Table S1 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

GSEA, gene set enrichment analysis; RBM39, RNA-binding motif protein 39; NES, Normalized Enrichment Score.

Table S2 Correlation between RBM39 expression and clinical characteristics of 66 HCC patients

Characteristic	Low expression of RBM39	High expression of RBM39	P
Gender, n (%)			>0.99
Female	5 (7.58)	4 (6.06)	
Male	28 (42.42)	29 (43.94)	
Age, n (%)			0.196
≤60	24 (36.36)	19 (28.79)	
>60	9 (13.64)	14 (21.21)	
Pathological stage, n (%)			0.284
I–II	21 (31.82)	25 (37.88)	
III	12 (18.18)	8 (12.12)	
T stage, n (%)			0.428
T1	21 (31.82)	24 (36.36)	
T2–T3	12 (18.18)	9 (13.64)	
N stage, n (%)			>0.99
N0	32 (48.48)	33 (50.00)	
N1	1 (1.52)	0 (0.00)	
M stage, n (%)			>0.99
M0	33 (50.00)	32 (48.48)	
M1	0 (0.00)	1 (1.52)	
Clinical stage, n (%)			>0.99
I–II	28 (42.42)	29 (43.94)	
III–IV	5 (7.58)	4 (6.06)	
Recurrence, n (%)			0.460
No recurrence	18 (27.27)	15 (22.73)	
Relapse	15 (22.73)	18 (27.27)	

RBM39, RNA-binding motif protein 39; HCC, hepatocellular carcinoma.