

Table S1 Primers for qPCR used in the current study

Primer	Sequence
CP F	CTTCACAAATCGAAAGGAGAGAG
CP R	TGGGTCCACAGCAGAATAATAC
EREG F	GTGATTCCATCATGTATCCCAGG
EREG R	GCCATTCATGTCAGAGCTACACT
PADI1 F	AGGTCTTCATGGTCTACAACCG
PADI1 R	CATCAGTGTCTAGCGGCCAA
FAM83A F	ACCGTCAAGCACACAACATCA
FAM83A R	CCAGGAGCACACAAACGAACAC
DLGAP5 F	AGGAAAGGTGCCAAGTAAAGGA
DLGAP5 R	TGTAAGTGGGTGTCAAAAAGC
GALNT5 F	GCGGATAGGATTCAGAGTTCAG
GALNT5 R	GCTTGTTAGGAGTCACAGGGAG
LAMA3 F	TGTTAATCGGGCAACACAAAGC
LAMA3 R	CTGGAAAAGTCACCTGAAGGCA
MET F	TCAGTGAGAAGGCTAAAGGAAAC
MET R	GCATGGACATACTTAATGGGGTA
Internal reference GAPDH F	CCCATCACCATCTTCCAGG
Internal reference GAPDH R	CATCAGGCCACAGTTTCCC

qPCR, quantitative polymerase chain reaction.

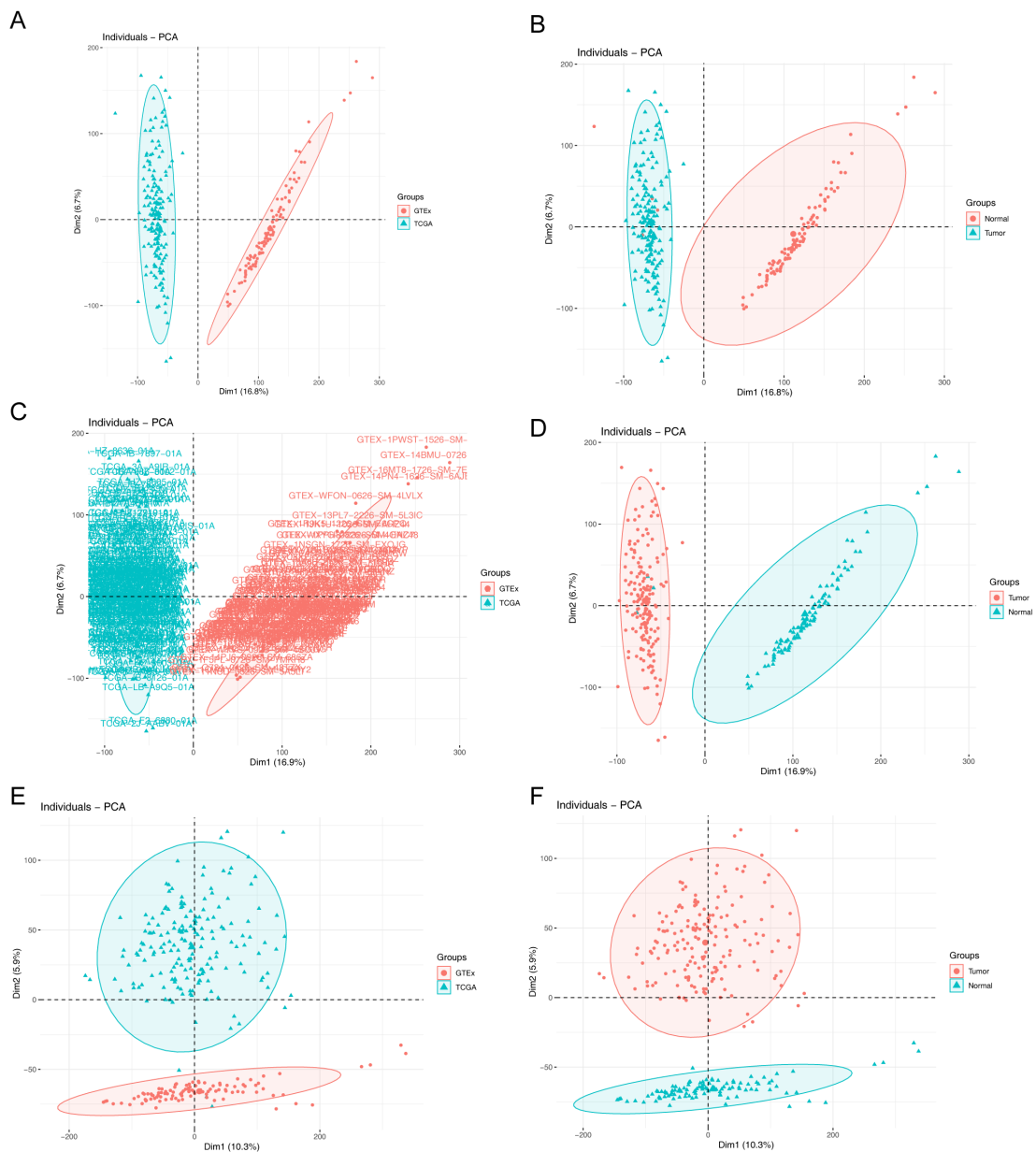


Figure S1 The distribution of TCGA and GTEx samples. (A-D) The distribution of TCGA and GTEx samples before correction. (E,F) The distribution of TCGA and GTEx samples after correction. PCA, principal component analysis; TCGA, The Cancer Genome Atlas.

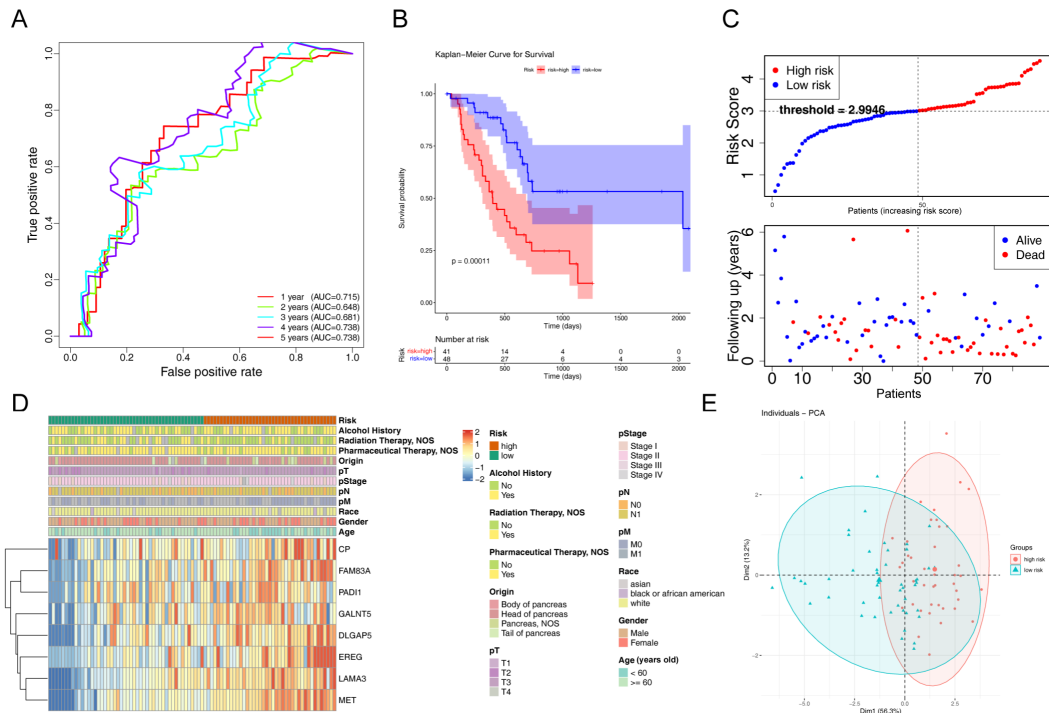


Figure S2 The validation results of the internal sets. (A) ROC curves for 1- to 5-year survival in the internal sets. (B) K-M curves of the high- and low-risk groups in the internal sets. (C,D) The distribution of the clinicopathological variables and eight model genes in the high- and low-risk groups. (E) PCA of the high- and low-risk groups in the internal sets. AUC, area under the curve; NOS, not otherwise specified; ROC, receiver operating characteristic; K-M, Kaplan-Meier; PCA, principal component analysis.

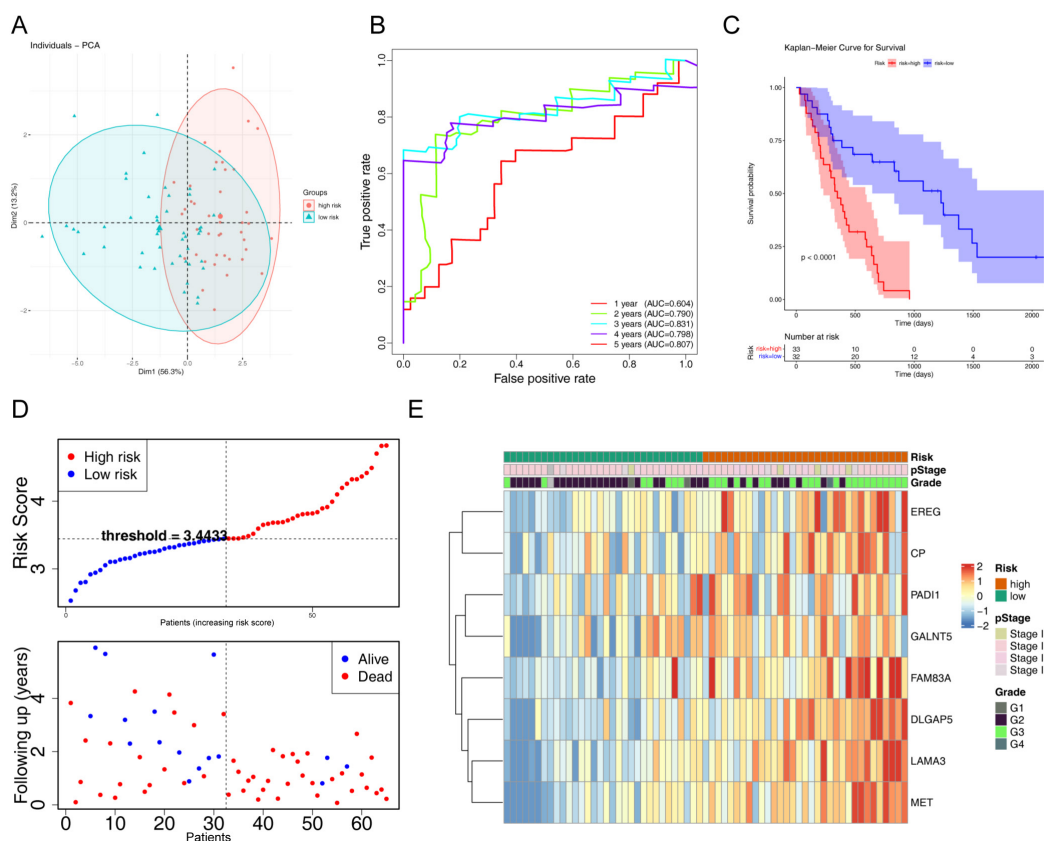


Figure S3 The validation results of the external sets (GSE62452). (A) PCA of the high- and low-risk groups in the external sets (GSE62452). (B) ROC curves for 1- to 5-year survival in the external sets (GSE62452). (C) K-M curves of the high- and low-risk groups in the external sets (GSE62452). (D,E) The distribution of the clinicopathological variables and eight model genes in the high- and low- risk groups. PCA, principal component analysis; AUC, area under the curve; ROC, receiver operating characteristic; K-M, Kaplan-Meier.

Table S2 Relative mRNA expression of 8 model genes in PAAD cells

Genes	HPDE6-C7	sw1990	panc-1	bx-pc-3	f value	P value
<i>CP</i>	1.0018±0.0753	4.7948±1.2983	4.8458±1.7937	6.5634±0.3579	11.51	0.0067
<i>EREG</i>	1.0005±0.0389	2.0977±0.4727	7.9414±0.2436	3.3860±1.4599	41.92	0.0002
<i>PADI1</i>	1.0035±0.1017	4.8502±0.0976	0.3584±0.0593	2.8659±0.1221	1058	<0.0001
<i>FAM83A</i>	1.0006±0.0425	34.4236±1.8429	55.1464±13.7139	92.5007±5.6939	85.35	<0.0001
<i>DLGAP5</i>	1.0121±0.1848	2.6225±0.5780	1.1783±0.1618	3.7211±1.3538	7.334	0.0197
<i>GALNT5</i>	1.0001±0.0208	5.8808±0.4615	10.4284±0.3443	4.4470±0.2005	372.1	<0.0001
<i>LAMA3</i>	1.0004±0.0327	8.1477±0.2953	2.6731±0.7056	7.8772±0.0667	286.4	<0.0001
<i>MET</i>	1.0007±0.0460	2.2837±0.7986	2.2844±1.5057	2.1386±0.0360	1.897	0.2312

PAAD, pancreatic adenocarcinoma.