

Table S1 The training and validation cohorts in this study

	TCGA	GSE15459	GSE13861	GSE66229
No. of patients	348	190	64	300
Gender				
Female	123 (35.34%)	67 (35.26%)	19 (29.69%)	101 (33.67%)
Male	225 (64.66%)	123 (64.74%)	45 (70.31%)	199 (66.33%)
Age				
<65	149 (42.82%)	83 (43.68%)	39 (60.94%)	216 (72.00%)
≥65	196 (56.32%)	107 (56.32%)	25 (39.06%)	84 (28.00%)
Stage				
I	46 (13.22%)	31 (16.32%)	12 (18.75%)	30 (10.00%)
II	110 (31.61%)	29 (15.26%)	11 (17.19%)	97 (32.33%)
III	144 (41.38%)	71 (37.37%)	25 (39.06%)	96 (32.00%)
IV	34 (9.77%)	59 (31.05%)	16 (25.00%)	77 (25.67%)
Molecular classification				
EBV	26 (7.47%)	–		
CIN	180 (51.72%)	–		
MSI	57 (16.38%)	–		
GS	63 (18.1%)	–		
<i>H. pylori</i> infection				
Negative	139 (39.94%)	–		
Positive	18 (5.17%)	–		
With radiation therapy				
No	229 (65.8%)	–		
Yes	45 (12.93%)	–		

TCGA, The Cancer Genome Atlas; EBV, Epstein-Barr virus; CIN, chromosomal instability; MSI, microsatellite instability; GS, genomically stable; *H. pylori*, *Helicobacter pylori*.

Table S2 The 11 DEGs used for calculating the risk score

Symbol	Description	Regression coefficient (β_i)
<i>SERPINE1</i>	serpin family E member 1	0.19
<i>CREB3L3</i>	cAMP responsive element binding protein 3 like 3	0.09
<i>ADAMTS12</i>	ADAM metalloproteinase with thrombospondin type 1 motif 12	0.043
<i>APOD</i>	apolipoprotein D	0.038
<i>GFRA1</i>	GDNF family receptor alpha 1	0.021
<i>KIT</i>	KIT proto-oncogene, receptor tyrosine kinase	0.011
<i>ZFP36</i>	ZFP36 ring finger protein	0.0077
<i>APOA1</i>	apolipoprotein A1	0.007
<i>DNMT1</i>	DNA methyltransferase 1	-0.059
<i>PVT1</i>	Pvt1 oncogene	-0.11
<i>TNFAIP2</i>	TNF alpha induced protein 2	-0.14

DEG, differentially expressed gene; AMP, Adenosine monophosphate; ADAM, a disintegrin and metalloproteinase; TS-1, thrombospondin type 1; GDNF, glial cell line-derived neurotrophic factor; *KIT*, kitproto-oncogeneprotein; *ZFP36*, zinc finger protein 36; *PVT1*, plasmacytoma variant translocation 1; TNF, tumor necrosis factor.

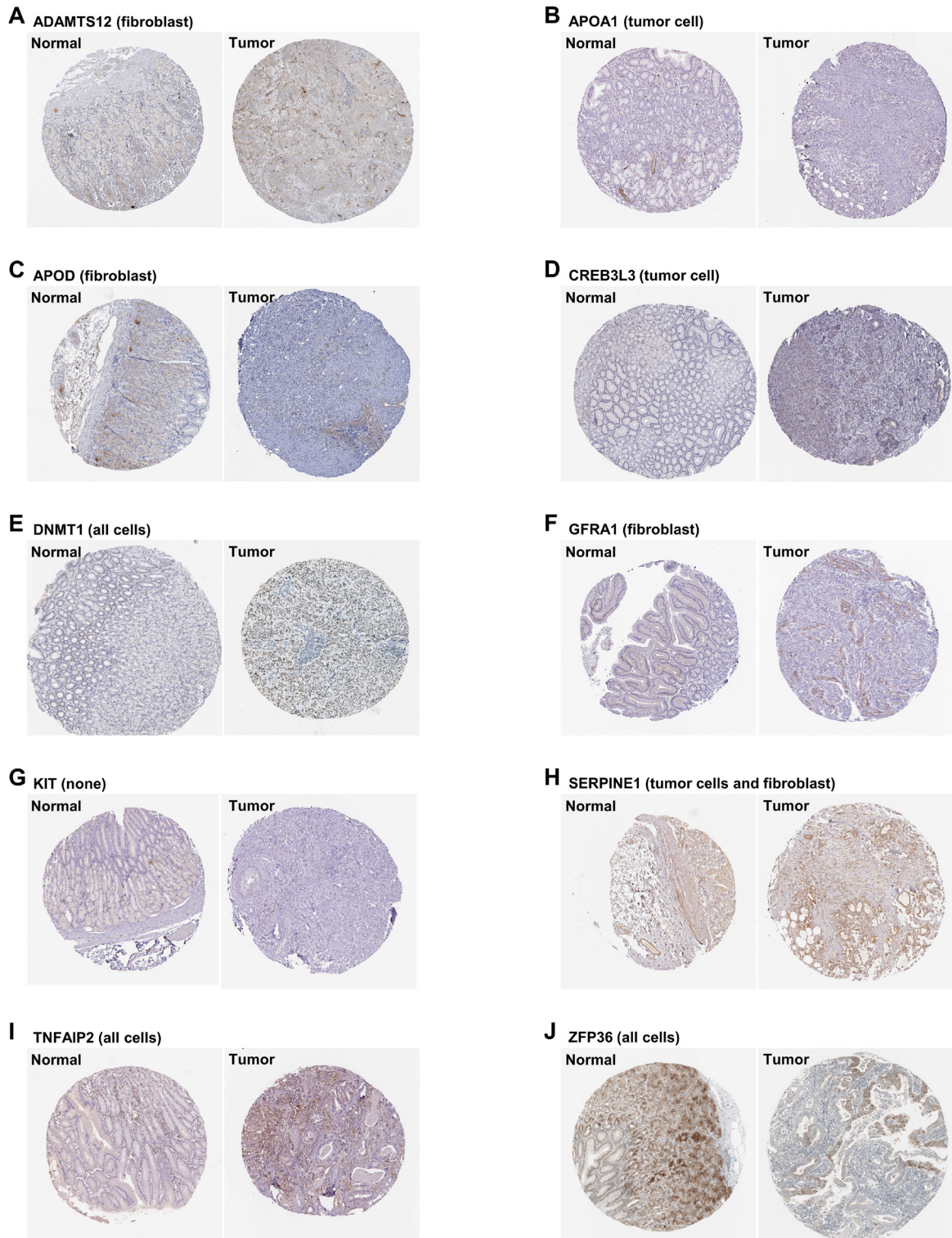


Figure S1 Expression levels of the inflammatory-related genes between tumor and normal tissues. Immunohistochemistry (IHC) staining samples of normal tissue (left) and GC (right) samples, including ADAMTS12 (A, normal, https://images.proteinatlas.org/35973/73527_A_2_1.jpg; tumor, https://images.proteinatlas.org/35973/73526_B_3_4.jpg), APOA1 (B, normal, https://images.proteinatlas.org/46715/126224_A_2_1.jpg; tumor, https://images.proteinatlas.org/46715/126237_B_2_8.jpg), APOD (C, normal, https://images.proteinatlas.org/40520/85189_A_1_1.jpg; tumor, https://images.proteinatlas.org/40520/85190_B_1_1.jpg), CREB3L3 (D, normal, https://images.proteinatlas.org/56228/163167_A_5_1.jpg; tumor, https://images.proteinatlas.org/40671/163174_B_1_2.jpg), DNMT1 (E, normal, https://images.proteinatlas.org/2694/8662_A_6_1.jpg; tumor, https://images.proteinatlas.org/5876/14025_B_3_2.jpg), GFRA1 (F, normal, https://images.proteinatlas.org/43829/99317_A_5_1.jpg; tumor, https://images.proteinatlas.org/43829/99327_B_3_2.jpg), KIT (G, normal, https://images.proteinatlas.org/72867/156398_A_3_1.jpg; tumor, https://images.proteinatlas.org/72867/156396_B_1_2.jpg), SERPINE1 (H, normal, https://images.proteinatlas.org/68501/149553_A_1_1.jpg; tumor, https://images.proteinatlas.org/68501/149552_B_2_7.jpg), TNFAIP2 (I, normal, https://images.proteinatlas.org/4598/155681_A_6_1.jpg; tumor, https://images.proteinatlas.org/4598/155679_B_1_1.jpg), and ZFP36 (J, normal, https://images.proteinatlas.org/6009/20650_A_5_1.jpg; tumor, https://images.proteinatlas.org/6009/20651_B_2_8.jpg). All IHC images were downloaded from the Human Protein Atlas database (Human Protein Atlas v22.0. [proteinatlas.org](https://www.proteinatlas.org/), <https://www.proteinatlas.org/>). GC, gastric cancer.

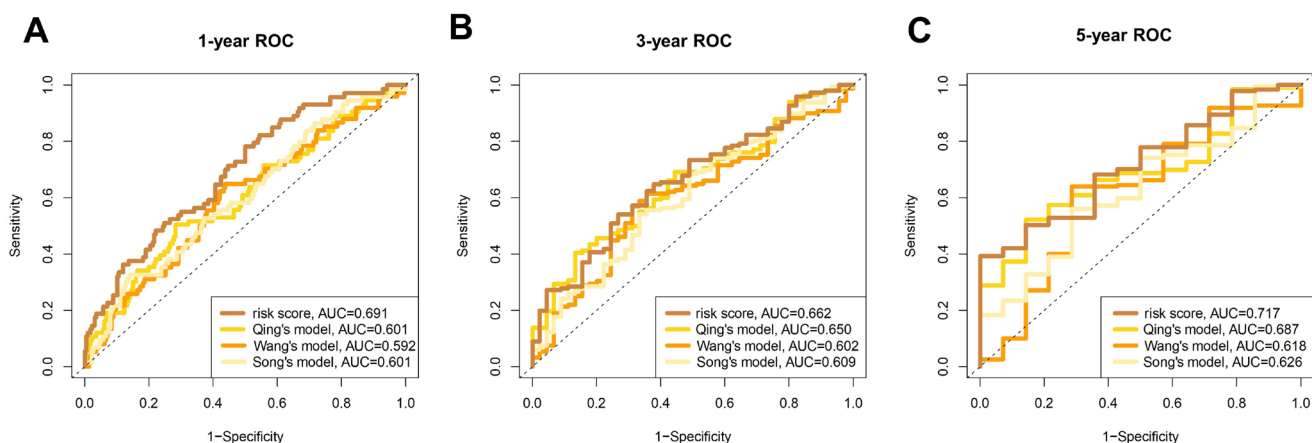


Figure S2 Performance comparison between the risk score and 3 previous models. ROC curves for predicting 1- (A), 3- (B), and 5-year (C) OS in TCGA-STAD cohort. ROC, receiver operating characteristic; OS, overall survival; TCGA-STAD, The Cancer Genome Atlas stomach adenocarcinoma.

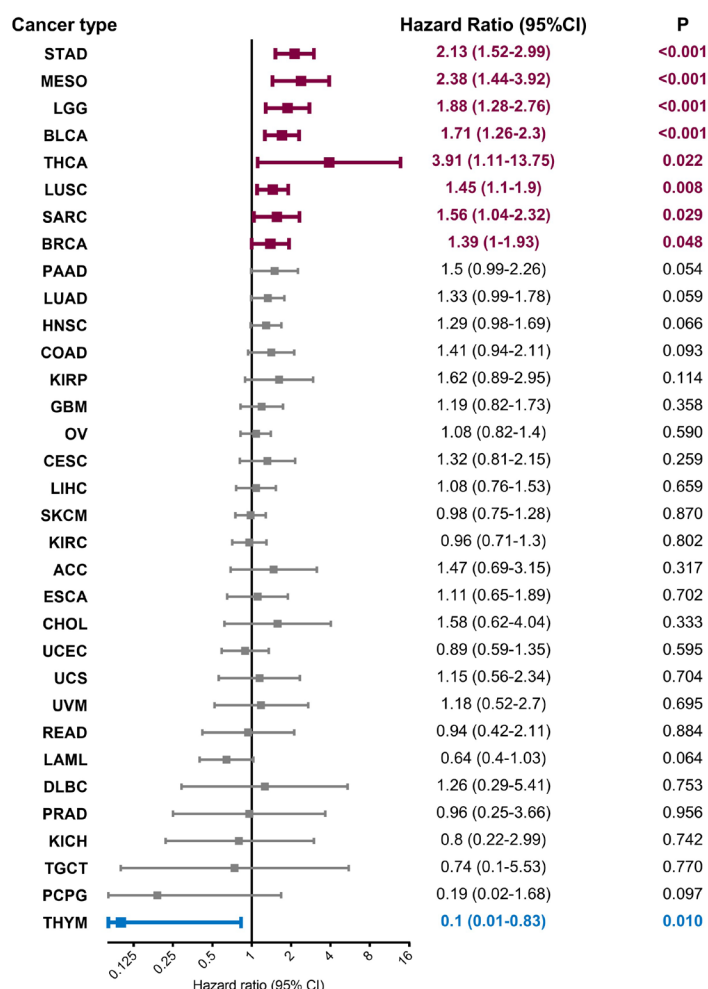


Figure S3 Prognostic value of the risk score in TCGA pan-cancer data set. ACC, adrenocortical cancer; BLCA, bladder cancer; BRCA, breast cancer; CESC, cervical cancer; CHOL, bile duct cancer; COAD, colon cancer; DLBC, large B-cell lymphoma; ESCA, esophageal cancer; GBM, glioblastoma; HNSC, head and neck cancer; KICH, kidney chromophobe; KIRC, kidney clear cell carcinoma; KIRP, kidney papillary cell carcinoma; LAML, acute myeloid leukemia; LGG, lower grade glioma; LIHC, liver cancer; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; OV, ovarian cancer; PAAD, pancreatic cancer; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate cancer; READ, rectal cancer; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach cancer; TGCT, testicular cancer; THCA, thyroid cancer; THYM, thymoma; UCEC, endometrioid cancer; UCS, uterine carcinosarcoma; UVM, ocular melanoma; HR, hazard ratio; 95% CI, 95% confidence interval.

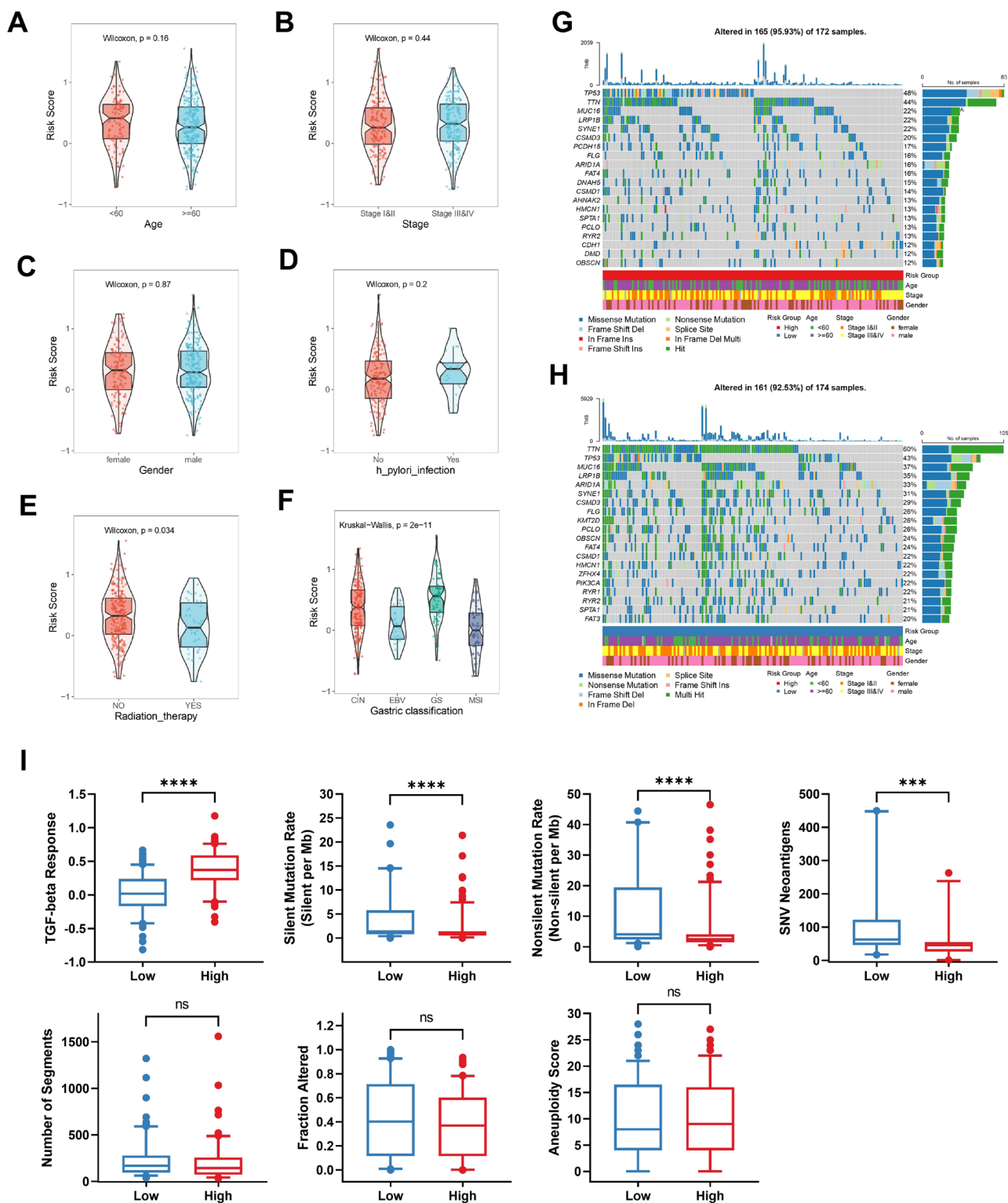


Figure S4 Association between the risk score and clinical features. (A-F) Comparison of the risk score between patient groups with different clinical characteristics in TCGA cohort. (G,H) Somatic mutation landscapes of high-risk and low-risk patients in TCGA cohort. (I) Comparison of tumor mutational burden (TMB)-related characteristics between high-risk and low-risk groups in TCGA cohort. ns, non-significant; *** $P < 0.001$; and **** $P < 0.0001$ by Mann-Whitney test.

Table S4 Detailed data of the correlates between the immune cell fraction and the gene expression/risk score

Cell Types	Riskscore		<i>SERPINE1</i>		<i>CREB3L3</i>		<i>ADAMTS12</i>		<i>APOD</i>		<i>GFRA1</i>		<i>KIT</i>		<i>ZFP36</i>		<i>APOA1</i>		<i>DNMT1</i>		<i>PVT1</i>		<i>TNFAIP2</i>	
	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)	Rho	-log (Q)
Activated CD4+ memory T cells	-0.154881156	1.782430021	0.133268602	1.398485406	-0.146695258	1.626059627	0.170568066	2.11730288	-0.227894306	3.644088927	-0.27992313	5.383196862	-0.176150636	2.231997676	-0.063668573	0.39632078	-0.214584125	3.22806624	0.343906882	8.330405412	0.205168841	2.968874365	0.191716858	2.612140544
Activated dendritic cells	-0.016336596	0.08543526	0.056022344	0.34360665	-0.028983698	0.139591666	-0.179725253	2.317748263	-0.10970854	0.981345128	0.024683201	0.121879264	0.08351754	0.607757788	0.05880395	0.35041775	0.029345131	0.140145918	-0.126425347	1.273055021	0.020870179	0.105555755	0.109251106	0.976449092
Activated mast cells	0.069362659	0.452495208	0.292803585	5.884305167	-0.048174451	0.273666601	0.173810487	2.185916797	-0.249378841	4.341440638	-0.291628298	5.859629739	-0.248623224	4.326641448	0.079106878	0.556626914	-0.009851159	0.055085336	0.024969122	0.121879264	-0.035343725	0.16792619	0.147533458	1.640916399
Activated NK cells	-0.043027376	0.227556061	-0.078421015	0.552445177	-0.038710572	0.188931213	0.010990835	0.057075157	0.141364934	1.526296074	0.175826104	2.231997676	0.138605259	1.490686628	0.162896265	1.951349713	-0.020952425	0.105555755	-0.092583432	0.718051067	-0.087671987	0.653478019	0.053218852	0.315097102
CD4+ naïve T cells	-0.05683463	0.345396558	-0.078847752	0.555772329	0.009730302	0.055085336	-0.076457621	0.528366248	-0.024217239	0.121879264	-0.026357875	0.124375474	-0.02086456	0.105555755	-0.03404645	0.16442421	0.020610636	0.105290265	0.054267343	0.325062989	0.063903158	0.396712049	-0.024130137	0.121879264
CD8+ T cells	0.019026436	0.0978365	0.112873689	1.033608486	0.021353311	0.105555755	0.035416098	0.16792619	0.131888456	1.376799141	0.231678832	3.743442943	0.204108878	2.947711985	0.21846888	3.337909343	-0.071997688	0.480778532	0.059680389	0.358732451	-0.017078113	0.089469119	0.171619555	2.139307543
Eosinophils	0.097424297	0.793854617	0.107636553	0.950238698	0.003865978	0.0198443	0.10507184	0.907164666	0.031184081	0.147924855	-0.011686054	0.059014518	0.0920592	0.717550487	0.086726853	0.641797647	0.031281659	0.147924855	-0.088458946	0.662728073	-0.051815228	0.303477871	-0.024541354	0.121879264
Follicular helper T cells	-0.058108276	0.350159926	0.100642715	0.842548056	0.006245942	0.032456331	0.010198258	0.055085336	0.017741159	0.090455895	0.04796596	0.273666601	0.030987397	0.147924855	0.159439111	1.874350395	-0.048125206	0.273666601	0.152242845	1.728390651	0.075603702	0.526025195	0.236767748	3.903705033
Macrophages M0	0.049178298	0.280379427	0.162928984	1.951349713	0.059996785	0.360113249	0.206259425	2.994441965	-0.056341854	0.345060992	-0.211800607	3.155925728	-0.115139518	1.069628063	-0.098531493	0.809412057	0.021749047	0.105555755	0.211817856	3.155925728	-0.05642568	0.345060992	0.173330042	2.179380801
Macrophages M1	0.017516028	0.090455895	0.208358462	3.052776713	-0.035571282	0.16792619	0.27389881	5.200502539	0.05014891	0.286728116	0.034373399	0.165473273	0.02469021	0.121879264	0.139025428	1.491501399	-0.169194609	2.094214748	0.273652714	5.200502539	0.07995976	0.565523052	0.199565267	2.818933048
Macrophages M2	0.277498226	5.301069302	0.343350306	8.330405412	-0.040089753	0.200755358	0.447785838	15.08098816	0.289084518	5.770243595	0.253224325	4.477908603	0.30422632	6.364075273	0.141778331	1.531059193	-0.024652446	0.121879264	-0.043471934	0.229357409	-0.191059542	2.60051936	0.136607399	1.459253274
Memory B cells	0.013219961	0.068641007	-0.110043621	0.983954679	0.057482193	0.346721242	-0.158371643	1.858623158	0.160448135	1.894276212	0.255626315	4.55812057	0.120912094	1.164228273	-0.029297998	0.140145918	0.00133756	0.005127054	-0.18186968	2.354758865	-0.019410901	0.099138822	-0.019533246	0.099138822
Monocytes	0.276492343	5.280485852	0.217637862	3.320563372	0.092289995	0.718051067	0.085175738	0.623948338	0.263045117	4.809590896	0.341675355	8.278037863	0.270608752	5.089918822	0.199152568	2.818933048	0.140259576	1.510362422	-0.18010405	2.319436226	-0.144216241	1.577770856	-0.014372866	0.075590346
Naïve B cells	0.116830033	1.09110069	0.148517856	1.659297589	0.065976645	0.418458209	-0.034565476	0.165473273	0.228261763	3.644088927	0.44910026	15.08945473	0.371461986	9.834440165	0.261862987	4.795512092	0.017428286	0.090455895	0.031667227	0.148119653	-0.036005848	0.16792619	0.104658278	0.903243329
Neutrophils	-0.029263801	0.140145918	0.136818156	1.459656008	-0.127958709	1.301172094	0.152815177	1.737027971	-0.185085176	2.432030175	-0.235873474	3.883977852	-0.115990968	1.078574344	-0.064683874	0.404190867	-0.063413339	0.395654055	-0.058274484	0.350159926	-0.057966176	0.350159926	0.168518354	2.087148528
Plasma cells	-0.010949327	0.057075157	-0.031892924	0.14816745	0.130252186	1.345747375	-0.18072864	2.329753366	0.049332225	0.280379427	0.056768969	0.345396558	0.137382964	1.467910633	0.069332503	0.452495208	0.149847401	1.68603955	-0.026177079	0.124375474	0.009858227	0.055085336	0.067486265	0.433902666
Regulatory T cells	-0.035063501	0.16792619	-0.000822115	0.00351393	0.060972154	0.369764199	-0.000216346	0.001352558	0.226124466	3.592816053	0.242570537	4.107783544	0.179533159	2.317748263	0.158746432	1.862483509	0.014993119	0.078574561	-0.038373251	0.187720667	-0.052653802	0.310856557	0.228124121	3.644088927
Resting CD4+ memory T cells	0.270039238	5.084931002	0.199014342	2.818933048	0.140944672	1.521349801	0.117614595	1.102614754	0.303566673	6.364075273	0.525942277	21.50956027	0.423788366	13.314439	0.138595284	1.490686628	0.175725499	2.231997676	-0.142766092	1.549007387	-0.203930623	2.947711985	0.079909486	0.565523052
Resting dendritic cells	0.101102412	0.847146996	0.075903279	0.527475401	0.08435403	0.614854569	0.151779297	1.722376988	0.150698625	1.701402781	0.132504593	1.386028937	0.156718835	1.822655858	0.134021095	1.410730123	0.004499345	0.02237146	-0.075280975	0.524236463	-0.146140939	1.61791306	0.03331253	0.159495373
Resting mast cells	0.139106278	1.491501399	-0.076364834	0.528366248	0.114806427	1.066927235	-0.061362719	0.372098967	0.366748652	9.602827931	0.493928717	18.84453543	0.502073538	19.43671926	0.015586377	0.081381278	0.068466545	0.443522649	-0.1978565	2.791369825	-0.115670918	1.076154207	-0.076040079	0.527475401
Resting NK cells	0.092366176	0.718051067	0.262234919	4.795512092	-0.026198843	0.124375474	0.169191749	2.094214748	-0.134065744	1.410730123	-0.169010319	2.094214748	-0.08107543	0.576890688	-0.086144398	0.635861039	-0.02102134	0.105555755	0.182969914	2.378647764	0.027103769	0.124721178	0.067344146	0.433902666
γδT cells	0.025292803	0.121879264	0.056857632	0.345396558	-0.035242226	0.16792619	0.042880659	0.227556061	0.081631923	0.582206293	-0.071119319	0.471412547	-0.045651946	0.250510483	0.058144041	0.350159926	-0.030522608	0.145652419	0.101390464	0.848733256	0.084181881	0.614854569	-0.026734039	0.124375474

CD4, cluster of differentiation antigen 4; NK cell, natural killer cell.

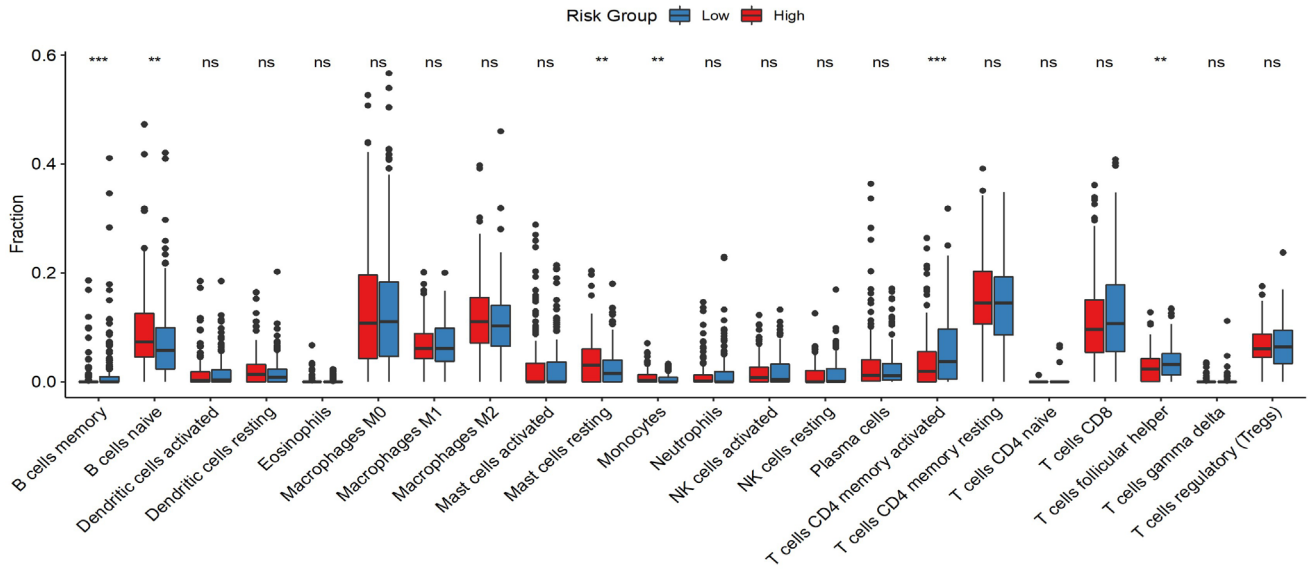


Figure S5 Comparison of the fractions of different immune cells between high-risk and low-risk groups in TCGA-STAD cohort. ns, non-significant; **P<0.01; and ***P<0.001 by Mann-Whitney test.