Table S1. Sequences of primers used in the PCR array

Gene name	MT	Length	Sequence
CD276	81.7	117	forward 5’-TCTCCAAAGGATGCGATACAC-3’
			reverse 5’-GTTGTGGGTGGTCTGTTCATT-3’
LGALS9	79.9	84	forward 5’-CCACCTGACCAGAGTGTTCTC-3’
			reverse 5’-GTGCCAACAAGCATTTTCATT-3’
CTLA4	82.7	136	forward 5’-TTGTGCTGAGTTGGTGTTG-3’
			reverse 5’-CTGGAGTAAGCCATTGTCTTC-3’
LAG3	84.3	82	forward 5’-ACTGGAGACAATGGCGACT-3’
			reverse 5’-GATGGATATGGCAGGTGTAGG-3’
CD86	82.9	105	forward 5’-CCTCTGTCAGGGTCAGTA AGG-3’
			reverse 5’-TCCAGGTTCTATCTCTGCCTC-3’
CD48	79.3	82	forward 5’-TAAGGTCCAGAAAGAGGACAA-3’
			reverse 5’-CTTGATCTTCCATTCTTGCTC-3’
HAVCR2	83.1	169	forward 5’-CCAACAGAGTTACCCAACCCAG-3’
			reverse 5’-CCTCAGCACCCAGTTTTCCCTA-3’
PDCD1	80.3	69	forward 5’-TTCCACATACCTCAAGTCCAA-3’
			reverse 5’-GGCGACCCCATAGATGATT-3’
TIGIT	81.8	133	forward 5’-ATCTGCCCTCAAGAACTTACA-3’
			reverse 5’-CCTATGCCAACTACCTCACC-3’
RPS3A	78	107	forward 5’-AAAAGGGAGCCAAGAAGAA-3’
			reverse 5’-GACGAGCGTCTTTCCAATAT-3’
GAPDH	86	158	forward 5’-ACAGGCAACTTGGCAAATC-3’
			reverse 5’-AAGGGCAGGAGTAAAGGTCAG-3’

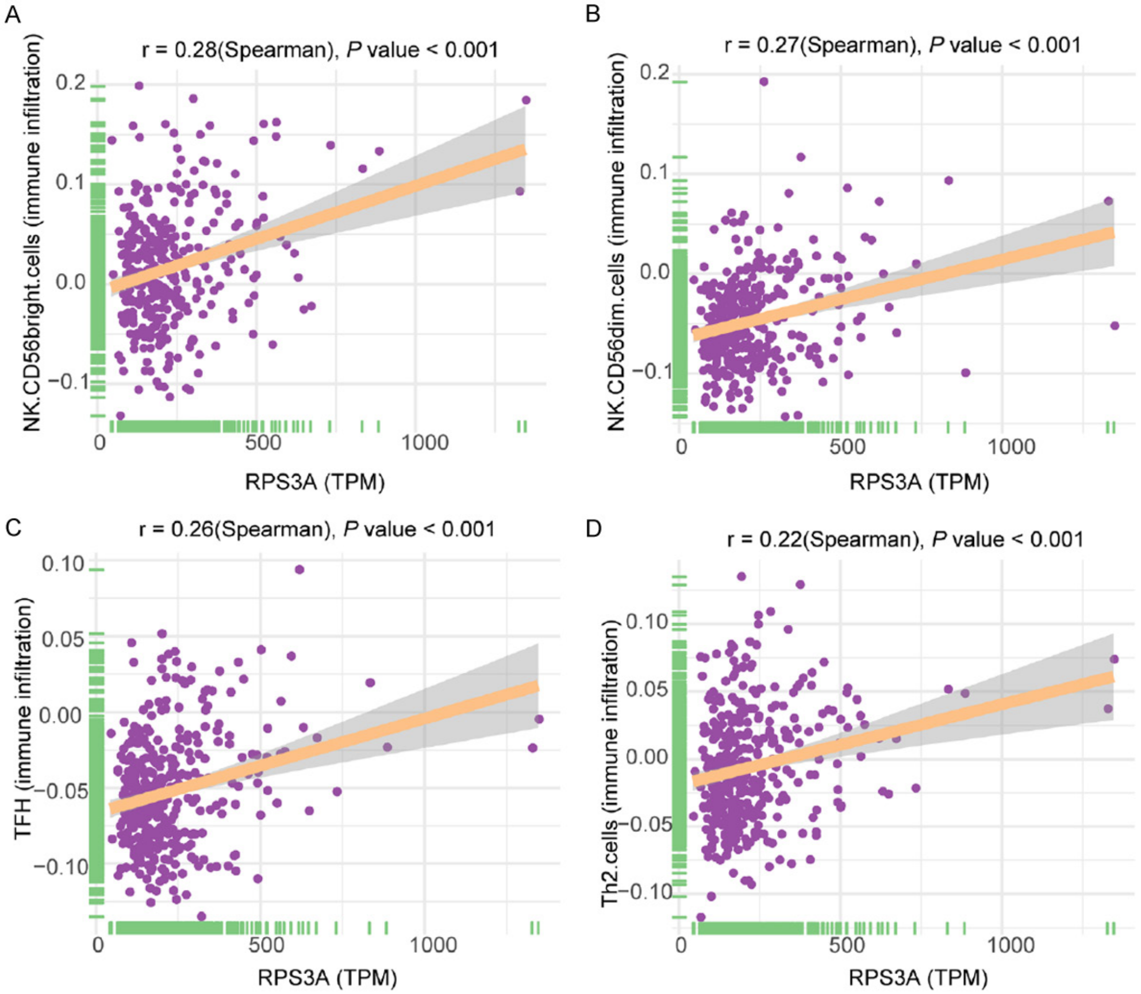

Figure S1. Correlation of RPS3A expression with the HCC infiltration of NK CD56^{bright} cells (A), NK CD56^{dim} cells (B), T follicular helper cells (C), and Th2 cells (D).

Table S2. Relationship between tumor RPS3A expression and immune checkpoint molecules expression in HCC patients in TCGA (n = 356)

Gene name	Gene name	r	*P* value
RPS3A	CD276	0.363217	1.53E-12
RPS3A	LGALS9	0.216578	3.77E-05
RPS3A	CTLA4	0.213689	4.81E-05
RPS3A	LAG3	0.212769	5.19E-05
RPS3A	CD86	0.195671	0.000203
RPS3A	CD48	0.187006	0.000389
RPS3A	HAVCR2	0.184702	0.00046
RPS3A	PDCD1	0.17371	0.000998
RPS3A	TIGIT	0.169156	0.001358
RPS3A	CD274	0.100316	0.058642
RPS3A	CD80	0.080507	0.129491
RPS3A	CD244	0.078762	0.138033
RPS3A	BTLA	0.06285	0.236868
RPS3A	IDO1	0.040675	0.444228
RPS3A	CD47	0.033558	0.527955

RPS3A	PVR	-0.0074	0.88928
RPS3A	TNFRSF14	-0.0585	0.270967
RPS3A	SIRPA	-0.06327	0.233741
RPS3A	CD160	-0.07341	0.166922
RPS3A	CEACAM1	-0.30193	6.13E-09

Spearman correlation test was used to determine the relationship between RPS3A expression and immune checkpoint molecules expression levels.

Table S3. Correlation of tumor RPS3A expression with clinicopathologic characteristics of 154 HCC patients

Characteristics		Patients	RPS3A expression		*P*
		Number (%)	Low (*n* = 75)	High (*n* = 79)	
Age, years	≤ 50	64 (41.56)	32	32	0.87
	> 50	90 (58.44)	43	47	
Gender	Female	18 (11.69)	7	11	0.456
	Male	136 (88.31)	68	68	
HBsAg	Negative	26 (16.88)	14	12	0.668
	Positive	128 (83.12)	61	67	
AFP, ng/ml	≤ 20	57 (37.01)	36	21	0.008*
	> 20	97 (62.99)	39	58	
CEA, ng/ml	≤ 5	141 (91.56)	71	70	0.248
	> 5	13 (8.44)	4	9	
CA19-9, U/ml	≤ 36	120 (77.92)	63	57	0.084
	> 36	34 (22.08)	12	22	
Ascites	Absent	145 (94.16)	70	75	0.741
	Present	9 (5.84)	5	4	
Liver cirrhosis	No	24 (15.58)	17	7	0.025*
	Yes	130 (84.42)	58	72	
Tumor number	Single	128 (83.12)	61	67	0.668
	Multiple	26 (16.88)	14	12	
Tumor size, cm	≤ 5	77 (50.00)	38	39	1
	> 5	77 (50.00)	37	40	
Tumor encapsulation	Complete	86 (55.84)	43	43	0.747
	None	68 (44.16)	32	36	
Tumor differentiation	I-II	97 (62.99)	53	44	0.067
	III-IV	57 (37.01)	22	35	
Microvascular invasion	Absent	89 (57.79)	46	43	0.418
	Present	65 (42.21)	29	36	
ALT, U/L	≤ 40	92 (59.74)	49	43	0.191
	> 40	62 (40.26)	26	36	
AST, U/L	≤ 37	109 (70.78)	60	49	0.021*
	> 37	45 (29.22)	15	30	
BCLC stage	0+A	78 (50.65)	40	38	0.524
	B+C	76 (49.35)	35	41	
TNM stage	I+II	117 (75.97)	56	61	0.851
	III+IV	37 (24.03)	19	18	

**P* value < 0.05 was considered statistically significant. *P* values were calculated using the Pearson chi-square test.