

Figure S1. Overlap genes between DEGs and expressed genes.

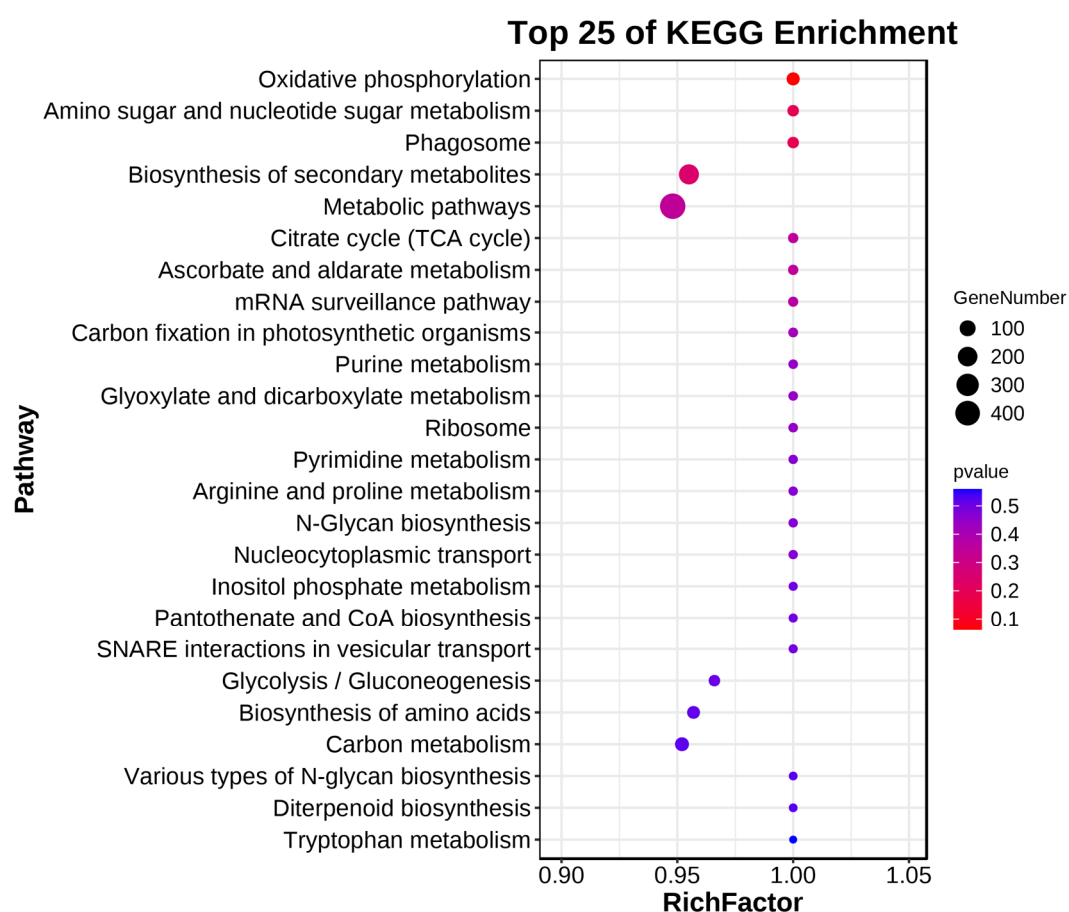
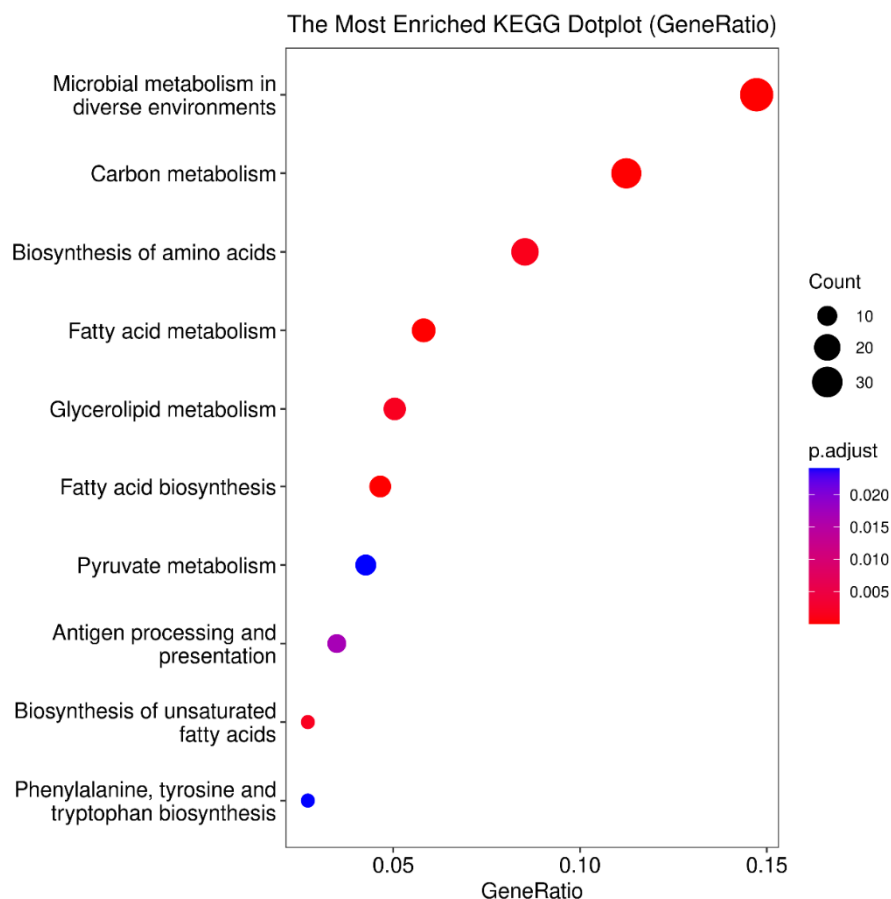
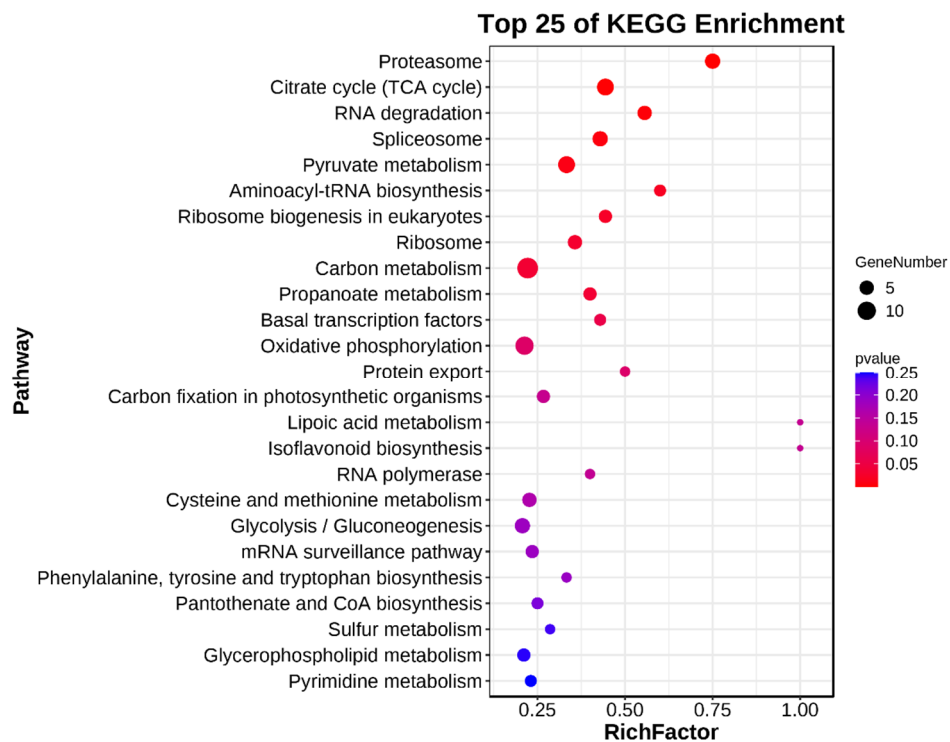


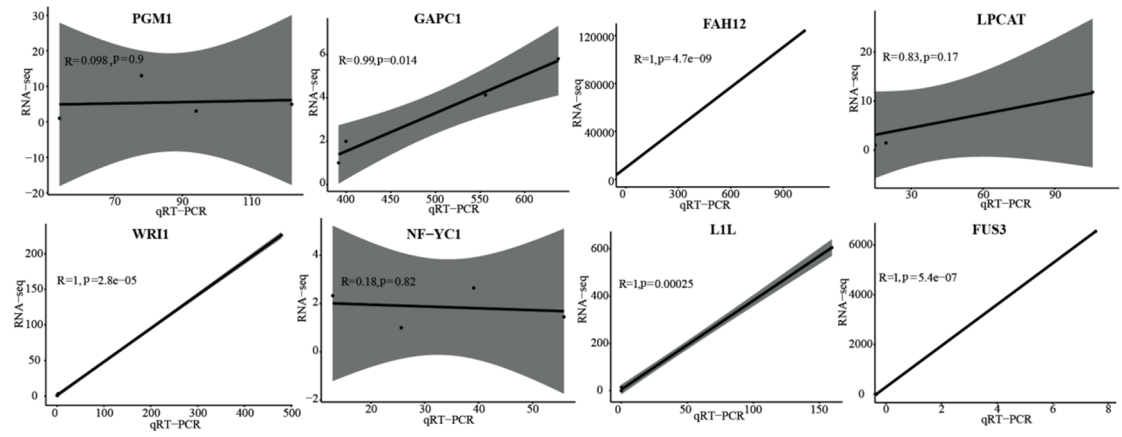
Figure S2. KEGG enrichment analysis of 13,194 differently expressed genes.



**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.**