

Supplementary Table 1

279 senescence-related genes list collected from CELLAGE dataset

[\(\[genomics.senescence.info/download.html#cellage\]\(http://genomics.senescence.info/download.html#cellage\)\)](http://genomics.senescence.info/download.html#cellage)

ACLY	CPEB1	ID1	MAPK14	PPM1B
AAK1	CSNK1A1	ID4	MAST1	PPM1D
ABI3	CTNNAL1	IGFBP1	MATK	PRMT6
ADCK5	CSNK2A1	IFNG	MCL1	PRKCH
AKR1B1	CXCL1	IGFBP3	MDH1	PRKCD
AGT	DDB2	IGFBP6	MCRS1	PROX1
AKT1	CYR61	IGFBP5	MECP2	PRPF19
ALOX15B	DEK	IL1A	MOB3A	PSMB5
AR	DGCR8	IL8	MMP9	PTRF
ARPC1B	DHCR24	ING1	MORC3	PTTG1
ASF1A	DLX2	ING2	MORF4	PSMD14
ASPH	DHX9	IRF3	MXD4	RAD21
ATF7IP	DPY30	IRF5	MVK	RAF1
ATM	DUSP3	IRF7	MYC	RB1
AURKA	DUSP16	ITPK1	MYLK	RBP2
AXL	E2F1	ITGB4	NADK	RBX1
BAG3	EHF	ITPKB	NANOG	RNASEL
BHLHE40	ENDOG	ITSN2	NDRG1	RPS6KA6
BCL6	EPHA3	KCNJ12	NEK1	RSL1D1
BLK	ERRFI1	KDM4A	NEK4	RUNX1
BLVRA	ETS1	KDM5B	NEK6	RUVBL2
BMI1	ETS2	KIAA1524	NFE2L2	SENP1
BRAF	EWSR1	KL	NINJ1	SENP2
BRD7	FASTK	KSR2	NOTCH3	SENP7
BRCA1	EZH2	LATS1	NOX4	SERPINE1
BTG3	FBXO31	LEO1	NR2E1	SFN
C11orf31	FOXM1	LGALS3	NTN4	SIK1
CAV1	FOS	LIMA1	NUAK1	SGK1
CBX7	FOXO3	LIMK1	OTX2	SIN3B
CBX8	FXR1	MAGEA2	P3H1	SIRT1
CCND1	G6PD	MAGOH	PATZ1	SIRT6
CDK1	GAPDH	MAD2L1	PAK4	SIX1
CDK18	GKN1	MAGOHB	PBRM1	SLC13A3
CDK2AP1	GATA4	MAP2K1	PCGF2	SLC16A7
CDK6	GNG11	MAP2K3	PDCD10	SMARCA4
CDK4	GLB1	MAP2K2	PDIK1L	SMG1
CDKN1A	GRK6	MAP2K6	PDZD2	SMARCB1

CDKN1C	HDAC4	MAP3K6	PDPK1	SMURF2
CDKN1B	HDAC1	MAP2K7	PEBP1	SNAI1
CDKN2A	HEPACAM	MAP4K1	PEX19	SOCS1
CDKN2AIP	HJURP	MAP3K7	PIAS4	SOD1
CDKN2B	HIVEP1	MAPK12	PIK3R5	SORBS2
CENPA	HK3	MAPKAPK5	PIK3C2A	SOX2
CEBPB	HMGB1	5-Mar	PIM1	SPIN1
CHEK1	HRAS	TPR	PLA2R1	SOX5
CKB	HSPA5	TP53	PKM	SP1
USP1	HSPB2	TRIM28	PML	SPOP
VEGFA	TFAP4	TRPM8	PNPT1	SRC
WNT16	TFDP1	TXN	PMVK	SREBF1
WNT2	TGFB1I1	TXNIP	POT1	SRSF1
WRN	TLR3	UBTD1	POU5F1	STAT5B
WT1	TMSB4X	TYK2	ZFP36	STK32C
XAF1	TNFSF13	VENTX	ZMAT3	STK40
WWP1	TNFSF15	TBX2	ZNF148	SUPT5H
YAP1	TOP1	TERF2	TACC3	SYK
YPEL3	TP63	TERT	TERC	

Supplementary Table 2 Complete baseline information of the 4 extracted datasets:

Parameters	TCGA (n=406)	GSE13507 (n=165)	GSE32894 (n=221)	GSE31684 (n=90)
Cohort				
Survival status				
Alive	177 (43.7%)	96 (58.1%)	196 (88.8%)	63 (70%)
Dead	229 (56.3%)	69 (41.8%)	25 (11.1%)	27 (30%)
Follow-up(day)	803.53±828.72	1451.45±1131.13	1196.98±766.65	1471±890.40
Age	68.10 ± 11.46	65.18 ± 12.34	69.43 ± 11.94	69.14 ± 12.20
Gender				
Female	105 (26.2%)	30 (18.1%)	61 (27.2%)	25 (27.7%)
Male	301 (73.7%)	135 (81.8%)	160 (72.7%)	68 (62.3%)
Grade				
Low	19 (5.0%)	105 (63.6%)	-	6 (93.4%)
High	384 (94.2%)	60 (36.3%)	-	84 (6.6%)
Unknown	3 (0.8%)	0 (0.0%)	-	0 (0%)
Pathological Stage				
I	2 (0.5%)	-	-	-
II	129 (31.7%)	-	-	-
III	140 (34.2%)	-	-	-
IV	133 (33.1%)	-	-	-
Unknown	2 (0.5%)	-	-	-

T stage				
T0	1 (0.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Ta	0 (0.0%)	23 (13.9%)	108 (49.1%)	8 (0.0%)
T1	3 (0.7%)	81 (49.0%)	62 (28.1%)	19 (21.1%)
T2	120(29.1%)	31 (18.7%)	43 (19.1%)	52 (57.2%)
T3	193 (47.5%)	19 (11.5%)	7 (3.1%)	10 (11.1%)
T4	57 (14.3%)	11 (6.6%)	1 (0.4%)	1 (1.1%)
Unknown	32 (8.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
M stage				
M0	193 (47.7%)	158 (95.7%)	-	-
M1	11 (2.4%)	7 (4.2%)	-	-
Unknown	202 (49.8%)	0 (0.0%)	-	-
N stage				
N0	236 (58.0%)	149 (90.3%)	26 (12.0%)	-
N1	46 (11.4%)	8 (4.8%)	3 (1.3%)	-
N2	75 (18.4%)	6 (3.6%)	10 (4.4%)	-
N3	8 (2.0%)	1 (0.6%)	0 (0.0%)	-
Unknown	41 (10.2%)	1 (0.6%)	182 (82.1%)	-

TNM stage, tumor-node-metastasis grading criterion; TCGA, The Cancer Genome Atlas; ILMRS, immune micro environment and lipid metabolism risk score; BCa, bladder cancer.