

Lists of figures

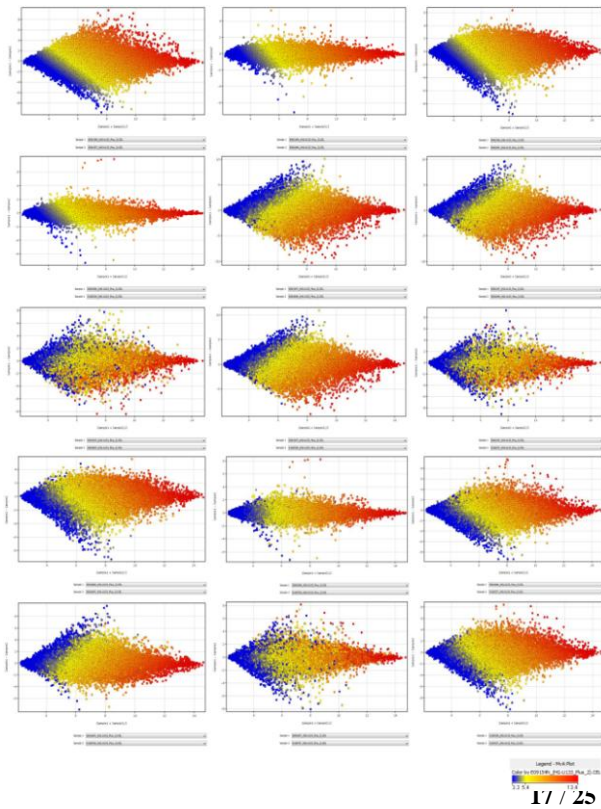
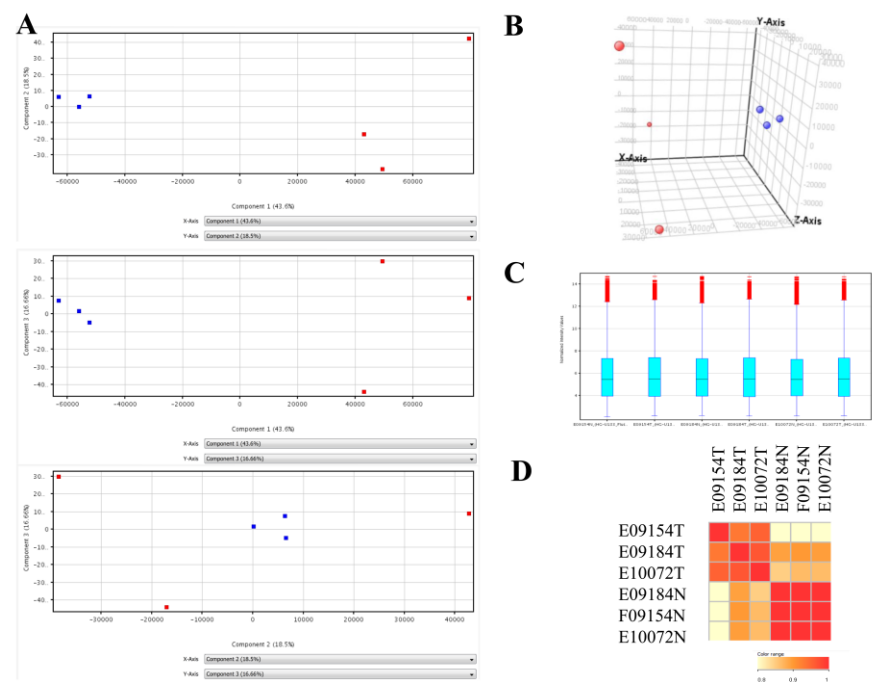


Figure S2: MvA plot of SCEC group.

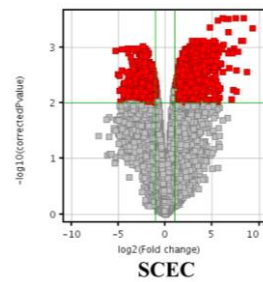


Figure S3: Volcano plots of probe sets differing between SCEC and matched normal tissues.

Fold change (X axis) is plotted against statistical significance (Y axis) for each probe sets. Genes altered with a fold change ≥ 2 and FDR < 0.01 are depicted in red. Grey represents genes in the arrays that were not found to differ significantly between cancerous samples and matched normal samples.

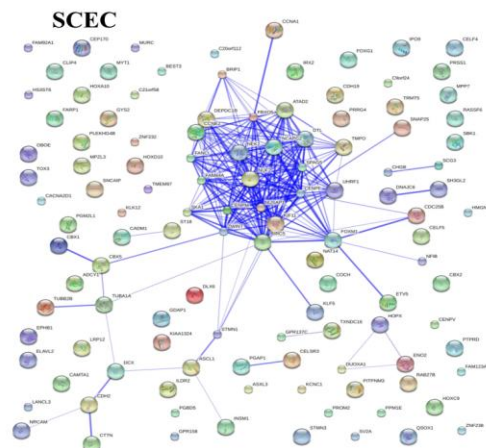


Figure S4: Gene regulatory network plotted by the top 120 DEGs (ranked by FDR) of SCEC groups.

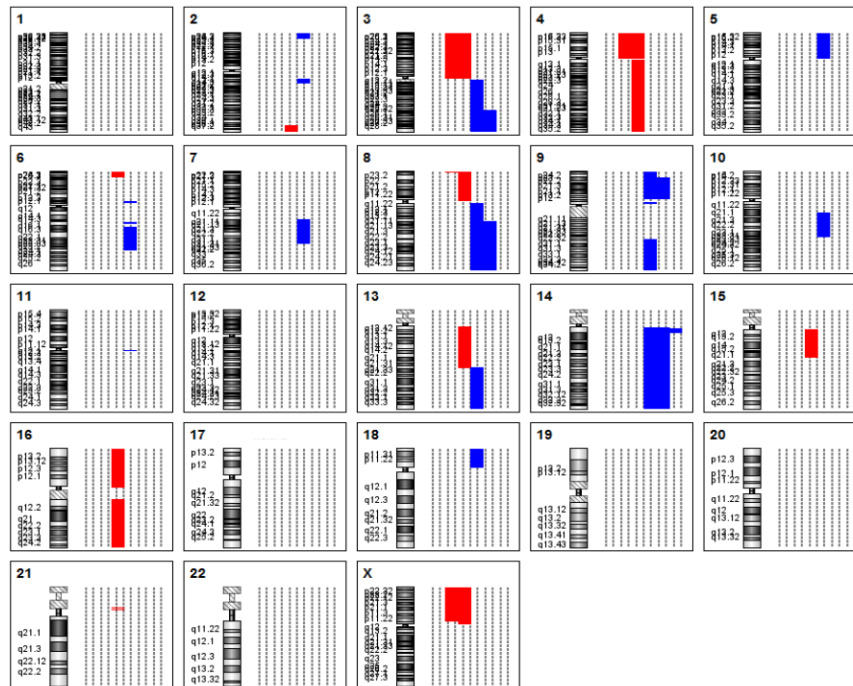


Figure S5: DNA copy number change profiles in 3 pairs of SCEC samples. The CNVs frequency of the whole genome was analyzed by aCGH. Gains were marked in red and losses in blue.

Lists of tables

Table S1. Primers used in qRT-PCR for microarray gene expression validation

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')	Product
β -actin	AAGGTGACAGCAGTCGGTT	TGTGTGGACTTGGGAGAGG	195bp
INSM1	GTATTCGCTGTGTTTCATGGTC	CGCTACATACATAGAGAGCAGAG	79bp
ASCL1	AACTCCCATCACCTCTAACA	TGAGACGAAAGACACCAACT	120bp
NRCAM	GATGGCGAAGAATGAAGTT	ACAGTGAGGGATAAGGTGTG	141bp
NUF2	ATGATGCCAGTGAAGTCTGAA	GACTTGTCCGTTTTGCTTTTG	160bp

SNAP25	CCTGGATATGGGCAATGAGAT	ACACGGGTGGGCACACTTA	146bp
PTP4A3	GCTTCCTCATCACCCACAA	CCGTACTTCTTCAGGTCCTCA	70bp
RFC4	CACCCGATTCTGTCTTATCTG	TCCTTCTTGGCAATGTCTAGT	135bp
REST	TTTAAGAGAAGAGGCATCAG	GATATTAGCAGCAAGACCAG	127bp
APEH	GTATTACCGTGCCCTCAAGAC	AAGTGTGTGCGTAGCCAGA	135bp
FBLN2	AGACCCCAACTCTGTCCATTC	CTCCAGGCACTCGTCATTGT	121bp

Table S2. List of regulatory network genes in SCEC group

Gene symbol	Gene title	Probe set	FC	p value	FDR
<i>INSM1</i>	Insulinoma-associated 1	206502_s_at	321	1.60E-08	2.91E-04
<i>ASCL1</i>	Achaete-scute complex homolog 1	209988_s_at	619	7.48E-08	4.55E-04
<i>TUBB2B</i>	Tubulin, beta 2B class IIb	214023_x_at	102	9.67E-08	5.29E-04
<i>NUSAP1</i>	Nucleolar and spindle associated protein 1	219978_s_at	13.1	2.14E-07	7.65E-04
<i>DCX</i>	Doublecortin	204851_s_at	261	2.47E-07	7.65E-04
<i>NRCAM</i>	Neuronal cell adhesion molecule	204105_s_at	24.8	3.26E-07	8.11E-04
<i>SNAP25</i>	Synaptosomal-associated protein	202508_s_at	74.7	3.79E-07	9.01E-04
<i>CCNE2</i>	Cyclin E2	205034_at	13.0	4.46E-07	9.39E-04
<i>CENPF</i>	Centromere protein F	207331_at	7.44	5.25E-07	9.49E-04
<i>CCNA1</i>	Cyclin A1	205899_at	17.3	4.98E-07	9.49E-04
<i>TUBA1A</i>	Tubulin, alpha 1a	209118_s_at	6.12	5.38E-07	9.49E-04
<i>NUF2</i>	NDC80 kinetochore complex component, homolog	223381_at	11.7	1.38E-06	1.06E-03
<i>FAM64A</i>	Family with sequence similarity 64, member A	221591_s_at	9.13	1.30E-06	1.06E-03
<i>NEK2</i>	NIMA (never in mitosis gene a)-related kinase 2	204641_at	10.1	9.34E-07	1.06E-03
<i>SKA1</i>	Spindle and kinetochore associated complex subunit 1	217640_x_at	5.34	6.67E-07	1.06E-03
<i>SPAG5</i>	Sperm associated antigen 5	203145_at	9.23	6.83E-07	1.06E-03
<i>TMPO</i>	Thymopoietin	209754_s_at	8.36	9.86E-07	1.06E-03
<i>CDC25B</i>	Cell division cycle 25 homolog B	201853_s_at	5.53	1.16E-06	1.06E-03
<i>NFIB</i>	Nuclear factor I/B	209289_at	4.76	1.18E-06	1.06E-03
<i>CBX1</i>	Chromobox homolog 1	201518_at	4.28	1.46E-06	1.06E-03
<i>CDH2</i>	Cadherin 2, type 1, N-cadherin	203440_at	50.0	1.54E-06	1.07E-03
<i>ETV5</i>	Ets variant 5	203348_s_at	4.93	1.61E-06	1.07E-03
<i>FBXO5</i>	F-box protein 5	218875_s_at	8.89	1.65E-06	1.07E-03
<i>DTL</i>	Denticleless E3 ubiquitin protein ligase homolog	222680_s_at	10.6	1.63E-06	1.07E-03
<i>KIF11</i>	Kinesin family member 11	204444_at	6.79	1.79E-06	1.07E-03
<i>KLF5</i>	Kruppel-like factor 5	209211_at	-4.07	1.97E-06	1.13E-03

<i>FANCI</i>	Fanconi anemia, complementation group I	213007_at	5.58	1.98E-06	1.13E-03
<i>STMN1</i>	Stathmin 1	200783_s_at	11.7	2.59E-06	1.15E-03
<i>CTTN</i>	Cortactin	214073_at	-5.24	2.29E-06	1.15E-03
<i>FOXM1</i>	Forkhead box M1	202580_x_at	8.26	2.47E-06	1.15E-03
<i>ZWINT</i>	ZW10 interactor	204026_s_at	6.47	2.68E-06	1.16E-03
<i>CBX5</i>	Chromobox homolog 5	231862_at	4.95	2.73E-06	1.17E-03
<i>CENPM</i>	Centromere protein M	218741_at	4.58	2.88E-06	1.20E-03
<i>NCAPG2</i>	Non-SMC condensin II complex, subunit G2	219588_s_at	5.19	3.01E-06	1.21E-03
<i>ATAD2</i>	ATPase family, AAA domain containing 2	228401_at	6.57	3.11E-06	1.21E-03
<i>UHRF1</i>	Ubiquitin-like with PHD and ring finger domains 1	225655_at	10.7	3.22E-06	1.23E-03
<i>DEPDC1B</i>	DEP domain containing 1B	226980_at	11.9	3.31E-06	1.24E-03
<i>BRIP1</i>	BRCA1 interacting protein C-terminal helicase 1	235609_at	7.85	3.56E-06	1.25E-03
<i>BIRC5</i>	Baculoviral IAP repeat containing 5	202095_s_at	7.13	3.63E-06	1.25E-03

Abbreviations: FC= fold change; FDR= false discover rate.

Table S3. DAVID annotation of regulatory network genes in SCEC group

Database	Name	Count	Benjamini <i>p</i> value
REACTOME	Cell Cycle, Mitotic	12	3.47E-36
GO BP5	Mitosis	14	3.82E-12
	M phase of mitotic cell cycle	14	2.42E-12
	M phase	15	9.29E-12
	Spindle organization	5	5.12E-04
	Regulation of mitotic cell cycle	6	0.00352
	Cell cycle checkpoint	5	0.00556
GO MF5	Tubulin binding	5	0.00731
	Microtubule binding	5	0.0287
	Cytoskeletal protein binding	7	0.0262

Abbreviations: GO= gene ontology; BP= biological process; MF= molecular function.

Table S4. DAVID annotation of genes changed consistently between copy number and mRNA expression in SCEC

Database	Name	Count	<i>p</i> value
KEGG	DNA replication	6	1.42E-04
	P53 signaling pathway	6	0.00274
	Cell cycle	7	0.00868
BBID	RBphosphoE2F	5	0.0195
REACTOME	Cell Cycle, Mitotic	17	1.34E-05
	DNA Repair	7	0.00556

PANTHER GO BP (TOP10)	Cell Cycle Checkpoints	7	0.00872
	DNA Replication	6	0.0193
	P53 pathway	6	0.0269
	DNA replication	15	8.85E-06
	DNA metabolic process	24	4.43E-05
	Mitotic sister chromatid segregation	6	4.39E-04
	DNA repair	14	0.00197
	Mitosis	12	0.00219
	M phase of mitotic cell cycle	12	0.00251
	DNA replication initiation	5	0.00274
GO MF	Cell cycle checkpoint	7	0.00604
	M phase	14	0.00682
	Ras guanyl-nucleotide exchange factor activity	7	0.00278
	Adenyl ribonucleotide binding	32	0.0457

^a DAVID annotation results of genes changed consistently between copy number and mRNA expression were highly concordant with biological processes or pathways annotated by DEGs in SCEC groups (in bold).

Table S5. List of 39 possibly cancer-associated genes in SCEC

Gene symbol	Gene title	Cytoband	Re-gulation	CNV -FC	Pearson r	p value
<i>GTF2A1</i>	General transcription factor IIA, 1	14q24.3-q31.3	Up	2.02	0.9997	0.015
<i>TCTEX1D2</i>	Tctex1 domain containing 2	3q28 - q29	Up	8.51	0.9996	0.018
<i>PDIA5</i>	Protein disulfide isomerase family A, member 5	3q11.1 - q29	Up	35.47	0.9992	0.026
<i>YEATS2</i>	YEATS domain containing 2	3q25.31 - q29	Up	4.76	0.9992	0.026
<i>PIGX</i>	Phosphatidylinositol glycan anchor biosynthesis, class X	3q28 - q29	Up	15.51	0.9992	0.026
<i>IKBKAP</i>	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	9q22.32 - q34.3	Up	9.45	0.9991	0.027
<i>LRCH3</i>	Leucine-rich repeats and calponin homology (CH) domain containing 3	3q28 - q29	Up	153.3	0.9990	0.028
<i>ZNF704</i>	Zinc finger protein 704	5q21.11 - q24.3	Up	2.96	0.9989	0.030
<i>RFC4</i>	Replication factor C 4	3q25.31 - q29	Up	3.59	0.9989	0.030
<i>PAIP1</i>	Poly(A) binding protein interacting protein 1	5p15.33 - p11	Up	3.81	0.9986	0.034
<i>LSG1</i>	Large subunit GTPase 1 homolog	3q28 - q29	Up	231.2	0.9984	0.036
<i>PTP4A3</i>	Protein tyrosine phosphatase type IVA, member 3	8q21.11 - q24.3	Up	2136	0.9983	0.037
<i>C9orf72</i>	Chromosome 9 open reading frame 72	9p23 - p21.1	Up	134.5	0.9981	0.040
<i>DZIP3</i>	DAZ interacting protein 3, zinc finger	3q11.1 - q29	Up	64.25	0.9981	0.040
<i>CAMK2N2</i>	Calcium/calmodulin-dependent protein kinase II inhibitor 2	3q25.31 - q29	Up	5.76	0.9980	0.041
<i>EXOSC3</i>	Exosome component 3	9p23 - p13.1	Up	3.40	0.9975	0.045
<i>ZNF7</i>	Zinc finger protein 7	8q21.11 - q24.3	Up	18.07	0.9971	0.048
<i>C3orf33</i>	Chromosome 3 open reading frame 33	3q11.1 - q29	Up	527.1	0.9980	0.049
<i>IP6K2</i>	Inositol hexakisphosphate kinase 2	3p26.3 - p11.1	Down	3.00	0.9999	0.004
<i>GNRHR</i>	Gonadotropin-releasing hormone receptor	4q11 - q25	Down	24.84	0.9998	0.011

<i>APEH</i>	N-acylaminoacyl-peptide hydrolase	3p26.3 - p11.1	Down	2.72	0.9998	0.013
<i>STAP1</i>	SH3 and cysteine rich domain	4q11 - q25	Down	4.59	0.9997	0.015
<i>GBA3</i>	Glucosidase, beta, acid 3 (cytosolic)	4p16.3 - p11	Down	97.96	0.9997	0.015
<i>TMEM42</i>	Transmembrane protein 40	3p26.3 - p11.1	Down	2.77	0.9997	0.017
<i>WNT5A</i>	Wingless-type MMTV integration site family, member 5A	3p26.3 - p11.1	Down	10.04	0.9996	0.018
<i>UQCRC1</i>	Ubiquinol-cytochrome c reductase core protein I	3p26.3 - p11.1	Down	3.44	0.9996	0.019
<i>C3orf38</i>	Chromosome 3 open reading frame 38	3p26.3 - p11.1	Down	16.85	0.9995	0.019
<i>RPL29</i>	Ribosomal protein L29	3p26.3 - p11.1	Down	4.98	0.9993	0.024
<i>PRKAR2A</i>	Protein kinase, cAMP-dependent, regulatory, type II, alpha	3p26.3 - p11.1	Down	3.56	0.9986	0.034
<i>MAP4</i>	Microtubule-associated protein 4	3p26.3 - p11.1	Down	4.53	0.9986	0.034
<i>AZI2</i>	5-azacytidine induced 2	3p26.3 - p11.1	Down	38.52	0.9985	0.039
<i>ALAS1</i>	Aminolevulinate, delta-, synthase 1	3p26.3 - p11.1	Down	4.99	0.9982	0.038
<i>GOLGA4</i>	Golgin A4	3p26.3 - p11.1	Down	4.53	0.9979	0.041
<i>FBLN2</i>	Fibulin 2	3p26.3 - p11.1	Down	144.08	0.9979	0.041
<i>SH3TC1</i>	SET domain and mariner transposase fusion gene	4p16.3 - p11	Down	5.35	0.9976	0.044
<i>REST</i>	RE1-silencing transcription factor	4q11 - q25	Down	4.35	0.9975	0.045
<i>FBXO25</i>	F-box protein 25	8p23.3 - p23.2	Down	3.32	0.9974	0.046
<i>SHQ1</i>	SH3 domain and tetratricopeptide repeats 1	3p26.3 - p11.1	Down	4.70	0.9971	0.049
<i>ATG7</i>	Autophagy related 7	3p26.3 - p11.1	Down	22.22	0.9970	0.049

Abbreviations: CNV-FC= Copy number associated aberration in gene expression.