

Figure S1. Functional annotation of the longest unigene collection based on gene ontology (GO) categorization.

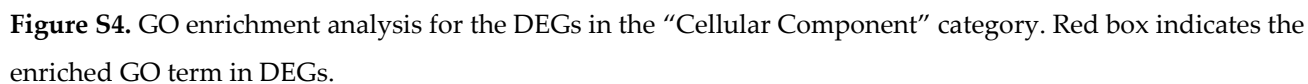


Figure S4. GO enrichment analysis for the DEGs in the “Cellular Component” category. Red box indicates the enriched GO term in DEGs.