

Table S1 Primer sequences used in this study

Targets	Name	Sequence (5'-3')
LINC00662	Forward	TGGACATCTGTCTGGAGG
	Reverse	GGCTGAGGCATAAGAATCG
hsa-miR-101-3p	Forward	TGCCCTGGCTCAGTTATCAC
	Reverse	TGCCATCCTTCAGTTATCACAGTAC
RAC1	Forward	CTGTTTCTCTGCAGTTTTCTCAG
	Reverse	TATGATTCAAGGATTTATTAAGTCATACATGC
GAPDH	Forward	CTCCCCTACCCTCTCAA
	Reverse	CGATTCTTCCTCATCTTCT
U6	Forward	GCTTCGGCAGCACATATACTAAAAT
	Reverse	CGCTTCACGAATTTGCGTGTGCAT

Table S2 Clinicopathological characteristics of high- and low-RAC1 expression groups

Characteristic	Low expression of RAC1	High expression of RAC1	P
n	185	186	
Age, n (%)			0.405
≤60 years	84 (22.7%)	93 (25.1%)	
>60 years	101 (27.3%)	92 (24.9%)	
Gender, n (%)			0.684
Female	58 (15.6%)	63 (17%)	
Male	127 (34.2%)	123 (33.2%)	
Race, n (%)			0.769
Asian	75 (20.9%)	83 (23.1%)	
Black or African American	9 (2.5%)	8 (2.2%)	
White	94 (26.2%)	90 (25.1%)	
T stage, n (%)			0.022
T1	104 (28.3%)	77 (20.9%)	
T2	41 (11.1%)	53 (14.4%)	
T3	31 (8.4%)	49 (13.3%)	
T4	6 (1.6%)	7 (1.9%)	
N stage, n (%)			1.000
N0	119 (46.5%)	133 (52%)	
N1	2 (0.8%)	2 (0.8%)	
M stage, n (%)			0.625
M0	126 (46.7%)	140 (51.9%)	
M1	1 (0.4%)	3 (1.1%)	
Pathologic stage, n (%)			0.052
Stage I	97 (28%)	74 (21.3%)	
Stage II	39 (11.2%)	47 (13.5%)	
Stage III	34 (9.8%)	51 (14.7%)	
Stage IV	2 (0.6%)	3 (0.9%)	
Tumor status, n (%)			0.025
Tumor free	112 (31.8%)	89 (25.3%)	
With tumor	65 (18.5%)	86 (24.4%)	
Histologic grade, n (%)			< 0.001
G1	41 (11.2%)	14 (3.8%)	
G2	97 (26.5%)	80 (21.9%)	
G3	42 (11.5%)	80 (21.9%)	
G4	3 (0.8%)	9 (2.5%)	
AFP (ng/mL), n (%)			< 0.001
≤400	127 (45.7%)	86 (30.9%)	
>400	19 (6.8%)	46 (16.5%)	
Vascular invasion, n (%)			0.043
No	115 (36.5%)	91 (28.9%)	
Yes	47 (14.9%)	62 (19.7%)	
OS event, n (%)			< 0.001
Alive	136 (36.7%)	105 (28.3%)	
Dead	49 (13.2%)	81 (21.8%)	
DSS event, n (%)			0.039
Alive	151 (41.6%)	133 (36.6%)	
Dead	31 (8.5%)	48 (13.2%)	

Table S3 Associations of RAC1 expression with clinicopathological characteristics of patients

Characteristics	Total (N)	Odds ratio (OR)	P value
T stage (T3&T4 vs. T1&T2)	368	0.592 (0.365-0.952)	0.032
N stage (N1 vs. N0)	256	0.895 (0.106-7.551)	0.912
M stage (M1 vs. M0)	270	2.700 (0.341-54.965)	0.392
Pathologic stage (Stage III & Stage IV vs. Stage I & Stage II)	347	1.686 (1.039-2.761)	0.036
Age (≤ 60 vs. >60 years)	370	1.215 (0.808-1.831)	0.349
Race (Asian & Black or African American vs. White)	359	1.131 (0.748-1.713)	0.559
Tumor status (With tumor vs. Tumor free)	352	1.665 (1.089-2.555)	0.019
Histologic grade (G3&G4 vs. G1&G2)	366	2.904 (1.871-4.554)	<0.001
AFP (ng/ml) (≤ 400 vs. >400)	278	0.280 (0.151-0.503)	<0.001
Vascular invasion (No vs. Yes)	315	0.600 (0.374-0.956)	0.032

Table S4 The potential upstream lncRNAs of hsa-miR-101-3p

miRNAname	geneID	geneName	geneType
hsa-miR-101-3p	ENSG00000233203	DHCR24-DT	lncRNA
hsa-miR-101-3p	ENSG00000281649	EBLN3P	lncRNA
hsa-miR-101-3p	ENSG00000204860	FAM201A	lncRNA
hsa-miR-101-3p	ENSG00000261824	LINC00662	lncRNA
hsa-miR-101-3p	ENSG00000231711	LINC00899	lncRNA
hsa-miR-101-3p	ENSG00000251562	MALAT1	lncRNA
hsa-miR-101-3p	ENSG00000245532	NEAT1	lncRNA
hsa-miR-101-3p	ENSG00000255717	SNHG1	lncRNA
hsa-miR-101-3p	ENSG00000224078	SNHG14	lncRNA
hsa-miR-101-3p	ENSG00000267322	SNHG22	lncRNA
hsa-miR-101-3p	ENSG00000245910	SNHG6	lncRNA
hsa-miR-101-3p	ENSG00000229807	XIST	lncRNA

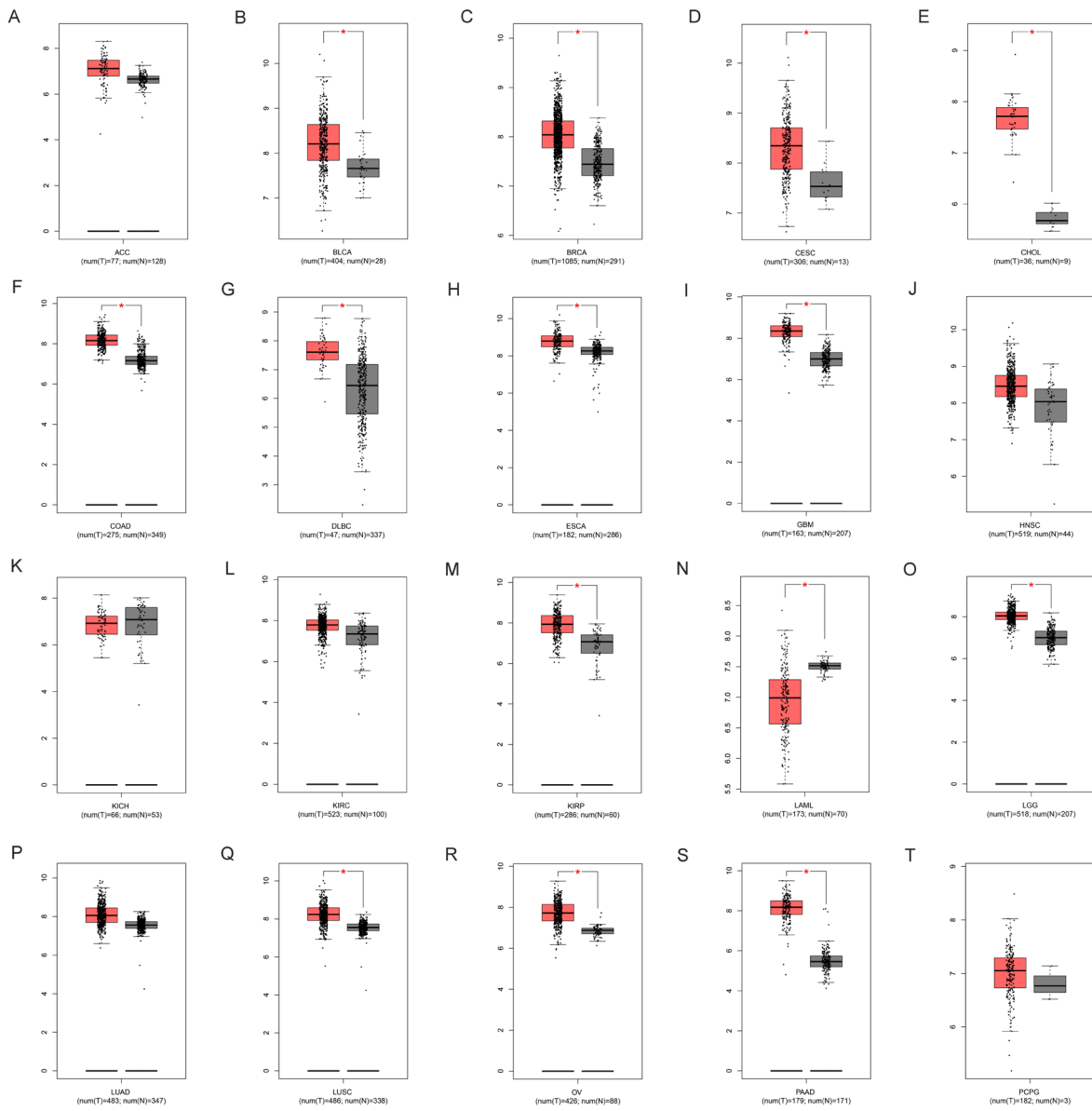


Figure S1 Expression analysis for RAC1 in multiple cancers. (A-T) RAC1 expression in TCGA ACC (A), BLCA (B), BRCA (C), CESC (D), CHOL (E), COAD (F), DLBC (G), ESCA (H), GBM (I), HNSC (J), KICH (K), KIRC (L), KIRP (M), LAML (N), LGG (O), LUAD (P), LUSC (Q), OV (R), PAAD (S) and PCPG (T) tissues compared with corresponding TCGA and GTEx normal tissues.

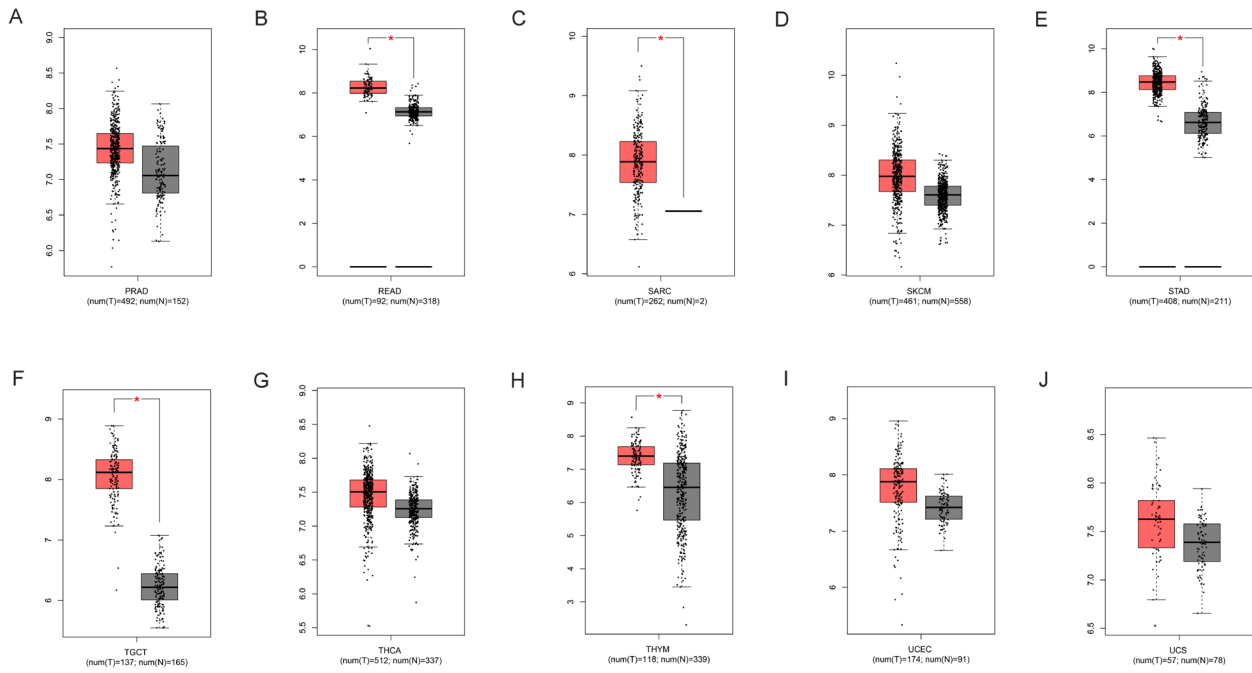


Figure S2 Expression analysis for RAC1 in multiple cancers. (A-J) RAC1 expression in TCGA PRAD (A), READ (B), SARC (C), SKCM (D), STAD (E), TGCT (F), THCA (G), THYM (H), UCEC (I) and UCS (J) tissues compared with corresponding TCGA and GTEx normal tissues.

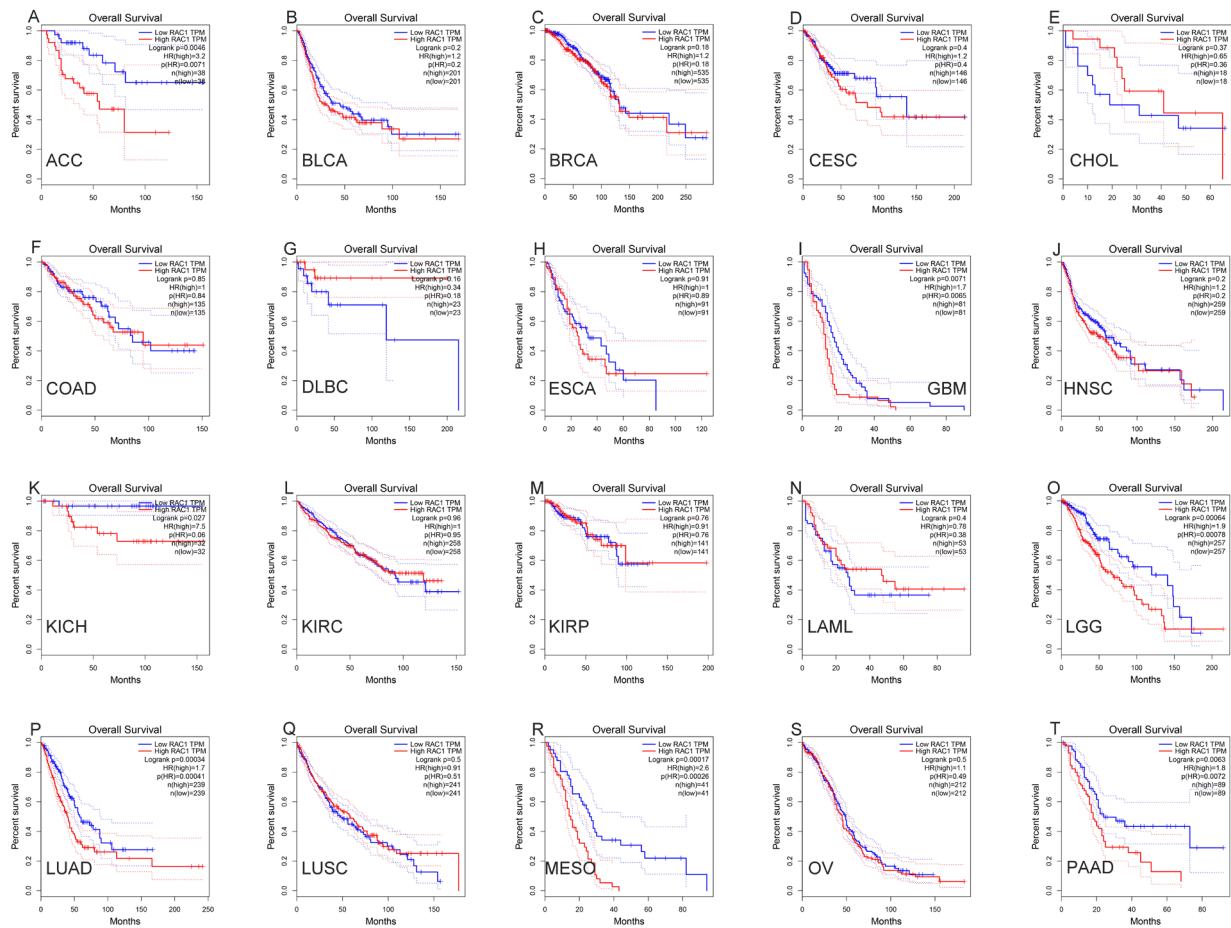


Figure S3 Prognosis of RAC1 in pan-cancers. (A-T) Overall survival of patients in ACC (A), BLCA (B), BRCA (C), CESC (D), CHOL (E), COAD (F), DLBC (G), ESCA (H), GBM (I), HNSC (J), KICH (K), KIRC (L), KIRP (M), LAML (N), LGG (O), LUAD (P), LUSC (Q), MESO (R), OV (S) and PAAD (T) with high versus low RAC1.

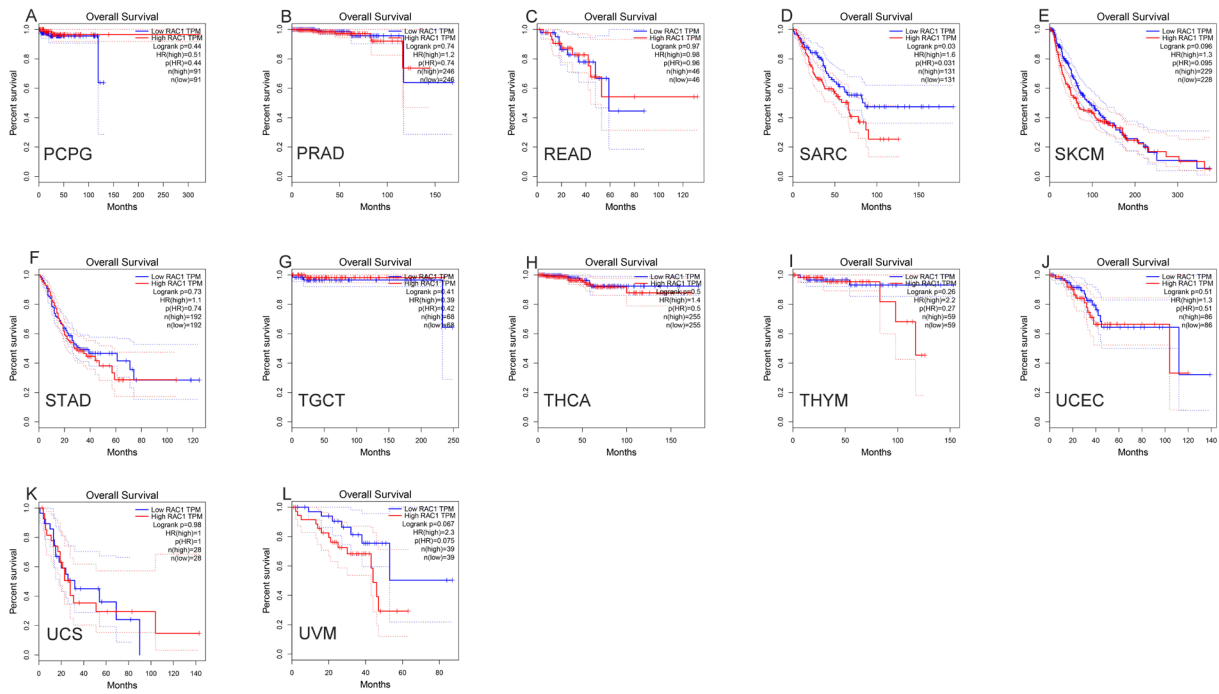


Figure S4 Prognosis of RAC1 in pan-cancers. (A-L) Overall survival of patients in PCPG (A), PRAD (B), READ (C), SARC (D), SKCM (E), STAD (F), TGCT (G), THCA (H), THYM (I), UCEC (J), UCS (K) and UVM (L) with high versus low RAC1.

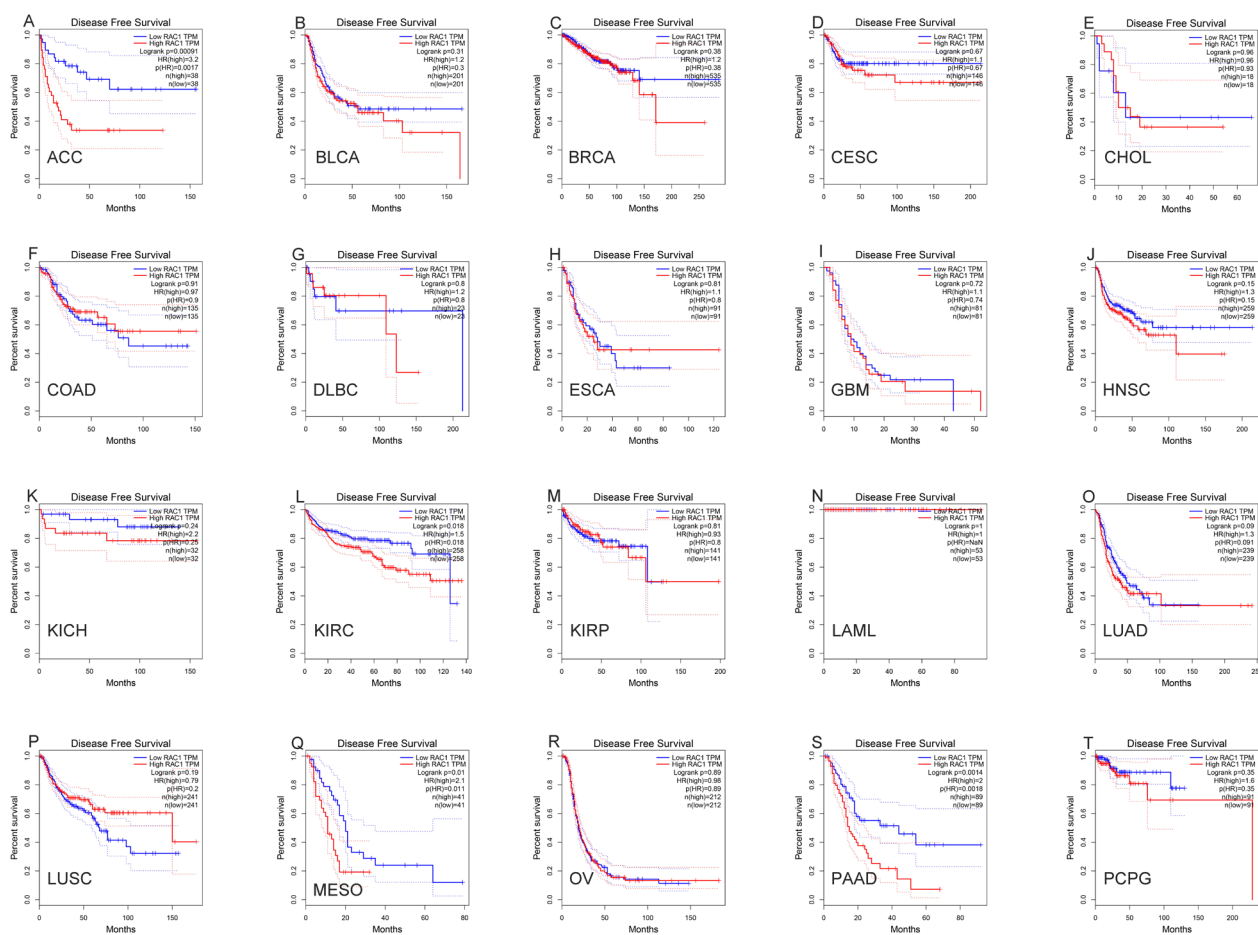


Figure S5 Prognosis of RAC1 in pan-cancers. (A-T) Disease free survival of patients in ACC (A), BLCA (B), BRCA (C), CESC (D), CHOL (E), COAD (F), DLBC (G), ESCA (H), GBM (I), HNSC (J), KICH (K), KIRC (L), KIRP (M), LAML (N), LUAD (O), LUSC (P), MESO (Q), OV (R), PAAD (S) and PCPG (T) with high versus low RAC1.

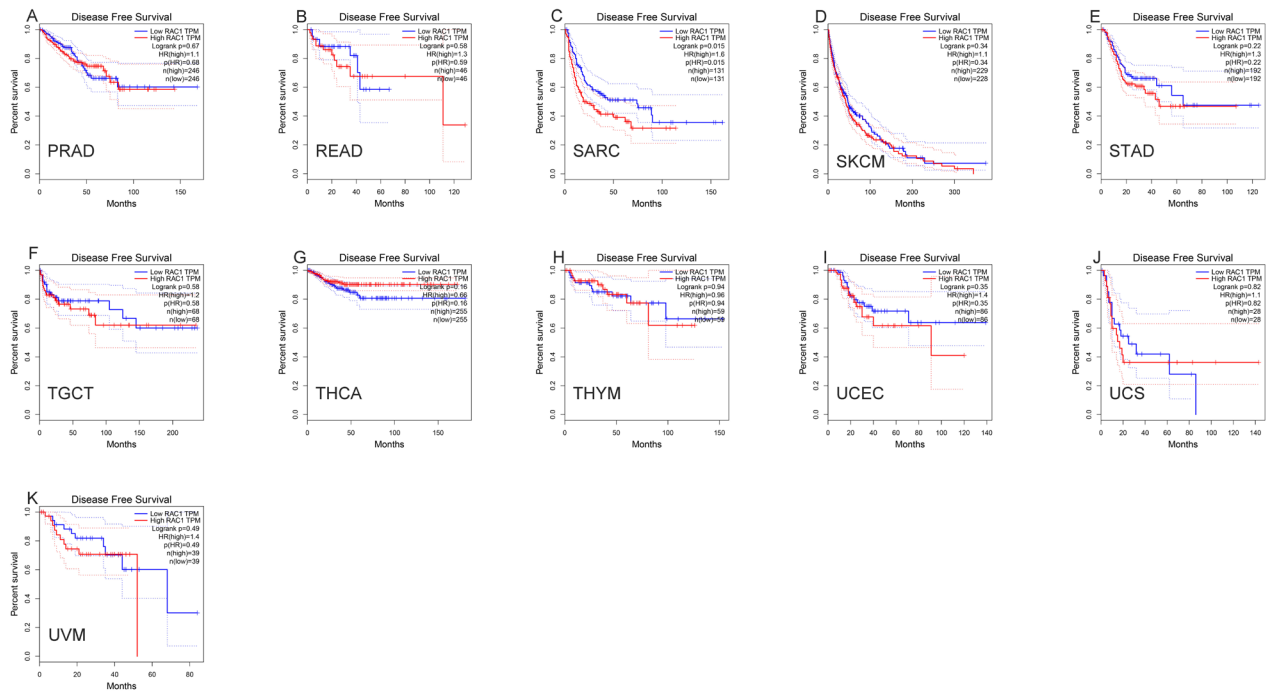


Figure S6 Prognosis of RAC1 in pan-cancers. (A-K) Disease free survival of patients in PRAD (A), READ (B), SARC (C), SKCM (D), STAD (E), TGCT (F), THCA (G), THYM (H), UCEC (I), UCS (J) and UVM (K) with high versus low RAC1.

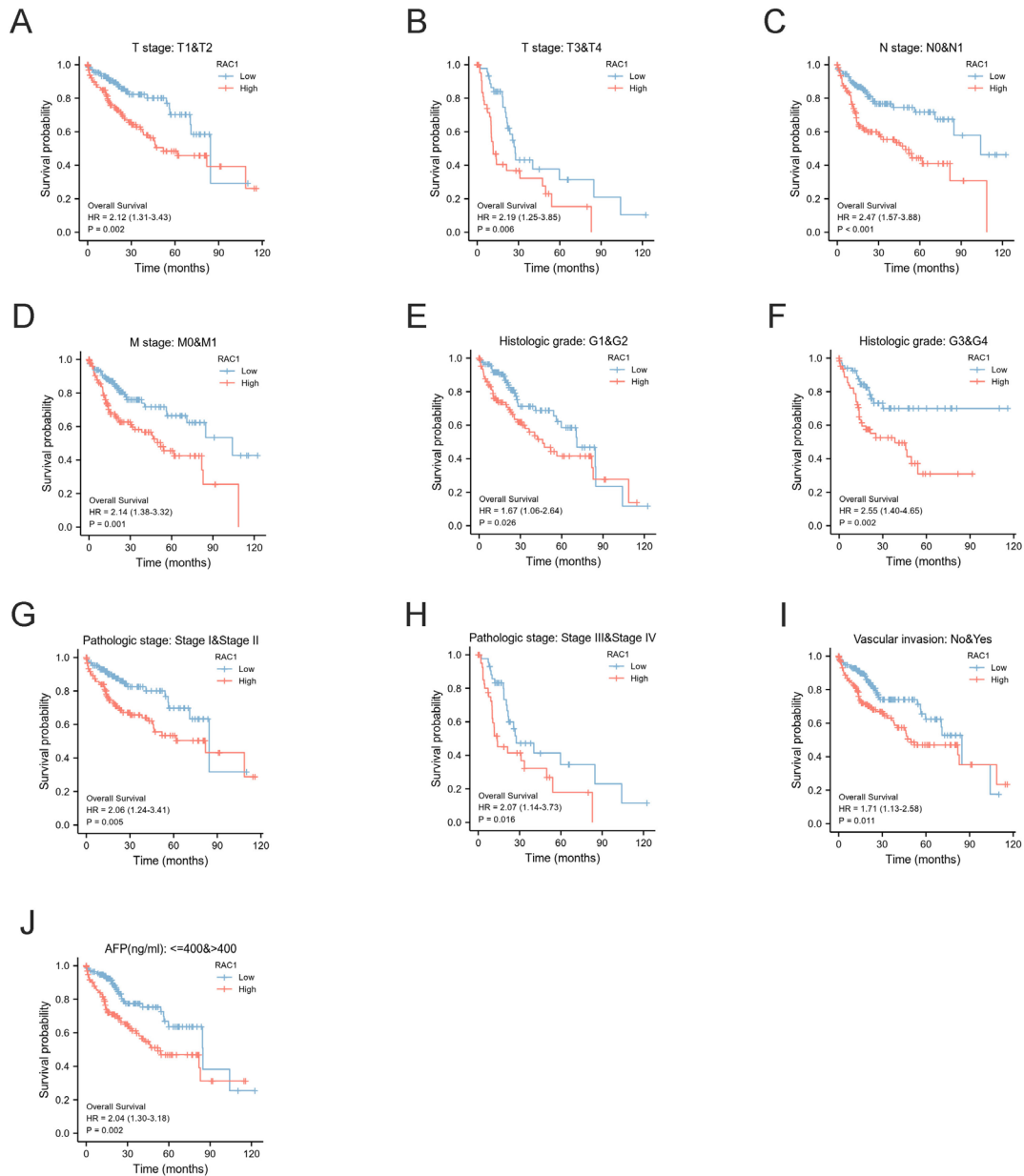


Figure S7 Prognostic values of RAC1 expression in patients with LIHC evaluated by the Kaplan-Meier method in different subgroups. (A-J) OS survival curves of T1 and T2, T3 and T4, N0 and N1, M0 and M1, G1 and G2, G3 and G4, stage I and II, stage III and IV, Vascular invasion, AFP >400 ng/mL between high- and low-RAC1 patients with LIHC.

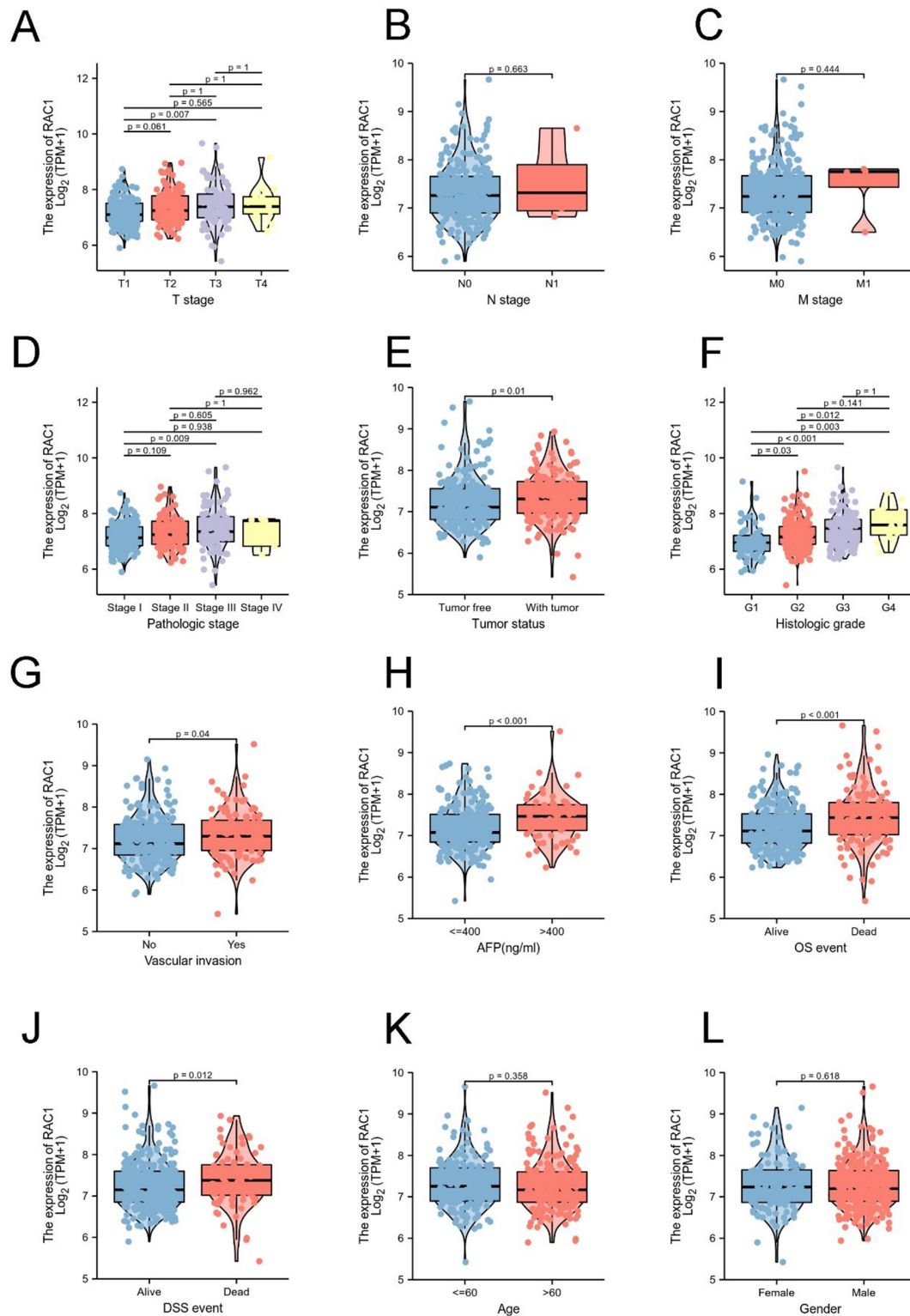


Figure S8 Associations between RAC1 expression and clinicopathological characteristics. (A-L) Data are shown for (A) T stage; (B) N stage; (C) M stage; (D) pathological stage; (E) tumor status; (F) histological grade; (G) vascular invasion; (H) AFP; (I) OS event; (J) DSS event; (K) age >0 years; (L) gender.

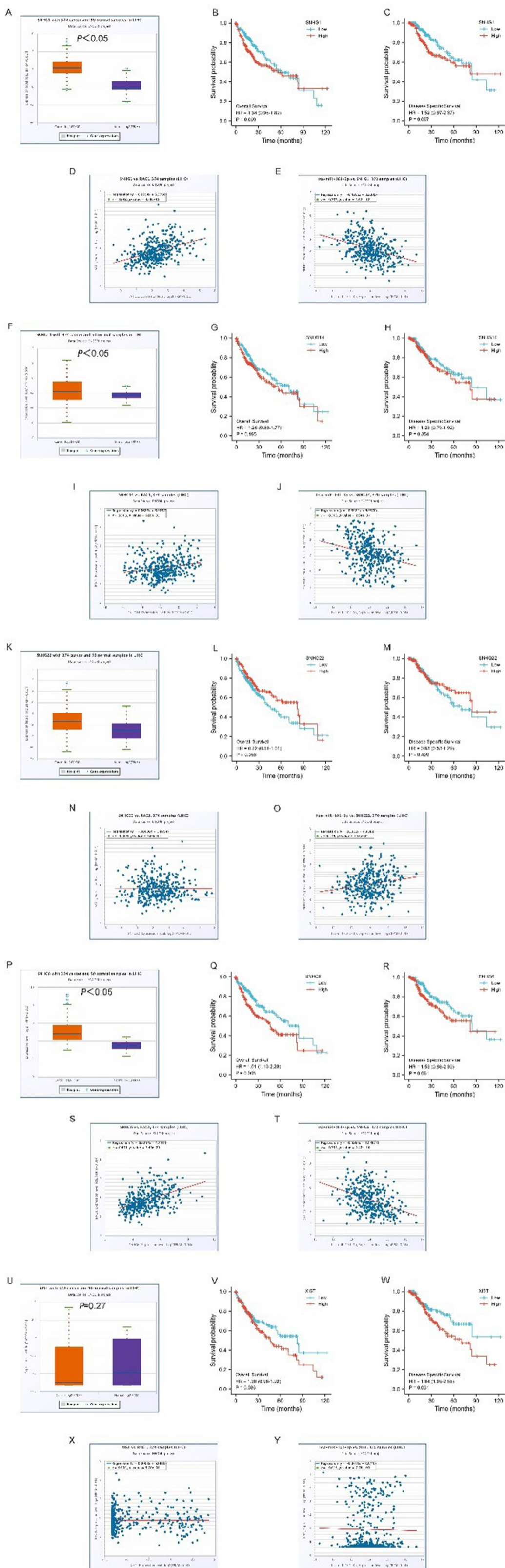


Figure S9 The expression, correlation of different LncRNAs with RAC1 and hsa-miR-101-3p in LIHC. (A-Y) The expression, the prognostic value of different LncRNAs, and the expression correlation of different LncRNAs with RAC1 and hsa-miR-101-3p in LIHC and control normal samples.

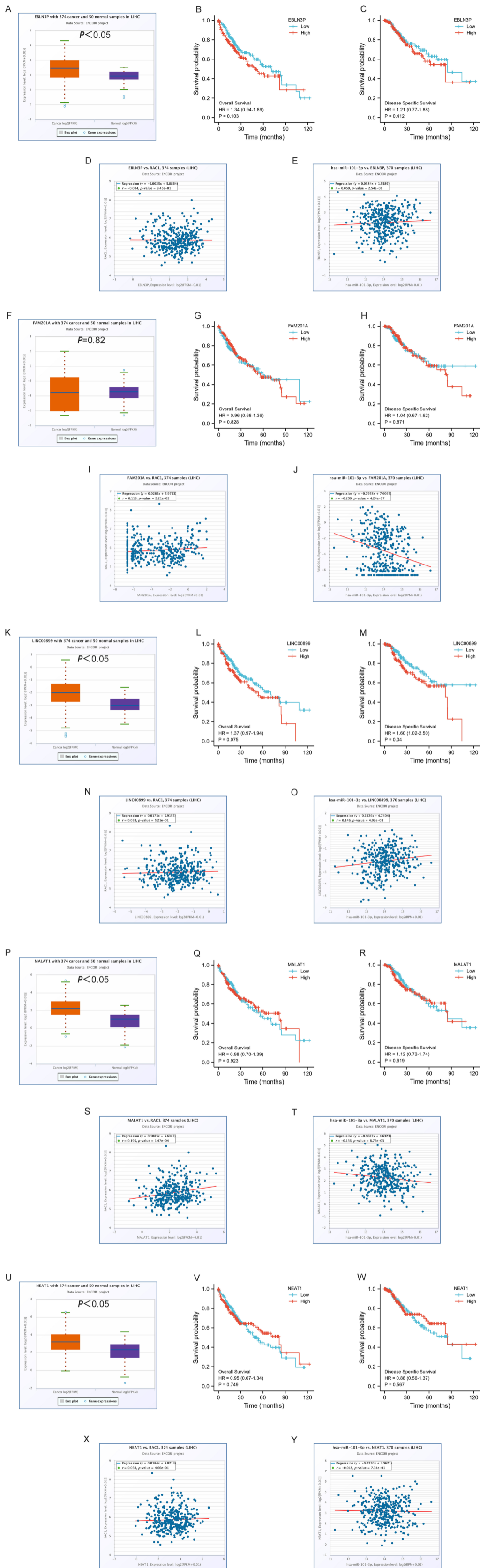


Figure S10 The expression, correlation of different LncRNAs with RAC1 and hsa-miR-101-3p in LIHC. (A-Y) The expression, the prognostic value of different LncRNAs, and the expression correlation of different LncRNAs with RAC1 and hsa-miR-101-3p in LIHC and control normal samples.