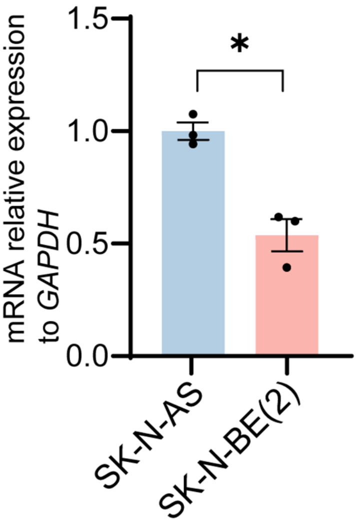

Figure S1 *MAPK8* expression in NB cell lines. Relative mRNA expression of *MAPK8* in the low-invasive SK-N-AS and high-invasive SK-N-BE(2) NB cell lines was measured by qRT-PCR. Expression levels were normalized to GAPDH. Data are presented as mean ± SEM from three independent experiments. Statistical significance was determined using an unpaired Student's *t*-test (*, P<0.05). mRNA, messenger RNA; NB, neuroblastoma; qRT-PCR, quantitative real-time polymerase chain reaction; SEM, standard error of the mean.

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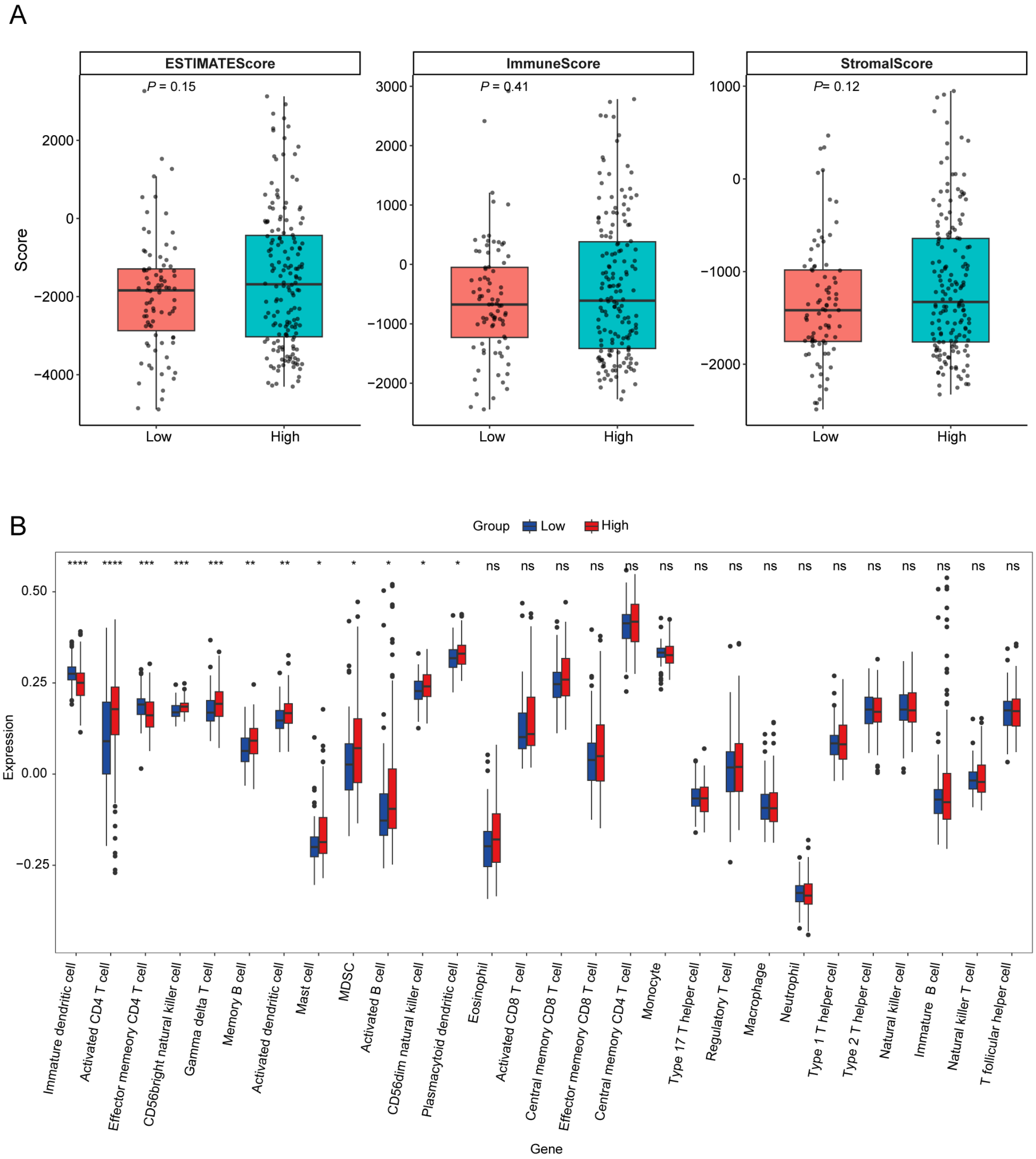

Figure S2 Association of the risk model with immune infiltration. (A) Comparison of ImmuneScore, StromalScore, and ESTIMATEScore between the high- and low-risk groups calculated using the ESTIMATE algorithm. (B) Relative enrichment scores of immune cell populations in the high- and low-risk groups as assessed by ssGSEA. *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001; ns, not significant (P>0.05). ssGSEA, single-sample gene set enrichment analysis.

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Table S1 Seventy-three ER stress-related genes in NB

Gene symbol	Description	Relevance score	Change
PPP1R15A	Protein phosphatase 1 regulatory subunit 15A	27.07	Down
MAPK8	Mitogen-activated protein kinase 8	26.08	Up
BCL2	BCL2 apoptosis regulator	25.77	Up
MAPT	Microtubule associated protein Tau	24.89	Up
CASP4	Caspase 4	23.07	Down
DSP	Desmoplakin	22.4	Down
HMOX1	Heme oxygenase 1	21.87	Down
CREB3L1	CAMP responsive element binding protein 3 like 1	18.62	Down
KCNH2	Potassium voltage-gated channel subfamily H member 2	18.4	Up
HFE	Homeostatic iron regulator	18.38	Down
EDN1	Endothelin 1	17.72	Down
SNAP25	Synaptosome associated protein 25	16.56	Up
SERPINH1	Serpin family H member 1	16.45	Down
CREB3L2	CAMP responsive element binding protein 3 like 2	15.07	Down
PARP1	Poly(ADP-ribose) polymerase 1	14.47	Up
IL6	Interleukin 6	14.43	Down
SERPINA3	Serpin family A member 3	14.36	Down
GJA1	Gap junction protein alpha 1	13.82	Down
C1S	Complement C1s	13.73	Down
PTGS2	Prostaglandin-endoperoxide synthase 2	13.69	Down
CIB1	Calcium and integrin binding 1	13.3	Down
BDNF	Brain derived neurotrophic factor	12.52	Down
ITPR3	Inositol 1,4,5-trisphosphate receptor type 3	12.43	Down
CKAP4	Cytoskeleton associated protein 4	12.23	Down
THBS1	Thrombospondin 1	12.15	Down
NR3C1	Nuclear receptor subfamily 3 group C member 1	12.01	Down
TGFB1	Transforming growth factor beta 1	11.86	Down
BCL2L1	BCL2 like 1	11.8	Down
STING1	Stimulator of interferon response CGAMP interactor 1	11.53	Down
CRYAB	Crystallin alpha B	11.46	Down
RRBP1	Ribosome binding protein 1	11.24	Down
MAP2	Microtubule associated protein 2	11.22	Up
VCL	Vinculin	11.13	Down
DYSF	Dysferlin	10.97	Down
TLR4	Toll like receptor 4	10.91	Down
CAV1	Caveolin 1	10.65	Down
PLOD2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	10.55	Down
COL1A1	Collagen type I alpha 1 chain	10.33	Down
BCL2L11	BCL2 like 11	10.05	Up
CDKN1A	Cyclin dependent kinase inhibitor 1A	10.04	Down
NUPR1	Nuclear protein 1, transcriptional regulator	9.57	Down
TRAM1	Translocation associated membrane protein 1	9.49	Down
TMED9	Transmembrane P24 trafficking protein 9	9.2	Down
FAS	Fas cell surface death receptor	9.19	Down
TRPC4	Transient receptor potential cation channel subfamily C member 4	9.1	Down
MAN2A1	Mannosidase alpha class 2A member 1	9.03	Down
C9orf72	C9orf72-SMCR8 complex subunit	8.93	Up
PON2	Paraoxonase 2	8.83	Down
ASPH	Aspartate beta-hydroxylase	8.78	Down
ANXA5	Annexin A5	8.73	Down
ITGB1	Integrin subunit beta 1	8.69	Down
PRKCD	Protein kinase C delta	8.69	Down
SCAMP5	Secretory carrier membrane protein 5	8.65	Up
NPY	Neuropeptide Y	8.63	Up
PIEZO1	Piezo type mechanosensitive ion channel component 1	8.57	Down
NGF	Nerve growth factor	8.42	Down
MGST1	Microsomal glutathione S-transferase 1	8.3	Down
PKD2	Polycystin 2, transient receptor potential cation channel	8.23	Down
TNFRSF1A	TNF receptor superfamily member 1A	7.79	Down
SLC2A1	Solute carrier family 2 member 1	7.75	Down
FURIN	Furin, paired basic amino acid cleaving enzyme	7.72	Down
FLNB	Filamin B	7.52	Down
JPH1	Junctophilin 1	7.52	Up
CPQ	Carboxypeptidase Q	7.41	Down
FOXRED2	FAD dependent oxidoreductase domain containing 2	7.39	Up
CTSD	Cathepsin D	7.38	Down
TPP1	Tripeptidyl peptidase 1	7.27	Down
PXN	Paxillin	7.21	Down
HEXA	Hexosaminidase subunit alpha	7.19	Down
QDPR	Quinoid dihydropteridine reductase	7.18	Up
MAPK8IP1	Mitogen-activated protein kinase 8 interacting protein 1	7.14	Up
SERPINE1	Serpin family E member 1	7.09	Down
FN1	Fibronectin 1	7	Down

ER, endoplasmic reticulum; NB, neuroblastoma.

Table S2 ER stress-related genes in GO analysis

Gene symbol	GO term	Relevance score	LogFC
Biological process			
MAPK8	Cellular response to abiotic stimulus	26.08	1.335753
PARP1	Cellular response to abiotic stimulus	14.47	1.001626
GJA1	Cellular response to abiotic stimulus	13.82	–5.42833
PTGS2	Cellular response to abiotic stimulus	13.69	–1.0654
BCL2L1	Cellular response to abiotic stimulus	11.8	–1.06928
CRYAB	Cellular response to abiotic stimulus	11.46	–4.16289
TLR4	Cellular response to abiotic stimulus	10.91	–3.38627
COL1A1	Cellular response to abiotic stimulus	10.33	–1.34231
CDKN1A	Cellular response to abiotic stimulus	10.04	–1.35523
FAS	Cellular response to abiotic stimulus	9.19	–3.68909
PRKCD	Cellular response to abiotic stimulus	8.69	–1.27502
PIEZO1	Cellular response to abiotic stimulus	8.57	–2.21335
PKD2	Cellular response to abiotic stimulus	8.23	–1.64434
TNFRSF1A	Cellular response to abiotic stimulus	7.79	–2.02325
SLC2A1	Cellular response to abiotic stimulus	7.75	–1.68337
PPP1R15A	Intrinic apoptotic signal pathway	27.07	–1.35245
BCL2	Intrinic apoptotic signal pathway	25.77	1.54263
CASP4	Intrinic apoptotic signal pathway	23.07	–3.18787
HMOX1	Intrinic apoptotic signal pathway	21.87	–1.47645
CREB3L1	Intrinic apoptotic signal pathway	18.62	–3.26865
PARP1	Intrinic apoptotic signal pathway	14.47	1.001626
PTGS2	Intrinic apoptotic signal pathway	13.69	–1.0654
BCL2L1	Intrinic apoptotic signal pathway	11.8	–1.06928
CAV1	Intrinic apoptotic signal pathway	10.65	–6.87448
BCL2L11	Intrinic apoptotic signal pathway	10.05	1.074993
CDKN1A	Intrinic apoptotic signal pathway	10.04	–1.35523
NUPR1	Intrinic apoptotic signal pathway	9.57	–3.75064
PRKCD	Intrinic apoptotic signal pathway	8.69	–1.27502
TNFRSF1A	Intrinic apoptotic signal pathway	7.79	–2.02325
MAPK8IP1	Intrinic apoptotic signal pathway	7.14	1.41689
DSP	Wound healing	22.4	–5.09746
HMOX1	Wound healing	21.87	–1.47645
EDN1	Wound healing	17.72	–2.91989
IL6	Wound healing	14.43	–2.3343
GJA1	Wound healing	13.82	–5.42833
THBS1	Wound healing	12.15	–5.32992
TGFB1	Wound healing	11.86	–2.4246
VCL	Wound healing	11.13	–2.63654
DYSF	Wound healing	10.97	–3.36192
TLR4	Wound healing	10.91	–3.38627
CAV1	Wound healing	10.65	–6.87448
COL1A1	Wound healing	10.33	–1.34231
CDKN1A	Wound healing	10.04	–1.35523
ANXA5	Wound healing	8.73	–1.53678
ITGB1	Wound healing	8.69	–1.21012
PRKCD	Wound healing	8.69	–1.27502
SERPINE1	Wound healing	7.09	–5.72952
FN1	Wound healing	7	–3.57186
Cellular component			
MAPT	Membrane raft	24.89	2.275015
HMOX1	Membrane raft	21.87	–1.47645
SERPINH1	Membrane raft	16.45	–1.89875
GJA1	Membrane raft	13.82	–5.42833
PTGS2	Membrane raft	13.69	–1.0654
CAV1	Membrane raft	10.65	–6.87448
FAS	Membrane raft	9.19	–3.68909
TRPC4	Membrane raft	9.1	–2.13766
ITGB1	Membrane raft	8.69	–1.21012
TNFRSF1A	Membrane raft	7.79	–2.02325
SLC2A1	Membrane raft	7.75	–1.68337
FURIN	Membrane raft	7.72	–2.33707
CTSD	Membrane raft	7.38	–1.92217
TPP1	Membrane raft	7.27	–1.32011
MAPT	Membrane microdomain	24.89	2.275015
HMOX1	Membrane microdomain	21.87	–1.47645
SERPINH1	Membrane microdomain	16.45	–1.89875
GJA1	Membrane microdomain	13.82	–5.42833
PTGS2	Membrane microdomain	13.69	–1.0654
CAV1	Membrane microdomain	10.65	–6.87448
FAS	Membrane microdomain	9.19	–3.68909
TRPC4	Membrane microdomain	9.1	–2.13766
ITGB1	Membrane microdomain	8.69	–1.21012
TNFRSF1A	Membrane microdomain	7.79	–2.02325
SLC2A1	Membrane microdomain	7.75	–1.68337
FURIN	Membrane microdomain	7.72	–2.33707
CTSD	Membrane microdomain	7.38	–1.92217
TPP1	Membrane microdomain	7.27	–1.32011
PPP1R15A	Organelle outer membrane	27.07	–1.35245
BCL2	Organelle outer membrane	25.77	1.54263
HMOX1	Organelle outer membrane	21.87	–1.47645
GJA1	Organelle outer membrane	13.82	–5.42833
PTGS2	Organelle outer membrane	13.69	–1.0654
ITPR3	Organelle outer membrane	12.43	–3.58176
BCL2L1	Organelle outer membrane	11.8	–1.06928
STING1	Organelle outer membrane	11.53	–2.04974
BCL2L11	Organelle outer membrane	10.05	1.074993
MGST1	Organelle outer membrane	8.3	–4.44987
Molecular function			
SERPINH1	Peptidase regulator activity	16.45	–1.89875
SERPINA3	Peptidase regulator activity	14.36	–1.3806
CAV1	Peptidase regulator activity	10.65	–6.87448
NGF	Peptidase regulator activity	8.42	–1.55651
FURIN	Peptidase regulator activity	7.72	–2.33707
SERPINE1	Peptidase regulator activity	7.09	–5.72952
FN1	Peptidase regulator activity	7	–3.57186
BCL2	Protease binding	25.77	1.54263
COL1A1	Protease binding	10.33	–1.34231
ITGB1	Protease binding	8.69	–1.21012
FURIN	Protease binding	7.72	–2.33707
SERPINE1	Protease binding	7.09	–5.72952
FN1	Protease binding	7	–3.57186
SERPINH1	Collagen binding	16.45	–1.89875
THBS1	Collagen binding	12.15	–5.32992
FN1	Collagen binding	7	–3.57186
ITGB1	Collagen binding	8.69	–1.21012

ER, endoplasmic reticulum; FC, fold change; GO, Gene Ontology.

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