Supplementary

Table S1 Abbreviation list

Abbreviation	Full term	Definition/context
HCC	Hepatocellular carcinoma	Primary liver cancer, the main research subject of this study
PRFs	Phagocytic regulatory factorsa	Factors regulating immune cells (e.g., macrophages) in the tumor microenvironment
PFRGs	Phagocytic regulatory factor-related genes	Genes related to phagocytic regulation, used to construct prognostic models
TAMs	Tumor-associated macrophages	Macrophages in tumor microenvironment, playing key roles in HCC immune suppression
TME	Tumor microenvironment	Cellular environment surrounding tumors, influencing HCC progression and therapy response
TCGA	The Cancer Genome Atlas	Database providing genomic and clinical data of HCC patients (primary data source)
GEO	Gene Expression Omnibus	Database for independent validation datasets (e.g., GSE76427)
FDR	False discovery rate	Multiple testing correction threshold (set as FDR <0.05 in this study)
FC	Fold change	Differential gene expression ratio (screening criteria: |logFC| >0.585)
GSEA	Gene set enrichment analysis	Identifies enriched biological pathways between experimental groups
ssGSEA	Single-sample gene set enrichment analysis	Method quantifying activity of gene sets in individual samples.
LASSO	Least absolute shrinkage and selection operator	Regression method selecting prognostic genes while preventing overfitting
DEGs	Differentially expressed genes	Genes differentially expressed between tumor/normal tissues
DEPFRGs	Differentially expressed PFRGs	Differentially expressed phagocytic regulatory factor-related genes
GO	Gene Ontology	Functional annotation system for biological processes/molecular functions
KEGG	Kyoto Encyclopedia of Genes and Genomes	Pathway database (e.g., cell adhesion molecule pathway)
ROC	Receiver operating characteristic	Curve evaluating model performance (1/3/5-year AUC values)
AUC	Area under the curve	Metric of model accuracy (AUC >0.7 indicates good performance)
K-M	Kaplan-Meier	Survival analysis comparing risk groups (log-rank P<0.05 as significant)
GSEA	Gene Set Enrichment Analysis	Identifies enriched biological pathways between risk groups
DCA	Decision curve analysis	Evaluates clinical utility and net benefit of nomograms.
IPS	Immunophenoscore	Predicts immunotherapy response based on immune infiltration/checkpoints
TCIA	The Cancer Immunome Atlas	Database for immunotherapy data (e.g., IPS scores used in this study)
TMB	Tumor mutational burden	Total mutation count in tumor genome (higher TMB may indicate better immunotherapy response)
IC50	Half-maximal inhibitory concentration	Drug sensitivity metric (lower IC50 =higher sensitivity)
DC	Dendritic cells	Antigen-presenting cells critical for T cell activation in tumor immunity
cDC1	Conventional dendritic cell type 1	Specialized subset of DCs for cross-presentation and anti-tumor immunity
ACT	Adoptive cell transfer	Immunotherapy involving infusion of engineered immune cells (e.g., CAR-T)
HDAC	Histone deacetylase	Epigenetic modifier enzyme family
ICIs	Immune checkpoint inhibitors	Therapeutics targeting PD-1/PD-L1 etc., used in HCC immunotherapy
M1/M2 macrophages	M1/M2 polarized macrophages	M1 (pro-inflammatory, anti-tumor) *vs.* M2 (anti-inflammatory, pro-tumor) phenotypes
CR/PR/SD/PD/NR/R	Complete response/partial response/stable disease/progressive disease/non-responders/responders	Immunotherapy efficacy criteria. NR (non-responders): SD + PD R (responders): CR + PR

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Table S2 The clinical baseline characteristics of patients in the high and low scoring groups

Variables	High (N=117)	Low (N=119)	P
Height, mean (SD)	165.01 (12.34)	167.26 (8.58)	0.11
Weight, mean (SD)	69.66 (16.02)	67.50 (15.90)	0.307
Race, n (%)			0.687
American indian or Alaska native	1 (0.9)	1 (0.8)	
Asian	75 (64.1)	74 (62.2)	
Black or african american	2 (1.7)	2 (1.7)	
Not reported	4 (3.4)	1 (0.8)	
White	35 (29.9)	41 (34.5)	
OS.time, mean (SD)	920.96 (730.76)	807.91 (862.26)	0.279
OS, n (%)			0.032
0	88 (75.2)	73 (61.3)	
1	29 (24.8)	46 (38.7)	
Age, n (%)			0.053
≤65	75 (64.1)	91 (76.5)	
>65	42 (35.9)	28 (23.5)	
Gender, n (%)			0.846
Female	35 (29.9)	38 (31.9)	
Male	82 (70.1)	81 (68.1)	
Grade, n (%)			0.926
G1	14 (12.0)	15 (12.6)	
G2	50 (42.7)	52 (43.7)	
G3	47 (40.2)	48 (40.3)	
G4	6 (5.1)	4 (3.4)	
Stage, n (%)			0.089
Stage I	64 (54.7)	51 (42.9)	
Stage II	23 (19.7)	27 (22.7)	
Stage III	30 (25.6)	37 (31.1)	
Stage IV	0 (0.0)	4 (3.4)	
T, n (%)			0.216
T1	65 (55.6)	51 (42.9)	
T2	24 (20.5)	28 (23.5)	
T3	23 (19.7)	35 (29.4)	
T4	5 (4.3)	5 (4.2)	
M, n (%)			0.135
M0	117 (100.0)	115 (96.6)	
M1	0 (0.0)	4 (3.4)	

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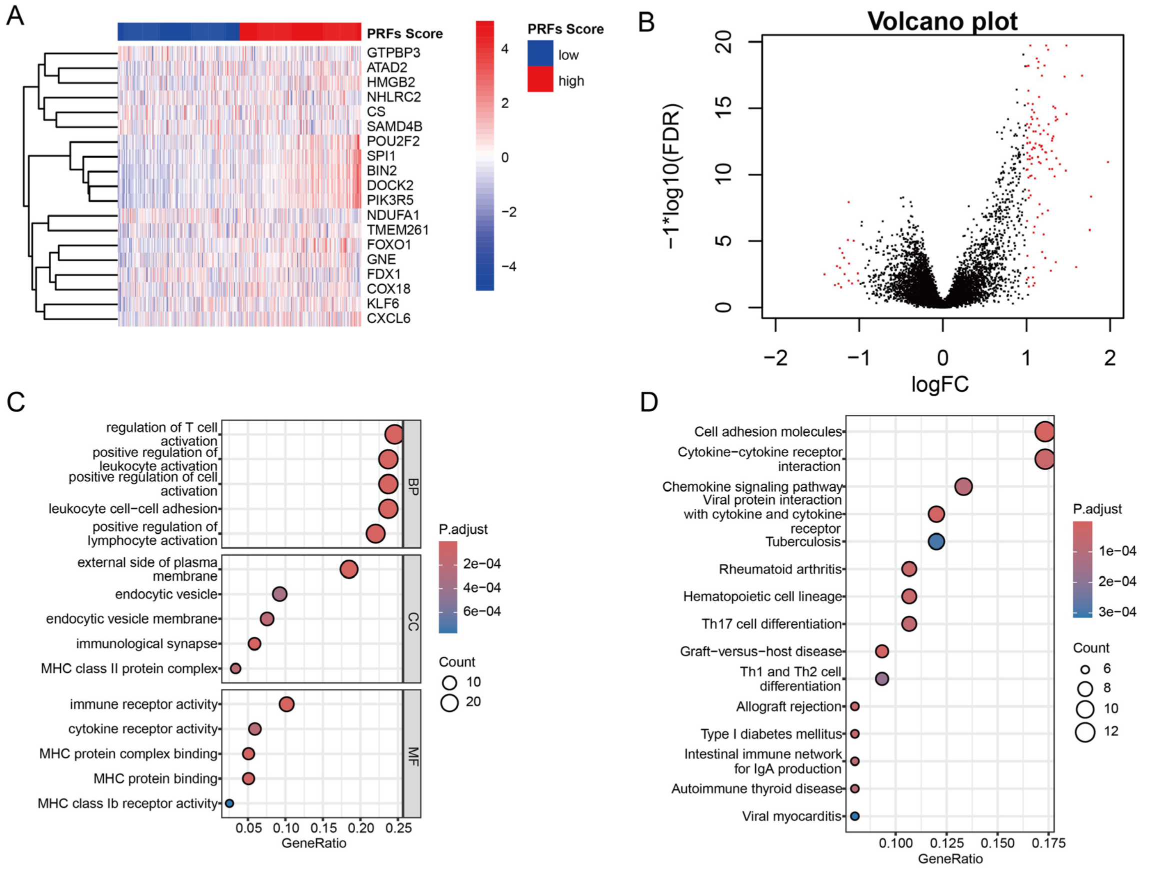

Figure S1 Feature of PRFs enrichment in TCGA-LIHC cohort. (A) The heatmap illustrates the expression levels of DEPFRGs in the different scoring groups. (B) The volcano plot represents the differentially expressed genes between the high and low enrichment score groups, with a total of 124 differentially expressed genes, including 106 upregulated genes and 18 downregulated genes. (C) GO enrichment analysis and (D) KEGG pathway analysis of DEGs in the scoring groups. PRFs, phagocytic regulatory factors; DEPFRGs, differentially expressed genes related to phagocytic regulatory factors; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table S3 Univariate regression analysis results (P<0.01)

Gene	HR	HR.95L	HR.95H	Z	P value
CD6	0.82916199115004	0.730110517375827	0.941651422909171	–2.886183148	0.0038994516642616
CD5L	0.899121488596289	0.849753843401906	0.951357216601902	–3.69065985	0.000223673076270821
CST7	0.796637875574032	0.689173838343673	0.92085896110675	–3.075136084	0.00210406526933759
ITM2A	0.823150253297483	0.725497423024342	0.933947272588695	–3.02057067	0.00252298823128821
SLA2	0.774141098180914	0.662463133733199	0.904645721967242	–3.220716446	0.0012787059448513
BIN2	0.779978620023402	0.645750741045297	0.942107548663171	–2.578879982	0.00991212180246402
ITK	0.800256205026791	0.706858647802308	0.905994424309554	–3.519109132	0.00043299855315133
SLAMF1	0.821037739426305	0.719978869963429	0.936281601703807	–2.942413858	0.00325664375936656
FLT3	0.811457332592956	0.720257835636693	0.914204566808785	–3.434605836	0.000593416294226791
ZNF831	0.800475999340183	0.715498728500512	0.895545722160157	–3.886663201	0.000101631607692562
GPR18	0.792366313778904	0.696804362975974	0.901033932293586	–3.549240992	0.000386343326611608
PTGER2	0.807188961717348	0.699730614885127	0.931149796876179	–2.938627985	0.00329668513614216
BCL11B	0.81063739130826	0.712762108324183	0.921952742033502	–3.197745735	0.00138506346334712
KLRD1	0.814020548090197	0.704037265454566	0.941185197469958	–2.778430164	0.00546222534014852
TESPA1	0.803696893644106	0.700146154779203	0.922562657016784	–3.105251615	0.00190117222366935
CTSV	1.13745633426787	1.06003673002558	1.22053026628133	3.58106449580181	0.000342197161283151
CD226	0.788247726685054	0.67912385348021	0.914905985763996	–3.129742263	0.00174959737416953
UBASH3A	0.788906882918229	0.692556909589526	0.898661267107469	–3.567700848	0.000360127317016484
IKZF3	0.797811181421643	0.693538120078217	0.917761638148474	–3.160824	0.00157323527336945
EOMES	0.820564680566815	0.726709045321089	0.926541921184174	–3.191063274	0.0014175023313815
TRAT1	0.846271613511629	0.759549283633699	0.942895555650291	–3.025914565	0.0024788233313466
XCR1	0.836891764284134	0.759446456574308	0.922234634270207	–3.59397034	0.000325676927702032
IKZF1	0.795417850658907	0.673208093597181	0.939812760963936	–2.689307274	0.00716004782277747
SPN	0.780837226582466	0.664082018499879	0.918119686171128	–2.993761088	0.00275561628504849
CD3E	0.849984735666156	0.753610149131464	0.958684077832706	–2.647149523	0.0081173452782582
KLRK1	0.777107308120718	0.682578992460411	0.884726566456195	–3.810769464	0.000138534914172617

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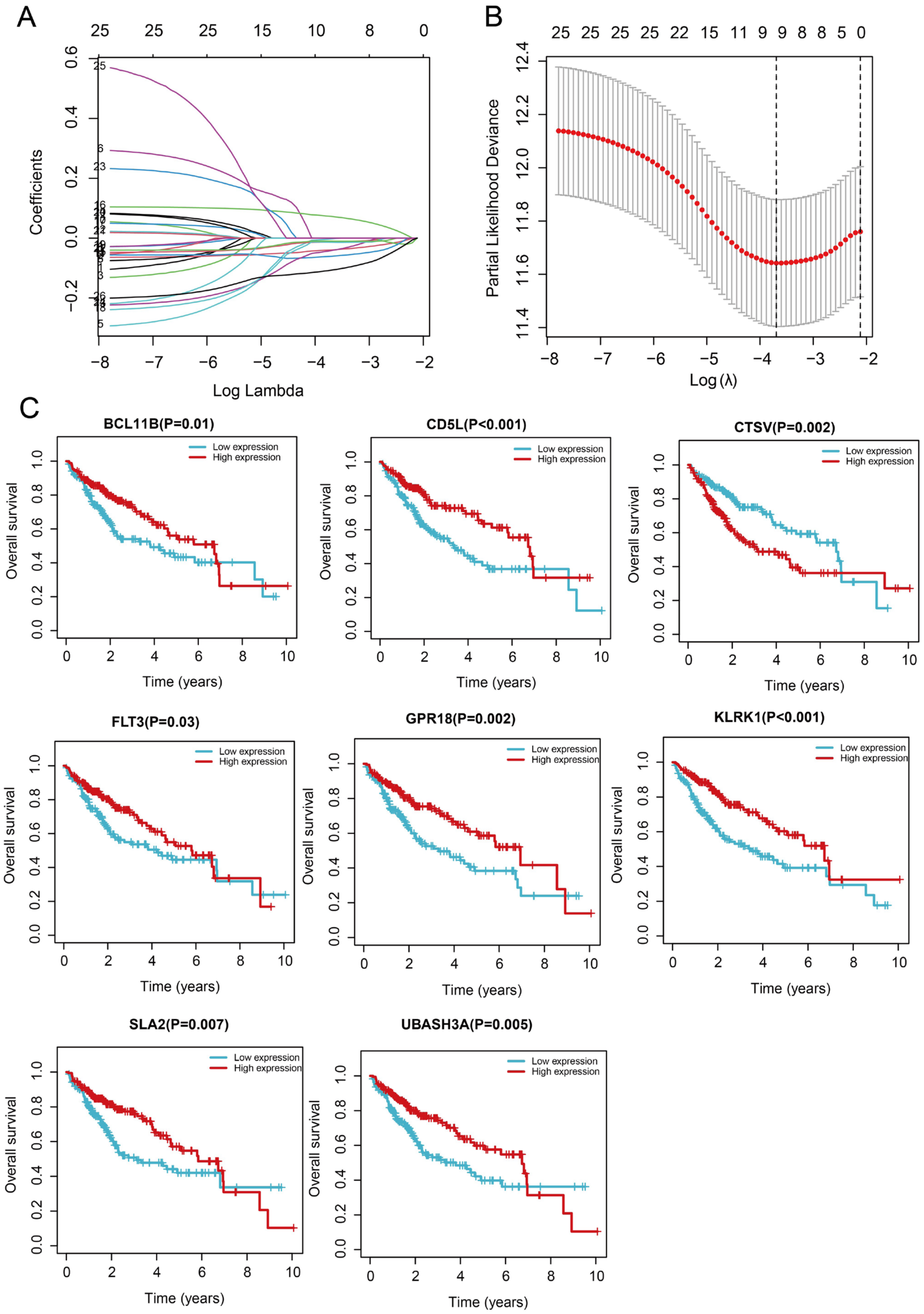

Figure S2 Results of LASSO regression analysis and survival analysis of feature genes. (A) LASSO regression coefficient path plot and (B) cross-validation results. (C) The results of the Kaplan-Meier (K-M) curve for the feature genes. LASSO, least absolute shrinkage and selection operator.

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Table S4 LASSO analysis results

Gene	Coef
CD5L	−0.038380731
SLA2	−0.001151068
FLT3	−0.012629193
GPR18	−0.059326499
BCL11B	−0.038636607
CTSV	0.0702825508173428
UBASH3A	−0.014539043
XCR1	−0.010620087
KLRK1	−0.104566836

Table S5 Results of multivariate regression analysis

ID	Coef	HR	HR.95L	HR.95H	Pvalue
CD5L	−0.0508	0.950441187328056	0.890746764481686	1.01413610084254	0.124581300801092
SLA2	−0.0178	0.982378311834265	0.75457562144877	1.27895352053573	0.894920026218819
FLT3	−0.0165	0.98359803983995	0.827345193327752	1.16936088077777	0.851371999420477
GPR18	−0.0749	0.927840276747769	0.771859129730948	1.11534287280564	0.425138820501199
BCL11B	−0.0720	0.930518574034982	0.777427471729553	1.11375639286041	0.432328684317125
CTSV	0.0909	1.09518832353563	1.01787431379876	1.17837482265607	0.0149220243682939
UBASH3A	−0.0113	0.98878231339826	0.772180379188789	1.26614258745648	0.928745315453685
XCR1	−0.0101	0.989989351229622	0.837801972881613	1.16982168492284	0.905955093427959
KLRK1	−0.1351	0.873655943317692	0.745639144823868	1.02365160492563	0.0947612318708252

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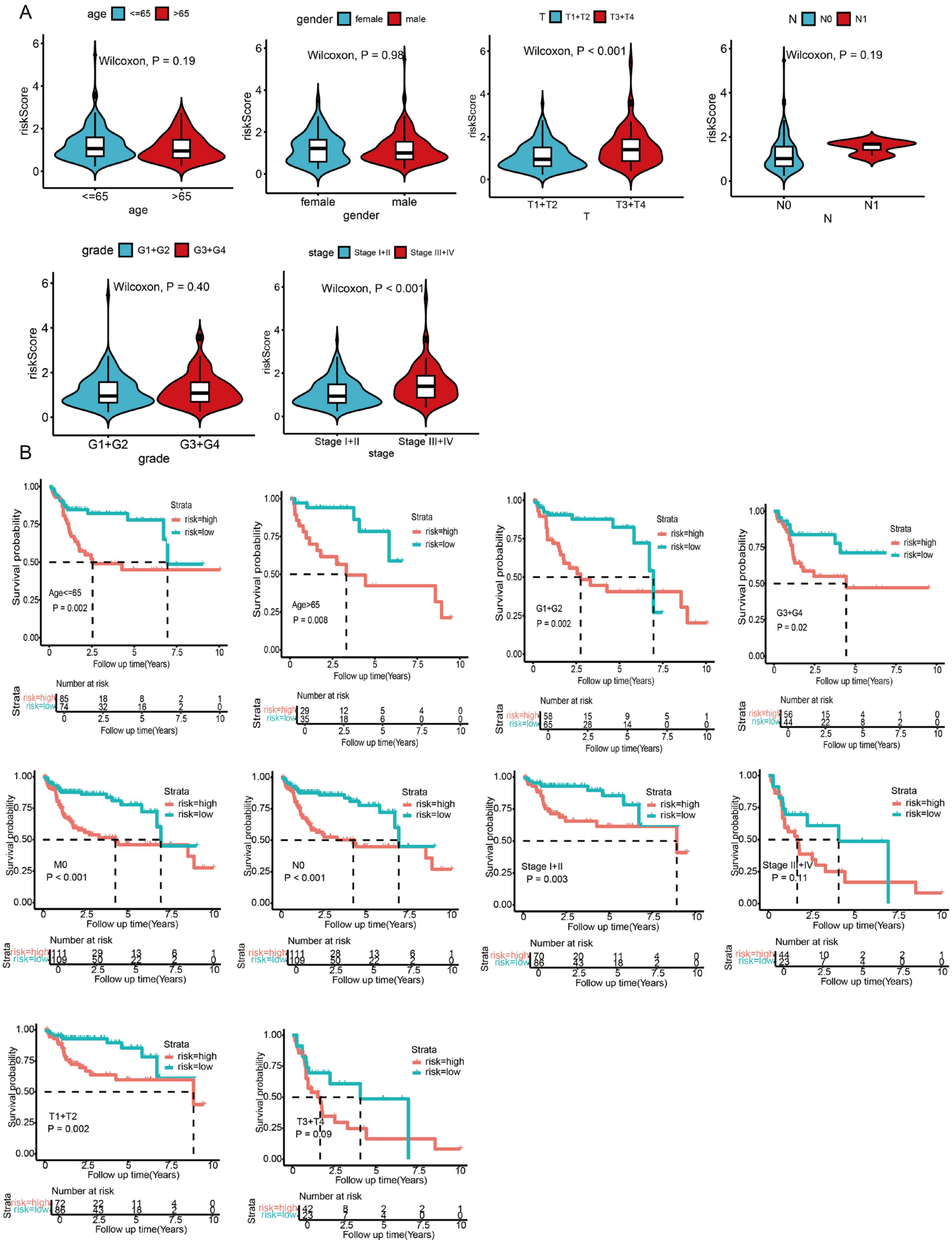

Figure S3 Subgroup analysis based on different clinical characteristics. (A) Evaluation of risk scores across patient subgroups based on clinical information. (B) Comparison of overall survival rates among various patient subgroups. P<0.05 indicates statistical significance.

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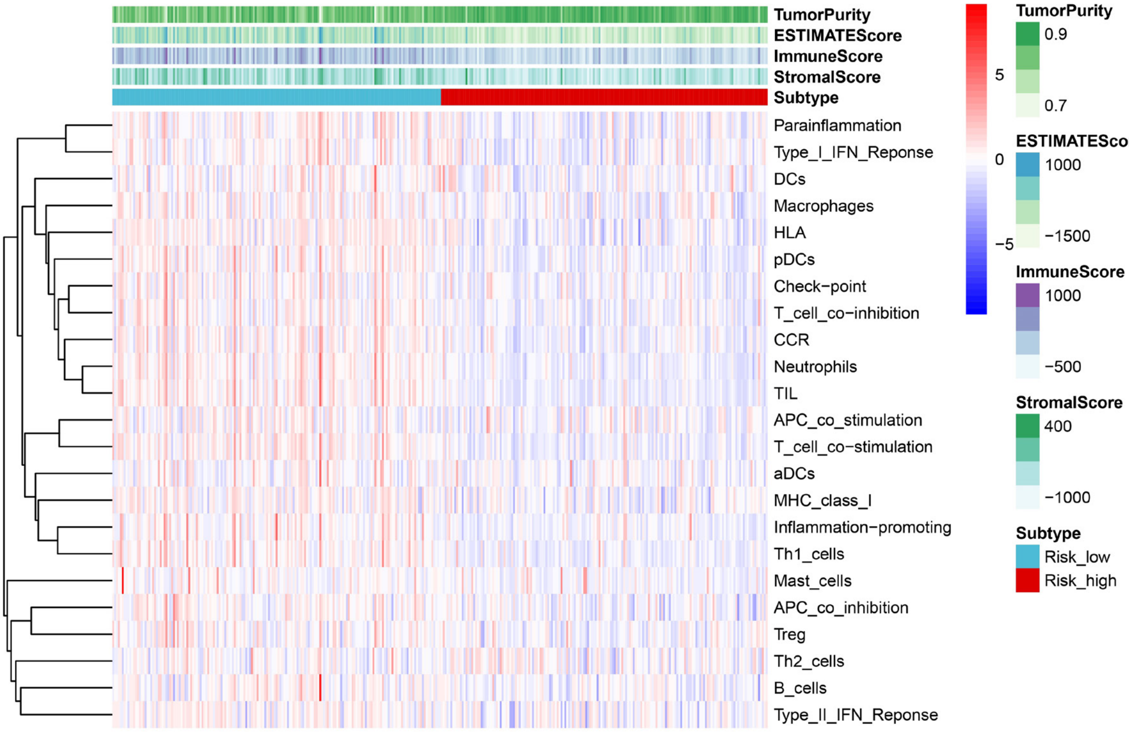

Figure S4 The heatmap depicts the disparity in the migration of numerous immune cells across different risk categories, as dissected via the ssGSEA technique.

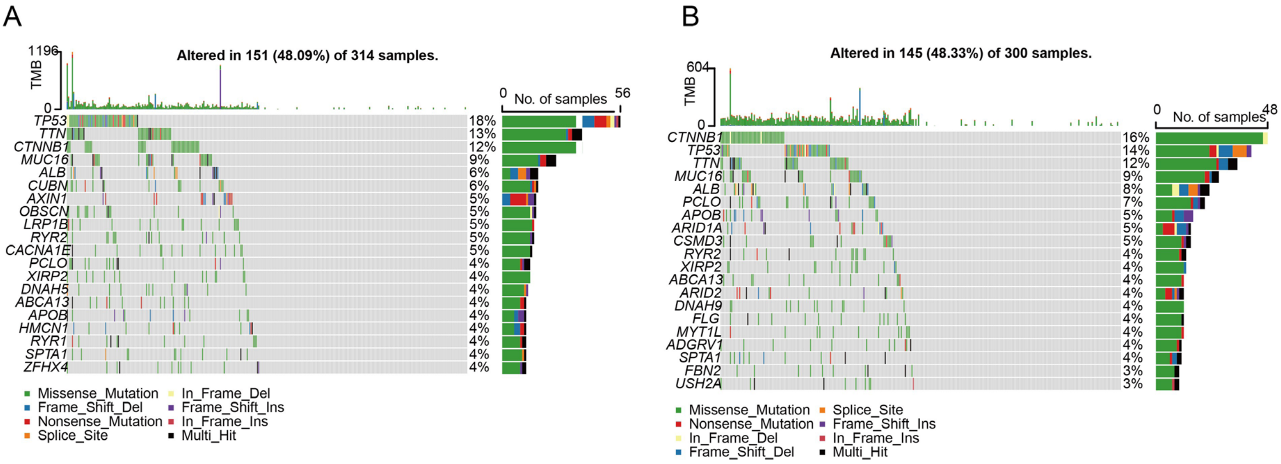

Figure S5 Evaluation of TMB sensitivity. (A) Waterfall plot depicting the TMB of the top 20 genes in the high-risk group. (B) Waterfall plot depicting the TMB of the top 20 genes in the low-risk category. TMB, tumor mutational burden.

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