

Insights into salvianolic acid B biosynthesis from chromosome-scale assembly of the *Salvia bowleyana* genome

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SUPPORTING INFORMATION

Supplementary Figures

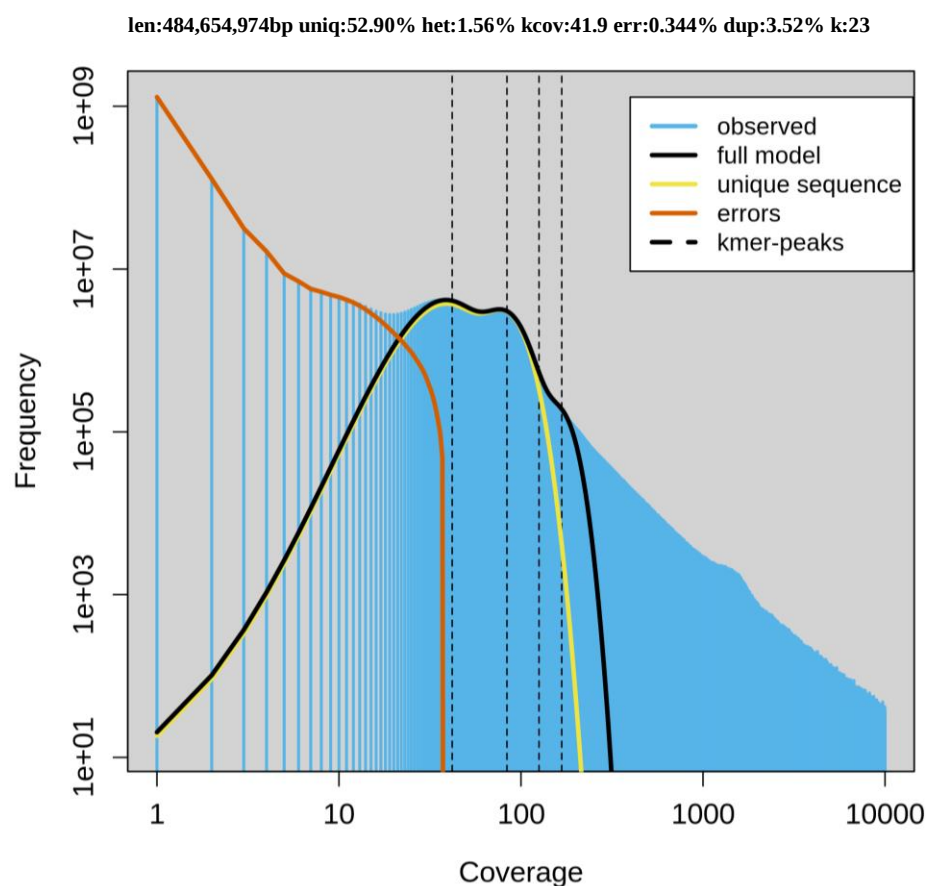


Figure S1. 23-K-mer count distribution for the *S. bowleyanae* genome size estimation

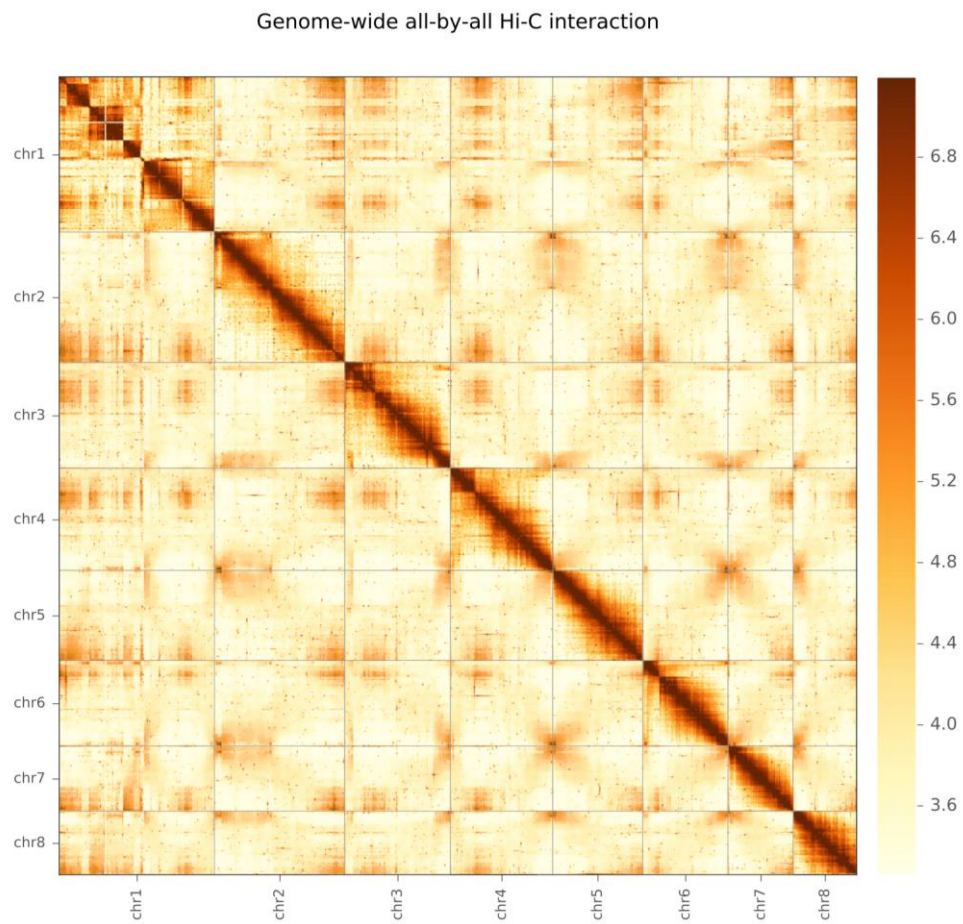


Figure S2. *S. bowleyanae* genome-wide all-by-all Hi-C interactions heat map

The map shows a high resolution of individual superscaffolds that are scaffolded and assembled independently.

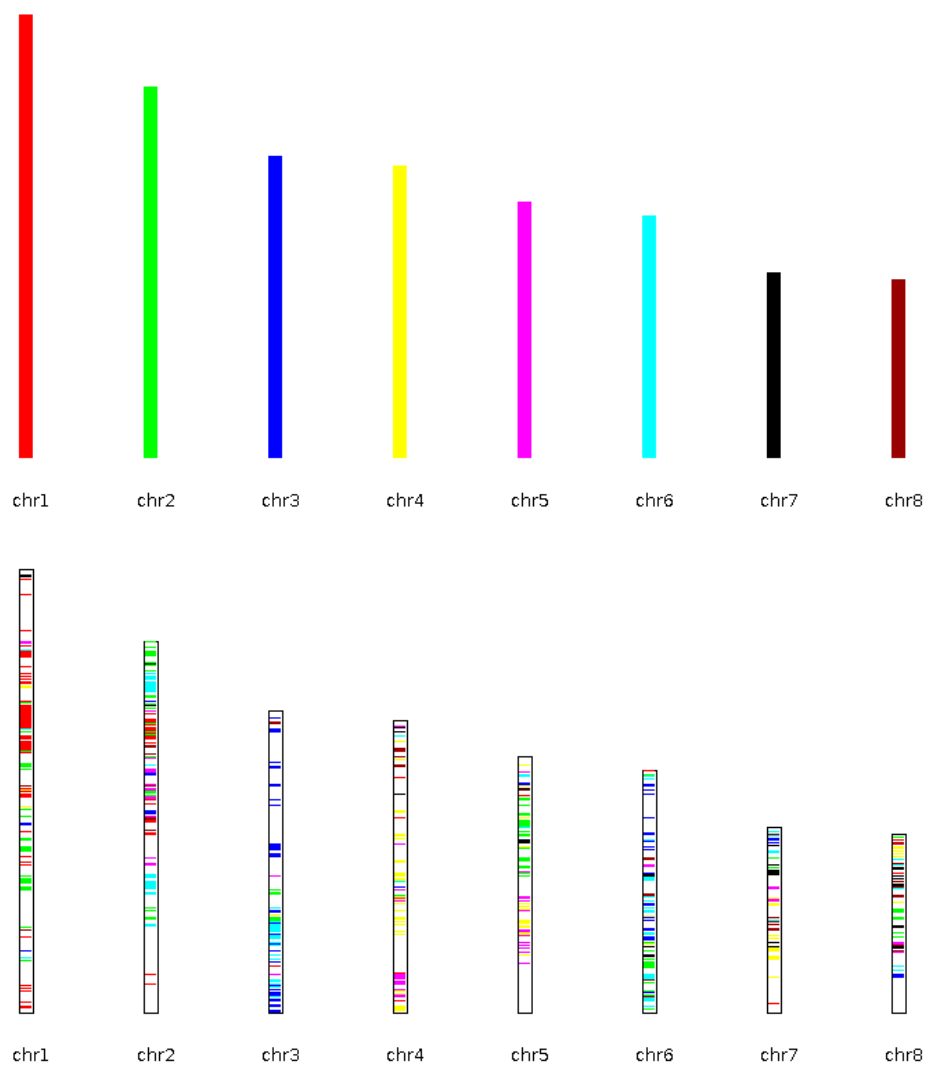


Figure S3. Syntenic analysis of *S. bowleyanae* genome

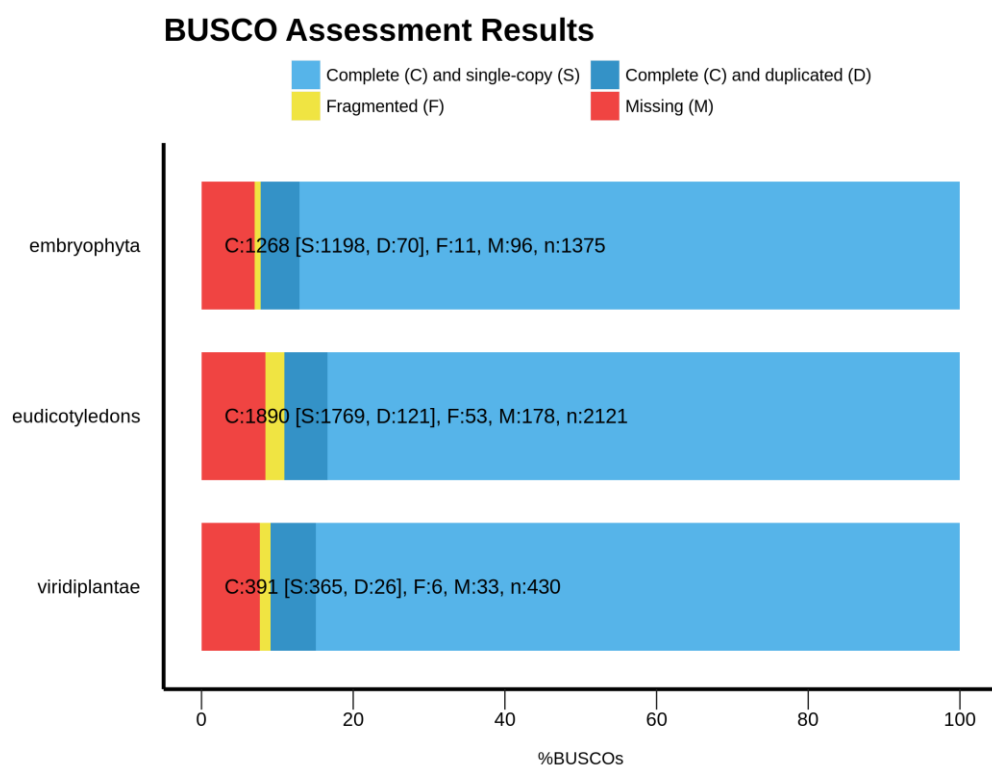


Figure S4. Assessment of the completeness of the *S. bowleyanae* genome assembly by BUSCO

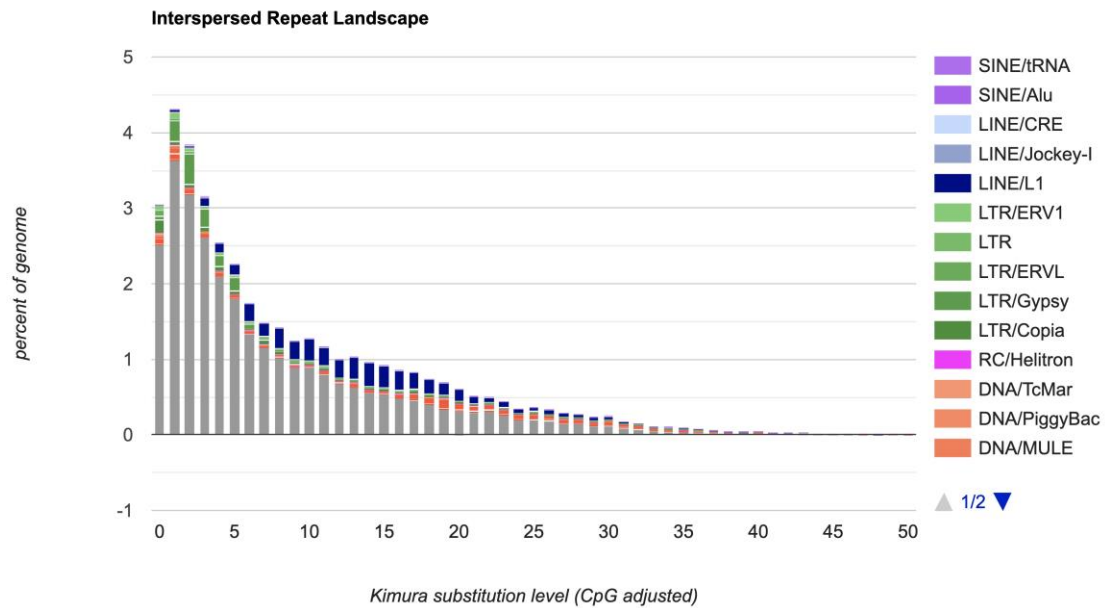


Figure S5. Kimura distance-based copy divergence analysis of transposable elements in *S. bowleyanae* genome

The graph represents percentage of genome (y-axis) for each type of TEs (SINE, LINE, LTR/Gypsy, LTR/Copia and DNA transposons), clustered according to Kimura distances to their corresponding consensus sequences (x-axis, K-value from 0 to 50)

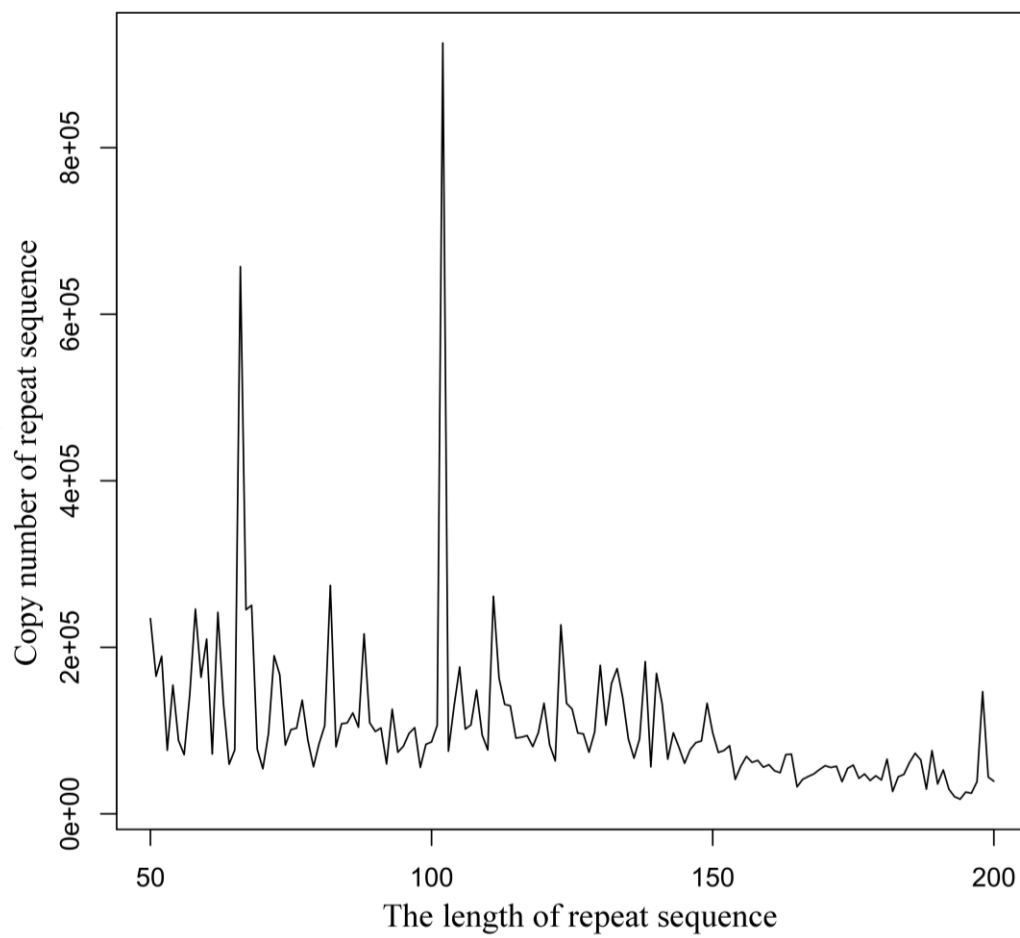


Figure S6. Prediction of centromere model

The centromere type of *S. bowleyanae* was monocentric.

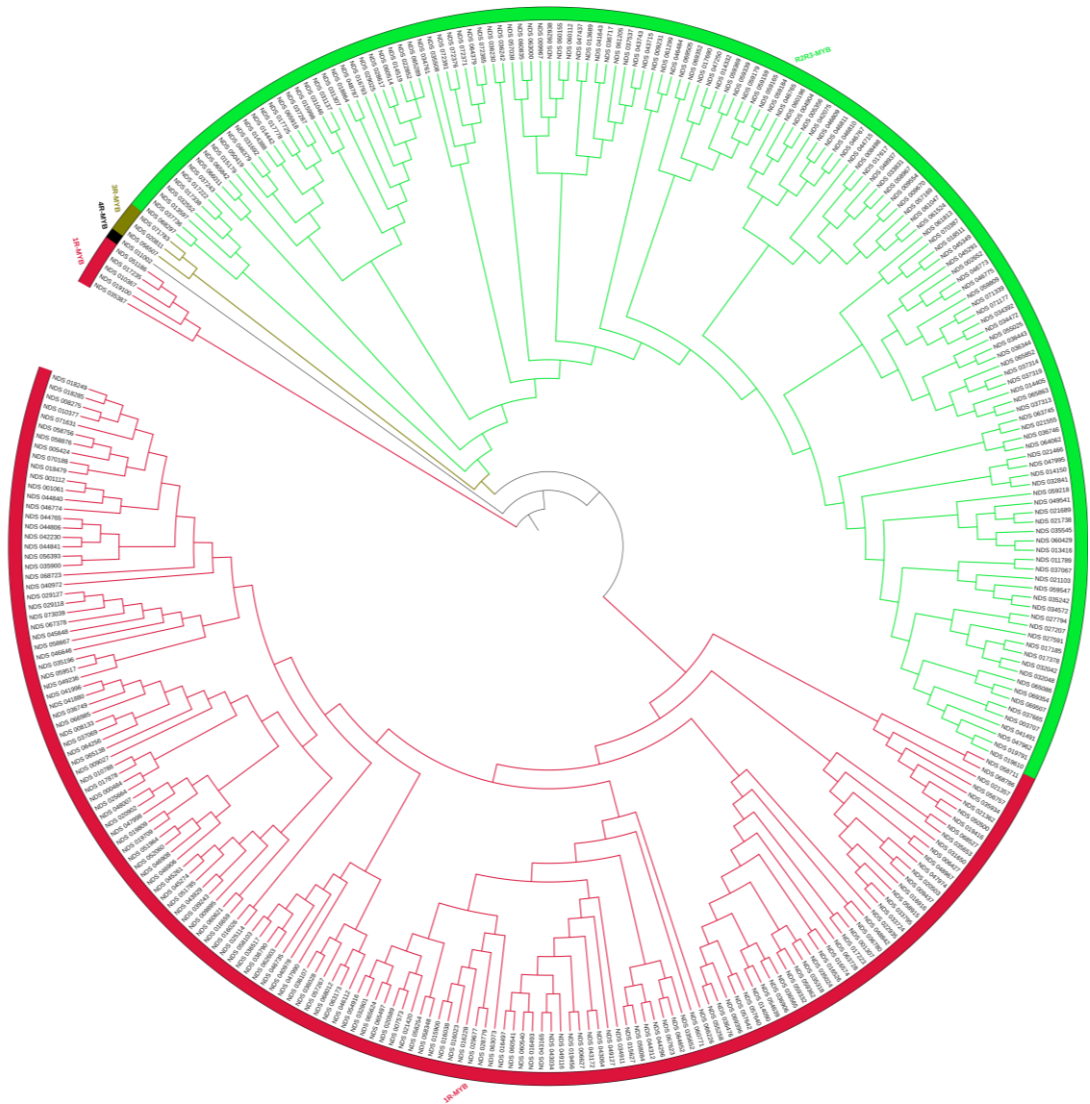


Figure S7. The evolutionary tree of MYB gene families in *S. bowleyanae*

Genes in the MYB families were clustered separately using MEGA7 software via the neighbor-joining method

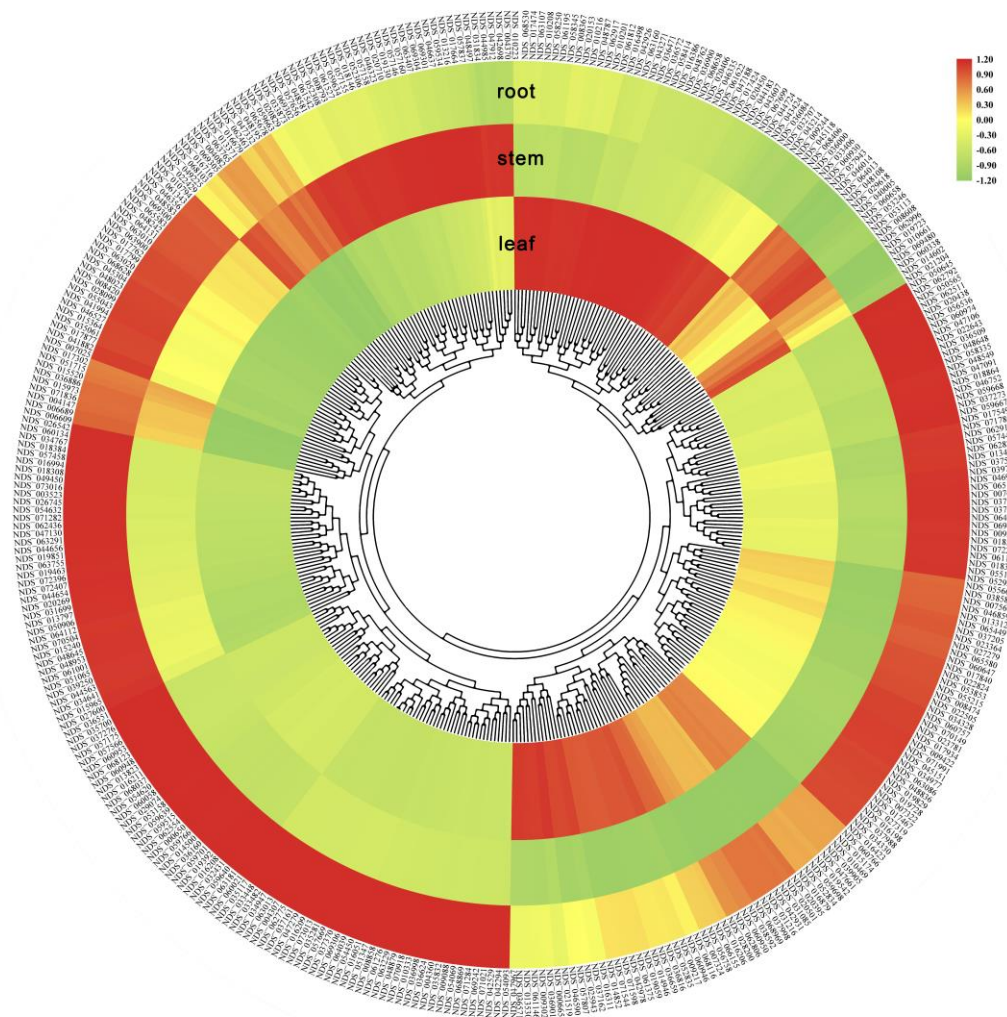


Figure S8. Heatmap showing the root-, stem- and leaf-specific gene expression

Each box represents an individual gene, and the red and green boxes represent relatively high levels and low levels of gene expression, respectively

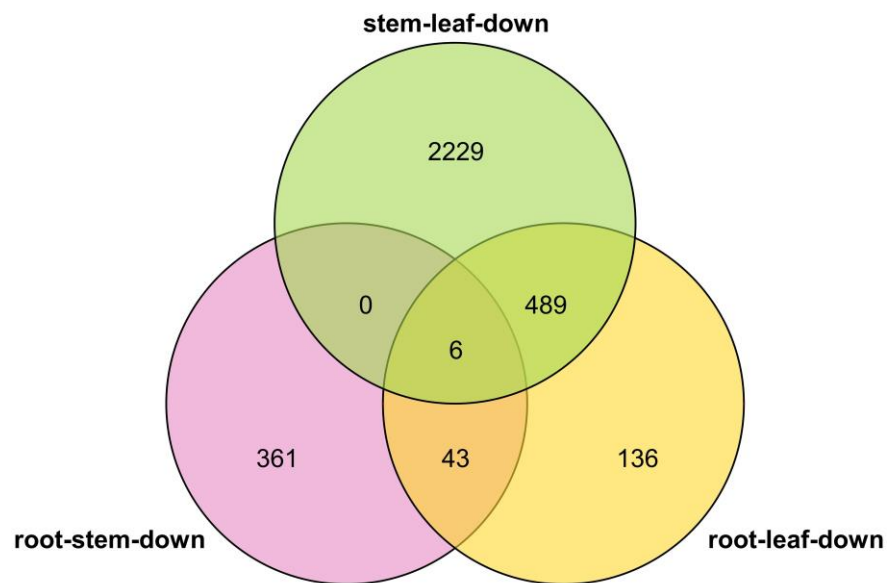


Figure S9. Venn diagram of the number of downregulated gene between root, stem and leaf.

The numbers of genes (clusters) are indicated for each DEGs intersection in root, stem and leaf

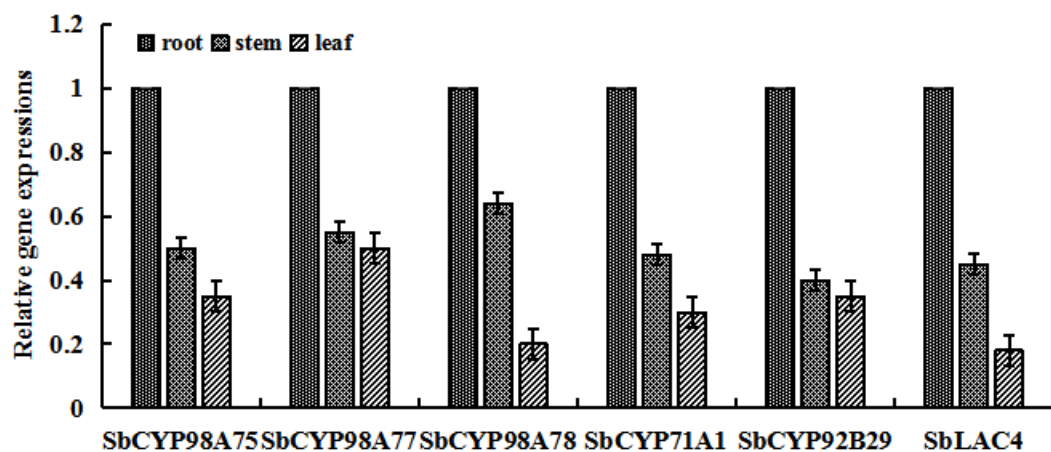


Figure S12. Real-time quantitative RT-qPCR confirmation of 6 genes at the root, stem and leaf

Relative gene expressions were analyzed using the $2^{-\Delta\Delta C_t}$ method. The expression values were adjusted by setting the expression of root to be 1 for each gene. Experiments were performed in triplicate. Error bars indicate standard deviation

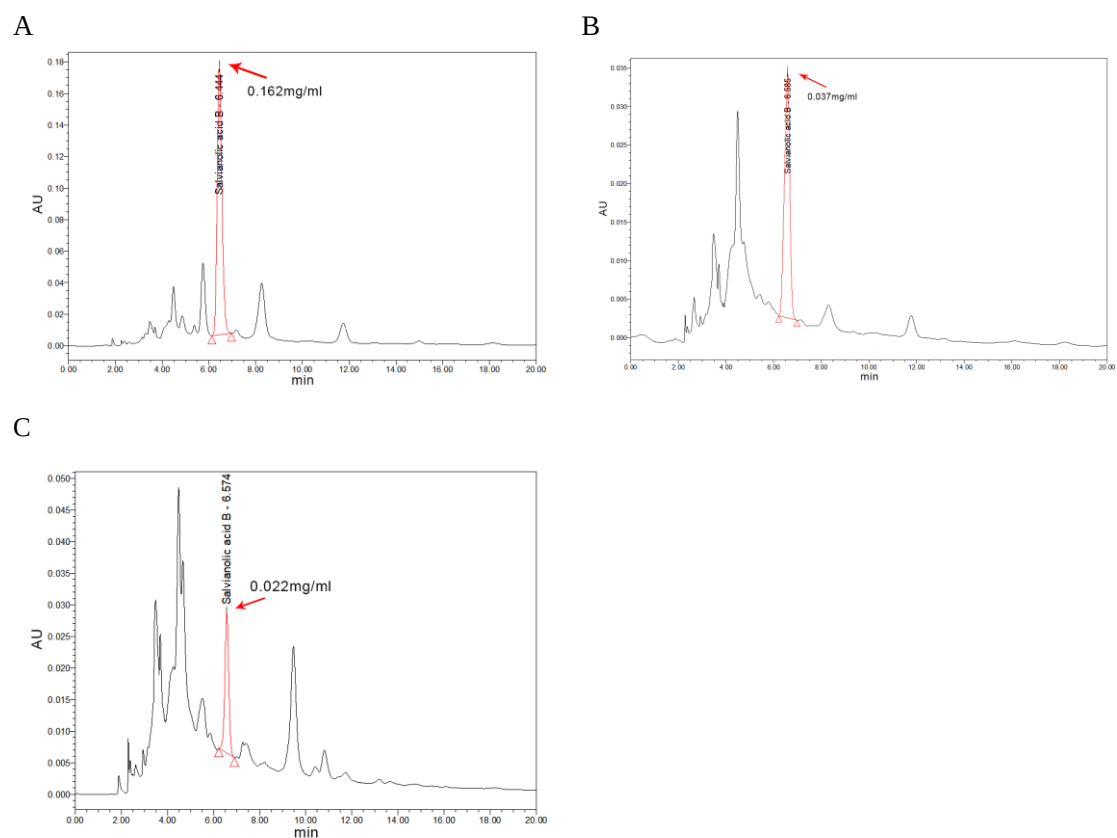


Figure S13. Determination of salvianolic acid B by HPLC in root (**A**), stem (**B**) and leaf (**C**) of *S.bowleyana*

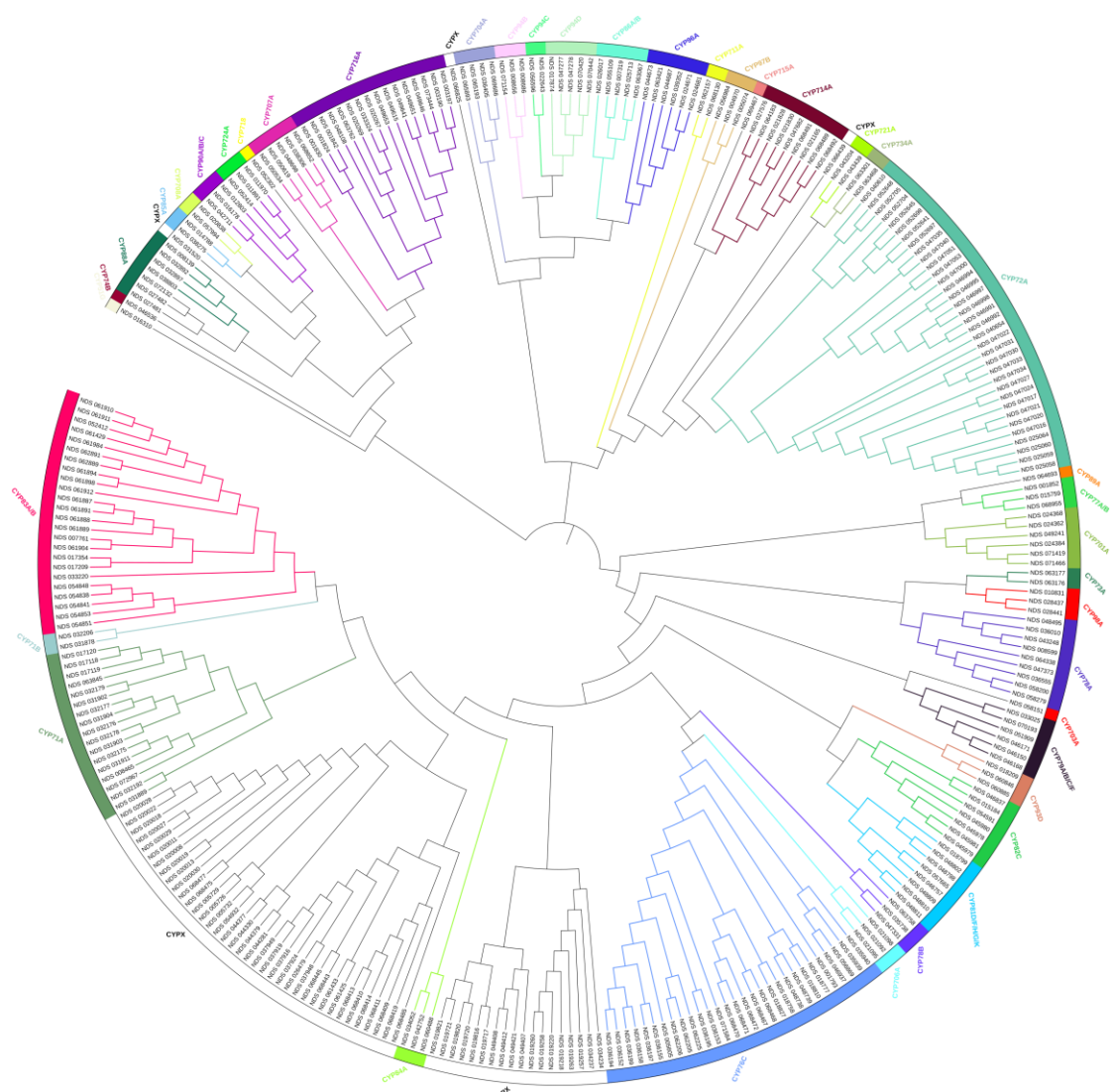


Figure S14. The evolutionary tree of CYP450 gene families in *S. bowleyanae*

Genes in the CYP450 families were clustered separately using MEGA7 software via the neighbor-joining method.

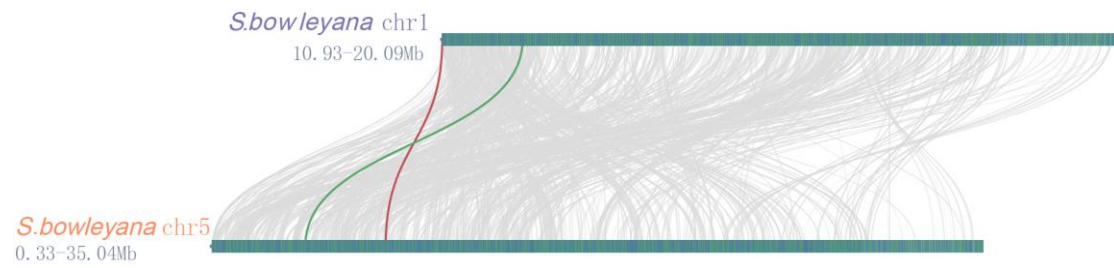


Figure S15. Syntenic analysis of SbCYP92B29 (NDS_049413) and SbCYP71A1 (NDS_002064) flanking region

CYPs gene paris were marked by green line.