Supplementary material

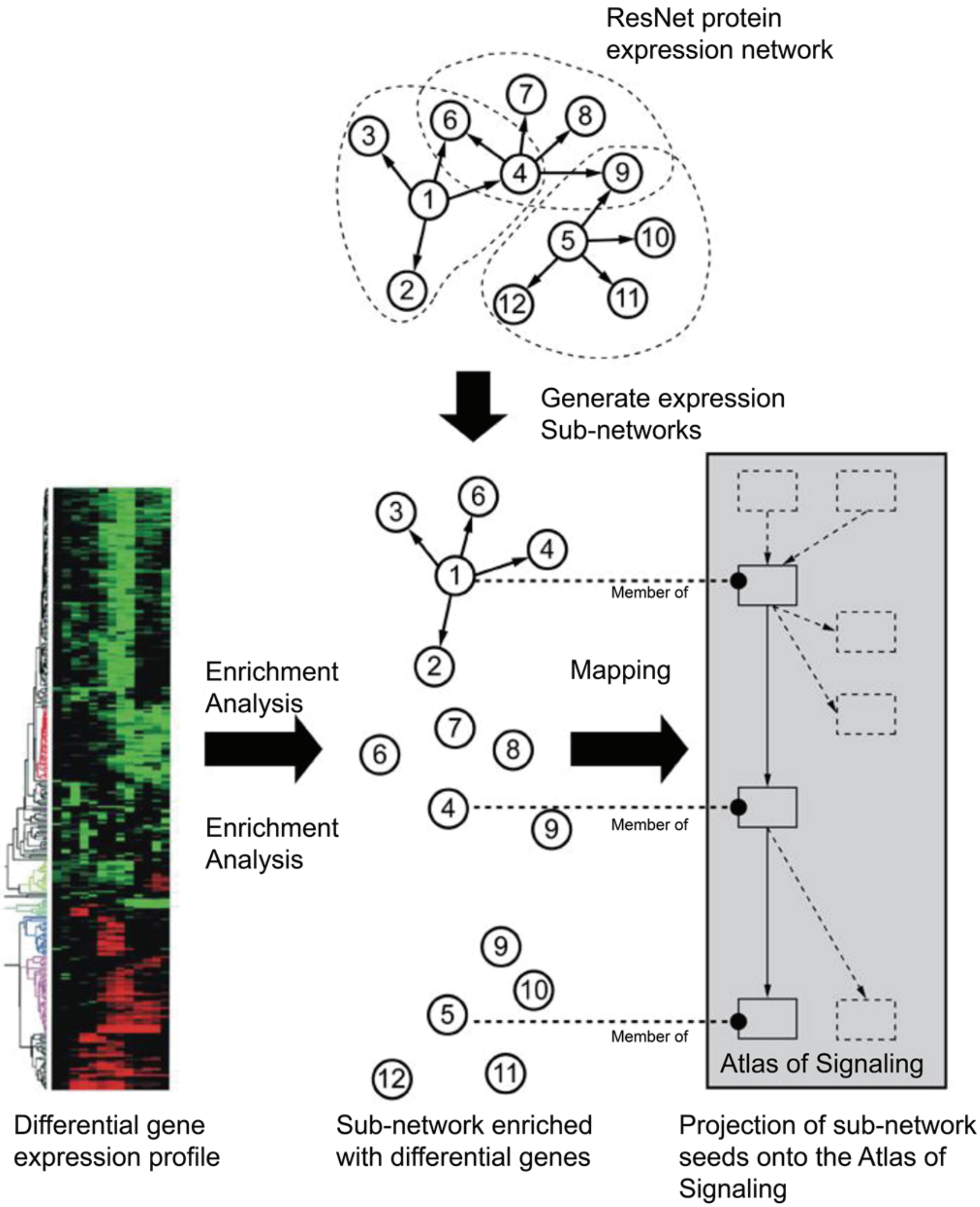

Figure S1. An overview of Sub-Network Enrichment Analysis (SNEA) algorithms

Table S1. Differential expression in DNA repair genes

Name	Description	SCC		ADC	
		fold-change	p-value	fold-change	p-value
RBBP8	Retinoblastoma binding protein 8	2.15	9.61×10^{-7}	1.26	5.34×10^{-2}
PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	2.14	3.89×10^{-7}	1.45	1.10×10^{-3}
SHFM1	Split hand/foot malformation (ectrodactyly) type 1	2.12	1.96×10^{-7}	1.34	1.61×10^{-1}
PCNA	Proliferating cell nuclear antigen	2.01	1.66×10^{-6}	1.43	4.79×10^{-4}
CHEK1	CHK1 checkpoint homolog (*S. Pombe*)	1.97	1.33×10^{-5}	1.35	1.20×10^{-4}
FANCI	Fanconi anemia, complementation group I	1.84	2.79×10^{-6}	1.29	4.88×10^{-3}
CHAF1A	Chromatin assembly factor 1, subunit A (p150)	1.82	2.55×10^{-7}	1.28	1.52×10^{-4}
EXO1	Exonuclease 1	1.79	7.13×10^{-7}	1.36	4.29×10^{-4}
CHEK2	CHK2 checkpoint homolog *(S. Pombe*)	1.73	9.38×10^{-6}	1.18	1.62×10^{-2}
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	1.73	6.67×10^{-7}	1.32	2.22×10^{-2}
BLM	Bloom syndrome, RecQ helicase-like	1.72	8.70×10^{-6}	1.25	1.41×10^{-4}
POLB	Polymerase (DNA directed), beta	1.59	8.74×10^{-5}	1.28	3.57×10^{-2}
BRCA1	Breast cancer 1, early onset	1.56	2.13×10^{-5}	1.11	1.25×10^{-1}
PMS2	PMS2 postmeiotic segregation increased 2 (*S. cerevisiae*)	1.54	3.87×10^{-4}	1.21	2.58×10^{-2}
PARP1	Poly (ADP-ribose) polymerase 1	1.54	3.11×10^{-4}	1.23	4.17×10^{-2}
CETN2	Centrin, EF-hand protein, 2	1.52	3.31×10^{-3}	-1.06	7.41×10^{-1}
CDK7	Cyclin-dependent kinase 7	1.50	1.53×10^{-4}	1.09	3.01×10^{-1}
MSH6	mutS homolog 6 (*E. Coli*)	1.49	1.29×10^{-3}	1.05	6.09×10^{-1}
ATR	Ataxia telangiectasia and Rad3 related	1.46	1.50×10^{-4}	1.10	2.66×10^{-1}
UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2	1.45	2.00×10^{-5}	1.11	1.28×10^{-1}

FEN1	Flap structure-specific endonuclease 1	1.45	4.79×10^{-7}	1.39	4.18×10^{-7}
PARP2	Poly (ADP-ribose) polymerase 2	1.44	2.05×10^{-3}	1.06	5.74×10^{-1}
FANCD2	Fanconi anemia, complementation group D2	1.44	6.33×10^{-6}	1.09	1.90×10^{-1}
FANCL	Fanconi anemia, complementation group L	1.41	3.93×10^{-2}	-1.08	5.57×10^{-1}
RAD54B	RAD54 homolog B (*S. cerevisiae*)	1.41	4.37×10^{-6}	1.15	4.16×10^{-3}
GTF2H3	General transcription factor IIH, polypeptide 3, 34 kDa	1.38	1.58×10^{-3}	1.19	3.65×10^{-3}
TDG	Thymine-DNA glycosylase	1.38	1.58×10^{-3}	1.16	5.83×10^{-2}
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	1.37	1.98×10^{-3}	1.07	3.63×10^{-1}
UNG	Uracil-DNA glycosylase	1.36	1.67×10^{-5}	1.13	5.20×10^{-2}
MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (*E. Coli*)	1.36	9.78×10^{-3}	1.26	1.49×10^{-3}
DDB1	Damage-specific DNA binding protein 1, 127 kDa	1.36	2.18×10^{-3}	1.12	2.29×10^{-1}
OBFC2B	Oligonucleotide/oligosaccharide-binding fold containing 2B	1.35	1.63×10^{-4}	1.15	9.60×10^{-3}
XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	1.34	3.81×10^{-3}	1.13	1.12×10^{-1}
TDP1	Tyrosyl-DNA phosphodiesterase 1	1.29	1.75×10^{-4}	1.13	2.73×10^{-2}
PALB2	Partner and localizer of BRCA2	1.28	1.88×10^{-3}	1.05	3.43×10^{-1}
GTF2H1	General transcription factor IIH, polypeptide 1, 62 kDa	1.27	5.39×10^{-2}	1.13	1.53×10^{-1}
PMS2L3	Postmeiotic segregation increased 2-like 3	1.27	2.48×10^{-2}	1.28	1.76×10^{-2}
APTX	Aprataxin	1.26	2.40×10^{-3}	1.09	1.33×10^{-1}
MNAT1	Menage a trois homolog 1, cyclin H assembly factor (*X. laevis*)	1.26	1.54×10^{-2}	-1.01	8.98×10^{-1}
RAD51	RAD51 homolog (RecA homolog, *E. Coli*) (*S. cerevisiae*)	1.25	4.56×10^{-3}	1.14	2.94×10^{-2}
FANCF	Fanconi anemia,	1.24	3.57×10^{-3}	1.11	5.48×10^{-2}

	complementation group F				
DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, *S. cerevisiae*)	1.24	2.93×10^{-3}	1.19	1.59×10^{-3}
RAD51C	RAD51 homolog C (*S. cerevisiae*)	1.24	3.84×10^{-3}	1.06	3.43×10^{-1}
RECQL	RecQ protein-like (DNA helicase Q1-like)	1.24	3.15×10^{-2}	1.04	5.70×10^{-1}
WRN	Werner syndrome, RecQ helicase-like	1.23	7.64×10^{-2}	-1.28	1.76×10^{-3}
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	1.22	2.27×10^{-2}	-1.02	8.53×10^{-1}
RAD18	RAD18 homolog (*S. cerevisiae*)	1.22	1.58×10^{-4}	1.12	1.57×10^{-2}
ERCC6	Excision repair cross-complementing rodent repair deficiency, complementation group 6	1.20	1.10×10^{-2}	-1.03	6.42×10^{-1}
POLQ	Polymerase (DNA directed), theta	1.20	1.45×10^{-2}	1.05	3.89×10^{-1}
CLK2	CDC-like kinase 2	1.19	6.15×10^{-3}	1.27	1.55×10^{-4}
FANCE	Fanconi anemia, complementation group E	1.18	4.80×10^{-3}	1.04	3.84×10^{-1}
FANCA	Fanconi anemia, complementation group A	1.18	2.57×10^{-3}	1.15	3.99×10^{-3}
NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	1.18	1.23×10^{-3}	1.15	1.33×10^{-2}
DUT	Deoxyuridine triphosphatase	1.18	4.96×10^{-3}	1.08	2.18×10^{-1}
TP53	tumor protein p53	1.18	6.27×10^{-2}	1.09	1.88×10^{-1}
RAD54L	RAD54-like (*S. cerevisiae*)	1.18	5.95×10^{-3}	1.16	9.38×10^{-3}
EME1	Essential meiotic endonuclease 1 homolog 1 (*S. Pombe*)	1.17	2.57×10^{-3}	1.14	3.56×10^{-2}
ERCC1	Excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	1.17	6.47×10^{-4}	1.03	5.51×10^{-1}
RAD23B	RAD23 homolog B (*S. cerevisiae*)	1.17	7.37×10^{-2}	1.09	2.50×10^{-1}
BRCA2	breast cancer 2, early onset	1.17	1.61×10^{-2}	1.02	6.07×10^{-1}

SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	1.16	1.41×10^{-2}	1.12	3.81×10^{-2}
MSH5	mutS homolog 5 (*E. Coli*)	1.16	2.48×10^{-3}	1.10	7.79×10^{-2}
NBN	Nibrin	1.16	2.26×10^{-1}	1.10	3.12×10^{-1}
FANCG	Fanconi anemia, complementation group G	1.16	5.29×10^{-4}	1.10	7.89×10^{-2}
LIG3	Ligase III, DNA, ATP-dependent	1.16	2.82×10^{-2}	1.15	6.57×10^{-3}
RAD1	RAD1 homolog (*S. Pombe*)	1.15	3.82×10^{-2}	1.14	5.71×10^{-2}
RAD50	RAD50 homolog (*S. cerevisiae*)	1.15	3.50×10^{-1}	-1.14	3.96×10^{-1}
FANCB	Fanconi anemia, complementation group B	1.14	4.52×10^{-2}	1.17	1.22×10^{-2}
DDB2	Damage-specific DNA binding protein 2, 48 kDa	1.14	3.45×10^{-2}	1.15	4.07×10^{-3}
GTF2H5	General transcription factor IIH, polypeptide 5	1.14	7.73×10^{-2}	1.11	2.18×10^{-1}
RAD23A	RAD23 homolog A (*S. cerevisiae*)	1.13	1.05×10^{-1}	1.03	6.54×10^{-1}
POLE	Polymerase (DNA directed), epsilon	1.12	2.41×10^{-2}	1.05	3.21×10^{-1}
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	1.11	3.77×10^{-2}	1.13	2.74×10^{-3}
MRE11A	MRE11 meiotic recombination 11 homolog A (*S. cerevisiae*)	1.10	4.23×10^{-1}	1.05	6.12×10^{-1}
FANCM	Fanconi anemia, complementation group M	1.10	7.10×10^{-2}	-1.02	6.83×10^{-1}
APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	1.10	5.71×10^{-2}	1.05	2.46×10^{-1}
PMS1	PMS1 postmeiotic segregation increased 1 (*S. cerevisiae*)	1.10	7.01×10^{-2}	1.09	6.87×10^{-2}
LIG1	Ligase I, DNA, ATP-dependent	1.09	4.08×10^{-2}	1.12	5.11×10^{-3}
NEIL3	nei endonuclease VIII-like 3 (*E. Coli*)	1.09	9.13×10^{-2}	1.12	6.20×10^{-2}
RPA1	Replication protein A1, 70 kDa	1.08	2.72×10^{-2}	1.08	4.27×10^{-2}
ALKBH2	alkB, alkylation repair homolog 2	1.08	1.96×10^{-1}	1.02	7.80×10^{-1}

	(*E. Coli*)				
ALKBH3	alkB, alkylation repair homolog 3 (*E. Coli*)	1.08	1.79×10^{-1}	1.08	2.22×10^{-1}
HUS1	HUS1 checkpoint homolog (*S. Pombe*)	1.08	2.59×10^{-1}	1.03	7.19×10^{-1}
UBE2A	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)	1.08	2.09×10^{-1}	-1.01	8.50×10^{-1}
ERCC4	Excision repair cross-complementing rodent repair deficiency, complementation group 4	1.07	2.51×10^{-1}	1.06	3.21×10^{-1}
MBD4	Methyl-CpG binding domain protein 4	1.07	4.14×10^{-1}	1.11	5.74×10^{-2}
MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	1.07	2.13×10^{-1}	1.12	3.10×10^{-2}
LIG4	Ligase IV, DNA, ATP-dependent	1.06	3.15×10^{-1}	1.11	7.92×10^{-2}
RAD52	RAD52 homolog (*S. cerevisiae*)	1.06	3.06×10^{-1}	-1.05	2.82×10^{-1}
MDC1	Mediator of DNA damage checkpoint 1	1.06	4.24×10^{-1}	1.03	6.25×10^{-1}
MUTYH	mutY homolog (*E. Coli*)	1.06	2.57×10^{-1}	1.05	3.47×10^{-1}
RPA3	Replication protein A3, 14 kDa	1.06	2.83×10^{-1}	1.14	5.66×10^{-3}
POLH	Polymerase (DNA directed), eta	1.06	4.73×10^{-1}	1.11	2.02×10^{-1}
POLN	Polymerase (DNA directed) nu	1.05	2.92×10^{-1}	1.12	1.98×10^{-2}
GTF2H4	General transcription factor IIH, polypeptide 4, 52 kDa	1.05	1.64×10^{-1}	1.06	2.92×10^{-1}
DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, *S. cerevisiae*)	1.05	4.68×10^{-1}	1.20	1.05×10^{-3}
XAB2	XPA binding protein 2	1.04	4.75×10^{-1}	1.07	1.75×10^{-1}
H2AFX	H2A histone family, member X	1.04	4.13×10^{-1}	1.25	4.58×10^{-6}
ERCC3	Excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	1.04	6.20×10^{-1}	-1.05	5.19×10^{-1}
RAD51L1	RAD51-like 1 (*S. cerevisiae*)	1.04	5.92×10^{-1}	1.06	3.94×10^{-1}
XRCC3	X-ray repair complementing defective repair in Chinese	1.04	4.91×10^{-1}	1.18	2.41×10^{-3}

	hamster cells 3				
RPA2	replication protein A2, 32 kDa	1.04	6.87×10^{-1}	1.02	8.38×10^{-1}
ATM	ataxia telangiectasia mutated	1.04	7.26×10^{-1}	-1.21	7.93×10^{-2}
RAD17	RAD17 homolog (*S. Pombe*)	1.04	6.98×10^{-1}	1.21	1.44×10^{-2}
REV1	REV1 homolog (*S. cerevisiae*)	1.03	6.98×10^{-1}	-1.09	2.49×10^{-1}
RAD51L3	RAD51-like 3 (*S. cerevisiae*)	1.03	5.07×10^{-1}	1.06	2.89×10^{-1}
UBE2B	Ubiquitin-conjugating enzyme E2B (RAD6 homolog)	1.03	6.85×10^{-1}	-1.20	7.78×10^{-2}
RDM1	RAD52 motif 1	1.02	6.46×10^{-1}	1.16	4.44×10^{-3}
MSH4	mutS homolog 4 (*E. Coli*)	1.02	7.35×10^{-1}	1.00	9.38×10^{-1}
RECQL4	RecQ protein-like 4	1.02	6.92×10^{-1}	1.12	3.02×10^{-2}
ERCC2	Excision repair cross-complementing rodent repair deficiency, complementation group 2	1.01	8.80×10^{-1}	1.18	8.45×10^{-4}
NTHL1	nth endonuclease III-like 1 (*E. Coli*)	1.00	9.79×10^{-1}	1.07	1.54×10^{-1}
POLM	Polymerase (DNA directed), mu	-1.00	9.79×10^{-1}	1.07	1.53×10^{-1}
MSH3	mutS homolog 3 (*E. Coli*)	-1.00	9.80×10^{-1}	-1.00	9.47×10^{-1}
ERCC5	Excision repair cross-complementing rodent repair deficiency, complementation group 5	-1.00	9.70×10^{-1}	-1.32	2.85×10^{-3}
EME2	Essential meiotic endonuclease 1 homolog 2 (*S. Pombe*)	-1.01	8.17×10^{-1}	-1.02	6.86×10^{-1}
PNKP	Polynucleotide kinase 3'-phosphatase	-1.01	7.46×10^{-1}	1.14	4.45×10^{-3}
XPA	Xeroderma pigmentosum, complementation group A	-1.01	8.65×10^{-1}	-1.08	2.43×10^{-1}
POLD1	Polymerase (DNA directed), delta 1, catalytic subunit 125 kDa	-1.02	7.40×10^{-1}	1.05	3.27×10^{-1}
TREX2	Three prime repair exonuclease 2	-1.02	6.83×10^{-1}	1.10	9.88×10^{-2}
POLL	Polymerase (DNA directed), lambda	-1.02	6.14×10^{-1}	1.03	6.11×10^{-1}
MMS19	MMS19 nucleotide excision repair	-1.02	5.25×10^{-1}	-1.03	4.03×10^{-1}

	homolog (*S. cerevisiae*)				
MPG	N-methylpurine-DNA glycosylase	-1.03	4.49×10^{-1}	1.11	2.26×10^{-3}
RAD9A	RAD9 homolog A (*S. Pombe*)	-1.03	5.52×10^{-1}	1.06	2.13×10^{-1}
TREX1	Three prime repair exonuclease 1	-1.03	4.99×10^{-1}	-1.06	2.04×10^{-1}
MUS81	MUS81 endonuclease homolog (*S. cerevisiae*)	-1.04	4.33×10^{-1}	1.10	3.02×10^{-2}
OGG1	8-oxoguanine DNA glycosylase	-1.05	3.02×10^{-1}	1.08	8.32×10^{-2}
RECQL5	RecQ protein-like 5	-1.05	2.99×10^{-1}	1.11	4.41×10^{-2}
POLI	Polymerase (DNA directed) iota	-1.05	6.10×10^{-1}	-1.12	3.06×10^{-1}
DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, *S. cerevisiae*)	-1.06	4.75×10^{-1}	1.11	1.35×10^{-1}
DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	-1.06	2.82×10^{-1}	1.07	2.07×10^{-1}
NEIL2	nei like 2 (*E. Coli*)	-1.07	1.90×10^{-1}	1.11	3.17×10^{-2}
POLK	Polymerase (DNA directed) kappa	-1.07	5.64×10^{-1}	-1.24	3.58×10^{-2}
ERCC8	Excision repair cross-complementing rodent repair deficiency, complementation group 8	-1.09	1.59×10^{-1}	1.05	3.57×10^{-1}
MGMT	O-6-methylguanine-DNA methyltransferase	-1.09	8.14×10^{-2}	1.05	1.79×10^{-1}
UBE2N	Ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	-1.09	1.84×10^{-1}	-1.11	8.47×10^{-2}
GTF2H2	General transcription factor IIH, polypeptide 2, 44 kDa	-1.10	5.17×10^{-1}	-1.20	2.56×10^{-1}
Hel308	Helicase, POLQ-like	-1.11	1.45×10^{-1}	-1.05	3.62×10^{-1}
SPO11	SPO11 meiotic protein covalently bound to DSB homolog (*S. cerevisiae*)	-1.11	1.26×10^{-1}	1.01	7.93×10^{-1}
MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (*E. Coli*)	-1.12	1.27×10^{-1}	-1.23	2.00×10^{-3}
POLG	polymerase (DNA directed), gamma	-1.12	1.54×10^{-2}	1.03	5.51×10^{-1}
RRM2B	Ribonucleotide reductase M2 B	-1.13	8.62×10^{-2}	1.09	2.92×10^{-1}

	(TP53 inducible)				
RPA4	Replication protein A4, 34 kDa	-1.14	2.69×10^{-2}	-1.11	4.93×10^{-2}
NEIL1	nei endonuclease VIII-like 1 (*E. Coli*)	-1.14	2.79×10^{-2}	-1.04	4.78×10^{-1}
XPC	Xeroderma pigmentosum, complementation group C	-1.14	2.71×10^{-2}	-1.11	1.05×10^{-1}
MLH3	mutL homolog 3 (*E. Coli*)	-1.16	1.25×10^{-2}	-1.10	1.44×10^{-1}
FANCC	Fanconi anemia, complementation group C	-1.21	3.49×10^{-3}	-1.14	2.08×10^{-2}
REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	-1.25	1.14×10^{-2}	-1.19	3.02×10^{-2}
PER1	Period homolog 1 (*Drosophila*)	-1.37	5.61×10^{-6}	-1.19	7.80×10^{-3}
CCNH	Cyclin H	-1.69	1.94×10^{-4}	-1.50	1.66×10^{-2}
A730011L01Rik	Hypothetical protein FLJ35220				
GEN1	Gen homolog 1, endonuclease (*Drosophila*)				
PMS2L4	Postmeiotic segregation increased 2-like 4 pseudogene				
ATRIP	ATR interacting protein				
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2				
C19orf40	Chromosome 19 open reading frame 40				

Table S2. Differential changes in cell cycle genes

Name	Description	SCC		ADC	
		fold-change	p-value	fold-change	p-value
TOP2A	Topoisomerase (DNA) II alpha 170 kDa	5.43	1.23×10^{-11}	2.92	7.95×10^{-9}
CCNB1	Cyclin B1	2.75	6.97×10^{-8}	1.56	4.82×10^{-5}
MELK	Maternal embryonic leucine zipper kinase	2.67	1.75×10^{-7}	1.45	3.21×10^{-6}
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	2.63	4.69×10^{-9}	1.38	2.05×10^{-4}
SFN	Stratifin	2.60	1.94×10^{-7}	1.43	1.28×10^{-5}
CDC6	Cell division cycle 6 homolog (*S. cerevisiae*)	2.54	3.24×10^{-9}	1.54	2.40×10^{-4}
ASPM	asp (abnormal spindle) homolog, microcephaly associated (*Drosophila*)	2.48	1.45×10^{-7}	1.57	7.97×10^{-5}
TOPBP1	Topoisomerase (DNA) II binding protein 1	2.02	5.03×10^{-6}	1.18	4.88×10^{-2}
CHEK1	CHK1 checkpoint homolog (*S. Pombe*)	1.97	1.33×10^{-5}	1.35	1.20×10^{-4}
CCNB2	Cyclin B2	1.93	1.69×10^{-6}	1.30	5.87×10^{-4}
CDC2	Cell division cycle 2, G1 to S and G2 to M	1.84	2.57×10^{-6}	1.37	7.20×10^{-5}
EZH2	Enhancer of zeste homolog 2 (*Drosophila*)	1.78	6.05×10^{-8}	1.24	8.23×10^{-3}
CHEK2	CHK2 checkpoint homolog (*S. Pombe*)	1.73	9.38×10^{-6}	1.18	1.62×10^{-2}
CDK4	Cyclin-dependent kinase 4	1.70	3.64×10^{-6}	1.34	3.85×10^{-3}
GMNN	Geminin, DNA replication inhibitor	1.65	1.07×10^{-4}	1.16	5.31×10^{-2}
NAE1	NEDD8 activating enzyme E1 subunit 1	1.59	1.64×10^{-3}	1.10	3.85×10^{-1}
BRCA1	Breast cancer 1, early onset	1.56	2.13×10^{-5}	1.11	1.25×10^{-1}
CDK6	Cyclin-dependent kinase 6	1.47	2.86×10^{-3}	-1.03	6.09×10^{-1}
ATR	Ataxia telangiectasia and Rad3 related	1.46	1.50×10^{-4}	1.10	2.66×10^{-1}

FANCD2	Fanconi anemia, complementation group D2	1.44	6.33×10^{-6}	1.09	1.90×10^{-1}
HDAC1	Histone deacetylase 1	1.44	1.11×10^{-3}	1.12	3.54×10^{-1}
MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (*E. Coli*)	1.36	9.78×10^{-3}	1.26	1.49×10^{-3}
BIRC5	Baculoviral IAP repeat-containing 5	1.35	1.93×10^{-7}	1.26	1.52×10^{-4}
BARD1	BRCA1 associated RING domain 1	1.33	9.99×10^{-4}	-1.04	3.95×10^{-1}
CDKN2A	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	1.32	2.06×10^{-2}	1.26	1.15×10^{-3}
RAD51	RAD51 homolog (RecA homolog, *E. Coli*) (*S. cerevisiae*)	1.25	4.56×10^{-3}	1.14	2.94×10^{-2}
TBPL1	TBP-like 1	1.23	1.50×10^{-2}	-1.07	3.51×10^{-1}
RINT1	RAD50 interactor 1	1.21	4.38×10^{-3}	1.03	5.78×10^{-1}
FANCA	Fanconi anemia, complementation group A	1.18	2.57×10^{-3}	1.15	3.99×10^{-3}
TP53	Tumor protein p53	1.18	6.27×10^{-2}	1.09	1.88×10^{-1}
CDC25A	Cell division cycle 25 homolog A (*S. Pombe*)	1.17	1.92×10^{-3}	1.05	5.00×10^{-1}
BRCA2	Breast cancer 2, early onset	1.17	1.61×10^{-2}	1.02	6.07×10^{-1}
NBN	Nibrin	1.16	2.26×10^{-1}	1.10	3.12×10^{-1}
RAD50	RAD50 homolog (*S. cerevisiae*)	1.15	3.50×10^{-1}	-1.14	3.96×10^{-1}
LIMK1	LIM domain kinase 1	1.15	1.34×10^{-3}	1.20	1.67×10^{-3}
MAPK14	Mitogen-activated protein kinase 14	1.14	2.18×10^{-1}	1.03	8.05×10^{-1}
TAOK1	TAO kinase 1	1.13	3.32×10^{-1}	-1.15	3.06×10^{-1}
CDK5	Cyclin-dependent kinase 5	1.12	6.26×10^{-2}	1.26	6.48×10^{-4}
TP53BP1	Tumor protein p53 binding protein 1	1.12	8.23×10^{-2}	1.02	8.03×10^{-1}
POLE	Polymerase (DNA directed), epsilon	1.12	2.41×10^{-2}	1.05	3.21×10^{-1}
MRE11A	MRE11 meiotic recombination 11 homolog A (*S. cerevisiae*)	1.10	4.23×10^{-1}	1.05	6.12×10^{-1}

ETV6	ets variant 6	1.10	3.89×10^{-1}	1.14	7.57×10^{-2}
E2F1	E2F transcription factor 1	1.08	7.91×10^{-2}	1.21	9.59×10^{-3}
HUS1	HUS1 checkpoint homolog (*S. Pombe*)	1.08	2.59×10^{-1}	1.03	7.19×10^{-1}
GADD45A	Growth arrest and DNA-damage-inducible, alpha	1.07	5.45×10^{-1}	-1.00	9.99×10^{-1}
CDC25B	Cell division cycle 25 homolog B (*S. Pombe*)	1.07	3.34×10^{-1}	1.06	4.34×10^{-1}
MDC1	Mediator of DNA damage checkpoint 1	1.06	4.24×10^{-1}	1.03	6.25×10^{-1}
TOP2B	topoisomerase (DNA) II beta 180 kDa	1.06	6.39×10^{-1}	-1.29	3.22×10^{-2}
UBA3	Ubiquitin-like modifier activating enzyme 3	1.05	5.31×10^{-1}	1.02	7.93×10^{-1}
TP73	Tumor protein p73	1.05	2.53×10^{-1}	1.06	1.64×10^{-1}
CDK2	Cyclin-dependent kinase 2	1.05	5.94×10^{-1}	-1.09	2.64×10^{-1}
DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, *S. cerevisiae*)	1.05	4.68×10^{-1}	1.20	1.05×10^{-3}
H2AFX	H2A histone family, member X	1.04	4.13×10^{-1}	1.25	4.58×10^{-6}
ATM	ataxia telangiectasia mutated	1.04	7.26×10^{-1}	-1.21	7.93×10^{-2}
RAD17	RAD17 homolog (*S. Pombe*)	1.04	6.98×10^{-1}	1.21	1.44×10^{-2}
TRAF2	TNF receptor-associated factor 2	1.02	6.59×10^{-1}	1.06	1.34×10^{-1}
UIMC1	Ubiquitin interaction motif containing 1	1.02	7.46×10^{-1}	1.09	1.30×10^{-1}
MAPKAPK 2	Mitogen-activated protein kinase-activated protein kinase 2	1.01	7.91×10^{-1}	1.02	7.06×10^{-1}
CDC25C	Cell division cycle 25 homolog C (*S. Pombe*)	1.01	8.74×10^{-1}	1.08	1.72×10^{-1}
TERF1	Telomeric repeat binding factor (NIMA-interacting) 1	1.01	9.26×10^{-1}	-1.02	8.44×10^{-1}
HDAC4	Histone deacetylase 4	1.01	8.64×10^{-1}	1.02	5.65×10^{-1}
MAP2K2	Mitogen-activated protein kinase kinase 2	1.00	9.69×10^{-1}	1.19	8.11×10^{-3}
SPDYA	Speedy homolog A (Xenopus	-1.01	8.79×10^{-1}	1.09	9.73×10^{-2}

	laevis)				
CEP164	Centrosomal protein 164 kDa	-1.01	8.19×10^{-1}	1.00	9.67×10^{-1}
CDKN1B	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-1.01	9.27×10^{-1}	-1.09	3.39×10^{-1}
PPP5C	Protein phosphatase 5, catalytic subunit	-1.01	8.02×10^{-1}	1.05	2.05×10^{-1}
CDKN2B	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-1.01	8.38×10^{-1}	1.20	3.78×10^{-3}
FAM175A	Family with sequence similarity 175, member A	-1.02	7.51×10^{-1}	-1.02	7.81×10^{-1}
RAD9A	RAD9 homolog A (*S. Pombe*)	-1.03	5.52×10^{-1}	1.06	2.13×10^{-1}
CDT1	Chromatin licensing and DNA replication factor 1	-1.03	6.54×10^{-1}	1.18	1.91×10^{-2}
HMGN1	High-mobility group nucleosome binding domain 1	-1.04	3.83×10^{-1}	1.18	5.14×10^{-3}
PPP2CB	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	-1.06	6.49×10^{-1}	-1.30	2.75×10^{-2}
MCPH1	Microcephalin 1	-1.07	2.65×10^{-1}	-1.00	9.96×10^{-1}
MAPK1	Mitogen-activated protein kinase 1	-1.08	4.32×10^{-1}	-1.26	1.93×10^{-2}
BTG3	BTG family, member 3	-1.09	4.16×10^{-1}	-1.07	4.18×10^{-1}
MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (*E. Coli*)	-1.12	1.27×10^{-1}	-1.23	2.00×10^{-3}
CCNG1	Cyclin G1	-1.14	2.93×10^{-1}	-1.01	9.02×10^{-1}
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-1.16	1.18×10^{-1}	1.01	9.32×10^{-1}
PPM1D	Protein phosphatase 1D magnesium-dependent, delta isoform	-1.20	9.29×10^{-3}	-1.04	3.42×10^{-1}
WEE1	WEE1 homolog (*S. Pombe*)	-1.21	3.05×10^{-1}	-1.25	2.52×10^{-1}
FANCC	Fanconi anemia, complementation group C	-1.21	3.49×10^{-3}	-1.14	2.08×10^{-2}
MAPK3	Mitogen-activated protein kinase 3	-1.23	1.58×10^{-4}	-1.08	2.10×10^{-1}
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-1.72	1.98×10^{-2}	-1.39	5.63×10^{-2}

KLF4	Kruppel-like factor 4 (gut)	-2.31	1.83×10^{-9}	-2.54	5.38×10^{-11}
CAV1	Caveolin 1, caveolae protein, 22 kDa	-4.24	2.78×10^{-10}	-4.80	3.59×10^{-12}
ATRIP	ATR interacting protein				

Table S3. Differential changes in apoptosis genes

Name	Description	SCC		ADC	
		fold-change	p-value	fold-change	p-value
Bim	BCL2-like 11 (apoptosis facilitator)	1.56	6.19×10^{-6}	1.04	4.42×10^{-1}
CYCS	Cytochrome c, somatic	1.49	1.46×10^{-3}	1.10	4.69×10^{-1}
ATR	Ataxia telangiectasia and Rad3 related	1.46	1.50×10^{-4}	1.10	2.66×10^{-1}
CAPN1	Calpain 1, (mu/I) large subunit	1.42	1.09×10^{-7}	1.21	1.46×10^{-3}
BIK	BCL2-interacting killer (apoptosis-inducing)	1.38	4.47×10^{-6}	1.21	1.73×10^{-3}
CASP3	Caspase 3, apoptosis-related cysteine peptidase	1.37	1.95×10^{-4}	1.08	2.50×10^{-1}
BIRC5	Baculoviral IAP repeat-containing 5	1.35	1.93×10^{-7}	1.26	1.52×10^{-4}
BAG1	BCL2-associated athanogene	1.23	1.19×10^{-1}	-1.08	4.39×10^{-1}
BIRC4	X-linked inhibitor of apoptosis	1.22	1.26×10^{-2}	-1.01	9.11×10^{-1}
TP53	Tumor protein p53	1.18	6.27×10^{-2}	1.09	1.88×10^{-1}
DFFA	DNA fragmentation factor, 45 kDa, alpha polypeptide	1.18	2.40×10^{-2}	1.09	1.07×10^{-1}
AIFM1	Apoptosis-inducing factor, mitochondrion-associated, 1	1.15	5.22×10^{-2}	1.09	1.77×10^{-1}
BAK1	BCL2-antagonist/killer 1	1.13	1.08×10^{-1}	1.06	6.30×10^{-1}
ENDOG	Endonuclease G	1.12	5.69×10^{-3}	1.11	6.11×10^{-2}
BAX	BCL2-associated X protein	1.10	5.67×10^{-2}	1.21	4.78×10^{-4}
GZMK	Granzyme K (granzyme 3; tryptase II)	1.08	5.59×10^{-1}	-1.17	2.67×10^{-1}
DIABLO	Diablo homolog (*Drosophila*)	1.08	2.01×10^{-1}	1.09	1.01×10^{-1}
CASP6	Caspase 6, apoptosis-related cysteine peptidase	1.07	4.09×10^{-1}	1.16	7.90×10^{-2}
MDM2	Mdm2 p53 binding protein homolog (mouse)	1.05	5.56×10^{-1}	-1.04	8.03×10^{-1}
GZMB	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated	1.05	6.19×10^{-1}	-1.18	1.08×10^{-3}

	serine esterase 1)				
ATM	Ataxia telangiectasia mutated	1.04	7.26×10^{-1}	-1.21	7.93×10^{-2}
AKT1	v-akt murine thymoma viral oncogene homolog 1	1.03	6.06×10^{-1}	1.14	1.98×10^{-2}
BOK	BCL2-related ovarian killer	1.01	8.26×10^{-1}	1.11	6.98×10^{-2}
BID	BH3 interacting domain death agonist	1.01	8.65×10^{-1}	1.05	2.70×10^{-1}
BCL2L2	BCL2-like 2	1.01	9.44×10^{-1}	-1.12	1.09×10^{-1}
BMF	Bcl2 modifying factor	-1.00	9.97×10^{-1}	1.12	3.21×10^{-2}
BCL2L1	BCL2-like 1	-1.01	8.91×10^{-1}	-1.02	8.72×10^{-1}
BCL2	B-cell CLL/lymphoma 2	-1.04	4.97×10^{-1}	1.08	8.44×10^{-2}
CASP7	Caspase 7, apoptosis-related cysteine peptidase	-1.04	4.80×10^{-1}	1.02	7.05×10^{-1}
BBC3	BCL2 binding component 3	-1.05	3.36×10^{-1}	1.12	8.96×10^{-3}
DFFB	DNA fragmentation factor, 40 kDa, beta polypeptide (caspase-activated DNase)	-1.05	2.89×10^{-1}	1.03	6.72×10^{-1}
APAF1	Apoptotic peptidase activating factor 1	-1.05	2.49×10^{-1}	-1.04	3.48×10^{-1}
BCL2L10	BCL2-like 10 (apoptosis facilitator)	-1.06	2.93×10^{-1}	1.10	1.04×10^{-1}
CASP9	Caspase 9, apoptosis-related cysteine peptidase	-1.08	1.61×10^{-1}	1.04	4.76×10^{-1}
BIRC2	Baculoviral IAP repeat-containing 2	-1.11	1.48×10^{-1}	-1.30	6.32×10^{-3}
CASP10	Caspase 10, apoptosis-related cysteine peptidase	-1.12	1.46×10^{-1}	1.01	8.79×10^{-1}
BCL2A1	BCL2-related protein A1	-1.12	3.60×10^{-1}	-1.20	5.64×10^{-2}
CASP4	Caspase 4, apoptosis-related cysteine peptidase	-1.13	2.69×10^{-1}	-1.13	2.76×10^{-1}
BAD	BCL2-associated agonist of cell death	-1.14	2.46×10^{-2}	1.06	1.96×10^{-1}
CASP8	Caspase 8, apoptosis-related cysteine peptidase	-1.16	3.38×10^{-2}	-1.20	1.48×10^{-2}

NAIP	NLR family, apoptosis inhibitory protein	-1.23	2.90×10^{-2}	-1.17	6.10×10^{-2}
BIRC3	Baculoviral IAP repeat-containing 3	-1.27	1.25×10^{-1}	1.04	7.99×10^{-1}
CAPN2	Calpain 2, (m/II) large subunit	-1.41	2.71×10^{-4}	-1.22	1.81×10^{-1}
MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	-1.81	6.44×10^{-8}	-1.59	8.64×10^{-5}
CFLAR	CASP8 and FADD-like apoptosis regulator	-2.34	2.59×10^{-10}	-1.80	1.80×10^{-4}

Table S4. Differential changes in oncogenes

		SCC		ADC	
Name	Description	fold-change	p-value	fold-change	p-value
ECT2	Epithelial cell transforming sequence 2 oncogene	3.59	2.55×10^{-8}	1.54	4.55×10^{-3}
DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (*S. cerevisiae*)	2.66	4.00×10^{-7}	-1.06	4.63×10^{-1}
RAB10	RAB10, member RAS oncogene family	1.84	2.24×10^{-5}	1.13	4.28×10^{-1}
RAB25	RAB25, member RAS oncogene family	1.65	2.09×10^{-4}	1.78	1.55×10^{-7}
MET	met proto-oncogene (hepatocyte growth factor receptor)	1.60	8.63×10^{-3}	1.51	3.08×10^{-2}
NAE1	NEDD8 activating enzyme E1 subunit 1	1.59	1.64×10^{-3}	1.10	3.85×10^{-1}
RAP2B	RAP2B, member of RAS oncogene family	1.56	9.39×10^{-5}	1.14	1.07×10^{-2}
MCM3	Minichromosome maintenance complex component 3	1.56	4.24×10^{-5}	1.20	3.48×10^{-2}
SLC4A1AP	Solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.52	4.59×10^{-3}	1.05	7.03×10^{-1}
DEK	DEK oncogene	1.50	2.98×10^{-3}	-1.04	7.59×10^{-1}
RAB38	RAB38, member RAS oncogene family	1.49	4.24×10^{-4}	1.16	3.15×10^{-2}
HRASLS	HRAS-like suppressor	1.48	3.54×10^{-5}	1.36	1.94×10^{-4}
SET	SET nuclear oncogene	1.45	3.91×10^{-5}	1.06	5.01×10^{-1}
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1.45	1.11×10^{-3}	1.01	9.30×10^{-1}
NET1	Neuroepithelial cell transforming 1	1.42	2.25×10^{-4}	1.38	4.58×10^{-5}
P4HB	Prolyl 4-hydroxylase, beta polypeptide	1.42	5.22×10^{-5}	1.45	1.69×10^{-3}
EIF3E	Eukaryotic translation initiation factor 3, subunit E	1.41	6.90×10^{-3}	1.13	3.06×10^{-1}

PARK7	Parkinson disease (autosomal recessive, early onset) 7	1.40	4.04×10^{-4}	1.31	9.36×10^{-3}
TFG	TRK-fused gene	1.39	1.12×10^{-2}	1.21	3.35×10^{-2}
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	1.38	4.82×10^{-7}	1.21	2.09×10^{-3}
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	1.36	5.01×10^{-2}	-1.21	4.14×10^{-2}
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	1.36	8.49×10^{-6}	1.10	1.41×10^{-1}
CTTN	Cortactin	1.35	1.90×10^{-2}	1.22	8.26×10^{-2}
GNB2L1	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	1.32	6.89×10^{-3}	1.04	7.48×10^{-1}
LCN2	Lipocalin 2	1.31	2.80×10^{-2}	-1.00	9.66×10^{-1}
RAN	RAN, member RAS oncogene family	1.31	3.58×10^{-6}	1.28	3.71×10^{-6}
RAB18	RAB18, member RAS oncogene family	1.30	8.31×10^{-2}	-1.13	3.36×10^{-1}
BMI1	BMI1 polycomb ring finger oncogene	1.29	1.26×10^{-2}	1.03	8.21×10^{-1}
RAB30	RAB30, member RAS oncogene family	1.28	8.22×10^{-3}	1.12	1.69×10^{-1}
RAB11A	RAB11A, member RAS oncogene family	1.28	8.28×10^{-2}	-1.41	7.79×10^{-3}
RAB13	RAB13, member RAS oncogene family	1.26	3.18×10^{-2}	1.19	2.55×10^{-1}
RAB6B	RAB6B, member RAS oncogene family	1.26	5.74×10^{-3}	1.11	1.84×10^{-3}
YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	1.25	3.59×10^{-2}	-1.04	6.83×10^{-1}
PIM2	pim-2 oncogene	1.24	5.84×10^{-3}	1.23	1.27×10^{-3}
ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	1.24	1.80×10^{-2}	1.05	4.13×10^{-1}
MYB	v-myb myeloblastosis viral oncogene homolog (avian)	1.24	4.77×10^{-2}	-1.01	9.21×10^{-1}
HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	1.23	1.95×10^{-5}	1.19	6.43×10^{-5}

RAB15	RAB15, member RAS onocogene family	1.23	4.39×10^{-3}	1.13	4.13×10^{-2}
EGFR	Epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	1.22	1.90×10^{-2}	1.30	1.06×10^{-1}
RAB22A	RAB22A, member RAS oncogene family	1.21	8.18×10^{-3}	1.17	4.41×10^{-2}
TPR	Translocated promoter region (to activated MET oncogene)	1.19	1.23×10^{-1}	-1.04	7.82×10^{-1}
NRAS	Neuroblastoma RAS viral (v-ras) oncogene homolog	1.19	4.03×10^{-2}	1.11	1.30×10^{-1}
RAB9A	RAB9A, member RAS oncogene family	1.18	7.47×10^{-2}	1.03	7.55×10^{-1}
FGFR1OP	FGFR1 oncogene partner	1.18	2.39×10^{-3}	1.01	8.26×10^{-1}
NUP214	Nucleoporin 214 kDa	1.18	3.40×10^{-2}	-1.19	2.16×10^{-2}
RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	1.17	5.29×10^{-2}	1.02	8.17×10^{-1}
FGFR1OP2	FGFR1 oncogene partner 2	1.17	1.84×10^{-1}	1.04	7.76×10^{-1}
EWSR1	Ewing sarcoma breakpoint region 1	1.17	4.91×10^{-2}	-1.09	2.18×10^{-1}
RAB1A	RAB1A, member RAS oncogene family	1.17	2.81×10^{-1}	1.07	6.85×10^{-1}
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	1.16	9.99×10^{-2}	1.04	5.73×10^{-1}
RUNX1	runt-related transcription factor 1	1.16	3.46×10^{-2}	1.23	3.37×10^{-4}
RAB2A	RAB2A, member RAS oncogene family	1.16	1.31×10^{-1}	1.13	2.68×10^{-1}
FUS	Fusion (involved in t(12;16) in malignant liposarcoma)	1.16	1.21×10^{-1}	-1.02	8.58×10^{-1}
RAB3B	RAB3B, member RAS oncogene family	1.15	9.92×10^{-2}	1.19	3.84×10^{-2}
AKT2	v-akt murine thymoma viral oncogene homolog 2	1.14	9.05×10^{-3}	1.01	8.07×10^{-1}
RAB27B	RAB27B, member RAS oncogene family	1.14	1.22×10^{-1}	1.10	2.80×10^{-1}

HKR1	GLI-Kruppel family member HKR1	1.14	5.99×10^{-2}	1.11	1.08×10^{-2}
ITPA	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	1.13	2.09×10^{-2}	1.09	6.25×10^{-2}
MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	1.13	1.19×10^{-2}	1.18	1.35×10^{-2}
MERTK	c-mer proto-oncogene tyrosine kinase	1.13	2.82×10^{-1}	1.03	7.69×10^{-1}
BRI3BP	BRI3 binding protein	1.13	5.26×10^{-2}	1.23	4.03×10^{-4}
ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	1.13	1.89×10^{-1}	1.11	1.60×10^{-1}
RAB1B	RAB1B, member RAS oncogene family	1.12	2.26×10^{-1}	1.07	5.58×10^{-1}
SKIL	SKI-like oncogene	1.12	3.14×10^{-1}	-1.05	6.63×10^{-1}
RAB7A	RAB7A, member RAS oncogene family	1.12	2.95×10^{-1}	-1.27	1.11×10^{-1}
RAB40C	RAB40C, member RAS oncogene family	1.11	8.23×10^{-2}	1.32	1.24×10^{-4}
RAB12	RAB12, member RAS oncogene family	1.11	4.32×10^{-2}	-1.03	5.35×10^{-1}
IRF4	Interferon regulatory factor 4	1.11	1.93×10^{-1}	1.10	2.44×10^{-2}
ELK1	ELK1, member of ETS oncogene family	1.10	4.22×10^{-2}	1.15	6.63×10^{-3}
ETV6	ets variant 6	1.10	3.89×10^{-1}	1.14	7.57×10^{-2}
RAB40B	RAB40B, member RAS oncogene family	1.10	5.42×10^{-2}	1.15	1.38×10^{-3}
TET1	tet oncogene 1	1.10	2.30×10^{-1}	1.03	5.79×10^{-1}
RAB8A	RAB8A, member RAS oncogene family	1.08	4.70×10^{-1}	-1.26	1.09×10^{-1}
RABL4	RAB, member of RAS oncogene family-like 4	1.08	2.30×10^{-1}	1.12	8.22×10^{-2}
BLOC1S2	Biogenesis of lysosomal organelles complex-1, subunit 2	1.08	3.59×10^{-1}	1.01	8.43×10^{-1}
RAB3D	RAB3D, member RAS oncogene family	1.08	1.95×10^{-1}	1.08	2.11×10^{-1}

VAV2	vav 2 guanine nucleotide exchange factor	1.08	3.26×10^{-1}	1.01	8.41×10^{-1}
RAB7L1	RAB7, member RAS oncogene family-like 1	1.07	1.27×10^{-1}	-1.08	1.81×10^{-1}
MRPS11	Mitochondrial ribosomal protein S11	1.07	1.84×10^{-1}	1.17	5.48×10^{-3}
CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	1.07	1.83×10^{-1}	-1.03	5.84×10^{-1}
RAP2C	RAP2C, member of RAS oncogene family	1.07	2.09×10^{-1}	1.15	8.69×10^{-4}
RAB6A	RAB6A, member RAS oncogene family	1.07	4.65×10^{-1}	1.01	8.62×10^{-1}
RAB23	RAB23, member RAS oncogene family	1.07	5.96×10^{-1}	-1.32	2.63×10^{-2}
RAB3A	RAB3A, member RAS oncogene family	1.06	1.36×10^{-1}	1.10	7.76×10^{-2}
RAB21	RAB21, member RAS oncogene family	1.06	6.12×10^{-1}	-1.23	1.99×10^{-1}
TMEM50A	Transmembrane protein 50A	1.06	6.51×10^{-1}	-1.06	5.98×10^{-1}
RELB	v-rel reticuloendotheliosis viral oncogene homolog B	1.05	3.13×10^{-1}	1.12	6.33×10^{-2}
RAB26	RAB26, member RAS oncogene family	1.05	3.25×10^{-1}	1.21	1.53×10^{-3}
GLI3	GLI family zinc finger 3	1.05	5.64×10^{-1}	-1.03	6.47×10^{-1}
GLI4	GLI family zinc finger 4	1.04	4.00×10^{-1}	1.14	5.81×10^{-4}
RRAS2	Related RAS viral (r-ras) oncogene homolog 2	1.04	4.13×10^{-1}	1.20	1.64×10^{-4}
NR2F6	Nuclear receptor subfamily 2, group F, member 6	1.04	4.42×10^{-1}	1.23	4.71×10^{-5}
FGF3	Fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog)	1.04	4.62×10^{-1}	1.21	1.62×10^{-2}
PIM1	pim-1 oncogene	1.04	6.53×10^{-1}	1.07	1.13×10^{-1}
ZSCAN22	Zinc finger and SCAN domain containing 22	1.03	5.80×10^{-1}	1.06	2.53×10^{-1}
DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1.03	8.35×10^{-1}	-1.18	2.93×10^{-1}

RAB35	RAB35, member RAS oncogene family	1.03	7.65×10^{-1}	-1.09	3.27×10^{-1}
ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	1.03	5.53×10^{-1}	-1.09	8.34×10^{-2}
AKT1	v-akt murine thymoma viral oncogene homolog 1	1.03	6.06×10^{-1}	1.14	1.98×10^{-2}
RAB28	RAB28, member RAS oncogene family	1.03	7.67×10^{-1}	-1.13	3.06×10^{-1}
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	1.03	6.41×10^{-1}	1.22	2.29×10^{-4}
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	1.03	6.08×10^{-1}	1.10	2.20×10^{-2}
ETV7	ets variant 7	1.03	6.19×10^{-1}	-1.01	8.07×10^{-1}
RAB34	RAB34, member RAS oncogene family	1.03	5.98×10^{-1}	1.24	1.77×10^{-6}
MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	1.02	5.43×10^{-1}	1.04	2.90×10^{-1}
RAB14	RAB14, member RAS oncogene family	1.02	8.66×10^{-1}	-1.57	3.44×10^{-3}
RAB3C	RAB3C, member RAS oncogene family	1.02	7.84×10^{-1}	-1.05	4.08×10^{-1}
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	1.02	7.34×10^{-1}	-1.13	2.73×10^{-3}
RAB39B	RAB39B, member RAS oncogene family	1.02	7.28×10^{-1}	-1.02	7.92×10^{-1}
RET	ret proto-oncogene	1.02	6.56×10^{-1}	1.01	8.71×10^{-1}
RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	1.02	8.65×10^{-1}	-1.35	8.13×10^{-3}
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	1.02	6.52×10^{-1}	1.10	2.50×10^{-2}
TTC23	Tetratricopeptide repeat domain 23	1.02	7.68×10^{-1}	-1.03	4.95×10^{-1}
WNT3	Wingless-type MMTV integration site family, member 3	1.02	7.43×10^{-1}	1.20	5.90×10^{-4}
GLI1	GLI family zinc finger 1	1.02	7.63×10^{-1}	1.12	7.94×10^{-2}

GLI2	GLI family zinc finger 2	1.02	7.61×10^{-1}	1.11	3.29×10^{-2}
MAFA	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	1.01	8.88×10^{-1}	1.15	8.23×10^{-3}
RHOC	ras homolog gene family, member C	1.01	9.24×10^{-1}	1.08	2.34×10^{-1}
RAB24	RAB24, member RAS oncogene family	1.01	8.90×10^{-1}	1.06	1.48×10^{-1}
RAB33B	RAB33B, member RAS oncogene family	1.01	9.39×10^{-1}	1.11	1.03×10^{-1}
EPHA1	EPH receptor A1	1.00	8.99×10^{-1}	1.08	7.17×10^{-2}
RAB5B	RAB5B, member RAS oncogene family	1.00	9.91×10^{-1}	-1.11	3.12×10^{-1}
WNT1	Wingless-type MMTV integration site family, member 1	1.00	9.91×10^{-1}	1.13	2.91×10^{-2}
CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	-1.00	9.49×10^{-1}	1.06	3.64×10^{-1}
TCL1A	T-cell leukemia/lymphoma 1A	-1.00	9.51×10^{-1}	1.12	5.70×10^{-2}
RABL5	RAB, member RAS oncogene family-like 5	-1.01	9.11×10^{-1}	1.05	3.03×10^{-1}
RAB33A	RAB33A, member RAS oncogene family	-1.01	8.79×10^{-1}	1.08	2.20×10^{-1}
RAB5C	RAB5C, member RAS oncogene family	-1.01	9.07×10^{-1}	1.07	4.51×10^{-1}
MCF2	MCF.2 cell line derived transforming sequence	-1.01	8.35×10^{-1}	1.13	2.25×10^{-2}
MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.01	8.23×10^{-1}	1.16	1.08×10^{-2}
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	-1.01	8.34×10^{-1}	1.09	5.15×10^{-2}
FGF4	Fibroblast growth factor 4	-1.01	7.91×10^{-1}	1.13	1.70×10^{-2}
SSPN	Sarcospan (Kras oncogene-associated gene)	-1.01	8.01×10^{-1}	1.00	9.41×10^{-1}
MOS	v-mos Moloney murine sarcoma viral oncogene homolog	-1.02	8.30×10^{-1}	1.03	6.99×10^{-1}

RAB11B	RAB11B, member RAS oncogene family	-1.02	8.33×10^{-1}	-1.04	4.85×10^{-1}
RAB2B	RAB2B, member RAS oncogene family	-1.02	8.57×10^{-1}	-1.17	9.91×10^{-2}
ERAS	ES cell expressed Ras	-1.02	7.42×10^{-1}	1.13	1.49×10^{-2}
RGL2	ral guanine nucleotide dissociation stimulator-like 2	-1.02	7.53×10^{-1}	1.00	9.86×10^{-1}
RAB4B	RAB4B, member RAS oncogene family	-1.02	6.15×10^{-1}	1.06	2.23×10^{-1}
RABL3	RAB, member of RAS oncogene family-like 3	-1.02	8.66×10^{-1}	1.04	7.08×10^{-1}
RAB7B	RAB7B, member RAS oncogene family	-1.02	5.44×10^{-1}	1.02	5.34×10^{-1}
LCK	Lymphocyte-specific protein tyrosine kinase	-1.03	6.40×10^{-1}	1.06	2.08×10^{-1}
FEV	FEV (ETS oncogene family)	-1.03	6.62×10^{-1}	1.18	5.08×10^{-3}
RAB5A	RAB5A, member RAS oncogene family	-1.03	7.21×10^{-1}	-1.04	7.41×10^{-1}
NTRK1	Neurotrophic tyrosine kinase, receptor, type 1	-1.03	5.13×10^{-1}	1.09	7.97×10^{-2}
MMEL1	Membrane metallo-endopeptidase-like 1	-1.03	5.53×10^{-1}	1.07	1.92×10^{-1}
THPO	Thrombopoietin	-1.03	5.85×10^{-1}	1.04	4.43×10^{-1}
CALCA	Calcitonin-related polypeptide alpha	-1.03	5.76×10^{-1}	1.25	2.73×10^{-1}
BCL2	B-cell CLL/lymphoma 2	-1.04	4.97×10^{-1}	1.08	8.44×10^{-2}
CCND1	cyclin D1	-1.04	6.52×10^{-1}	1.06	4.94×10^{-1}
ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	-1.04	6.50×10^{-1}	1.00	9.81×10^{-1}
TLX1	T-cell leukemia homeobox 1	-1.04	6.24×10^{-1}	1.05	3.92×10^{-1}
ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-1.04	5.39×10^{-1}	1.12	1.47×10^{-2}
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	-1.04	4.91×10^{-1}	-1.01	8.22×10^{-1}

RAB6C	RAB6C, member RAS oncogene family	-1.04	6.76×10^{-1}	-1.25	1.04×10^{-1}
RAB36	RAB36, member RAS oncogene family	-1.05	3.46×10^{-1}	-1.09	7.18×10^{-2}
MAS1L	MAS1 oncogene-like	-1.05	4.83×10^{-1}	1.04	5.47×10^{-1}
RAB32	RAB32, member RAS oncogene family	-1.05	3.54×10^{-1}	1.11	5.44×10^{-2}
RAB39	RAB39, member RAS oncogene family	-1.05	4.87×10^{-1}	1.04	5.47×10^{-1}
MPL	Myeloproliferative leukemia virus oncogene	-1.06	1.56×10^{-1}	-1.02	5.97×10^{-1}
RAB43	RAB43, member RAS oncogene family	-1.06	4.88×10^{-1}	-1.00	9.83×10^{-1}
RAB40AL	RAB40A, member RAS oncogene family-like	-1.07	4.55×10^{-1}	1.02	7.75×10^{-1}
RAP2A	RAP2A, member of RAS oncogene family	-1.07	4.17×10^{-1}	-1.00	9.80×10^{-1}
FOXG1	Forkhead box G1	-1.07	1.79×10^{-1}	1.16	1.04×10^{-2}
RAB9B	RAB9B, member RAS oncogene family	-1.08	1.73×10^{-1}	-1.02	7.98×10^{-1}
TCL1B	T-cell leukemia/lymphoma 1B	-1.08	1.63×10^{-1}	1.11	1.35×10^{-1}
RAB41	RAB41, member RAS oncogene family	-1.08	1.18×10^{-1}	1.02	8.04×10^{-1}
MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	-1.09	2.72×10^{-1}	1.01	8.87×10^{-1}
BRAF	v-raf murine sarcoma viral oncogene homolog B1	-1.09	2.94×10^{-1}	-1.08	4.62×10^{-1}
PIM3	pim-3 oncogene	-1.09	1.28×10^{-1}	-1.02	6.60×10^{-1}
WNT7A	Wingless-type MMTV integration site family, member 7A	-1.10	1.56×10^{-1}	-1.01	7.82×10^{-1}
REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	-1.10	3.90×10^{-1}	-1.01	9.05×10^{-1}
CDON	Cdon homolog (mouse)	-1.10	9.39×10^{-2}	-1.10	1.27×10^{-1}
RAB20	RAB20, member RAS oncogene family	-1.10	1.83×10^{-1}	1.03	5.64×10^{-1}

MRAS	Muscle RAS oncogene homolog	-1.11	3.69×10^{-1}	-1.03	5.95×10^{-1}
CSF1R	Colony stimulating factor 1 receptor	-1.11	9.25×10^{-2}	1.02	6.44×10^{-1}
RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	-1.11	1.74×10^{-1}	-1.21	8.95×10^{-3}
ADRB1	Adrenergic, beta-1-, receptor	-1.11	9.67×10^{-2}	1.08	2.08×10^{-1}
SKI	v-ski sarcoma viral oncogene homolog (avian)	-1.11	3.55×10^{-2}	1.08	7.68×10^{-2}
THRB	Thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	-1.12	4.74×10^{-2}	-1.12	3.33×10^{-2}
FRAT1	Frequently rearranged in advanced T-cell lymphomas	-1.12	5.73×10^{-2}	1.01	8.37×10^{-1}
VAV1	vav 1 guanine nucleotide exchange factor	-1.13	3.25×10^{-2}	-1.00	9.95×10^{-1}
RAP1B	RAP1B, member of RAS oncogene family	-1.14	4.41×10^{-1}	-1.73	5.82×10^{-3}
RAB37	RAB37, member RAS oncogene family	-1.14	1.23×10^{-2}	1.08	2.00×10^{-1}
EEF1A1	Eukaryotic translation elongation factor 1 alpha 1	-1.14	2.38×10^{-1}	-1.16	8.13×10^{-2}
RAB42	RAB42, member RAS oncogene family	-1.14	1.74×10^{-1}	-1.01	8.90×10^{-1}
ABL1	c-abl oncogene 1, receptor tyrosine kinase	-1.14	1.85×10^{-2}	-1.08	2.07×10^{-1}
RABL2B	RAB, member of RAS oncogene family-like 2B	-1.15	1.66×10^{-2}	-1.20	4.97×10^{-3}
MAS1	MAS1 oncogene	-1.15	3.62×10^{-2}	1.02	8.03×10^{-1}
FES	Feline sarcoma oncogene	-1.16	6.14×10^{-3}	-1.05	2.91×10^{-1}
EVI1	Ecotropic viral integration site 1	-1.16	6.96×10^{-2}	-1.00	9.99×10^{-1}
RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	-1.17	3.54×10^{-2}	-1.15	2.36×10^{-2}
PEA15	Phosphoprotein enriched in astrocytes 15	-1.18	1.23×10^{-1}	-1.26	5.63×10^{-2}
CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating	-1.18	2.07×10^{-1}	1.14	2.77×10^{-1}

	activity, alpha)				
RAB40A	RAB40A, member RAS oncogene family	-1.19	2.68×10^{-3}	-1.05	3.04×10^{-1}
RAB31	RAB31, member RAS oncogene family	-1.20	1.56×10^{-1}	-1.09	4.61×10^{-1}
PDGFB	Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	-1.20	2.55×10^{-3}	-1.06	3.65×10^{-1}
RAP1A	RAP1A, member of RAS oncogene family	-1.21	6.05×10^{-2}	-1.27	1.90×10^{-2}
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	-1.21	1.81×10^{-3}	-1.01	9.02×10^{-1}
USP6	Ubiquitin specific peptidase 6 (Tre-2 oncogene)	-1.22	9.09×10^{-3}	-1.10	1.22×10^{-1}
RABL2A	RAB, member of RAS oncogene family-like 2A	-1.22	7.63×10^{-3}	-1.24	7.50×10^{-3}
RRAS	Related RAS viral (r-ras) oncogene homolog	-1.23	3.91×10^{-3}	-1.09	1.81×10^{-1}
VAV3	vav 3 guanine nucleotide exchange factor	-1.23	1.18×10^{-2}	-1.27	7.05×10^{-3}
SPAG9	Sperm associated antigen 9	-1.24	5.45×10^{-2}	-1.31	5.09×10^{-2}
RHOA	ras homolog gene family, member A	-1.24	3.95×10^{-3}	-1.29	4.22×10^{-3}
RASEF	RAS and EF-hand domain containing	-1.25	3.74×10^{-3}	1.07	4.46×10^{-1}
THRA	Thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	-1.26	6.05×10^{-3}	-1.19	2.69×10^{-2}
MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	-1.26	1.63×10^{-2}	-1.09	2.27×10^{-1}
AXL	AXL receptor tyrosine kinase	-1.26	7.17×10^{-6}	-1.12	2.65×10^{-2}
RBM6	RNA binding motif protein 6	-1.27	4.86×10^{-2}	-1.29	7.04×10^{-2}
USP4	Ubiquitin specific peptidase 4 (proto-oncogene)	-1.28	2.69×10^{-3}	-1.39	9.25×10^{-4}
RAB17	RAB17, member RAS oncogene family	-1.30	1.70×10^{-4}	1.02	6.96×10^{-1}

FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	-1.31	1.67×10^{-4}	-1.08	8.29×10^{-2}
CXCL3	Chemokine (C-X-C motif) ligand 3	-1.32	7.93×10^{-4}	1.11	8.52×10^{-2}
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	-1.34	1.16×10^{-2}	1.02	8.30×10^{-1}
NR2F1	Nuclear receptor subfamily 2, group F, member 1	-1.36	2.47×10^{-6}	-1.10	6.90×10^{-2}
MAP3K8	Mitogen-activated protein kinase kinase kinase 8	-1.36	7.46×10^{-5}	-1.22	9.21×10^{-3}
FYN	FYN oncogene related to SRC, FGR, YES	-1.38	6.05×10^{-4}	-1.62	3.58×10^{-5}
MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	-1.40	5.49×10^{-4}	-1.03	6.47×10^{-1}
RAB27A	RAB27A, member RAS oncogene family	-1.42	6.41×10^{-4}	-1.12	3.27×10^{-1}
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	-1.43	6.51×10^{-3}	-1.48	3.45×10^{-2}
JUND	jun D proto-oncogene	-1.44	1.75×10^{-8}	-1.13	5.28×10^{-3}
RHOB	ras homolog gene family, member B	-1.45	1.96×10^{-7}	-1.08	2.13×10^{-1}
ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-1.58	6.93×10^{-6}	-1.43	1.35×10^{-2}
JUNB	jun B proto-oncogene	-1.60	9.51×10^{-4}	-1.35	2.70×10^{-2}
FER	fer (fps/fes related) tyrosine kinase	-1.61	1.72×10^{-4}	-1.52	1.50×10^{-3}
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	-1.67	1.63×10^{-4}	-1.63	1.55×10^{-4}
FLI1	Friend leukemia virus integration 1	-1.68	1.69×10^{-8}	-1.63	7.05×10^{-6}
ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	-1.72	4.38×10^{-8}	-1.36	2.34×10^{-3}
RAB8B	RAB8B, member RAS oncogene family	-1.76	1.24×10^{-3}	-1.92	3.62×10^{-4}
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	-1.84	2.08×10^{-4}	-1.34	4.29×10^{-2}
AKAP13	A kinase (PRKA) anchor protein	-1.87	3.77×10^{-10}	-1.57	1.75×10^{-4}

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AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-1.88	4.68×10^{-4}	-1.83	2.81×10^{-4}
KLF6	Kruppel-like factor 6	-1.97	6.09×10^{-9}	-1.46	2.99×10^{-4}
JUN	jun oncogene	-2.30	7.39×10^{-9}	-1.72	1.19×10^{-4}
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	-2.80	7.18×10^{-7}	-2.02	9.18×10^{-4}
ROS1	c-ros oncogene 1 , receptor tyrosine kinase	-2.97	8.79×10^{-9}	-1.22	3.44×10^{-1}
CXCL2	Chemokine (C-X-C motif) ligand 2	-3.65	2.45×10^{-8}	-1.69	4.68×10^{-4}
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-4.65	1.60×10^{-9}	-2.14	4.87×10^{-4}

Table S5. Differential changes in tumor suppressors

Name	Description	SCC		ADC	
		fold-change	p-value	fold-change	p-value
DLG1	Discs, large homolog 1 (*Drosophila*)	2.41	3.46×10^{-5}	-1.15	3.72×10^{-1}
DLGAP5	Discs, large (*Drosophila*) homolog-associated protein 5	2.35	4.22×10^{-7}	1.42	1.13×10^{-4}
FAT	FAT tumor suppressor homolog 1 (*Drosophila*)	1.95	1.64×10^{-5}	1.34	2.29×10^{-2}
TRIM59	Tripartite motif-containing 59	1.55	8.23×10^{-5}	1.21	4.97×10^{-6}
FAT2	FAT tumor suppressor homolog 2 (*Drosophila*)	1.52	3.83×10^{-5}	1.10	6.39×10^{-2}
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	1.48	3.47×10^{-5}	1.10	1.62×10^{-1}
CDKN2A	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	1.32	2.06×10^{-2}	1.26	1.15×10^{-3}
TUSC3	Tumor suppressor candidate 3	1.29	4.14×10^{-2}	-1.01	9.36×10^{-1}
ING2	Inhibitor of growth family, member 2	1.25	7.19×10^{-2}	1.18	2.65×10^{-1}
ST13	Suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	1.25	7.53×10^{-2}	-1.10	4.53×10^{-1}
EXT1	Exostoses (multiple) 1	1.19	1.50×10^{-1}	-1.07	3.64×10^{-1}
TP53	Tumor protein p53	1.18	6.27×10^{-2}	1.09	1.88×10^{-1}
VHL	von Hippel-Lindau tumor suppressor	1.17	1.60×10^{-2}	1.20	1.02×10^{-3}
BRCA2	Breast cancer 2, early onset	1.17	1.61×10^{-2}	1.02	6.07×10^{-1}
RB1	Retinoblastoma 1	1.15	1.57×10^{-1}	-1.40	1.93×10^{-3}
LATS1	LATS, large tumor suppressor, homolog 1 (*Drosophila*)	1.15	3.78×10^{-2}	-1.15	2.59×10^{-2}
POU6F2	POU class 6 homeobox 2	1.14	3.07×10^{-2}	1.10	1.35×10^{-1}
CELSR2	Cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo	1.12	9.52×10^{-3}	1.10	4.80×10^{-3}

	homolog, *Drosophila*)				
PDGFRL	Platelet-derived growth factor receptor-like	1.12	1.91×10^{-1}	1.15	1.60×10^{-2}
BAX	BCL2-associated X protein	1.10	5.67×10^{-2}	1.21	4.78×10^{-4}
EXT2	Exostoses (multiple) 2	1.09	1.17×10^{-1}	1.00	9.21×10^{-1}
RARB	Retinoic acid receptor, beta	1.09	2.37×10^{-1}	-1.12	9.82×10^{-2}
ING1	Inhibitor of growth family, member 1	1.08	1.68×10^{-1}	1.10	2.26×10^{-2}
FH	Fumarate hydratase	1.07	3.18×10^{-1}	1.06	4.42×10^{-1}
EAF2	ELL associated factor 2	1.07	3.09×10^{-1}	1.06	2.95×10^{-1}
ING4	Inhibitor of growth family, member 4	1.07	2.85×10^{-1}	-1.01	8.93×10^{-1}
FAM123B	Family with sequence similarity 123B	1.06	2.78×10^{-1}	1.06	2.86×10^{-1}
ST7L	Suppression of tumorigenicity 7 like	1.05	2.52×10^{-1}	-1.04	2.28×10^{-1}
STEAP3	STEAP family member 3	1.05	2.84×10^{-1}	1.15	3.35×10^{-3}
SMAD2	SMAD family member 2	1.04	7.32×10^{-1}	1.04	7.07×10^{-1}
FAM10A4	Family with sequence similarity 10, member A4 pseudogene	1.04	5.94×10^{-1}	1.00	9.97×10^{-1}
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	1.02	6.95×10^{-1}	1.30	3.27×10^{-5}
MN1	Meningioma (disrupted in balanced translocation) 1	1.02	7.36×10^{-1}	1.16	7.45×10^{-3}
PTCH1	Patched homolog 1 (*Drosophila*)	1.01	8.18×10^{-1}	-1.04	3.97×10^{-1}
Pinx1	PIN2-interacting protein 1	1.01	9.32×10^{-1}	1.09	1.86×10^{-1}
TUSC2	Tumor suppressor candidate 2	1.00	9.53×10^{-1}	1.15	4.09×10^{-3}
DLEU1	Deleted in lymphocytic leukemia 1 (non-protein coding)	-1.00	1.00	-1.01	9.22×10^{-1}
LZTS2	Leucine zipper, putative tumor suppressor 2	-1.00	9.07×10^{-1}	1.02	6.23×10^{-1}
GLTSCR1	Glioma tumor suppressor candidate region gene 1	-1.00	9.22×10^{-1}	1.11	4.39×10^{-2}

CDKN1B	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-1.01	9.27×10^{-1}	-1.09	3.39×10^{-1}
CDKN2B	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-1.01	8.38×10^{-1}	1.20	3.78×10^{-3}
TUSC4	Tumor suppressor candidate 4	-1.02	6.06×10^{-1}	1.09	3.35×10^{-2}
OVCA2	Candidate tumor suppressor in ovarian cancer 2	-1.03	4.47×10^{-1}	1.06	7.07×10^{-2}
ARL11	ADP-ribosylation factor-like 11	-1.03	5.57×10^{-1}	-1.02	7.04×10^{-1}
TUSC1	Tumor suppressor candidate 1	-1.04	4.24×10^{-1}	1.10	2.77×10^{-2}
RPH3AL	Rabphilin 3A-like (without C2 domains)	-1.05	2.56×10^{-1}	1.23	1.24×10^{-4}
RASSF5	Ras association (RalGDS/AF-6) domain family member 5	-1.05	3.58×10^{-1}	-1.04	5.09×10^{-1}
SMAD4	SMAD family member 4	-1.05	5.53×10^{-1}	-1.25	3.24×10^{-2}
TUSC5	Tumor suppressor candidate 5	-1.06	4.42×10^{-1}	1.06	3.31×10^{-1}
CDK2AP2	Cyclin-dependent kinase 2 associated protein 2	-1.08	2.48×10^{-1}	1.21	4.60×10^{-4}
RASSF4	Ras association (RalGDS/AF-6) domain family member 4	-1.09	3.73×10^{-1}	1.07	1.88×10^{-1}
NKX3-1	NK3 homeobox 1	-1.09	1.07×10^{-1}	1.04	4.59×10^{-1}
LZTS1	Leucine zipper, putative tumor suppressor 1	-1.09	1.90×10^{-1}	1.08	1.94×10^{-1}
APC	Adenomatous polyposis coli	-1.09	3.95×10^{-1}	-1.29	9.09×10^{-4}
PTEN	Phosphatase and tensin homolog	-1.09	3.01×10^{-1}	-1.03	6.85×10^{-1}
CYB561D2	Cytochrome b-561 domain containing 2	-1.10	1.39×10^{-1}	1.04	5.50×10^{-1}
VHLL	von Hippel-Lindau tumor suppressor-like	-1.13	5.81×10^{-2}	-1.04	5.23×10^{-1}
FLCN	Folliculin	-1.13	2.29×10^{-2}	1.04	3.91×10^{-1}
RASSF1	Ras association (RalGDS/AF-6) domain family member 1	-1.15	4.18×10^{-2}	1.06	1.81×10^{-1}
LATS2	LATS, large tumor suppressor, homolog 2 (*Drosophila*)	-1.15	2.82×10^{-3}	1.02	5.47×10^{-1}
RPL10	Ribosomal protein L10	-1.17	1.78×10^{-1}	1.05	7.52×10^{-1}

GLTSCR2	Glioma tumor suppressor candidate region gene 2	-1.18	2.94×10^{-3}	-1.13	6.14×10^{-2}
SPI1	Spleen focus forming virus (SFFV) proviral integration oncogene spi1	-1.20	4.56×10^{-3}	1.05	2.56×10^{-1}
HYAL1	Hyaluronoglucosaminidase 1	-1.20	5.25×10^{-4}	-1.10	4.64×10^{-2}
FAT3	FAT tumor suppressor homolog 3 (*Drosophila*)	-1.20	5.88×10^{-4}	-1.07	2.91×10^{-1}
MTUS1	Mitochondrial tumor suppressor 1	-1.25	4.10×10^{-2}	-1.08	5.09×10^{-1}
DCC	Deleted in colorectal carcinoma	-1.27	1.47×10^{-3}	-1.14	4.26×10^{-2}
FAT4	FAT tumor suppressor homolog 4 (*Drosophila*)	-1.44	1.87×10^{-7}	-1.43	3.55×10^{-7}
CADM1	Cell adhesion molecule 1	-1.98	1.00×10^{-7}	-1.24	3.08×10^{-2}
TGFBR2	Transforming growth factor, beta receptor II (70/80 kDa)	-2.09	1.85×10^{-11}	-1.81	2.09×10^{-7}