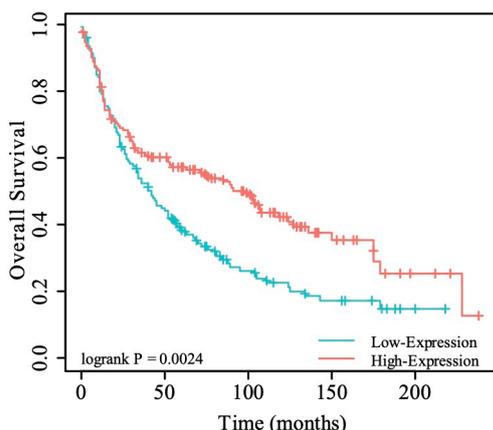
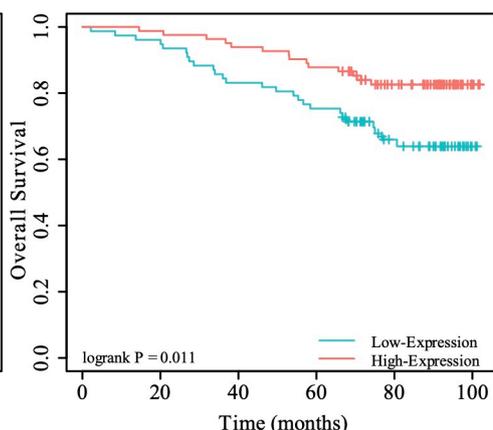


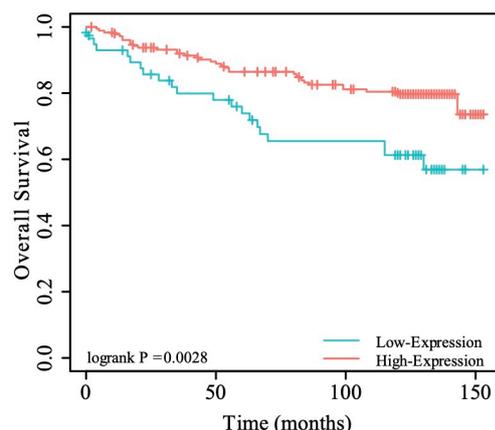
GSE30219 Kaplan-Meier Survival Curve



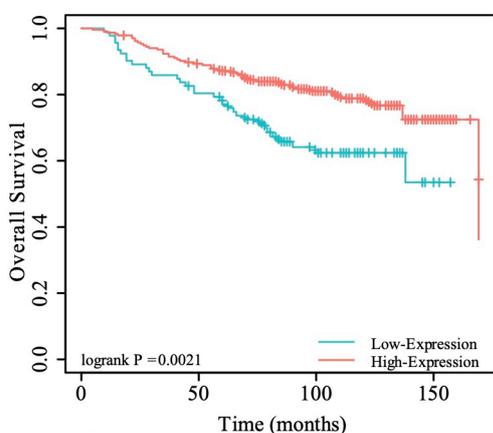
GSE1456 Kaplan-Meier Survival Curve



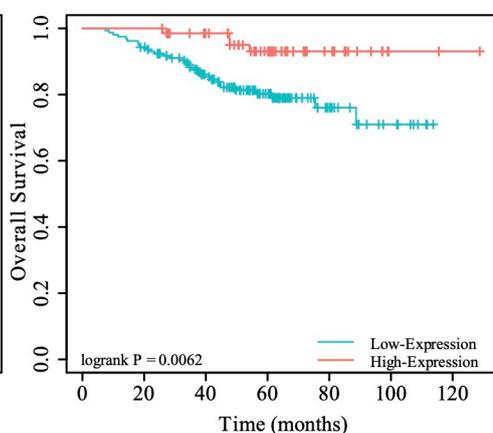
GSE3494 Kaplan-Meier Survival Curve



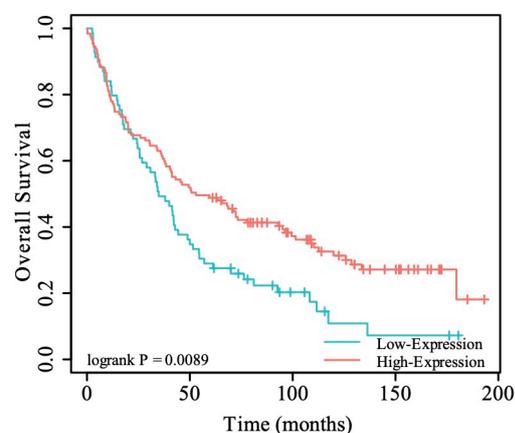
GSE20685 Kaplan-Meier Survival Curve



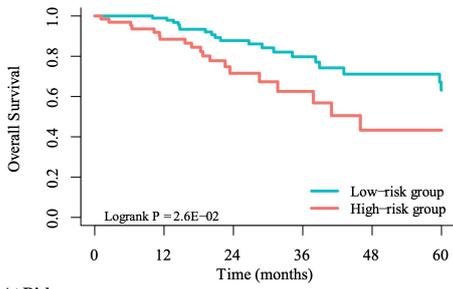
GSE31210 Kaplan-Meier Survival Curve



GSE37745 Kaplan-Meier Survival Curve

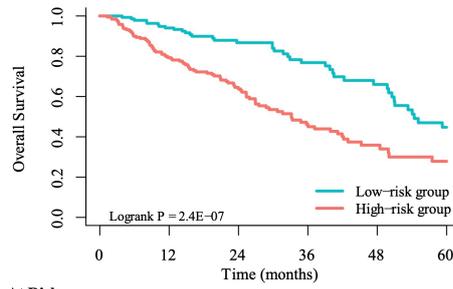


A TCGA-LUAD T1 Kaplan-Meier Survival Curve



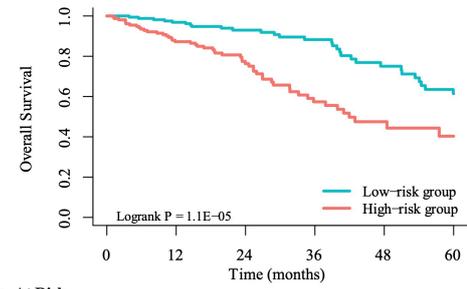
No. At Risk		0	12	24	36	48	60
Low-risk group	101	93	53	31	21	16	
High-risk group	65	50	21	12	5	3	

B TCGA-LUAD Tothers Kaplan-Meier Survival Curve



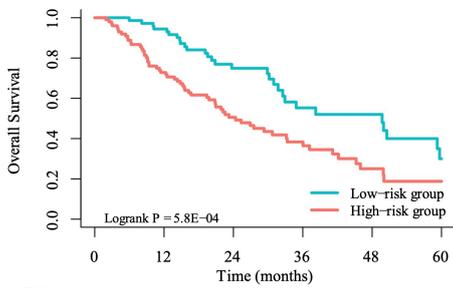
No. At Risk		0	12	24	36	48	60
Low-risk group	142	123	74	50	32	20	
High-risk group	193	139	82	42	20	13	

C TCGA-LUAD N0 Kaplan-Meier Survival Curve



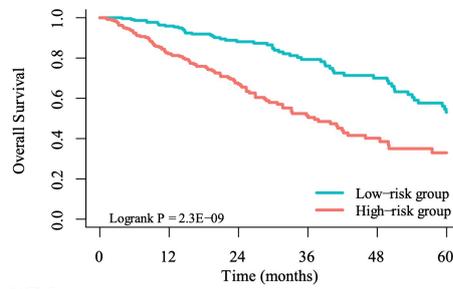
No. At Risk		0	12	24	36	48	60
Low-risk group	169	149	90	63	40	30	
High-risk group	157	122	65	34	16	10	

D TCGA-LUAD Nothers Kaplan-Meier Survival Curve



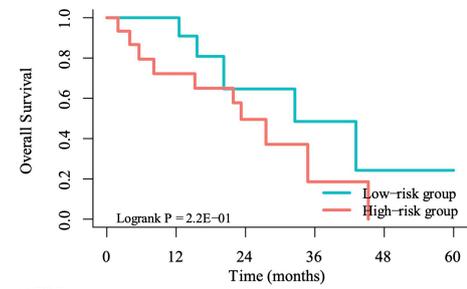
No. At Risk		0	12	24	36	48	60
Low-risk group	74	67	37	18	13	6	
High-risk group	101	67	38	20	9	6	

E TCGA-LUAD M0 Kaplan-Meier Survival Curve



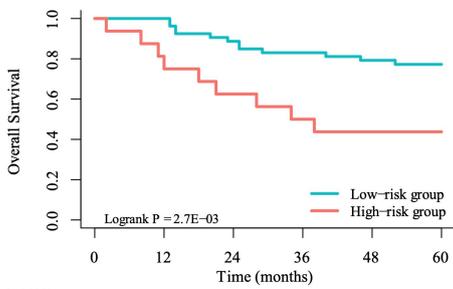
No. At Risk		0	12	24	36	48	60
Low-risk group	231	205	123	78	52	35	
High-risk group	243	179	98	53	25	16	

F TCGA-LUAD Mothers Kaplan-Meier Survival Curve



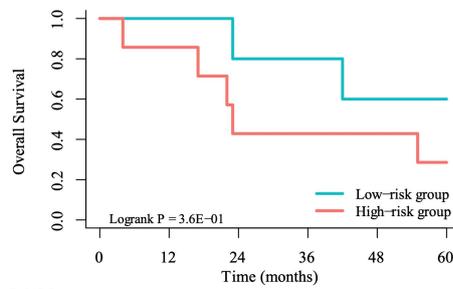
No. At Risk		0	12	24	36	48	60
Low-risk group	12	11	4	3	1	1	
High-risk group	15	10	5	1	0	0	

G GSE30219 T1 Kaplan-Meier Survival Curve



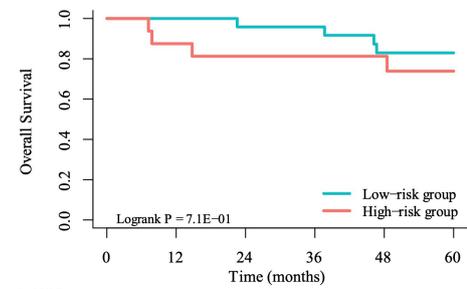
No. At Risk		0	12	24	36	48	60
Low-risk group	53	53	47	44	42	34	
High-risk group	16	13	10	8	7	7	

H GSE30219 T2 Kaplan-Meier Survival Curve



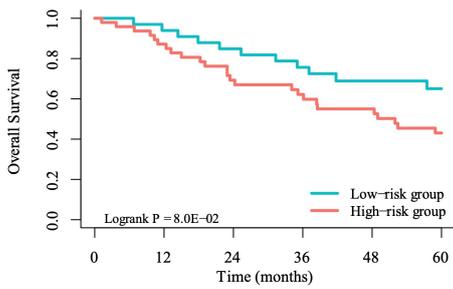
No. At Risk		0	12	24	36	48	60
Low-risk group	5	5	4	4	3	3	
High-risk group	7	6	3	3	3	2	

I GSE50081 T1 Kaplan-Meier Survival Curve



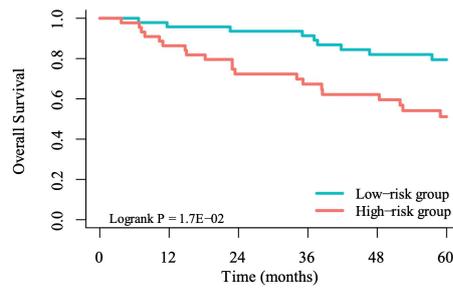
No. At Risk		0	12	24	36	48	60
Low-risk group	27	26	23	23	19	14	
High-risk group	16	14	12	11	11	6	

J GSE50081 Tothers Kaplan-Meier Survival Curve



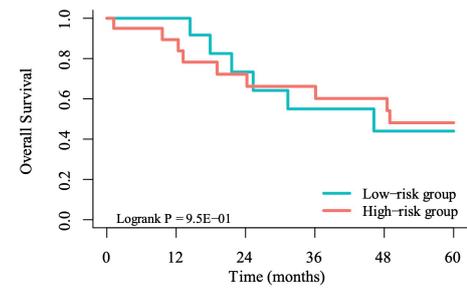
No. At Risk		0	12	24	36	48	60
Low-risk group	35	31	28	24	19	17	
High-risk group	49	40	30	26	23	18	

K GSE50081 N0 Kaplan-Meier Survival Curve

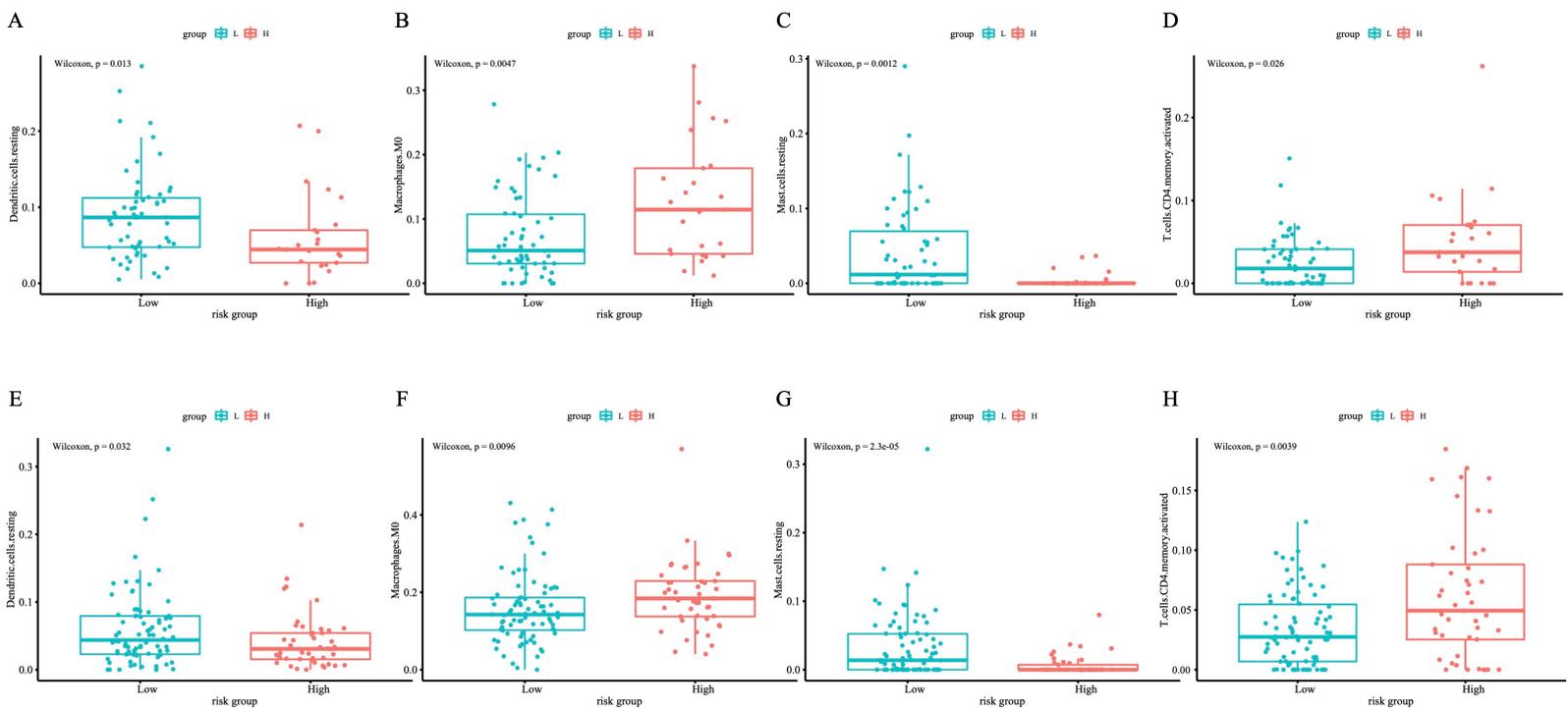


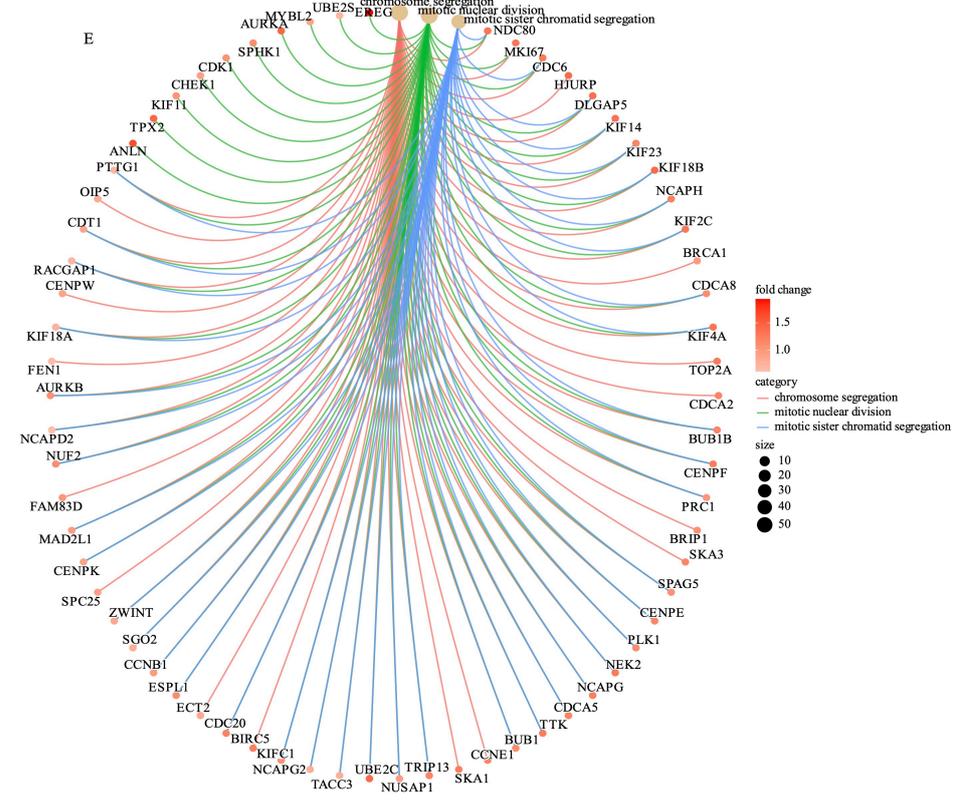
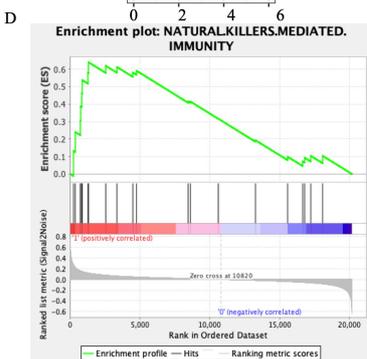
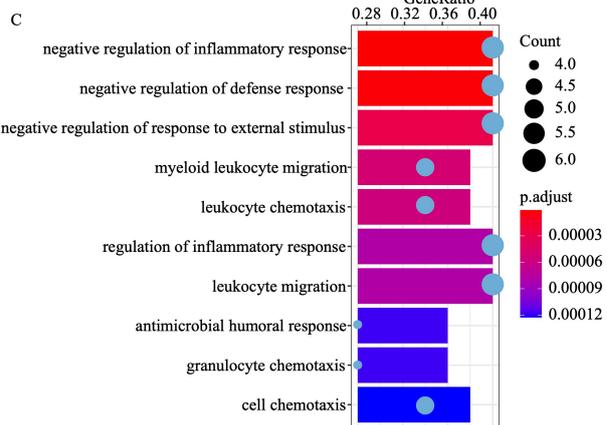
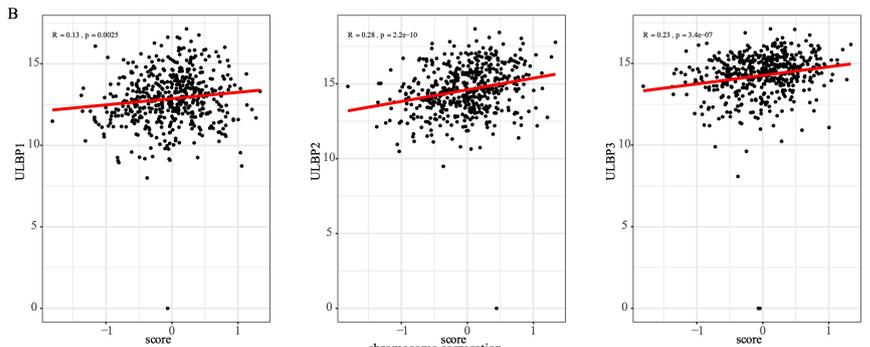
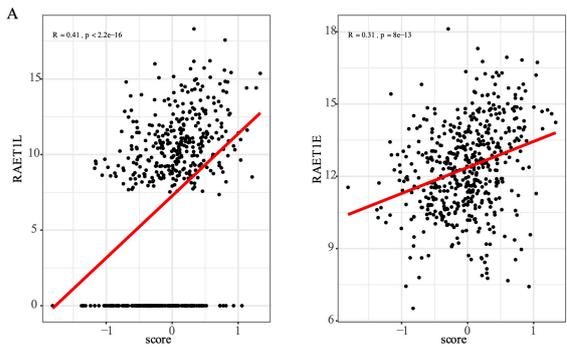
No. At Risk		0	12	24	36	48	60
Low-risk group	50	45	43	41	34	27	
High-risk group	44	38	30	26	24	17	

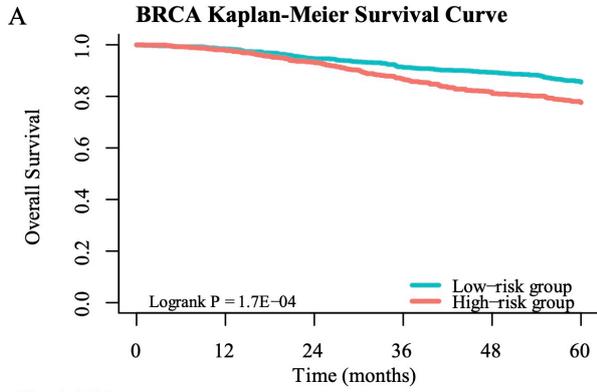
L GSE50081 Nothers Kaplan-Meier Survival Curve



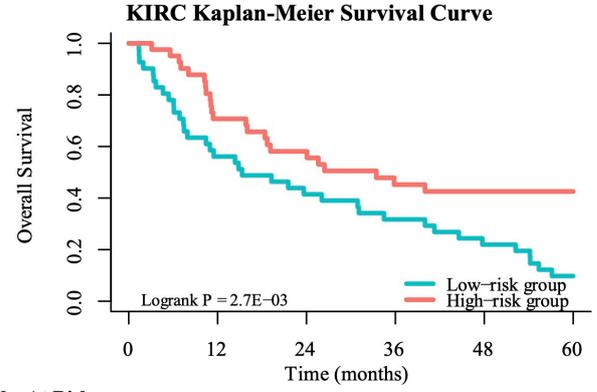
No. At Risk		0	12	24	36	48	60
Low-risk group	12	12	8	6	4	4	
High-risk group	21	16	12	11	10	7	



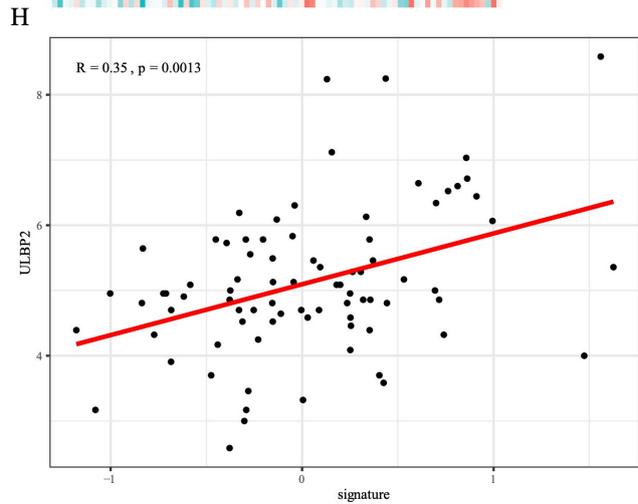
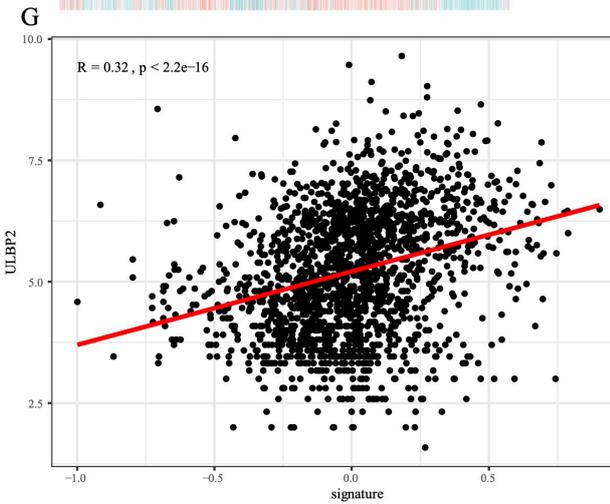
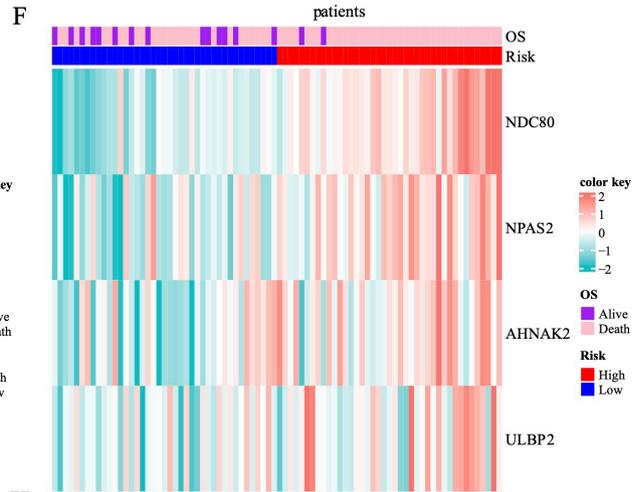
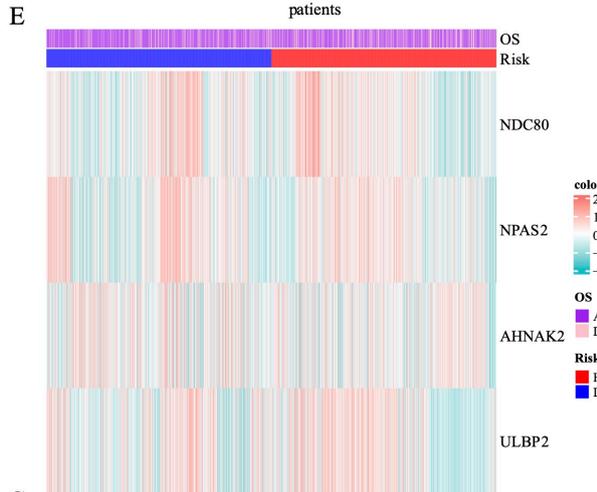
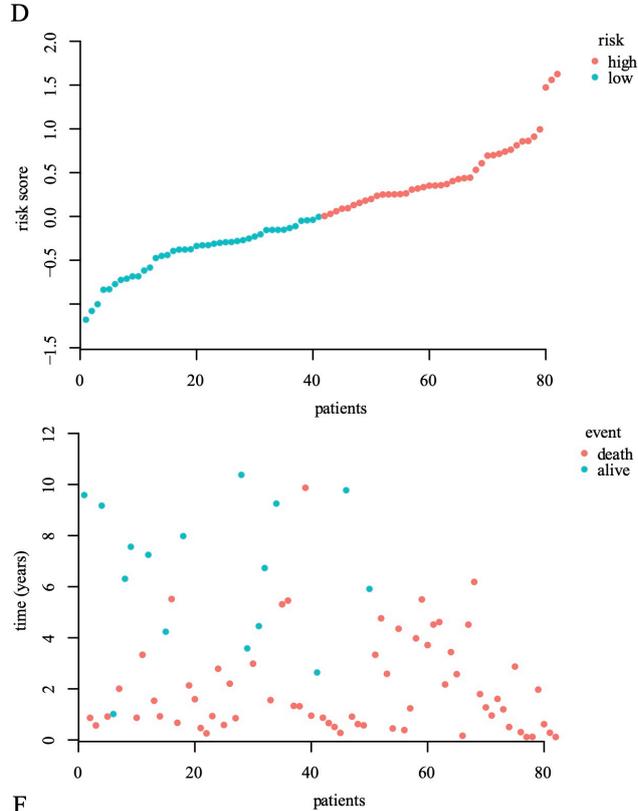
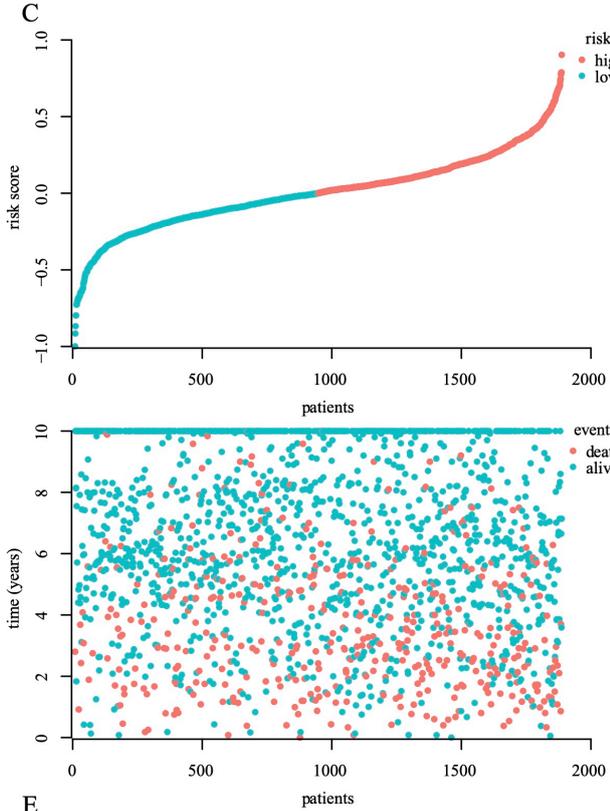




No. At Risk		0	12	24	36	48	60
Low-risk group	940	915	863	801	749	659	
High-risk group	939	909	834	731	643	534	



No. At Risk		0	12	24	36	48	60
Low-risk group	41	23	17	13	9	4	
High-risk group	41	29	23	17	15	13	



Supplementary Table 1 The primers used to amplify specific genes in CHCAMS and FUSCC cohorts

Gene symbol	Primer name	Sequence
NDC80	NDC80 F	TTC AGT TTC CAG CGG TGG TG
	NDC80 R	TCC GGG ATC CAT GTC CAC TA
NPAS2	NPAS2 F	CGT GTT GGA AAA GGT CAT CGG
	NPAS2 R	TCC AGT CTT GCT GAA TGT CAC
AHNAK2	AHNAK2 F	GTG CAG AAA CGG AAG ATG ACC
	AHNAK2 R	GCC TCA GTC GTG TAT TCG TAG A
ULBP2	ULBP2 F	AGC AAC TGC GTG ACA TTC AG
	ULBP2 R	GCC ATC CTA TAC AGT CTC CCA

CHCAMS, Cancer Hospital Chinese Academy of Medical Sciences; FUSCC, Fudan University Shanghai Cancer Center; NDC80, NDC80 kinetochore complex component; NPAS2, neuronal PAS domain protein 2; AHNAK2, AHNAK nucleoprotein 2; ULBP2, UL16 binding protein 2;

Supplementary Table 4 Univariate Cox regression for overall survival in CHCAMS and FUSCC cohorts.

Characteristics	CHCAMS		FUSCC	
	HR (95% CI)	p value	HR (95% CI)	p value
Age		0.001		0.33
<60	1		1	
≥60	3.049 (1.569-5.923)		0.648 (0.272-1.548)	
Gender		0.004		0.57
Female	1		1	
Male	2.570 (1.356-4.873)		0.768 (0.310-1.900)	
Primary site		\		0.04
Left			1	
Right			0.349 (0.130-0.936)	
T stage		0.37		0.72
T0 and T1	1		\	
T2	1.191 (0.814-1.741)	0.37	\	
T3	2.382 (0.407-3.482)	0.36	1	
T4	3.573 (0.271-5.223)	0.40	1.165 (0.511-2.655)	
TX			\	
N stage		0.04		\
N0	1			
N1	1.740 (0.837-3.616)	0.13		
N2	0.546 (0.237-1.258)	0.16		
N3				
NX				
M stage		\		\
M0				
M1				
MX				
Risk group		<0.001		0.006
Low risk	1		1	
High risk	3.062 (1.536-6.104)		2.958 (1.312-6.669)	

CHCAMS, Cancer Hospital Chinese Academy of Medical Sciences; FUSCC, Fudan University Shanghai Cancer Center; HR, hazard ratio; CI, confidence interval;

Supplementary Table 5 Prediction performance of ROC analysis in the training and validation cohorts

Characteristics	TCGA-LUAD			Validation cohorts (signature)				
	signature	TNM system	nomogram	GSE30219	GSE50081	GSE39582	CHCAMS	FUSCC
C-index	0.646	0.666	0.705	0.796	0.648	0.642	0.783	0.685
95% CI	0.597-0.759	0.573-0.750	0.621-0.789	0.700-0.890	0.528-0.747	0.467-0.766	0.696-0.869	0.591-0.770
Sensitivity	0.835	0.794	0.758	0.824	0.874	0.838	0.600	0.615
Specificity	0.528	0.600	0.660	0.722	0.422	0.583	0.878	0.860
Best cutoff	8.716	\	62.03	3.163	2.583	3.420	1.722	0.644

ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma; TNM, tumor–node–metastasis; CHCAMS, Cancer Hospital Chinese Academy of Medical Sciences; FUSCC, Fudan University Shanghai Cancer Center; CI, confidence interval