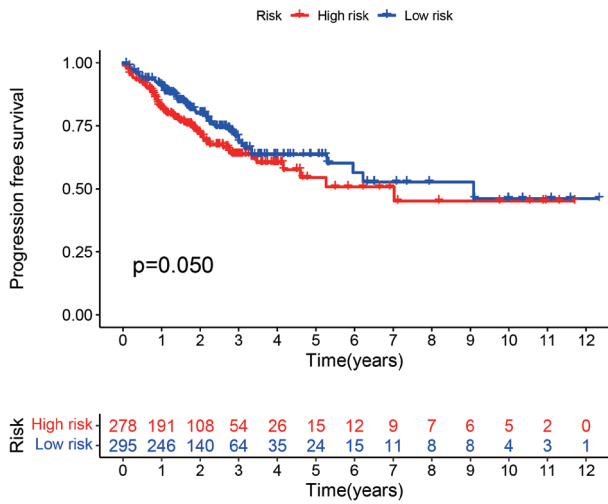


Table S1 Abnormal expression of senescence-related transcripts in tumor and normal tissues

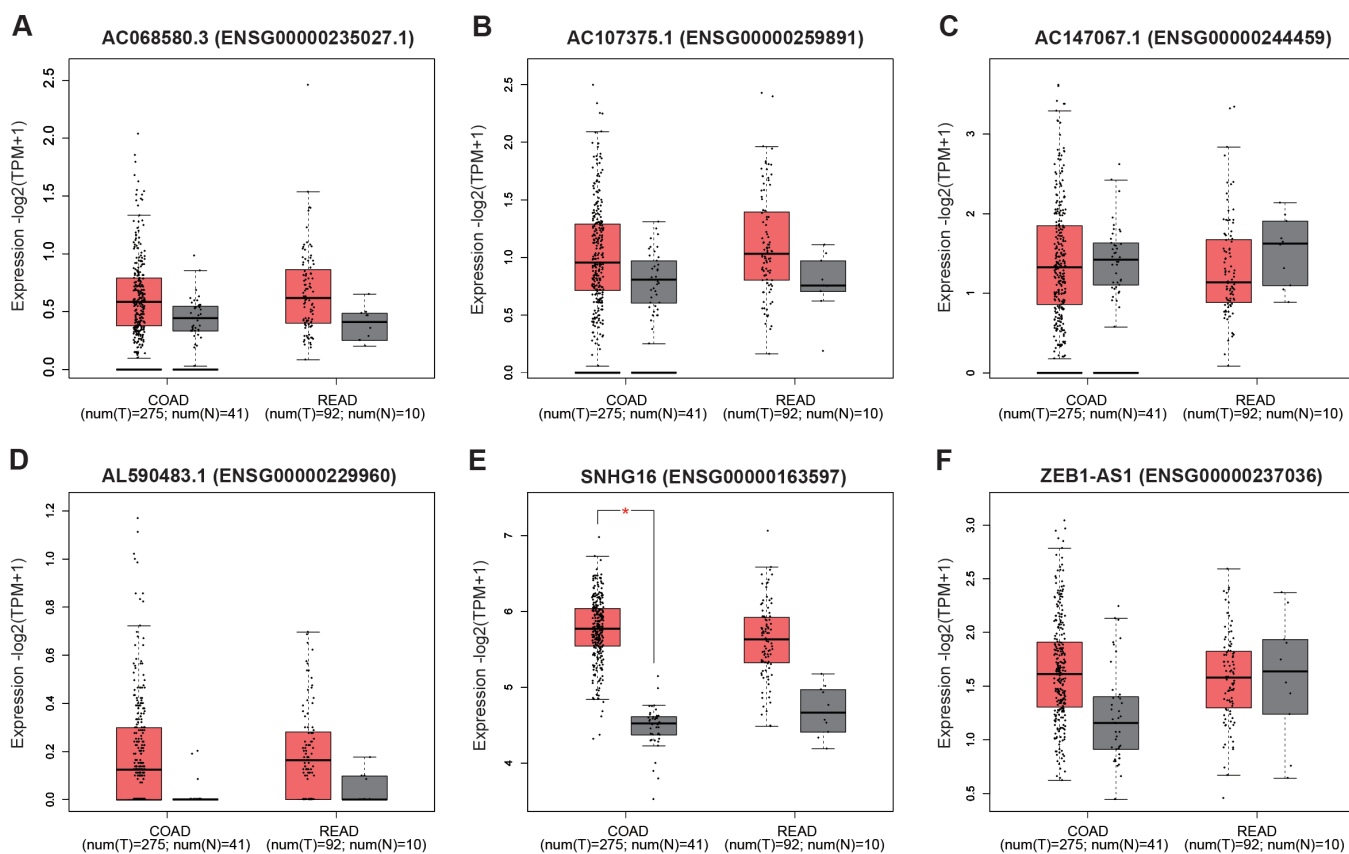
Gene	conMean	treatMean	logFC	pValue	fdR
MYLK	45.43049286	4.835150165	-3.232028356	1.60E-25	1.62E-24
CPEB1	0.402928334	0.046320615	-3.120796942	7.98E-29	2.23E-27
CDKN2B	32.37764714	3.990329208	-3.020418469	2.06E-30	1.13E-28
SGK1	25.31700027	4.163838381	-2.604120498	7.06E-22	3.71E-21
BLK	1.029332885	0.196936563	-2.385906734	4.56E-22	2.55E-21
HEPACAM	0.067705676	0.014976986	-2.176529439	2.58E-29	9.28E-28
CAV1	42.28390084	10.5726715	-1.999768514	2.15E-21	1.09E-20
SORBS2	5.663105863	1.523380725	-1.894316952	6.05E-15	1.71E-14
TLR3	5.301437431	1.450407288	-1.869925505	4.68E-28	7.86E-27
IGFBP6	28.20628039	7.76090572	-1.861719494	2.40E-25	2.32E-24
CBX7	8.159114235	2.515163023	-1.697760627	4.68E-28	7.86E-27
AR	0.492513069	0.161111414	-1.612103299	5.36E-17	1.69E-16
HSPB2	1.021621635	0.343481753	-1.572555617	6.15E-18	2.28E-17
TXNIP	322.4641176	122.5332253	-1.395965639	5.88E-25	4.94E-24
TGFB111	14.43172265	5.521799767	-1.386033039	3.37E-08	6.03E-08
CKB	590.5438782	231.3862979	-1.351740824	5.19E-17	1.66E-16
KL	0.796593584	0.313891708	-1.343576942	6.40E-22	3.43E-21
LIMA1	61.89995059	25.37560233	-1.28649619	2.47E-26	2.96E-25
MAP4K1	2.885565627	1.216850354	-1.245702384	2.16E-16	6.65E-16
SOX5	0.253704752	0.114198858	-1.151602321	4.44E-19	1.78E-18
EPHA3	1.387124029	0.637708422	-1.121127953	1.06E-09	1.99E-09
RNASEL	4.587609235	2.133236738	-1.104698431	5.62E-25	4.88E-24
GNG11	8.266570039	3.892514827	-1.086586317	6.15E-15	1.72E-14
LGALS3	696.0402706	335.7918113	-1.051603729	5.08E-22	2.78E-21
NDRG1	79.36151608	38.96538565	-1.026246491	9.78E-12	2.22E-11
RPS6KA6	1.869534325	0.923512447	-1.017475649	5.96E-16	1.81E-15
CDKN1A	106.8041535	52.85281501	-1.014915535	1.84E-18	7.14E-18
RSL1D1	18.31646357	36.74097013	1.004248737	1.73E-22	1.02E-21
PKM	76.27061373	153.3521255	1.007648949	2.96E-21	1.46E-20
TFDP1	23.21378549	47.2365147	1.024920718	4.13E-25	3.71E-24
ETS2	64.17043941	131.9216884	1.039701001	3.30E-17	1.11E-16
TRIM28	54.49911569	115.3215212	1.081357046	8.02E-27	1.12E-25
MAGOHB	1.82170582	3.866682047	1.085806136	3.40E-21	1.62E-20
STK32C	1.71506149	3.721296257	1.117544947	3.60E-10	7.15E-10
IFNG	0.153445475	0.334741148	1.125319804	0.000286479	0.000396663
RUVBL2	19.48998235	42.60548464	1.128306377	3.50E-25	3.26E-24
LIMK1	3.59932498	7.896085601	1.133411262	1.43E-25	1.50E-24
PNPT1	4.671970941	10.26929847	1.136234423	5.11E-24	3.68E-23
TACC3	5.017636157	11.1207995	1.148180745	9.05E-21	4.07E-20
UBTD1	2.300482882	5.537005343	1.267169193	6.77E-18	2.47E-17
BHLHE40	21.12079437	52.25496747	1.306904093	3.46E-20	1.48E-19
CHEK1	1.966428306	4.915463019	1.321749732	9.71E-25	7.65E-24
P3H1	1.78372751	4.463144372	1.323165235	2.01E-26	2.53E-25
CDK4	15.04297863	37.6590247	1.323905377	3.23E-27	4.79E-26
BRCA1	1.355655716	3.510378074	1.372635584	3.48E-23	2.19E-22
EZH2	3.315433688	8.820953632	1.411737034	3.04E-28	6.38E-27
PTTG1	8.478121627	22.87020411	1.431652673	1.75E-23	1.19E-22
FOXM1	5.200558059	14.32978034	1.462278146	8.87E-24	6.21E-23
NOTCH3	3.358027027	9.352483484	1.477735671	4.57E-17	1.48E-16
MMP9	8.783467414	24.50809334	1.480395767	1.40E-06	2.23E-06
MAD2L1	3.306140698	9.5602395	1.531898638	2.64E-23	1.71E-22
CENPA	2.2021113	6.483885238	1.557971168	4.61E-26	5.28E-25
RUNX1	1.856034906	5.497674539	1.566597659	3.40E-28	6.58E-27
TFAP4	1.376152371	4.156225451	1.594633697	2.24E-30	1.13E-28
CDK1	5.810577349	17.62087894	1.600532464	2.61E-23	1.71E-22
TNFSF15	0.796106263	2.415190295	1.601103948	9.52E-27	1.26E-25
CEBPB	11.47580922	36.32114263	1.6622137	5.63E-26	6.17E-25
VEGFA	4.248134569	13.5360475	1.671905164	7.12E-29	2.23E-27
AURKA	6.110931647	19.71822997	1.690065803	1.10E-27	1.74E-26
CCND1	15.33640988	53.10542678	1.791898496	2.20E-30	1.13E-28
HJURP	2.111342704	7.444368887	1.817988777	5.40E-30	2.27E-28
TERT	0.176508797	0.62915223	1.833669048	1.22E-12	2.94E-12
CBX8	1.153757884	4.172307006	1.854504811	4.45E-31	5.61E-29
SNAI1	1.1937992	4.346164595	1.86418262	6.73E-25	5.47E-24
E2F1	3.845043569	15.03910215	1.967646589	1.09E-28	2.75E-27
PROX1	1.216173559	5.064445645	2.058055231	1.89E-18	7.21E-18
MYC	25.8873938	108.7104266	2.070168683	2.96E-28	6.38E-27
SERPINE1	3.787122227	16.47001324	2.120667825	1.47E-17	5.08E-17
AGT	2.876721755	14.71928098	2.355209608	1.09E-20	4.81E-20
IL1A	0.222925151	1.485337668	2.736159641	1.38E-16	4.31E-16
CXCL1	8.824251016	70.13724454	2.990635017	2.44E-24	1.81E-23
CDKN2A	0.292369631	2.457387506	3.071260004	5.61E-21	2.57E-20
NOX4	0.057027145	0.497853395	3.126000245	1.86E-22	1.07E-21
TERC	0.019464609	0.209878939	3.430632144	0.000147604	0.000206645
SIX1	0.013375334	0.190589077	3.832818599	5.18E-23	3.19E-22
VENTX	0.133137618	2.004532996	3.912276002	1.90E-10	3.87E-10
IGFBP1	0.041727639	0.633491403	3.924249828	3.72E-05	5.48E-05
SLC13A3	0.08482972	1.771167386	4.383986957	1.83E-14	5.00E-14
WT1	0.017495718	0.600501925	5.101095062	7.73E-18	2.78E-17
WNT2	0.070308335	3.466901798	5.62380744	2.62E-32	6.59E-30



**Figure S1** Progression-free survival (PFS) analysis by the SenALSig model using the TCGA-CRC samples. The P value was generated by the log-rank test.

**Table S2** The qPCR primer sequences of the six lncRNAs in the SenALSig model

LncRNA	Forward	Reverse
AC068580.3	CCATTGGGTTAAGATACGAGAGTC	AGGGAGGGGACACCCAAAT
SNHG16	AAGACATGGCCACTCCAGTC	AGGCTGACTGCACCATCATC
AL590483.1	AGACTCCAAATACCTTGAGCATGT	AGGGGCCAGATGAAATGATCC
ZEB1-AS1	GGCTGATTCTCCCTGTACCC	GGTTCTACGCGAGGAAGAGG
AC107375.1	ACTTCTCTCGCCCTGAGGAT	GTTGGCTTCCTGCACACAAG
AC147067.1	AGAGGATAGGCAGGTGCAGA	AGTCGGGGTCGATGGTTCTA



**Figure S2** The online tool GEPIA2 ([gepia2.cancer-pku.cn](http://gepia2.cancer-pku.cn)) is used to analyze the different expressions of the six lncRNAs in the CRC data set of TCGA. COAD, colon adenocarcinoma; READ, rectum adenocarcinoma; num, sample size number; T, tumor tissues; N, normal tissues. \*, P value <0.05.