

Table S1 List of genes that were related to cellular senescence

MARCH5
AAK1
ABI3
ACLY
ADCK5
AGT
AKR1B1
AKT1
ALOX15B
AR
ARPC1B
ASF1A
ASPH
ATF7IP
ATM
AURKA
AXL
BAG3
BCL6
BHLHE40
BLK
BLVRA
BMI1
BRAF
BRCA1
BRD7
BTG3
SELENOH
CAV1
CBX7
CBX8
CCND1
CDK1
CDK18
CDK2AP1
CDK4
CDK6
CDKN1A
CDKN1B
CDKN1C
CDKN2A
CDKN2B
CEBPB
CENPA
CHEK1
CKB
CPEB1
CSNK1A1
CSNK2A1
CXCL1
CCN1
DDB2
DEK
DGCR8
DHCR24
DHX9
DLX2
DPY30
DUSP16
DUSP3
E2F1
EHF
ENDOG
EPHA3
ERRFI1
ETS1
ETS2
EWSR1
EZH2
FASTK
FBXO31
FOS
FOXM1
FOXO3
FXR1
G6PD
GAPDH
GATA4
GKN1
GLB1
GNG11
GRK6
HDAC1
HDAC4
HIVEP1
HJURP
HK3
HMGB1
HRAS
HSPA5
HSPB2
ID1
ID4
IFNG
IGFBP1
IGFBP3
IGFBP5
IGFBP6
IL1A
CXCL8
ING1
ING2
IRF3
IRF5
IRF7
ITGB4
ITPK1
ITPKB
ITSN2
KCNJ12
KDM4A
KDM5B
CIP2A
KL
KSR2
LATS1
LEO1
LGALS3
LIMA1
LIMK1
MAD2L1
MAGEA2
MAGOH
MAGOHB
MAP2K1
MAP2K2
MAP2K3
MAP2K6
MAP2K7
MAP3K6
MAP3K7
MAP4K1
MAPK12
MAPK14
MAST1
MATK

Table S1 (continued)

Table S1 (continued)

MCL1
MCRS1
MDH1
MECP2
MMP9
MOB3A
MORC3
MORF4
MVK
MXD4
MYC
MYLK
NADK
NANOG
NDRG1
NEK1
NEK4
NEK6
NFE2L2
NINJ1
NOTCH3
NOX4
NR2E1
NTN4
NUAK1
OTX2
P3H1
PAK4
PATZ1
PBRM1
PCGF2
PDCD10
PDIK1L
PDPK1
PDZD2
PEBP1
PEX19
PIAS4
PIK3C2A
PIK3R5
PIM1
PKM
PLA2R1
PML
PMVK
PNPT1
POT1
POU5F1
PPM1B
PPM1D
PRKCD
PRKCH
PRMT6
PROX1
PRPF19
PSMB5
PSMD14
CAVIN1
PTTG1
RAD21
RAF1
RB1
RBP2
RBX1
RNASEL
RPS6KA6
RSL1D1
RUNX1
RUVBL2
SENP1
SENP2
SENP7
SERPINE1
SFN
SGK1
SIK1
SIN3B
SIRT1
SIRT6
SIX1
SLC13A3
SLC16A7
SMG1
SMURF2
SNAI1
SOCS1
SOD1
SORBS2
SOX2
SOX5
SP1
SPIN1
SPOP
SRC
SREBF1
SRSF1
STAT5B
STK32C
STK40
SUPT5H
SYK
TACC3
TBX2
TERC
TERF2
TERT
TFAP4
TFDP1
TGFB111
TLR3
TMSB4X
TNFSF13
TNFSF15
TOP1
TP53
TP63
TPR
TRIM28
TRPM8
TXN
TXNIP
TYK2
UBTD1
USP1
VEGFA
VENTX
WNT16
WNT2
WRN
WT1
WWP1
XAF1
YAP1
YPEL3
ZFP36
ZMAT3
ZNF148

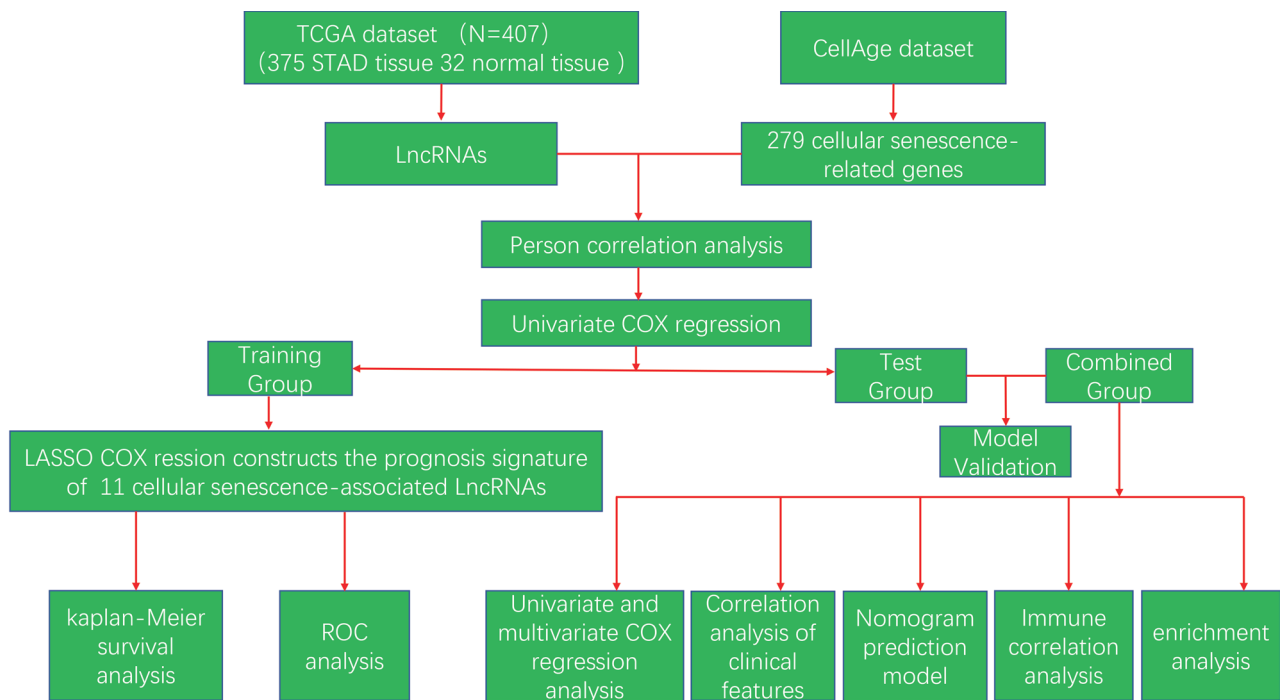


Figure S1 The detailed process of this analysis. TCGA, The Cancer Genome Atlas; STAD, stomach adenocarcinoma; lncRNAs, long non-coding RNAs; LASSO, least absolute shrinkage and selection operator; ROC, receiver operating characteristic.

Table S2 Through GSEA enrichment analysis, Screening of classical pathways enriched in high-risk groups

Pathway	Size	ES	NES	NOM P value	FDR q value	Leading edge
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	102	0.58	2.11	0.004	0.002	Tags =34%, list =12%, signal =39%
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	46	0.76	2.05	0.002	0.004	Tags =63%, list =11%, signal =71%
KEGG_AUTOIMMUNE_THYROID_DISEASE	50	0.69	2.02	0.002	0.006	Tags =50%, list =19%, signal =62%
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	132	0.54	1.95	0.006	0.01	Tags =43%, list =18%, signal =53%
KEGG_JAK_STAT_SIGNALING_PATHWAY	155	0.5	1.92	0.002	0.013	Tags =37%, list =18%, signal =45%
KEGG_MAPK_SIGNALING_PATHWAY	267	0.48	1.92	0	0.013	Tags =30%, list =13%, signal =34%
KEGG_RENAL_CELL_CARCINOMA	70	0.55	1.88	0.004	0.016	Tags =39%, list =16%, signal =46%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	108	0.56	1.87	0.006	0.017	Tags =37%, list =12%, signal =42%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	75	0.59	1.8	0.02	0.027	Tags =43%, list =13%, signal =49%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	96	0.52	1.79	0.01	0.029	Tags =34%, list =12%, signal =39%
KEGG_MELANOMA	71	0.5	1.77	0.008	0.033	Tags =30%, list =12%, signal =33%
KEGG_BASAL_CELL_CARCINOMA	55	0.54	1.76	0.013	0.033	Tags =29%, list =7%, signal =31%
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	79	0.48	1.75	0.004	0.034	Tags =30%, list =12%, signal =34%

GSEA, gene set enrichment analysis; KEGG, Kyoto Encyclopedia of Genes and Genomes; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table S3 GSEA enrichment analysis for screening the enriched classical pathways in the low-risk groups

Pathway	Size	ES	NES	NOM P value	FDR q value	Leading edge
KEGG_SPLICEOSOME	127	-0.71	-2.15	0.002	0.006	Tags =72%, list =19%, signal =88%
KEGG_PYRIMIDINE_METABOLISM	98	-0.6	-2.02	0.002	0.015	Tags =58%, list =16%, signal =69%
KEGG_RNA_POLYMERASE	29	-0.7	-1.98	0.002	0.02	Tags =62%, list =16%, signal =74%
KEGG_BASE_EXCISION_REPAIR	35	-0.7	-1.98	0.006	0.017	Tags =57%, list =15%, signal =67%
KEGG_HOMOLOGOUS_RECOMBINATION	28	-0.72	-1.95	0.004	0.019	Tags =71%, list =20%, signal =89%
KEGG_DNA_REPLICATION	36	-0.78	-1.92	0.004	0.022	Tags =89%, list =19%, signal =110%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-0.72	-1.89	0.002	0.028	Tags =71%, list =17%, signal =85%
KEGG_CELL_CYCLE	125	-0.59	-1.89	0.014	0.026	Tags =53%, list =14%, signal =61%
KEGG_MISMATCH_REPAIR	23	-0.74	-1.83	0.01	0.039	Tags =78%, list =16%, signal =93%
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	-0.75	-1.82	0.002	0.038	Tags =80%, list =20%, signal =99%
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	-0.63	-1.82	0.014	0.035	Tags =64%, list =22%, signal =82%
KEGG_RNA_DEGRADATION	59	-0.59	-1.78	0.018	0.045	Tags =47%, list =15%, signal =56%
KEGG_PROTEASOME	46	-0.67	-1.77	0.026	0.046	Tags =63%, list =20%, signal =78%

GSEA, gene set enrichment analysis; KEGG, Kyoto Encyclopedia of Genes and Genomes; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.