

Figure S1. Expression levels of candidate genes that associated with callus adventitious rooting in the cotyledon-derived callus. The genes expression as determined by qRT-PCR.

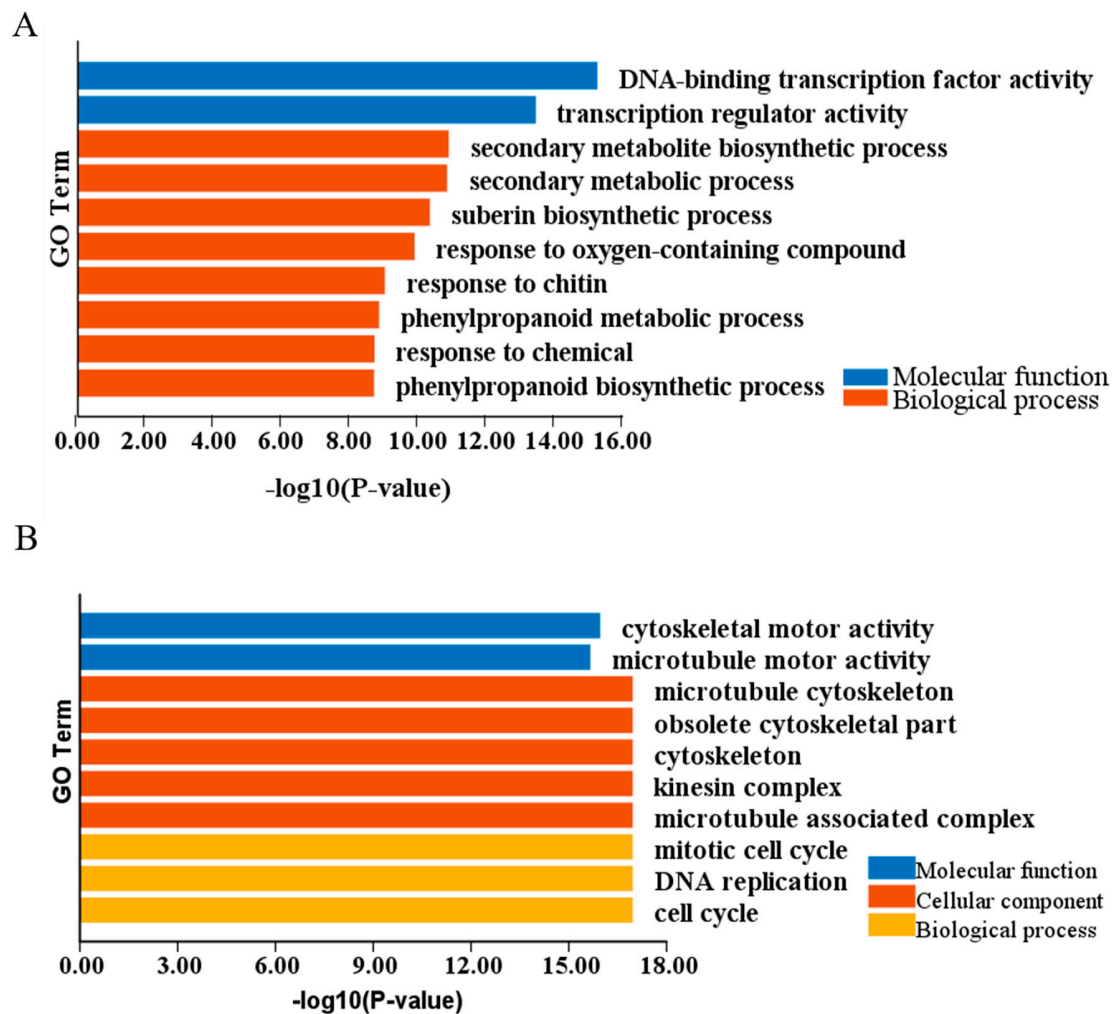


Figure S2. Gene ontology (GO) enrichment. **(A)** Ten enriched GO terms were identified by based on 1621 up-regulated DEGs. **(B)** Ten enriched GO terms were identified by based on 1120 down-regulated DEGs.