Supplementary

Table S1 Univariate Cox proportional hazard regression analysis results of immunogenic cell death-related lncRNAs in endometrial carcinoma

id	HR	HR.95L	HR.95H	P value
AC004585.1	0.137544605	0.028907838	0.654442514	0.01
SCARNA9	0.609948644	0.375630052	0.990435524	0.046
FAM198B-AS1	0.038476824	0.003259061	0.454261509	0.01
FKBP14-AS1	6.85210706	1.262031183	37.20301987	0.03
DLEU2	2.951432972	1.008909633	8.634030548	0.048
AC010615.2	2.235437172	1.103270917	4.529421806	0.03
AL035530.2	6.488149496	1.171351622	35.9380421	0.03
AC007611.1	0.109107868	0.014086926	0.845076266	0.03
SOCAR	0.007758384	0.000123896	0.485829692	0.02
UNQ6494	0.000839063	2.03E–06	0.347128919	0.02
AC012645.3	0.042936915	0.002151408	0.856917101	0.04
AC007996.1	1.566942263	1.016678532	2.415028919	0.042
FBXO30-DT	6.908472159	1.039536648	45.91178932	0.045
LINC01943	0.063296412	0.006455071	0.620664841	0.02
AL161431.1	1.459764949	1.04847224	2.032398784	0.03
AC006369.1	0.016749967	0.000316831	0.885524833	0.043

lncRNAs, long non-coding RNAs; HR, hazard ratio; 95L, the lowest value of the 95% confidence interval; 95H, the highest value of the 95% confidence interval.

Table S2 qRT-PCR primers used in this study

Gene name	Forward primer	Reverse primer
SCARNA9	5'-AAG GGC ATA TGT CTG GTG TGT GTG-3'	5'-CCC CAC CCT CAA TCT CAT TCA TTC C-3'
FAM198B-AS1	5'-GGA ATG AAG CCA CCC TTG ACT GAG-3'	5'-GTC TTC TGT GCC GTG TCT CCT TG-3'
FKBP14-AS1	5'-CGA GAC CAG CCT GAC CAA CAT G-3'	5'-CTA CAG ACA CAT GCC ACC ACA CTC-3'
FBXO30-DT	5'-ACC AGG GTC TGC TTC TGT GAG G-3'	5'-CAG TTT GGC ATG GCT GGA GAG G-3'
LINC01943	5'-TGG CAT CAG TCT GGT TGG ATT ACA C-3'	5'-CAG CAG GTA TCA GGC ACA GCA TC-3'
AL161431.1	5'-GGC TCT CTG GCA AGA ACC ACA AG-3'	5'-GAA CGG TGT TGG GTC TGT CAG TAG-3'
β-actin	5'-ACC GAG CGT GGC TAC AGC TTC ACC-3'	5'-AGC ACC CGT GGC CAT CTC TTT CTC G-3'

qRT-PCR, quantitative real-time polymerase chain reaction.

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Table S3 ShRNA sequences used for cell transfection

ShRNA	Sequence (5'-3')
sh-FKBP14-AS1-1	F-CCG GAG AAT CAG ACA GAA AAT CCC TCG AGG GAT TTT CTG TCT GAT TCT TTT TTG
	R-AAT TCA AAA AAA GAA TCA GAC AGA AAA TCC CTC GAG GGA TTT TCT GTC TGA TTC T
sh-FKBP14-AS1-2	F-CCG GAG ACC AAA ACA GTA TTT TAC TCG AGT AAA ATA CTG TTT TGG TCT TTT TTG
	R-AAT TCA AAA AAA GAC CAA AAC AGT ATT TTA CTC GAG TAA AAT ACT GTT TTG GTC T
sh-FKBP14-AS1-3	F-CCG GTC TAC TAA AAA TAC AAA AAC TCG AGT TTT TGT ATT TTT AGT AGA TTT TTG
	R-AAT TCA AAA AAT CTA CTA AAA ATA CAA AAA CTC GAG TTT TTG TAT TTT TAG TAG A
sh-FBXO30-DT-1	F-CCG GGG ACC TTT TTT CCT TTC GAC TCG AGT CGA AAG GAA AAA AGG TCC TTT TTG
	R-AAT TCA AAA AAG GAC CTT TTT TCC TTT CGA CTC GAG TCG AAA GGA AAA AAG GTC C
sh-FBXO30-DT-2	F-CCG GAG AAG CAT AAG CTG CAA TAC TCG AGT ATT GCA GCT TAT GCT TCT TTT TTG
	R-AAT TCA AAA AAA GAA GCA TAA GCT GCA ATA CTC GAG TAT TGC AGC TTA TGC TTC T
sh-FBXO30-DT-3	F-CCG GGC TGC AAT AAA AAT TTG GTC TCG AGA CCA AAT TTT TAT TGC AGC TTT TTG
	R-AAT TCA AAA AAG CTG CAA TAA AAA TTT GGT CTC GAG ACC AAA TTT TTA TTG CAG C
sh-AL161431.1-1	F-CCG GGG AAA TAT CCC ATT AGA TTC TCG AGA ATC TAA TGG GAT ATT TCC TTT TTG
	R-AAT TCA AAA AAG GAA ATA TCC CAT TAG ATT CTC GAG AAT CTA ATG GGA TAT TTC CTT TTT G
sh-AL161431.1-2	F-CCG GGC TAG GAT ACA AGA GAA ACC TCG AGG TTT CTC TTG TAT CCT AGC TTT TTG
	R-AAT TCA AAA AAG CTA GGA TAC AAG AGA AAC CTC GAG GTT TCT CTT GTA TCC TAG C
sh-AL161431.1-3	F-CCG GGC CTG AAA TCA TTT ATT TCC TCG AGG AAA TAA ATG ATT TCA GGC TTT TTG
	R-AAT TCA AAA AAG CCT GAA ATC ATT TAT TTC CTC GAG GAA ATA AAT GAT TTC AGG C

ShRNA, short hairpin RNA.

Table S4 The risk model for immunogenic cell death-related lncRNAs

Immunogenic cell death-related lncRNA	Coefficient
SCARNA9	−0.401528645653866
FAM198B-AS1	−1.90526441273924
FKBP14-AS1	2.21856134166291
FBXO30-DT	1.63157340507073
LINC01943	−2.36050864717649
AL161431.1	0.600416817300287

lncRNAs, long non-coding RNAs.

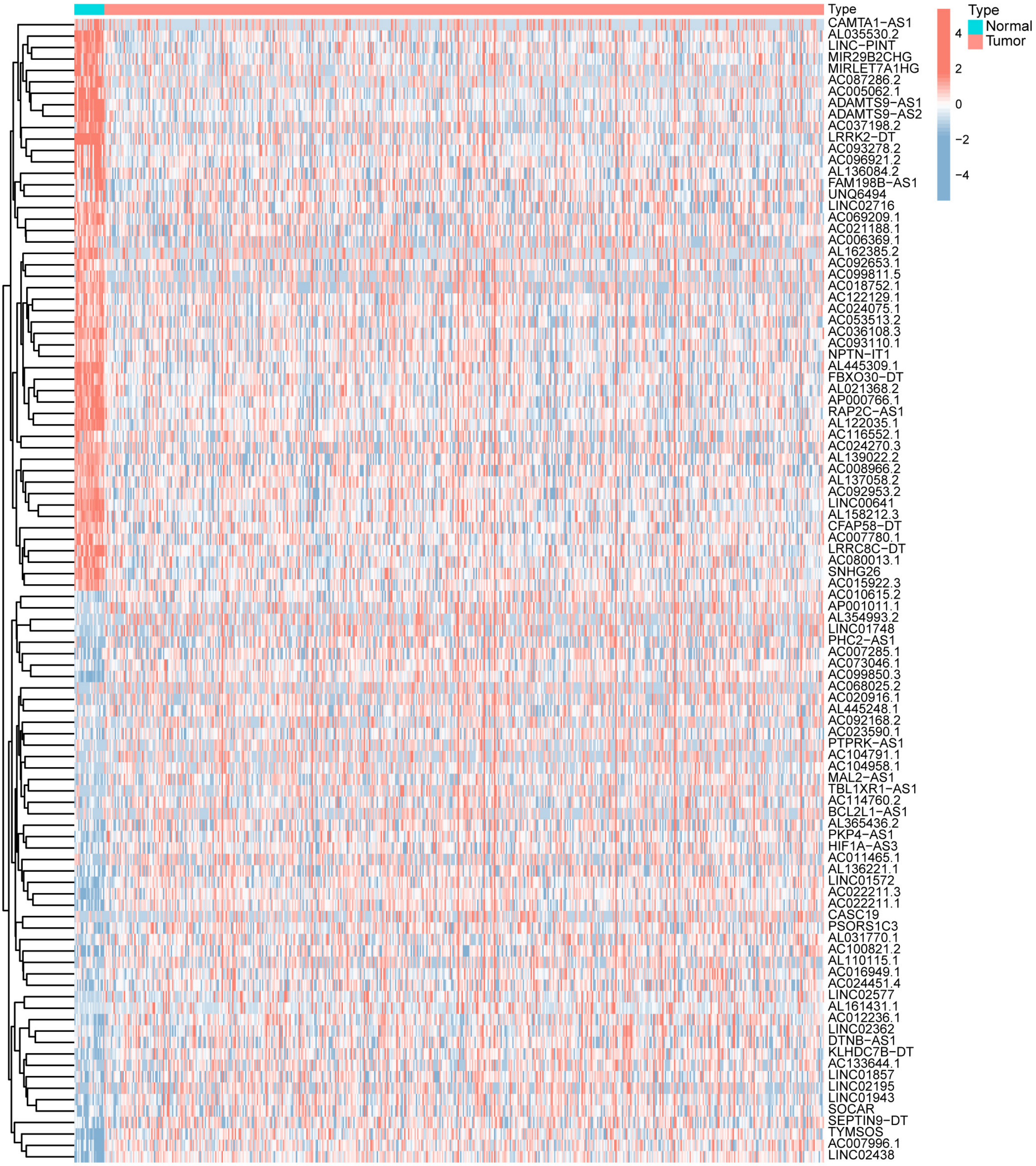

Figure S1 Heatmap shows differential expression of immunogenic cell death-related lncRNAs in tumor tissues and normal tissues. lncRNAs, long non-coding RNAs.

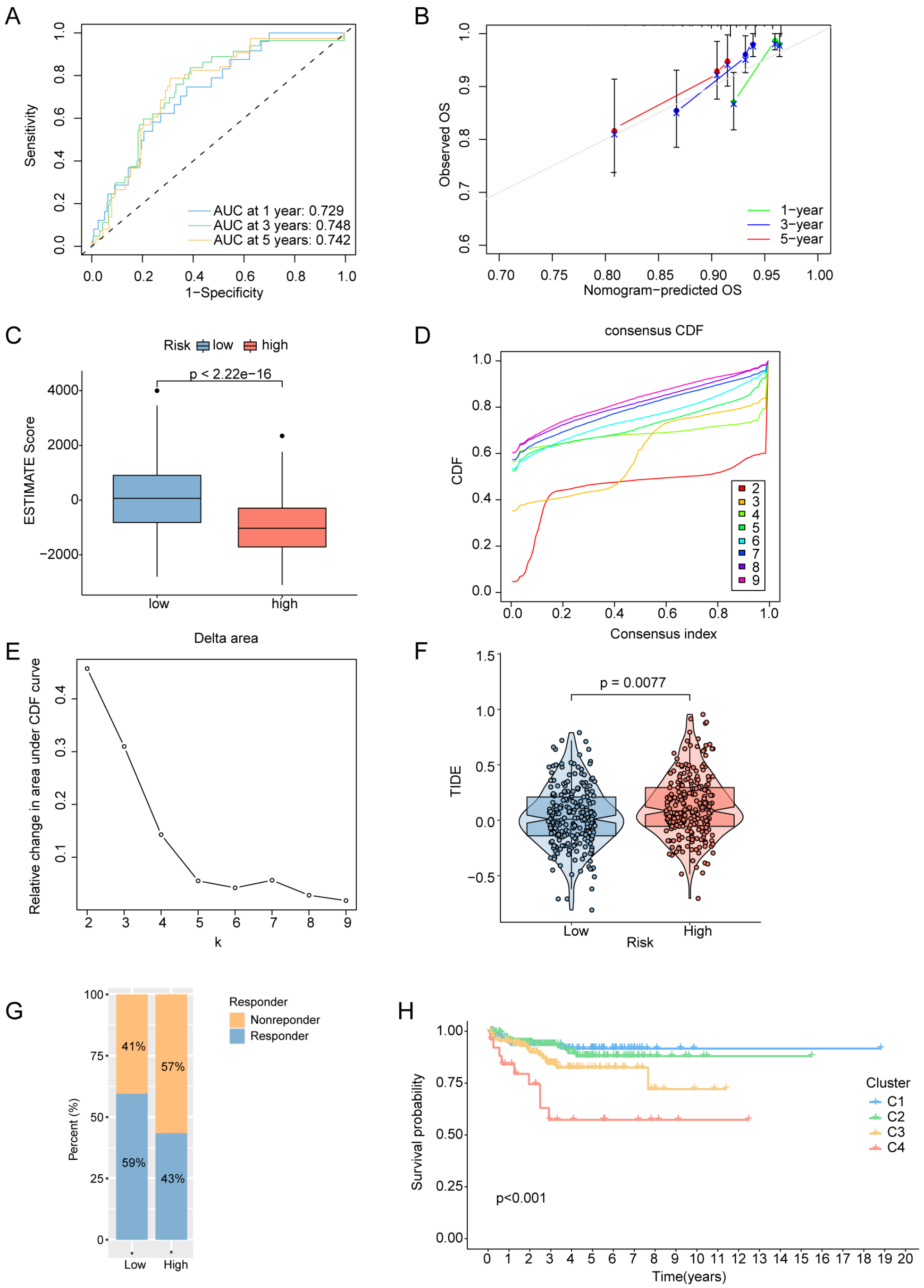

Figure S2 The validation curve of the predictive model, immune scores for high and low-risk groups, and the survival curve of four clusters. (A) ROC curve at 1, 3, 5 years. (B) The calibration curve of the nomogram. (C) Box plots of ESTIMATE score for the low- and high-risk groups. (D) The CDF curves when k =2–9. (E) Relative changes in area under CDF curves. (F) The TIDE scores between high- and low-risk groups. (G) In high- and low-risk groups, the ICI therapy responders was predicted by the TIDE algorithm. (H) The survival curve of 4 subtypes. AUC, area under the curve; OS, overall survival; ESTIMATE, Estimation of STromal and Immune cells in MAlignant Tumour tissues using Expression data; CDF, cumulative distribution function; ROC, receiver operating characteristic; TIDE, Tumor Immune Dysfunction and Exclusion; ICI, immune checkpoint inhibitor.

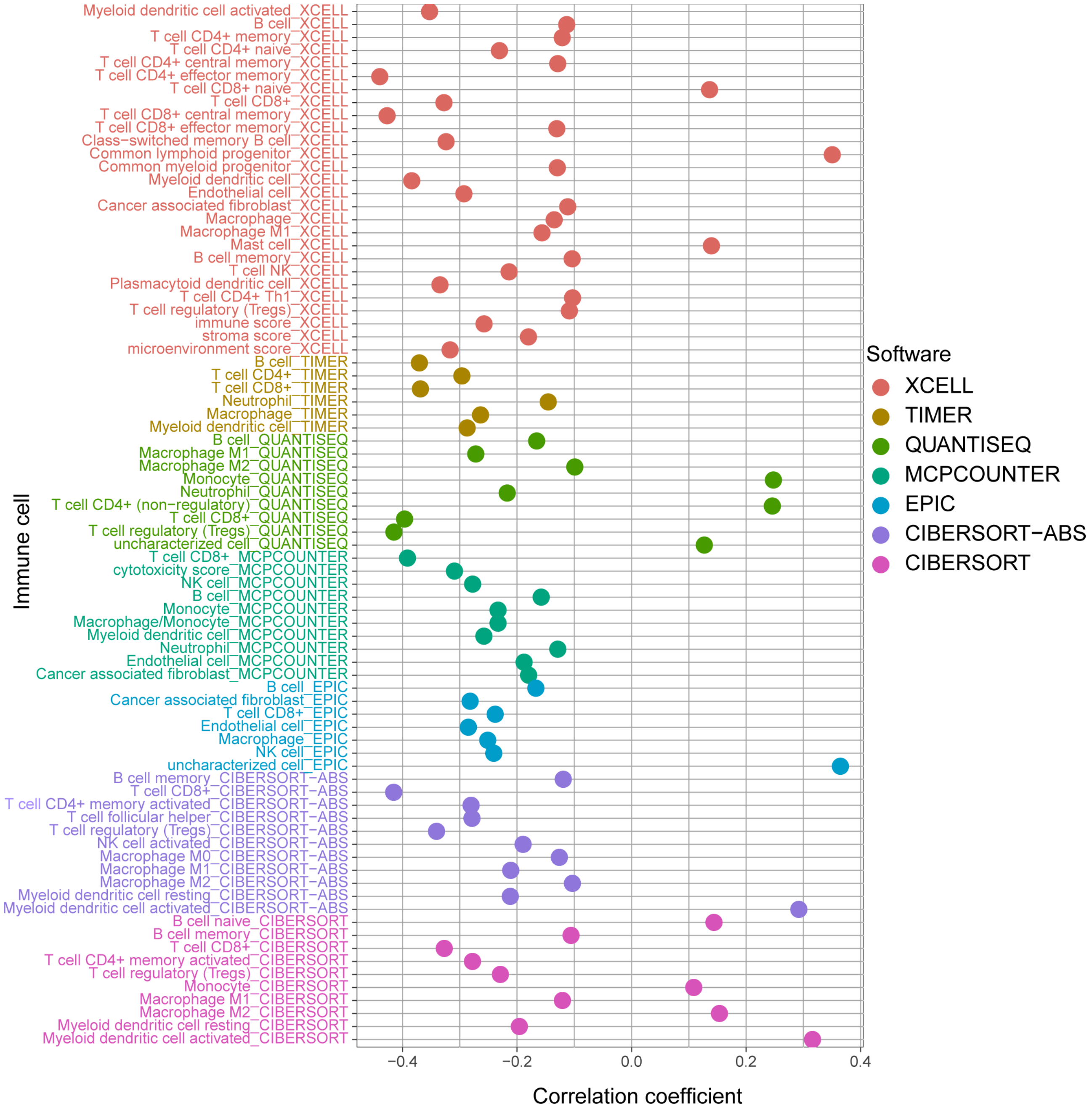

Figure S3 The bubble gram of immune cells in low- and high-risk groups.

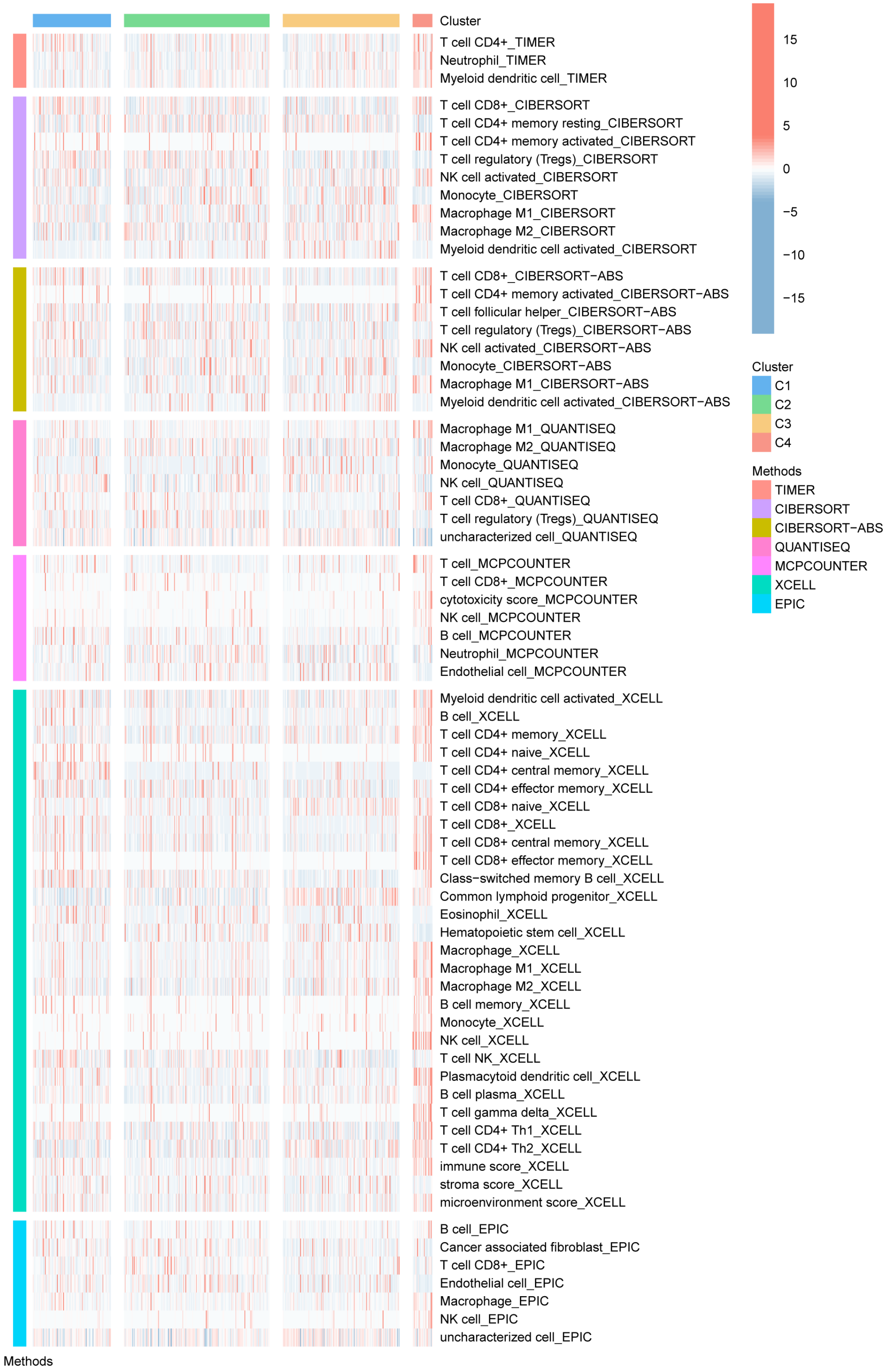

Figure S4 The heat map of immune cell infiltration in 4 clusters.

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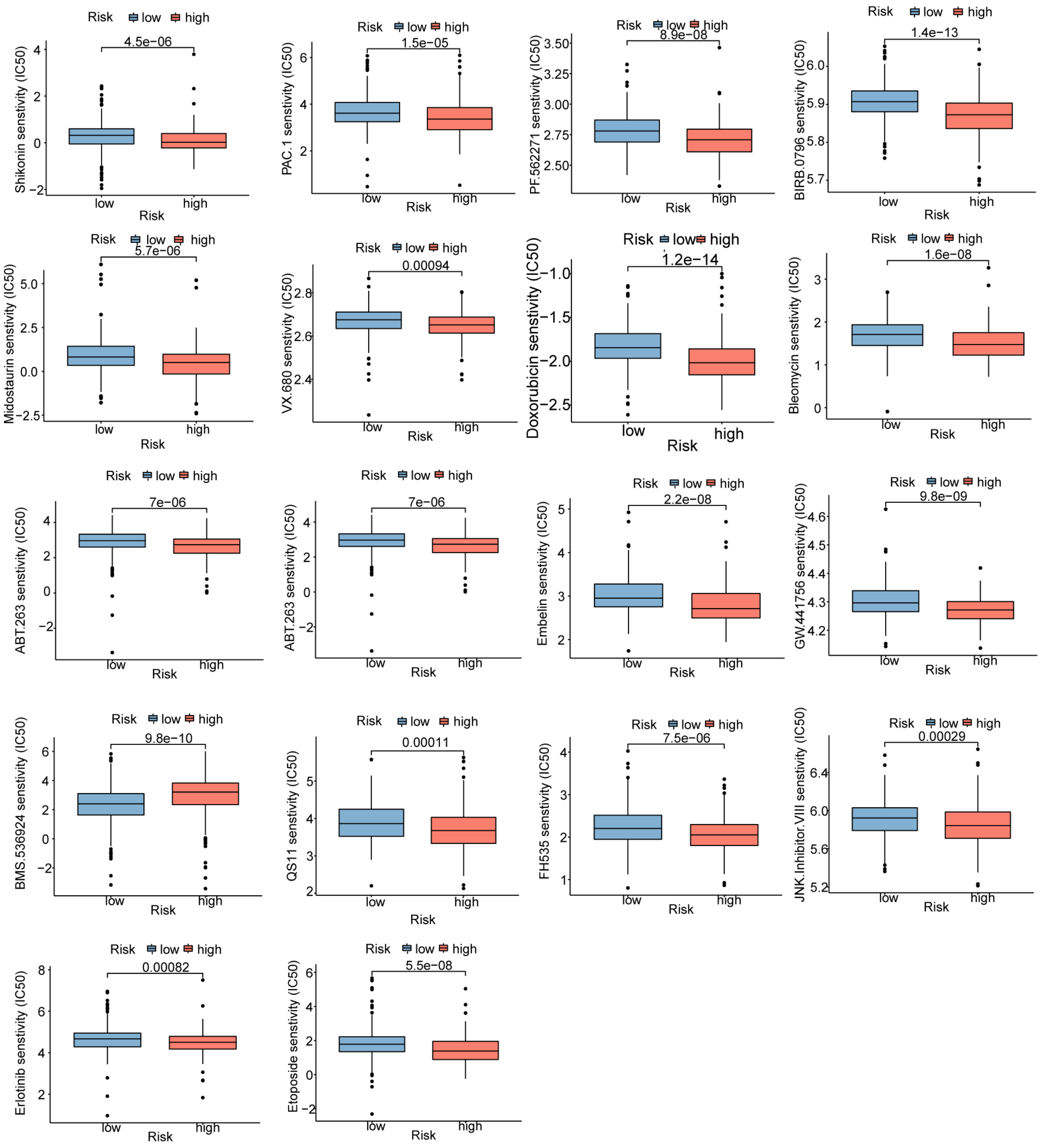

Figure S5 Compounds with IC50 in the high-risk group. IC50, half inhibitory centration.

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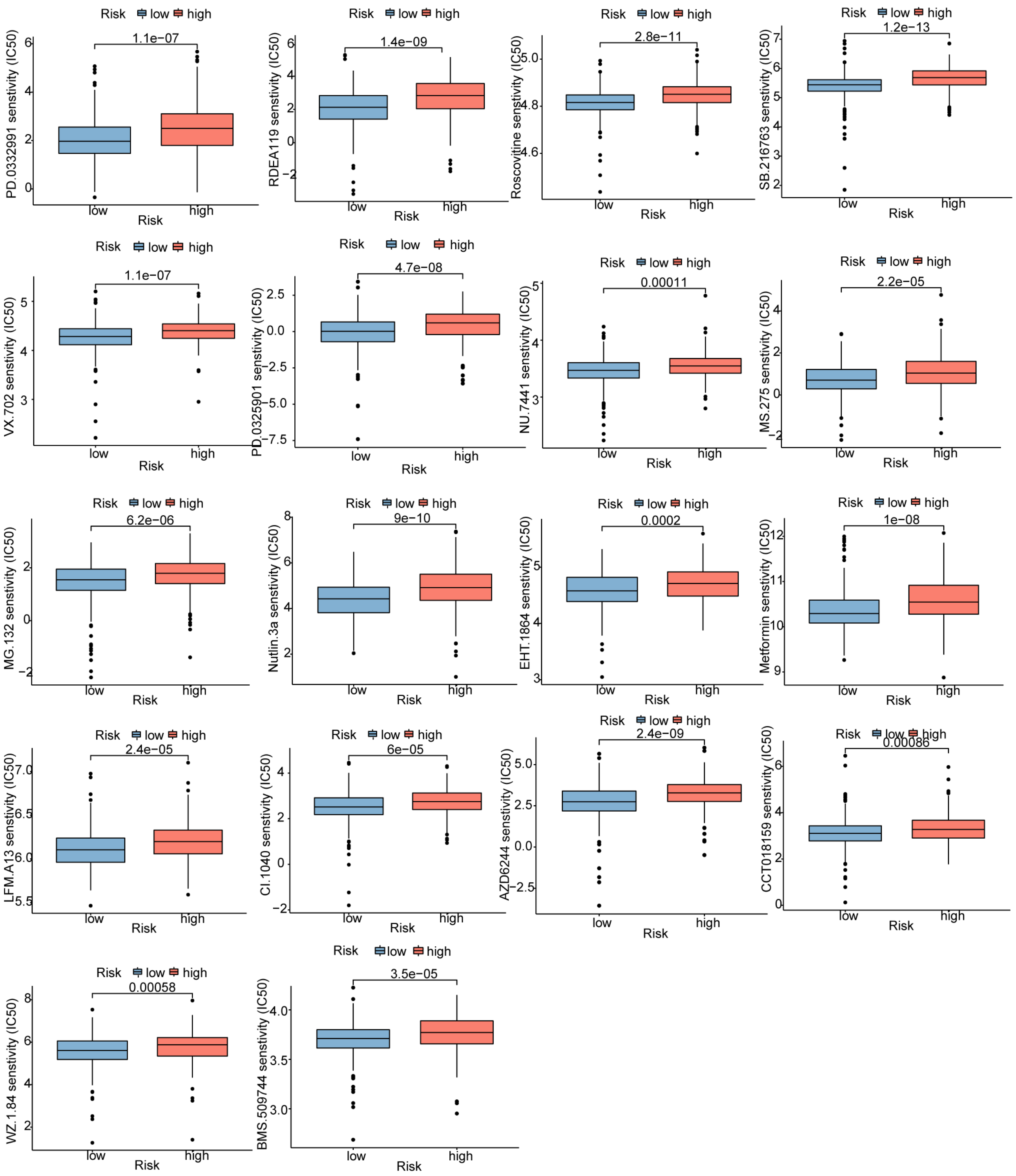

Figure S6 Compounds with lower IC50 in low-risk group. IC50, half inhibitory centration.

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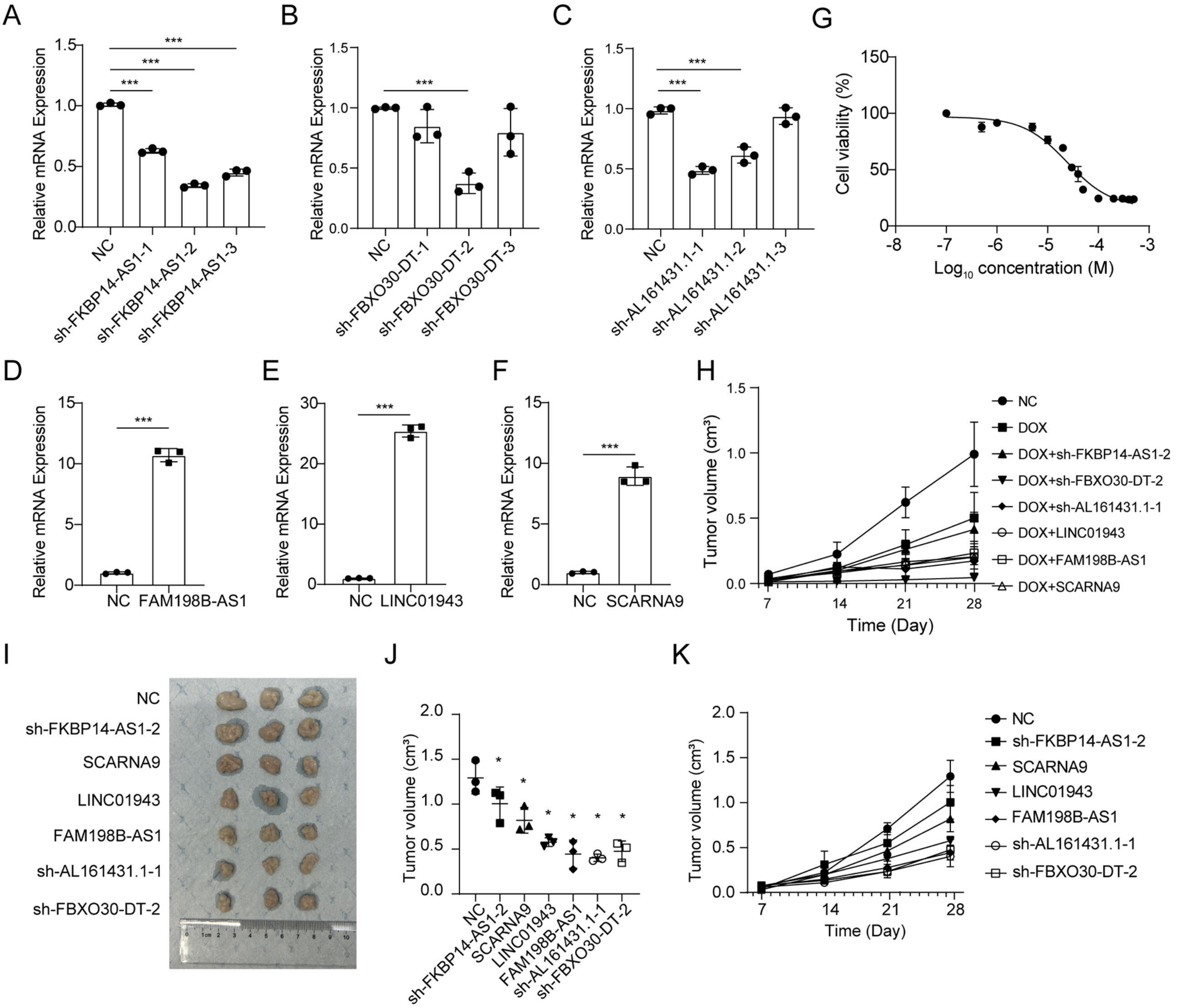

Figure S7 *In vivo* and *in vitro* experiments. (A-C). The efficiency of knocked down. (D-F) The efficiency of overexpression. (G) Viability of KLE cells after 48 h incubation with different DOX formulations. (H) Growth curves of the tumor measured in BALB/c nude mice. (I) Xenograft tumors without DOX treatment at the endpoint. (J) Tumor volume measured in BALB/c nude mice without DOX treatment. (K) Growth curves of the tumor measured in BALB/c nude mice without DOX treatment. *, P<0.05; ***, P<0.001. NC, negative control; DOX, doxorubicin.