

Supplementary

Table S1 Clinical characteristics of TCGA and GEO cohorts

Clinical characteristics	TCGA cohorts	GSE68465 cohorts
Total cases	486	443
Survival status		
Alive	328 (67.5%)	207 (46.7%)
Dead	158 (32.5%)	236 (53.3%)
Age, years		
<65	215 (44.2%)	214 (48.3%)
≥65	271 (55.8%)	229 (51.7%)
Gender		
Male	225 (46.3%)	223 (50.3%)
Female	261 (53.7%)	220 (49.7%)
Stage		
Stage I	258 (53.1%)	
Stage II	116 (23.9%)	
Stage III	79 (16.3%)	
Stage IV	25 (5.1%)	
Unknow	8 (1.6%)	443 (100.0%)
T		
T1	163 (33.5%)	150 (33.9%)
T2	259 (53.3%)	251 (56.7%)
T3	43 (8.8%)	28 (6.3%)
T4	18 (3.7%)	12 (2.7%)
TX	3 (0.6%)	2 (0.5%)
N		
N0	312 (64.2%)	299 (67.5%)
N1	93 (19.1%)	88 (19.9%)
N2	68 (14.0%)	53 (12.0%)
N3	2 (0.4%)	3 (0.7%)
NX	11 (2.3%)	0
M		
M0	322 (66.3%)	
M1	24 (4.9%)	
MX	140 (28.8%)	443 (100.0%)

TCGA, The Cancer Genome Atlas; GEO, Gene-Expression Omnibus.

Table S2 The top 10 GO enrichment terms of immune-related RBPs

Term	ID	Description	Count	P.adjust
BP	GO:0034660	ncRNA metabolic process	48	1.23E-19
BP	GO:0008380	RNA splicing	46	1.88E-18
BP	GO:0022613	Ribonucleoprotein complex biogenesis	42	2.35E-15
BP	GO:0034470	ncRNA processing	38	3.14E-15
BP	GO:0006401	RNA catabolic process	36	3.34E-13
BP	GO:0090501	RNA phosphodiester bond hydrolysis	23	1.70E-12
BP	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	33	1.21E-11
BP	GO:0000398	mRNA splicing, via spliceosome	33	1.21E-11
BP	GO:0000375	RNA splicing, via transesterification reactions	33	1.35E-11
BP	GO:0009451	RNA modification	22	3.59E-11
CC	GO:0005681	Spliceosomal complex	19	7.99E-08
CC	GO:0000313	Organellar ribosome	13	1.99E-07
CC	GO:0005761	Mitochondrial ribosome	13	1.99E-07
CC	GO:0000932	P-body	12	1.08E-06
CC	GO:0009897	External side of plasma membrane	24	2.62E-06
CC	GO:0000315	Organellar large ribosomal subunit	9	1.78E-05
CC	GO:0005762	Mitochondrial large ribosomal subunit	9	1.78E-05
CC	GO:0036464	Cytoplasmic ribonucleoprotein granule	16	2.05E-05
CC	GO:1902555	Endoribonuclease complex	7	2.27E-05
CC	GO:0035770	Ribonucleoprotein granule	16	3.04E-05
MF	GO:0140098	Catalytic activity, acting on RNA	44	1.47E-19
MF	GO:0004540	Ribonuclease activity	20	6.87E-12
MF	GO:0003730	mRNA 3'-UTR binding	17	1.41E-10
MF	GO:0003725	Double-stranded RNA binding	15	8.44E-10
MF	GO:0140101	Catalytic activity, acting on a tRNA	18	1.17E-09
MF	GO:0004518	Nuclease activity	22	3.26E-09
MF	GO:0004521	Endoribonuclease activity	13	1.02E-08
MF	GO:0004519	Endonuclease activity	17	1.34E-08
MF	GO:0019955	Cytokine binding	17	1.35E-08
MF	GO:0035925	mRNA 3'-UTR AU-rich region binding	9	2.86E-08

GO, Gene Ontology; RBP, RNA-binding protein; BP, biological process; CC, cellular component; MF, molecular function; ncRNA, non-coding RNA.

Table S3 The top 10 KEGG pathway enrichment terms of immune-related RBPs

Term	ID	Description	Count	P.adjust
KEGG	hsa04060	Cytokine-cytokine receptor interaction	25	4.17E-06
KEGG	hsa04061	Viral protein interaction with cytokine and cytokine receptor	12	0.000354355
KEGG	hsa05323	Rheumatoid arthritis	10	0.004139102
KEGG	hsa04062	Chemokine signaling pathway	14	0.007427762
KEGG	hsa04380	Osteoclast differentiation	11	0.007427762
KEGG	hsa03040	Spliceosome	12	0.007427762
KEGG	hsa03013	RNA transport	12	0.041508323
KEGG	hsa05167	Kaposi sarcoma-associated herpesvirus infection	12	0.048966089
KEGG	hsa05140	Leishmaniasis	7	0.048966089
KEGG	hsa04060	Cytokine-cytokine receptor interaction	25	4.17E-06

KEGG, Kyoto Encyclopedia of Genes and Genomes; RBP, RNA-binding protein.

Table S4 The immune-related RBPs with LUAD patients' survival by univariate cox regression analysis

ID	HR	95% CI of HR	P value
ZC3H12C	1.491	1.085–2.050	0.014
ZC3H12D	0.466	0.280–0.744	0.003
OAS1	1.180	1.020–1.346	0.026
OAS3	1.225	1.035–1.449	0.018
CIRBP	0.712	0.575–0.881	0.002
PNRC2	0.610	0.419–0.888	0.010
RNPC3	0.629	0.452–0.876	0.006
AGO4	0.669	0.469–0.952	0.026
HEATR1	1.535	1.070–2.201	0.020
R3HDM1	1.614	1.064–2.447	0.024
PRIM1	1.410	1.128–1.762	0.003
PCF11	0.570	0.365–0.890	0.013
TLR7	0.753	0.573–0.989	0.041
BRCA1	1.362	1.058–1.752	0.016
EXO1	1.452	1.204–1.752	<0.001

RBP, RNA-binding protein; LUAD, lung adenocarcinoma; HR, hazard ratio; CI, confidence interval.

Table S5 Coefficients and multivariable cox model results of each gene in risk signature

ID	HR	95% CI of HR	P value	Coefficient
OAS3	1.203	0.994–1.456	0.006	0.185096493
PCF11	0.679	0.446–1.033	0.007	-0.387198866
TLR7	0.859	0.710–1.039	0.012	-0.151663163
EXO1	1.239	0.996–1.542	0.005	0.214581606

HR, hazard ratio; CI, confidence interval.

Table S6 Univariate and multivariate cox regression analysis of OS of LUAD patients

Parameter	Univariate analysis			Multivariate analysis		
	HR	95% CI of HR	P	HR	95% CI of HR	P
Age	1.000	0.980–1.019	0.976	1.012	0.992–1.033	0.231
Gender	1.005	0.692–1.461	0.977	0.915	0.627–1.335	0.644
Stage	1.672	1.411–1.981	<0.001*	1.786	1.093–2.918	0.021*
T	1.612	1.286–2.019	<0.001*	1.213	0.942–1.561	0.134
M	1.776	0.951–3.319	0.072*	0.464	0.131–1.649	0.235
N	1.806	1.467–2.222	0.072*	1.047	0.688–1.592	0.830
Risk score	2.110	1.508–2.954	<0.001*	1.862	1.292–2.683	<0.001*

*, P<0.05. OS, overall survival; LUAD, lung adenocarcinoma; HR, hazard ratio; CI, confidence interval.

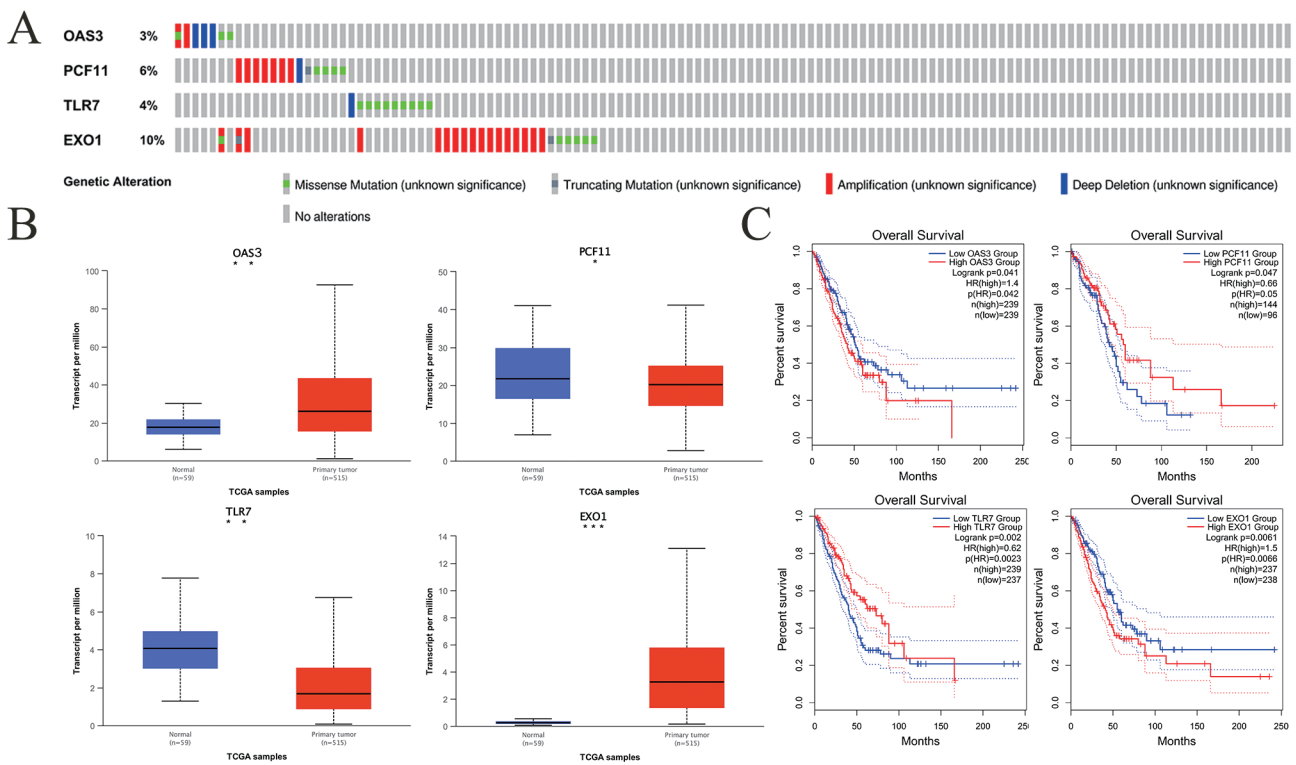


Figure S1 Mutation rate, expression level and prognostic status of risk genes in LUAD patients. (A) Mutation rate of risk genes in LUAD patients; (B) mRNA expression of risk genes in LUAD tissues and adjacent normal tissues. OAS and EXO1 were highly expressed in tumor tissues. PCF11 and TLR7 were lowly expressed in tumor tissues. (C) OS of the risk genes in LUAD patients. *, P<0.05; **, P<0.005; ***, P<0.0005. HR, hazard ratio; LUAD, lung adenocarcinoma; OS, overall survival; TCGA, The Cancer Genome Atlas.

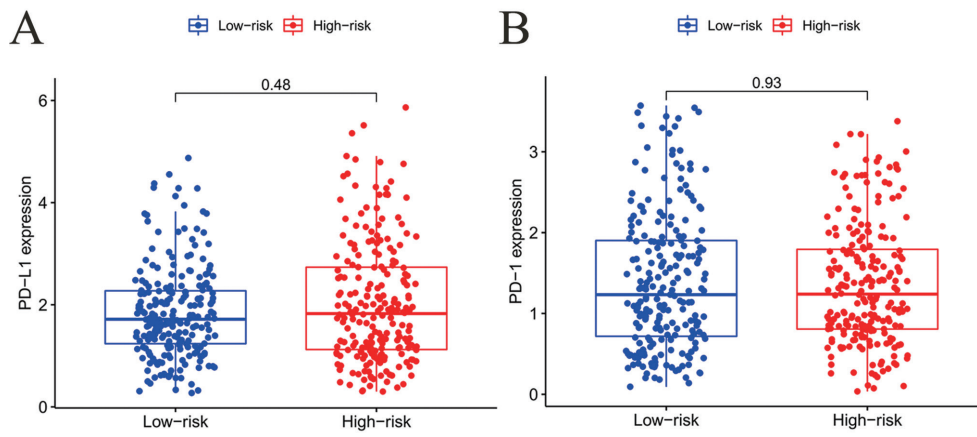


Figure S2 Immune checkpoints in low- and high-risk groups. (A) PD-L1. (B) PD-1.