

Supplementary Figure

KEGG Enrichment based Functional Annotation of of miRNA-Target Genes

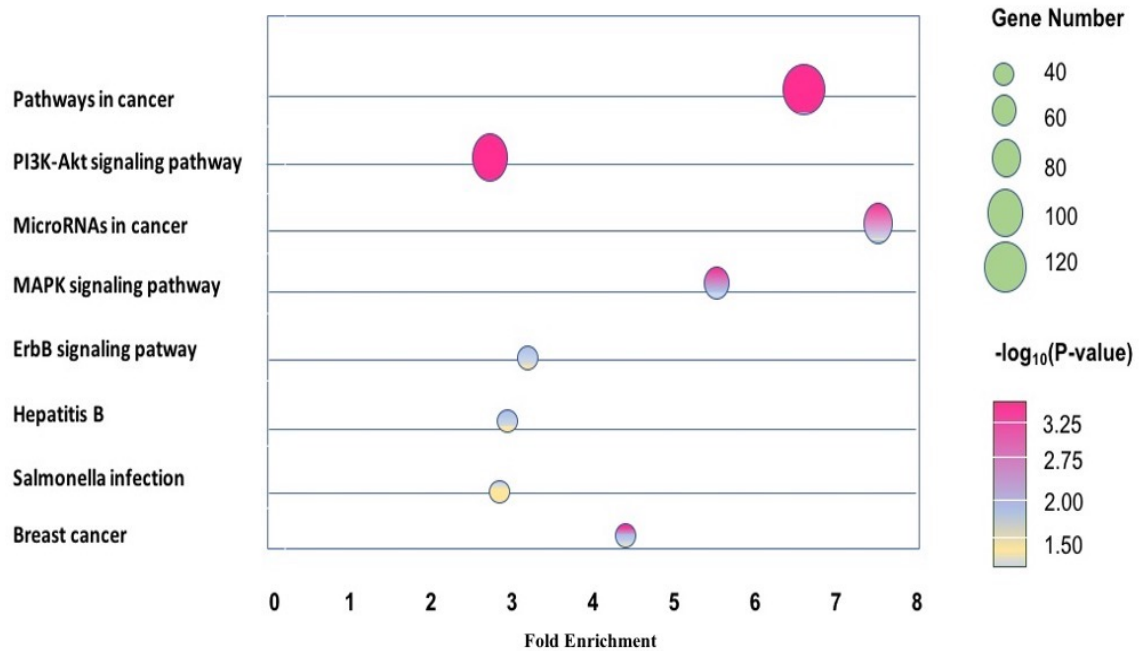


Figure S1. Represents functional enrichment analysis based on Kyoto Encyclopedia of Genes and Genomes analysis (KEEG) using DAVID online tools, revealing top eight highly enriched pathways

Gene Ontology analysis of candidate miRNA-Target Genes

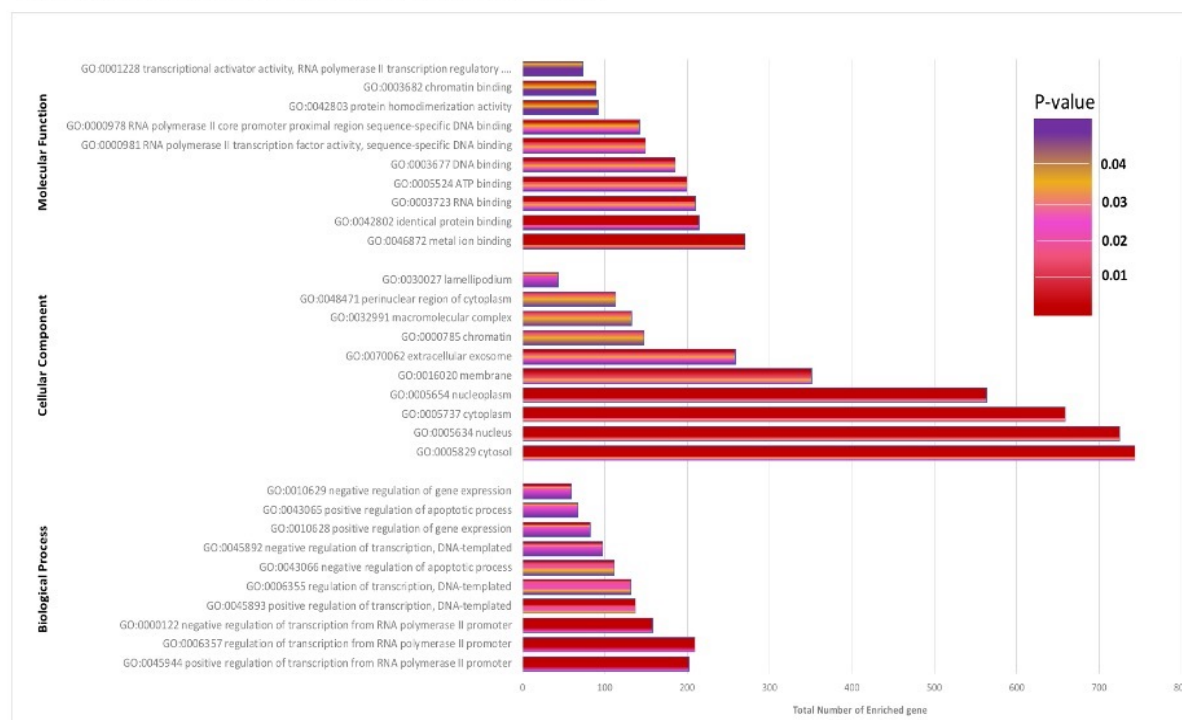


Figure S2. Represents functional enrichment analysis based on Gene Ontology analysis, revealing top ten highly enriched term of miRNA-target genes in Molecular Function, Biological Process and Cellular Component