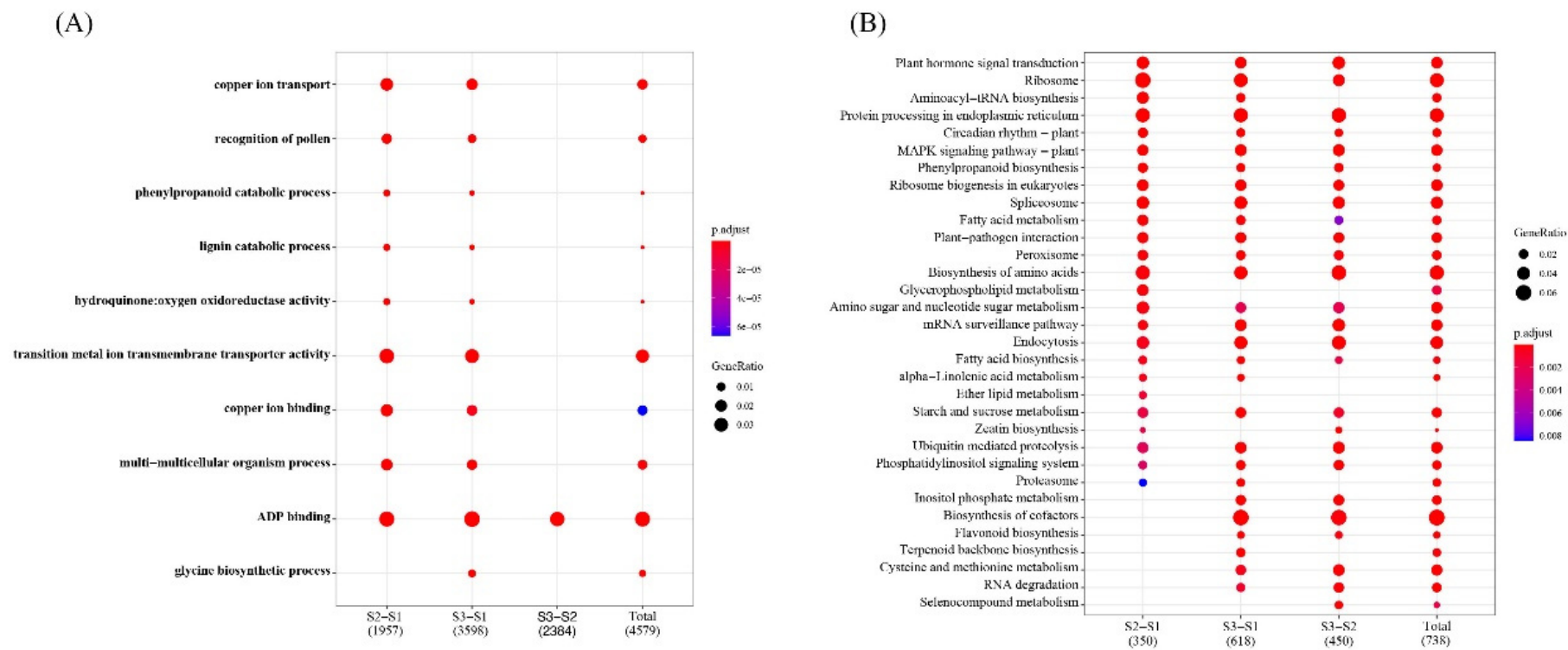
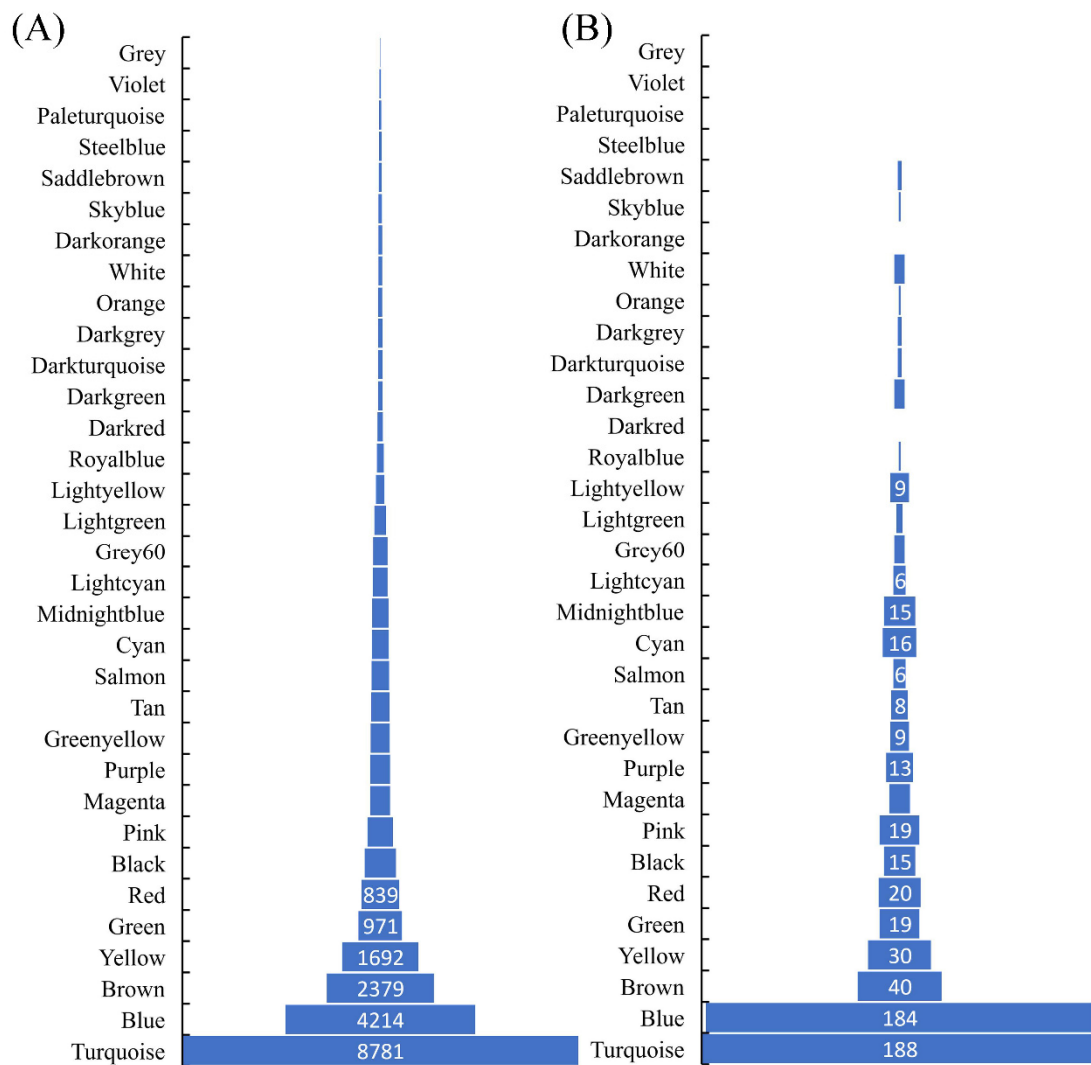


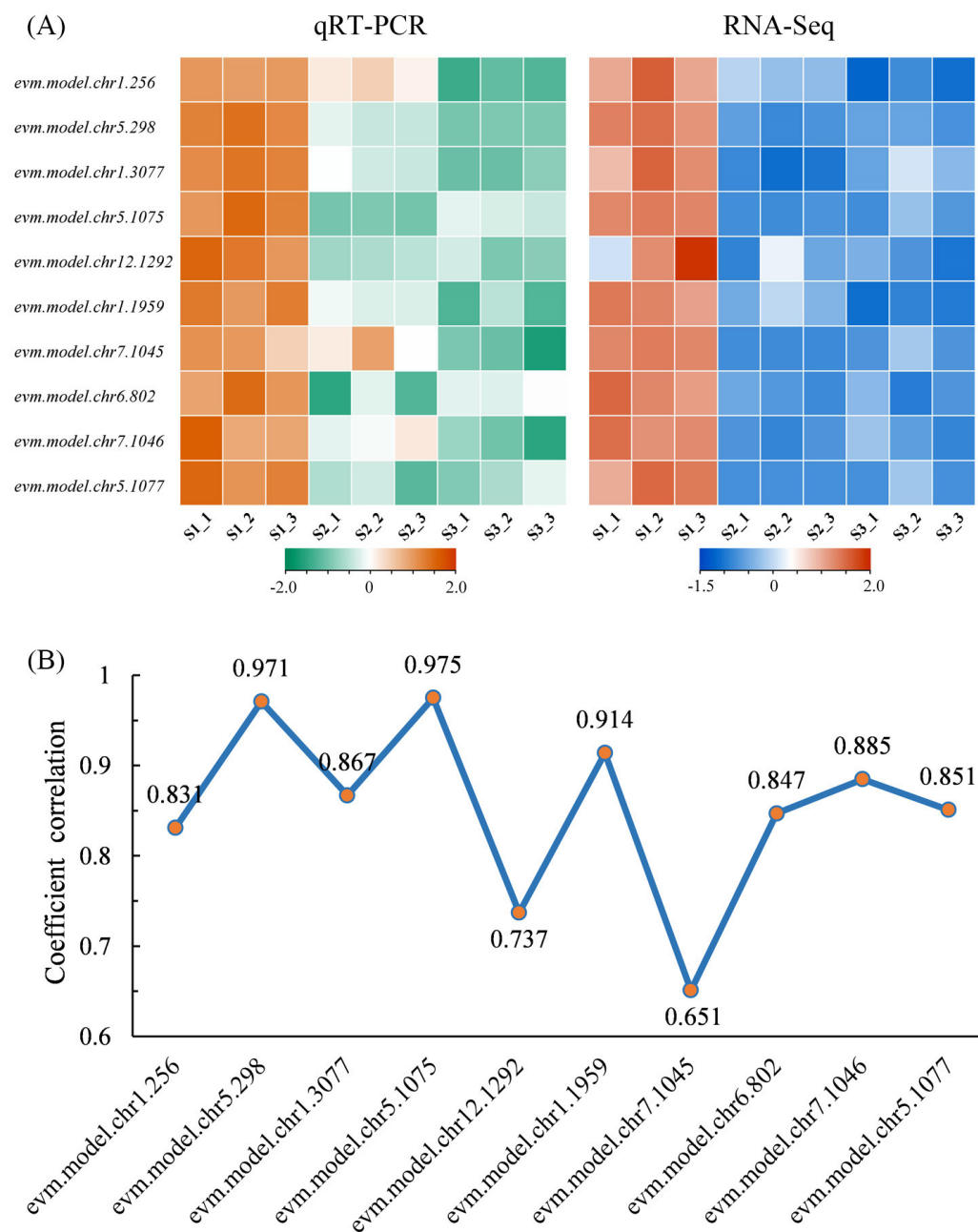
**Figure S1.** Differential expression genes (DEGs) analysis (A). The gene ontology (B) and KEGG pathway (C) of DEGs



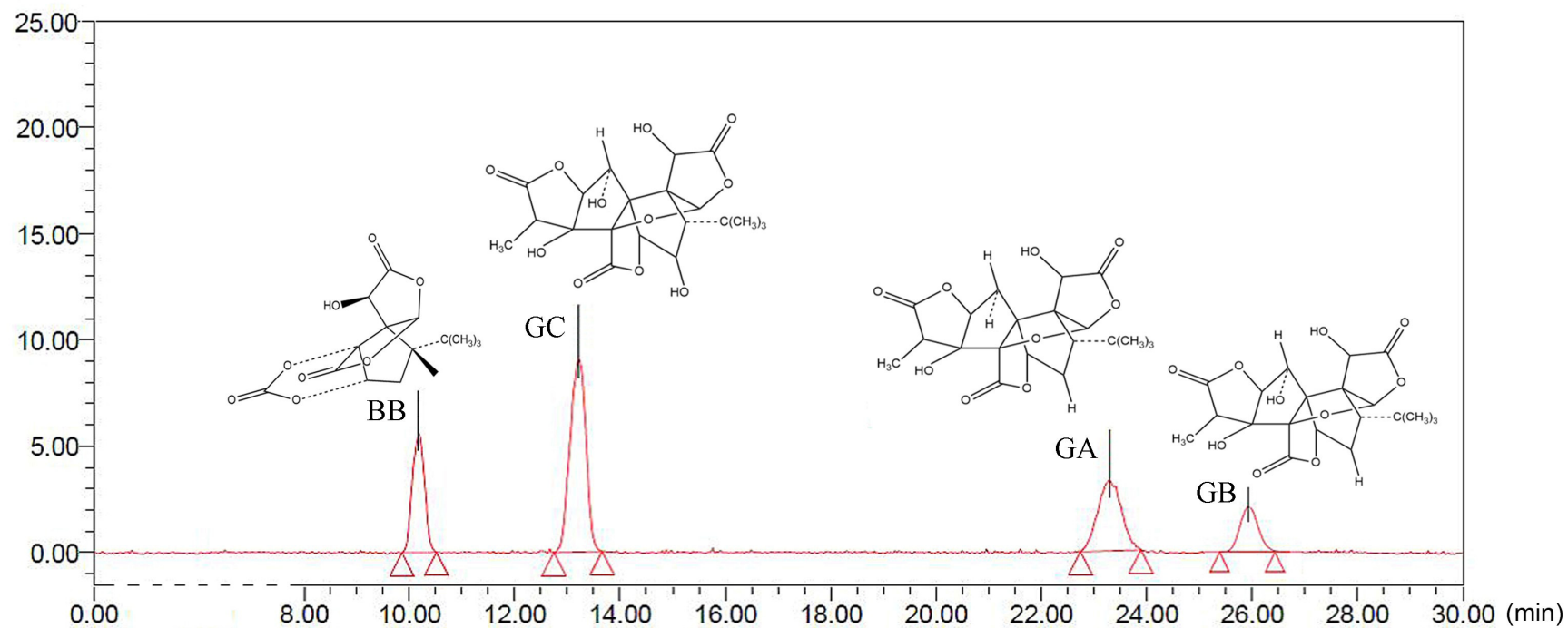
**Figure S2.** The gene ontology (A) and KEGG pathway (B) of the target genes of differentially expressed miRNAs (DEMs)



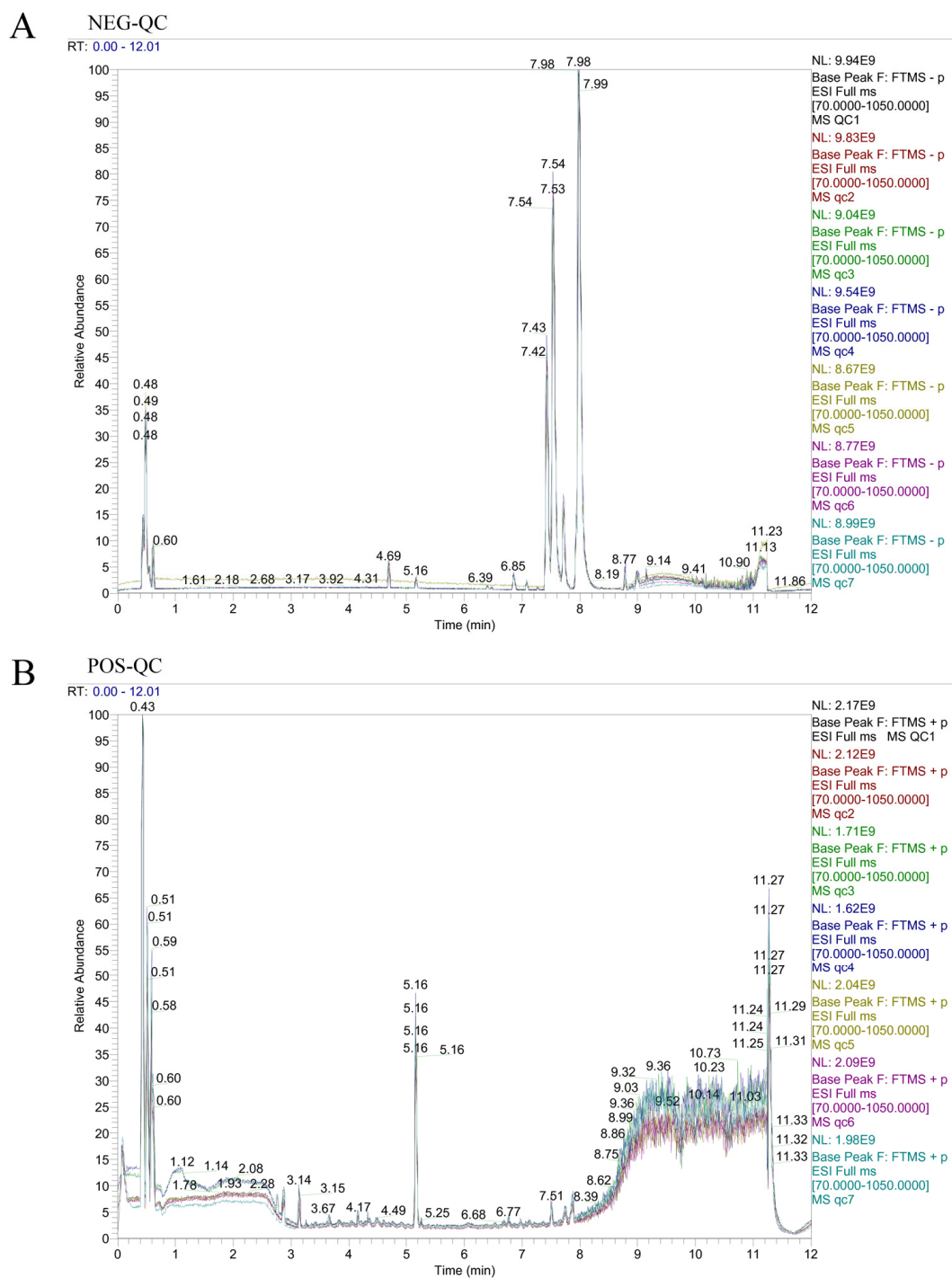
**Figure S3.** The number of gene (A) and transcription factor (B) in each module based on co-expression network analysis



**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)



**Figure S6.** The mass spectrum of the QC samples with negative ion mode (A) and positive ion mode (B)