

Figure S1. GO functional annotation of all the transcripts.

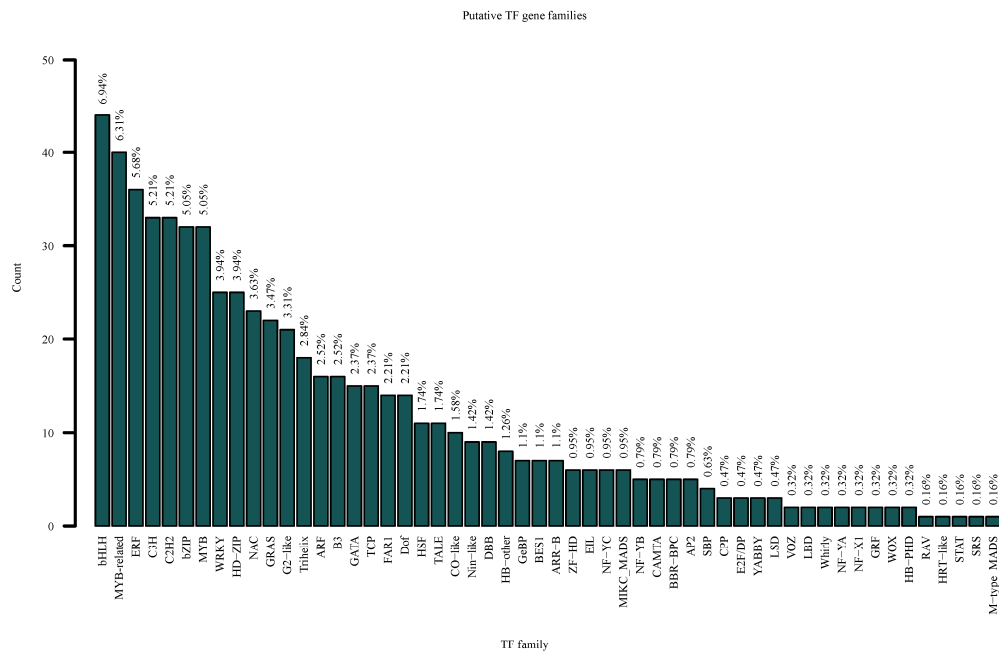


Figure S2. Transcription factor family classification.

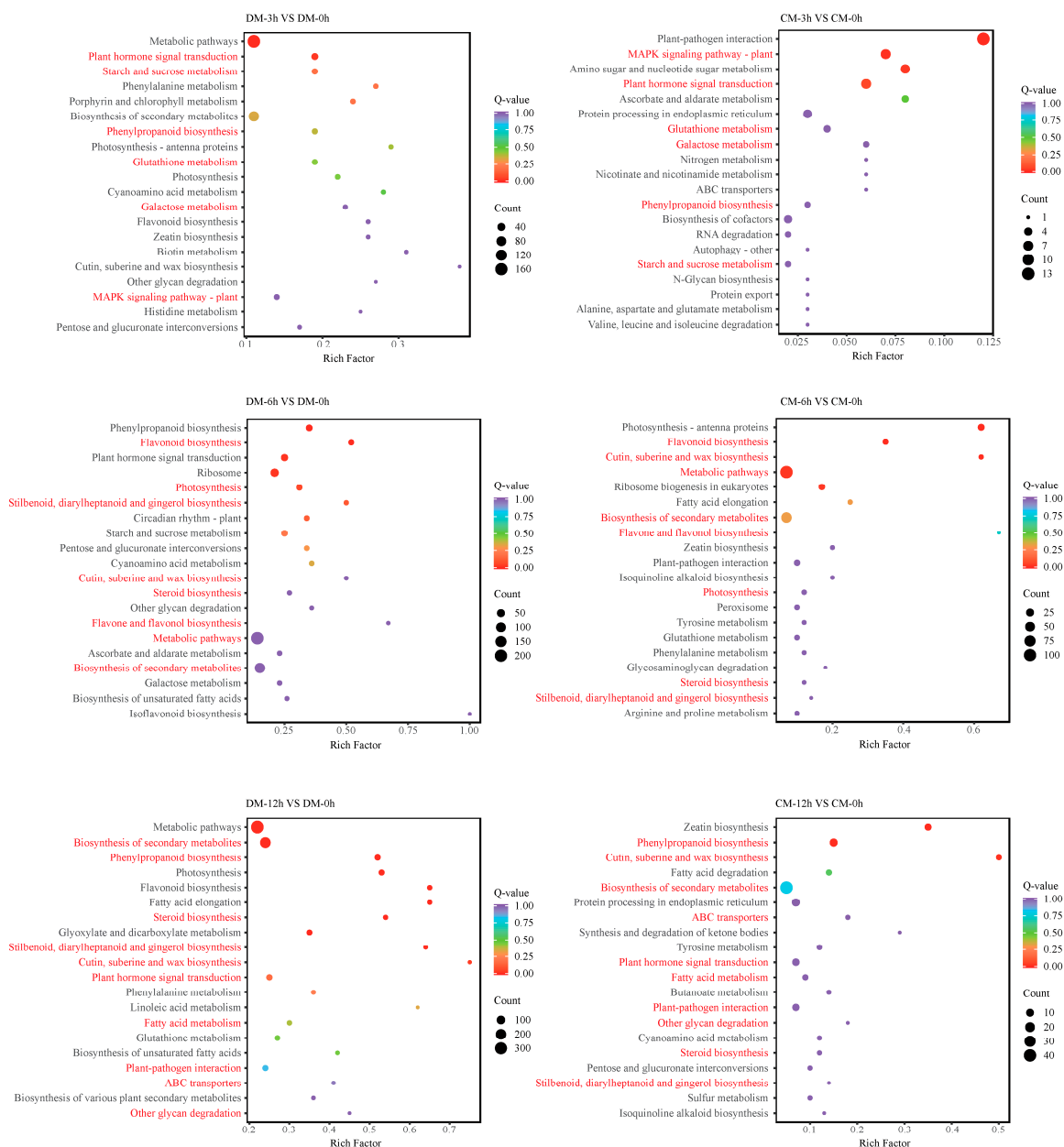


Figure S3. KEGG pathway enrichment analysis of the DEGs identified in DM and CM