

Supplementary Results

RNA-Seq was conducted to compare gene expression in parental Suit2 cells with two isogenic, metastatic Suit2 subclones, S2-013 and S2-LM7AA. In addition, ST6Gal-I was overexpressed (OE) in Suit2 parental cells, and gene expression in OE cells compared with control, empty vector (EV)-transduced Suit2 cells. Data from these experiments are included in the following Supplementary Tables:

Supplementary Table 1. Genes altered in S2-013 and S2-LM7AA cells relative to Suit2 EV cells.

This table lists the top 50 upregulated and downregulated genes in the two metastatic subclones compared to parental, poorly-metastatic Suit2 cells.

Supplementary Table 2. IPA Upstream Regulators altered in S2-013 and S2-LM7AA cells relative to Suit2 EV cells.

In this table, the Ingenuity Pathway Analysis (IPA) Upstream Regulators module was used to identify the pathways either activated or inhibited in the two metastatic subclones as compared with parental Suit2 cells.

Supplementary Table 3. Genes altered in Suit2 OE versus Suit2 EV cells

This table lists the top 50 upregulated and downregulated genes in Suit2 OE cells as compared to Suit2 EV cells.

Supplementary Table 4. IPA Upstream Regulators altered in Suit2 OE relative to Suit2 EV cells.

In this table, the IPA Upstream Regulators module was used to identify the pathways either activated or inhibited in Suit2 OE cells as compared to Suit2 EV cells.

Supplementary Table 1. Genes altered in S2-013 and S2-LM7AA relative to Suit2 EV cells

A Top 50 upregulated genes

S2-013		S2-LM7AA	
gene name	Z Score	gene name	Z Score
CHST9	4.9791565	CHRM3	4.848015
BOC	4.967989	EPHA7	4.834556
TRABD2B	4.9650354	SETBP1	4.8167334
CRMP1	4.9584484	GJA1	4.7665424
SPOCK1	4.953624	LDLRAD4	4.741674
ERBB4	4.953421	P2RY1	4.71017
SLC17A3	4.9468355	WFDC1	4.6820936
RGS4	4.9465475	AUTS2	4.635952
EVC	4.943861	PLAT	4.589742
EPHA7	4.9315243	KCNJ15	4.5756273
PTGER2	4.9291673	CALD1	4.5452437
ISM1	4.918633	LRIG1	4.5425453
PCYT1B	4.9124303	GRID1	4.493754
ENOX1	4.9119964	KCNJ12	4.4503117
DNAJC5B	4.906601	KCNJ4	4.3913965
TNFAIP6	4.899787	CAMK4	4.3471484
LNCAROD	4.8977523	HLX	4.339615
KCNJ15	4.890724	FEZ1	4.3220263
WFDC1	4.8895035	BVES	4.2801723
CRYAB	4.880079	NTF3	4.2795386
EPHB1	4.8786187	TMEFF2	4.273749
HES7	4.873289	DSCAML1	4.2371936
SEMA6A	4.8631697	PDGFD	4.2251496
VAV3	4.8450937	VCAM1	4.2105227
NTNG2	4.834516	ADGRA2	4.192516
AFF3	4.8277216	ASB9	4.1669703
FAM155A	4.826208	NACAD	4.1570516
SEMA6B	4.81453	CD226	4.144238
MIOX	4.8108425	LPAR3	4.1395035
CALD1	4.8006387	ISM1	4.121965
PRDM16	4.800318	HLA-DPB1	4.108773
GPC4	4.7849913	LYPD6	4.085726
SMIM32	4.7691774	CNIH3	4.0844517
PLCB4	4.7635036	TIMP3	4.063056
HLF	4.752887	LZTS1	4.0617776
ALPK2	4.743556	SGK1	4.0599556
TSPAN7	4.7234907	ANGPTL2	4.0381
INHBB	4.715522	RNVU1-4	4.029565
PRR16	4.70858	P3H3	4.0244584
STK32B	4.703925	SRPX	4.009984
DCDC2	4.7028785	TSHZ3	4.007069
HRK	4.701378	TRIM22	3.9996552
DPF3	4.6949487	OSBPL6	3.9904444
SLC16A7	4.6945863	NLGN1	3.987834
MITF	4.694077	CLDN16	3.9798505
FXD2	4.6820965	PAK3	3.9570365
SLC6A15	4.679244	NKAIN	3.9442637
AQP1	4.6703873	SUSD5	3.9180527
ADGRA2	4.663525	FLT1	3.9056764
OTOP1	4.663312	AK5	3.898411

B Top 50 downregulated genes

S2-013		S2-LM7AA	
gene name	Z Score	gene name	Z Score
C4BPB	-4.9913206	GALNT3	-4.851432
CDH2	-4.9894357	CEACAM6	-4.8127456
TMEM176A	-4.989257	PHACTR3	-4.7663064
CCDC152	-4.981356	MAL2	-4.7495804
UGT1A8	-4.978773	SCEL	-4.73677
ADH1C	-4.978284	BSPRY	-4.709945
TBX2	-4.9756083	MYO1D	-4.6571813
TMEM176B	-4.97384	FGF19	-4.6166573
CYP2C18	-4.9592485	STX19	-4.616506
TSPAN8	-4.954827	DAPP1	-4.588257
HSD17B2	-4.9410048	EPHB6	-4.573664
TM4SF20	-4.928785	PAG1	-4.521394
NRIP3	-4.9246254	RAB25	-4.390008
CLRN3	-4.919323	ZNF334	-4.375597
SERPINB5	-4.906589	SPNS2	-4.3255653
SERPINE2	-4.9061775	TMEM30B	-4.3226357
GASK1B	-4.883624	WNT10A	-4.288116
MUC13	-4.8676414	FAM131B	-4.2616997
HHLA2	-4.8645015	ESRP1	-4.205865
CLCN1	-4.8588605	BHLHE41	-4.1997476
AGR2	-4.8586965	GPX2	-4.1956625
GPA33	-4.8570194	FOXJ1	-4.177557
ZNF334	-4.838888	EPN3	-4.1530743
RASGEF1B	-4.824592	KDF1	-4.1398654
AKR1C2	-4.8205986	CBLC	-4.133392
IKZF2	-4.7992053	ITGB6	-4.1187105
UGT1A10	-4.7964425	AKR1B10	-4.114817
PKIA	-4.778929	MARVELD3	-4.099542
CEACAM6	-4.7645407	MPP7	-4.073924
KCNJ3	-4.740252	CDH1	-4.070056
KIAA0040	-4.7266226	FAM83F	-4.068028
STEAP1	-4.7240286	FAM83A	-4.055757
FGF19	-4.692759	TRBC2	-3.991412
RASSF9	-4.660843	TMPRSS13	-3.9877846
ANPEP	-4.647873	CYP2C18	-3.9834173
SNAI2	-4.641878	RBBP8NL	-3.9809165
HAS2	-4.6326146	ANO1	-3.9807398
SPINK7	-4.624757	FUT2	-3.9651875
VSTM2L	-4.622706	KCNJ3	-3.949789
MOB3B	-4.6150417	MPZL2	-3.947292
XYLT1	-4.6099906	MACC1	-3.942559
CGREF1	-4.601841	ENPP5	-3.9124942
ADH6	-4.597636	ANKRD22	-3.8937342
CYP4F3	-4.5905004	CYP2C9	-3.887514
SLC38A11	-4.58188	NCMAP	-3.8839972
B3GALT1	-4.563985	SPRR1B	-3.8657577
MXRA5	-4.5547056	OVOL1	-3.855813
PLA2R1	-4.552125	P2RY2	-3.8537807
OMP	-4.5512743	RAB11FIP4	-3.8528874
CXCL1	-4.5478554	TSPAN2	-3.8372097

Supplementary Table 2. IPA Upstream Regulators altered in S2-013 and S2-LM7AA relative to Suit2 EV cells

A Upstream Regulators with predicted activation

S2-013		S2-LM7AA	
Regulator	Z Score	Regulator	Z Score
DSCAM	4.122	TGFB1	4.557
TEAD4	4.086	MRTFB	4.182
TEAD1	3.979	Tgf beta	4.016
NRG1	3.729	NRG1	3.789
CCR2	3.687	MRTFA	3.491
SIM1	3.637	F2	3.441
TEAD3	3.578	WNT3A	3.388
ARNT2	3.569	EDN1	3.378
NSUN6	3.5	LLGL2	3.317
MRTFB	3.466	CCR2	3.111
DSCAML1	3.452	SMARCA4	3.071
Tgf beta	3.452	CTNNB1	3.043
CBX5	3.317	SHH	2.95
TEAD2	3.3	BDNF	2.914
TGFB1	3.141	NSUN6	2.887
MAPK1	3.046	EPAS1	2.881
BDNF	2.943	D-glucose	2.861
LLGL2	2.887	MAPK1	2.852
glucocorticoid	2.863	FGF8	2.815
NOTCH1	2.842	ROR1	2.813
SMAD3	2.796	SMAD1	2.805
DLX5	2.789	SMAD3	2.791
Wnt	2.739	AGER	2.787
Tcf7	2.709	GLI1	2.787
WWTR1	2.697	NORAD	2.714
HIF1A	2.695	TWIST1	2.709
BMP6	2.664	DSCAM	2.683
TFAP2A	2.59	ROCK1	2.621
D-glucose	2.569	ATF2	2.615
LATS2	2.534	IPMK	2.611
CTNNB1	2.493	Interferon α	2.576
KMT2D	2.468	RUNX1	2.563
FBXO32	2.467	IgG	2.542
TAZ	2.467	TEAD2	2.53
F2	2.45	cyclic AMP	2.528
EDNRA	2.449	ETS1	2.523
ARRB1	2.433	NOTCH3	2.513
GLI1	2.433	F3	2.466
WBP2	2.419	MTPN	2.459
NFIC	2.414	SP1	2.435
VDR	2.385	CBX5	2.414
STK40	2.384	GDF9	2.392
NCOA4	2.383	FEV	2.357
PLAG1	2.377	IL6	2.34
TP53	2.35	ARNT2	2.335
SNAI2	2.343	CYP1B1	2.333
STAT5B	2.336	RETNLB	2.331
MET	2.325	LEF1	2.314
JAG1	2.315	progesterone	2.311
BRD4	2.273	TEAD1	2.309
CIITA	2.27	CG	2.268
WNT1	2.245	MAPK14	2.268
Growth hormone	2.226	IFNAR1	2.249
DLX6	2.219	KDM3A	2.241
TEK	2.219	HRG	2.236
MMP7	2.213	JAG1	2.223
KDM3A	2.197	IFNA2	2.212
NMNAT1	2.197	WBP2	2.212
IL1R2	2.186	EGF	2.207
ROCK1	2.178	GAB2	2.201
PPP1CA	2.176	Fgf	2.2
TET3	2.176	PDGFC	2.198
APLN	2.164	Tnf receptor	2.19
TRIM59	2.157	TGFBR1	2.181
HRG	2.138	BRD4	2.178
NORAD	2.138	Secretase gamma	2.177
IL10	2.115	MYOD1	2.166
GLI2	2.103	RAF1	2.163
CSF1	2.089	RAC1	2.152
ERBB3	2.084	TEAD4	2.137
LEF1	2.083	VCAN	2.126
ROR1	2.074	CLEC4G	2.121
JAK1/2	2.065	CYP1A2	2.121
EBI3	2.06	TEAD3	2.111
FOXC2	2.048	PTK2	2.103
EGR2	2.025	Ap1	2.086
II3	2.025	ZEB1	2.06
EREG	2.012	WWTR1	2.041
HCAR1	2	SIM1	2.038
SMC3	2	TCF7L2	2.01
		β catenin/TCF	2
		Endothelin	2
		RXFP2	2

B Upstream Regulators with predicted inhibition

S2-013		S2-LM7AA	
Regulator	Z Score	Regulator	Z Score
RUNX3	-3.665	RUNX3	-3.969
EGLN	-3.344	SPDEF	-3.771
PTPN1	-3.293	PKD1	-3.573
FAS	-3.132	Alpha catenin	-3.386
HRAS	-3.016	estrogen receptor	-3.375
NR1H4	-2.999	FGF1	-3.347
OGA	-2.898	FAS	-3.231
IKZF3	-2.605	CR1L	-3.121
SFTPA1	-2.578	ALDH1A2	-2.985
GFI1	-2.505	SMAD7	-2.75
CXCR3	-2.425	GFI1	-2.693
IL17R	-2.414	DICER1	-2.649
TNFSF12	-2.393	GAPDH	-2.621
TRADD	-2.345	FBN1	-2.607
FOSL1	-2.286	REST	-2.414
NCOR1	-2.236	HNF1A	-2.391
PTPRE	-2.236	SOCS1	-2.311
SAV1	-2.236	CIP2A	-2.309
SPDEF	-2.226	KRAS	-2.3
SFRP1	-2.214	ABCB4	-2.294
RORC	-2.213	Atrial Natri.Peptide	-2.236
KMT5B	-2.2	SPINT1	-2.224
LTF	-2.2	NOSTRIN	-2.208
NFKBIZ	-2.193	MED16	-2.205
RIPK2	-2.134	TNFRSF1A	-2.191
IL36A	-2.072	HNF1B	-2.176
DL-fructose	-2.046	DKK1	-2.172
FGF1	-2.039	FOXA3	-2.122
DICER1	-2.027	GPX1	-2.07
CLOCK	-2.024	TAF4	-2.007
GATA6	-2.006	CHD1	-2
Atrial Natri.Peptide	-2	GLIS2	-2
CISH	-2	SFRP4	-2
FAF1	-2		
LGALS8	-2		
MEDAG	-2		

Supplementary Table 3. Genes altered in Suit2 OE versus Suit2 EV cells

A Top 50 upregulated genes

Suit2 OE vs. Suit EV	
gene name	Z Score
BASP1	4.9322567
STK32B	4.8835506
EPHB1	4.7745857
ST6GAL1	4.7094207
KCNMA1	4.5498943
KCNJ15	4.4093223
PDGFD	4.2174225
CALD1	4.172452
WFDC1	3.9941797
P2RY1	3.9835193
ANXA8L1	3.9461062
SLC16A7	3.8598228
DPF3	3.8140402
ALPK2	3.775378
ILDR2	3.7584732
SEMA6B	3.7221954
SNCG	3.6903024
PGBD5	3.6679268
DPYSL5	3.6629093
FXD2	3.6378546
WNT5A	3.6239634
IGFBP2	3.5305097
NEURL1	3.486795
AQP1	3.480325
SPOCK1	3.467746
BTNL8	3.4442382
FRMD3	3.4297755
DRAXIN	3.4053168
NUGGC	3.4053168
SLC6A15	3.3929842
TARID	3.3746426
AFF3	3.352433
RGS4	3.3237362
CCDC80	3.2820559
SPP1	3.2807908
SFTPD	3.2591472
CAMK4	3.2503872
HES7	3.2448862
SRPX	3.2286468
NLGN1	3.199847
LPAR3	3.1771877
TRIM9	3.162713
LOXL2	3.152729
LRIG1	3.1396716
SMIM32	3.138023
DCLK2	3.1370163
ANTXR1	3.127695
TNC	3.1158962
MITF	3.0908923
AUTS2	3.0765173

B Top 50 downregulated genes

Suit2 OE vs. Suit2 EV	
gene name	Z Score
GASK1B	-3.3527489
TCIM	-2.9040418
FCER1G	-2.8452768
ANGPTL7	-2.7785919
HHLA2	-2.7483401
ANXA10	-2.3554127
PRR35	-2.348888
CCDC175	-2.2943113
CYP2C18	-2.2828605
DHRS9	-2.250698
CIDEC	-2.1772063
SLC16A9	-2.1759825
AKR1B10	-2.0901911
SIDT1	-2.0725164
MMP1	-2.0614552
ZC3H11A	-2.0372212
FOXF1	-2.028866
BAMBI	-2.0213413
AKR1B15	-2.0111032
WNT7A	-2.007517
SULT1C2	-1.9560361
CLCN1	-1.9129947
GUCY1A1	-1.9120764
RGS2	-1.9100358
SNORA59B	-1.9020985
PKIA	-1.8948313
ERFL	-1.8901143
KRT17	-1.8871663
CYP2C9	-1.8866144
SLC9A2	-1.8684675
DPP4	-1.8655809
XK	-1.8138207
CEACAM6	-1.8080875
LRRN4CL	-1.797032
SNORA71B	-1.7757243
LNCAROD	-1.7651157
ABCC2	-1.750571
P2RY2	-1.749371
CES4A	-1.7472205
SPRR1B	-1.7442523
AGMAT	-1.6901253
IL1RL1	-1.6725954
H3C8	-1.6652617
S100P	-1.6648424
EVA1A	-1.648896
TFF1	-1.6450198
DDX4	-1.6357026
RAET1L	-1.6357026
CELA2B	-1.6357026
KYNU	-1.6319162

Supplementary Table 4. IPA Upstream Regulators altered in Suit2 OE relative to Suit2 EV cells

A Upstream Regulators with predicted activation

Suit2 OE vs. EV		Suit2 OE vs. EV (continued)	
Regulator	Z Score	Regulator	Z Score
ARNT2	4	NFAT5	2.592
TGFB1	3.943	SRC (family)	2.588
HIF1A	3.905	BDNF	2.58
NRG1	3.696	Growth hormone	2.469
TP53	3.68	ZAP70	2.449
SMARCA4	3.669	CD247	2.449
SIM1	3.615	TEAD4	2.449
STAT3	3.546	KDM3A	2.433
Tgf beta	3.543	JUN	2.433
NFKBIA	3.537	ROCK1	2.425
WNT3A	3.535	cholesterol	2.395
KLF4	3.358	BMP2	2.381
SP1	3.327	IL27	2.359
EHMT1	3.317	KITLG	2.343
DSCAML1	3.3	glucocorticoid	2.332
SMAD3	3.296	SOX4	2.331
F2R	3.265	SOX11	2.306
AGT	3.131	CCN2	2.297
VitaminD3-VDR-RXR	3.127	CG	2.287
cyclic AMP	3.105	SMAD4	2.264
JAG1	3.086	AR	2.237
SMARCB1	3.053	IFNAR1	2.236
WBP2	3.036	TIMP1	2.236
LEF1	3.026	ROR1	2.236
MTPN	2.97	THRB	2.234
aldosterone	2.962	ERG	2.228
TGFBR1	2.942	OTX2	2.216
RAF1	2.936	FGF10	2.213
VEGFA	2.935	Complement	2.213
MRTFB	2.883	GLI1	2.208
FEV	2.828	ARID1A	2.2
RETNLB	2.828	TAF7L	2.2
MAFB	2.789	RARB	2.197
F2	2.787	CEBPB	2.193
PDGFB	2.777	FOXC2	2.169
APLN	2.728	Brd4	2.138
GDF2	2.718	F3	2.135
TGM2	2.692	D-glucose	2.118
SHH	2.689	TP73	2.096
DSCAM	2.688	MRTFA	2.078
NFkB (complex)	2.671	IL13	2.068
SGK1	2.646	STAT1	2.038
NORAD	2.646	SMAD1	2.038
NSUN6	2.646	CNR1	2.027
LLGL2	2.646	P38 MAPK	2.023
EPAS1	2.64	HOXB13	2
T3-TR-RXR	2.63	FHL2	2
BRD4	2.626	vitamin K2	2
CCL5	2.596	HRG	2

B Upstream Regulators with predicted inhibition

Suit2 OE vs. EV	
Regulator	Z Score
Alpha catenin	-3.894
EGLN	-3.773
ZNF217	-3.162
CBX5	-2.887
IKZF3	-2.828
FFAR3	-2.813
PSMB11	-2.714
SYK	-2.63
FAS	-2.614
SOX1	-2.53
SPDEF	-2.53
DNMT3B	-2.5
EED	-2.449
CR1L	-2.412
DKK1	-2.393
KDM1A	-2.341
KDM3B	-2.236
NPC2	-2.236
GMNN	-2.145
COL18A1	-2.143
REST	-2.135
CDKN1B	-2.132
CIP2A	-2.121
SOX3	-2.111
KRAS	-2.081
LRP1	-2
LATS1	-2