

Figure S1. Overlap genes between DEGs and expressed genes.

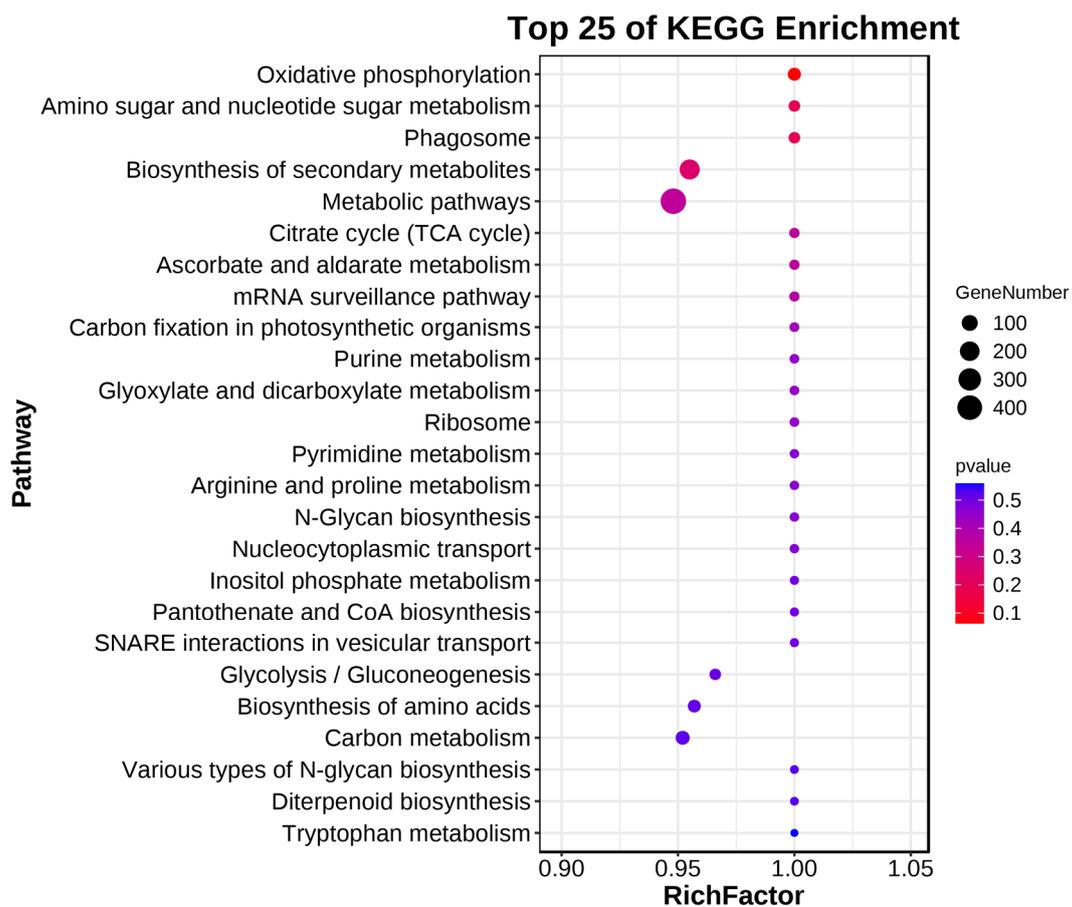


Figure S2. KEGG enrichment analysis of 13,194 differently expressed genes.

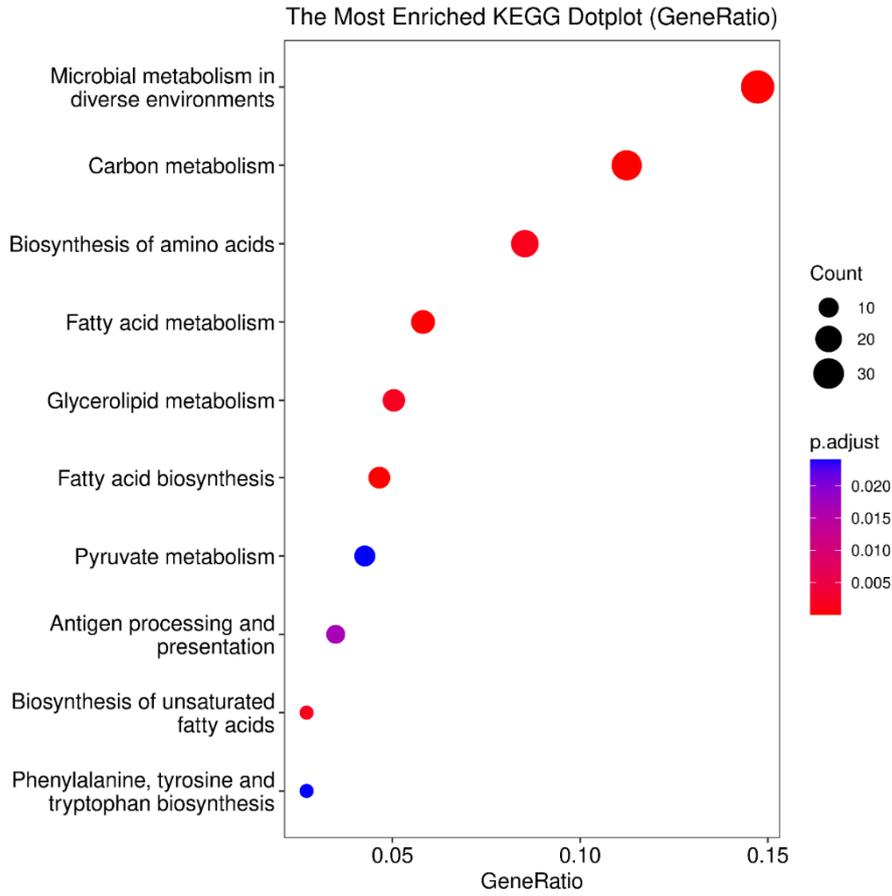


Figure S3. KEGG enrichment analysis of genes clustered in C5.

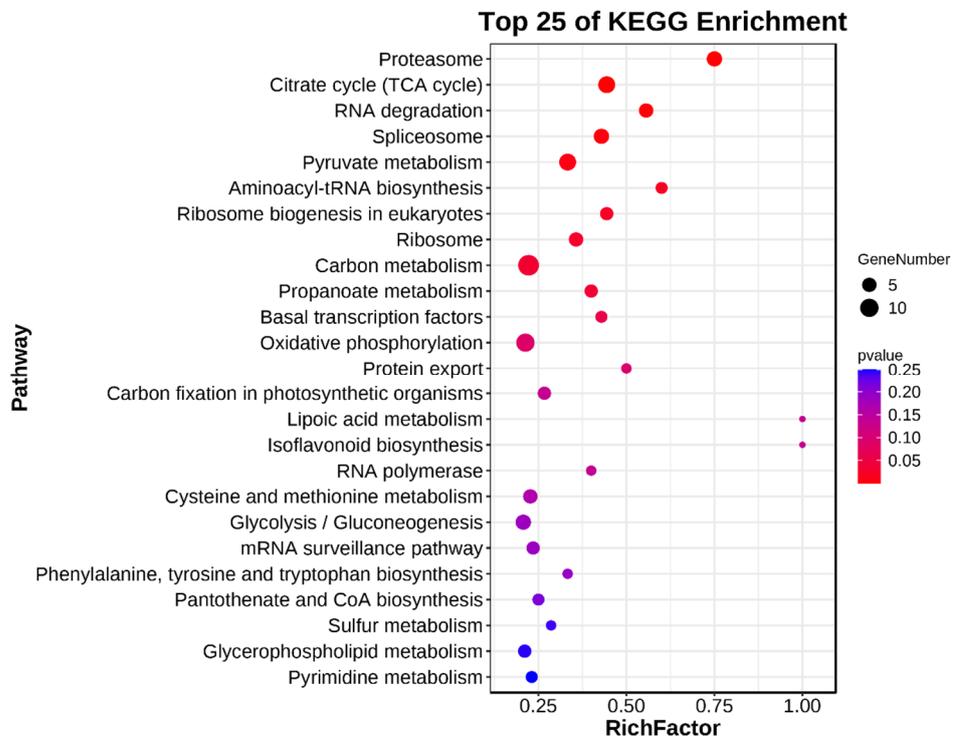


Figure S4. KEGG enrichment analysis of genes clustered in C2.

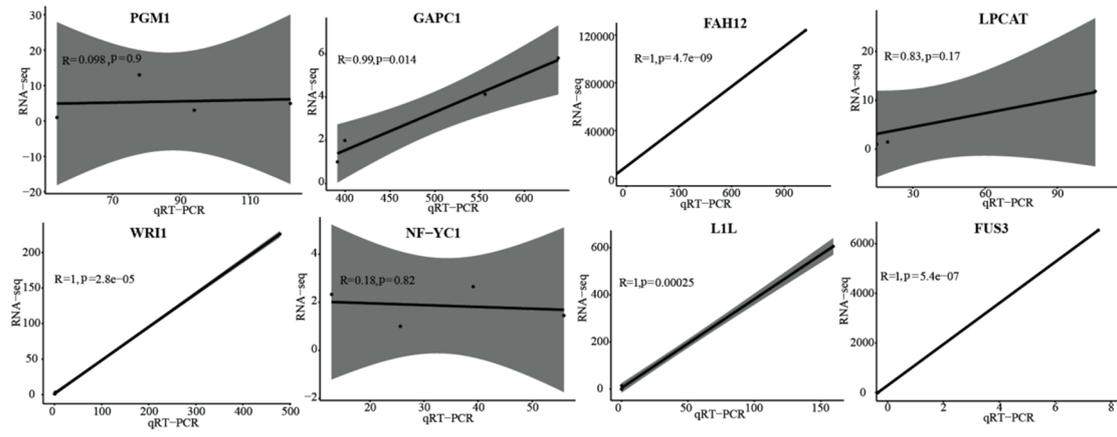


Figure S5. Correlation analysis of 8 genes involved in seed oil accumulation between RT-qPCR and RNA-Seq.