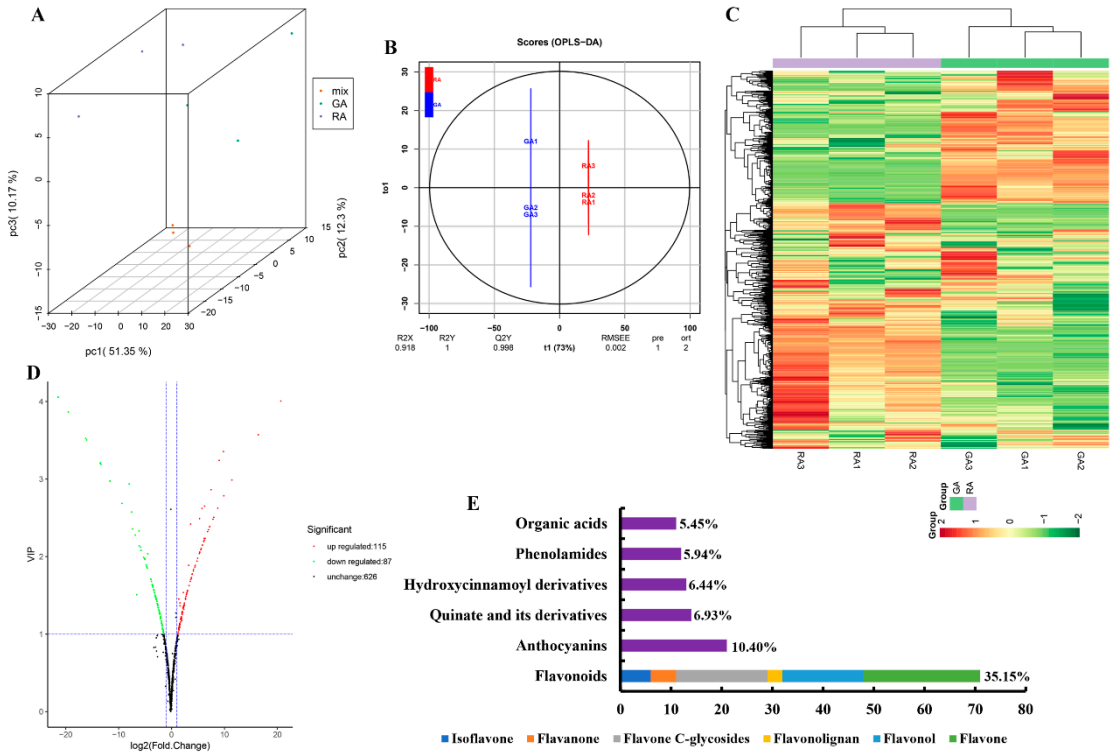


Figure S1. Differential metabolites analysis in GA and RA. (A) Principal component analysis (PCA) of the metabolic datasets. (B) The OPLS-DA model of differential metabolites. (C) The hierarchical heatmap clustering analysis (HCA) of metabolites in all samples. (D) Volcano plot of metabolites analysis of GA vs. RA. (E) The class distribution of DAMs in GA and RA.

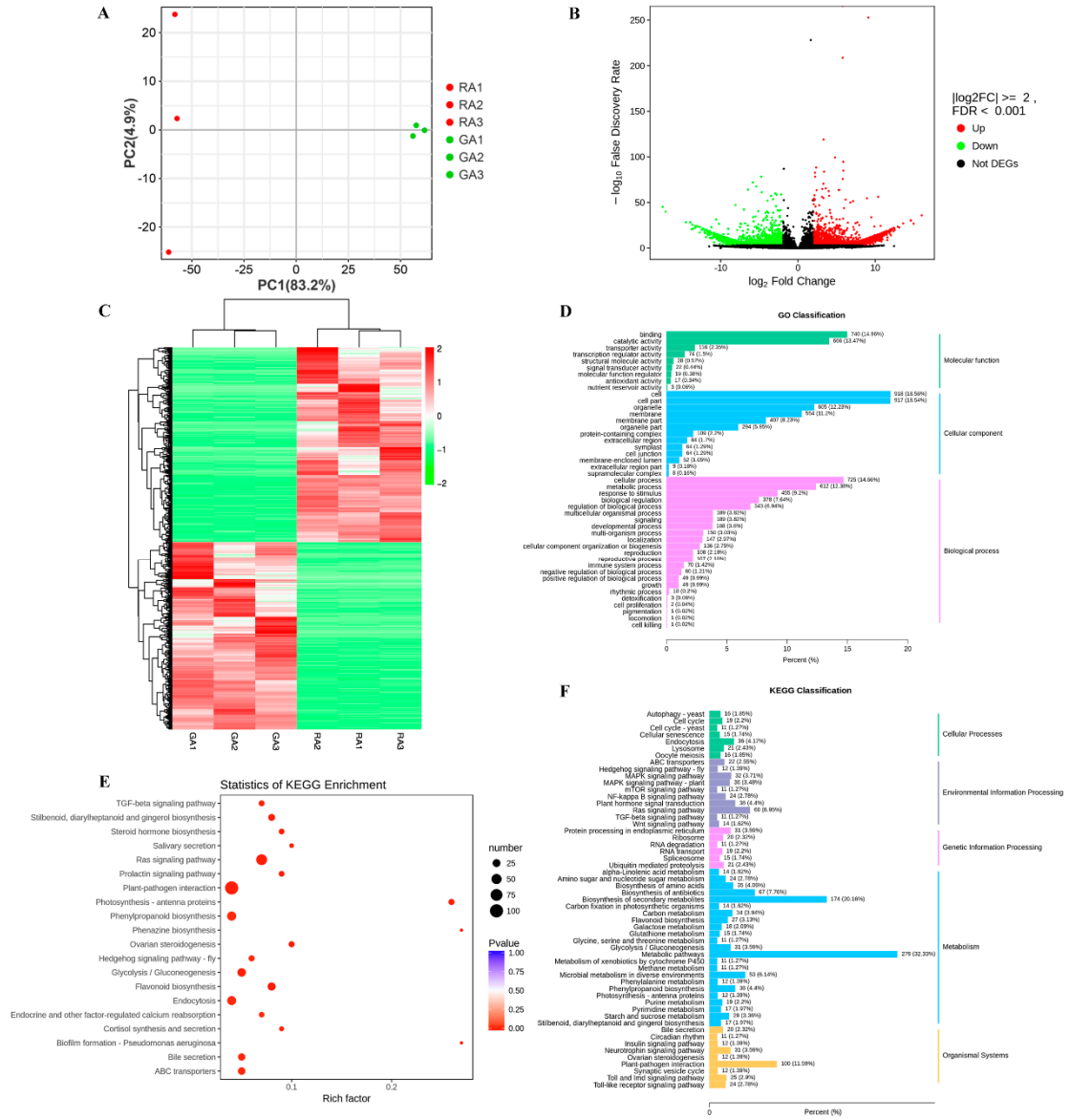


Figure S2. Analysis of DEGs in GA and RA. (A) Principal component analysis (PCA) of the transcriptomic datasets. (B) Volcano plot of gene differential analysis of GA and RA. (C) Overall cluster analysis of DEGs in the transcriptomic comparisons of GA and RA. FPKM was used to estimate the level of gene expression. (D) GO classification of DEGs. (E) Statistics of top 20 KEGG enrichment pathways of up- and down- regulated DEGs. (F) KEGG classification of DEGs.

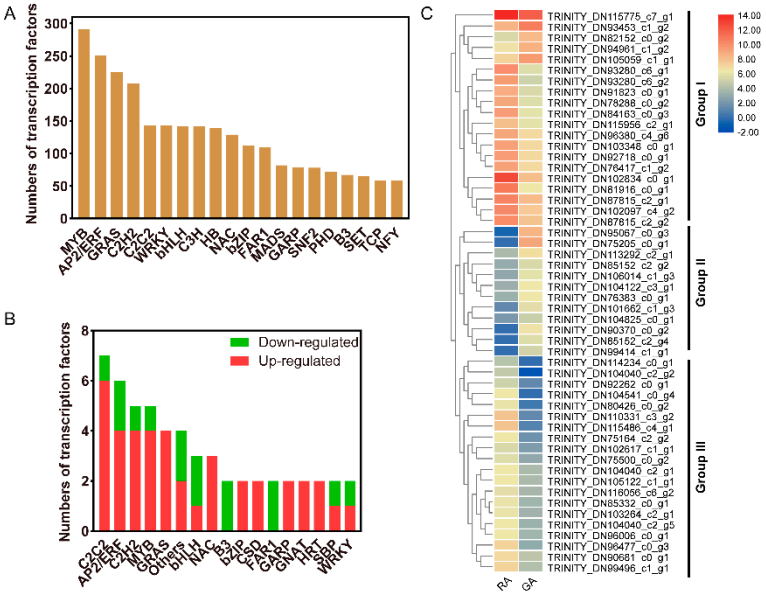


Figure S3. Analysis of TFs in GA and RA. (A) Numbers of each TF; (B) Differentially expressed TFs in GA and RA; (C) HCA of the differentially expressed TFs in GA and RA.

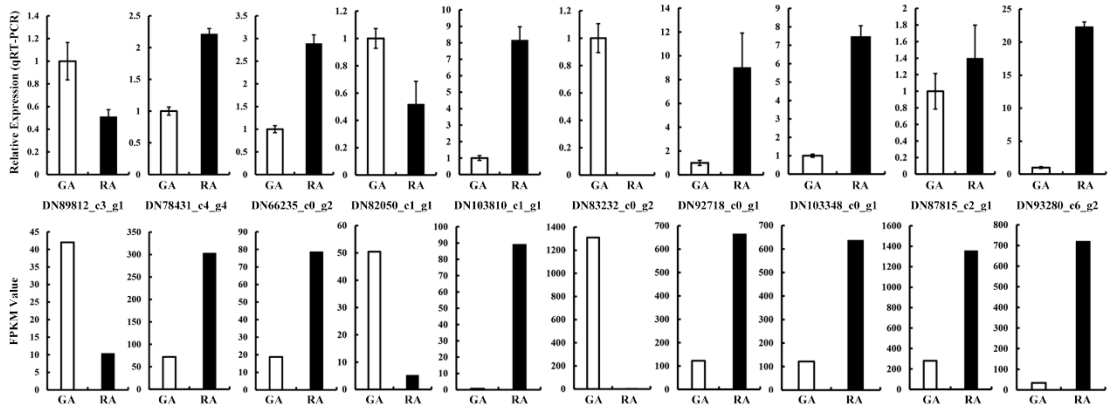


Figure S4. qPCR validation of transcript levels evaluated by RNA-seq.



Figure S5. The co-expression analysis between metabolite accumulation and differential gene expression. The red circles indicate up-regulated metabolites, the green circles indicate down-regulated metabolites. The red rectangles indicate up-regulated genes, the green rectangles indicate down-regulated genes.