

Table S1: RNA-seq data statistics

| Names | | GC Content | %≥Q30 |
|------------|------|------------|--------|
| Control | ck-1 | 46.6% | 93.95% |
| | ck-2 | 46.65% | 93.68% |
| | ck-3 | 46.43% | 93.6% |
| NaHCO3 3 h | N3-1 | 46.3% | 93.5% |
| | N3-2 | 46.49% | 92.83% |
| | N3-3 | 46.45% | 93.56% |
| NaHCO3 6 h | N6-1 | 46.44% | 92.8% |
| | N6-2 | 46.43% | 93.01% |
| | N6-3 | 46.45% | 93.54% |

Table S2 The alignment statistics of the sequencing data against the reference genome

| Names | | Total Reads | Mapped Reads | Uniq Mapped Reads | Multiple Map Reads | Reads Map to '+' | Reads Map to '-' |
|------------------------|------|-------------|------------------------|------------------------|----------------------|------------------------|------------------------|
| Control | ck-1 | 45,882,766 | 42,340,738 (92.28%) | 41,306,864 (90.03%) | 1,033,874 (2.25%) | 21,823,009 (47.56%) | 21,857,358 (47.64%) |
| | ck-2 | 44,678,562 | 41,588,698 (93.08%) | 40,602,072 (90.88%) | 986,626 (2.21%) | 21,400,152 (47.90%) | 21,439,696 (47.99%) |
| | ck-3 | 43,845,858 | 40,467,813 (92.30%) | 39,574,236 (90.26%) | 893,577 (2.04%) | 20,796,645 (47.43%) | 20,817,791 (47.48%) |
| NaHCO ₃ 3 h | N3-1 | 54,155,330 | 50,068,330 (92.45%) | 48,924,515 (90.34%) | 1,143,815 (2.11%) | 25,747,176 (47.54%) | 25,781,187 (47.61%) |
| | N3-2 | 41,592,742 | 38,457,038 (92.46%) | 37,573,043 (90.34%) | 883,995 (2.13%) | 19,779,094 (47.55%) | 19,804,249 (47.61%) |
| | N3-3 | 59,572,294 | 55,228,967 (92.71%) | 53,974,047 (90.60%) | 1,254,920 (2.11%) | 28,412,360 (47.69%) | 28,437,763 (47.74%) |
| NaHCO ₃ 6 h | N6-1 | 52,658,328 | 48,754,408 (92.59%) | 47,637,470 (90.47%) | 1,116,938 (2.12%) | 25,066,454 (47.60%) | 25,105,916 (47.68%) |
| | N6-2 | 49,886,458 | 46,068,439 (92.35%) | 44,949,505 (90.10%) | 1,118,934 (2.24%) | 23,731,050 (47.57%) | 23,772,214 (47.65%) |
| | N6-3 | 51,890,900 | 47,989,877 (92.48%) | 46,877,643 (90.34%) | 1,112,234 (2.14%) | 24,691,964 (47.58%) | 24,724,644 (47.65%) |

Table S4: The primer sequences used for qRT-PCR analyses

| Primer | Sequences(5'-3') | Amplicon length (bp) |
|---------------------|-----------------------|----------------------|
| Ubiquitin-F | GGAGGACAAGGTGGAGGG | 228 |
| Ubiquitin-R | GATTGAGGGGAGGGATGC | |
| α -tubulin-F | TGGCTCGAATGCACTGTTGG | 215 |
| α -tubulin-R | TCAACCGCCTTGTCTCTCAGG | |
| CYP82C2-F | GTGGAACAGGGACAT | 159 |
| CYP82C2-R | TTGGAAGAAAGAGCC | |
| WRKY70-F | CGATGATGTCACCCAC | 157 |
| WRKY70-R | ATCGGCAAAGTGGTC | |
| NAC9-F | TTTGTGCCGAGTGTA | 176 |
| NAC9-R | CTCCCGAGTAAGAAGT | |
| RLP53-F | GAAGGCTGAACACGC | 180 |
| RLP53-R | TGAAGCTGCTCCAAA | |
| ATJ11-F | CCATTCAGCGTATTCA | 159 |

| | | |
|----------|--------------------|-----|
| ATJ11-R | TCAGTCTCCCAGTTCC | |
| GSTF2-F | CACATACCTGCCTTCG | |
| GSTF2-R | GTGCCTCCACTTCCAT | 160 |
| XTH6-F | GCGATAGGGAACAAA | |
| XTH6-R | CATCTTCGGGTAGGG | 161 |
| XTH15-F | GGGAAATCAAAGGAA | |
| XTH15-R | TTGGGCATCTGTAGTT | 158 |
| PMEI7-F | AACCAGCTCAGCCAGTC | |
| PMEI7-R | TCGCCTTCAACTTTCC | 178 |
| WRKY41-F | AGATGCCATATCCTTT | |
| WRKY41-R | CTTGGAAGTTGCTCGT | 168 |
| BG2-F | GTGGAACAGGGACAT | |
| BG2-R | TTGGAAGAAAGAGCC | 177 |
| EARLI1-F | CTTCAACTTATGTCCCTT | |
| EARLI1-R | GGTTTCTTTGGTGGG | 187 |

Table S5 Primers used for the construction of birch plants overexpressing *WRKY70* and *NAC9*

| Primer | Sequences(5'-3') | Amplicon length (bp) |
|-------------------|--|----------------------|
| WRKY70-Infusion-F | GACTCTAGAGGATCCCCGGGATGGAGTCTTCTTG GCC | |
| WRKY70-Infusion-R | ATTCGAGCTCGGTACCCGGGTAAAAAGAAAAG GCACCC | 924 |
| NAC9-Infusion-F | GACTCTAGAGGATCCCCGGGATGGAGGAATTCG CACC | |
| NAC9-Infusion-R | ATTCGAGCTCGGTACCCGGGTAAAGCCAATTCA GTTGT | 744 |

Table S6 Primer sequences of *SOD* and *POD* used in qRT-PCR analyses

| Primer | Sequences(5'-3') | Amplicon length (bp) |
|--------|-----------------------|----------------------|
| SOD1-F | CCGTGGTTGTTCTTGGCAAC | |
| SOD1-R | CCAGCAGGATTGAAATGTGGC | 190 |
| SOD2-F | TGCTCCTAAAGCGGTGGTTC | |
| SOD2-R | GGGTTGAAATGAGGGCCAGT | 195 |
| SOD3-F | GAAGCCGCACTAGTAGCCAT | |
| SOD3-R | ACGACAGTGAGTGGTTTGGC | 191 |
| SOD4-F | CGGAGGTCATATCAACCACTC | |
| SOD4-R | CAGACCAAGCCACACCCAT | 190 |
| SOD5-F | ATGTAGGTCTGGTGGTGCTTC | 195 |

| | | |
|--------|------------------------|-----|
| SOD5-R | AGAGAAAGTGTGTGGATGGCTC | |
| SOD6-F | CTTTGCTCTTTCCTCACTCT | |
| SOD6-R | ACAACCCTCGCATTTCAT | 247 |
| POD1-F | ACTAAATCTACCACCACCC | |
| POD1-R | TGTATCGCCCTTTCCAG | 172 |
| POD2-F | AGCATAAAAGAGCATCCCTC | |
| POD2-R | CACATCCAGACCCAGAAATT | 179 |
| POD3-F | TTCATTGCGAGGGTTTG | |
| POD3-R | TGCTTGAGAAGGCAGATAG | 248 |
| POD4-F | TACTGGACGCAAAGATGG | |
| POD4-R | AGGAAGGAAAGCGGAAT | 244 |
| POD5-F | TGAGGTGAATGGGAAGAATG | |
| POD5-R | AGGTGATGTGGTTGGTGC | 154 |
| POD6-F | CAAGTCGGCAGTTGAGAAT | |
| POD6-R | TGGAAAGGCCACATTAC | 227 |
| POD7-F | ACATCTTAGCCGTTGTTGC | |
| POD7-R | GGCAGTGAGACCTTTGTTT | 182 |
| POD8-F | TGTCAACAATTCTGGGCTAC | |
| POD8-R | CCACCCTACAGTTCTTCCT | 191 |
