Research Square

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Potential Diagnostic and Therapeutic Targets for Hepatocellular Carcinoma Based on Exosome-Derived Competitive Endogenous RNA Network

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Abstract

Background: Hepatocellular carcinoma (HCC) is one of the most malignant tumors in the world. The pathogenesis of HCC is complex and closely related to chronic uncontrollable inflammation. As a bridge between inflammation and cancer, circulating exosomes play a vital role in early tumorigenesis, metastasis, and immune escape. Studies have shown that exosomes containing specific RNAs may be potential diagnostic and therapeutic targets for HCC. Purpose The current research investigated key circRNA through exosome-derived competitive endogenous RNA network based on the ExoRBase database.

Methods: The circRNA, lncRNA, and mRNA expression profiles of human blood samples were downloaded from the ExoRBase database. At the standard of $P<0.05$ and log FC>0, differentially expressed genes (DEGs) were further identified between normal human and HCC patients. The co-expressed pairs of DEGs were predicted by TargetScan, miRcode, and StarBase databases. The ceRNA network was constructed by Cytoscape software. Subsequently, target genes corresponding to circRNA in the ceRNA network were annotated and analyzed by Gene Ontology (GO) and Kyoto Encyclopedia of Gene and Genome (KEGG). The potential transcription factors were screened by FunRich database.

Results: At the criterion of $P<0.05$ and log FC>0, 13 differentially expressed circRNAs(DECs) were identified with 9 up-regulated and 4 down-regulated. The co-expressed differentially expressed miRNAs-mRNAs (DEMis-DEMs) (620 pairs), differentially expressed miRNAs- LncRNAs (DEMis-DElncRNA) (684 pairs) and DEMis-DECs (53 pairs) were finally predicted to construct the ceRNA network. The GO analysis indicated that target genes in the ceRNA network were mainly enriched in the molecular function of protein serine/threonine kinase activity. KEGG pathway analysis suggested target genes were enriched in two pathways of MAPK and central carbon metabolism.

Conclusion: The study provides a valuable reference for HCC through the ceRNA network in exosomes. Besides, hsa_circ_0000284 may be potential diagnostic markers of HCC.

Full Text

This preprint is available for download as a PDF.

Figures

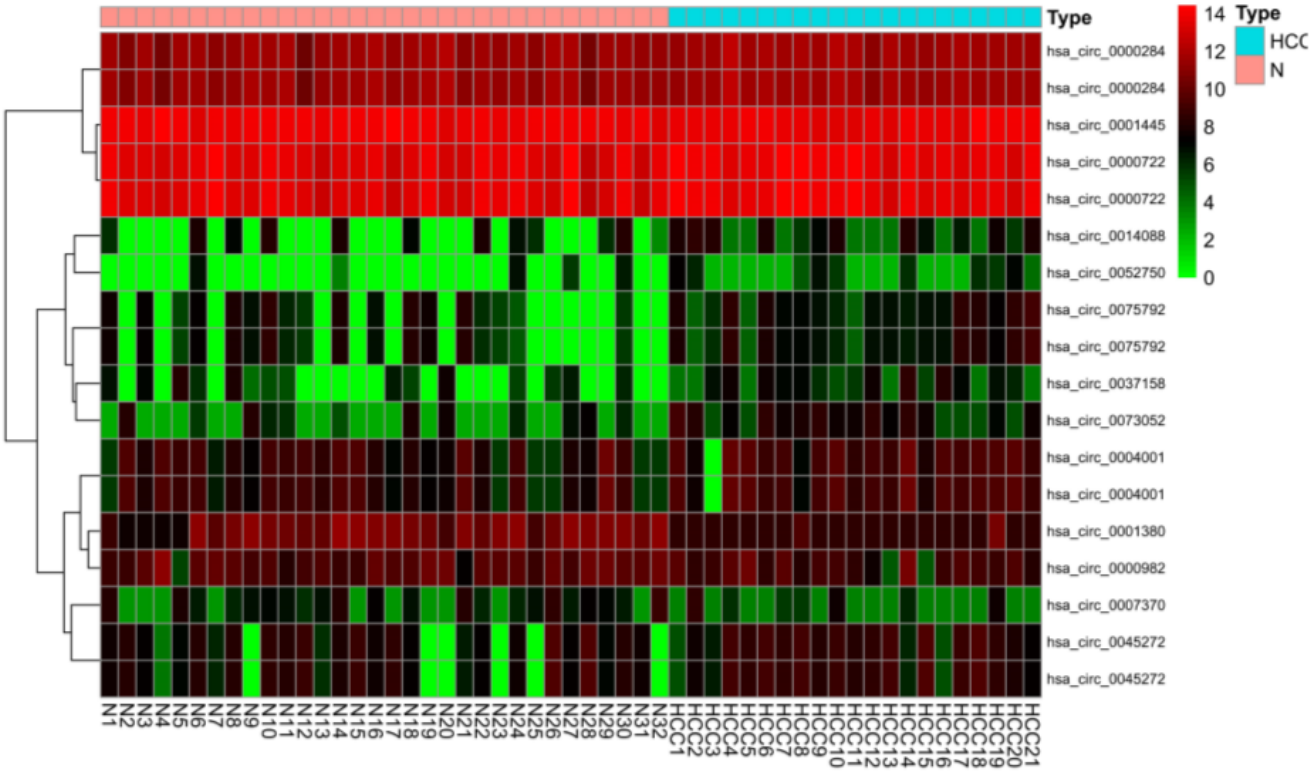

Figure 1

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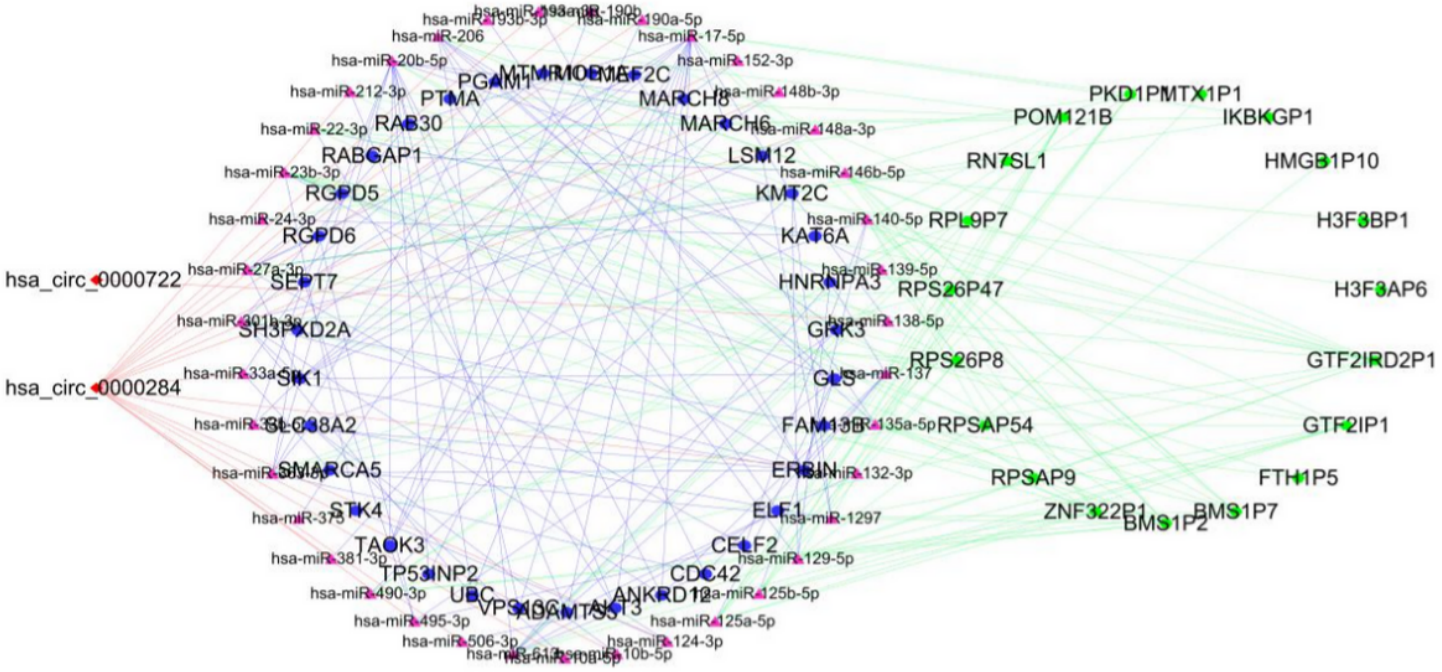

Figure 2

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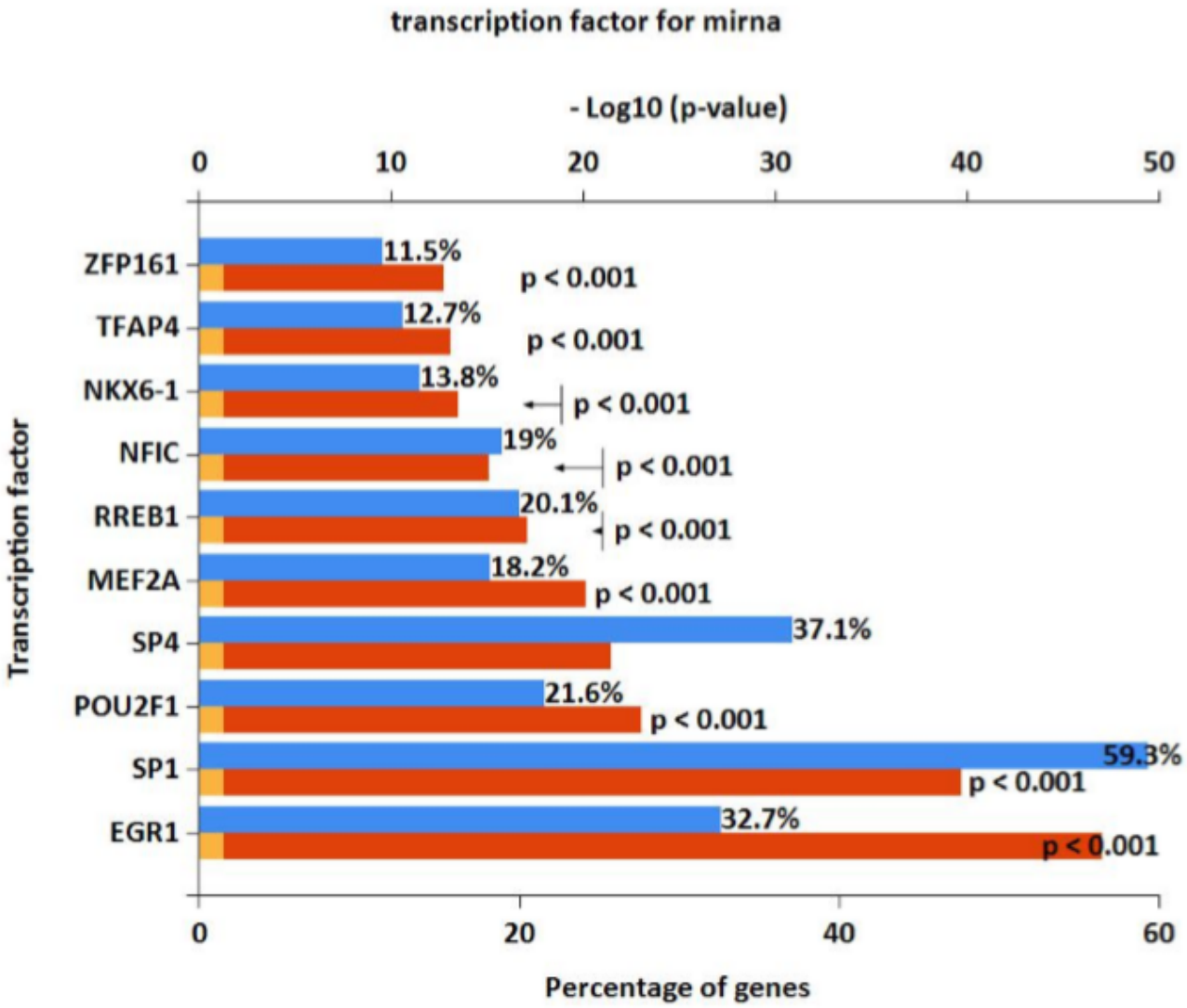

Figure 3

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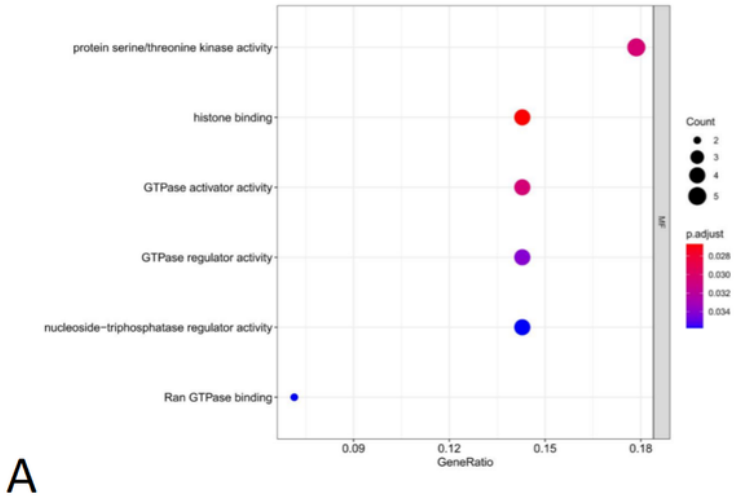
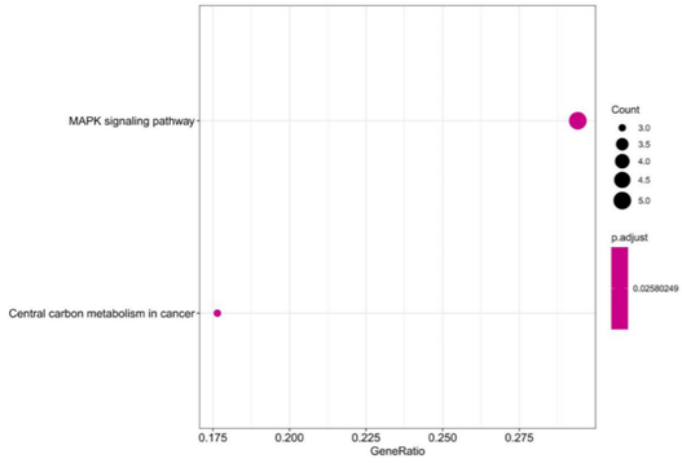


A



B

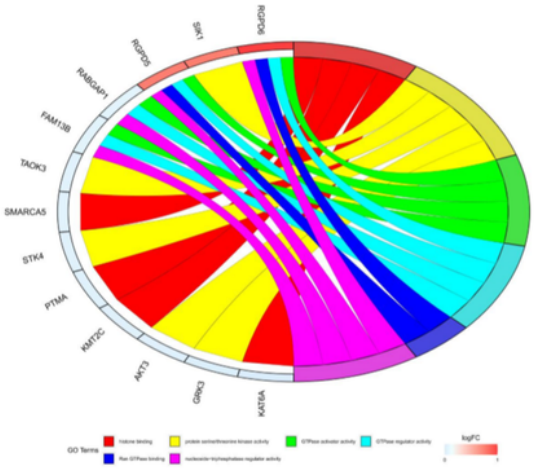


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Figure 4

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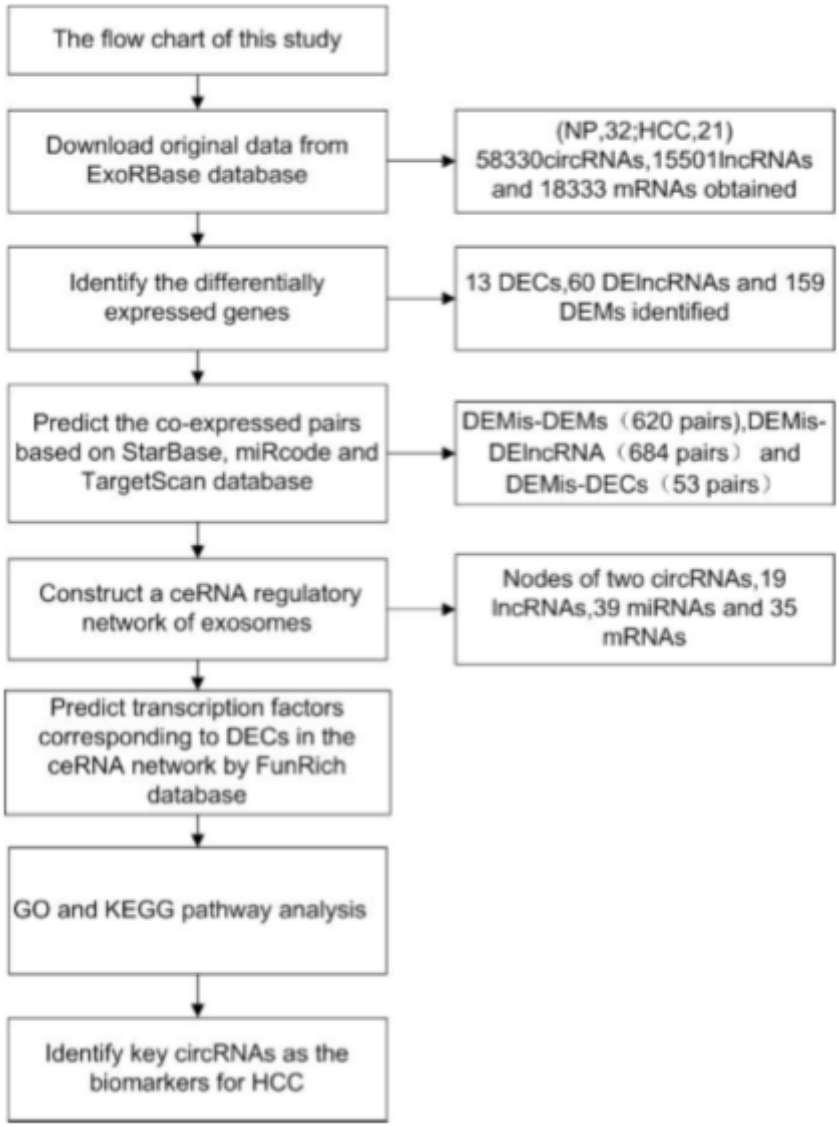

Figure 5

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