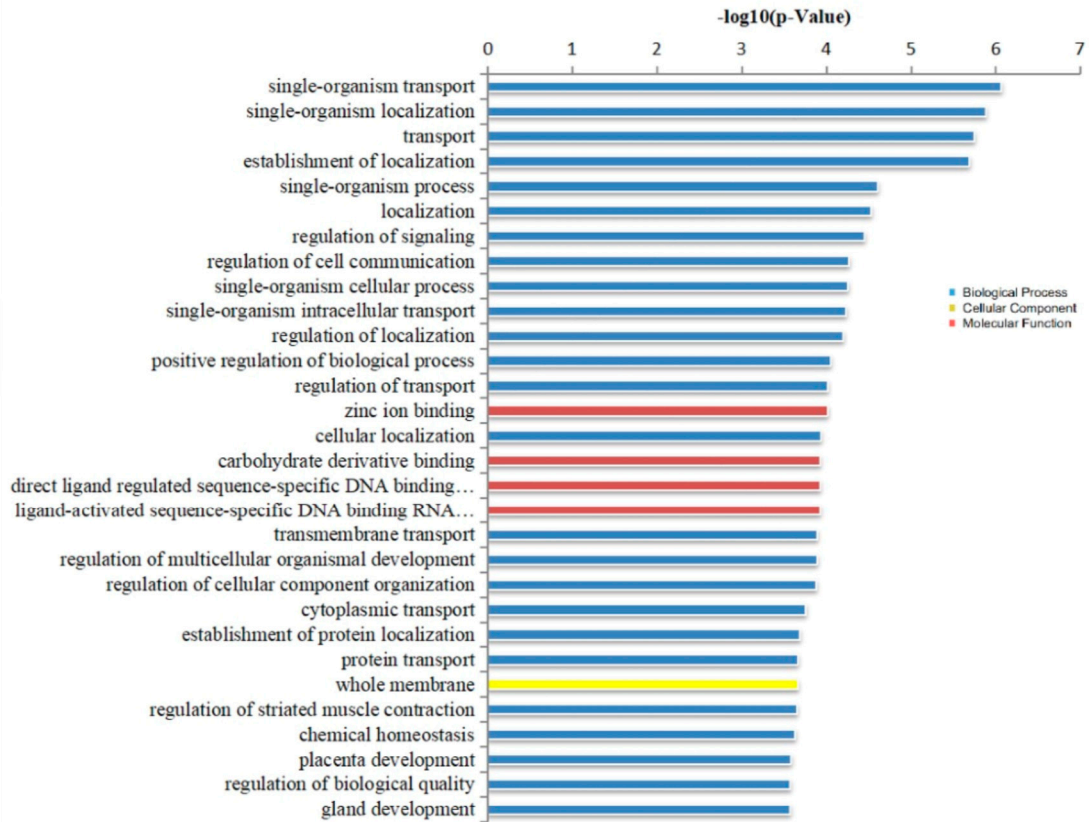
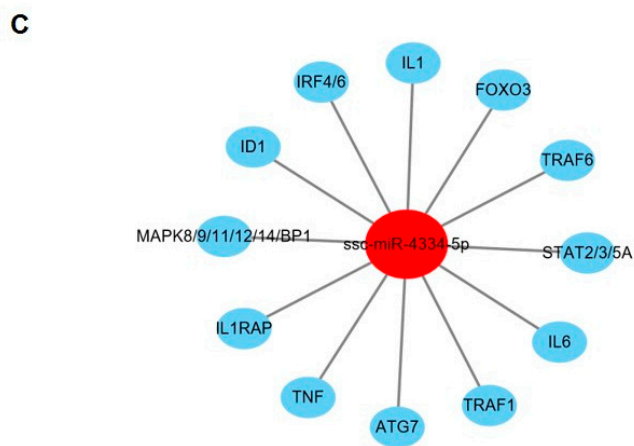
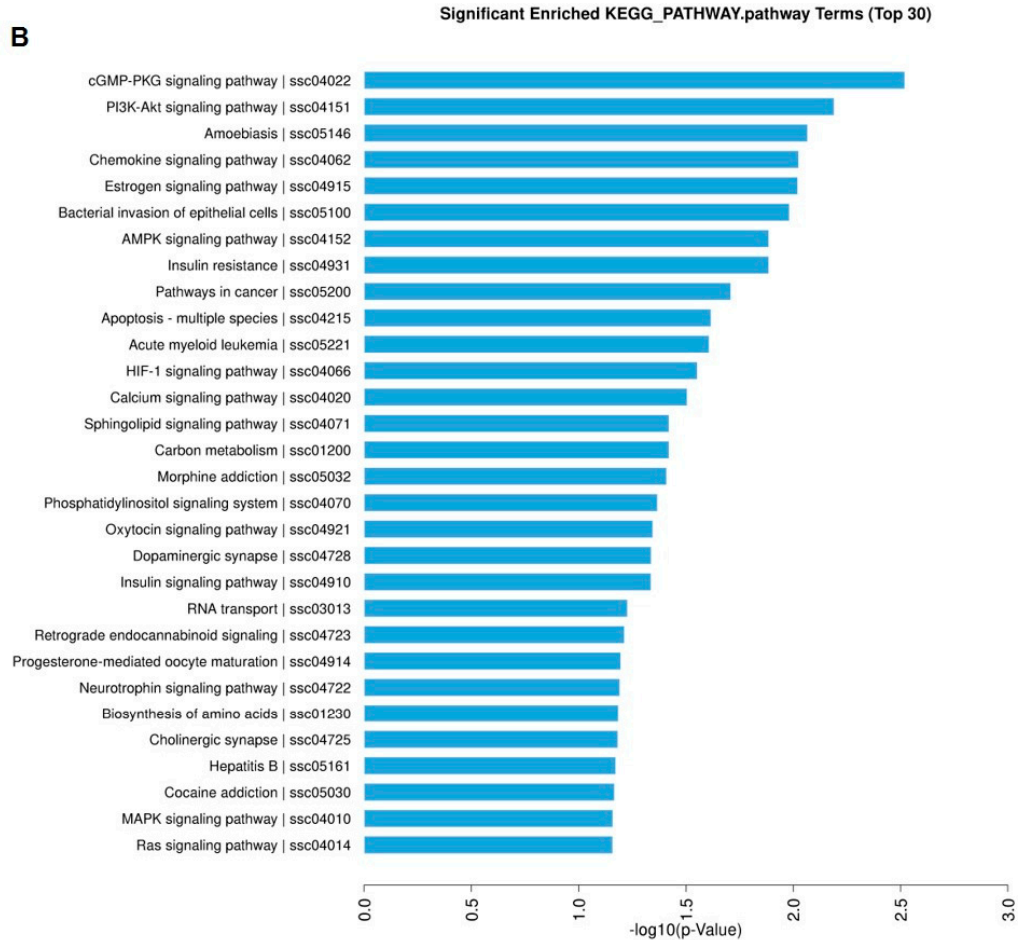


A

Significant Enrichment GO Terms(Top 30)





Supplemental Figure 1. Bioinformatics analysis demonstrated miR-4334-5p participated in interferon regulation.

(A). Top 30 significantly enriched gene ontology (GO) terms of miR-4334-5p. The blue bars represent biological process. The yellow bars represent cellular component. The red bars represent molecular function. The ordinate is the GO terms, and the abscissa is the $-\log$ (P-value) of GO terms. The length of the bar represents the $-\log$ (P-value); credibility increases with bar length. (B). Top 30 significantly enriched pathways of Differentially expressed genes (DEGs) in miR-4334-5p. The ordinate is Kyoto Encyclopedia of Genes and Genomes (KEGG) signaling pathways, and the abscissa is the $-\log$ (P-value) of pathways. (C). The target genes

prediction of miR-4334-5p and microRNA-gene interaction networks analysis by software shown in materials and methods. The red dot represents miRNA. Blue dots represent its target genes. Lines represent the regulation relationship of miRNA-target gene.