

Supplementary Materials: Assessing the Genetic Diversity and Genealogical Reconstruction of Cypress (*Cupressus funebris* Endl.) Breeding Parents Using SSR Markers

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Table S1. Nucleotide sequences of the 17 primer pairs used in this study.

| Locus | Motif | Allele Size (bp) | Forward Primer Sequence 5'-3' | Reverse Primer Sequence 5'-3' |
|---------------------|---|------------------|-------------------------------|-------------------------------|
| Cf01 ^a | (TG) ₂₀ -(TA) ₆ | 98–132 | ACACCCCTAATTTAACTAACA | AGAGTAGTCCACCCAATGTAT |
| Cf02 ^a | (GT) ₇ | 110–154 | ATGTTCTTGTTTTGGTCA | CACGATGTTGATGGAGATA |
| Cf03 ^a | (CA) ₇ | 118–136 | CTTCTCATCCTTCTACTCAA | ATTGGCCCAACCTAATAGTG |
| Cf04 ^a | (TC) ₁₃ -(CA) ₁₆ | 126–188 | GATGTAAACTCGGAACAAC | TGAGAATTCACCAAAGCAC |
| Cf09 ^a | (AC) ₁₄ GTG(CA) ₈ (AC) ₆ | 140–152 | CACATCACATAGTTTAGTTGTT | GTTGTAACCTGTATTGTGGTCA |
| Cf11 ^a | (CT) ₂₁ -(TG) ₄ | 116–158 | AATAGAACCACCTTAGAAGC | TGTTGAGAGAGACACACAC |
| Cf12 ^a | (GT) ₂₉ | 102–146 | ATTGGTCAAAATAAGGTGTG | ACCTCTCTGTCACTAAATGT |
| Cuc1 ^b | (CA) ₁₈ | 113–153 | CGTTCTCATCCTCGTCTCTGATCTC | CATGCTGGGATGAAATATGTAAACA |
| Cuc2 ^b | (CA) ₂₇ -(CA) ₆ | 152–178 | CGCTATCATCCTCATCTCTGATCTC | CCATGCTGGGATGAAATATGTAAAC |
| Cuc3 ^b | (AC) ₄ -(GT) ₉ | 150–180 | CGTTCTCATCCTCGTCTCTGATCTC | CATGCTGGGATGAAATATGTAAACA |
| Cuc4 ^b | (AT) ₄ -(GT) ₉ | 118–131 | CATTCAAGGTGATCAAGTCATCCTGG | CCTGAATGAATGCCATTGCCGTC |
| Cuc6 ^b | (TG) ₁₇ -(GC) ₄ | 79–95 | GAACATGGGTCCATATCAAGTAG | CACCCACACACCCACAC |
| Cuc7 ^b | (TG) ₂₅ | 109–228 | ACTATGGAGCACGCAAAATGCCAAG | TAGTTCCTGCTCTGCTTATCGTC |
| Cuc8 ^b | (TG) ₁₉ | 110–188 | AACACGGAAGCAAGAAAAAATGAAG | CACACATTCCACCTCCACACCACT |
| Cyp52 ^b | (GT) ₂₁ | 121–187 | CATCCACTGCCAATACTTTT | AGCATCTTCCCATTACTTGA |
| Cyp84 ^b | (GT) ₁₃ (TC) ₂₃ | 188–266 | CATTTCAATTTGCATAAGTTCT | GCAATGGGATGACTACAAAA |
| Cyp101 ^c | (GT) ₁₂ | 175–209 | AGGCCACACTCAAACCTTATG | ATGACAATGGGTGAAGTCAT |

^a [20], ^b [21], ^c [22].

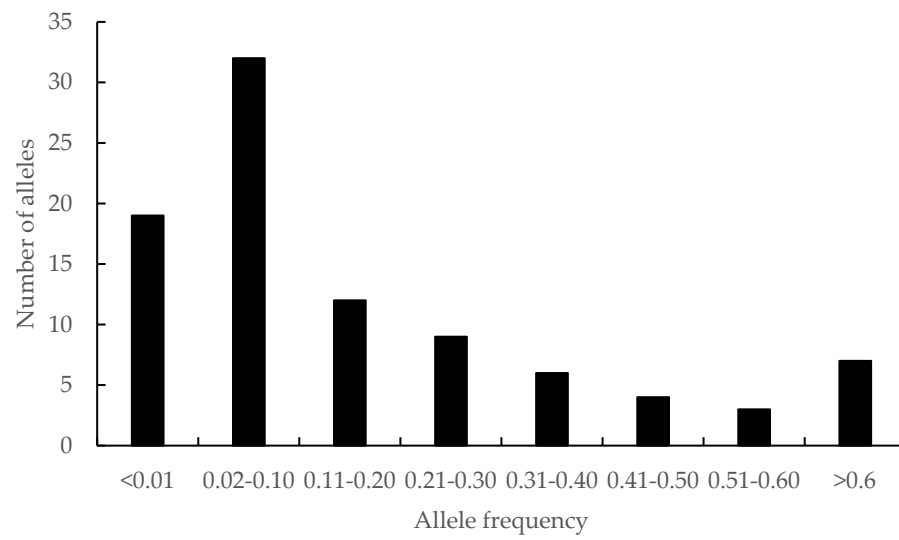


Figure S1. Histogram of allele frequency distribution.