

**Table S1** The 11 primers of the prognostic OS-DEGs

Species	Gene name	Gene ID	Primer-F (5'-3')	Primer-R (5'-3')	Length (bp)
Human	<i>LDHA</i>	3939	CAGCCCGATTCCGTTACCTAA	GAGACACCAGCAACATTCATTCC	130
Human	<i>PTPRN</i>	5798	CGGGACACATGATTCTGGCAT	CTGCTTGGTAGGCACAGAGG	93
Human	<i>TRAP1</i>	10131	TGCGAGATGTGGTAACGAAGTA	GTAGCGGTAGAACTCCTCATGT	143
Human	<i>GPR37</i>	2861	GTGACCAGTGATGACAATGACAA	CAGCAATGAGTTCCGACAGAAG	110
Human	<i>SIRPA</i>	140885	CCAACAACCACACGGAGTATG	ATGTCCAGGTCAGCATAGGTG	85
Human	<i>CDK1</i>	983	GGGTCAGCTCGTTACTCAACTC	GGAGTGCCCAAAGCTCTGAAA	140
Human	<i>ECT2</i>	1894	GGCTCAGTGGAGGGAAGAAGT	GACAAGGGAGGGAGAAGGGATAC	102
Human	<i>ADA</i>	100	TTGACTACTACATGCCTGCTATCG	ACATACACCACGCCCTCTTTG	100
Human	<i>COL1A1</i>	1277	TAGGGTCTAGACATGTTTCAGCTTTG	CGTTCTGTACGCAGGTGATTG	142
Human	<i>SESN3</i>	143686	CCTTCCTCTACCATACAGGCACTA	ACCATTCAACCACTCAGCAATACC	127
Human	<i>BTK</i>	695	GATGTATAGCAAGTTCAGCAGCAA	GGCAATGTGTTTCAGCAGTCTC	127

OS-DEGs, oxidative stress-related differentially expressed genes.

**Table S2** 74 genes were identified as OS-DEGs

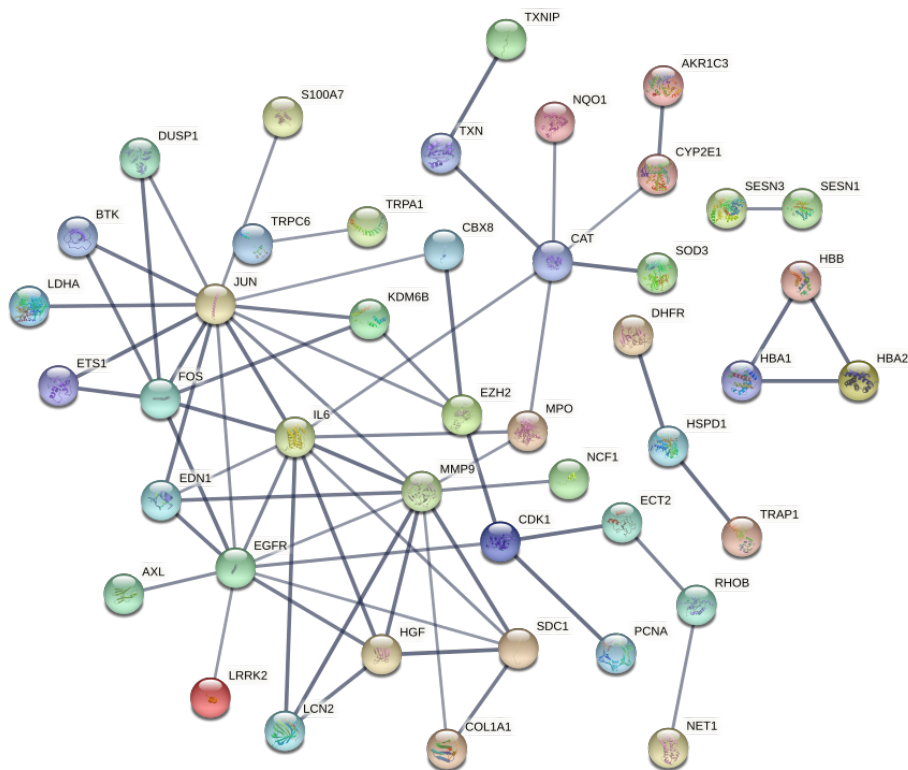
EntrezID	Gene	Log <sub>2</sub> FoldChange	P value	P <sub>adj</sub>	Direction
5831	<i>PYCR1</i>	3.336696	6.87E-251	6.16E-248	Up
2146	<i>EZH2</i>	2.908288	6.99E-207	2.13E-204	Up
983	<i>CDK1</i>	2.996593	1.44E-174	2.54E-172	Up
1894	<i>ECT2</i>	2.763503	2.69E-162	3.79E-160	Up
847	<i>CAT</i>	-2.00266	2.26E-155	2.73E-153	Down
8692	<i>HYAL2</i>	-1.49078	4.90E-131	3.82E-129	Down
3040	<i>HBA2</i>	-4.27436	1.35E-124	9.28E-123	Down
3039	<i>HBA1</i>	-4.77027	1.34E-120	8.54E-119	Down
3043	<i>HBB</i>	-4.44424	3.62E-119	2.24E-117	Down
10131	<i>TRAP1</i>	1.2559	2.87E-106	1.34E-104	Up
27244	<i>SESN1</i>	-1.52721	4.02E-102	1.71E-100	Down
3329	<i>HSPD1</i>	1.443673	1.09E-97	4.32E-96	Up
57332	<i>CBX8</i>	1.364132	3.46E-93	1.24E-91	Up
6278	<i>S100A7</i>	7.627122	7.58E-92	2.64E-90	Up
948	<i>CD36</i>	-2.92453	2.51E-87	7.89E-86	Down
5111	<i>PCNA</i>	1.546974	3.06E-83	8.59E-82	Up
10516	<i>FBLN5</i>	-2.27056	2.47E-79	6.22E-78	Down
3939	<i>LDHA</i>	1.390294	3.50E-76	8.06E-75	Up
10365	<i>KLF2</i>	-2.25447	4.86E-76	1.11E-74	Down
10105	<i>PPIF</i>	1.546297	1.01E-73	2.17E-72	Up
1728	<i>NQO1</i>	2.907394	1.47E-69	2.83E-68	Up
10276	<i>NET1</i>	1.35415	2.74E-67	4.96E-66	Up
3741	<i>KCNA5</i>	-2.64665	8.86E-65	1.50E-63	Down
5798	<i>PTPRN</i>	3.569865	2.56E-62	4.06E-61	Up
8013	<i>NR4A3</i>	-2.66461	1.22E-61	1.90E-60	Down
3373	<i>HYAL1</i>	-2.31031	4.63E-60	6.86E-59	Down
3569	<i>IL6</i>	-2.88615	7.26E-60	1.07E-58	Down
1906	<i>EDN1</i>	-2.08122	1.05E-59	1.55E-58	Down
1843	<i>DUSP1</i>	-2.02746	4.88E-59	7.04E-58	Down
695	<i>BTK</i>	-1.69577	2.75E-56	3.66E-55	Down
2113	<i>ETS1</i>	-1.47924	3.49E-54	4.37E-53	Down
655	<i>BMP7</i>	3.361854	1.49E-53	1.83E-52	Up
6770	<i>STAR</i>	3.702938	5.23E-53	6.34E-52	Up
23135	<i>KDM6B</i>	-1.06663	1.07E-50	1.21E-49	Down
2353	<i>FOS</i>	-2.01246	1.11E-49	1.22E-48	Down
1719	<i>DHFR</i>	1.014932	3.87E-49	4.17E-48	Up
1277	<i>COL1A1</i>	2.153711	5.66E-48	5.88E-47	Up
1263	<i>PLK3</i>	-1.13655	8.49E-48	8.78E-47	Down
120892	<i>LRRK2</i>	-2.58981	1.03E-47	1.06E-46	Down
8989	<i>TRPA1</i>	3.022744	6.46E-46	6.31E-45	Up
4151	<i>MB</i>	2.687459	3.55E-45	3.39E-44	Up
4318	<i>MMP9</i>	2.208829	4.79E-45	4.56E-44	Up
2861	<i>GPR37</i>	2.365341	1.28E-42	1.13E-41	Up
6382	<i>SDC1</i>	1.293357	2.37E-42	2.08E-41	Up
664	<i>BNIP3</i>	1.218884	1.65E-41	1.41E-40	Up
8644	<i>AKR1C3</i>	2.827991	1.12E-40	9.34E-40	Up
9314	<i>KLF4</i>	-1.69333	5.76E-40	4.68E-39	Down
100	<i>ADA</i>	1.615126	2.36E-39	1.88E-38	Up
3725	<i>JUN</i>	-1.13911	2.18E-37	1.64E-36	Down
6649	<i>SOD3</i>	-1.59754	7.77E-36	5.53E-35	Down
10628	<i>TXNIP</i>	-1.32583	1.54E-35	1.09E-34	Down
7356	<i>SCGB1A1</i>	-3.58406	4.33E-35	3.02E-34	Down
358	<i>AQP1</i>	-2.13428	8.25E-35	5.69E-34	Down
653361	<i>NCF1</i>	-1.37665	6.17E-34	4.13E-33	Down
7226	<i>TRPM2</i>	1.172667	5.29E-33	3.43E-32	Up
7295	<i>TXN</i>	1.215444	1.55E-32	9.84E-32	Up
140885	<i>SIRPA</i>	-1.09725	1.64E-32	1.04E-31	Down
558	<i>AXL</i>	-1.17266	4.48E-32	2.81E-31	Down
283120	<i>H19</i>	2.923638	4.87E-31	2.94E-30	Up
6546	<i>SLC8A1</i>	-1.14853	1.55E-29	8.90E-29	Down
388	<i>RHOB</i>	-1.1199	2.88E-26	1.47E-25	Down
3934	<i>LCN2</i>	1.997659	3.39E-24	1.61E-23	Up
8807	<i>IL18RAP</i>	-1.22721	6.63E-23	2.98E-22	Down
3082	<i>HGF</i>	-1.39694	2.17E-22	9.51E-22	Down
4541	<i>ND6</i>	-1.14073	7.89E-20	3.14E-19	Down
8877	<i>SPHK1</i>	1.145564	2.17E-19	8.50E-19	Up
143686	<i>SESN3</i>	1.16616	2.55E-19	9.93E-19	Up
1571	<i>CYP2E1</i>	1.421226	5.14E-19	1.98E-18	Up
5076	<i>PAX2</i>	2.811937	3.02E-15	9.84E-15	Up
4353	<i>MPO</i>	-1.05348	5.04E-14	1.56E-13	Down
7225	<i>TRPC6</i>	-1.10913	1.18E-13	3.61E-13	Down
9283	<i>GPR37L1</i>	1.116013	1.37E-13	4.16E-13	Up
1956	<i>EGFR</i>	1.040976	1.89E-13	5.72E-13	Up
337	<i>APOA4</i>	2.430688	2.15E-05	4.15E-05	Up

OS-DEGs, oxidative stress-related differentially expressed genes.

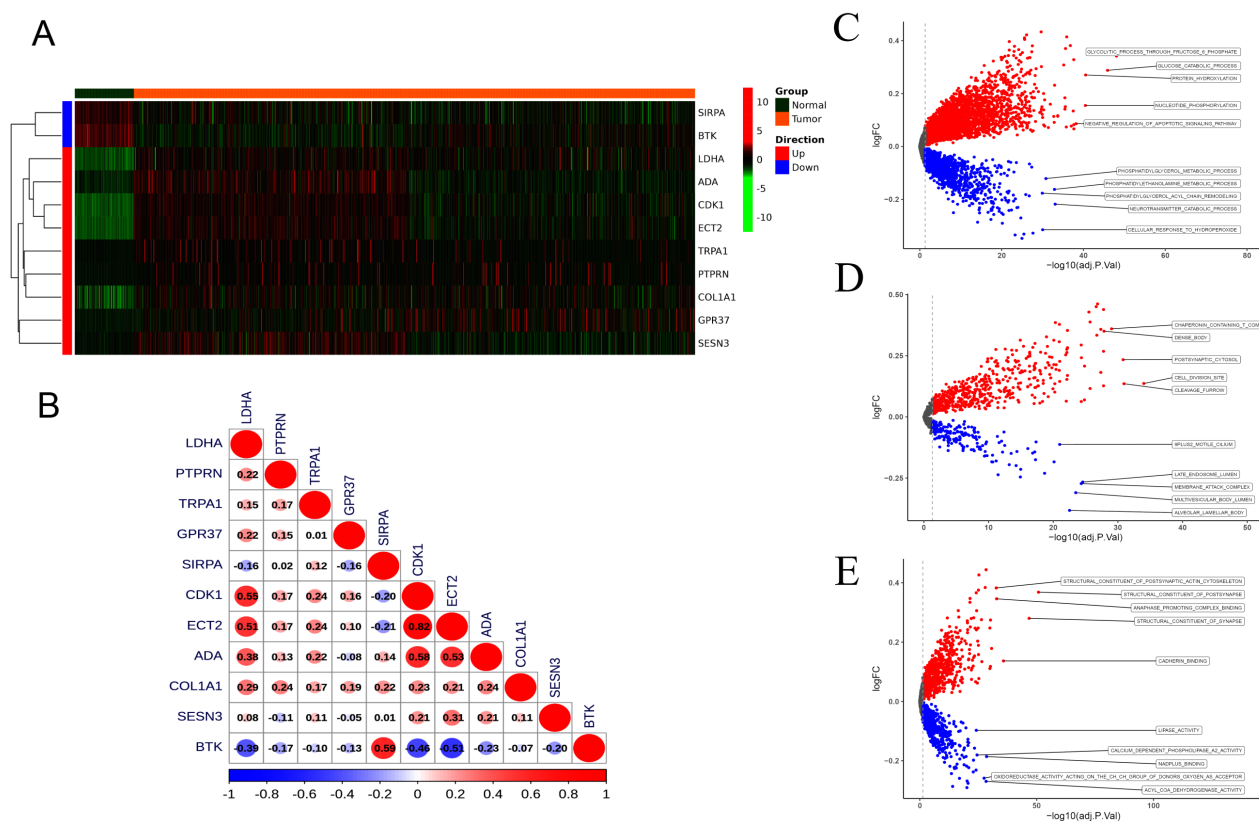
**Table S3** 34 key ICI genes were selected for further research

Gene	P value	P <sub>adj</sub>
<i>PD-1</i>	0.88	>0.99
<i>PD-L1</i>	0.001	0.03
<i>PD-L2</i>	0.002	0.07
<i>CTLA4</i>	0.02	0.59
<i>CD80</i>	0.08	>0.99
<i>CD86</i>	0.56	>0.99
<i>CD28</i>	<0.001	<0.001
<i>CD112</i>	0.13	>0.99
<i>CD155</i>	<0.001	<0.001
<i>TIGIT</i>	0.03	>0.99
<i>CD27</i>	<0.001	<0.001
<i>CD134</i>	0.18	>0.99
<i>TIM3</i>	0.69	>0.99
<i>LAG3</i>	0.03	>0.99
<i>BTLA</i>	<0.001	<0.001
<i>CD160</i>	<0.001	<0.001
<i>CDK4</i>	<0.001	<0.001
<i>FOXP3</i>	0.75	>0.99
<i>FAS</i>	0.89	>0.99
<i>CD40L</i>	<0.001	<0.001
<i>CD244</i>	<0.001	0.03
<i>CD137</i>	0.001	0.04
<i>FASL</i>	0.20	>0.99
<i>CD270</i>	<0.001	<0.001
<i>B7H3</i>	<0.001	<0.001
<i>B7H4</i>	0.97	>0.99
<i>B7H5</i>	0.90	>0.99
<i>ICOSL</i>	0.06	>0.99
<i>GEM</i>	<0.001	<0.001
<i>CD134L</i>	<0.001	<0.001
<i>CD137L</i>	<0.001	0.002
<i>CD48</i>	<0.001	<0.001
<i>IDO1</i>	0.16	>0.99
<i>CD83</i>	<0.001	0.004

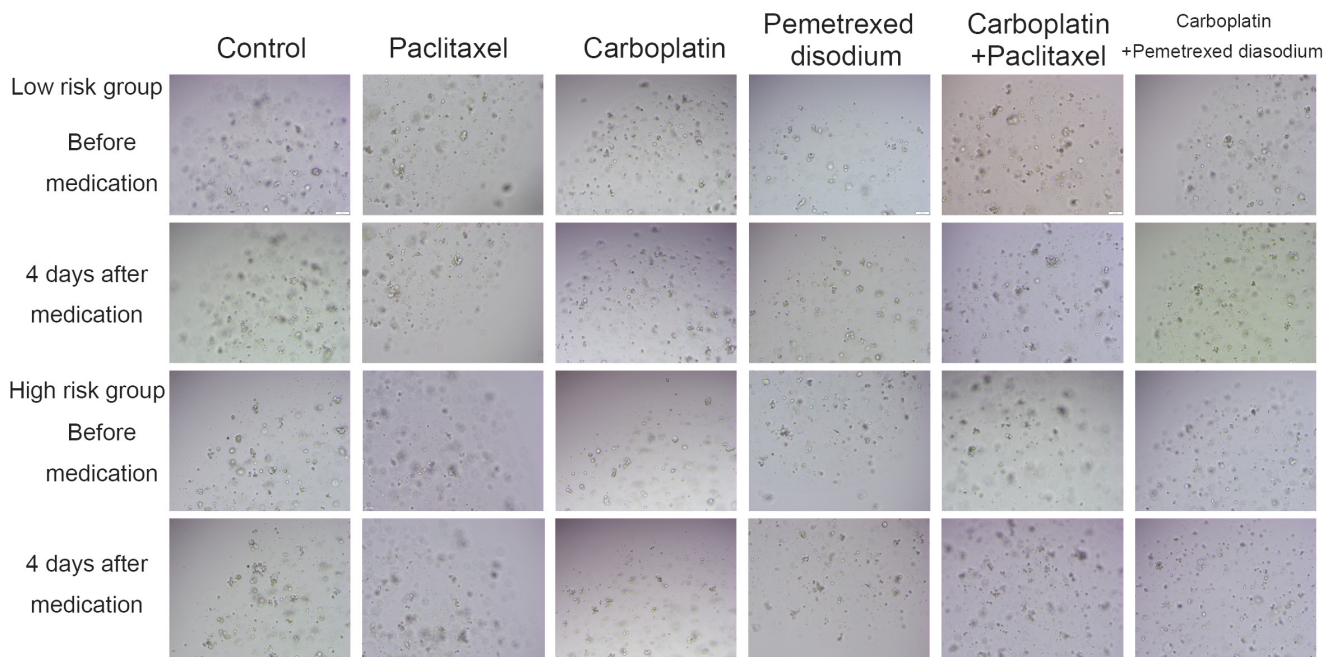
ICI, immune checkpoint inhibitor.



**Figure S1** Protein-protein interaction network. The interactions among the candidate genes were explored using the registration information in the STRING database. Outliers without connections were removed.

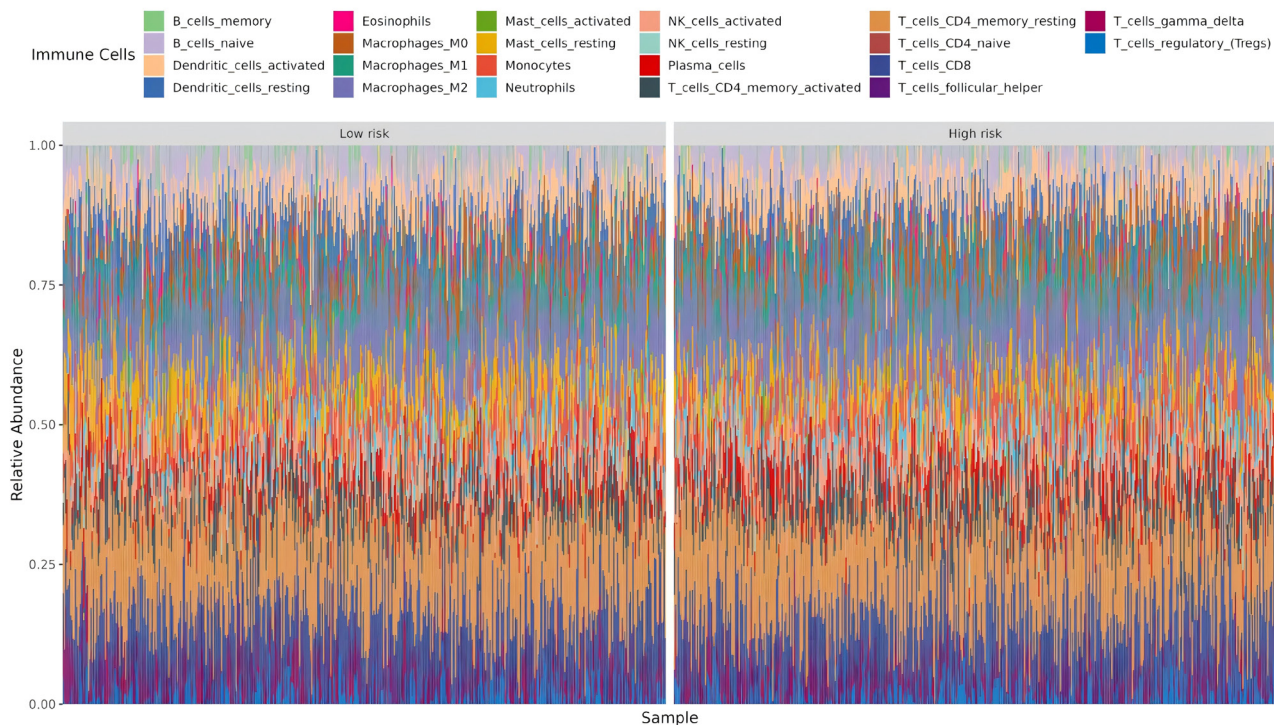


**Figure S2** Analysis of model gene expression, and GSEA of GO. (A) The expression levels of 11 prognostic OS-DEGs were visualized. (B) Correlation analysis of the 11 model genes. (C) GSEA for GO BPs. (D) GSEA for GO CCs. (E) GSEA for GO MFs. Pathways significantly activated in the high-risk group are represented in red, while those significantly activated in the low-risk group are shown in blue, and the groups with non-significant expression are represented in black. GSEA, gene set variation analysis; GO, Gene Ontology; OS, oxidative stress; DEG, differentially expressed gene; BP, biological process; CC, cellular component; MF, molecular function; FC, fold change.

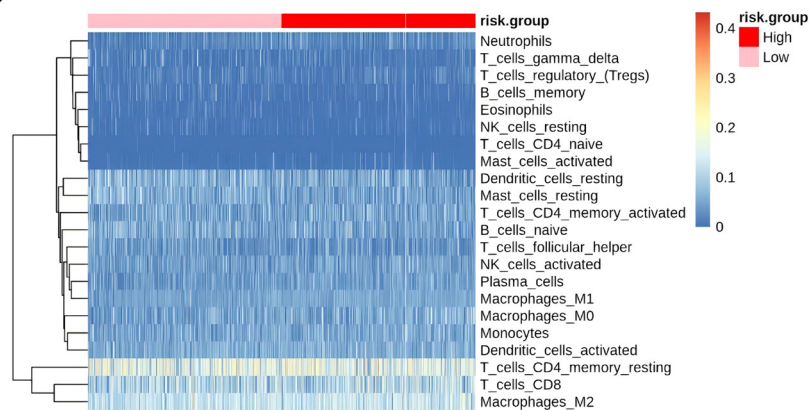


**Figure S3** Organoid drug sensitivity test. Organoid drug sensitivity test with high- or low-risk patients showing the microscopic findings before and after treatment with drugs. Image magnification of 10 $\times$ .

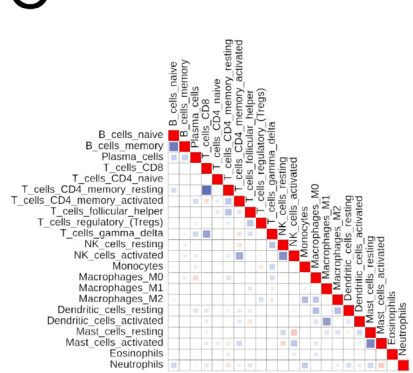
**A**



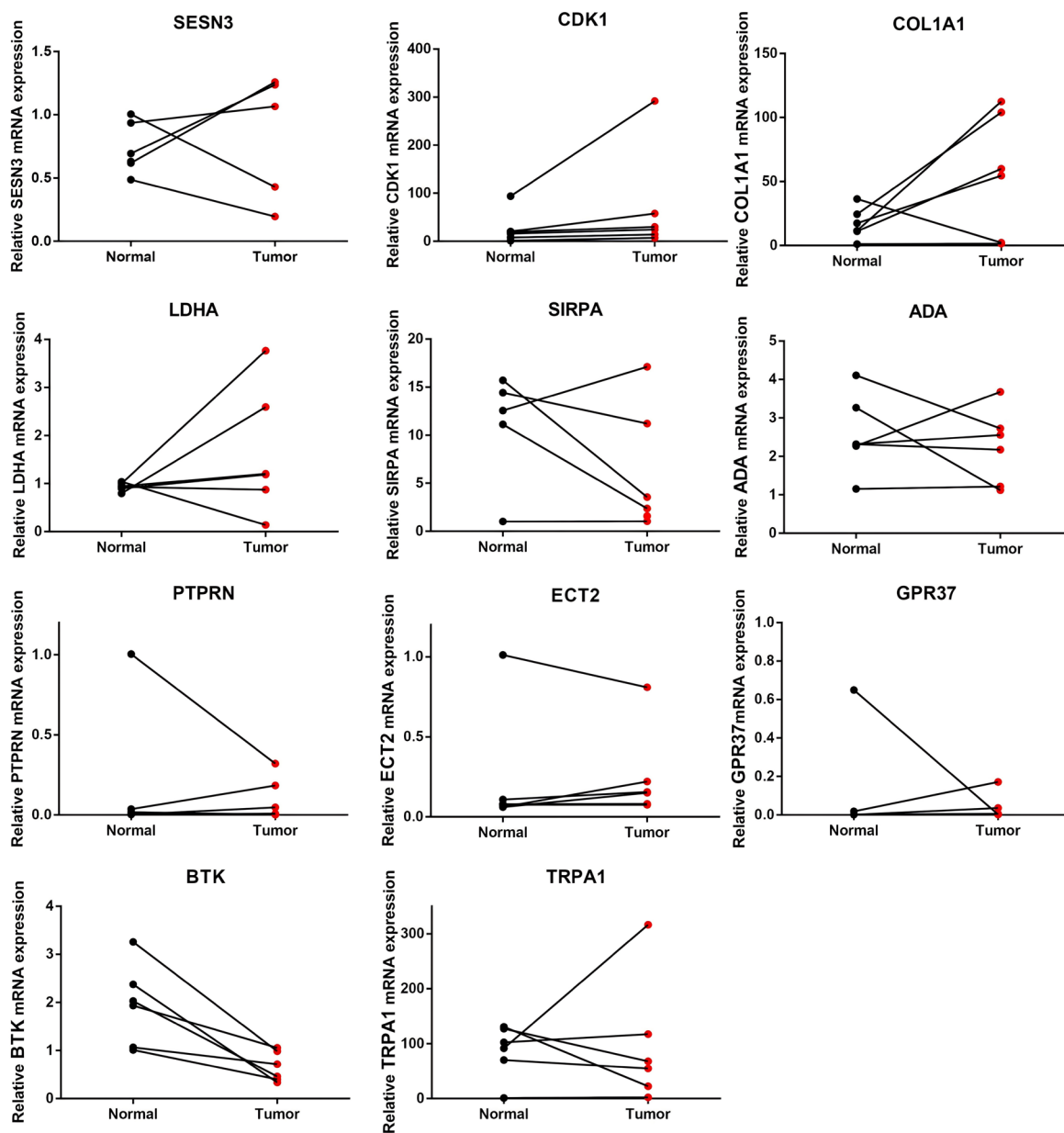
**B**



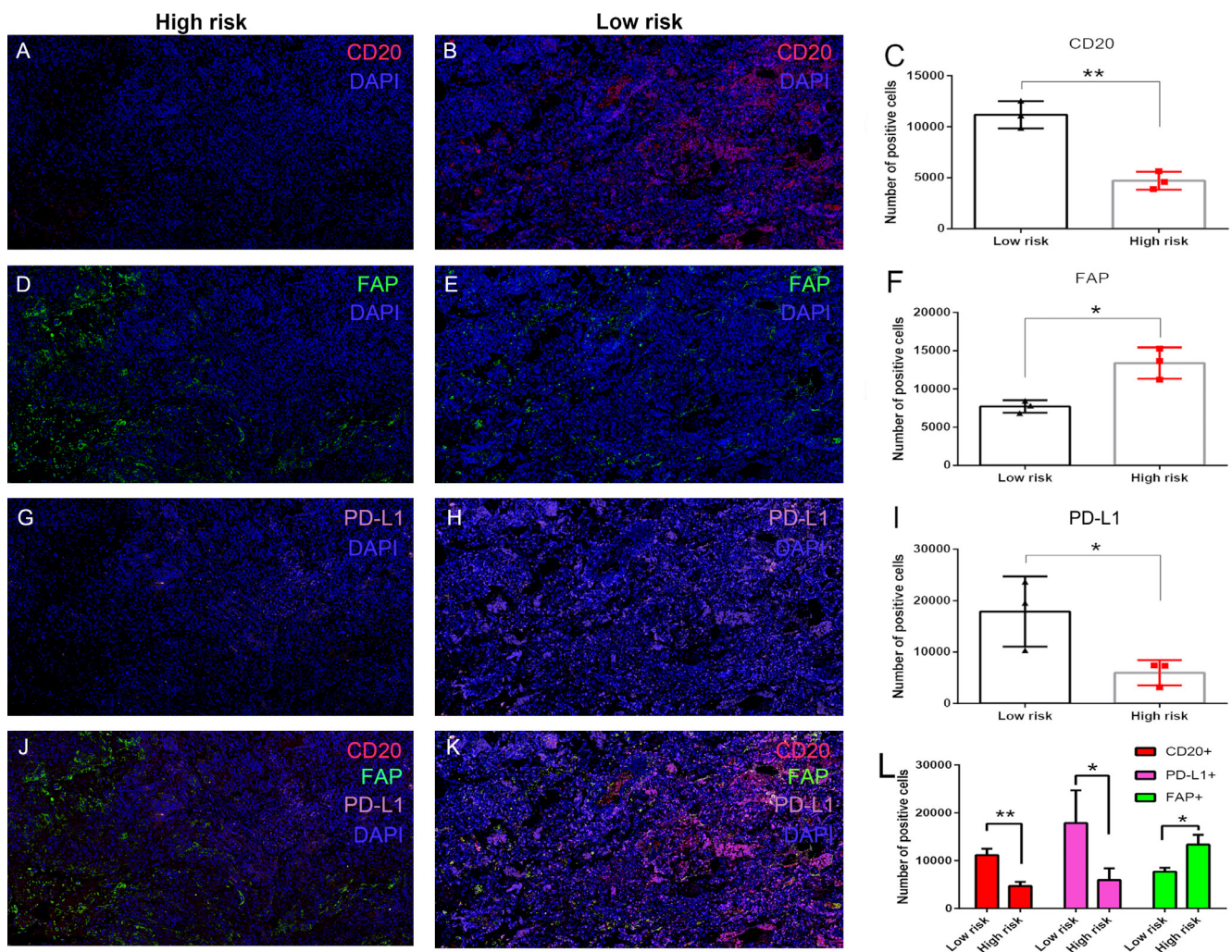
**C**



**Figure S4** Immune cell analysis. (A) Stacking plot map of immune cells; CIBERSORT was used to analyze the infiltration of 22 kinds of immune cells. (B) Heatmap of 22 immune cell infiltrates in the samples analyzed by CIBERSORT. (C) The correlation between immune cells as analyzed by CIBERSORT.

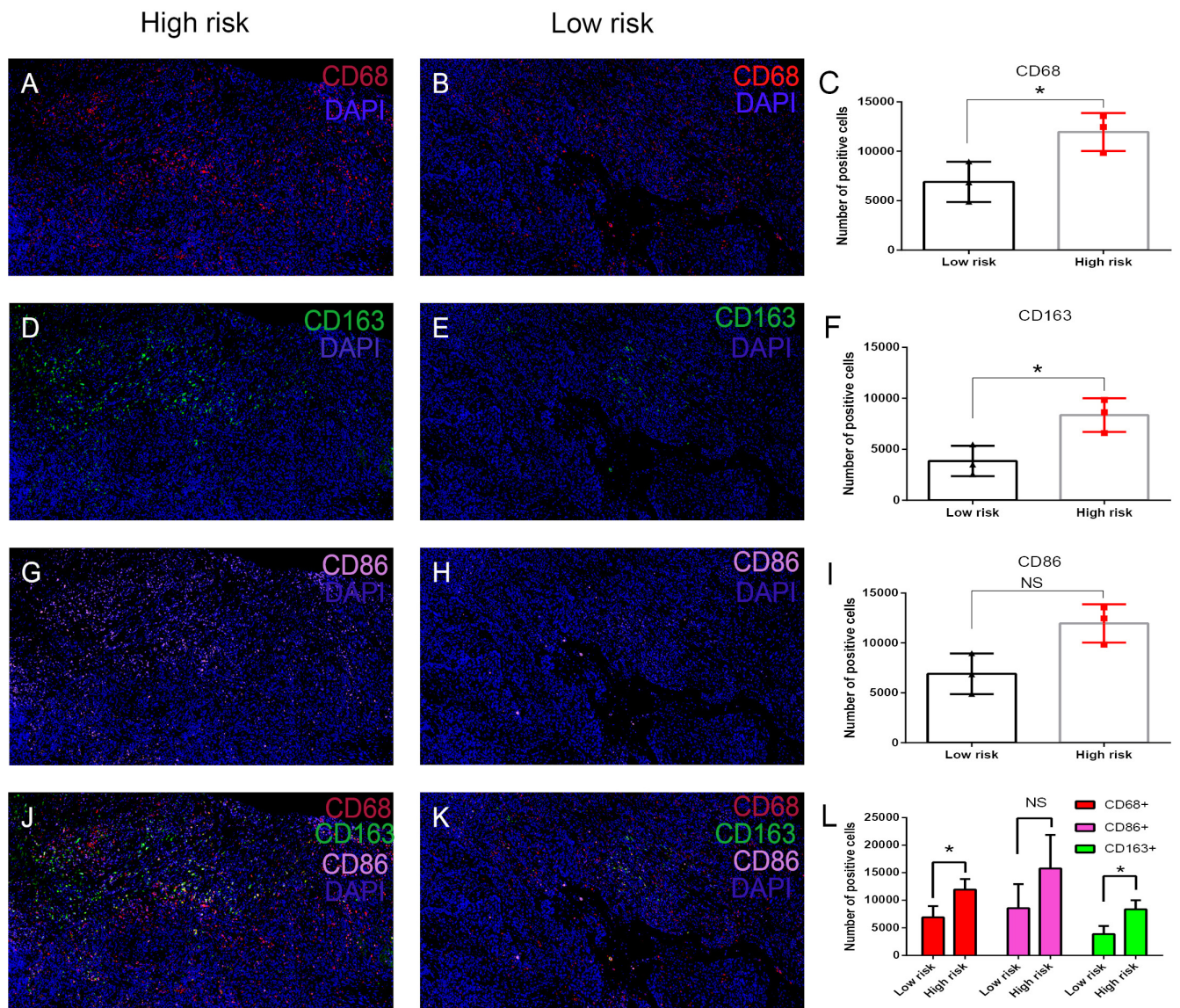


**Figure S5** qRT-PCR. Expression level of OS-related genes in tumor samples of NSCLC and adjacent control normal samples. The messenger RNA values were normalized by the expression of the housekeeping gene GAPDH. qRT-PCR, quantitative real-time polymerase chain reaction; OS, oxidative stress; NSCLC, non-small cell lung cancer; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.



**Figure S6** Multiple immunofluorescence staining of high- and low-risk NSCLC specimens. (A-C) CD20<sup>+</sup> cells were highly expressed in the low-risk group compared with the high-risk group. (D-F) FAP<sup>+</sup> cells were highly expressed in the high-risk group compared with the low-risk group. (G-I) PD-L1<sup>+</sup> cells were highly expressed in the low-risk group compared with the high-risk group. (J-L) Merge of CD20<sup>+</sup>, FAP<sup>+</sup>, and PD-L1 immunofluorescence staining. \*, P<0.05; \*\*, P<0.01. NSCLC, non-small cell lung cancer. The organoids were stained with propidium iodide (red indicating dead cells), and calcein (green indicating live cells). Image magnification of 10 $\times$ .





**Figure S7** Multiple immunofluorescence staining of macrophages in high- and low-risk NSCLC specimens. (A-C) CD68<sup>+</sup> cells were highly expressed in the high-risk group compared with the low-risk group. (D-F) CD163<sup>+</sup> cells were highly expressed in the high-risk group compared with the low-risk group. (H-I) There was no significant difference in the CD86<sup>+</sup> cells between the high-risk group and the low-risk group. (J-L) Merge of CD68<sup>+</sup>, CD163<sup>+</sup> and CD86<sup>+</sup> cell immunofluorescence staining. \*, P<0.05, NS, not significant. NSCLC, non-small cell lung cancer. The organoids were stained with propidium iodide (red indicating dead cells), and calcein (green indicating live cells). Image magnification of 10x.