**S3 Table.** Primer sequences and final markers based on microsatellite loci.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Marker** | **Primer sequences (5‘ – 3‘)** | **SSR motif** | **Expected** **amplicon size [bp]** | **Number of alleles** | **DH14 contig** |
| *obm21* | GTATGGTTTGAGGGGTGGTCTA | (CT)9 | 115 | - | 000403 |
| TTGACATTTTCTACTTCGCCCT |
| *obm22* | CCTAGTTTTGTGCACCAGCA | (GAAAAA)9 | 150 | -a | 000935 |
| GGGTGAAACGGGCTGATAG |
| *obm23* | CGATCGCGTTTACTAGGTCA | (AT)19 | 108 | - | 001220 |
| TCCGGCACTGTAATGTGGTA |
| *obm24* | TCATGCCTCTTGGGTTTAGG | (ATAC)16 | 129 | 5 | 004927 |
| CTTGAAGCAAGCAATGGACA |
| *obm25* | CCAATTGGAACTCAACAAATG | (AT)11 | 88 | - | 006229 |
| AACTGAGTTAATGACTGTTGAGGA |
| *obm26* | TAGGCAGAGAGGACCTGCAT | (TAA)10 | 121 | -\* | 002485 |
| CCTGTTCTGATCTGCACTCAA |
| *obm27* | AGCAATAGCATCTTCAGTTTTGA | (GT)9 | 97 | 3 | 003803 |
| CATGTCCTTACATAGTCGCAGA |
| *obm28* | GGCGTGACTGCGGTAACTAT | (CA)9 | 78 | 3 | 004468 |
| CGAGTCGAAGAACTGGATCG |
| *obm29* | GAGGAGCCCAATGTGCTAGA | (CACT)9 | 105 | 7 | 005093 |
| AGGATACAGGGAGGATTCAGG |
| *obm30* | TGGAGAGAGAATTCCTCAATCTAAA | (AT)10 | 98 | - | 005649 |
| TTCAGGTCACAGGGAGAATCTT |

a Too complex patterns, irreproducible