**Table 4:** List of primers used in the PCR with their 5’-3’ sequence, repeat motif’s, chromosomal location and annealing temperature.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Primer** | **5’-3’ sequence of FWD/REV primer** | **SSR repeat motif** | **Chromosomal location** | **Annealing temperature** |
| RM5 | FWD: TGCAACTTCTAGCTGCTCGA | (GA)14 | 1 |  |
| REV: GCATCCGATCTTGATGGG | 55 |
| RM6 | FWD: TGCAACTTCTAGCTGCTCGA | (AG)16 | 2 |  |
| REV: TCGTCTACTGTTGGCTGCAC | 55 |
| RM11 | FWD: TCTCCTCTTCCCCCGATC | (GA)17 | 7 |  |
| REV: ATAGCGGGCGAGGCTTAG | 55 |
| RM14 | FWD: CCGAGGAGAGGAGTTCGAC | (GA)17 | 1 |  |
| REV: GTGCCAATTTCCTCGAAAAA | 55 |
| RM17 | FWD: TGCCCTGTTATTTTCTTCTCTC | (GA)21 | 12 |  |
| REV: GGTGATCCTTTCCCATTTCA | 55 |
| RM19 | FWD: CAAAAACAGAGCAGATGAC | (ATC)10 | 12 |  |
| REV: CTCAAGATGGACGCCAAGA | 55 |
| RM21 | FWD: ACAGTATTCCGTAGGCACGG | (GA)21 | 11 |  |
| REV: GCTCCATGAGGGTGGTAGAG | 55 |
| RM22 | FWD: GGTTTGGGAGCCCATAATCT | (GA)22 | 3 |  |
| REV: CTGGGCTTCTTTCACTCGTC | 55 |
| RM23 | FWD: CATTGGAGTGGAGGCTGG | (GA)15 | 1 |  |
| REV: GTCAGGCTTCTGCCATTCTC | 55 |
| RM24 | FWD: GAAGTGTGATCACTGTAACC | (GA)29 | 1 |  |
| REV: TACAGTGGACGGCGAAGTCG | 55 |
| RM25 | FWD: GGAAAGAATGATCCTTTTCATGG | (GA)18 | 8 |  |
| REV: CTACCATCAAAACCAATGTTC | 55 |
| RM26 | FWD: GAGTCGACGAGCGGCAGA | (GA)15 | 5 |  |
| REV: CTGCGAGCGACGGTAACA | 55 |
| RM29 | FWD: CAGGGACCCACCTGTCATAC | (GA)7-18(GA)5(AG)4 | 2 |  |
| REV: AACGTTGGTCATATCGGTGG | 55 |
| RM30 | FWD: GGTTAGGCATCGTCACGG | (AG)9A(AGA)12 | 6 |  |
| REV: TCACCTCACCACACGACACG | 55 |
| RM31 | FWD: GATCACGATCCACTGGAGCT | (GA)15 | 5 |  |
| REV: AAGTCCATTACTCTCCTCCC | 55 |
| RM42 | FWD: ATCCTACCGCTGACCATGAG | (AG)5(GA)(AG)2T(GA)A(AG)5 | 8 |  |
| REV: TTTGGTCTACGTGGCGTACA |  | 55 |
| RM44 | FWD: ACGGGCAATCCGAACAACC | (GA)16 | 8 |  |
| REV: TCGGGAAAACCTACCCTACC | 55 |
| RM49 | FWD: TTCGGAAGTTGGTTACTGATCA | (GA)27 | 3 |  |
| REV: TTGGAGCGGATTCGGAGG | 55 |
| RM50 | FWD: ACTGTACCGGTCGAAGACG | (CTAT)4(CT)15 | 6 |  |
| REV: AAATTCCACGTCAGCCTCC | 55 |
| RM55 | FWD: CCGTCGCCGTAGTAGAGAAG | (GA)17 | 3 |  |
| REV: TCCCGGTTATTTTAAGGCG | 55 |
| RM60 | FWD: AGTCCCATGTTCCACTTCCG | (AATT)5AATCT(AATT) | 3 |  |
| REV: ATGGCTACTGCCTGTACTAC | 55 |
| RM80 | FWD: TTGAAGGCGCTGAAGGAG | (TCT)25 | 8 |  |
| REV: CATCAACCTCGTCTTCACCG | 55 |
| RM84 | FWD: TAAGGGTCCATCCACAAGATG | (TCT)10 | 1 |  |
| REV: TTGCAAATGCAGCTAGAGTAC |  | 55 |
| RM105 | FWD: GTCGTCGACCCATCGGAGCCAC | (CCT)6 | 10 |  |
| REV: TGGTCGAGGTGGGGATCGGGTC |  |  | 55 |
| RM110 | FWD: TCGAAGCCATCCACCAACGAAG | (GA)15 | 2 |  |
| REV: TCCGTACGCCGACGAGGTCGAG | 55 |
| RM118 | FWD: CCAATCGGAGCCACCGGAGAGC | (GA)8 | 7 |  |
| REV: CACATCCTCCAGCGACGCCGAG | 67 |
| RM125 | FWD: ATCAGCAGCCATGGCAGCGACC | (GCT)8 | 7 | 55 |
| REV: AGGGGATCATGTGCCGAAGGCC |
| RM126 | FWD: CGCGTCCGCGATAAACACAGGG | (GA)7 | 8 |  |
| REV: TCGCACAGGTGAGGCCATGTCG |  |  | 55 |
| RM129 | FWD: TCTCTCCGGAGCCAAGGCGAGG |  |  |  |
| REV: CGAGCCACGACGCGATGTACCC | (CGG)8 | 1 | 55 |
| RM133 | FWD: TTGGATTGTTTTGCTGGCTCGC | (CT)8 | 6 |  |
| REV: GGAACACGGGGTCGGAAGCGAC | 60 |
| RM134 | FWD: ACAAGGCCGCGAGAGGATTCCG |  |  |  |
| REV: GCTCTCCGGTGGCTCCGATTGG | (CCA)7 | 7 | 55 |
| RM136 | FWD: GAGAGCTCAGCTGCTGCCTCTAGC | (AGG)7 | 6 |  |
| REV: GAGGAGCGCCACGGTGTACGCC |  |  | 55 |
| RM144 | FWD: TGCCCTGGCGCAAATTTGATCC | (ATT)11 | 11 |  |
| REV: GCTAGAGGAGATCAGATGGTAGTGCATG | 57 |
| RM152 | FWD: GAAACCACCACACCTCACCG | (GGC)10 | 8 |  |
| REV: CCGTAGACCTTCTTGAAGTAG | 55 |
| RM159 | FWD: GGGGCACTGGCAAGGGTGAAGG | (GA)19 | 8 |  |
| REV: GCTTGTGCTTCTCTCTCTCTCTCTCTCTC |  |  | 55 |
| RM161 | FWD: TGCAGATGAGAAGCGGCGCCTC | (AG)20 | 5 |  |
| REV: TGTGTCATCAGACGGCGCTCCG | 57 |
| RM162 | FWD: GCCAGCAAAACCAGGGATCCGG | (AC)20 | 6 |  |
| REV: CAAGGTCTTGTGCGGCTTGCGG | 61 |
| RM171 | FWD: AACGCGAGGACACGTACTTAC | (GATG)5 | 10 |  |
| REV: ACGAGATACGTACGCCTTTG | 55 |
| RM184 | FWD: ATCCCATTCGCCAAAACCGGCC | (CA)7 | 10 | 55 |
| REV: TGACACTTGGAGAGCGGTGTGG |
| RM205 | FWD: CTGGTTCTGTATGGGAGCAG | (GA)25 | 9 |  |
| REV: CTGGCCCTTCACGTTTCAGTG | 55 |
| RM207 | FWD: CCATTCGTGAGAAGATCTGA | (CT)25 | 2 |  |
| REV: CACCTCATCCTCGTAACGCC | 55 |
| RM209 | FWD: ATATGAGTTGCTGTCGTGCG | (CT)18 | 11 |  |
| REV: CAACTTGCATCCTCCCCTCC | 55 |
| RM212 | FWD: CCACTTTCAGCTACTACCAG | (GA)24 | 1 |  |
| REV: CACCCATTTGTCTCTCATTATG | 55 |
| RM213 | FWD: ATCTGTTTGCAGGGGACAAG | (CT)17 | 2 | 55 |
| REV: AGGTCTAGACGATGTCGTGA |  |
| RM215 | FWD: CAAAATGGAGCAGCAAGAGC | (GA)16 | 9 |  |
| REV: TGAGCACCTCCTTCTCTGTAG | 55 |
| RM219 | FWD: CGTCGGATGATGTAAAGCCT | (GA)17 | 9 |  |
| REV: CATATCGGCATTCGCCTG | 55 |
| RM220 | FWD: GGAAGGTAACTGTTTCCAAC | (CT)17 | 1 |  |
| REV: GAAATGCTTCCCACATGTCT | 55 |
| RM224 | FWD: ATCGATCGATCTTCACGAGG | (AAG)8(AG)13G(AG) | 11 |  |
| REV: TGCTATAAAAGGCATTCGGG | 55 |
| RM225 | FWD: TGCCCATATGGTCTGGATG | (CT)18 | 6 |  |
| REV: GAAAGTGGATCAGGAAGGC | 55 |
| RM333 | FWD: GTACGACTACGAGTGTCACCAA | (TAT)19(CTT)19 | 10 | 55 |
| REV: GTCTTCGCGATCACTCGC |  |  |  |
| RM337 | FWD: GTAGGAAAGGAAGGGCAGAG | CTT64 8 (CTT)4-19-(CTT)8 | 8 | 55 |
| REV: CGATAGATAGCTAGATGTGGCC |  |  |  |
| RM153 | FWD: GCCTCGAGCATCATCATCAG | (GAA)9 | 5 | 55 |
| REV: ATCAACCTGCACTTGCCTGG |  |  |  |
| RM154 | FWD: ACCCTCTCCGCCTCGCCTCCTC | (GA)21 | 2 | 61 |
| REV: CTCCTCCTCCTGCGACCGCTCC |  |  |  |
| RM164 | FWD: TCTTGCCCGTCACTGCAGATATCC | (GT)16TT(GT)4 | 6 | 55 |
| REV: GCAGCCCTAATGCTACAATTCTTC |  |  |  |
| RM180 | FWD: CTACATCGGCTTAGGTGTAGCAACACG | (ATT)10 | 7 | 55 |
| REV: ACTTGCTCTACTTGTGGTGAGGGACTG |  |  |  |
| RM206 | FWD: TAGTTTAACCAAGACTCTC | (GA)19 | 2 | 55 |
| REV: GGTTGAACCCAAATCTGCA |  |  |  |
| RM307 | FWD: GTACTACCGACCTACCGTTCAC | (AT)14(GT)21 | 4 | 55 |
| REV: CTGCTATGCATGAACTGCTC |  |  |  |
| RM322 | FWD: CAAGCGAAAATCCCAGCAG | (CAT)7 | 2 | 55 |
| REV: GATGAAACTGGCATTGCCTG |  |  |  |
| RM1 | FWD: GCGAAAACACAATGCAAAAA | (GA)26 | 1 | 55 |
| REV: GCGTTGGTTGGACCTGAC |  |  |  |
| RM211 | FWD: CCGATCTCATCAACCAACTG | (TC)3A(TC)18 | 2 | 55 |
| REV: CTTCACGAGGATCTCAAAGG |  |  |  |
| RM251 | FWD: GAATGGCAATGGCGCTAG | (CT)29 | 3 | 55 |
| REV: ATGCGGTTCAAGATTCGATC |  |  |  |
| RM263 | FWD: CCCAGGCTAGCTCATGAACC | (CT)34 | 2 | 55 |
| REV: GCTACGTTTGAGCTACCACG |  |  |  |
| RM167 | FWD: GATCCAGCGTGAGGAACACGT | GGAA(GA)16GGGG | 11 | 55 |
| REV: AGTCCGACCACAAGGTGCGTTGTC |  |  |  |
| RM216 | FWD: TTCCCCAATGGAACAGTGAC | (CT)18 | 10 | 55 |
| REV: AGGGTCTACCACCCGATCTC |  |  |  |
| RM475 | FWD: CCTCACGATTTTCCTCCAAC | (TATC)8 |  |  |
| REV: ACGGTGGGATTAGACTGTGC |  | 2 | 55 |
| RM6344 | FWD: ACACGCCATGGATGATGAC | (GAA)8 | 7 | 55 |
| REV: TGGCATCATCACTTCCTCAC |  |  |  |
| RM335 | FWD: GTACACACCCACATCGAGAAG | (CTT)25 | 4 | 55 |
| REV: GCTCTATGCGAGTATCCATGG |  |  |  |