



Supplementary Material

Identification of SET7/9-E2F1 as Novel Therapeutic Biomarkers in Hepatocellular Carcinoma

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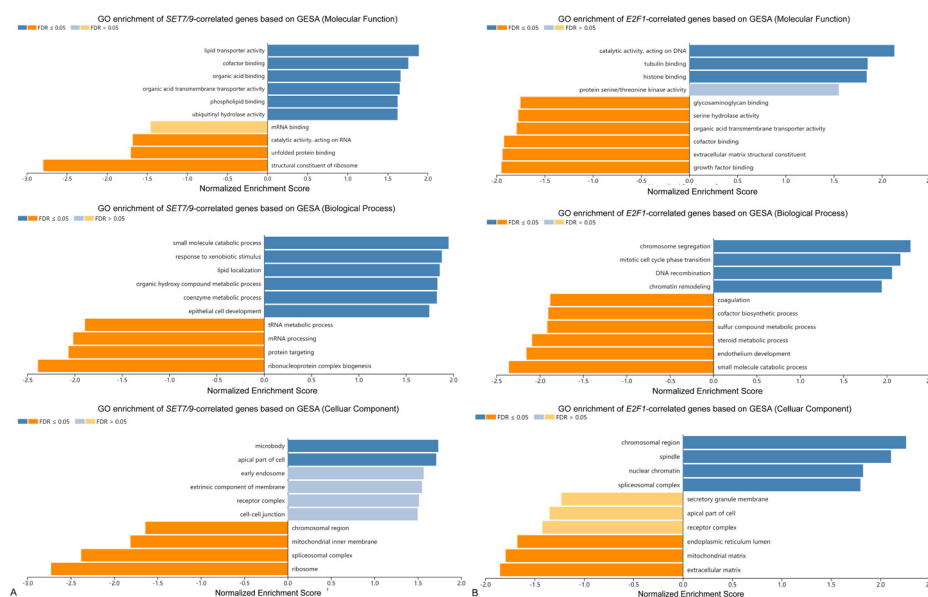
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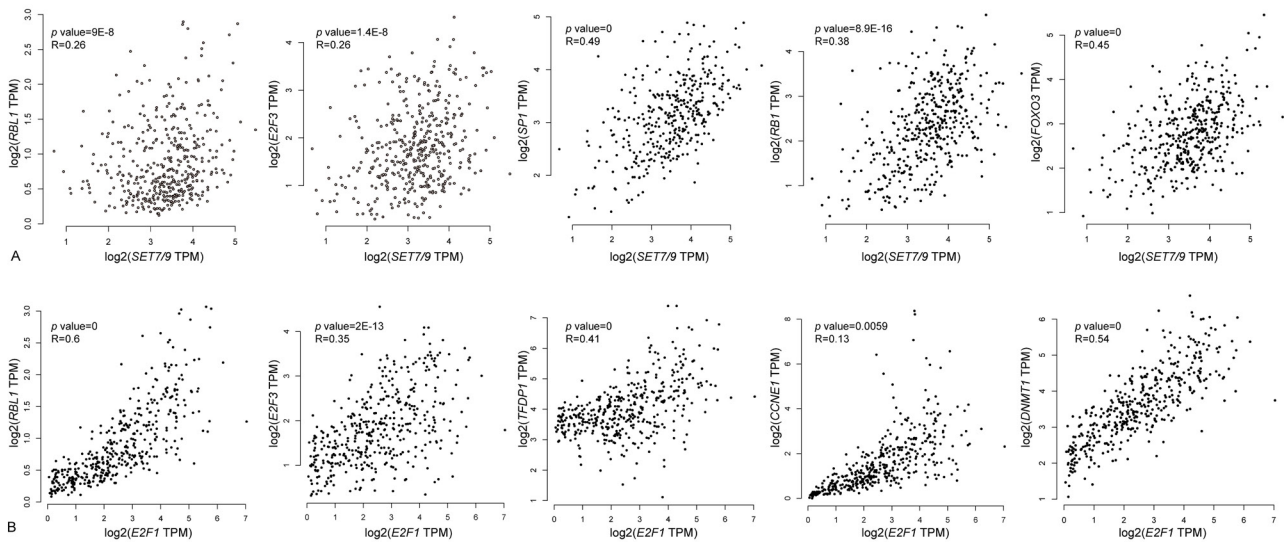
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Supplementary Fig. S1. GO enrichment analysis of SET7/9- and E2F1-correlated genes in HCC. (A) Top enriched GO terms of SET7/9-correlated genes based on Gene Set Enrichment Analysis (GSEA). (B) Top enriched GO terms of E2F1-correlated genes based on Gene Set Enrichment Analysis (GSEA). GO terms of positively and negatively correlated genes of SET7/9 and E2F1 are shown by blue and yellow bars, respectively.

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0030-9923/2023/0004-1553 \$ 9.00/0





Supplementary Fig. S2. Correlation analyses between *SET7/9* and *E2F1* mRNA expression levels with their co-expressed genes in HCC. (A) Correlation between *SET7/9* and the top five significant correlated genes *RBL1*, *E2F3*, *SP1*, *RBL1*, and *FOXO3*. (B) Correlation between *E2F1* and the top five significant correlated genes *RBL1*, *E2F3*, *TFDP1*, *CCNE1*, and *DNMT1*.

Supplementary Table SI. A list of *SET7/9* and *E2F1*-correlated proteins in PPI networks for functional enrichment analyses.

Supplementary Table SII. All the significantly enriched KEGG and GO terms of *SET7/9*- and *E2F1*-correlated proteins identified in the PPI network.