**Table S3.** **Flanking sequences of targeted SNPs in eastern white pine**. The two alleles at each focal SNP are located between parentheses.

|  |  |
| --- | --- |
| **SNP** | **Flanking sequence** |
| RPSS03\_05 | TCAGGGGAGTACCACATGGGAAACCCGGACGCTGGAGTACTGAAATGATGTCAGCTACCC**[T/G]**GTGAAATGAATGGTCAGTATGTTGTCTCCATTCCTTCCTCGAGTCTTTTAGAACGTCGTG |
| RPSS04\_02 | GGTGTTTGCATGGGTTTGCCTTGGTATCGCGTTCATACCGTCGTATTGAATGATCCTGGC**[C/G]**GATTAATTTCTGTACATATAATGCATACAGCTCTAGTTGCTGGTTGGGCCGGTTCAATGA |
| RPSS04\_03 | CGTGCGTTTTACAACGTCGTGGAGTACATAGGGACTCGGGATAGACTCCATGAATGCAAT**[A/G]**ATGACTCAACTTGGATGCTCTAAACAAGGGTGACTCGATGGTGCTGCCACACATCAAAGG |
| RPSS05\_01 | GATTCCGGCAGGGATGATCACGAGATCCATTCCCACCAACG**[T/C]**TGCTTCCAGCTGCCTCTTTGCCCACAAATCCACGCACACTAGAAAACACA |
| RPSS05\_04 | CCACAAATCCACGCACACTAAAAAACACAAAAATCGTTCCGATTAAGACCTAAAATGAA**[A/G]**CAAATAAAAAAGCCCCATTTTTCAAAATTGTACATACAACGGTGGTGGTGTCCATATGGC |
| RPSS05\_05 | ATGAAACAAATAAGAAAGCCCCATTTTTCAAAATTGTACATACAACGGTGGTGGTGTCC**[A/T]**TATGGCTGATATCTGCAGTGACGCCGAGGGTATTGACAACATCATAGAGGTGAAGGAATG |
| RPSS06\_03 | ATCGCCAATCACCTTCTCTCGTCGTTTTACAACGTCGTGACAAAACTTGCGAGTTCGATA**[A/T]**CGTCATAGGCAATCACCTTCTCTCGTCTTTTTAGAACGACATGATTTTCCAACACAAATA |
| RPSS08\_01 | ACCGTCGTATTGAATGATCCTGGCCGATTAATTTCTGTACATATAATGCATACAGCTCTA**[T/G]**TTGCTGGTTGGGCCGGTTCAATGACTCTGTATGAATTAACAGTTTTTGATCCATCCGACC |
| RPSS08\_03 | GATTAATTTCTGTACATATAATGCAGACAGCTCTAGTTGCTGGTTGGGCCGGTTCAATGAA**[A/T]**CTGTATGAATTAACAGTTTTTGATCCATCCGACCCTGTTCTTGATCCAATGTGGAGACAA |
| RPSS12\_01 | GCTAATTTCATAAATTGAACCTTATCTCAAATTGATCCGTATTCCCATCTTGCACCAC**[C/A]**AGAGATATCCCTTTATCTCCTCCCTATTGAAATAACATTCCCTTCAGATAAGTTAAGTAT |
| RPSS12\_03 | CTTTATCTCCTCCCTATTGAAATAACATTCCCTTCAGATAAGTTAAGTATGGAGAAATTA**[A/T]**GAGAAAAAAAAAAACAAAAATTCCATTGTATTTACCCTTTACAAAAGAAAAAGGGGAAGA |
| RPSS14\_03 | CATTTCTCCCAGTTTGAATGGTTAGTGTGTCTATGGCCATACCTTCAAGGTTTCTAACTG**[C/T]**TATTCTACCTTCACTTGGCCAAGAGACAGGAAGTCTGCTGCTTTCTATAATTGCCGGAGG |
| RPSS14\_06 | AATAAAGTCGGAGAGATTGCATTGCCATTGCACCAAAAATACTTGACAAGATGTAAGTGA**[A/G]**AGTGCATAAGAAAGAGCAAGACCCGCAAATGTCGTTTTACAAACGTCGTGAGATCTCATC |
| RPSS16\_01 | GGGTTGCTTAGCGGCACTTGGTGTCATATTAAAGTTGTCACCAGCTTTATTGGGTCTGAC**[A/G]**GTATTGGCTTGGGGAAATTCCATTGGGGATCTAGTTGCAGATGTTGCAGTTGCAAAAGCT |
| RPSS16\_03 | TGGTTTTCTGTTTTTGAGCTTACTTGGCTCATTATTTGTGATAACATGGTCAAGATTTCA**[C/G]**GTTCCTCGATTCTGGGGATTTTTCCTTATTGGTCGTTTTACAACGTCGTG |
| RPSS19\_02 | AGTTACATAGTGTCTACTTTTTCCGATAAAGGGGTGTTTGCATGGGTTTGCCTTGGTATC**[T/G]**CGTTCATACCGTCGTATTGAATGATCCTGGCCGATTAATTTCTGTACATATAATGCATAC |
| RPSS19\_03 | CATATAATGCATACAGCTCTAGTTGCTGGTTGGGCCGGTTCAATGACTCTGTATGAATTA**[A/G]**CAGTTTTTGATCCATCCGACCCTGTTCTTGATCCAATGTGGAGACAAGGTATGTTCGTTA |
| RPSS19\_04 | TGACTCTGTATGAATTAGCAGTTTTTGATCCATCCGACCCTGTTCTTGATCCAATGTGGA**[T/G]**ACAAGGTATGTTCGTTATACCCTTTATGACTCGTTTGGGAATAAAGGGTCGTTTTACAAC |
| RPSS19\_06 | ACATATAATGCATACAGCTCTAGTTGCTGGTTGGGCCGGTTCAATGACTCTGTATGAAT**[T/G]**AGCAGTTTTTGATCCATCCGACCCTGTTCTTGATCCAATGTGGAGACAAGGTATGTTCGT |
| RPSS28\_04 | GATTGCTTGTCTTTGTGTTTGATACCCATCAAGAATAGTCAGCAGTGTGGTGGTTGTGAA**[T/C]**TGTGTGTGAAGATAGATTTATTAATGATGCAATTGATGCTGTTACTGTTGTTCCGTTTCA |
| RPSS28\_06 | TAAGGTTAGACAAACAGAGTTGGAATGATTGCTTGTCTTTGTGTTTGATACCCATCAAGA**[A/G]**TAGTCAGCAGTGTGGTGGTTGTGAACTGTGTGTGAAGATAGATTTATTAATGATGCAATT |
| RPSS30\_01 | CTTTACCGTGAAGGCGGAGGGCACGAACAAGAACCTTCCACCGGACTTCCAGAAGACGAA**[C/G]**CTCATGACACGGCTGACCTACACGCTGGACGAGATCCGCCCGCTGGAAGTCTCTTCGGAT |
| RPSS30\_02 | GCTGGAAGTCTCTTCGGATGGCAAGCTCATGTTTGAAGAGAAGGATGACATCGACTACGC**[C/G]**GCGGTCACTGTTCATCTGCCCAAAGGTGAGCGCCTGCCCTTCCTGTTCACCGTCAGTCGT |
| RPSS31\_01 | AGGCGGAGGGCACGAACAAGAACCTTCCACCGGACTTCCAGAAGACGAAGCTCATGACAC**[T/G]**GCTGACCTACACACTGGACGAGATCGGCCCGCTGGAAGTCTCTTCGGATGGCAAGCTCAT |
| RPSS31\_02 | AACAAGAACCTTCCACCGGACTTCCAGAAGACGAAGCTCATGACACGGCTGACCTACACA**[T/C]**TGGACGAGATCGGCCCGCTGGAAGTCTCTTCGGATGGCAAGCTCATGTTTGAGGAGAAGG |
| RPSS32\_03 | GTTGGTCCTGATGCTAGACCATCCATGGGTGAGAGAAGATGGTGAGGCACCAGACAAACC**[A/T]**CTTGACAGTGCTGTATTAGTTAGGATGAAGCAATTCAGGGCAATGAACAAGCTTAAAAAA |
| RPSS33\_01 | TGCACGATACGCCAAACATTCTGTTCGCAATTTCAAAAGTCGTTTTACAACGTCGTGACA**[A/G]**TGGAAGAGATCTTATGGGTGAAAGAAAAACTGGCGGAAGCCAAACAGCAACTACGTAACG |
| RPSS36\_05 | TATCTGCCTGCAAGCGTGGCCTGGCGGCAGAAAGAGCAGTTCTCCGATGGCGTCGGTTAC**[A/T]**GTTGGATCGGAGGAGATTTGGTCGTTTTACAACGTCGTGATAATATGAACACACTAAGAT |
| RPSS47\_04 | CTGATATGACAGATGAACCCTGTACATGAGCTTACACTGAGTTGATTGAACGGAACCTTA**[T/C]**AATAAATGAGGTATTGGTAATGTGACTTTCAAATTATCTTTGGCAGAGATGAATTTTGCA |
| RPSS61\_02 | GAGTTGACAGTCTCATCATATCAATGTCAGAGACCGGAATTTTGCTGAATTGTTGTTTCA**[A/T]**AACTTCATTTGTGTCAGACTGAACATTCAATCTTTCTTTGTACTCTTGCATTTCCTTTTT |
| RPSS61\_03 | TGTCAGAGACCGGAATTTTGCTGAATTGTTGTTTCAAAACTTCATTTGTGTCAGACTGAA**[A/C]**ATTCAATCTTTCTTTGTACTCTTGCATTTCCTTTTTGTACCTTTCCTTGTCCTTCAATCC |
| RPSS61\_05 | AATCCAAAATCTTGATAAACCTGCAATCATAAGGCAAAATCCTCAGCTATGTCCTGGAGC**[T/C]**CGCTAATGCATGAAACTATGTCCTATGTGCCCGCTACATGCAGGTTGTCATAGTACAAAA |
| RPSS61\_06 | TACATGCAGGTTGTCATAGTACAAAAGAATTTTGTCTAAGCTTCATTTGAAAGAATCCTA**[T/G]**AGACACCATATGCACATCAGACCAATATCTTACCCCTCTTTCCTCTTCACTGAGTTTATT |
| RPSS62\_01 | CTCTGAGGAACGGCCTGAGAACAGGAATGAAGTCACCATAGTTATACTCGAAGCTCTGAG**[A/C]**CAGGCGGCTCCTCTCGCCATTGAGTGCCTTGAGGCGGAGGAAGAGCGGGTCGTCCTCGCT |
| RPSS62\_02 | TTGAGTGCCTTGAGGCGGAGGAAGAGCGGGTCGTCCTCGCTCTCGAACCTCCTGTCAAAC**[A/T]**TCATCCTGTACATGATATTATACATCACAAGCTGCAGGCGCCTCCTGATCACAATCCCCG |
| RPSS66\_04 | GTACTCTTCCGTACGGACGATCCTTGCTCTCTCACCGCAGATGGGGTGGCACATTCATCA**[A/G]**ATGGATGTGAAGACTGCGTTCCTCATTGGAGTTATTGAGGAAGAGGTGTACATAGAGCAG |
| RPSS71\_02 | TTTGGCTCTGGTGGAGGCTAATATGGATTTGATGATGGTGATAAATATTTAAGACTGTTT**[C/G]**AACACTAATTTTTAGGATTTTTGAGCCCTGACTCTGGCTCATTTTTTTGAATAATGAGTT |
| RPSS77\_04 | GAAAGAATCAAATGAATTTGCAGTATCAGGCTTCTGCAAAAGAACAGTCTTTATAGCCTT**[A/G]**CAAAATCTCTTCCACTGTCCTCCCAGTACCAATATAATTGGCAATTACTTCCCACCTTTG |
| RPSS86\_01 | CTTATTAGAGCTTGAGAGAGCGTGCAGAAGAAAAGAATTTGAGAAGATTCAAGCACACCA**[A/G]**CTTGAAACACTGGAGGTAATTATAGCAAGAGCCTTCCAACAGAAAGAGCTGGGGATCCAA |
| RPSS86\_02 | ACTGGAGGTAATTATAGCAAGAGCCTTCCAACAGAAAGAGCTGGGGATCCAACCAGGCAG**[A/C]**AAATGGGATGGCAACACAATCCAGAAAGACTCCAAGAAAAGAGGTCGGAAAACAGATCTG |
| RPSS86\_04 | CCAGAAAGACTCCAAGAAAAGAGGTCGGAAAACAGATCTGGAGAGAACAATCACAGTGGG**[A/C]**AAAATCCTGGTTGATTCTGGAAGATATGCTAAATTGACAAAGTACTATAAGCCCCTCCCA |
| RPSS 86\_06 | TCCTGGTTGATTCTGGAAGATATGCTAAATTGACAAAGTACTATAAGCCCCTCCCAAACA**[A/G]**TGAATCATGAAGCTCACATCATGGAATACTAGAGGACTCAACTGTCCCGGGAAACACAGG |
| RPSS87\_05 | GTACCACCCACTCCCTGACTGACAATTACGTTAGCATCTGCGGATCATGCTAAAATCGCG**[A/G]**CCTGACAATTATTCACTCAAGGCACGATCATGGCAAAAACAGCAGCAGCACTGCATATCC |
| RPSS96\_02 | ATGTTATCACGGGAGACACACGGCGGGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCC**[A/G]**GACCGCCAGCTAAGGTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGAC |