



**Supplementary Fig. 1.** Modular analysis of common differentially expressed genes (DEGs). (A) The protein-protein interaction (PPI) network constructed by string database and Cytoscape. (B, C, D) Module 1, 2, and 3 gene cluster of the PPI network were calculated by MCODE maximal clique centrality (MCC) method. (E) The count of DEGs from Module 1, 2, and 3 in each term, enriched by Gene Ontology (GO) biological process enrichment.