Figure S1. Phylogenetic relationships, motif pattern, domain pattern, and gene structure of R2R3-MYB transcription factors in *C. oleifera*. (**A**) Phylogenetic tree constructed by NJ method with 128 *Camellia* R2R3-MYB proteins (1000 bootstraps). (**B**) Conserved motif patterns of 128 *Camellia* R2R3-MYB proteins. Different colors represent different motif sequences, and the detailed sequence of each motif is shown in Table S4. (**C**) SMART conserved structure of 128 *Camellia* R2R3-MYB proteins. The green and yellow boxes represent the SANT domain (R2, R3) and the low complexity region, respectively. (**D**) Gene structure of 128 *Camellia* R2R3-MYB proteins. Pink boxes, light green boxes, and black lines represent the CDS, untranslated regions (UTR), and introns of each MYB gene, respectively.

Figure S2. Predicted cis-acting elements of promoters of 128 *R2R3-MYB* genes in *C. oleifera*. Different

colored rectangles represent different cis-acting elements.

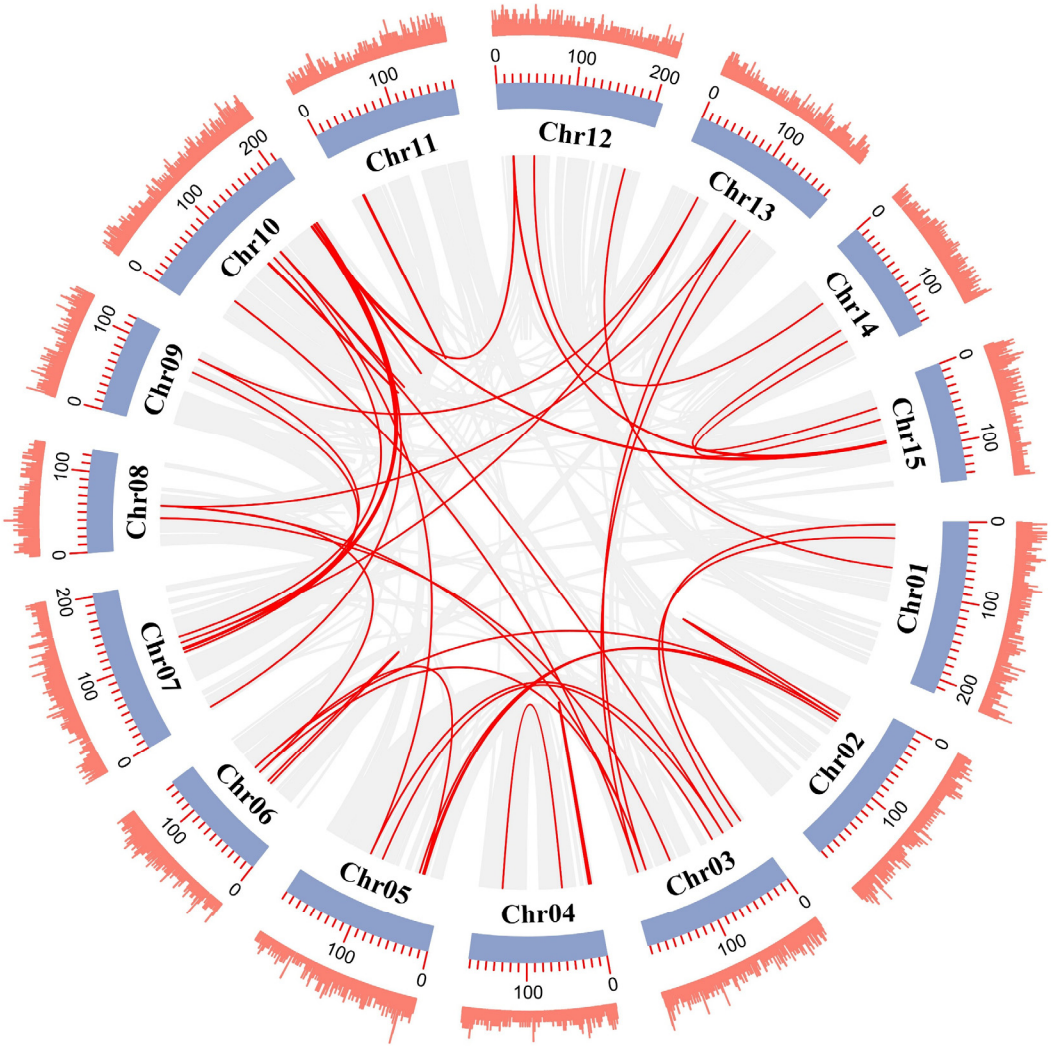

Figure S3. Schematic diagram of the colinear relationship within *C. oleifera*. The gray lines in the background represent intergenomic colinear blocks, and the red lines represent intraspecies collinearity *R2R3-MYB* gene pairs. The innermost purple arc represents the chromosome. The red bars in the Circos diagram represent gene density.

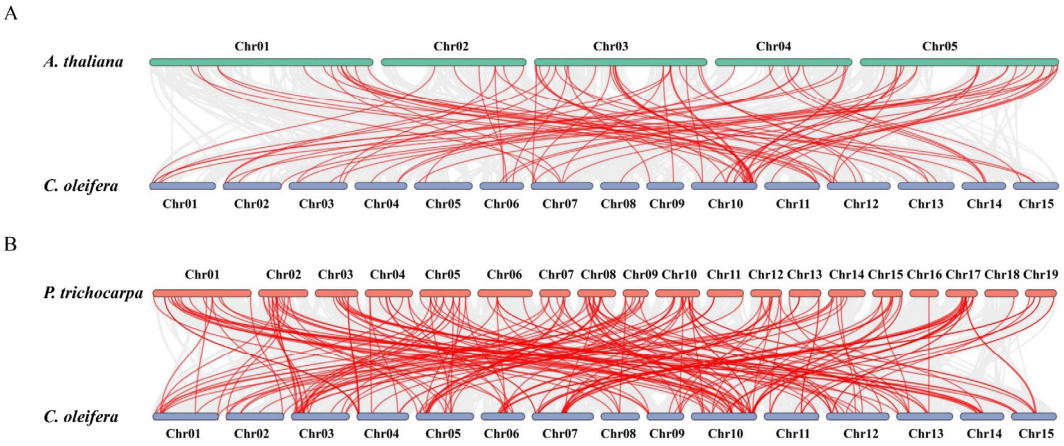

Figure S4. Synteny analyses of the *C. oleifera* with Poplar and *Arabidopsis*. (**A**) Schematic diagram of the colinear relationship between *C. oleifera* and *Arabidopsis thaliana*. (**B**) Schematic diagram of the colinear relationship between *C. oleifera* and *Populus trichocarpa*. The gray lines in the background represent intergenomic colinear blocks, and the red lines represent the collinearity of *R2R3-MYB* gene pairs.

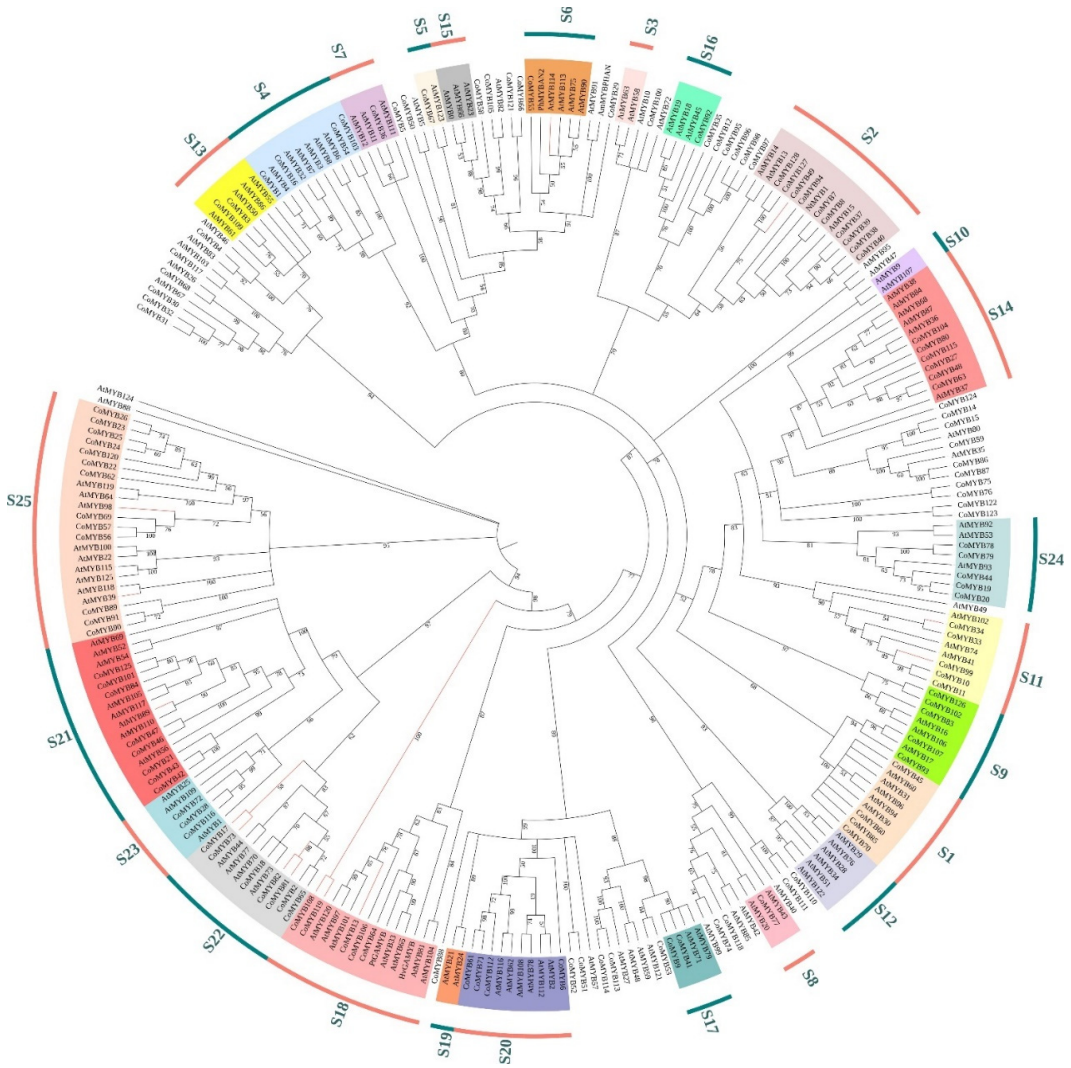

Figure S5. Phylogenetic tree of R2R3-MYB transcription factors from *C. oleifera*, *A. thaliana*, and five other

species. The number on the branch represents the bootstrap value. Different colored backgrounds and strips represent different subgroups. The red branches represent genes on this branch that do not have the conserved motif characteristic of this subgroup.

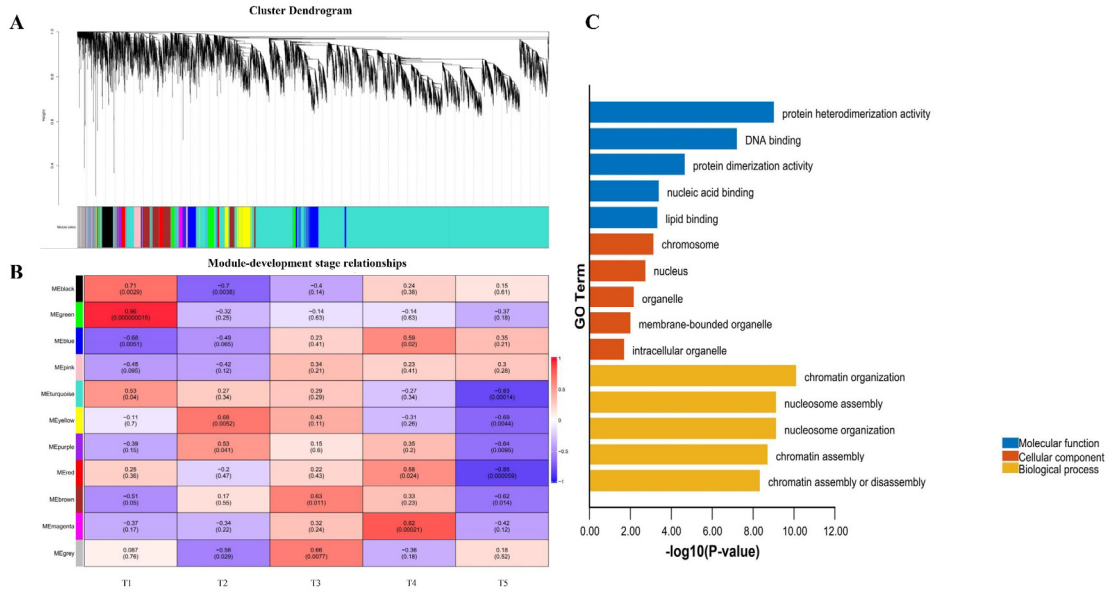

Figure S6. Weighted gene co-expression network analysis of (WGCNA) of transcriptome and GO enrichment of 7 *CoMYB* genes and their co-expression genes. (**A**) Clustering dendrograms of genes. The 11 co-expression modules are displayed in different colors. (**B**) Correlation analysis of 11 co-expression modules and 5 seed different developmental stages of *C. oleifera*. Red represents a positive correlation, purple represents a negative correlation, and the greater the absolute value, the stronger the correlation. (**C**) GO enrichment of 7 *CoMYB* genes and their co-expression genes. Three colors represent the three parts of GO, respectively.