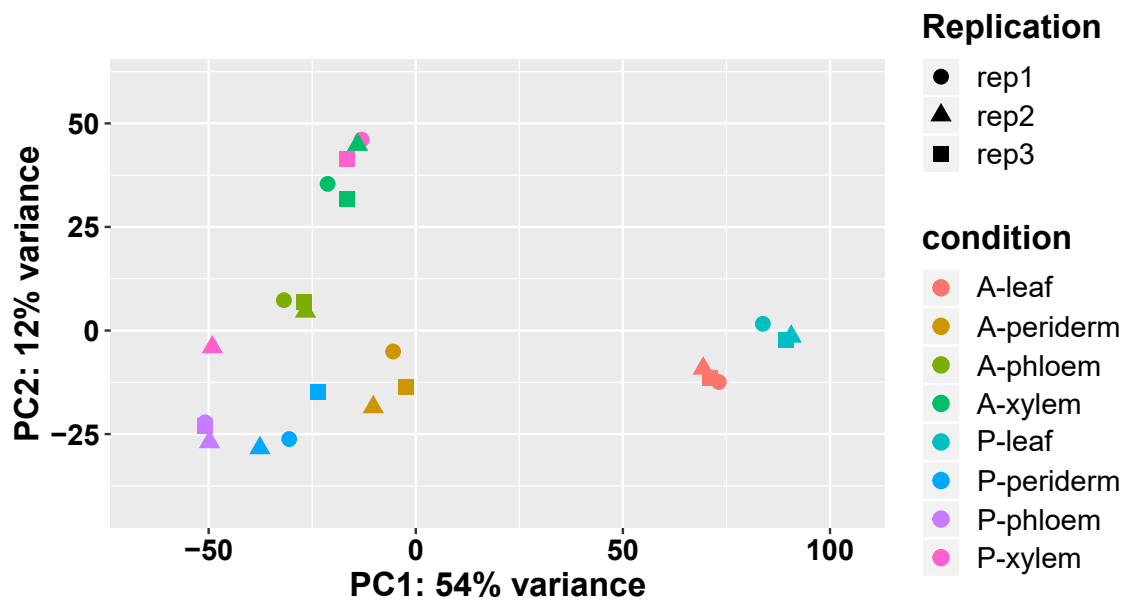
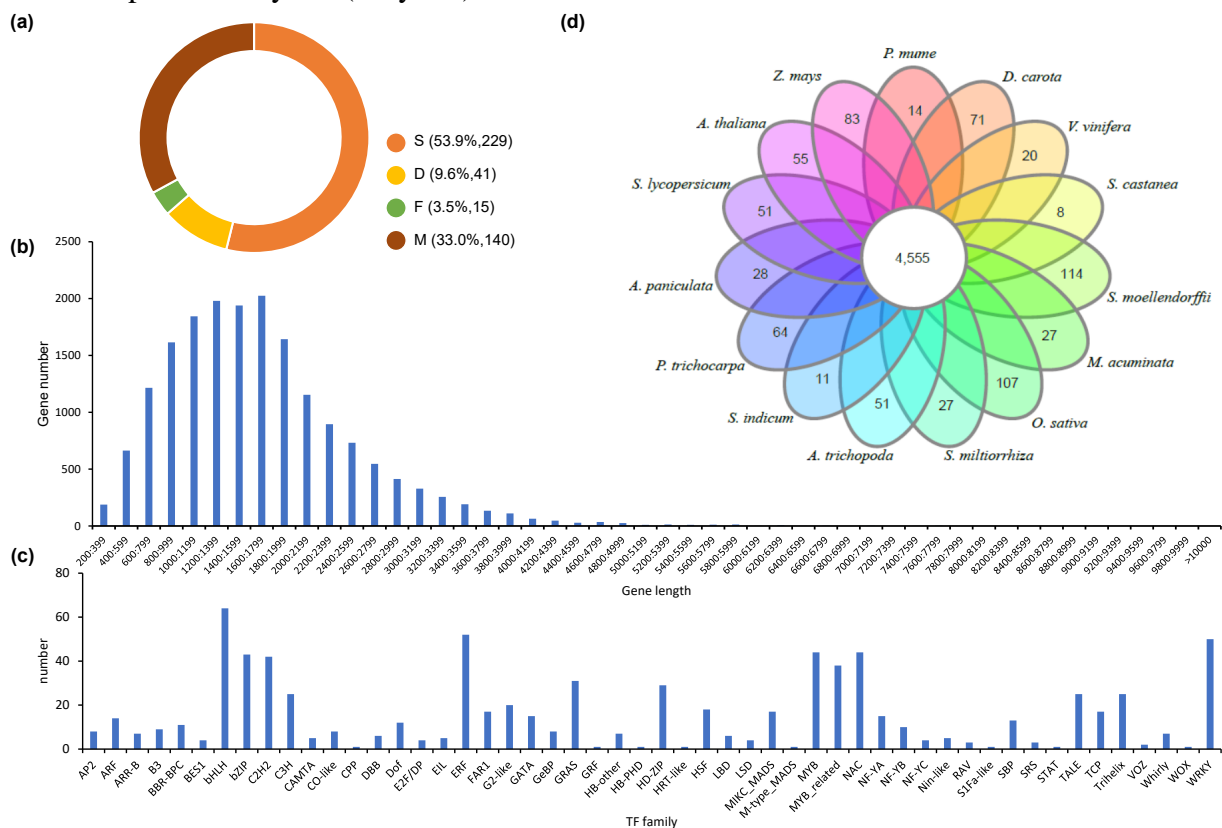


## Supplementary figures

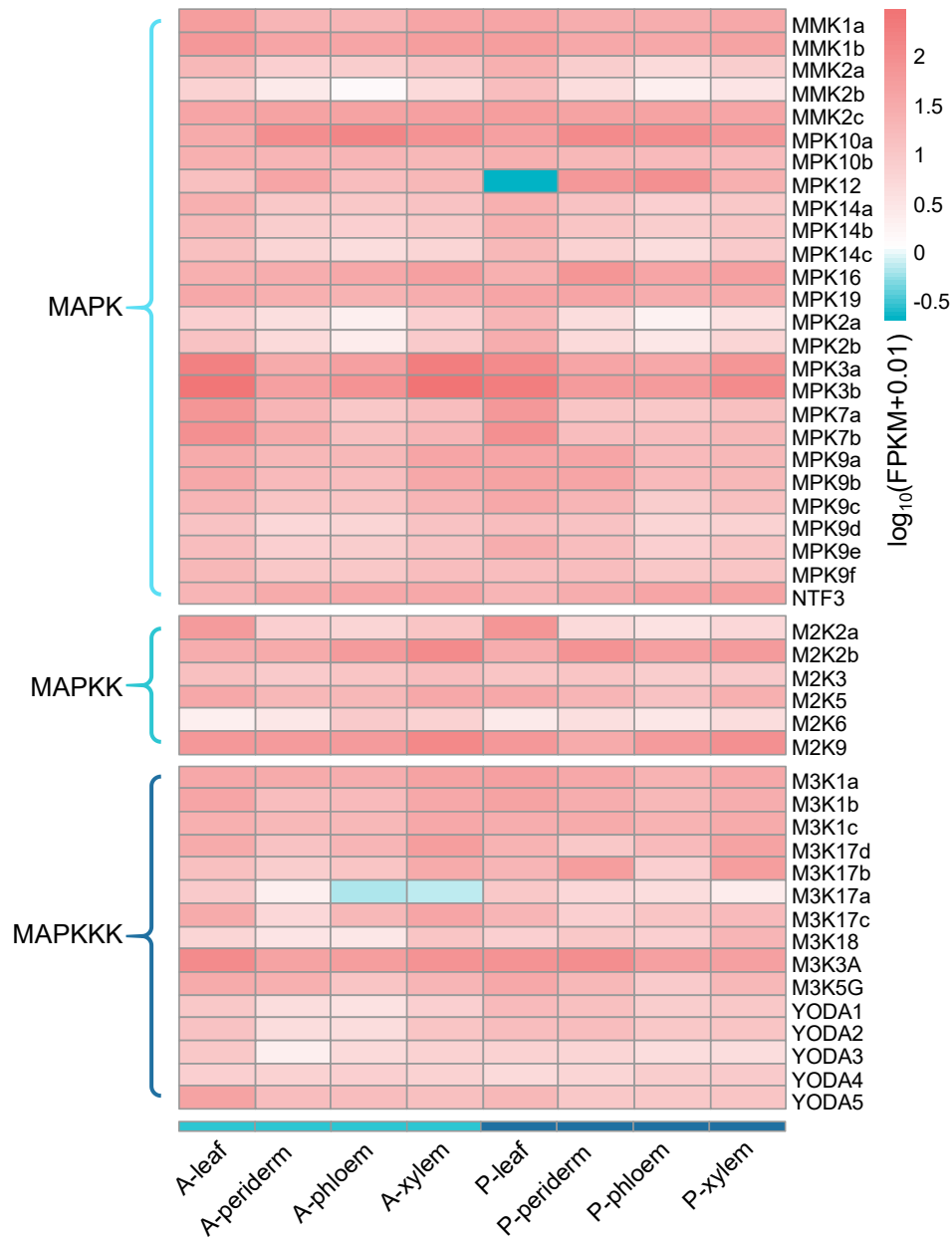


**Fig. S1** Principal component analysis (PCA) of gene expression profiles in 8 tissues for three biological replicates. Eight tissues were including annual leaf (A-leaf), annual periderm (A-periderm), annual phloem (A-phloem), annual xylem (A-xylem), perennial leaf (P-leaf), perennial periderm (P-periderm), perennial phloem (P-phloem), and perennial xylem (P-xylem)

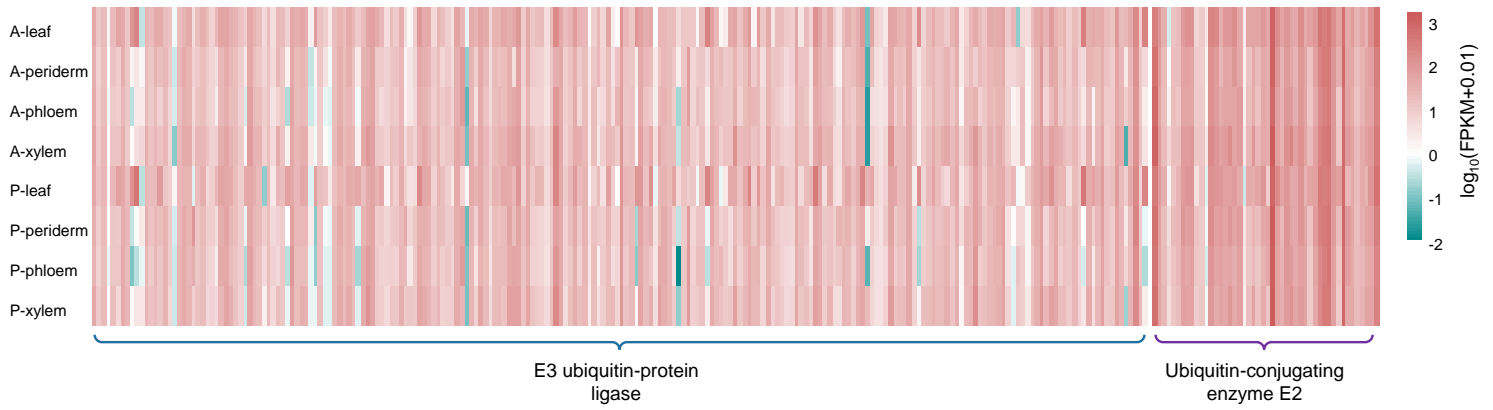


**Fig. S2** Genes and OGGs identified from full-length transcriptome in *Salvia castanea*. (a) BUSCO completeness of full-length transcriptome. (b) Basic information of genes

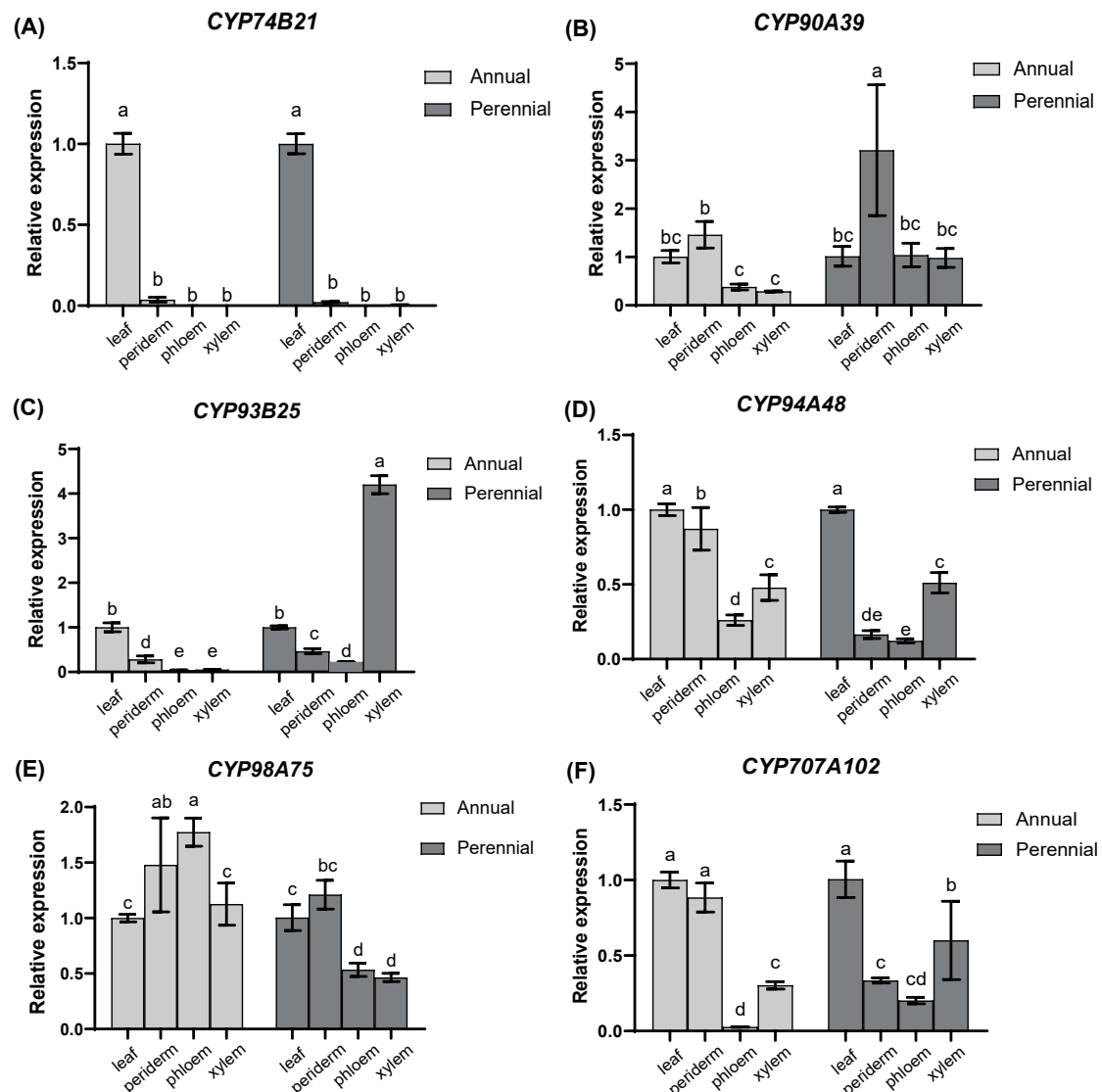
assembled from full-length transcriptome in *Salvia castanea*. (c) 52 distinct TFs identified in *S. castanea*. (d) Venn diagram showed the shared and specific gene families distributed among *S. castanea* and 14 representative plant species. Each value in parentheses represented the number of genes within corresponding families (without parentheses).



**Fig. S3** Expressions of 47 MAPK genes in 8 tissues of *Salvia castanea*. Eight tissues were including annual leaf (A-leaf), annual periderm (A-periderm), annual phloem (A-phloem), annual xylem (A-xylem), perennial leaf (P-leaf), perennial periderm (P-periderm), perennial phloem (P-phloem), and perennial xylem (P-xylem)



**Fig. S4** Expressions of genes in ubiquitin (Ub)-proteasome system (UPS) including 49 Ub conjugating enzyme (E2) and 224 Ub ligase (E3) 8 tissues of *Salvia castanea*. Eight tissues were including annual leaf (A-leaf), annual periderm (A-periderm), annual phloem (A-phloem), annual xylem (A-xylem), perennial leaf (P-leaf), perennial periderm (P-periderm), perennial phloem (P-phloem), and perennial xylem (P-xylem)



**Fig. S5** qRT-PCR results for six P450 genes. Normalized expression levels of these

genes were presented in 8 tissues for three biological replicates. Eight tissues were including annual leaf, annual periderm, annual phloem, annual xylem, perennial leaf, perennial periderm, perennial phloem, and perennial xylem. The relative expression levels were calculated by  $2^{-\Delta\Delta Ct}$  method comparing with that of *actin* gene with three replicates. Data are the means of three replicates (mean  $\pm$  SE). Values followed by different letters indicated significant differences at  $P < 0.05$  levels.