

Figure S1 Kaplan-Meier (K-M) survival curve of differential expression groups in 16 genes out of 50 immune-related hub genes.

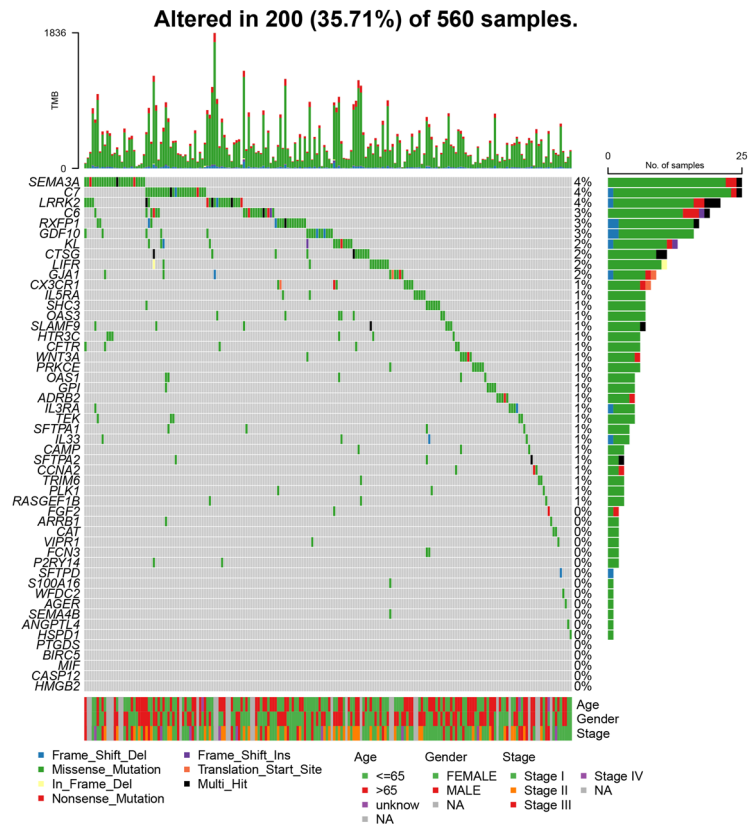


Figure S2 Oncoplot displaying the mutation status of 50 immune-related hub genes in The Cancer Genome Atlas (TCGA) cohort. Mutated genes are ordered by mutation numbers of the whole sample, the colors represent the mutation type. TMB, tumor mutation burden.

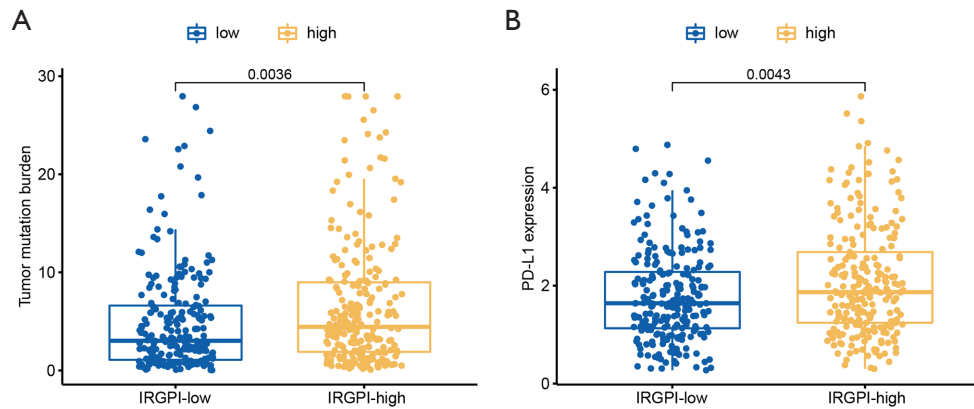


Figure S3 The relationship between immune-related gene prognostic index (IRGPI) and tumor mutation burden and programmed death-ligand 1 (PD-L1) expression. (A) Differential analysis of tumor mutation burden in 2 IRGPI subgroups. (B) Differential analysis of PD-L1 expression in 2 IRGPI subgroups.

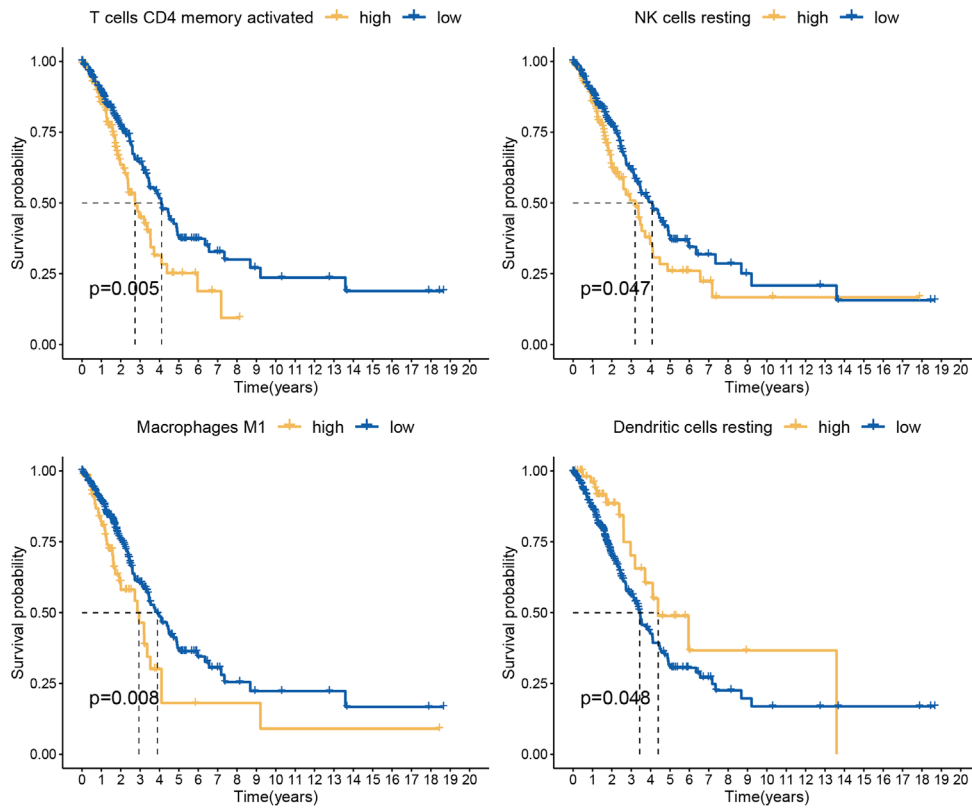


Figure S4 Kaplan-Meier (K-M) survival analysis of immune cells with different distributions in 2 immune-related gene prognostic index (IRGPI) subgroups.

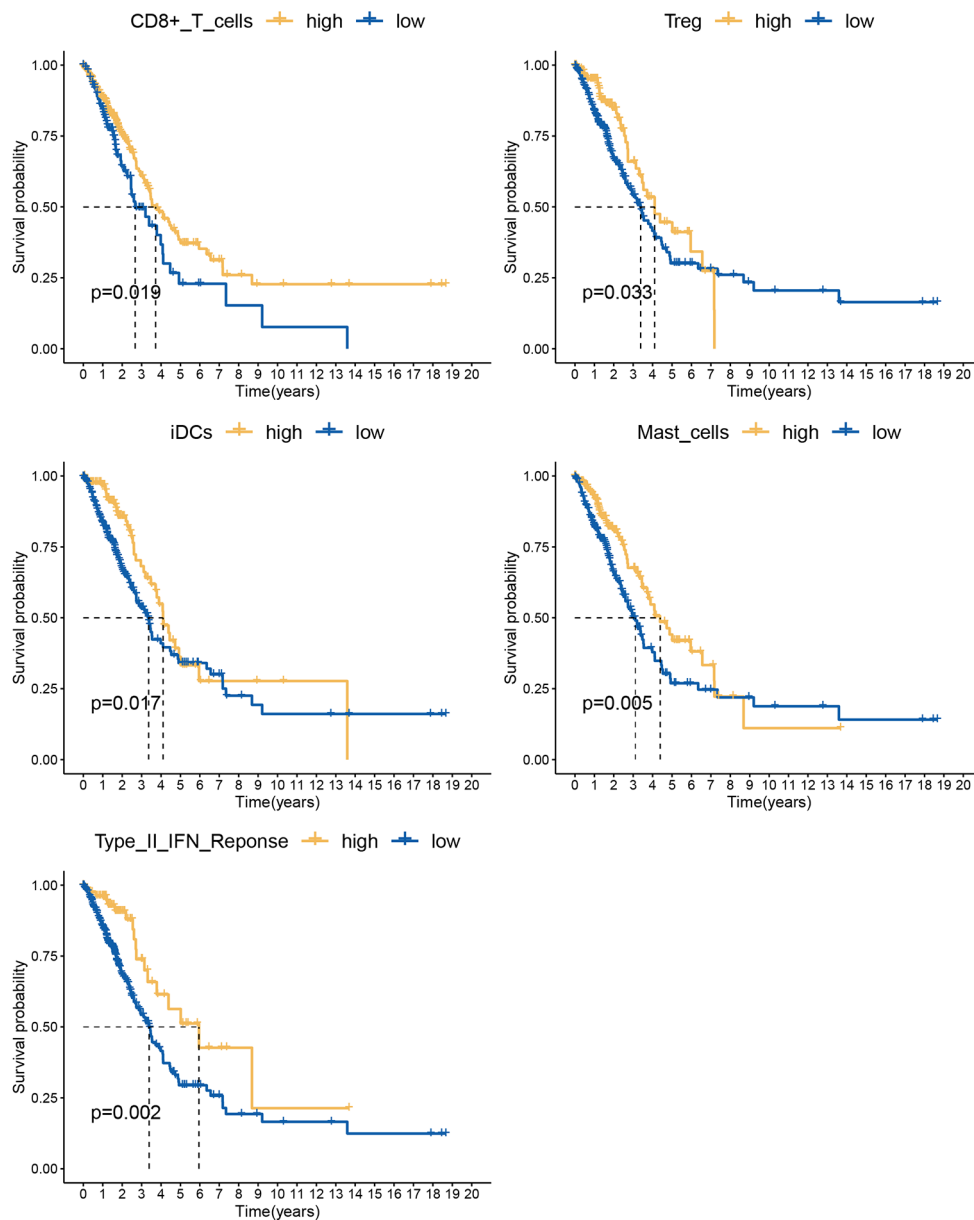


Figure S5 Kaplan-Meier (K-M) survival analysis of immune-related functions with different expressions in 2 immune-related gene prognostic index (IRGPI) subgroups.

Table S1 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways enriched in immune-related differentially expressed genes (DEGs)

ID	Description	GeneRatio	BgRatio	P value	P. adjust
hsa04060	Cytokine-cytokine receptor interaction	89/394	295/8091	2.42E-48	6.04E-46
hsa04061	Viral protein interaction with cytokine and cytokine receptor	37/394	100/8091	1.09E-23	1.36E-21
hsa04080	Neuroactive ligand-receptor interaction	54/394	341/8091	4.54E-15	3.76E-13
hsa04062	Chemokine signaling pathway	37/394	192/8091	2.86E-13	1.78E-11
hsa04630	JAK-STAT signaling pathway	32/394	162/8091	6.27E-12	3.12E-10
hsa04657	IL-17 signaling pathway	21/394	94/8091	2.88E-09	1.20E-07
hsa05323	Rheumatoid arthritis	19/394	93/8091	7.74E-08	2.75E-06
hsa04610	Complement and coagulation cascades	18/394	85/8091	9.58E-08	2.98E-06
hsa05417	Lipid and atherosclerosis	29/394	215/8091	5.02E-07	1.39E-05
hsa04064	NF-kappa B signaling pathway	18/394	104/8091	2.24E-06	5.58E-05
hsa05171	Coronavirus disease - COVID-19	28/394	232/8091	7.32E-06	0.000165615
hsa04380	Osteoclast differentiation	19/394	128/8091	1.22E-05	0.000253638
hsa04010	MAPK signaling pathway	32/394	294/8091	1.44E-05	0.000276659
hsa04668	TNF signaling pathway	17/394	112/8091	2.61E-05	0.000458062
hsa04621	NOD-like receptor signaling pathway	23/394	184/8091	2.76E-05	0.000458062
hsa04151	PI3K-Akt signaling pathway	35/394	354/8091	4.52E-05	0.00070387
hsa04014	Ras signaling pathway	26/394	232/8091	5.70E-05	0.000834168
hsa04360	Axon guidance	22/394	182/8091	6.89E-05	0.000953554
hsa04015	Rap1 signaling pathway	24/394	210/8091	8.05E-05	0.001054898
hsa04933	AGE-RAGE signaling pathway in diabetic complications	15/394	100/8091	8.92E-05	0.001110638
hsa05144	Malaria	10/394	50/8091	0.000119246	0.001355588
hsa05169	Epstein-Barr virus infection	23/394	202/8091	0.000119771	0.001355588
hsa05218	Melanoma	12/394	72/8091	0.000162323	0.001710843
hsa04350	TGF-beta signaling pathway	14/394	94/8091	0.000164901	0.001710843
hsa05133	Pertussis	12/394	76/8091	0.00027485	0.002737505
hsa05418	Fluid shear stress and atherosclerosis	17/394	139/8091	0.000397396	0.003667049
hsa01521	EGFR tyrosine kinase inhibitor resistance	12/394	79/8091	0.000397632	0.003667049
hsa04620	Toll-like receptor signaling pathway	14/394	104/8091	0.000482954	0.004294839
hsa04650	Natural killer cell mediated cytotoxicity	16/394	131/8091	0.000593909	0.005099427
hsa04614	Renin-angiotensin system	6/394	23/8091	0.000638591	0.005300309
hsa04024	cAMP signaling pathway	22/394	219/8091	0.000963935	0.007742578
hsa05167	Kaposi sarcoma-associated herpesvirus infection	20/394	194/8091	0.001180665	0.00918705
hsa04020	Calcium signaling pathway	23/394	240/8091	0.001411756	0.010652344
hsa04924	Renin secretion	10/394	69/8091	0.001729835	0.0126685
hsa05150	Staphylococcus aureus infection	12/394	96/8091	0.002302274	0.016286295
hsa04066	HIF-1 signaling pathway	13/394	109/8091	0.002354645	0.016286295
hsa04012	ErbB signaling pathway	11/394	85/8091	0.002627403	0.017681713
hsa04145	Phagosome	16/394	152/8091	0.002891555	0.018947294
hsa05219	Bladder cancer	7/394	41/8091	0.003289964	0.021005154
hsa05146	Amoebiasis	12/394	102/8091	0.003831773	0.023852788
hsa04625	C-type lectin receptor signaling pathway	12/394	104/8091	0.004493435	0.027289397
hsa04270	Vascular smooth muscle contraction	14/394	133/8091	0.005171768	0.030364107
hsa04928	Parathyroid hormone synthesis, secretion and action	12/394	106/8091	0.005243601	0.030364107
hsa05161	Hepatitis B	16/394	162/8091	0.005423714	0.030693293
hsa05226	Gastric cancer	15/394	149/8091	0.005864391	0.032402127
hsa05134	Legionellosis	8/394	57/8091	0.005985935	0.032402127
hsa05207	Chemical carcinogenesis - receptor activation	19/394	212/8091	0.007361743	0.039001573
hsa05162	Measles	14/394	139/8091	0.007608567	0.039469439
hsa05223	Non-small cell lung cancer	9/394	72/8091	0.007875125	0.040018494
hsa05143	African trypanosomiasis	6/394	37/8091	0.00827002	0.0411847
hsa04640	Hematopoietic cell lineage	11/394	99/8091	0.008465363	0.041330888
hsa04672	Intestinal immune network for IgA production	7/394	49/8091	0.009008454	0.043136636
hsa05340	Primary immunodeficiency	6/394	38/8091	0.009428056	0.044294073
hsa04926	Relaxin signaling pathway	13/394	129/8091	0.009882914	0.045571216
hsa05214	Glioma	9/394	75/8091	0.010229837	0.045687772
hsa05166	Human T-cell leukemia virus 1 infection	19/394	219/8091	0.010275161	0.045687772

Table S2 Univariate and multivariate cox regression analysis of immune-related gene prognostic index (IRGPI) and clinical factors [age, gender, tumor (T), metastasis (M), and lymph node (N)]

Variables	Univariate Cox analysis				Multivariate Cox analysis			
	HR	HR95L	HR95H	p-value	HR	HR95L	HR95H	P value
Age	1.004	0.985	1.023	0.7	1.013	0.994	1.033	0.195
Gender	1.078	0.749	1.55	0.687	0.92	0.632	1.339	0.662
T	1.631	1.314	2.025	<0.001	1.241	0.978	1.576	0.075
M	1.78	0.976	3.242	0.06	1.717	0.917	3.214	0.091
N	1.794	1.462	2.201	<0.001	1.623	1.29	2.041	<0.001
IRGPI	1.098	1.068	1.129	<0.001	1.078	1.046	1.111	<0.001

Table S3 Enriched pathways of immune-related differentially expressed genes (DEGs) in gene set enriched analysis (GSEA)

Description	setSize	enrichmentScore	NES	P value	P. adjust
SYSTEMIC_LUPUS_ERYTHEMATOSUS	108	-0.700210169	-2.236714273	1.00E-10	1.84E-08
CELL_CYCLE	121	0.574703456	2.19402952	4.03E-07	3.70E-05
FOCAL_ADHESION	177	0.490064778	1.970109543	3.85E-06	0.000235869
PROTEASOME	42	0.693281363	2.206226372	5.07E-05	0.002332459
ECM_RECEPTOR_INTERACTION	71	0.592614811	2.049230703	6.34E-05	0.002332829
PATHWAYS_IN_CANCER	288	0.371385484	1.543639028	0.000209649	0.006429231
REGULATION_OF_ACTIN_CYTOSKELETON	175	0.412060839	1.665088775	0.000944204	0.024819067
SMALL_CELL_LUNG_CANCER	79	0.510180417	1.823864275	0.001846318	0.042465306
DNA_REPLICATION	35	0.626889593	1.913638336	0.002571949	0.052582077
ASTHMA	20	-0.730757742	-1.762992145	0.002863025	0.052679661
PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	19	-0.730437212	-1.727719996	0.003633549	0.06077936
PATHOGENIC_ESCHERICHIA_COLI_INFECTION	49	0.537429773	1.739493574	0.007362404	0.11289019
CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	193	0.359432836	1.455147952	0.008425906	0.117256955
P53_SIGNALING_PATHWAY	65	0.485176919	1.677399639	0.008943621	0.117256955
AXON_GUIDANCE	111	0.422190879	1.593107835	0.009985658	0.117256955
ADIPOCYTOKINE_SIGNALING_PATHWAY	59	-0.539358508	-1.574700597	0.010196257	0.117256955
SPLICEOSOME	125	0.40663282	1.564202992	0.011162246	0.117806307
NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	104	0.418019857	1.53885823	0.011559573	0.117806307
MELANOMA	54	0.481120743	1.605560995	0.012317879	0.117806307
HOMOLOGOUS_RECOMBINATION	26	0.625166147	1.835475822	0.012805033	0.117806307
OOCYTE_MEIOSIS	94	0.448305493	1.635022164	0.014123624	0.12374985
ALPHA_LINOLENIC_ACID_METABOLISM	15	-0.724497581	-1.634535987	0.015027571	0.125685142
ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	58	0.467601692	1.588697323	0.016563866	0.132510926
LINOLEIC_ACID_METABOLISM	17	-0.696664401	-1.597793528	0.018117388	0.138899978
ADHERENS_JUNCTION	69	0.441414319	1.540072764	0.024371308	0.179372827
PYRIMIDINE_METABOLISM	90	0.408774297	1.4872183	0.034616773	0.244980241
PPAR_SIGNALING_PATHWAY	55	-0.495789945	-1.422290124	0.03974359	0.262503671
PENTOSE_PHOSPHATE_PATHWAY	23	0.567769515	1.599608724	0.039946211	0.262503671
GLIOMA	58	0.42900605	1.45756693	0.044950999	0.281226567
FC_EPSILON_RI_SIGNALING_PATHWAY	69	-0.465332046	-1.390163002	0.045962733	0.281226567
RENAL_CELL_CARCINOMA	67	0.413786129	1.43035015	0.048223898	0.281226567