

Supplementary Information for

The effect of key DNA methylation in different regions on gene expression in hepatocellular carcinoma

Fig. S1 Kaplan-Meier curve analysis of the high expression group and low expression group of four key genes.

Table S1 Clinical information of LIHC patients in this study

Clinical character		Number	Percent (%)
Age	<=50	76	20.88
	>50	288	79.12
Gender	Male	245	67.31
	Female	119	32.69
Pathologic M	M0	262	71.98
	M1	3	0.82
	Unknown	99	27.20
Pathologic N	N0	247	67.86
	N1	4	1.10
	Unknown	113	31.04
Pathologic T	T1	179	49.18
	T2	91	25.00
	T3	78	21.43
	T4	13	3.57
	Unknown	3	0.82
Pathologic stage	I	169	46.43
	II	84	23.08
	III	83	22.80
	IV	4	1.10
	Unknown	24	6.59
Vital status	Dead	130	35.71
	Alive	234	64.29

Abbreviations: LIHC: Liver hepatocellular carcinoma.

Table S2 Univariate Cox regression analyses of gene associated with survival prognosis in HCC

Gene	Coefficient	HR (95% CI for HR)	P value
------	-------------	--------------------	---------

<i>CDC20</i>	0.340	1.40 (1.20-1.60)	8.60E-08
<i>RRM2</i>	0.340	1.40 (1.20-1.70)	2.70E-05
<i>SPP1</i>	0.130	1.10 (1.10-1.20)	3.70E-06
<i>MAD2L1</i>	0.540	1.70 (1.30-2.20)	1.10E-05
<i>LAPTM4B</i>	0.280	1.30 (1.20-1.50)	4.30E-05
<i>SFN</i>	0.150	1.20 (1.10-1.30)	0.00022
<i>UBE2C</i>	0.270	1.30 (1.20-1.50)	2.00E-05
<i>KIF15</i>	0.590	1.80 (1.40-2.30)	1.00E-05
<i>SLC22A1</i>	-0.120	0.89 (0.83-0.95)	0.00047
<i>FEN1</i>	0.360	1.40 (1.20-1.70)	0.00017
<i>GRM4</i>	2.900	19.0 (4.20-82.0)	0.00011
<i>ROBO1</i>	0.190	1.20 (1.10-1.40)	0.0052
<i>CDKN2C</i>	0.260	1.30 (1.10-1.50)	0.0019
<i>EGF</i>	0.480	1.60 (1.20-2.20)	0.0035
<i>AKR1B10</i>	0.077	1.10 (1.00-1.10)	0.0061
<i>MMP3</i>	0.500	1.60 (1.20-2.30)	0.0026
<i>CDKN3</i>	0.260	1.30 (1.10-1.50)	0.0010
<i>E2F1</i>	0.220	1.20 (1.10-1.40)	0.0011
<i>FRAS1</i>	0.300	1.40 (1.10-1.70)	0.0032
<i>GRM8</i>	0.560	1.80 (1.20-2.50)	0.0014
<i>CSMD1</i>	0.680	2.00 (1.20-3.20)	0.0063

Abbreviations: HCC: Hepatocellular carcinoma. HR: hazard ratio. CI: confidence interval.