_2(CA)_5$ | 135 | 23 | 16 | 129–187 | 0.957/0.912 | 0.780 |
| *Soc696* | GAAAATGGTGAAAACCCTGA<br>CAAAATGGAGAAGCCTGAAG | $(CA)_{31}$ | 207 | 23 | 21 | 191–253 | 1.000/0.954 | 0.937 |
| *Soc*697 | AAGCACGCAATCTATGAAACAC<br>TGTGGGAAAACATCCAGAGG | $(CA)_{10}$ | 166 | 22 | 7 | 183–199 | 0.682/0.744 | 0.421 |
| *Soc*698 | TCTCAAATCTTCCAATCAGCAG<br>CGACAGGGAGTGACCAACAG | $(CA)_{11}$ | 133 | 22 | 9 | 152–172 | 0.818/0.819 | 0.684 |
| *Soc*699 | AGCCAGCAACTGAATACCA<br>CAAAGCCACCTCCTGATTT | $(CA)_{13}$ | 163 | 23 | 15 | 170–224 | 0.783/0.853 | 0.218 |
| *Soc700* | GCTGAACTGTGAGGCAGATGA<br>CGTAAATAAGGGAAACAAACAAGA | $(CA)_{28}$ | 245 | 22 | 22 | 249–305 | 0.955/0.946 | 0.701 |
| *Soc*701 | ATCCAGGTTTAGAGGCTGTCA<br>TTCAGGAAAAGTCCACACAGA | $(CA)_6(N)_2(CA)_{15}$ | 120 | 23 | 12 | 129–169 | 0.739/0.846 | 0.034 |
| *Soc*703 | TCTCCGTGTAAAGATGATGGTC<br>GAGGGCGAACAAACTGCTAA | $(CA)_{18}$ | 235 | 23 | 16 | 236–278 | 0.913/0.923 | 0.910 |
| *Soc*704 | CCCAGCGTTTCCCCTAAT<br>ACATCCCCTCTGTTCCTCCT | $(GA)_{15}$ | 237 | 22 | 12 | 254–302 | 0.682/0.722 | 0.303 |
| *Soc*705[2] | CTGCCTGGATTGCCTTTTAG<br>TTCTGCTGTTGAGGACGATG | $(CA)_7(N)_{28}(CA)_4$ | 215 | 23 | 9 | 235–246 | 0.826/0.752 | 0.755 |
| *Soc*706 | ACTCTGTTGCTCCACTACCCA<br>GCTCTTCTCCTGTTTGTGTGA | $(CA)_5(N)_2(CA)_8$ | 150 | 24 | 2 | 170–176 | 0.042/0.042 | na |
| *Soc707* | TTCCTCTCTTCACTCCTGGT<br>CAACACTGCCTCCCTATGG | $(CA)_{21}$ | 156 | 23 | 18 | 173–217 | 0.870/0.932 | 0.287 |

*continued*

**Table 1 (continued)**

| Micro–satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*708 | TTCCCACTAGAGCTGTGATTGA<br>TCTGACTTCCTCTGCCCATT | $(CA)_{17}$ | 130 | 23 | 9 | 139–157 | 0.870/0.878 | 0.258 |
| *Soc*709 | CTGATGAATGGACTGAACAC<br>TGTGAGAGGAACAGAGACG | $(CA)_{22}$ | 200 | 22 | 7 | 201–221 | 0.682/0.740 | 0.261 |
| *Soc*710 | TGTGTGAGTGAAAGGCAAACC<br>TGGCAGGGAGAATAGAGGAA | $(CA)_{18}(N)_2(CA)_4$ | 102 | 22 | 10 | 107–131 | 0.591/0.674 | 0.033 |
| *Soc*711 | CCTCCCCACCCTCTCTCTG<br>AGTCGCTGCTGTGTGTTTGT | $(CA)_5(N)_2(CA)_{14}$ | 244 | 23 | 10 | 262–288 | 0.783/0.807 | 0.552 |
| *Soc*712 | CAGCAGAGGGCAAAAATGA<br>AGGGTGGGTGGTGTTGTCA | $(GA)_{14}$ | 84 | 23 | 7 | 95–111 | 0.652/0.557 | 0.836 |
| *Soc*713 | AATAGTTTCCTCTGGATTGACG<br>TGGCTTAGACAAGTGGTGCT | $(CA)_{18}$ | 189 | 24 | 11 | 189–211 | 1.000/0.888 | 0.919 |
| *Soc*715 | TTTCCCTCTCTTTCCCACAG<br>GCAACACAGTCAGCCCACA | $(CA)_{10}$ | 98 | 24 | 4 | 114–124 | 0.583/0.666 | 0.716 |
| *Soc*716[2] | ATGGTGTTTGGCTTGCTGAG<br>AGAGCGGCAGTCATCTGTTC | $(CA)_{10}(N)_2(CA)_6$ | 144 | 24 | 15 | 146–186 | 0.833/0.921 | 0.040 |
| *Soc*717 | ACGGCAACTGGGGTCAAC<br>TTCCATCGTGTAGGTCACAAAC | $(CA)_6(N)_2(CA)_5$ | 241 | 22 | 3 | 260–264 | 0.636/0.609 | 0.818 |
| *Soc*718 | CCCTCTGTTTTCTCTGGGATTT<br>CTTTGGTGTGTGCGTGTTTCT | $(CA)_{16}$ | 190 | 23 | 9 | 203–223 | 0.783/0.796 | 0.041 |
| *Soc*719 | CACCTTCTACTCCCCATTCA<br>CCTCCTTCTTGGCTTCATA | $(CA)_{27}$ | 183 | 24 | 17 | 190–230 | 1.000/0.917 | 0.397 |
| *Soc*721 | GGTAAAGTGTAAAATGCCAATAG<br>AGGGAAACGAAAAGAGGAAA | $(CA)_{10}(N)_{24}(CA)_{12}$ | 203 | 23 | 10 | 209–229 | 0.783/0.847 | 0.142 |
| *Soc*723 | CAGATGGCACTAACTAAGGAGA<br>CAGATAAGTAGAGGTGGAAGACA | $(CA)_7(N)_2(CA)_{24}$ | 170 | 24 | 19 | 183–245 | 0.833/0.940 | 0.171 |
| *Soc*724 | GTATTTTGAGCCTGCGTTGTA<br>CATGAACCCGTCTATTTGC | $(CA)_{22}$ | 194 | 24 | 11 | 198–234 | 0.833/0.892 | 0.021 |
| *Soc*725 | GAAGCGAAAATAAGGCTGA<br>GTTTAGTTTGGTCTGTTCAATC | $(CA)_{15}$<br>$(CA)_{15}(N)_2(CA)_4$ | 88 | 22 | 9 | 101–123 | 0.773/0.841 | 0.088 |
| *Soc*726 | GCTTTCTATTGATTCTGCCTGTC<br>CAAGGTGGGGAGGAGAGACA | $(N)_2(CA)_{11}$ | 146 | 24 | 16 | 140–184 | 0.958/0.918 | 0.270 |
| *Soc*727[1] | AGGCATCATTTACACGCTCA<br>AACCAACACACGAGGCTGA | $(CA)_{17}$ | 138 | 22 | 8 | 136–164 | 0.591/0.779 | 0.071 |
| *Soc*729 | CTTCTTCCACCTGTAACTGAATC<br>CTTTGTCCTCCGCTTGTTTC | $(CA)_9(N)_2(CA)_4$ | 137 | 23 | 13 | 156–184 | 0.913/0.930 | 0.810 |
| *Soc*730 | GCACAGGGAGATAAACACAG<br>CTGAAGAAAAGCCAGAGTGAA | $(CA)_{14}$ | 92 | 24 | 4 | 109–115 | 0.333/0.487 | 0.019 |

*continued*

**Table 1 (continued)**

| Micro-satellite | Primer sequence (5′–3′) | Repeat sequence | Cloned allele | $N$ | $N_A$ | Size range | $H_O/H_E$ | $P_{HW}$ |
|---|---|---|---|---|---|---|---|---|
| *Soc*731 | CAACCGATGAGAGCAGAGACT<br>TGTGTGTAGGTGAGACAAAAGAA | $(CA)_{22}$ | 224 | 23 | 9 | 220–254 | 0.391/0.484 | 0.133 |
| *Soc*733 | GCTGATGATGAACTGGTGCT<br>TTTCTTGTATGCTCTGTTTGC | $(CA)^{12}$ | 158 | 23 | 3 | 176–188 | 0.130/0.127 | 1.000 |
| *Soc*734 | CAGATTGGAACTGACACACAC<br>AAGCCCCTTCTTGGAGATT | $(CA)_{10}(N)_2(CA)_3$ | 90 | 22 | 1 | 109 | 0/0 | — |
| *Soc*735 | CCATCAGGAGGCTTTTGTCA<br>AAGAAGTAGGGTCAGCACACTGT | $(CA)_{31}$ | 187 | 23 | 23 | 164–244 | 1.000/0.965 | 1.000 |
| *Soc*736 | GAACCACCACTGCGAAACT<br>GCCTACAGATTGAGAACCACT | $(CA)_3(N)_2(CA)_9(N)_2(CA)_6$ | 168 | 22 | 3 | 188–196 | 0.136/0.132 | 1.000 |
| *Soc*737 | TCCAGGAAGTGGTCGGTTT<br>GGGAGAATGTGTGAATGCTTG | $(CA)_6(N)_2(CA)_{19}$ | 197 | 22 | 12 | 203–247 | 0.818/0.869 | 0.242 |
| *Soc*738 | TGTAACAGCAGAGACTGAAGC<br>CTGGGTGAAAGGCAGAGTA | $(CA)_{28}$ | 117 | 23 | 21 | 116–170 | 1.000/0.949 | 0.651 |
| *Soc*739 | TTGTGTTTTCCCTCTGCTG<br>TGTTGTTATGTTGGTGTGGTG | $(CA)_3(N)_2(CA)_3(N)_2(CA)_{10}$ | 188 | 23 | 16 | 201–251 | 1.000/0.938 | 0.894 |

[1] Microsatellites where occurrence of null alleles was indicated by analysis with MICRO-CHECKER
[2] Microsatellites with observed alleles differing by only a single base

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