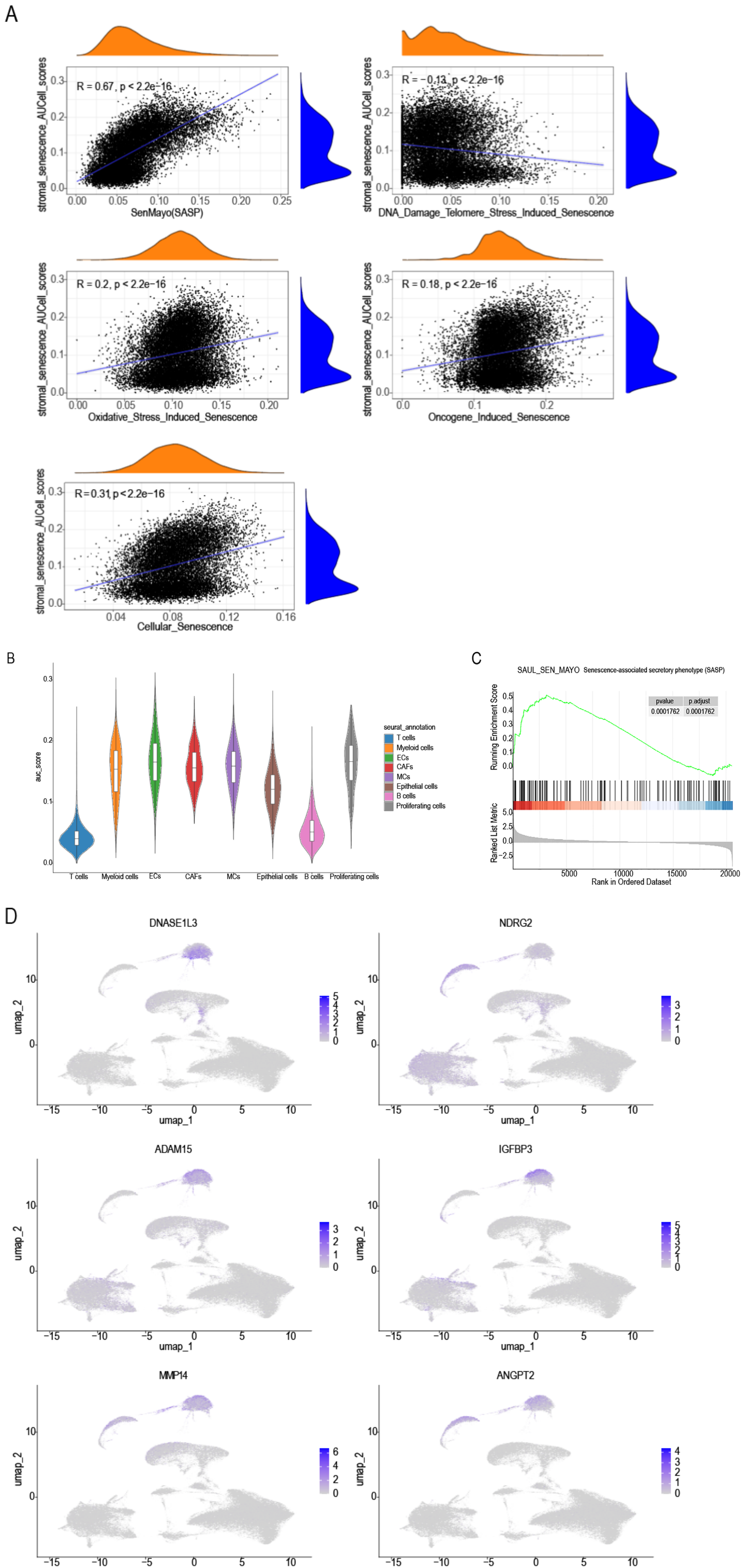

Cell localization and expression analyses of 6 modeling genes

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster
DNASE1L3	1.67E-88	5.480366	0.344	0.035	5.62E-84	Stromal cells
NDRG2	1.47E-49	2.59221	0.364	0.138	4.95E-45	Stromal cells
ADAM15	8.08E-52	2.969135	0.312	0.104	2.72E-47	Stromal cells
IGFBP3	8.52E-53	4.250753	0.268	0.058	2.87E-48	Stromal cells
MMP14	5.12E-92	2.391665	0.250	0.044	1.72E-87	Stromal cells
ANGPT2	2.75E-97	6.265862	0.332	0.019	9.26E-93	Stromal cells

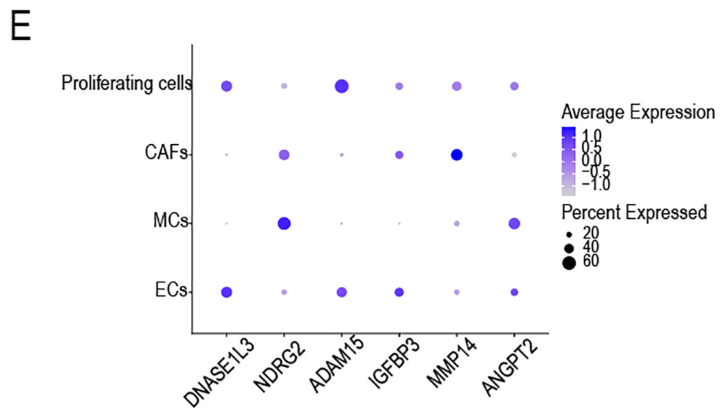

Figure S1 (A) Correlation analysis between stromal senescence AUCell scores and senescence pathways. (B) Violin plots depicting the distribution of senescence scores across characterized cell types. (C) Enrichment plots illustrating the transcriptional signatures of SAUL_SEN_MAYO (SASP). (D) UMAP visualizations showing the differential expression of *DNASE1L3*, *NDRG2*, *ADAM15*, *MMP14*, and *ANGPT2*. (E) Bubble plot illustrating the stromal senescence-associated genes for each characterized cell subtype. AUCell, Area Under the Curve Cell; CAF, cancer-associated fibroblast; EC, endothelial cell; FC, fold change; UMAP, Uniform Manifold Approximation and Projection.

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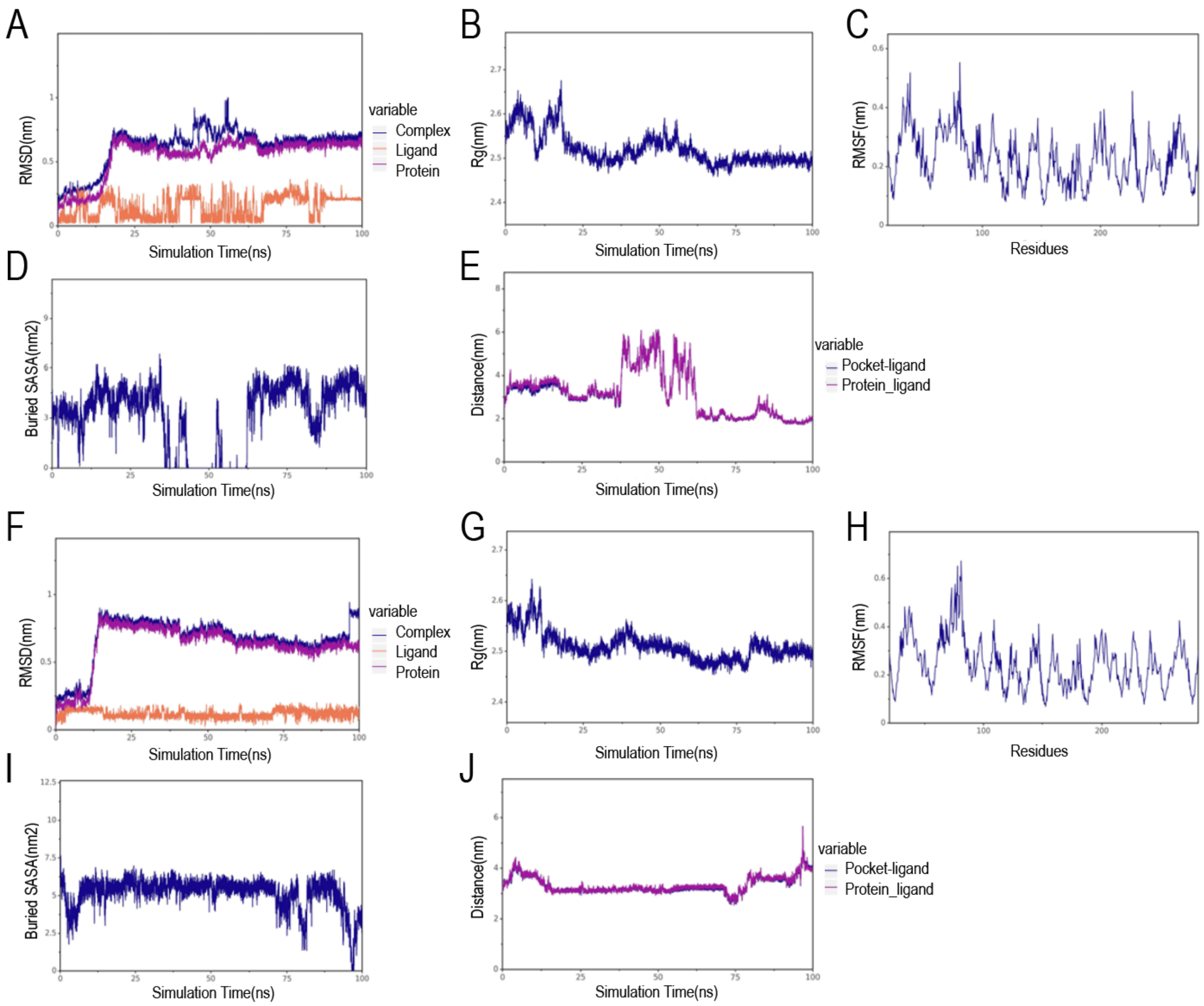

Figure S2 (A-E) 100-ns all-atom MD simulation confirms the stability of the DNASE1L3-ligand STK119225 complex: (A) RMSD values remain low. (B) Rg suggests a compact protein structure. (C) RMSF shows low flexibility at the binding interface. (D) SASA remains consistent. (E) Center-of-mass distance between ligand and protein remains stable, indicating sustained binding throughout the simulation. (F-J) 100-ns all-atom MD simulation confirms the stability of the DNASE1L3-ligand STK598132 complex: (F) RMSD values remain low. (G) Rg suggests a compact protein structure. (H) RMSF shows low flexibility at the binding interface. (I) SASA remains consistent. (J) Center-of-mass distance between ligand and protein remains stable, indicating sustained binding throughout the simulation. MD, molecular dynamics; Rg, radius of gyration; RMSD, root mean square deviation; RMSF, root mean square fluctuation; SASA, solvent-accessible surface area.

Table S1 CellAge senescence genes

AAK1, CBX8, DYRK1A, HDAC3, LEO1, NCAPG2, PPP2R5A, SLC13A3, TPP1, ABCB1, CCL2, E2F1, HDAC4, LGALS3, NCAPH2, PRKAA2, SLC16A7, TPR, ABCC6, CCN2, E2F3, HDAC7, LIMA1, NDRG1, PRKCD, SLC25A5, TPX2, ABI3, CCN6, E2F7, HELLS, LIMK1, NDST2, PRKCH, SLC31A2, TRA2B, ABI3BP, CCNA2, ECT2, HEPACAM, LIN52, NEDD4, PRKD1, SLC52A1, TRDMT1, ACER2, CCNB1, EEF1E1, HIF1A, LIN54, NEK1, PRKD2, SLC5A2, TRIM28, ACKR1, CCND1, EGFR, HIPK2, LIN9, NEK2, PRKDC, SMAD1, TRPM7, ACLY, CCND3, EGLN1, HIRA, LMNA, NEK4, PRKN, SMAD2, TRPM8, ADCK5, CD28, EGR2, HIVEP1, LMNB1, NEK6, PRMT1, SMAD3, TRRAP, AGO2, CD34, EHF, HJURP, LNCTAM34A, NEK9, PRMT6, SMAD5, TSC22D1, AGR2, CD40LG, EHMT2, HK3, LOX, NF1, PRODH, SMAD6, TTK, AGT, CD82, EID3, HMGA1, LOXL2, NF2, PROX1, SMARCA2, TWIST1, AHR, CDC25A, EIF2AK2, HMGA2, LPAR1, NFE2L2, PRPF19, SMARCA4, TWIST2, AKAP4, CDC45, EIF2AK3, HMGB1, LPAR3, NFKB2, PSMA2, SMARCB1, TXN, AKR1B1, CDC6, EIF4E, HMGB2, LRRK2, NFKBIA, PSMA5, SMARCD1, TXNIP, AKT1, CDC7, EIF4EBP1, HMGB3, LY6D, NHEJ1, PSMB1, SMC1A, TYK2, AKT1S1, CDCA2, EIF4G2, HMGCR, MAD1L1, NINJ1, PSMB5, SMC2, TYMS, AKT3, CDCA4, ELAVL1, HNRNPA1, MAD2L1, NIPA2, PSMD14, SMG1, UBE2C, AKTIP, CDH1, ELOA, HNRNPA3, MAEL, NLK, PTEN, SMURF2, UBE2I, ALDH2, CDK1, ENDOG, HNRNPAB, MAF, NLRX1, PTGS2, SNAI1, UBE2N, ALDOA, CDK18, ENG, HNRNPC, MAGEA2, NOLC1, PTK2, SOCS1, UBE2V1, ALKBH3, CDK2, ENO1, HNRNPD, MAGOHB, NOTCH1, PTPN1, SOD1, UBE2V2, ALOX15B, CDK2AP1, ENTPD7, HOPX, MAP2K1, NOTCH3, PTPN6, SOD2, UBE3A, ANAPC1, CDK4, EP300, HOXA9, MAP2K2, NOX1, PTTG1, SORBS2, UBTD1, ANLN, CDK5, EPAS1, HRAS, MAP2K3, NOX4, PURB, SOX1, UHRF1, ANXA5, CDK5R1, EPHA3, HS2ST1, MAP2K6, NPM1, PYGL, SOX2, ULK3, APEX1, CDK6, EPHA5, HSF1, MAP2K7, NQO1, RACGAP1, SOX4, USP1, AR, CDKN1A, EPOR, HSP90AA1, MAP3K14, NR1H2, RACK1, SOX5, USP28, ARF1, CDKN1B, ERBB2, HSP90AB1, MAP3K5, NR2E1, RAD21, SP1, UTP6, ARG2, CDKN1C, ERCC1, HSPA1A, MAP3K6, NRAS, RAD23B, SPAG9, VCAN, ARID1A, CDKN2A, ERRFI1, HSPA2, MAP3K7, NRF1, RAD51C, SPARC, VDR, ARID1B, CDKN2AIP, ERVW-1, HSPA5, MAP4K1, NRSN2, RAF1, SPHK1, VEGFA, ARID3A, CDKN2B, ESPL1, HSPA9, MAPK1, NSUN2, RAN, SPI1, VENTX, ARID4B, CEACAM1, ESR1, HSPB1, MAPK12, NTN4, RANBP9, SPIN1, WEE1, ARPC1B, CEBPB, ESRRB, HTRA1, MAPK14, NUAK1, RAP1GAP, SPOP, WIF1, ARRB1, CEBPG, ETS1, HYOU1, MAPK9, NUAK2, RAPGEF4, SRC, WIPI1, ASAH1, CENPA, ETS2, ID1, MAPKAPK5, NUDT5, RARB, SREBF1, WNT16, ASF1A, CHAF1B, ETV6, IFI16, MARCHF5, NUTF2, RASSF1, SRF, WNT2, ASPH, CHD5, EWSR1, IFNG, MARCKS, OGG1, RASSF4, SRSF1, WNT5A, ASXL2, CHEK1, EZH2, IGFBP1, MAST1, OGT, RASSF5, SRSF2, WNT7B, ATF3, CHEK2, FANCD2, IGFBP3, MATK, OPA1, RB1, SRSF3, WRN, ATF6, CHUK, FASN, IGFBP5, MAVS, ORAI1, RBBP4, SSX2, WSB1, ATF7IP, CIP2A, FASTK, IGFBP7, MCAM, ORC1, RBL1, STAG2, WT1, ATG10, CIT, FBXO22, IKBKG, MCL1, OTX2, RBL2, STAT1, WWP1, ATG12, CKAP2, FBXO31, IL1A, MCM3AP, OXTR, RBM38, STAT3, XAF1, ATG16L1, CKB, FBXO4, IL1R1, MCM7, P2RY14, RBM39, STAT5A, XIAP, ATG4D, CLCA2, FBXO5, IL1RN, MCRS1, P3H1, RBP1, STAT5B, XPC, ATG5, CLPP, FBXW11, IL24, MCU, PAK2, RBP2, STAT6, XPO1, ATG7, CLSPN, FDPS, IL6, MDC1, PAK4, RBPJ, STIM1, YAP1, ATM, CLU, FERMT1, ILF3, MDH1, PAPSS2, RBX1, STK32C, YBX1, ATP6V0A2, CNOT6, FERMT2, ILK, MDK, PARK7, RCC1, STK4, YEATS4, ATP6V0C, CNOT6L, FGF21, IMMT, MDM2, PARP1, RECK, STK40, YPEL3, ATR, COX5B, FGFR1, INCENP, MDP1, PATZ1, RECQL4, STN1, YWHAB, ATRAID, CPEB1, FGFR2, ING1, ME1, PAX8, RELA, STUB1, YWHAZ, ATRX, CPT1C, FGFR3, ING2, ME2, PBRM1, RELB, SUMO2, YY1, ATXN10, CREG1, FIS1, ING5, MECP2, PCGF2, RHOA, SUMO3, ZCCHC10, AURKA, CRISPLD2, FLT1, INPP4B, MED12, PDCD10, RNASEH2A, SUPT5H, ZDHHC3, AURKB, CSNK1A1, FNTB, IRAK4, MEF2A, PDCD11, RNASEH2B, SUV39H1, ZEB1, AXL, CSNK2A1, FOS, IRF1, MEIS2, PDCD4, RNASEL, SUZ12, ZFP36, BAG3, CTH, FOXA1, IRF3, MEN1, PDGFB, ROMO1, SYK, ZFX, BAP1, CTNNAL1, FOXD1, IRF5, MEOX1, PDIK1L, RPL11, SYT1, ZMAT3, BAZ1A, CTNNB1, FOXM1, IRF7, MET, PDPK1, RPS14, SYT7, ZMPSTE24, BCL11B, CTSB, FOXO1, ITGB3, METTL14, PDZD2, RPS6KB1, TACC3, ZMYND11, BCL2, CTSD, FOXO3, ITGB4, MIF, PEA15, RPS9, TAGLN, ZNF148, BCL2L1, CUL4B, FOXO4, ITPK1, MINK1, PEBP1, RPTOR, TBK1, ZNF207, BCL2L2, CUX1, FOXP1, ITPKB, MITF, PELP1, RRAD, TBPL1, ZNF217, BCL3, CXCL1, FOXP3, ITPR1, MKRN1, PES1, RRAS2, TBX2, BCL6, CXCR2, FOXQ1, ITPR2, MME, PEX19, RRM1, TBX3, BCLAF1, CYB5R3, FSCN1, ITPR3, MMP7, PGR, RRM2, TEAD1, BECN1, CYBB, FXN, ITSN2, MMP9, PHB, RRM2B, TEAD4, BHLHE40, CYP26A1, FXR1, JAK2, MNX1, PHB2, RRP8, TERF2, BIN1, DAO, G6PD, JPT1, MOB3A, PHGDH, RTN4, TERT, BIRC5, DDAH2, GADD45G, JUN, MORC3, PI4KB, RUNX1, TFDP1, BLK, DDB1, GAPDH, JUNB, MORF4L1, PIK3C2A, RUVBL2, TFG, BLVRA, DDB2, GATA4, KAT5, MOS, PIK3CA, S100A6, TGFB1I1, BMI1, DDIT4, GDF15, KCNA1, MRTFA, PIK3R5, SALL1, TGFB2, BMP4, DEK, GEMIN2, KCNJ12, MRTFB, PIM1, SAMHD1, TGFBI, BMPR2, DEPTOR, GGCT, KDM1A, MSN, PIN1, SAT2, TGFBR1, BMS1, DGCR8, GJA1, KDM2B, MST1, PINK1, SDC1, TGFBR2, BNIP3L, DHCR24, GKN1, KDM4A, MT1G, PINX1, SELENBP1, THRB, BRAF, DHRS2, GLI1, KDM4C, MTDH, PIR, SELENOH, TIGAR, BRCA1, DHX9, GMNN, KDM5B, MTHFD2, PITX1, SENP1, TIMELESS, BRD4, DICER1, GMPS, KDM6B, MTOR, PLA2G2A, SENP7, TLR10, BRD7, DIDO1, GNG11, KDR, MUC4, PLA2R1, SERPINB2, TLR2, BRIP1, DIRAS3, GNMT, KEAP1, MUS81, PLD2, SERPINE1, TLR3, BTG1, DKC1, GPC3, KIF11, MVK, PLK1, SETD1A, TLR4, BTG2, DLC1, GRIK2, KIF20A, MVP, PML, SFN, TLR8, BTG3, DMTF1, GRK4, KIF2C, MXD4, PMVK, SFRP1, TMEM9B, BUB1, DNMT1, GRK6, KIFC1, MYBBP1A, PNPT1, SGK1, TNFSF13, BUB1B, DNMT3A, GRN, KL, MYBL2, PON1, SIAH1, TNFSF15, CALR, DNMT3B, GRPR, KLF4, MYC, POT1, SIK1, TOM1, CAPNS1, DOT1L, GRSF1, KNDC1, MYCN, POU3F1, SIN3B, TOP1, CARF, DPP4, GSK3A, KRT19, MYD88, POU5F1, SIRT1, TOP3A, CARM1, DPY30, GSK3B, KSR2, MYLK, PPARG, SIRT2, TOPBP1, CASP2, DTL, GTSE1, LAMP2, NACC1, PPARGC1A, SIRT3, TP53, CAV1, DUSP1, HAS1, LATS1, NADK, PPIB, SIRT6, TP53BP1, CAVIN1, DUSP16, HAUS4, LATS2, NAMPT, PPM1B, SIRT7, TP53BP2, CBS, DUSP21, HBP1, LAYN, NANOG, PPM1D, SIX1, TP53I3, CBX5, DUSP3, HDAC1, LBR, NBN, PPP1R13B, SIX6, TP53INP1, CBX7, DUSP6, HDAC2, LCN2, NBR1, PPP2R1A, SKP2, TP63

Table S2 The differential expression of 93 senescence genes in HCC at the single-cell level

Gene	P_val	Avg_log$_2$FC	Pct.1	Pct.2	P_val_adj	Cluster
RACK1	1.82767E−70	2.790849956	0.412	0.108	6.14809E−66	T cells
CCND3	1.60221E−48	2.081488547	0.32	0.193	5.38966E−44	T cells
PRKCH	1.12227E−43	2.866054871	0.26	0.081	3.77519E−39	T cells
CLU	3.186E−252	3.905160565	0.882	0.252	1.0717E−247	Epithelial cells
AGT	8.7407E−243	3.93267564	0.86	0.19	2.9403E−238	Epithelial cells
PEBP1	5.1308E−175	2.27353943	0.902	0.547	1.7259E−170	Epithelial cells
PON1	1.9313E−141	4.731589734	0.506	0.035	6.4967E−137	Epithelial cells
DHCR24	8.5482E−134	3.800494701	0.544	0.053	2.8755E−129	Epithelial cells
MDK	7.1915E−132	3.43606838	0.7	0.178	2.4192E−127	Epithelial cells
SELENBP1	3.3179E−112	3.307248411	0.484	0.049	1.1161E−107	Epithelial cells
PROX1	5.61341E−98	3.221465643	0.346	0.016	1.88829E−93	Epithelial cells
SDC1	4.98139E−95	3.180155942	0.494	0.081	1.67569E−90	Epithelial cells
GPC3	2.66384E−93	3.246823622	0.468	0.072	8.96088E−89	Epithelial cells
ALDH2	2.47621E−86	2.458361417	0.608	0.164	8.32972E−82	Epithelial cells
IGFBP1	1.34363E−79	4.923247543	0.386	0.056	4.51983E−75	Epithelial cells
MST1	4.02725E−78	4.155344113	0.302	0.018	1.35473E−73	Epithelial cells
FASN	1.0721E−70	3.134321978	0.338	0.037	3.60644E−66	Epithelial cells
ABCC6	1.75832E−70	3.890582534	0.25	0.011	5.9148E−66	Epithelial cells
HMGB3	8.61046E−69	2.589761148	0.462	0.1	2.89647E−64	Epithelial cells
ERRFI1	2.52834E−68	2.472775759	0.454	0.096	8.5051E−64	Epithelial cells
CKB	6.07253E−64	3.53432431	0.374	0.064	2.04274E−59	Epithelial cells
GDF15	1.99391E−57	3.13718964	0.322	0.048	6.70731E−53	Epithelial cells
GMNN	1.3209E−53	2.179567638	0.384	0.083	4.44338E−49	Epithelial cells
PHGDH	1.22928E−51	2.261336676	0.336	0.062	4.13516E−47	Epithelial cells
PIR	9.32988E−51	2.892625302	0.284	0.04	3.13848E−46	Epithelial cells
NQO1	2.39612E−50	3.123257712	0.324	0.098	8.0603E−46	Epithelial cells
WEE1	2.28275E−41	2.064598045	0.26	0.046	7.67895E−37	Epithelial cells
CDKN2A	4.30203E−31	2.037058607	0.27	0.068	1.44716E−26	Epithelial cells
CTSB	0	4.129970396	0.898	0.378	0	Myeloid cells
CYBB	3.866E−180	4.854363498	0.608	0.04	1.3005E−175	Myeloid cells
GRN	2.2377E−171	2.556063883	0.848	0.422	7.5275E−167	Myeloid cells
SPI1	9.1438E−167	4.265871076	0.598	0.058	3.0759E−162	Myeloid cells
SOD2	2.937E−161	3.037221534	0.836	0.355	9.8798E−157	Myeloid cells
CTSD	6.3542E−160	2.81982566	0.852	0.45	2.1375E−155	Myeloid cells
ASAH1	2.043E−130	2.482293045	0.736	0.321	6.8724E−126	Myeloid cells

Table S2 (*continued*)

Table S2 (*continued*)

Gene	P_val	Avg_$\log_2$FC	Pct.1	Pct.2	P_val_adj	Cluster
NAMPT	1.1654E−122	2.553603495	0.768	0.308	3.9204E−118	Myeloid cells
TGFBI	8.2102E−122	3.293261917	0.584	0.114	2.7618E−117	Myeloid cells
NFKBIA	9.0548E−120	2.58044406	0.832	0.502	3.046E−115	Myeloid cells
CREG1	1.5024E−113	3.255762222	0.558	0.152	5.054E−109	Myeloid cells
NINJ1	1.0557E−107	2.686135931	0.64	0.22	3.5512E−103	Myeloid cells
SGK1	3.1965E−104	2.765571708	0.634	0.167	1.0753E−99	Myeloid cells
LGALS3	4.0334E−102	2.435024846	0.706	0.26	1.35679E−97	Myeloid cells
IL1RN	3.60954E−84	4.994128682	0.344	0.036	1.21421E−79	Myeloid cells
TLR2	5.42653E−84	5.361985266	0.284	0.01	1.82543E−79	Myeloid cells
MARCKS	7.42766E−80	2.017576856	0.672	0.265	2.49859E−75	Myeloid cells
TPP1	2.58731E−79	2.148648739	0.612	0.218	8.70344E−75	Myeloid cells
SAMHD1	3.03697E−79	2.559514968	0.538	0.144	1.02161E−74	Myeloid cells
SLC31A2	2.87535E−74	3.301050006	0.38	0.065	9.67241E−70	Myeloid cells
PTGS2	3.29132E−71	4.550373181	0.282	0.02	1.10717E−66	Myeloid cells
KLF4	4.67131E−68	2.126346487	0.542	0.155	1.57138E−63	Myeloid cells
CEBPB	1.09856E−66	2.233610183	0.586	0.246	3.69544E−62	Myeloid cells
MMP9	2.07122E−65	4.863337616	0.268	0.024	6.96737E−61	Myeloid cells
RB1	4.61563E−55	2.518457984	0.39	0.091	1.55265E−50	Myeloid cells
RASSF4	9.58503E−48	2.495961584	0.354	0.093	3.22431E−43	Myeloid cells
SYK	2.77415E−47	3.07583066	0.27	0.041	9.33198E−43	Myeloid cells
VEGFA	2.27996E−26	0.714446583	0.292	0.116	7.66956E−22	Epithelial cells
BLVRA	3.04898E−40	2.03752065	0.398	0.146	1.02565E−35	Myeloid cells
RUNX1	8.45874E−30	2.269460439	0.26	0.072	2.84544E−25	Myeloid cells
BAG3	5.39181E−28	2.000110145	0.348	0.194	1.81375E−23	Myeloid cells
SPARC	0	7.404351511	0.894	0.078	0	Stromal cells
IGFBP7	0	7.234162297	0.892	0.134	0	Stromal cells
GNG11	2.7806E−281	6.257233865	0.772	0.063	9.3535E−277	Stromal cells
CAV1	6.0135E−231	4.964143475	0.698	0.111	2.0229E−226	Stromal cells
EPAS1	2.1515E−207	5.152727438	0.656	0.088	7.2374E−203	Stromal cells
ENG	7.7059E−163	4.869898845	0.566	0.076	2.5922E−158	Stromal cells
TSC22D1	2.0289E−153	3.332284962	0.686	0.212	6.825E−149	Stromal cells
TAGLN	1.8418E−147	7.762580156	0.472	0.062	6.1956E−143	Stromal cells
MCAM	5.1958E−120	6.977629545	0.358	0.009	1.7478E−115	Stromal cells
CD34	6.9514E−120	6.89696683	0.36	0.011	2.3384E−115	Stromal cells

Table S2 (*continued*)

Table S2 (*continued*)

Gene	P_val	Avg_$\log_2$FC	Pct.1	Pct.2	P_val_adj	Cluster
IGFBP5	1.3402E−114	7.185805258	0.372	0.021	4.5083E−110	Stromal cells
NOTCH3	1.0083E−105	6.4151669	0.322	0.007	3.3919E−101	Stromal cells
ID1	2.6473E−105	4.919648637	0.408	0.053	8.9052E−101	Stromal cells
KDR	1.4208E−104	8.451040382	0.298	0.003	4.7796E−100	Stromal cells
TGFB1I1	1.6147E−103	6.437083498	0.33	0.014	5.4318E−99	Stromal cells
FLT1	1.7282E−100	5.724231776	0.354	0.024	5.81352E−96	Stromal cells
MYLK	6.3645E−97	4.701585732	0.396	0.054	2.14095E−92	Stromal cells
DLC1	1.95758E−94	5.335695226	0.334	0.02	6.5851E−90	Stromal cells
TGFBR2	1.03669E−78	2.956781956	0.472	0.156	3.48733E−74	Stromal cells
PTK2	7.63467E−68	3.387546802	0.358	0.076	2.56823E−63	Stromal cells
FERMT2	9.22847E−67	3.4637552	0.344	0.062	3.10437E−62	Stromal cells
CYB5R3	1.22046E−66	2.027045174	0.558	0.263	4.1055E−62	Stromal cells
LIMA1	1.28521E−59	3.003263096	0.368	0.085	4.3233E−55	Stromal cells
BMPR2	1.77069E−54	3.381401518	0.314	0.062	5.95643E−50	Stromal cells
CCND1	2.8401E−54	2.728867759	0.392	0.124	9.55383E−50	Stromal cells
ZEB1	7.42077E−54	2.961498805	0.338	0.068	2.49627E−49	Stromal cells
IGFBP3	8.52128E−53	4.250753053	0.268	0.058	2.86647E−48	Stromal cells
PIK3C2A	4.4624E−45	3.047552562	0.286	0.078	1.50111E−40	Stromal cells
DUSP6	1.36775E−42	2.751849032	0.318	0.101	4.60098E−38	Stromal cells
RBP1	1.99747E−40	2.619758051	0.308	0.079	6.71928E−36	Stromal cells
HTRA1	3.50305E−39	2.942870492	0.256	0.057	1.17839E−34	Stromal cells
FSCN1	6.05402E−35	2.569297722	0.264	0.066	2.03651E−30	Stromal cells
HDAC7	7.27136E−32	2.443191461	0.26	0.067	2.44601E−27	Stromal cells
SORBS2	3.41273E−54	1.406509545	0.348	0.075	1.14801E−49	Epithelial cells

FC, fold change; HCC, hepatocellular carcinoma.

Table S3 The intersection of senescence-related genes used for AUCell scoring with SASP genes, validated senescence regulators, and stromal markers

The intersection of senescence-related genes used for AUCell scoring with SenMayo (SASP)
ANG, CCL20, CXCL1, EGFR, IGF1, IL1A, MMP12, PTGES, VEGFC, ANGPT1, CCL26, CXCL10, EREG, IGFBP1, IL1B, MMP14, SEMA3F, ANGPTL4, CCL3, CXCL12, ESM1, IGFBP3, IL6, MMP2, SERPINE1, AXL, CCL3L1, CXCL16, ETS2, IGFBP4, INHA, MMP9, SPP1, BMP2, CCL7, CXCL2, FGF2, IGFBP5, ITGA2, NRG1, SPX, C3, CCL8, CXCL3, FGF7, IGFBP6, ITPKA, PGF, TIMP2, CCL13, CD9, CXCL8, GDF15, IGFBP7, KITLG, PLAT, TNFRSF10C, CCL16, CSF2RB, DKK1, HGF, IL10, MMP1, PLAU, TNFRSF11B, CCL2, CTSB, EDN1, ICAM1, IL18, MMP10, PLAUR, VEGFA
The intersection of senescence-related genes used for AUCell scoring with CellAge
YAP1, TBX2, SERPINE1, PON1, MITF, IL6, FLT1, CXCL1, BCL2L2, WNT5A, TAGLN, SELENBP1, PLA2G2A, MET, IL1RN, FGFR3, CTSD, AXL, VEGFA, SYT7, SDC1, PIR, MEIS2, IL1A, FGFR2, CTSB, ASPH, VCAN, SYT1, SALL1, PINK1, ME1, IGFBP7, FGF21, CRISPLD2, ASAH1, UBTD1, SYK, RRAD, PDZD2, MDK, IGFBP5, FERMT2, CREG1, AR, TSC22D1, SRC, RBP2, PDGFB, MCAM, IGFBP3, FERMT1, CPT1C, ALOX15B, TNFSF15, SPI1, RBP1, PCGF2, MARCKS, IGFBP1, ETS2, CLU, ALDH2, TNFSF13, SPHK1, RASSF4, PAPSS2, MAPK12, ID1, ERRFI1, CKB, AGT, TLR8, SPARC, RARB, NUAK1, MAEL, HTRA1, EPHA3, CDKN1C, AGR2, TLR4, SOX5, RAPGEF4, NTN4, LRRK2, HMGA2, EPAS1, CDK2AP1, ACKR1, TLR2, SOX2, RAP1GAP, NQO1, LPAR1, HK3, ENG, CDK18, ABCC6, THRB, SORBS2, PYGL, NOX4, LOXL2, GRN, EHF, CDH1, TGFBI, SOD2, PTK2, NOTCH3, LOX, GPC3, EGFR, CD34, TGFB2, SNAI1, PTGS2, NEK6, LCN2, GNG11, DUSP6, CCND1, TGFB1I1, SMAD6, PROX1, MYLK, LATS2, GJA1, DUSP3, CCL2, TERT, SLC31A2, PRKD1, MT1G, KRT19, GDF15, DLC1, CAVIN1, TEAD4, SLC13A3, PRKAA2, MST1, KLF4, GATA4, DHCR24, CAV1, TEAD1, SGK1, PPARGC1A, MMP9, KDR, FSCN1, DEPTOR, BMPR2, TBX3, SFRP1, PPARG, MMP7, ITGB4, FOXA1, CYBB, BMP4
The intersection of senescence-related genes used for AUCell scoring with stromal markers
A2M, CCND1, CRIM1, FAM167B, IGFBP4, MYO1C, PLAT, RCN1, TIMP3, ACTA2, CD151, CRIP2, FAM198B, IGFBP5, NCKAP1, PLK2, RDX, TINAGL1, ADAM15, CD34, CRYAB, FERMT2, IGFBP7, NDRG2, PLPP1, RGS5, TJP1, ADAMTS1, CD36, CSRP2, FILIP1, IL33, NDUFA4L2, PLPP3, RRAS, TM4SF1, ADAMTS4, CD59, CTGF, FILIP1L, INSR, NFIA, PLS3, S100A16, TM4SF18, ADAMTS9, CD9, CXorf36, FKBP10, JAG1, NFIB, PLVAP, SDPR, TMEM47, ADGRF5, CD93, CYR61, FLT1, KDR, NGFRAP1, PLXND1, SEPT10, TMEM88, ADGRL4, CDC42EP1, CYYR1, FRZB, LAMA4, NID1, PMP22, SEPT4, TNS1, ADIRF, CDH13, DCN, FSCN1, LAMB2, NNMT, PODXL, SLC9A3R2, TNS2, AKAP12, CDH5, DLC1, FSTL1, LAMC1, NOTCH3, PPFIBP1, SMTN, TPM1, ANGPT2, CLDN5, DNASE1L3, FXYD6, LDB2, NOTCH4, PPIC, SNCG, TPM2, APLNR, CLEC14A, DUSP6, GAS6, LHFP, NPDC1, PPP1R14A, SOD3, TPPP3, APP, CLIC4, EBF1, GJA4, LIMCH1, NR2F2, PRKCDBP, SORBS2, TSC22D1, AQP1, CNN3, EDNRB, GNG11, LRRC32, NRP1, PRSS23, SPARC, TUBB6, ARHGAP29, COL15A1, EFEMP2, GPX3, MAP1B, OAZ2, PTK2, SPARCL1, UACA, ARHGEF12, COL18A1, EFNB2, GSN, MCAM, PALLD, PTP4A3, SPRY1, VWF, BCAM, COL1A1, EGFL7, HES1, MEF2C, PALMD, PTPRB, STC1, WBP5, BGN, COL1A2, EHD2, HES4, MFGE8, PCAT19, PTPRG, SWAP70, WWTR1, BMPR2, COL3A1, EMCN, HIGD1B, MGLL, PCDH17, PTRF, SYNPO, YBX3, C10orf10, COL4A1, EMP1, HSPG2, MGP, PDGFRB, PVRL2, TAGLN, ZFHX3, C11orf96, COL4A2, EMP2, HTRA1, MMP14, PDLIM1, RAMP2, TCF4, C8orf4, COL6A1, ENG, HYAL2, MMRN2, PDLIM3, RAMP3, TGFB1I1, CALCRL, COL6A2, EPAS1, ID1, MTUS1, PDLIM7, RBMS3, TGM2, CALD1, COLEC11, EPS8, IFI27, MYCT1, PGF, RBP1, THY1, CAV1, COX7A1, ESAM, IFITM3, MYL9, PKIG, RBP7, TIE1, CAV2, CPE, FABP4, IGFBP3, MYLK, PLAC9, RBPMS, TIMP1

AUCell, Area Under the Curve Cell.