

Figure S1. RT-qPCR verification of expression level of 16 DEGs related to the monolignol, cellulose and hemicellulose synthesis identified by RNA sequencing in stem xylem tissue. The Y-axis on the right indicates the relative gene expression levels analyzed by qRT-PCR, while the Y-axis on the left represents the FPKM value obtained by RNA-seq. The X-axis represents the samples under different treatments. Error bars indicate mean \pm SE (n = 3) from three independent trials. Two - tailed Student's t-test; * P<0.05 and ** P<0.01.

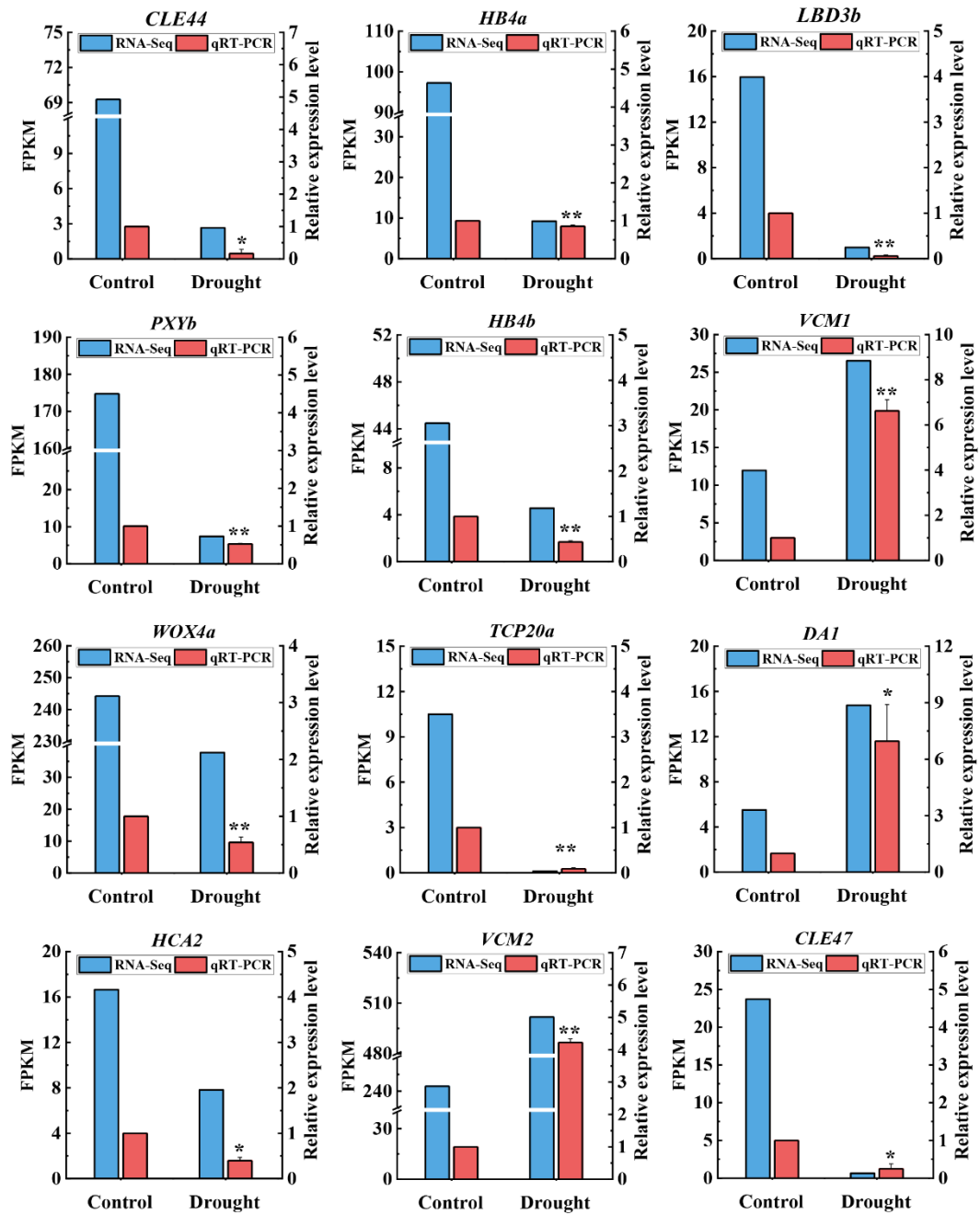


Figure S2. RT-qPCR verification of expression level of 12 DEGs related to cambium activity identified by RNA sequencing in stem cambium tissue. The Y-axis on the right indicates the relative gene expression levels analyzed by qRT-PCR, while the Y-axis on the left represents the FPKM value obtained by RNA-seq. The X-axis represents the samples under different treatments. Error bars indicate mean \pm SE (n = 3) from three independent trials. Two-tailed Student's t-test; * P<0.05 and ** P<0.01.

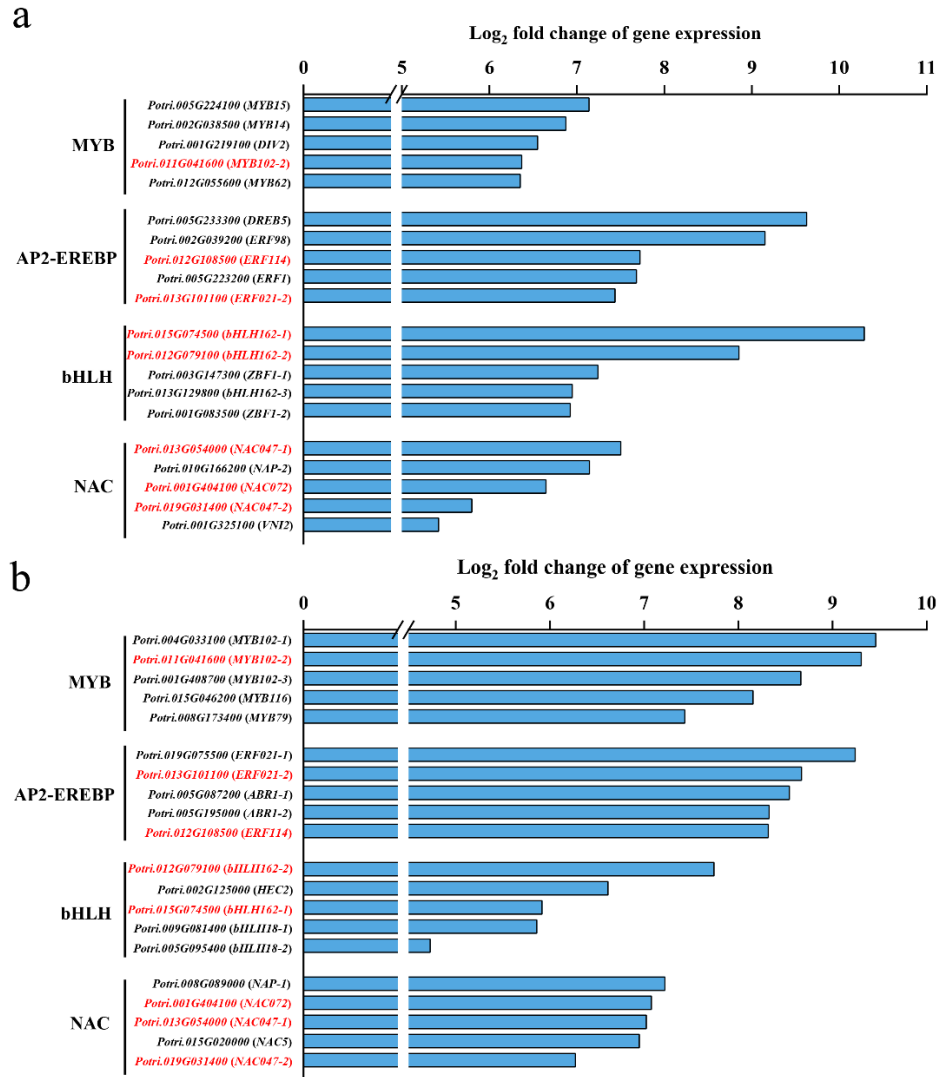


Figure S3. Identification of transcription factor genes from MYB, AP2-EREBP, bHLH, NAC families. (a) Top five differentially expressed TF genes from four TF families ranked by log₂(fold-change values) in xylem. (b) Top five differentially expressed TF genes from four TF families ranked by log₂(fold-change values) in cambium.