Supplemental Tables

Supplemental Table 1. Univariate Cox regression results for the LUAD-specific risk score.

	coef	HR	p_value	CI_lower	CI_upper
IGHA2	0.000145841643868081	1.00014585227928	0.0426608234126501	1.00000482430081	1.00028690014654
G0S2	0.000395200679536257	1.00039527878161	0.0482627071839404	1.00000301825632	1.00078769317476
GZMB	0.00387102228234246	1.00387852436622	0.12360005794142	0.998944393638581	1.00883702646647
ITM2C	0.000917453334091772	1.00091787432314	0.128602756890522	0.999734194264204	1.00210295585307
IRF7	0.00249929837100679	1.00250242422078	0.142884673515669	0.999156247980495	1.00585980681188
MNDA	-0.00451950701368103	0.995490690589645	0.193314589898088	0.98873490317328	1.00229263867402
PLEK	-0.00309590300584986	0.99690888436018	0.24330265259084	0.991737863519018	1.00210686742344
TSPAN13	0.000301772135343397	1.00030181767313	0.287008690793717	0.999746287455758	1.00085765658265
LGALS2	0.00627155929534086	1.00629126670052	0.299527718769727	0.994438732054797	1.01828506955412
PLAC8	0.00300006788848262	1.00300457259217	0.404386922669457	0.995956286593624	1.0101027386268
CSF3R	-0.00261765493583128	0.997385768135392	0.413981475400963	0.991141408855643	1.00366946793958
FGL2	0.00221847417762559	1.00222093681222	0.467257913297362	0.996244194832301	1.00823353490542
IGHA1	7.69624840273102e-06	1.00000769627802	0.502315104333195	0.999985210951412	1.00003018211022
FCGR3A	0.000391470458749339	1.00039154709331	0.58447277663962	0.998988947087897	1.00179611637654
NAAA	0.00412830321516422	1.00413683639736	0.58950055916235	0.989190987519219	1.01930850455763
FKBP11	0.00344643604171092	1.00345238183104	0.606243358060872	0.990387915734953	1.01668918471725
C1QA	-7.32249348331382e-05	0.999926777746047	0.672025930688067	0.999587869262867	1.00026580113554
AIF1	-	0.9993994677	0.6803313047	0.99654763043080	1.0022594661248

	0.000600712689513189	02231	22224	1	
C5AR1	-0.00117295728901572	0.998827730356499	0.694511709470924	0.992998039266439	1.00469164638645
IGHG2	3.10456577830352e-05	1.0000310461397	0.696361378205291	0.999875126706081	1.00018698988723
CCL3	-0.0111005578331148	0.988960826017376	0.710091223460598	0.932740538756974	1.04856975199166
C1QB	-5.55037438938689e-05	0.99994449779641	0.730855575587967	0.999628317540687	1.00026077805926
FCER1G	-0.000204172849939136	0.999795847991919	0.739972848753944	0.998591082940497	1.00100206655004
DUSP4	0.000426107713273948	1.00042619851006	0.753257688759787	0.997771796066596	1.00308766254052
IL1B	0.00155522651956643	1.00155643651152	0.779242764520609	0.990724014230111	1.01250729881335
C1orf54	0.00128620066150703	1.00128702817232	0.826611271567696	0.98982989461339	1.01287677634524
FPR1	-0.000853912316668975	0.999146452162701	0.853759373147507	0.990115392451406	1.00825988615091
BCL2A1	0.000401157021206843	1.00040123749545	0.880715903504722	0.99517331101045	1.00565662775487

Supplemental Table 2. Univariate Cox regression results for the LUSC-specific risk score.

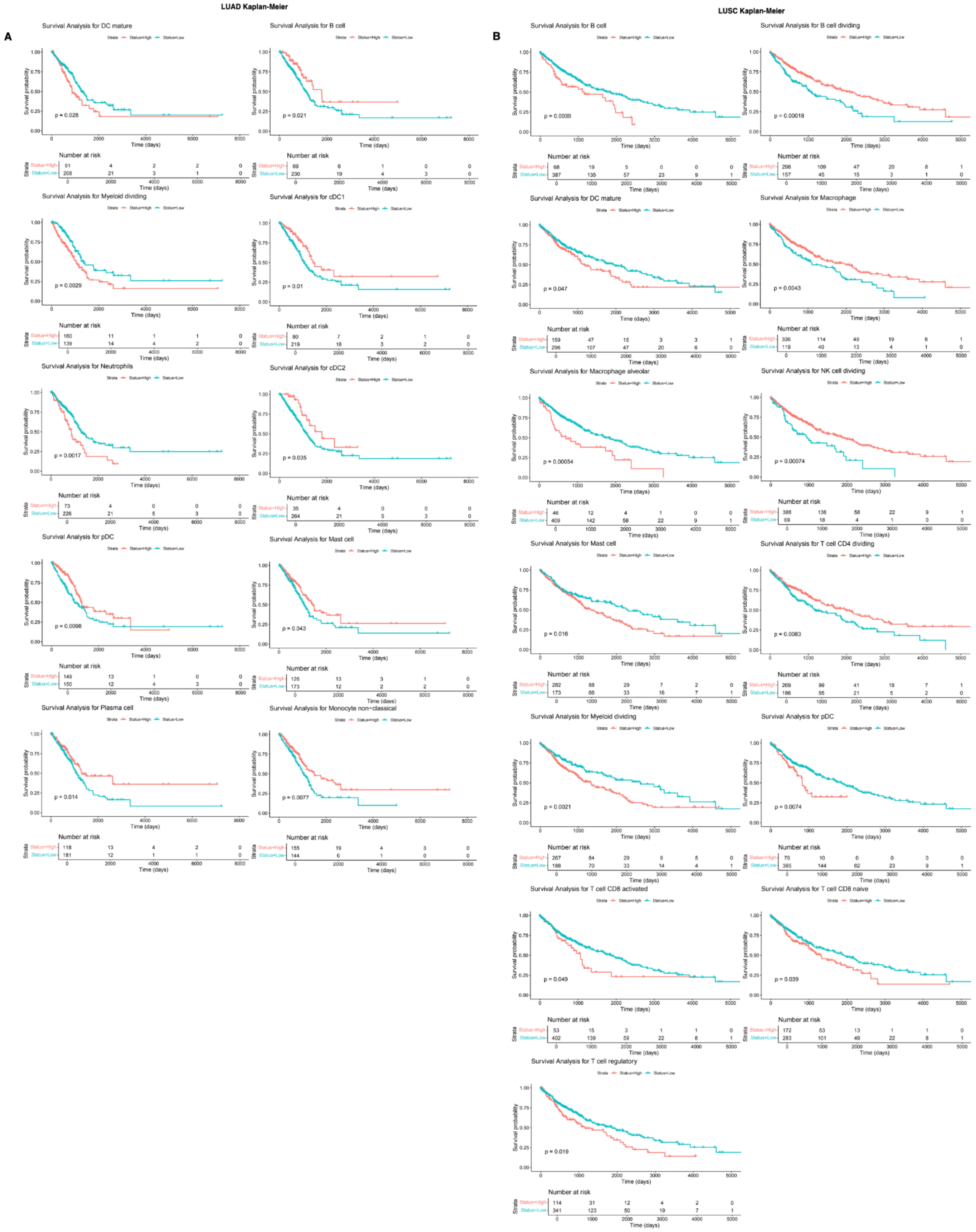
	coef	HR	p_value	CI_lower	CI_upper
TYROBP	0.000992932753201803	1.00099342587413	0.00254162200302142	1.00034823122437	1.00163903665511
GZMB	-0.000142868359653168	0.999857141845545	0.950906741064306	0.995320037508418	1.00441492828992
CD79A	-0.000450447933726892	0.999549653502712	0.635033886181865	0.997692206469892	1.00141055862557
SPOCK2	0.000950953433988135	1.00095140573357	0.028986443166616	1.00009742547764	1.00180611520073
CD69	0.0121039052870115	1.01217745399124	0.0199794027269908	1.00190979801616	1.02255033376933

CD83	0.00358814913528315	1.00359459424876	0.00136729508071408	1.00139242407325	1.00580160723451
CD2	0.000951322730236786	1.00095177538123	0.730076123810592	0.995557085221311	1.00637569810085
CENPF	-0.00378182174506384	0.996225320336595	0.307805703517032	0.989010947000328	1.00349231915976
SPP1	4.42702720013657e-05	1.00004427125194	0.260371879122512	0.999967178703113	1.00012136974423
DUSP4	0.00533622411556926	1.00535048711838	0.0497839120493073	1.00000503753158	1.01072451039253
CLU	0.000445164418014301	1.0004452635184	0.398773065789907	0.999411335351836	1.00148026132207
APOE	-1.67392079391209e-06	0.999998326080607	0.990938672836272	0.999709485337046	1.00028725027739
APOC1	0.0004871715289461	1.00048729021627	0.482296759094054	0.999128569735612	1.00184785842844
JCHAIN	8.98442678429627e-05	1.00008984830396	0.263052986120701	0.999932510188443	1.00024721117643
GPNMB	-0.000106484162562276	0.999893521506675	0.262774148106887	0.999707191276166	1.00007988646631
IRF8	0.0102951493143942	1.01034832669712	0.0550419173225965	0.999777766376471	1.02103064860045
S100A8	-3.4497347719963e-05	0.999965503247307	0.218184514698299	0.999910597434399	1.00002041207513
GZMA	-0.000563077870277967	0.999437080628316	0.699049144063846	0.996588125851694	1.00229417973569
MKI67	-0.00561805722171023	0.99439769454984	0.0998336366166988	0.987766344844429	1.00107356368957
MS4A1	-0.000859078890493613	0.99914129001213	0.886489065733335	0.987425308896006	1.01099628337787
FCER1G	0.0012434419040838	1.00124421529849	0.0200837355004736	1.00019514604139	1.00229438488717
S100A9	-9.19757271171775e-06	0.999990802469586	0.225662230538842	0.99997592422347	1.00000568093707
CPA3	0.00193911054356775	1.00194099183423	0.119295469366711	0.999499423874168	1.00438852403395
PCLAF	-	0.971538366703	0.01829143653	0.9485146793	0.995120917498

	0.0288745187126179	215	74588	50323	988
C15orf48	-0.00082775373696955	0.999172588756648	0.662864754648327	0.995461221702805	1.0028977928592
IL7R	0.00308657707061506	1.00309134545435	0.0251763683431381	1.00038436016116	1.00580565570151
GPR183	0.00289320108236758	1.00289739042785	0.33637286496662	0.996999204562526	1.00883046959735
TPSAB1	0.00194391930259253	1.0019458099386	0.30477602243309	0.998232907878189	1.00567252204435
C1QB	0.000476000455417827	1.00047611376161	0.00132827391578808	1.00018536283497	1.00076694920869
C1QA	0.000462768275676182	1.00046287536943	0.00259447830746319	1.00016165939762	1.00076418205765
MARCKSL1	-7.68705348870637e-05	0.999923132419577	0.714053130612615	0.999512069377808	1.00033436451666
IRF7	0.00298243004758645	1.00298688191678	0.241113037310809	0.997997737778254	1.00800096755396
HLA_DQA1	0.00128845109118677	1.0012892815009	0.0836244027243314	0.999828772252385	1.00275192420199
TPSB2	0.00252011610444264	1.00252329426625	0.0657227559234597	0.999836159366189	1.00521765104352
TRBC2	0.000359981256949752	1.00036004605798	0.760926298989532	0.998043027956177	1.00268244325941
IGHM	4.10718885708197e-05	1.00004107273203	0.0953277915313236	0.999992809111406	1.00008933868205
LTB	-8.04535459135235e-05	0.999919549690386	0.954777516603718	0.997142986234332	1.00270384453976
CCL5	-0.000305968210365879	0.999694078593133	0.576443652641195	0.998621404892265	1.00076790451131

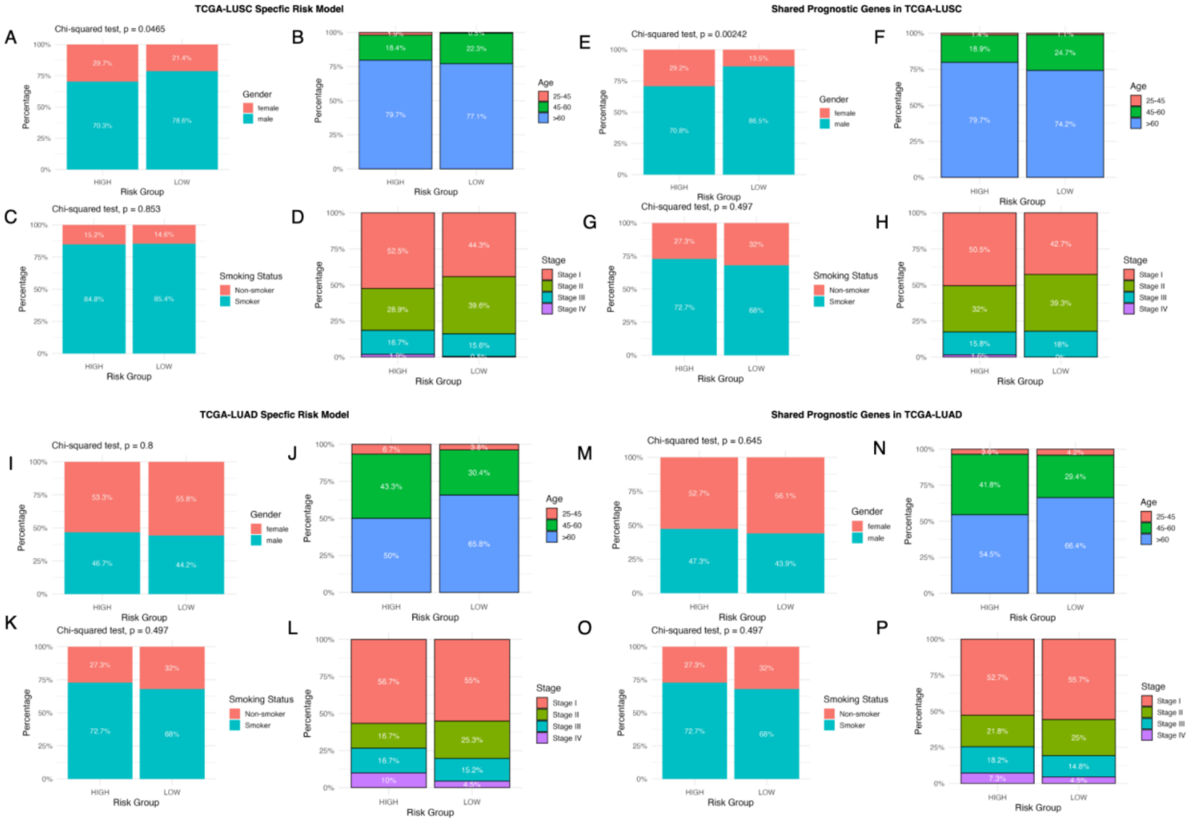
Supplemental Figures

Supplemental Figure 1



Supplemental Figure 1. Kaplan–Meier survival analysis of immune cell types in LUAD and LUSC cohorts. (A) Survival curves for selected immune cell types in the LUAD cohort based on cell fraction estimates obtained from CIBERSORTx deconvolution. Cell types include DC mature, B cell, Myeloid dividing, cDC1, cDC2, Macrophage alveolar, Mast cell, Plasma cell, Monocyte non-classical, and others. (B) Survival curves for selected immune cell types in the LUSC cohort. Cell types include B cell, B cell dividing, DC mature, Macrophage alveolar, Macrophage, NK cell dividing, Mast cell, Myeloid dividing, cDC, T cell CD8 activated, and T cell regulatory.

Supplemental Figure 2



Supplemental Figure 2. Distribution of clinical and demographic variables between low- and high-risk patient groups for LUAD and LUSC risk models derived from all prognostic genes and from shared prognostic genes. (A–D) LUAD-specific risk model (all prognostic genes): (A) smoking status, (B) tumor stage, (C) gender, (D) age. (E–H) LUSC-specific risk model (all prognostic genes): (E) smoking status, (F) tumor stage, (G) gender, (H) age. (I–L) LUAD-specific risk model (shared prognostic genes): (I) smoking status, (J) tumor stage, (K) gender, (L) age. (M–P) LUSC-specific risk model (shared prognostic genes): (M) smoking status, (N) tumor stage, (O) gender, (P) age. Percentages are shown within each bar. Associations between categorical variables and risk groups were evaluated using Chi-squared tests.
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Table 3. Genes included in the LUAD and LUSC risk models. Official gene symbols, full names, associated cancer subtype(s) (LUAD, LUSC, or both), and overlap status between models.

Gene name	Cell type	**Full gene name**	**LUAD/LUSC**
AIF1	Myeloid dividing	Allograft Inflammatory Factor 1	LUAD
BCL2A1	Monocyte non-classical	BCL2 Related Protein A1	LUAD
C1orf54	cDC1	Chromosome 1 Open Reading Frame 54	LUAD
CCL3	Myeloid dividing	C-C Motif Chemokine Ligand 3	LUAD
C5AR1	Neutrophils	Complement C5a Receptor 1	LUAD
FCGR3A	Monocyte non-classical	Fc Gamma Receptor IIIa	LUAD
CSF3R	Neutrophils	Colony Stimulating Factor 3 Receptor	LUAD
G0S2	Monocyte non-classical	G0/G1 Switch 2	LUAD
FGL2	cDC1	Fibrinogen Like 2	LUAD
FKBP11	Plasma	FKBP Prolyl Isomerase 11	LUAD
FPR1	Neutrophils	Formyl Peptide Receptor 1	LUAD
IGHA1	Plasma	Immunoglobulin Heavy Constant Alpha 1	LUAD
IGHG2	Plasma	Immunoglobulin Heavy Constant Gamma 2	LUAD
ITM2C	pDC	Integral Membrane Protein 2C	LUAD
IGHA2	Plasma	Immunoglobulin Heavy Constant Alpha 2	LUAD
MNDA	Myeloid dividing	Myeloid Cell Nuclear Differentiation Antigen	LUAD
PLEK	Neutrophils	Pleckstrin	LUAD
IL1B	Monocyte non-classical	Interleukin 1 Beta	LUAD
LGALS2	cDC1	Galectin 2	LUAD
NAAA	Monocyte non-classical	N-Acylethanolamine Acid Amidase	LUAD
TSPAN13	pDC	Tetraspanin 13	LUAD
PLAC8	pDC	Placenta Associated 8	LUAD
CLU	Mast	Clusterin	LUSC
APOE	Macrophage	Apolipoprotein E	LUSC
C15orf48	Macrophage	Chromosome 15 Open Reading Frame 48	LUSC
APOC1	Macrophage alveolar	Apolipoprotein C1	LUSC
CCL5	NK cell dividing	C-C Motif Chemokine Ligand 5	LUSC
CD2	T cell regulatory	CD2 Molecule	LUSC
CD69	Mast	CD69 Molecule	LUSC

CD79A	B cell dividing	CD79a Molecule	LUSC
CD83	Mast	CD83 Molecule	LUSC
CENPF	NK cell dividing	Centromere Protein F	LUSC
CPA3	Mast	Carboxypeptidase A3	LUSC
GPNMB	Macrophage	Glycoprotein Nmb	LUSC
GPR183	pDC	G Protein-Coupled Receptor 183	LUSC
GZMA	NK cell dividing	Granzyme A	LUSC
HLA-DQA1	B cell	Major Histocompatibility Complex, Class II, DQ Alpha 1	LUSC
IGHM	B cell	Immunoglobulin Heavy Constant Mu	LUSC
IL7R	T cell regulatory	Interleukin 7 Receptor	LUSC
IRF8	B cell	Interferon Regulatory Factor 8	LUSC
JCHAIN	pDC	Joining Chain Of Multimeric IgA And IgM	LUSC
LTB	B cell dividing	Lymphotoxin Beta	LUSC
MARCKSL1	B cell dividing	MARCKS Like 1	LUSC
MKI67	B cell dividing	Marker Of Proliferation Ki-67	LUSC
MS4A1	B cell dividing	Membrane Spanning 4-Domains A1	LUSC
PCLAF	B cell dividing	PCNA Clamp Associated Factor	LUSC
S100A8	Macrophage	S100 Calcium Binding Protein A8	LUSC
S100A9	Macrophage	S100 Calcium Binding Protein A9	LUSC
SPOCK2	T cell regulatory	SPARC (Osteonectin), Cwcv And Kazal Like Domains Proteoglycan 2	LUSC
SPP1	Myeloid dividing	Secreted Phosphoprotein 1	LUSC
TPSAB1	Mast	Tryptase Alpha/Beta 1	LUSC
TPSB2	Mast	Tryptase Beta 2	LUSC
TRBC2	T cell regulatory	T Cell Receptor Beta Constant 2	LUSC
TYROBP	pDC	Transmembrane Immune Signaling Adaptor TYROBP	LUSC
C1QA	Macrophage alveolar	Complement C1q A Chain	Shared by both
C1QB	Macrophage alveolar	Complement C1q B Chain	Shared by both
FCER1G	Neutrophils	Fc Epsilon Receptor Ig	Shared by both
DUSP4	cDC1	Dual Specificity Phosphatase 4	Shared by both
GZMB	pDC	Granzyme B	Shared by both
IRF7	pDC	Interferon Regulatory Factor 7	Shared by both