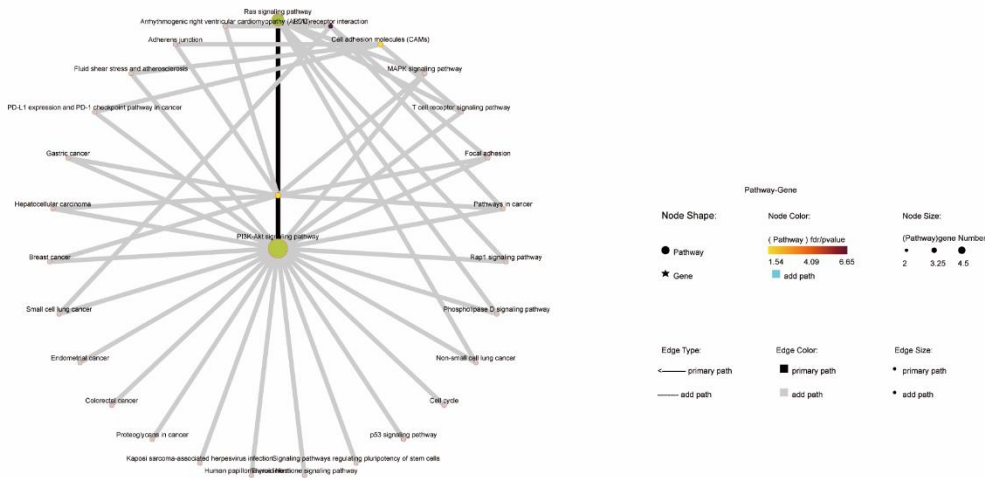


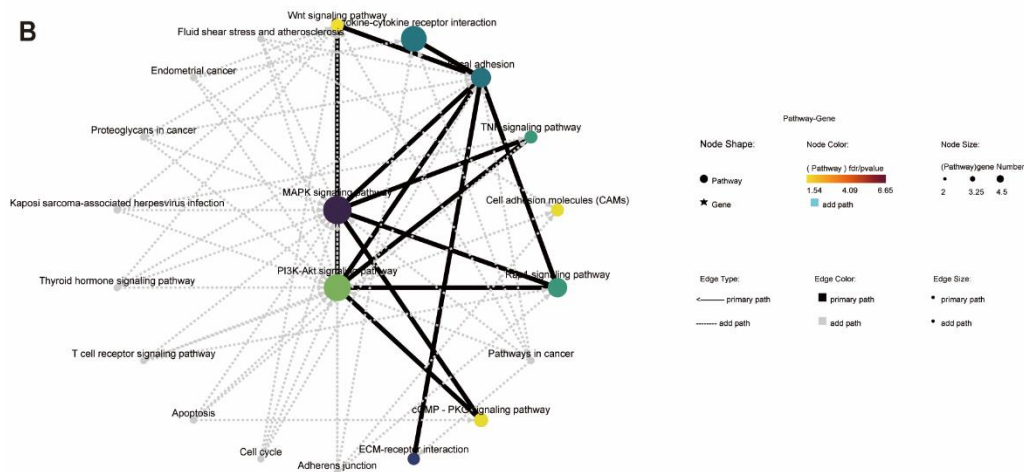
## Supplementary Material

### 1.1 Supplementary Figures

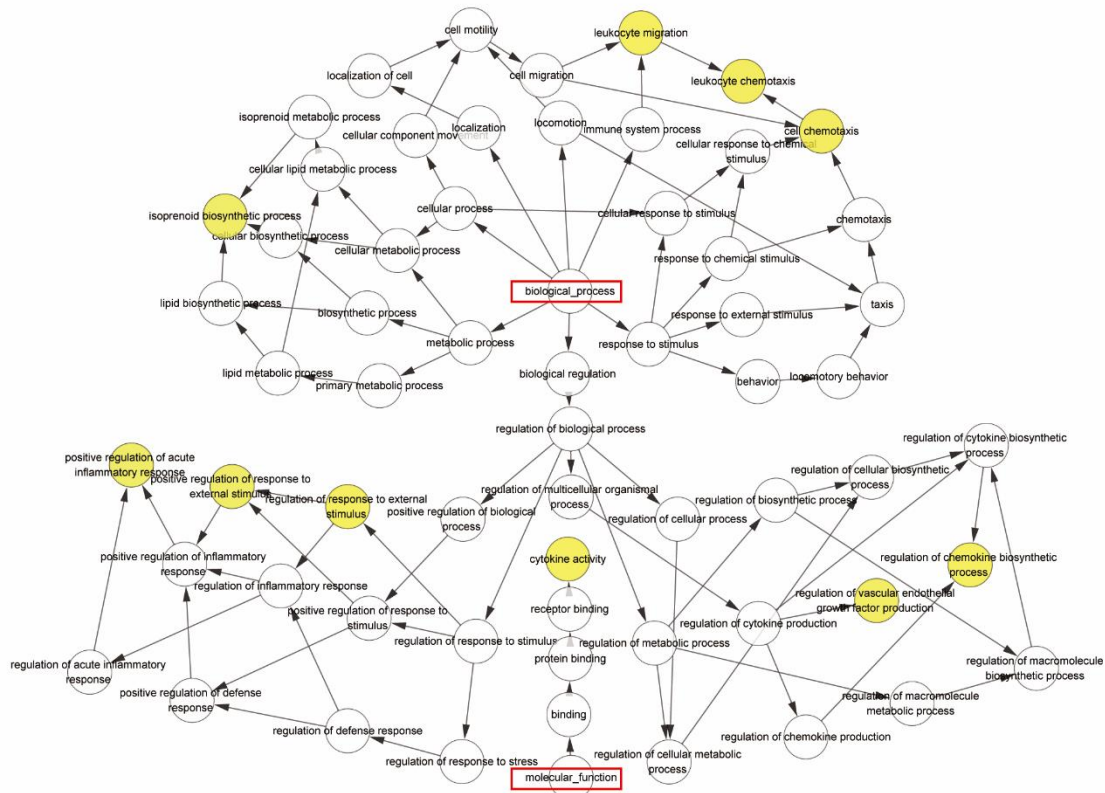
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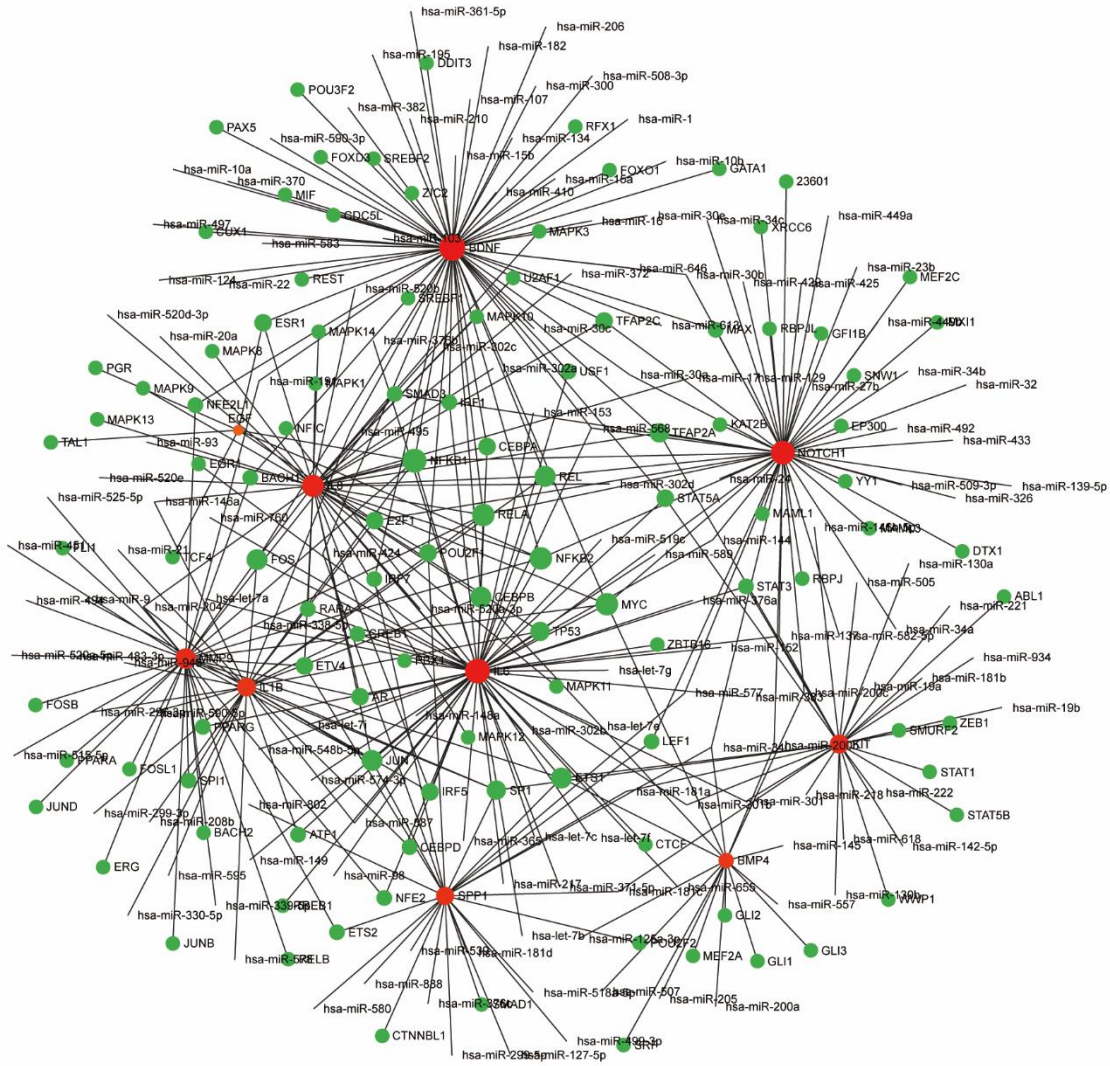
B



**Supplementary Figure 1.** KEGG network of DEGs identified in the 2D (A) and 3D (B) groups. Each node represents a KEGG pathway; the size of the node represents the number of genes enriched in the pathway; the color of the node indicates the  $p$ -value, and a grey node represents the supplementary adjacent pathway from the KEGG connection database. A solid line in the figure indicates that there is a connection between the enriched pathways; a dotted line indicates the connection between the supplementary pathway and the enriched pathway.



**Supplementary Figure 2.** GO\_FULL analysis of 10 hub genes. GO\_FULL analysis, including biological process, molecular function, and cellular component analyses of hub genes, were performed using BiNGO. The yellow nodes represent the top 10 terms having the highest corrected *p*-values of ontologies. *p* < 0.01 was considered statistically significant.



**Supplementary Figure 3.** TF-miRNA coregulatory network. The network consists of 266 nodes and 364 edges including 148 TF-genes, 107 miRNAs, and 9 hub genes. The nodes in red are the hub genes, a green node represents TF-genes, and other nodes indicate miRNAs.