

| Marker       | Locus     | Forward primer                | Reverse primer         | $T_a$<br>(°C) | $A$ | $L$<br>(bp) | $E_a$  | $E_l$ |
|--------------|-----------|-------------------------------|------------------------|---------------|-----|-------------|--------|-------|
| <b>nSSR</b>  | Se-116    | CCTTCTGGTTGATTTGGCTAAGC(FAM)  | AGAAGTGCACATTTGAAGCCTG | 48            | 22  | 370-432     | 0.000  | 0.000 |
|              | Se-136    | CAAAGGTAGGATGATGTGAAGCTC(FAM) | TCTTGTTGGGTCAATGCTCG   | 51            | 74  | 257-358     | 0.069  | 0.083 |
|              | Se-138    | ACTTCGTGGGCCATTCCAG(VIC)      | CTTCCTGCATAACATCCACCAC | 58            | 30  | 123-185     | 0.044  | 0.086 |
|              | Se-176(a) | AGCATAGTGCAAGCATGTTTCG(FAM)   | CTTTGATGTTGGCTGCAATGC  | 60            | 29  | 185-245     | 0.007  | 0.014 |
|              | Se-194    | GTCGCAGTACCGTCACTG(VIC)       | GAGCAGCAGACAACGACAC    | 58            | 9   | 307-318     | 0.031  | 0.061 |
|              | Se-208    | TTTTGGGCAGGCCATATCC(NED)      | AGTGTCTCCACGGTTGTCG    | 55            | 61  | 264-360     | 0.020  | 0.040 |
|              | Se-220    | AACTCGACCAGTCCTCAGC(NED)      | GTCACACTGGAACCCAACTG   | 58            | 23  | 115-175     | 0.033  | 0.039 |
| <b>cpSSR</b> | Ccmp1     | CAGGTAAACTTCTCAACGGA(VIC)     | CCGAAGTCAAAAGAGCGATT   | 50            | 3   | 159-161     | 0.053* |       |
|              | Ccmp2     | GATCCCGGACGTAATCCTG(PET)      | TCGTACCGAGGGTTCGAAT    | 50            | 3   | 217-219     | 0.043* |       |
|              | Ccmp5     | TGTTCCAATATCTTCTGTCAATTT(FAM) | AGGTTCATCGGAACAATTAT   | 50            | 2   | 112-115     | 0.000* |       |

\*Error rate per locus and per allele are the same in haploid genomes