Figure S1. The entire analytical process of the study.

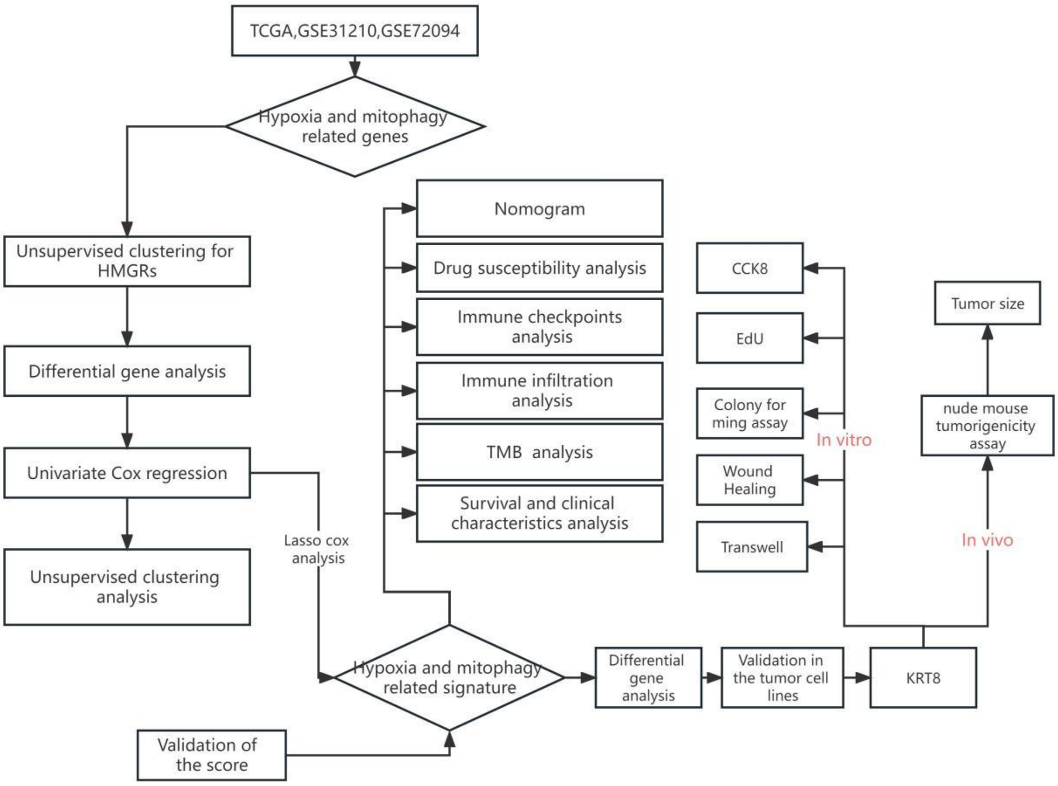

Figure S2

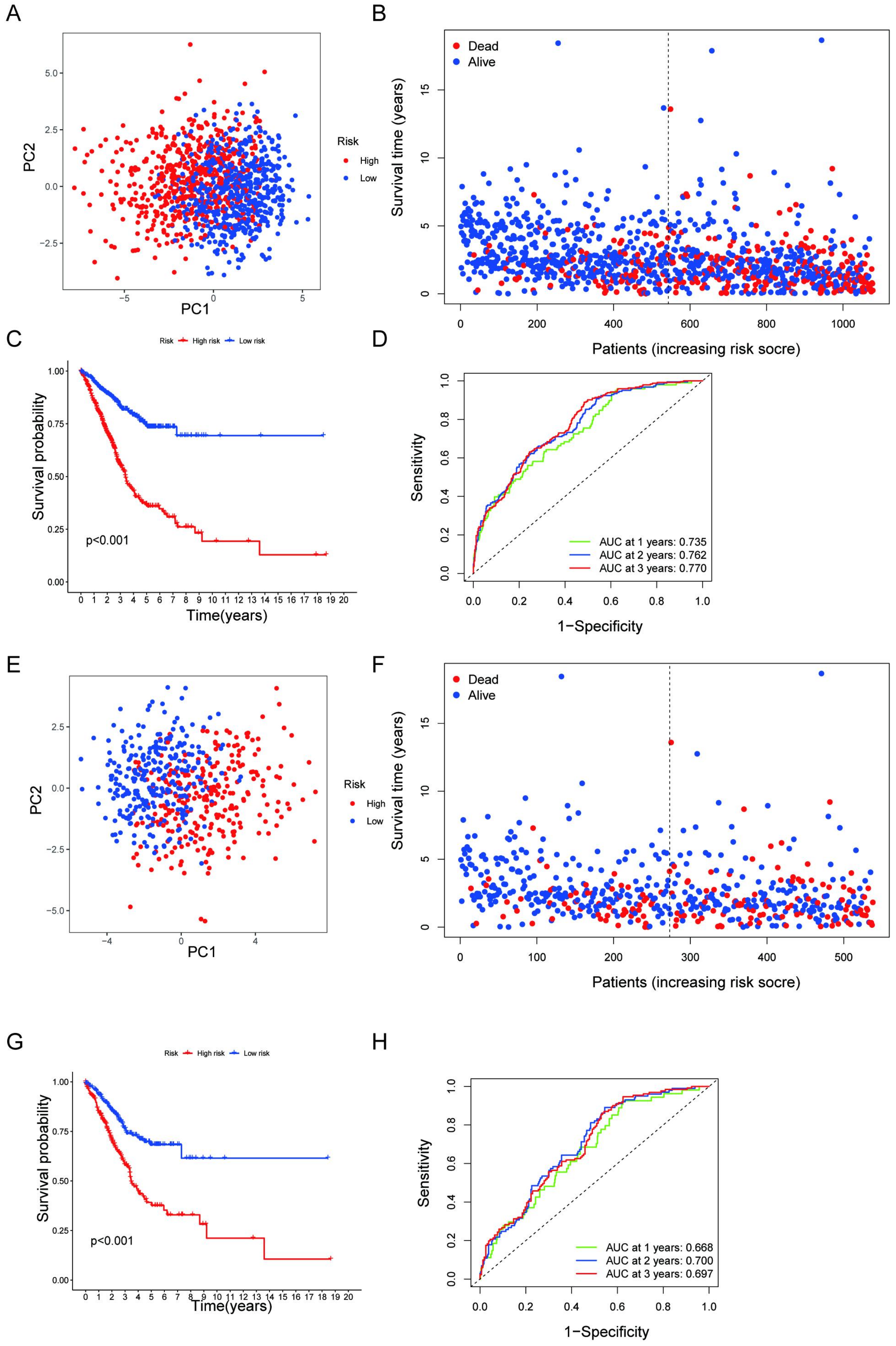

Figure S2: (A) PCA analysis demonstrating significant differences between high-risk and low-risk patients in the test cohort. (B, C) Distribution of OS status and OS of patients between high-risk and low-risk groups, with patients in the high-risk group showing higher score values and mortality in the test cohort. (D) Time-independent ROC analysis of the risk score for predicting OS, with the area under the curve for 1, 2, and 3 years reaching 0.735, 0.762, and 0.770, respectively, in the test cohort. (E) PCA analysis showing significant differences between high-risk and low-risk patients in the entire cohort. (F, G) Distribution of OS status and OS of patients between high-risk and low-risk groups, with patients in the high-risk group having higher score values and mortality in the entire cohort. (H) Time-independent ROC analysis of the risk score for predicting OS, with the area under the curve for 1, 2, and 3 years reaching 0.668, 0.700, and 0.697, respectively, in the entire cohort.

Table S1. Summary of hypoxia-related genes.

Hypoxia-related genes				
ACKR3	CSRP2	HDLBP	NDRG1	S100A4
ADM	CXCR4	HEXA	NDST1	SAP30
ADORA2B	DCN	HK1	NDST2	SCARB1
AK4	DDIT3	HK2	NEDD4L	SDC2
AKAP12	DDIT4	HMOX1	NFIL3	SDC3
ALDOA	DPYSL4	HOXB9	NOCT	SDC4
ALDOB	DTNA	HS3ST1	NR3C1	SELENBP1
ALDOC	DUSP1	HSPA5	P4HA1	SERPINE1
AMPD3	EDN2	IDS	P4HA2	SIAH2
ANGPTL4	EFNA1	IER3	PAM	SLC25A1
ANKZF1	EFNA3	IGFBP1	PCK1	SLC2A1
ANXA2	EGFR	IGFBP3	PDGFB	SLC2A3
ATF3	ENO1	IL6	PDK1	SLC2A5
ATP7A	ENO2	ILVBL	PDK3	SLC37A4
B3GALT6	ENO3	INHA	PFKFB3	SLC6A6
B4GALNT2	ERO1A	IRS2	PFKL	SRPX
BCAN	ERRFI1	ISG20	PFKP	STBD1
BCL2	ETS1	JMJD6	PGAM2	STC1
BGN	EXT1	JUN	PGF	STC2
BHLHE40	F3	KDELR3	PGK1	SULT2B1
BNIP3L	FAM162A	KDM3A	PGM1	TES
BRS3	FBP1	KIF5A	PGM2	TGFB3
BTG1	FOS	KLF6	PHKG1	TGFBI
CA12	FOSL2	KLF7	PIM1	TGM2
CASP6	FOXO3	KLHL24	PKLR	TIPARP
CAV1	GAA	LALBA	PKP1	TKTL1

CAVIN1
CAVIN3
CCN1
CCN2
CCN5
CCNG2
CDKN1A
CDKN1B
CDKN1C
CHST2
CHST3
CITED2
COL5A1
CP
GALK1
GAPDH
GAPDHS
GBE1
GCK
GCNT2
GLRX
GPC1
GPC3
GPC4
GPI
GRHPR
GYS1
HAS1
LARGE1
LDHA
LDHC
LOX
LXN
MAFF
MAP3K1
MIF
MT1E
MT2A
MXI1
MYH9
NAGK
NCAN
PLAC8
PLAUR
PLIN2
PNRC1
PPARGC1A
PPFIA4
PPP1R15A
PPP1R3C
PRDX5
PRKCA
PYGM
RBPJ
RORA
RRAGD
TMEM45A
TNFAIP3
TPBG
TPD52
TPI1
TPST2
UGP2
VEGFA
VHL
VLDLR
WSB1
XPNPEP1
ZFP36
ZNF292

Table S2. Summary of mitophagy-related genes.

mitophagy-related genes

ATG12
ATG5
CSNK2A1
CSNK2A2
CSNK2B
FUNDC1
MAP1LC3A
MAP1LC3B
MFN1
MFN2
MTERF3
PGAM5
PINK1
PRKN
RPS27A
SQSTM1
SRC
TOMM20
TOMM22
TOMM40
TOMM5
TOMM6
TOMM7
TOMM70
UBA52
UBB
UBC
ULK1
VDAC1

Table S3. Composition and correlation coefficients of the model genes.

Gene	Coef
RSPO2	0.024492365
SCARNA17	-0.056782396
IGLC1	-0.03907669
E2F7	0.039422522
ATP8A1	-0.012155166
PMEPA1	0.021919653
RRM1	0.025439152
KRT8	0.055842854
RHOV	0.100350605
DDIT4	0.028346796
AMT	-0.077985661
ABCD1	0.062979162
LINC00324	-0.038423804
CD99	0.190942904

IL27RA	-0.023125091
TXNDC11	-0.014783862
PSMB7	0.128662048
ANO1	0.010028674
C1orf105	0.021486414
MGAT5B	0.037014019
RSAD1	-0.026144302
IGFBP1	0.091480139
FJX1	0.088488225
SPAG8	-0.001316037
SARM1	-0.22639413
BCAP31	0.209184934
GALT	-0.051968202
ASCC1	0.312490847
TBC1D10C	-0.054093371
IKZF3	-0.002042239
CSNK1E	0.08868312

Table S4. Primers used in this study.

Gene	Forward primer	Reverse primer
RSPO2	GACGCAGTAAGCGAGCTAGTT	ACATCGGCTACACCCATTGTC
E2F7	AGGCAGCCCAGACTAGATTTT	GCTGGCAGCACTAATGAGCA
KRT8	CAGAAGTCCTACAAGGTGTCCA	CTCTGGTTGACCGTAACTGCG
RHOV	CCTCATCGTCAGCTACACCTG	GAACGAAGTCGGTCAAAATCCT
DDIT4	TGAGGATGAACACTTGTGTGC	CCAACTGGCTAGGCATCAGC
C1orf105	ATTCACTACAGACTGCCCATTCT	CGTTGTCTTGCCTATTGGTTCC
SPAG8	AGACCAACGAGTCTACGGAGG	GACCTGGGACTGTCATCTGAA