

**Table S2.** Characteristics of SSR markers for *Arabidopsis thaliana*.

| Marker   | Chr. | Physical position (bp) | Motif | Product size in Col-0 (bp) | Primer sequence forward | Primer sequence reverse |
|----------|------|------------------------|-------|----------------------------|-------------------------|-------------------------|
| F21M12   | 1    | 3212191                | GAAA  | 201                        | GGCTTTCTCGAAATCTGTCC    | TTACTTTTTGCCTCTTGTCATTG |
| MSAT1.10 | 1    | 7296649                | AT    | 235                        | ATGGTGAGATACTGAGATTAT   | CGAGAAGGTCTAAAGGTA      |
| T27K12   | 1    | 15926702               | AT    | 146                        | GGAGGCTATACGAATCTTGACA  | GGACAACGTCTCAAACGGTT    |
| NGA128   | 1    | 20633251               | AG    | 180                        | GGTCTGTTGATGTCGTAAGTCG  | ATCTTGAAACCTTTAGGGAGGG  |
| F5I14    | 1    | 24374008               | A     | 196                        | CTGCCTGAAATTGTCGAAAC    | GGCATCACAGTTCTGATTCC    |
| NGA692   | 1    | 28841544               | GA    | 119                        | TTTAGAGAGAGAGAGCGCGG    | AGCGTTTAGCTCAACCCTAGG   |
| MSAT2.38 | 2    | 2457014                | AT    | 180                        | TGTAACGCTAATTTAATTGG    | CGCTCTTTCGCTCTG         |
| MSAT2.36 | 2    | 8685521                | AG    | 158                        | GATCTGCCTCTTGATCAGC     | CCAAGAACTCAAACCGTT      |
| MSAT2.22 | 2    | 19632943               | AT    | 248                        | CGATCCAATCGGTCTCTCT     | TGGTAACATCCCGAACTTC     |
| NGA172   | 3    | 786303                 | AG    | 166                        | CATCCGAATGCCATTGTTC     | AGCTGCTTCCTTATAGCGTCC   |
| NT204    | 3    | 5570082                | TA    | 150                        | TGGAAGCTCTAGAAACGATCG   | ACCACCTAAACCGAGAATTGG   |
| MSAT3.10 | 3    | 17255200               | AT    | 293                        | CTCCATTGGGCAGAGAGAAC    | TGGCATTGTCCCTATGGG      |
| MSAT3.18 | 3    | 21387949               | AT    | 267                        | TACCTCAAAGAGCAAACA      | TCATACCTACATATTGCCCT    |

Table S2 continued.

|          |   |          |     |     |                        |                        |
|----------|---|----------|-----|-----|------------------------|------------------------|
| MSAT4.8  | 4 | 407010   | AG  | 202 | GTTGGGTTTAGTTGGTAACA   | CGGGTAAAGACAGAGCAT     |
| NGA8     | 4 | 5628810  | AG  | 157 | GAGGGCAAATCTTTATTTCGG  | TGGCTTTCGTTTATAAACATCC |
| MSAT4.15 | 4 | 9362588  | AG  | 174 | TTTCTTGTCTTTCCCCTGAA   | GACGAAGAAGGAGACGAAAA   |
| MSAT4.13 | 4 | 15297044 | AG  | 226 | GGAACAAGAACACAGTGAA    | ATAAATCTAGGCAGGACAAG   |
| MSAT4.37 | 4 | 18336495 | AT  | 139 | CGTTTCATCAAGTTCCGA     | TAGGAGGTTATCATGCGTG    |
| NGA249   | 5 | 2770217  | AG  | 125 | TACCGTCAATTTTCATCGCC   | GGATCCCTAACTGTAAAATCCC |
| MSAT5.14 | 5 | 7498509  | AT  | 221 | AACAACCCTATCTTCTTCTG   | TGTGACCCCTTACTCAATA    |
| NGA76    | 5 | 10418614 | GA  | 250 | GGAGAAAATGTCACTCTCCACC | AGGCATGGGAGACATTTACG   |
| ATHS0191 | 5 | 15021915 | ATG | 166 | TGATGTTGATGGAGATGGTCA  | CTCCACCAATCATGCAAATG   |
| MSAT5.5  | 5 | 22491371 | AG  | 154 | CGATCATATAAATTCGAATCC  | GATTATCTCGCATGTTTATCA  |
| MSAT5.19 | 5 | 25924795 | AT  | 208 | AACGCATTTGCTGTTTCCCA   | ATGGTTATCTCATCTGGTCT   |