

Figure S1. The top 30 comparative analysis of Gene Ontology category of DEGs at different time points after GA₃ treatment in *J. curcas*.

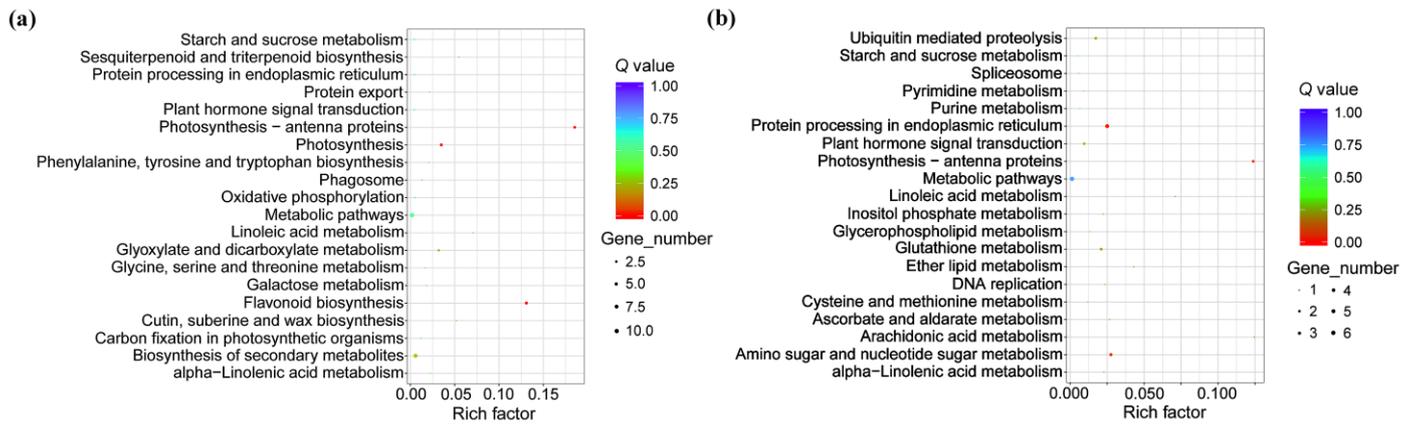


Figure S3 The KEGG enrichment pathways involved in male floral differentiation after GA₃ treatment in *J. curcas*. The Rich factor indicated the percentages of DEGs belong to the corresponding pathway. The left y-axis represented the enrichment pathways. The sizes of bubble represent the number of DEGs in the corresponding pathway, and the colors of the bubble represent the enrichment Q value of the corresponding pathway. (a) KEGG enrichment pathways of the DEGs co-detected in STD1 vs. IND and GA₃ treatment. (b) KEGG enrichment pathways of the DEGs co-detected in STD1 vs. IND & STD2 vs. STD1 and GA₃ treatment, STD2 vs. STD1 and GA₃ treatment.

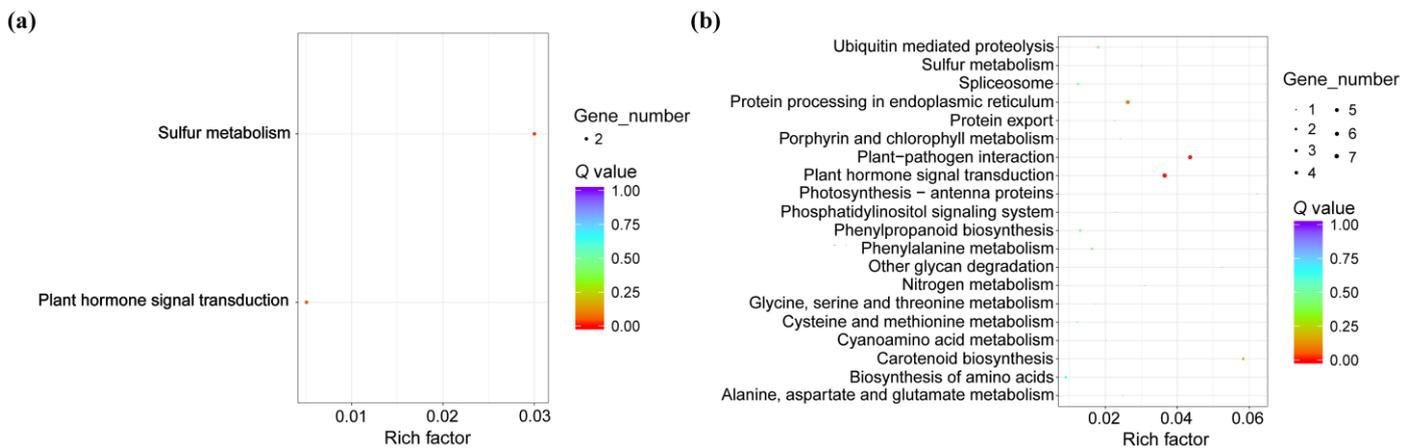


Figure S4 The KEGG enrichment pathways involved in female floral differentiation after GA₃ treatment in *J. curcas*. The Rich factor indicated the percentages of DEGs belong to the corresponding pathway. The left y-axis represented the enrichment pathways. The sizes of bubble represent the number of DEGs in the corresponding pathway, and the colors of the bubble represent the enrichment Q value of the corresponding pathway. (a) KEGG enrichment pathways of the DEGs co-detected in PID1 vs. IND and GA₃ treatment. (b) KEGG enrichment pathways of the DEGs co-detected in PID1 vs. IND & PID2 vs. PID1 and GA₃ treatment, PID2 vs. PID1 and GA₃ treatment.