

Figure S1. Differential expression genes (DEGs) analysis (A). The gene ontology (B) and KEGG pathway (C) of DEGs

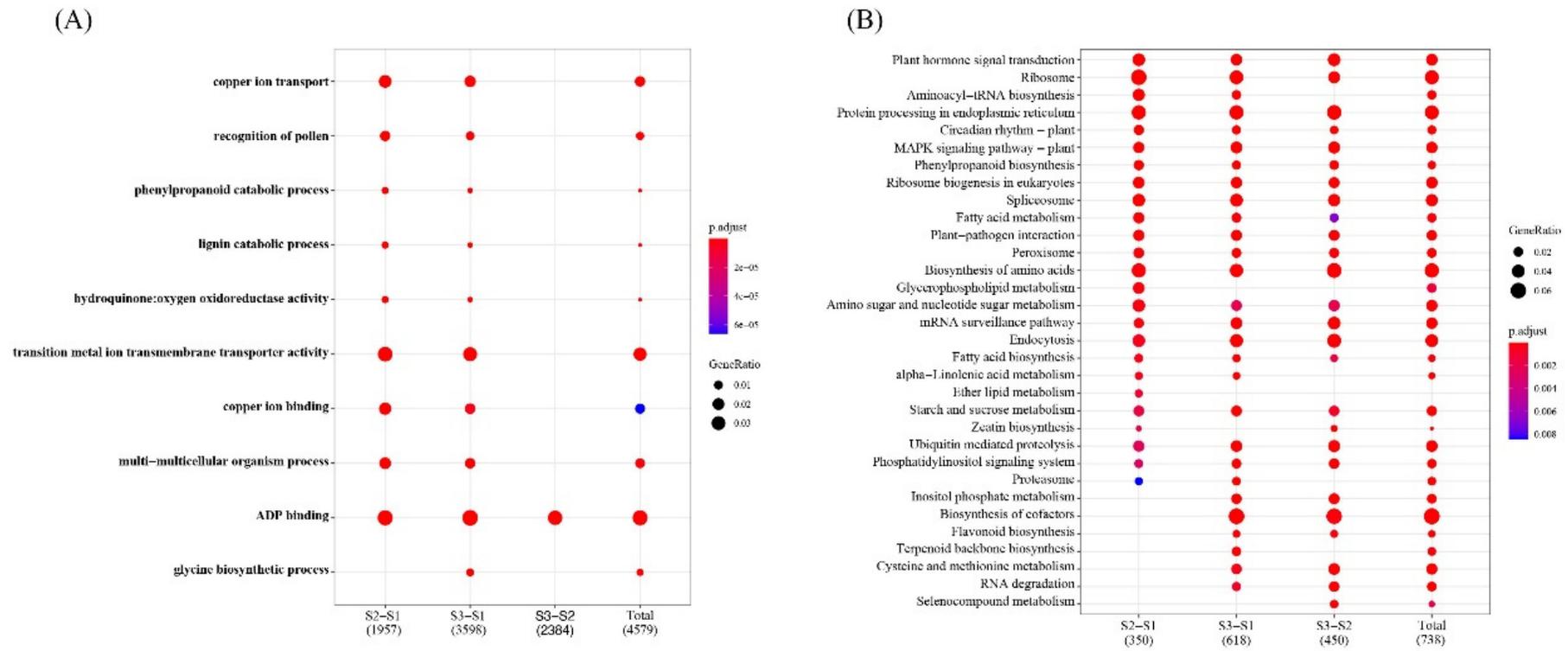


Figure S2. The gene ontology (A) and KEGG pathway (B) of the target genes of differentially expressed miRNAs (DEMs)

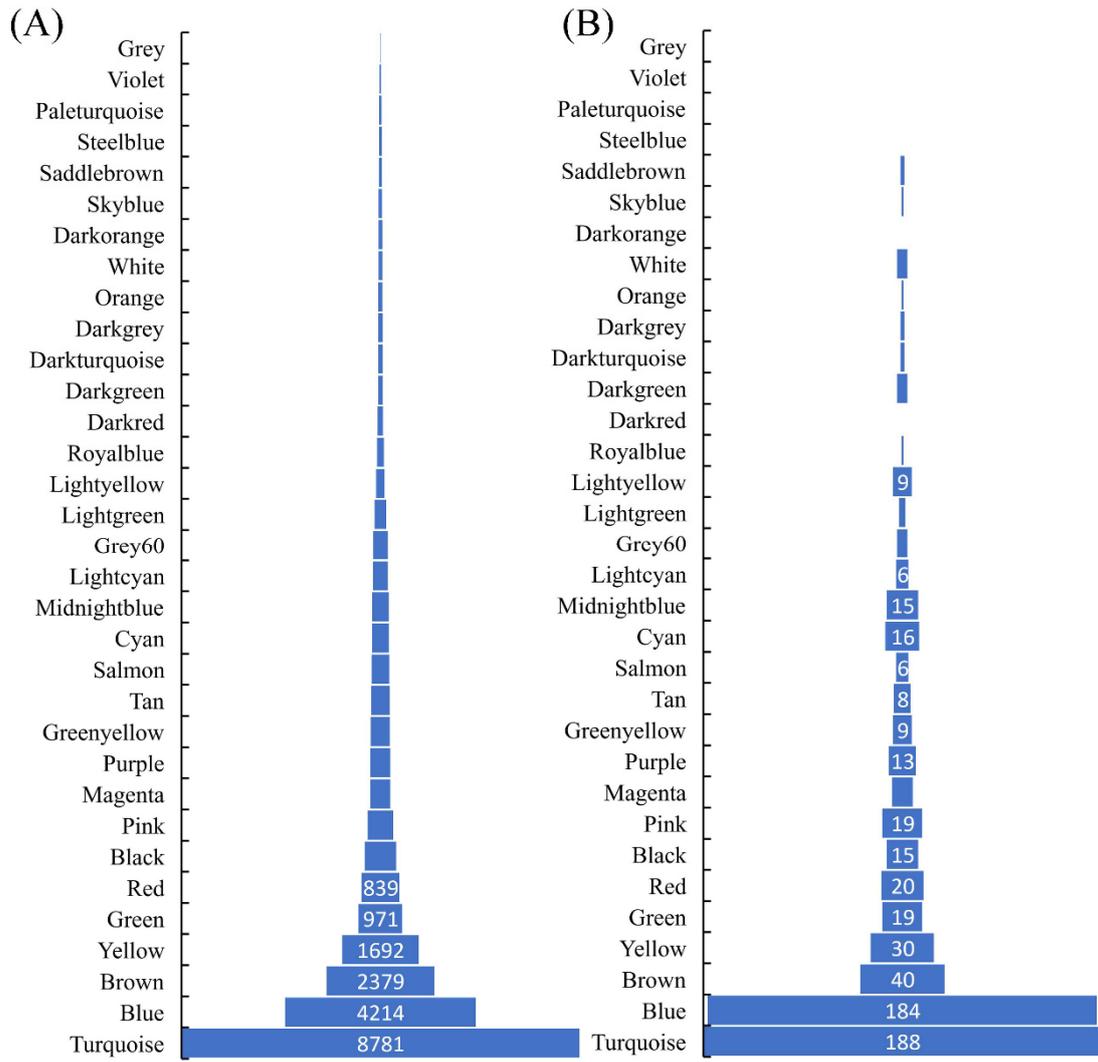


Figure S3. The number of gene (A) and transcription factor (B) in each module based on co-expression network analysis

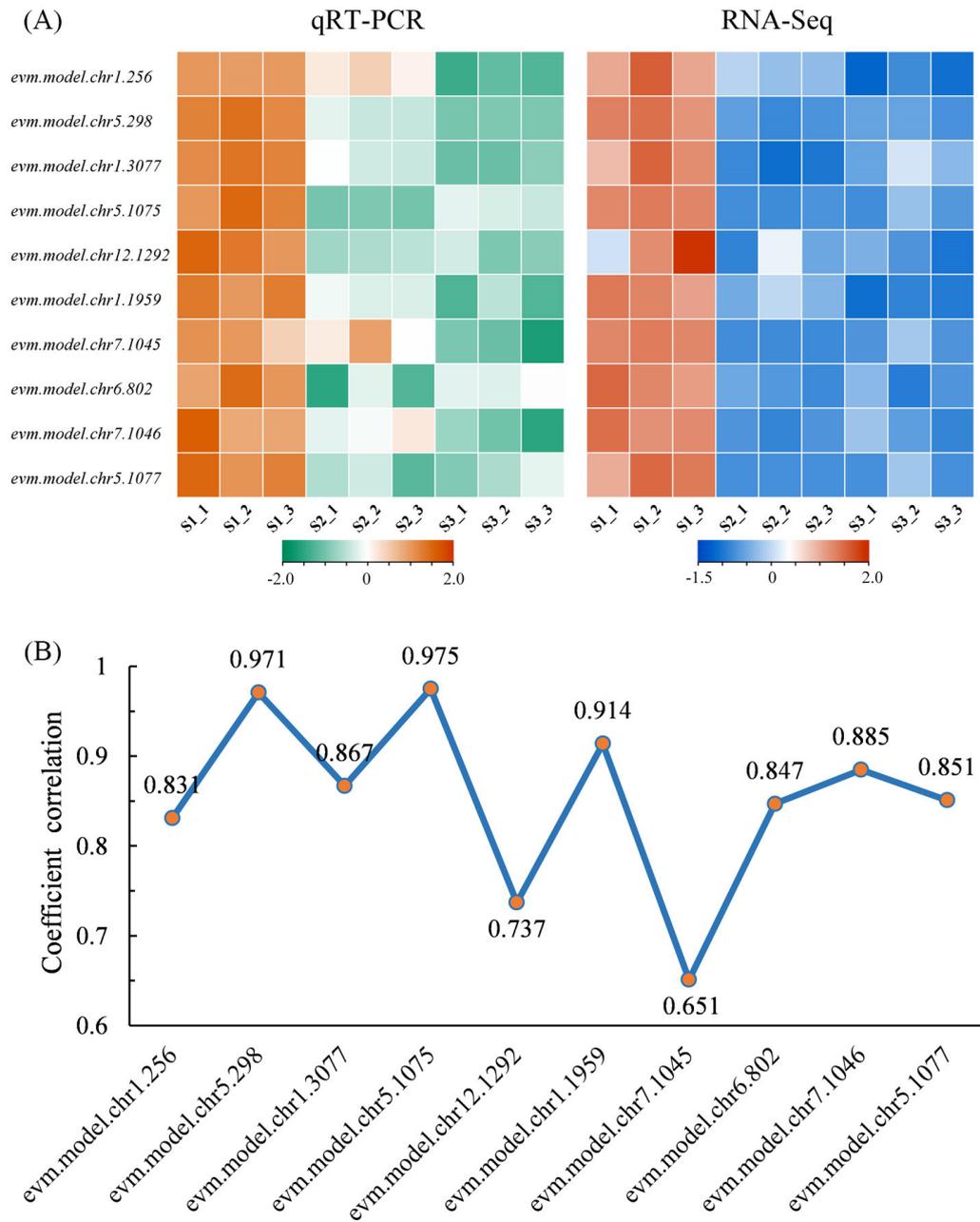


Figure S4. The qRT-PCR analysis of ten TTL-related genes (A) and correlation analysis with expression patterns based RNA sequencing (B)

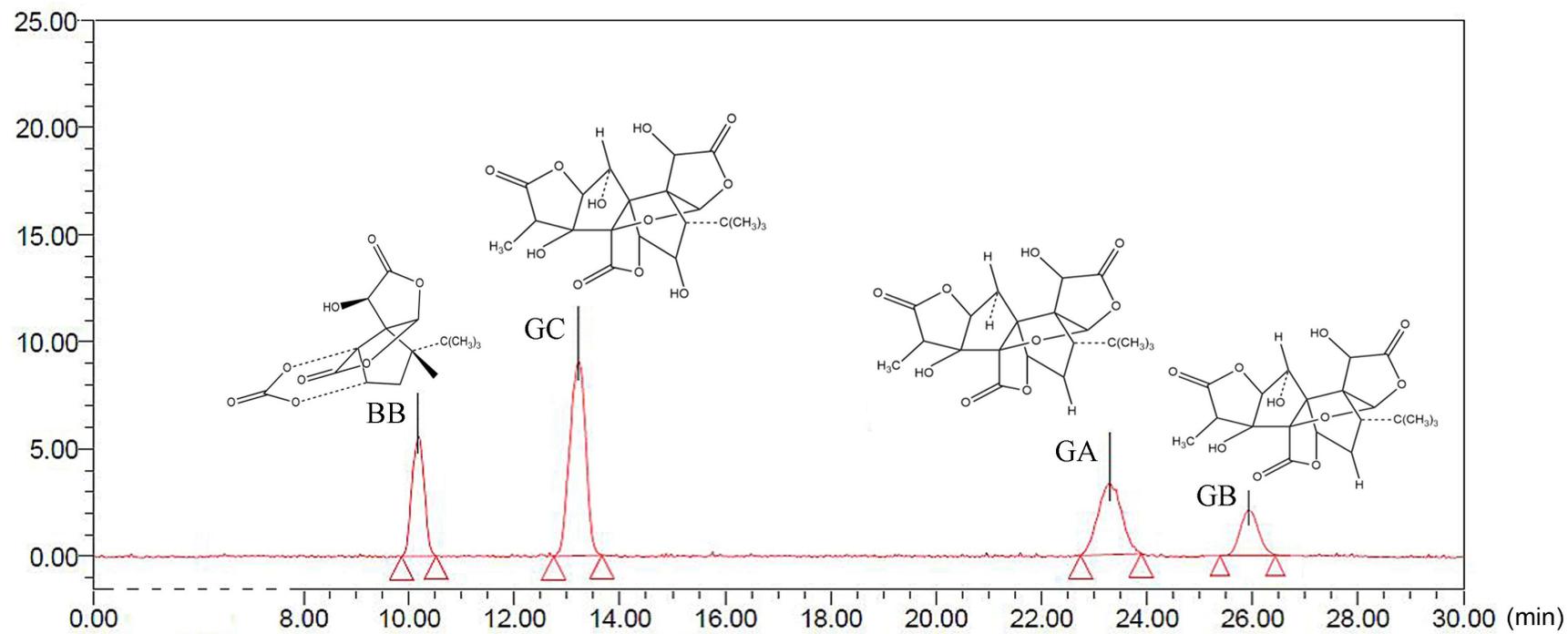


Figure S5. The HPLC chromatograms of the four standards (ginkgolide A, B, C, and bilobalide)

