

Table S1 All datasets used in this study

Accession number	Data type	Platform	Platform code	DNA chip	Total patients	Patients with prognosis information	Patients without chemotherapy
GSE96058	RNAseq	Illumina HiSeq 2000	GPL11154	–	3,273	3,273	1,973
TCGA	RNAseq	Illumina HiSeq	–	–	1,095	773	763
GSE7390	Microarray	Affymetrix	GPL96	HG-U133A	198	198	198
GSE124647	Microarray	Affymetrix	GPL570	HG-U133_Plus_2	140	140	140
GSE42568	Microarray	Affymetrix	GPL570	HG-U133_Plus_2	121	104	104
GSE20711	Microarray	Affymetrix	GPL570	HG-U133_Plus_2	90	88	88
GSE48391	Microarray	Affymetrix	GPL570	HG-U133_Plus_2	81	81	81
GSE20685	Microarray	Affymetrix	GPL570	HG-U133_Plus_2	327	327	59

RNAseq, RNA sequencing; TCGA, The Cancer Genome Atlas.

Table S2 IRGPs of the Cox regression model

IRG1	IRG2	Coefficient
A2M	CLDN4	0.282349
A2M	NDRG1	0.130049
ADIPOR2	MSR1	0.274064
ADIPOR2	SEMA3F	0.299172
AHNAK	CDH1	0.441029
AHNAK	HMOX1	0.316474
AHNAK	NDRG1	0.147511
AHNAK	PLTP	0.308854
BMP1	COLEC12	0.261746
BMP1	TNFAIP3	0.351643
BST2	PIK3R1	0.070978
BST2	RABEP1	0.147772
BST2	SPP1	0.423874
BST2	TNFSF10	0.098549
C3	FCER1G	-0.0116
CALCRL	FCER1G	-0.12911
CALCRL	IGF1R	-0.42733
CALCRL	MX1	0.559984
CCL5	COLEC12	0.029377
CCL5	CXCL9	0.298755
CD14	DDX58	-0.10417
CD14	HLA-DQA1	-0.23676
CD14	IL1R1	0.260254
CD14	S100A10	-0.24603
CD320	RORC	0.257753

Table S2 (continued)

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IRG1	IRG2	Coefficient
CD320	TNFRSF21	0.119847
CD4	CYBB	0.45898
CDH1	PRLR	0.629915
CLDN4	S100A13	0.040821
COLEC12	HLA-DOA	-0.17594
COLEC12	OSMR	-0.12973
CRIM1	FGFR1	0.106655
CRIM1	LYN	0.099633
CRIM1	NR1D2	-0.05094
CRIM1	TGFBR1	-0.04757
CSF1	NRP2	0.169575
CSF1	TNFRSF21	0.216225
CYBB	PTPRC	-0.20826
CYBB	RAC2	-0.06914
EDNRA	LTBP1	0.183387
EDNRA	MX1	-0.07353
FCER1G	FYN	0.415989
FCER1G	MDK	-0.32189
FCER1G	SPP1	0.061659
FCER1G	TCF7L2	0.26156
FGFR1	PTPRC	-0.4665
FYN	NRP2	0.191294
GBP2	ICAM1	0.175022
GBP2	NRP1	0.279443
GREM1	LTBP2	-0.16645

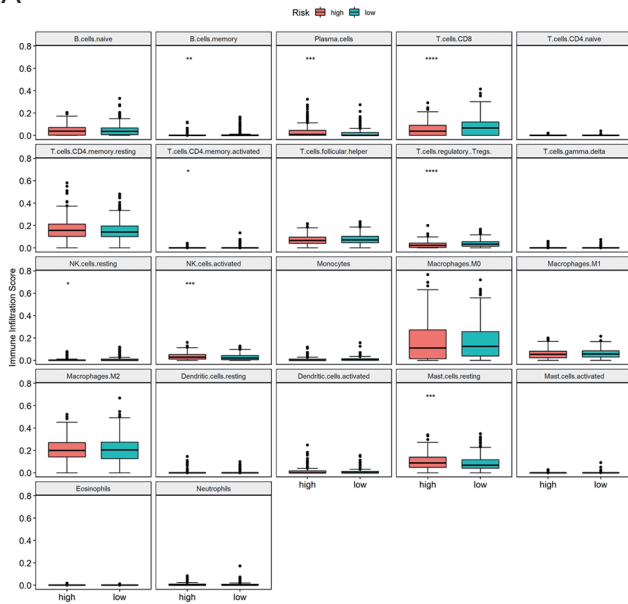
Table S2 (continued)

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IRG1	IRG2	Coefficient
<i>HLA-DPB1</i>	<i>SPP1</i>	-0.0709
<i>IGF1R</i>	<i>NR1D2</i>	-0.0714
<i>IGF1R</i>	<i>PLXNB1</i>	0.250375
<i>IKBKB</i>	<i>NRP2</i>	0.302683
<i>IKBKB</i>	<i>PDGFRB</i>	-0.00531
<i>IL32</i>	<i>IRF1</i>	0.040111
<i>IL4R</i>	<i>LTBP1</i>	0.197219
<i>IL4R</i>	<i>NR2F2</i>	0.830174
<i>IL4R</i>	<i>OAS1</i>	0.263039
<i>INHBB</i>	<i>PIK3R1</i>	-0.17934
<i>IRF1</i>	<i>ITGB2</i>	-0.18168
<i>IRF1</i>	<i>VCAM1</i>	-0.64962
<i>IRF7</i>	<i>NR2F2</i>	-0.42777
<i>JAG1</i>	<i>NR1D2</i>	0.103694
<i>JAG1</i>	<i>TNFRSF21</i>	0.025046
<i>KITLG</i>	<i>RARA</i>	-0.51714
<i>KITLG</i>	<i>STC1</i>	0.237533
<i>LTBP1</i>	<i>LTBP2</i>	0.080745
<i>LTBP1</i>	<i>SDC2</i>	-0.01819
<i>LTBP1</i>	<i>SPP1</i>	-0.53269
<i>LTBP2</i>	<i>SDC1</i>	-0.35911
<i>LTBP2</i>	<i>SEMA4A</i>	-0.00054
<i>LYN</i>	<i>PTPRC</i>	-0.37115
<i>MDK</i>	<i>NDRG1</i>	0.033879
<i>MDK</i>	<i>PLXNB1</i>	-0.09229
<i>MSR1</i>	<i>TGFBR2</i>	0.015669
<i>NR1D2</i>	<i>PIK3R3</i>	-0.25647
<i>NR2F2</i>	<i>SEMA3F</i>	0.101798
<i>NR2F2</i>	<i>TNFRSF21</i>	0.074551
<i>NR4A1</i>	<i>TCF7L2</i>	0.36575
<i>OAS1</i>	<i>TRIM22</i>	-0.48104
<i>OAS1</i>	<i>UNC93B1</i>	-0.10061
<i>OSMR</i>	<i>TNFRSF21</i>	-0.00249
<i>PIK3R3</i>	<i>TNFRSF21</i>	0.172928
<i>S100A10</i>	<i>SPP1</i>	0.21671
<i>S100A13</i>	<i>THBS1</i>	0.012698
<i>SDC4</i>	<i>TNFSF10</i>	0.228961
<i>SPP1</i>	<i>TYROBP</i>	0.112062
<i>TNFAIP3</i>	<i>VCAM1</i>	-0.22958

IRG, immune-related gene; IRGPs, immune-related gene pairs.

A BRCA Immune Cell Infiltration



B GSE96058 Immune Cell Infiltration

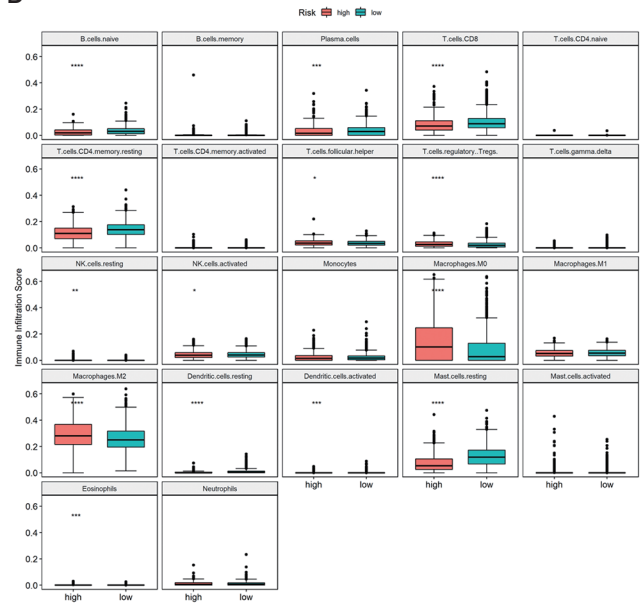


Figure S1 Infiltration of 22 types of immune cells in the high-risk and low-risk groups, analyzed with CIBERSORT. (A) In TCGA-BRCA dataset; (B) in GSE96058 dataset. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$. BRCA, breast cancer; TCGA, The Cancer Genome Atlas.