Figure S1. Flowchart of the bioinformatics analytical methods. GO annotation and KEGG analysis are two important databases in the DAVID database. The GO database mainly describes genes or gene products from different aspects. KEGG is mainly a database for analyzing gene functions, which links the information of the genome with gene functions, providing an intuitive understanding of the pathways. In the present study, DEGs were first screened out using the GEO2R online tool. In order to further understand the functions of these genes and the enriched pathways, GO function annotation and KEGG enrichment pathway analyses of these DEGs were conducted through the DAVID database. By adjusting the P-value and FDR, the enrichment pathway that is required can be selected. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DAVID, Database for Annotation, Visualization and Integrated Discovery; DEGs, differentially expressed genes; FDR, false discovery rate.