

Expression levels of m6A RNA methylation regulators in HCC at different tumor stages.



Kaplan–Meier overall survival curve for patients with HCC with high or low expression levels of m6A RNA methylation regulators.



Consensus clustering matrix for k = 4-9.



Heatmap and clinicopathological features of the two clusters defined by the consensus expression of m6A RNA methylation regulators in GSE62232.



Prognostic value of m6A RNA methylation regulators in HCC from GSE14520 The heatmap shows the expression of the four RNA methylation regulators in lowand high-risk groups. The distribution of clinicopathological features was compared between these two groups. (B-C) Univariate and multivariate Cox regression analyses of the association between clinicopathological factors (including the risk score) and OS of patients with HCC. (D) OS curves for patients in the GSE14520 dataset assigned to high- and low-risk groups based on the risk score.

Note: * P < 0.05, ** P < 0.01, *** P < 0.001





Prognostic value of m6A RNA methylation regulators in HCC from clinical samples collected in Xinqiao Hospital. The heatmap shows the expression of the five RNA methylation regulators in low- and high-risk groups. The distribution of clinicopathological features was compared between these two groups. (B-C) Univariate and multivariate Cox regression analyses of the association between clinicopathological factors (including the risk score) and OS of patients with HCC. (D) OS curves for clinical samples we collected assigned to high- and low-risk groups based on the risk score.

Note: * P < 0.05, ** P < 0.01, *** P < 0.001



Supplementary figure 7 The correlation of 13 m6A RNA methylation regulators.

Gene name	Forward Primer	Reverse Primer	
FTO	ACTTGGCTCCCTTATCTGACC	TGTGCAGTGTGAGAAAGGCTT	
WTAP	TTGTAATGCGACTAGCAACCAA	GCTGGGTCTACCATTGTTGATCT	
ALKBH5	CGGCGAAGGCTACACTTACG	CCACCAGCTTTTGGATCACCA	
ZC3H13	TGACCGGCGTCACGAAAGGA	AAACTCCTTTCGTGACGCCGGT	
YTHDF2	CCTTAGGTGGAGCCATGATTG	TCTGTGCTACCCAACTTCAGT	
METTL14	GAACACAGAGCTTAAATCCCCA	TGTCAGCTAAACCTACATCCCTG	
METTL3	CATTGCCCACTGATGCTGTG	AGGCTTTCTACCCCATCTTGA	
KIAA1429	CGATAACTTGATGACCCCAGAA	ATAACGGCAAGATTCCATTTC	
YTHDC1	AACTGGTTTCTAAGCCACTGAGC	GGAGGCACTACTTGATAGACGA	
HNRNPC	GCCAGCAACGTTACCAACAA	TGAACAGAGCAGCCCACAAT	
YTHDF1	ACCTGTCCAGCTATTACCCG	TGGTGAGGTATGGAATCGGAG	
YTHDC2	CAAAACATGCTGTTAGGAGCCT	CCACTTGTCTTGCTCATTTCCC	
RBM15	CACCGATTGACCAATGAGGTCTG	AAACCGCAGACCTCATTGGTCA	
GAPDH	CGCTGAGTACGTCGTGGAGTC	GCTGATGATCTTGAGGCTGTTGTC	

Supplementary Table 1. Primers used in qRT-PCR

Supplementary Table 2. Univariate analysis for survival analysis in GSE14520

	Univariate analysis			
Variables	HR	HR95%L	HR95%H	P value
Age	0.990449	0.97126306	1.010013766	0.336252123
Gender	1.694362	0.817532942	3.51161524	0.156148784
Stage	2.293942	1.729966003	3.041777358	8.06E-09
Risk score	53.9503	3.543541277	821.3916138	0.004096944

Abbreviations: HR, Hazard ratio; CI, confidence interval

Supplementary	Table 3	Multivariato	analycic f	for survival	analycic in	GSE14520
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	Multivariate analysis				
Variables	HR	HR95%L	HR95%H	P value	
Stage	2.318134	1.740963	3.086651	8.65E-09	
Risk score	56.44311	3.644262	874.203	0.003915	

Abbreviations: HR, Hazard ratio; CI, confidence interval

	Univariate analysis			
Variables	HR	HR95%L	HR95%H	P value
	1.012225	0.987563	1.037503	0.334281
Gender	0.435958	0.180495	1.052989	0.065008
Grade	0.84171	0.553252	1.280566	0.420895
Stage	2.406997	1.492711	3.881284	0.000314
Risk score	1.646967	1.035524	2.619446	0.035082

Supplementary Table 4. Univariate analysis for survival analysis in 60 clinical samples

Abbreviations: HR, Hazard ratio; CI, confidence interval

Supplementary Table 5. Multivariate analysis for survival analysis in 60 clinical samples

	Multivariate analysis			
Variables	HR	HR95%L	HR95%H	P value
Stage	2.173333045	1.362560531	3.466544	0.001119
Risk score	3.152811369	1.09492328	9.078462	0.033335

Abbreviations: HR, Hazard ratio; CI, confidence interval