

Figure S1. Uncropped western blot images. (A) Alix, MW, 97/80 kDa. (B) CD9, MW, 23-27 kDa. (C) HSP70, MW, 70 kDa. (D) Calnexin, MW, 90 kDa. MW, molecular weight; Alix, apoptosis-linked gene 2-interacting protein X; HSP70, heat shock protein 70 kDa.

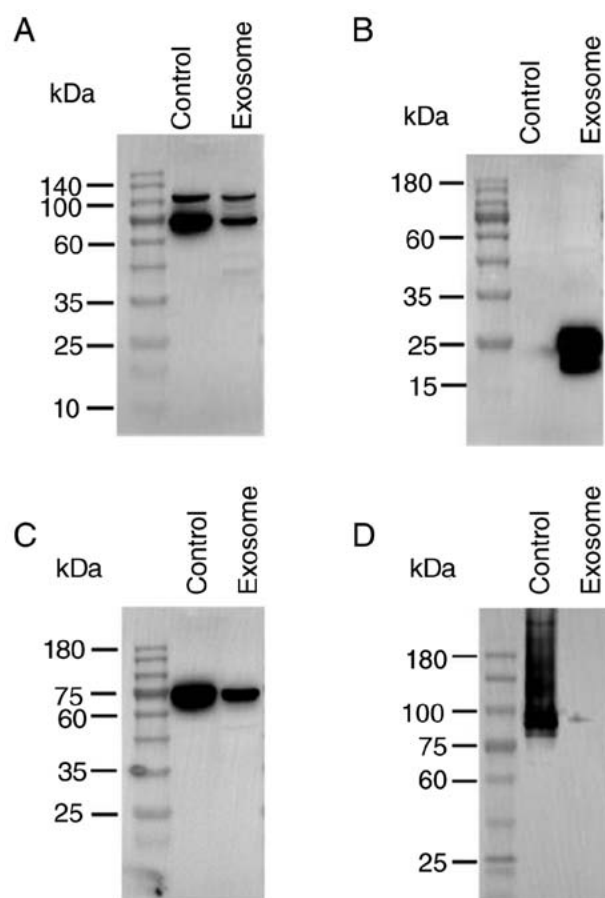


Figure S2. Gene Set Enrichment Analysis of the entire exosomal transcriptome on Gene Ontology items. (A) Biological processes. (B) Cellular components. (C) Molecular functions. $P < 0.001$, FDR < 0.05 .

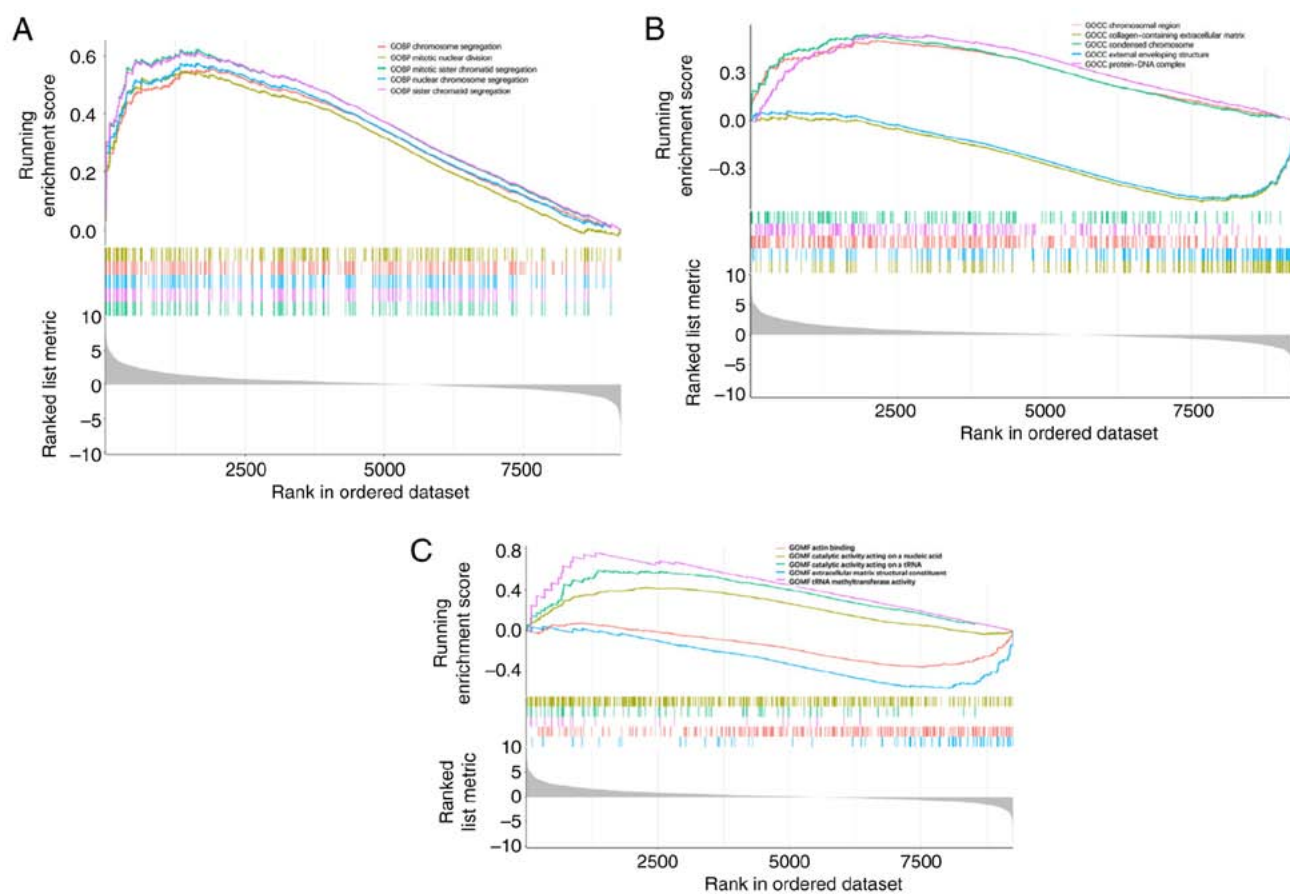


Figure S3. Gene Set Enrichment Analysis of the entire exosomal transcriptome on KEGG and Reactome database. (A) KEGG enrichment analysis. (B) Analysis of the Reactome database. $P < 0.001$, $FDR < 0.05$. KEGG, Kyoto Encyclopedia of Genes and Genomes.

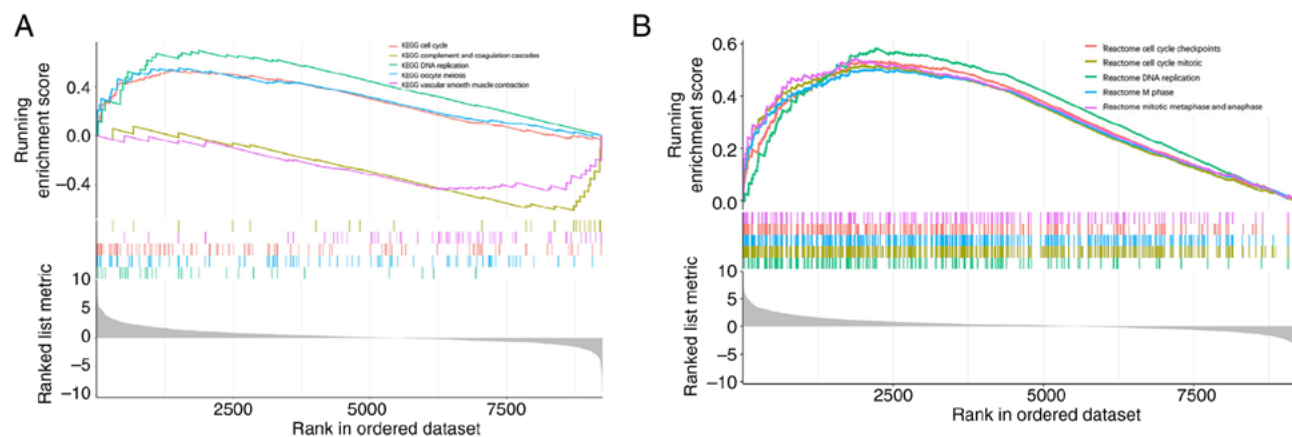


Figure S4. Gene set variation analysis of differentially expressed genes. (A) Hallmark gene set analysis. (B) Gene Ontology and (C) Kyoto Encyclopedia of Genes and Genomes term analysis. $P < 0.05$. NC, normal control; CRC, colorectal cancer.

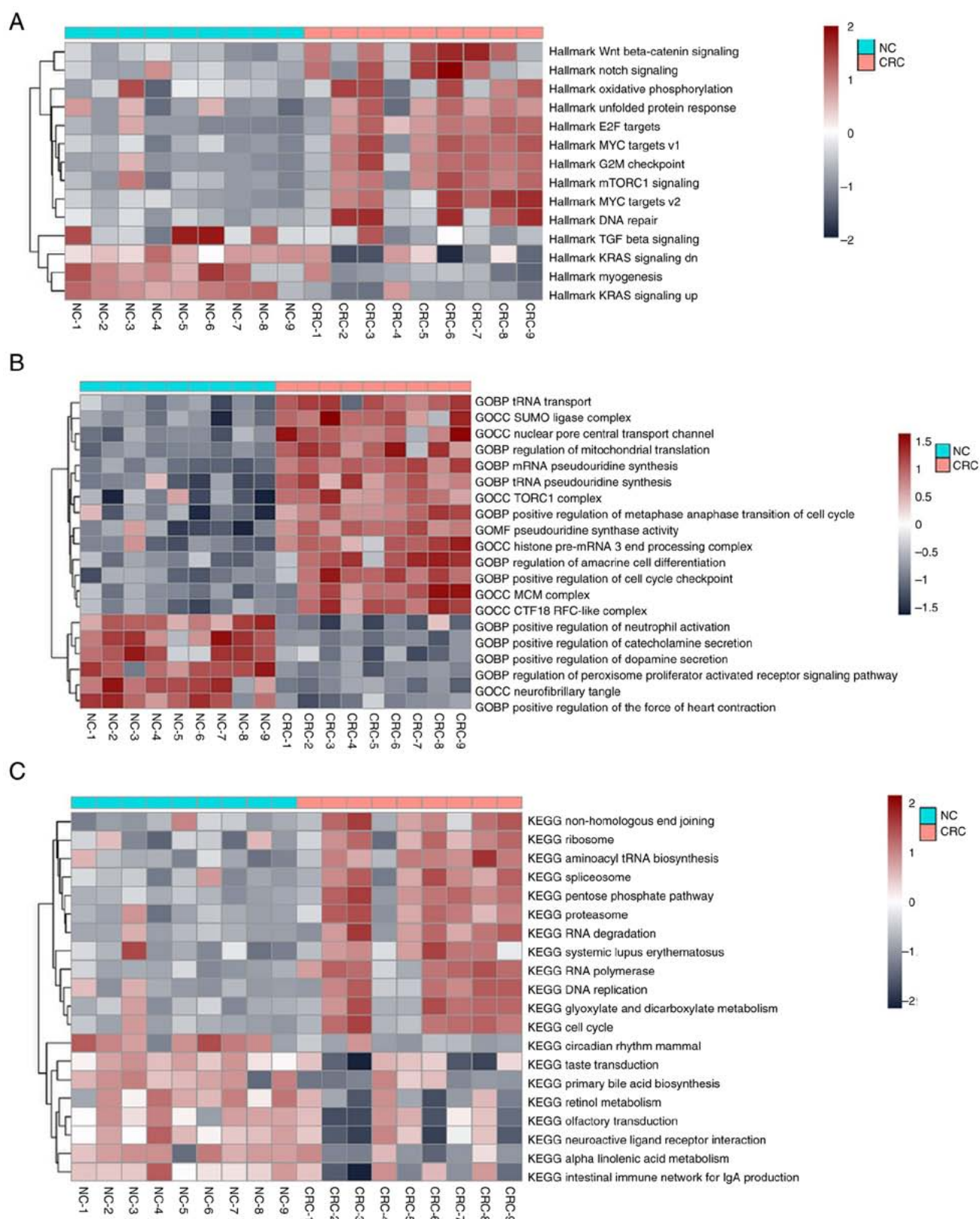


Figure S5. Modules with significant correlations with biological processes of colorectal cancer. Based on Gene Ontology, (A) cyan and (B) dark olive green modules were significantly correlated with biological processes of colorectal cancer.

