Figure S1. Analysis of enriched GO terms and KEGG pathways for Janus kinase genes using Database for Annotation, Visualization and Integrated Discovery. (A) Biological process results of GO functional enrichment analysis. (B) Cellular component results of GO functional enrichment analysis.

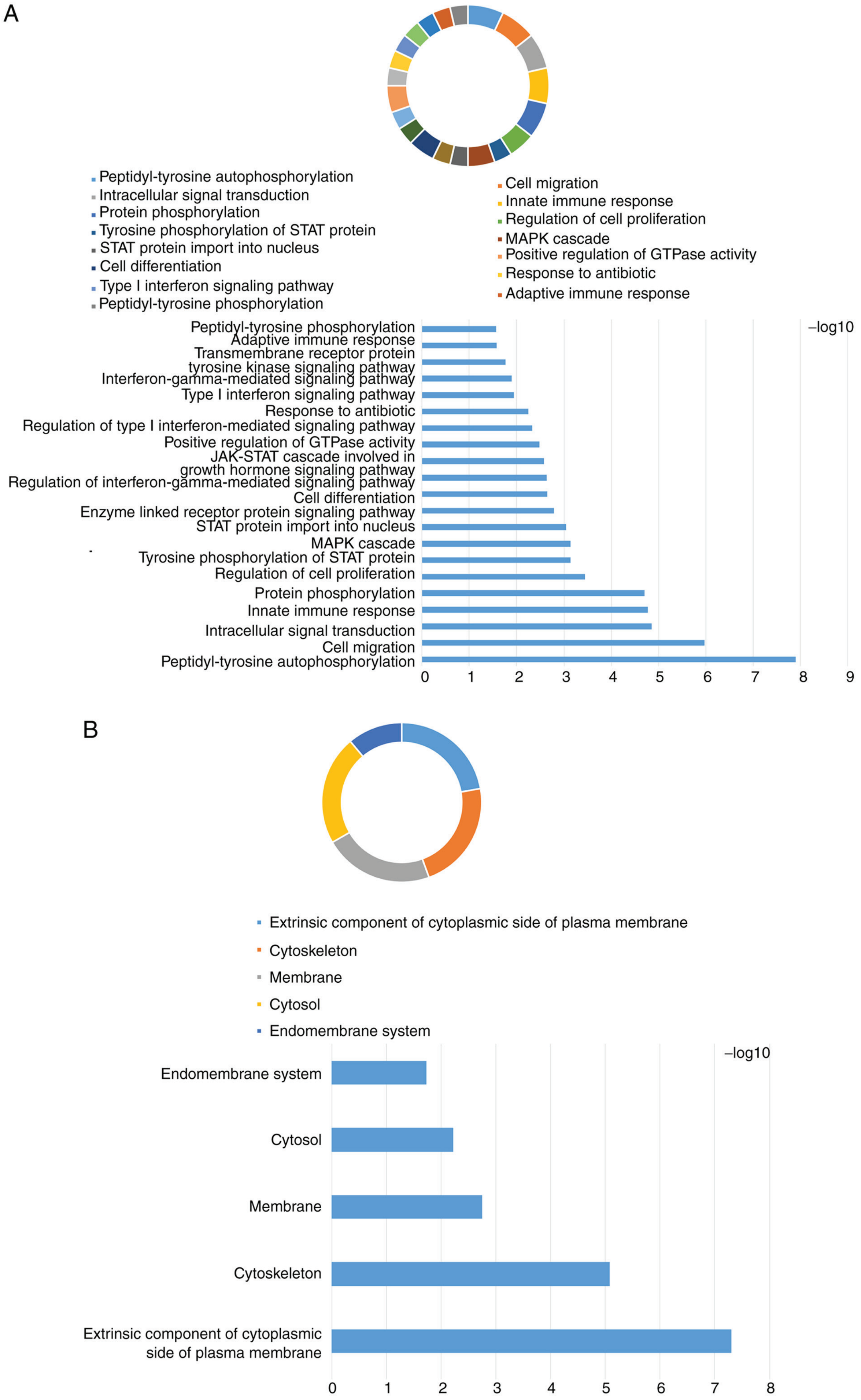

Figure S1. Continued. (C) Molecular function results of GO functional enrichment analysis. (D) KEGG pathway analysis results. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

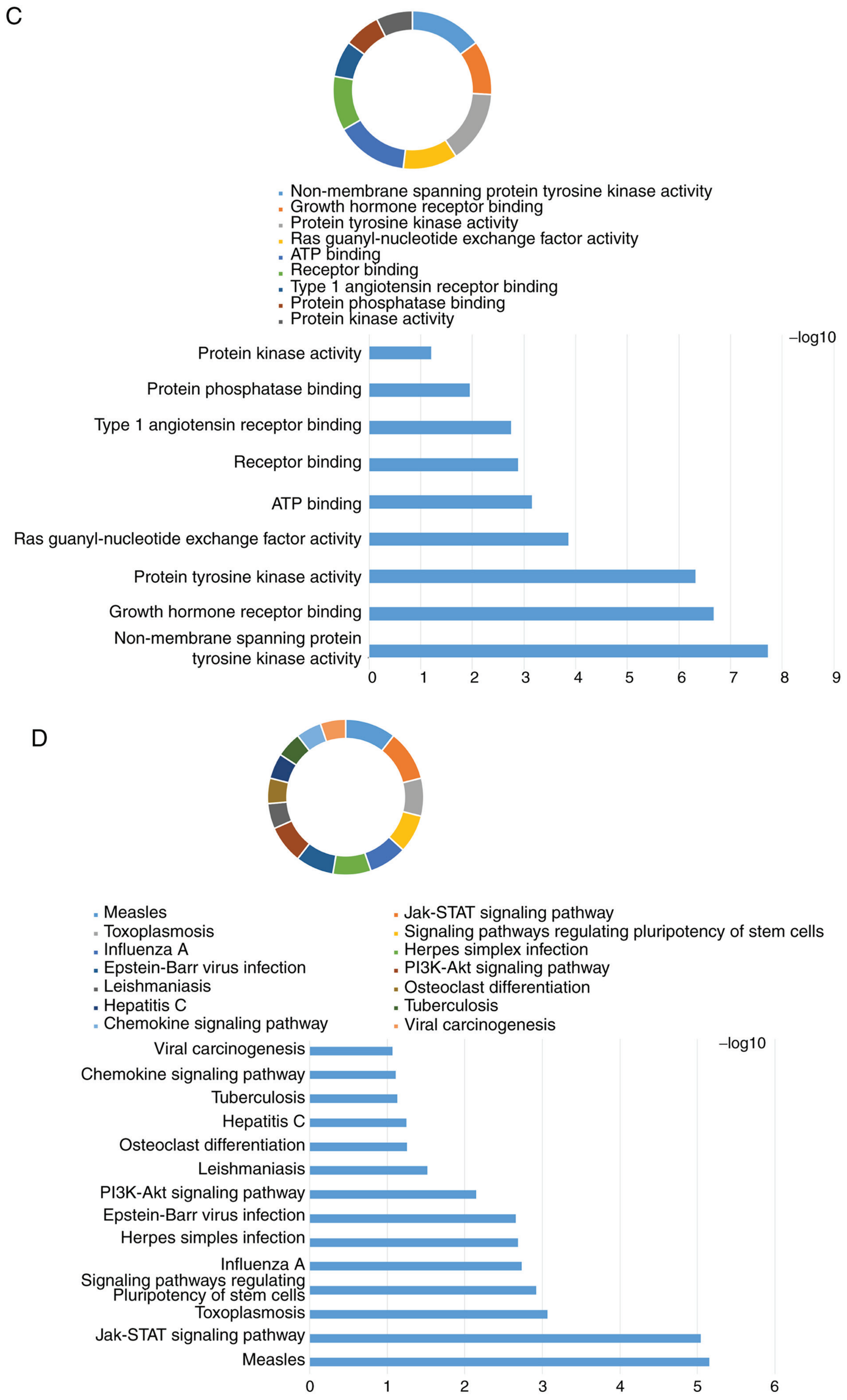

Figure S2. Analysis of enriched GO terms and KEGG pathways for signal transducer and activator of transcription genes using Database for Annotation, Visualization and Integrated Discovery. (A) Biological process results of GO functional enrichment analysis. (B) Cellular component results of GO functional enrichment analysis.

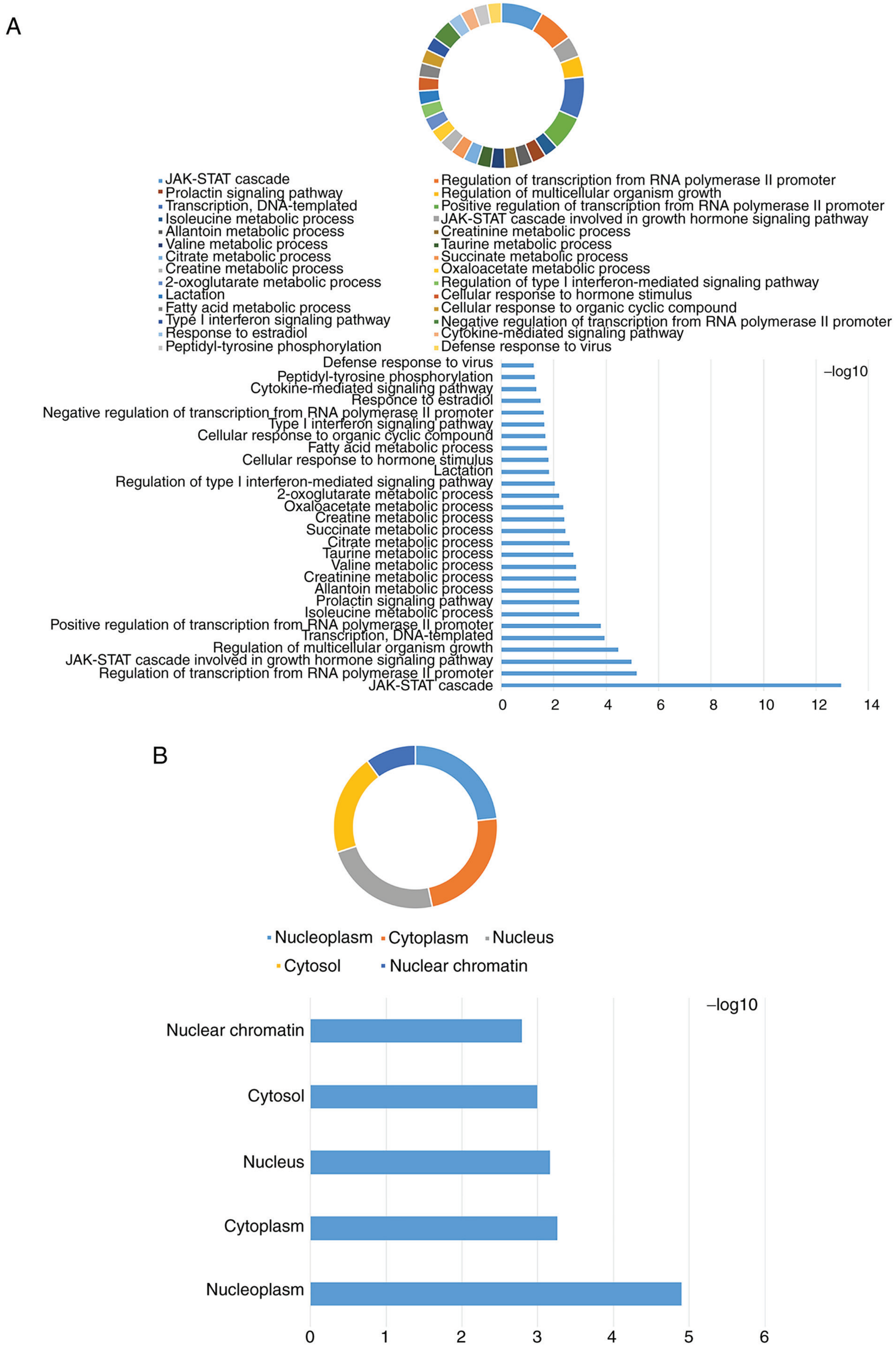

Figure S2. Continued. (C) Molecular function results of GO functional enrichment analysis. (D) KEGG pathway analysis results. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes. GO, gene ontology; KEGG, Kyoto encyclopedia of genes and genomes.

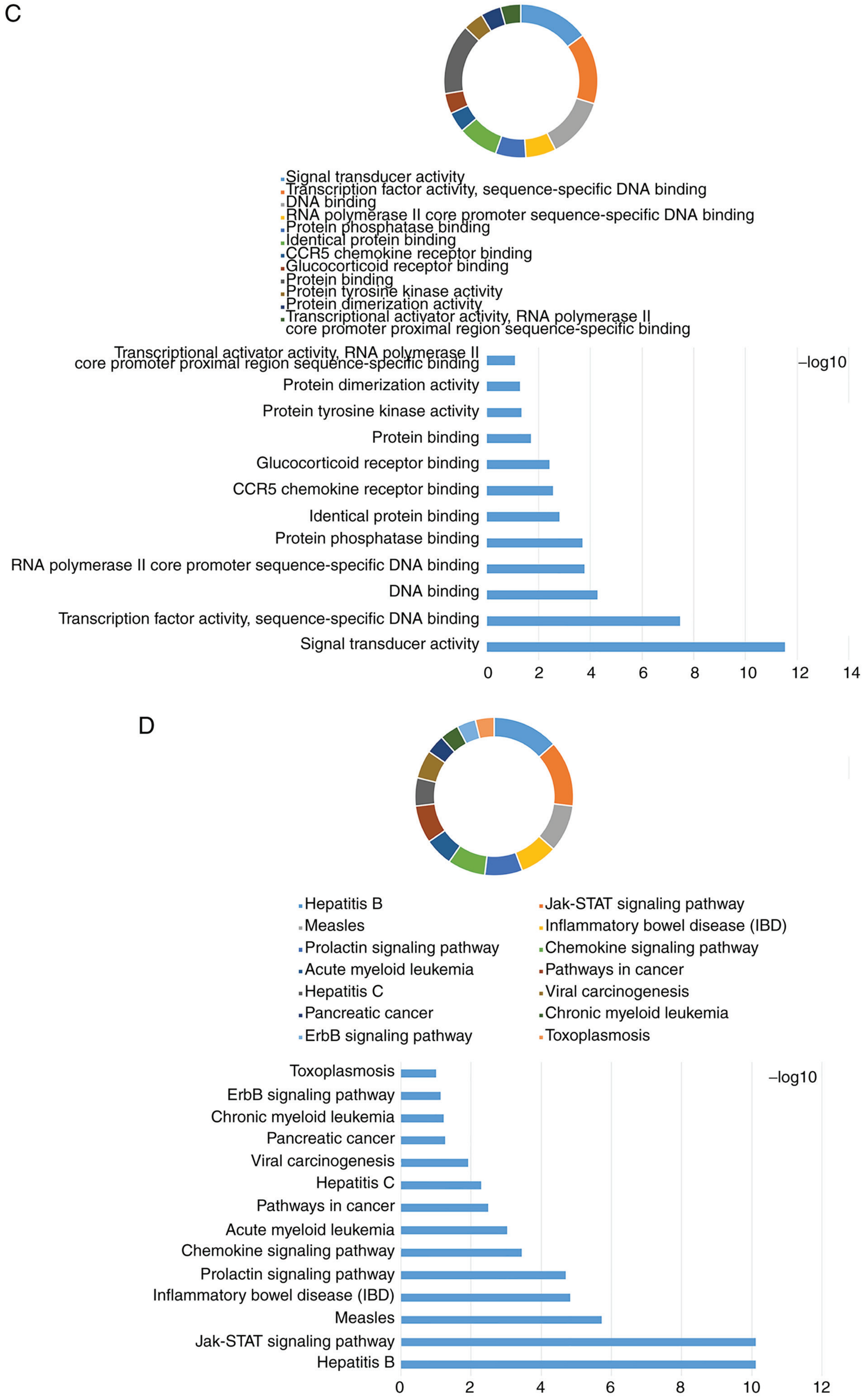

Figure S3. Gene interaction network of Janus kinase genes generated by gene multiple association network integration algorithm.

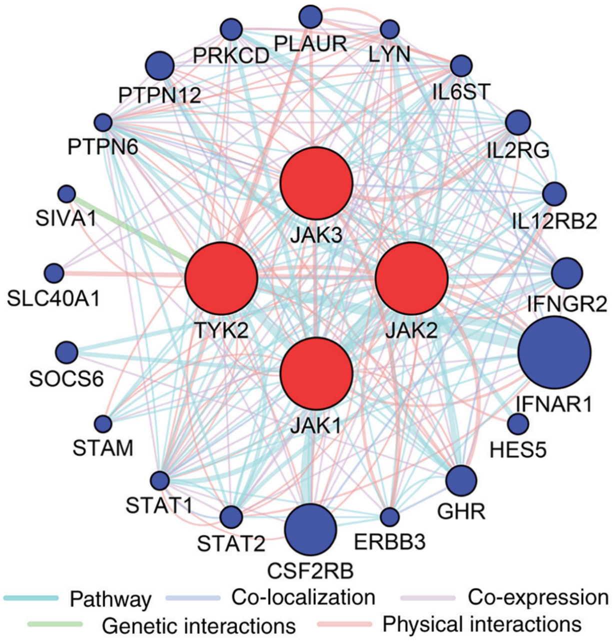

Figure S4. Gene interaction network of signal transducer and activator of transcription genes generated by gene multiple association network integration algorithm.