

Supplementary Material

RBM39 is a potential prognostic biomarker associated with immune infiltrates in hepatocellular carcinoma

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Supplementary Table1: GSEA analysis of genes associated with the expression of RBM39.

Description	NES	P. adjust	Q value	Core enrichment
KEGG_CELL_CYCLE	2.751	0.0286	0.0228	CDC45/CDC20/CCNB2/CCNA2/CDK1/MAD2L1/TTK/CHEK1/CCNB1/MCM5/PTTG1/MCM2/CDC25A/CDC6/PLK1/BUB1B/ESPL1/CCNE1/ORC6/ORC1/CCNE2/MCM6/MCM4/DBF4/SKP2/CDC25B/BUB1/MYC/PCNA/E2F1/CDKN2A/CDC7/MCM7/SFN/HDAC2/E2F3/CDKN2C/PKMYT1/CDC25C/CDK4/MCM3/RAD21/CHEK2/TFDP1/E2F5/YWHAZ
KEGG_DNA_REPLICATION	2.356	0.0286	0.0228	MCM5/MCM2/MCM6/MCM4/FEN1/RFC4/PCNA/RNASEH2A/DNA2/POLE2/POLA2/MCM7/RFC2/PRIM1/PRIM2/MCM3/POLD1/RFC3/POLD2/POLE3/RPA3
KEGG_P53_SIGNALING_PATHWAY	1.823	0.0286	0.0228	CCNB2/RRM2/CDK1/CHEK1/CCNB1/GTSE1/CCNE1/CCNE2/SERPINB5/CDKN2A/SFN/CYCS/CDK4/BID/ADGRB1/CHEK2
KEGG_PRIMARY_IMMUNODEFICIENCY	2.044	0.0286	0.0228	ICOS/TAP1/LCK/IL2RG/IL7R/CD3D/CD40LG/CD8A/PTPRC/CD3E/ADA/UNG/TAP2/CD19

Supplementary Table2:Correlation between RBM39 expression and clinical characteristics in 66 HCC patients

Characteristic	Low expression of RBM39	High expression of RBM39	P
Gender			1.000
female	5(7.58%)	4(6.06%)	
male	28(42.42%)	29(43.94%)	
age			0.196
≤60	24(36.36%)	19(28.79%)	
>60	9(13.64%)	14(21.21%)	
Pathological stage			0.284
I-II	21(31.82%)	25(37.88%)	
III	12(18.18%)	8(12.12%)	
T stage			0.428
T1	21(31.82%)	24(36.36%)	
T2-T3	12(18.18%)	9(13.64%)	
N stage			1.000
N0	32(48.48%)	33(50.00%)	
N1	1(1.52%)	0(0.00%)	
M stage			1.000
M0	33(50.00%)	32(48.48%)	
M1	0(0.0e+0%)	1(1.52%)	
Clinical stage			1.000
I-II	28(42.42%)	29(43.94%)	
III-IV	5(7.58%)	4(6.06%)	
recurrence			0.460
no recurrence	18(27.27%)	15(22.73%)	
relapse	15(22.73%)	18(27.27%)	