Table S6 Sequences of 103 polymorphic SSR markers used for genetic diversity analysis

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| NO | SSR name | SSR | FORWARD PRIMER1 (5'-3') | Tm | REVERSE PRIMER1 (5'-3') | Tm |
| 1 | T\_DN32469 | (TAA)8 | ACGGTTCCTTCTGGTTGTTG | 60  | TTTTTCGTAACGCCATCACA | 60  |
| 2 | T\_DN24459 | (CTC)5 | CCGCCATTCGGTGTATTTAG | 60  | GCCAAAAACTGCAACCATTT | 60  |
| 3 | T\_DN27482 | (GAA)5 | CAGCTCTCAAACCGTTCTCC | 60  | TTCCCAAACACTTCACTCCC | 60  |
| 4 | T\_DN22376 | (TA)8 | TGATTCCCACACAAACACTTG | 59  | AACGGTTGTCGAGGTTTCAC | 60  |
| 5 | T\_DN29279 | (TGA)5 | CCCTAGTTCACCACCAGGAA | 60  | GTGGCTTTGTACTTGGGGAA | 60  |
| 6 | T\_DN1835 | (GA)7 | TACCTGGGCTTGGCTTTATG | 60  | TTCTGTTAATGTTAGAATATGGACCC | 59  |
| 7 | T\_DN33317 | (TC)8 | GATCATGCAAAAAGCAAGCA | 60  | GAGAAAGTGGGTAGCTGGGA | 59  |
| 8 | T\_DN24385 | (GTT)6 | TAGCAGCGGAGGAGTAGGAA | 60  | AGAAAAGCACCTCTACCGCA | 60  |
| 9 | T\_DN26689 | (ACA)5 | AACACAACCACAAACCAGCA | 60  | TACCCCAGTCATTGCAACTT | 58  |
| 10 | T\_DN23895 | (TGA)6 | GCATCCTCTTCAACCAAAGC | 60  | TTGTCCAATCAATAACCGCA | 60  |
| 11 | T\_DN31712 | (CAT)5 | TTCACCTCCAATCTCCATCA | 59  | TGCTTTGATGGCATTTCAAC | 60  |
| 12 | T\_DN20824 | (GCG)5 | CCGTAGTTGACGCCGATATT | 60  | CTTCTATCAAATTCCCCGCA | 60  |
| 13 | T\_DN28915 | (CAT)7 | TGAAAACTCTTCCTCTCGGC | 60  | TGTGATGTTGATCATTGCCC | 60  |
| 14 | T\_DN32959 | (AG)7 | CTCGTTTTCTCCGATCCAAC | 60  | TTTGAGAAATACAAAATCAGTTGC | 58  |
| 15 | T\_DN24924 | (CT)10 | TCATGACAGTAACAACTGTAAAGAAGA | 59  | TGAAGTGAGAGAGTCGAGGGA | 60  |
| 16 | T\_DN27054 | (TTG)6 | TCATCCCTTGTCTCTCACCA | 59  | TCCATGGAAAACCAAAACAA | 59  |
| 17 | T\_DN27054 | (TTG)8 | TTTTGGTTTTCCATGGAGTTG | 60  | ACCCAAATGAAATCAGTGGC | 60  |
| 18 | T\_DN32461 | (AGA)5 | AAGACCATGAAGGCATGAGG | 60  | TCATCAATGGCTTCCACAAA | 60  |
| 19 | T\_DN32430 | (AAC)5 | AATCGGTGAAAACGAAAACG | 60  | AAAAGCCGGCACTATCACAG | 60  |
| 20 | T\_DN32302 | (AG)10 | GAGAGATTTTGCTTCCGTCG | 60  | TAACAAACTCGAGGCAGGCT | 60  |
| 21 | T\_DN23241 | (AG)21 | GCAACTTGTTCAGCGTTTGA | 60  | CCGAAGTAAAAGAGATTGAGCC | 59  |
| 22 | T\_DN29012 | (GAG)5 | TGTGAAGTCCGTGACACCAT | 60  | CTTTCCATCGCTTCACCTGT | 60  |
| 23 | T\_DN20702 | (AT)14 | TCATTTCAACGTACCAATGGAT | 59  | ATTTGGAGGGTTTTTGGGAC | 60  |
| 24 | T\_DN31208 | (TGA)5 | AGTTCCCTCTTTGGTCCCAT | 60  | GAGAGTGAAGGCGTGTGTTG | 59  |
| 25 | T\_DN24534 | (TG)10 | TGCACAGTCAAAGCATGTCA | 60  | AATCACAAGTGTCGGTGCAG | 60  |
| 26 | T\_DN7799 | (AC)6 | CCATCAACAACCTCACATGC | 60  | AGGCTCTGATACCACGCTGT | 60  |
| 27 | T\_DN20827 | (AAC)5 | CATCCAAACCATACCCAATCA | 60  | TGAAGTTAGCAATGGGGCTC | 60  |
| 28 | T\_DN23877 | (GAA)5 | GCGGAGGTTGAAATTTGTGT | 60  | CCCTCACTTTCCCATCCTTT | 60  |
| 29 | T\_DN27103 | (AG)11 | TGTTGCCAGATGAGACAAGG | 60  | CCTCTCTGCAAGCTGCTTTT | 60  |
| 30 | T\_DN19607 | (AG)6 | GAAAGGGACAACAAGAGAAGTCA | 60  | GATTGTGAATTGGGTGCTCA | 60  |
| 31 | T\_DN26771 | (ATC)6 | TTGAGACACTTCAGCTAGTATCACG | 60  | GAACCGACAATTGATCAGGAA | 60  |
| 32 | T\_DN27978 | (CCG)5 | CTCCCAACTTGCAAATCCTC | 60  | TAATAGCTGCCATGAGCGAA | 60  |
| 33 | T\_DN25216 | (AAC)5 | TGAAAGCAATTGCGTACGAG | 60  | TCACCATCTTCCGCAATACA | 60  |
| 34 | T\_DN30193 | (TCT)7 | ACTCCCCTTGCTCCTCATCT | 60  | CTCGAGCCACAACAACTCAA | 60  |
| 35 | T\_DN9246 | (GTT)6 | GCTAGTGGACCTCCCATTGA | 60  | TCCAATGCAAACTCTCCAAA | 59  |
| 36 | T\_DN19478 | (A)10 | GCAAACGAAGATAAACCACAAA | 59  | TTTGTGAAAGTGTGGGTGTGA | 60  |
| 37 | T\_DN34083 | (TTA)6 | ATCGTCGTCGTTTCTACGCT | 60  | TAGAATTTCCGAAAATGGCG | 60  |
| 38 | T\_DN9805 | (GT)7 | GCCTCGTTCTCGTATGTTTCA | 60  | GTCACCACAGTCCTAGGGGA | 60  |
| 39 | T\_DN30600 | (AC)9 | AGCCAATTTGACCCATCATT | 59  | TCCTCCCTTAGTGGCTCTTG | 59  |
| 40 | T\_DN9218 | (AC)6 | CCAGAAAACATCCTCAACCA | 59  | CCGAACCTAAGCCACGTTAC | 60  |
| 41 | T\_DN23793 | (TTG)5 | TGATCGGCTTTGACACAGAG | 60  | GGGCTTGCTTCCTAAAGAGG | 60  |
| 42 | T\_DN23793 | (GTC)5 | AACGCGTGATGCTTCTTCTT | 60  | TCCCACATTGCACTTCAAAA | 60  |
| 43 | T\_DN30269 | (TTG)7 | GGTTCGGAGTTAGGTGTGGA | 60  | AGCCATTCCATTCCCTCTTT | 60  |
| 44 | T\_DN26655 | (AG)6 | GGCTTGTACCGATCGTGTTT | 60  | CCCTTCCCTCAACCTCATTC | 61  |
| 45 | T\_DN18457 | (T)10 | TGGCAATGGAAAGTGAAAGA | 59  | TCCAAGGGTGGAAGTTTTTCT | 60  |
| 46 | T\_DN26075 | (ATC)7 | TTCACACACCCAACAAACAAA | 60  | GAATGGTGGTGGAGGAAGAA | 60  |
| 47 | T\_DN27071 | (CAA)6 | GATTCTCGCAGTTTCGGTTC | 60  | TGGGGTTGTTGTGTTGTTGT | 60  |
| 48 | T\_DN29286 | (A)10 | CGGGATAATTAGCACAAGCAA | 60  | AGGGGCCTCTCTATCCCATA | 60  |
| 49 | T\_DN32727 | (CATTA)5 | TGCCAAATTAACCTCATTCCTT | 60  | ATACGTGTGTGCCTGCAGAT | 59  |
| 50 | T\_DN29213 | (AAC)5 | TCATGATCGTGCCTTAGCAG | 60  | TTTGATCAATGTAGTAGCCGATTC | 60  |
| 51 | T\_DN33153 | (CT)7 | TCAAGGCTCTCTGCCATTTT | 60  | ATGCATCCGGTTATGGTGAT | 60  |
| 52 | T\_DN32381 | (TC)18 | TGAGGGACCATGGCAGTTAT | 60  | GCCACCACTGTGGAGTTCAT | 61  |
| 53 | T\_DN33688 | (CT)15 | GTTTCCCAACCCTCAATCAA | 60  | CCTTGGTGCATAATAGGGGA | 60  |
| 54 | T\_DN24007 | (AG)9 | ACCCATGACGGTGAATTGAT | 60  | AATCGAGCCAAAATAGCACG | 60  |
| 55 | T\_DN25422 | (CT)6 | GCCAACTCATACGACCGATT | 60  | TCTTGGTGATTCCTCTGCAA | 59  |
| 56 | T\_DN34120 | (GAA)6 | AAAGAAGCATGAAACTGGGG | 59  | CCTTGGCAAGCTGAAAGAAG | 60  |
| 57 | T\_DN29810 | (GTG)5 | GTGACTTGAGCGAATGCAAA | 60  | TGTTAACCTCAATGCCACCA | 60  |
| 58 | T\_DN30324 | (TC)7 | TTGGGGATGACAGTTTGAAT | 58  | GTTGCAGCGATGAAACAGAA | 60  |
| 59 | T\_DN26787 | (CCA)5 | CATAACCTTCACCATCGCCT | 60  | TTCATCGTCACCTAACAGCG | 60  |
| 60 | T\_DN32610 | (TGG)5 | AGCTTTCAGGGGGTTTGTTT | 60  | GGCACAACCTTGTAATGCCT | 60  |
| 61 | T\_DN16768 | (AT)6 | GTCTCAGGGAATTGATCGGA | 60  | TTATTACCTTCGAAAGCACGC | 59  |
| 62 | T\_DN26565 | (A)13 | AAGCTTAGAAGAAATTCAGCAAAAA | 59  | TCCACCACTACCAAACCCTC | 60  |
| 63 | T\_DN31063 | (AT)9 | TCCATCAAACTTGTGCATGA | 59  | TTCAGGCAAGTTAAGATTCTTGG | 60  |
| 64 | T\_DN22109 | (A)11 | CCATAGAAGAAACTAATTTGCCC | 58  | AGTTCGCGATACATCCCAAG | 60  |
| 65 | T\_DN28291 | (TC)6 | CATTGTGCATGTGCAGTAACA | 59  | TCTGAATCGCAAACAAGCTC | 59  |
| 66 | T\_DN23988 | (TTTC)6 | AAGGGGAAAAGGAAGGTGTG | 60  | CCTTAGGCATCACAGCACAA | 60  |
| 67 | T\_DN24104 | (CT)7 | AAGCACCCTTATTCCATCAAA | 59  | GTTGGATCCGGGTTTTCTCT | 60  |
| 68 | T\_DN29493 | (A)10 | TCGTGTTCATTCTGCCTGAG | 60  | TACTGCGCACATCCTAGTGG | 60  |
| 69 | T\_DN25939 | (AG)8 | TGTTTGGAAAAAGAAGGCACA | 61  | CCAAAACAAAAACCATTCCG | 60  |
| 70 | T\_DN34009 | (GATT)6 | GGAATTGAAGCCCTAAACCC | 60  | ACTTGAACCCCCTTTTTGCT | 60  |
| 71 | T\_DN25127 | (GA)9 | CCGCATTGAAGTTTTTAGCC | 60  | CATTCACCCCACGTTTCTCT | 60  |
| 72 | T\_DN33367 | (TG)6 | CTGGTCGTCTGAGTAAGGGG | 60  | CCACACCCAACCAAAATCTC | 60  |
| 73 | T\_DN28175 | (TTG)5 | ATGATGGTGGTGGTGAGGTT | 60  | ATATCAACCCGATCCTTCCC | 60  |
| 74 | T\_DN26387 | (ATC)5 | AAAAATCCCCCTGCATCTTC | 60  | AGGTGTTGCTCTGAATTGGC | 60  |
| 75 | T\_DN25712 | (CTT)5 | TGGTCATCTTCTTCAGCGTG | 60  | AAGAAGAAAAAGAAGCCCGC | 60  |
| 76 | T\_DN29236 | (A)11 | AAATTAGCATATGGAGCATAGTGAA | 58  | GCATTGATGCAAAAGGGAGT | 60  |
| 77 | T\_DN30971 | (GA)9 | TGTTGACGGTGGATGGAGTA | 60  | TGGATTCTCAACGTGACTCG | 60  |
| 78 | T\_DN28375 | (GA)8 | ACGCAAAGAAAGAACCGAGA | 60  | TTTCCACCACTCTCCTCCAC | 60  |
| 79 | T\_DN23472 | (AG)8 | GGTTTTTGTTTTGCTGCGAT | 60  | ACCAACGAATCATTCTGCAA | 59  |
| 80 | T\_DN28326 | (AG)6 | CTTGCGCATGTTGAAGAAAA | 60  | TGCAGCCACAATTCAACACT | 60  |
| 81 | T\_DN24259 | (A)10 | AGCCCCTCCTTTTCCAAATA | 60  | TGGTCTCAAATGTGGTGGAA | 60  |
| 82 | T\_DN30467 | (TC)10 | CACCACCAACTGCACCTTC | 60  | TCTCGCTTACGATTCTGGTG | 59  |
| 83 | T\_DN30467 | (AGA)5 | CACTGCAACCTTCACCTTCA | 60  | TGCTCAGGTTCGCCTTATCT | 60  |
| 84 | T\_DN12372 | (T)10 | AGGCATCAAAGAGGAACTGC | 59  | GCACATGGGTTAGCAGGATT | 60  |
| 85 | T\_DN25819 | (ATG)5 | GTTGTAAGGTCAGGGGCTCA | 60  | AAGGTTTTTGCAACACTTCCA | 60  |
| 86 | T\_DN28542 | (A)11 | TGGATTCCATCATATTCCGC | 61  | TGACTATGGGTGTGGGAAAA | 59  |
| 87 | T\_DN17703 | (AG)7 | TTGGAAGGAAGTGAACCACC | 60  | TTGTTCAGGTGATGCAAGAGA | 59  |
| 88 | T\_DN24002 | (TC)12 | CCCTCTCTCTTTTGCTTTCG | 59  | GAGACTGAGCGAGCCATACC | 60  |
| 89 | T\_DN30331 | (GAA)5 | CTAAGGCAAGAGCAACGGTC | 60  | CCCAAAGACAATCCAGTCCT | 59  |
| 90 | T\_DN23145 | (GAA)5 | CCCGAAAAATTTCGAGAAGA | 59  | TGACGGATCTAGGGTTCCAG | 60  |
| 91 | T\_DN33887 | (CAA)6 | CGAACAGTACCGGAACAAAAA | 60  | CACCACCATCCTTGCTCTTT | 60  |
| 92 | T\_DN25920 | (A)11 | GCCTACTTCTGAAGGCATGG | 60  | GGGCTTCCTCCTCAGTTTTC | 60  |
| 93 | T\_DN30840 | (TGT)6 | AGTGTGAGGGTGGTGGTAGC | 60  | GCCAAGTGGTGAACAAGGTT | 60  |
| 94 | T\_DN24924 | (AG)8 | GCAGCAAGAACGACCATTTT | 60  | ATGCATGAGTTTGTTTTGCG | 60  |
| 95 | T\_DN20915 | (TCA)5 | TCAGTTGGAGGCATAGGAGG | 60  | TCAAACTTCATGGCTTTCCC | 60  |
| 96 | T\_DN29632 | (T)11 | GTCGATGTTTCTTTTGCAGC | 59  | TTTGAATTCCTTTTCTTTTGTTTG | 59  |
| 97 | T\_DN15279 | (AT)8 | TCCGCCATGAATAATTTGGT | 60  | GCGAGCTAACGCTCAGAATC | 60  |
| 98 | T\_DN31937 | (CT)9 | AGATCAAGAACTCACCGCAAA | 60  | GATTCGCTGATGAAGGTGGT | 60  |
| 99 | T\_DN22251 | (A)10 | CATGTCAATCCACAATCTCTTCA | 60  | GTGTCATTGAGTGTCGGTGC | 60  |
| 100 | T\_DN32482 | (ACA)5 | TCCCCCAAAGCAATCAATAG | 60  | TTGTCCGGAGAGTTGTTTTTG | 60  |
| 101 | T\_DN32707 | (ACA)6 | GTGAGAATGGGGGATGAAAA | 60  | ATCGCCGGCTTAGTATGAAA | 60  |
| 102 | T\_DN34099 | (A)12 | TGTGAAAATAGGGGCCTCAG | 60  | AAGAGGCAACCCTAATCCGT | 60  |
| 103 | T\_DN29047 | (ATA)5 | TTTGCACCACTTTTATGCCA | 60  | AGAAGGAAAACCTGGACGGT | 60  |