**Description of Additional Supplementary Files**

**Supplementary Data 1:** The file describes detailed information on all 228 *S. polyrhiza* genotypes, including their sequencing statistics, sampling regions, and Accession number in NCBI.

**Supplementary Data 2:** The table contains the annotation of all SNPs. Each row records one annotated gene. The first column is the gene ID, and the following columns are the number of SNPs annotated as different categories.

**Supplementary Data 3:** The table contains all the annotation information of SVs.

**Supplementary Data 4:** The table contains gene families as well as members from each gene family identified in the *S. polyrhiza* genome.

**Supplementary Data 5:** The table contains results of enrichment analysis of small INDELs and SVs among all the gene families identified.

**Supplementary Data 6:** The table contains the grouping of clonal families of all 228 *S. polyrhiza* genotypes.

**Supplementary Data 7:** The file contains the alignment (against to the homologs from *Arabidopsis thaliana*) and expression of 34 candidate genes that were discussed in the manuscript.

**Supplementary Data 8:** The table contains the list of genes detected under positive selection at the species-wide level according to RAiSD, SweeD and LASSI.

**Supplementary Data 9:** This table contains the list of genes (rows) belonging to the top 1% CLR values of 3P-CLR and the population branches where they are under selection (columns). Fields with “1” indicate that a signature of selection was found, and fields with “0” indicate no signature of selection was found.