Table S2: Gene diversity among 19 EST-SSR loci used in this study.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | Na | Nef | *H*O | *H*S | *H*T | *G*ST | *G*IS | Microsatellite motif | Forward primer | Accession number | Reverse primer | Accession number | Origin |
| Aat01 | 5 | 3.054 | 0.675 | 0.68 | 0.681 | 0.002 | 0.007 | (GCG)10 | CCATGTCTCCGATTTCCAGT | KF304594 | GGCCTAACGAAAGCAGAATC | KF304594 | [23] |
| Aat02 | 11 | 1.172 | 0.147 | 0.149 | 0.151 | 0.015 | 0.011 | (CAG)7 | AGAAGATTTCCCGGCTTTTC | KF304595 | ATCCAGACAGCGAACTTTGG | KF304595 | [23] |
| Aat04 | 11 | 2.638 | 0.637 | 0.627 | 0.641 | 0.022 | -0.016 | (CAG)11 | CCATGTATGGTGCTCCTCCT | KF304597 | CCTTCATTGCAGAAAAGCAA | KF304597 | [23] |
| Aat05 | 11 | 1.307 | 0.243 | 0.237 | 0.245 | 0.031 | -0.026 | (GCA)7 | AGCATCCACATTCCGTAACC | KF304598 | AGTTGACCGTTGGAGAGCAG | KF304598 | [23] |
| Aat06 | 5 | 1.125 | 0.112 | 0.113 | 0.114 | 0.012 | 0.008 | (GCA)8 | TTATGCGGAGCAGTTCTGTG | KF304599 | TGTTGCTGGCGTACTGGTAG | KF304599 | [23] |
| Aat08 | 3 | 1.036 | 0.037 | 0.035 | 0.036 | 0.011 | -0.052 | (AT)9 | ACTCCATCACGGTGGTCTTC | KF304601 | GCCATTCAGGCTCTCAGTTC | KF304601 | [23] |
| Aat09 | 3 | 1.866 | 0.391 | 0.47 | 0.482 | 0.025 | 0.167 | (TCA)8 | CAGATCCTCCCACATCCAAC | KF304602 | TGACACCACAGGAAACCATC | KF304602 | [23] |
| Aat10 | 9 | 3.506 | 0.544 | 0.724 | 0.734 | 0.014 | 0.249 | (AT)12 | GAGCACGATGAAGAGGAAGC | KF304603 | AAAACCCCCACGCGGTAT | KF304603 | [23] |
| Aat11 | 5 | 1.099 | 0.088 | 0.091 | 0.092 | 0.012 | 0.033 | (AAC)9 | AGCGTTGATTGGAAGCAGTC | KF304604 | GAAGCATGGTGTCGTTGTTG | KF304604 | [23] |
| Aat13 | 3 | 1.376 | 0.272 | 0.276 | 0.28 | 0.014 | 0.015 | (AG)8 | ACTCAAAGCCAAGCTGGAGA | KF304606 | TGCATAAGACAGCCGAGTCA | KF304606 | [23] |
| Aat15 | 2 | 1.801 | 0.453 | 0.450 | 0.468 | 0.042 | -0.009 | (AGA)8 | AGGAGGAGGTTCAGCATGTC | KF304608 | CTTGCTCTCTGACCCAGTTG | KF304608 | [23] |
| Egm1005 | 5 | 1.932 | 0.378 | 0.489 | 0.496 | 0.016 | 0.227 | (TGC)7 | TGGTGGGAAAGCTTGAATGGAACC | LC514337 | GGCGGGTGGTTTCTGTTGAAGAAC | LC514338 | this study |
| Egm14860 | 7 | 1.047 | 0.046 | 0.045 | 0.046 | 0.004 | -0.020 | (CCG)7 | TGAATGGGAACTGTGGGTCTGCC | LC514339 | AACGTGGGCAGCTCCAAGGATC | LC514340 | this study |
| Egm16822 | 6 | 1.968 | 0.483 | 0.497 | 0.499 | 0.003 | 0.028 | (CAG)6 | GCACCGTGCGAAAGACGTCTAAG | LC514341 | TACAGAGTCTCGGACAAGAGGCC | LC514342 | this study |
| Egm26233 | 13 | 2.252 | 0.535 | 0.562 | 0.571 | 0.016 | 0.049 | (GGC)8 | GCTATGCGTTGCTCAGCAGTGTG | LC514343 | ACGCATCCCAGGTTGAGCAGTAG | LC514344 | this study |
| Egm4191 | 3 | 1.738 | 0.617 | 0.427 | 0.428 | 0.003 | -0.446 | (GAG)6 | TGTGGGACAGACAGAGCTCTCAATC | LC514345 | TCGGATCGTCCTCTGTACTCACGG | LC514346 | this study |
| Egm4389 | 4 | 1.884 | 0.469 | 0.474 | 0.485 | 0.022 | 0.012 | (ATG)6 | ATTCTGAGAGCTGTGCGGACCAG | LC514347 | TCACCTGCTTCGACTGAACCCAC | LC514348 | this study |
| Egm5979 | 9 | 2.116 | 0.527 | 0.533 | 0.538 | 0.010 | 0.012 | (CCT)8 | GCAAAGCCATTCCCAGAAGTCGC | LC514349 | TCTTCTTGGTCATCGTCTCCAGGG | LC514350 | this study |
| Egm55338 | 11 | 3.010 | 0.674 | 0.675 | 0.689 | 0.021 | 0.002 | (CAC)6 | ATTCTCTGTGCCAACGACCACGG | LC514351 | TGGCCAGCAATAGGAGCCCTTTC | LC514352 | this study |
| Overall |  | 1.891 | 0.386 | 0.398 | 0.404 | 0.016 | 0.03 |  |  |  |  |  |  |