SUPPLEMENTARY INFORMATION

Recurrent somatic mutation of *FAT1* in multiple human cancers leads to aberrant Wnt activation

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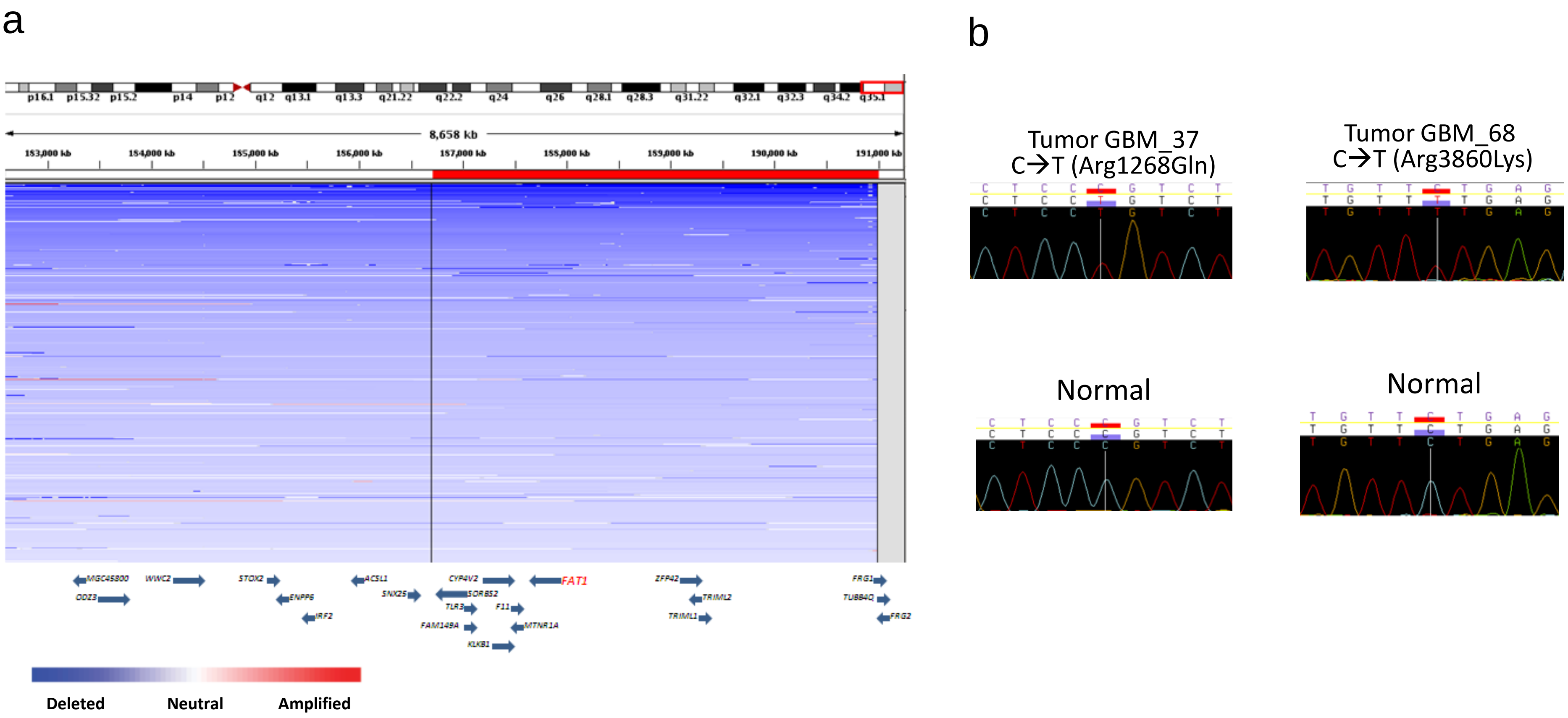
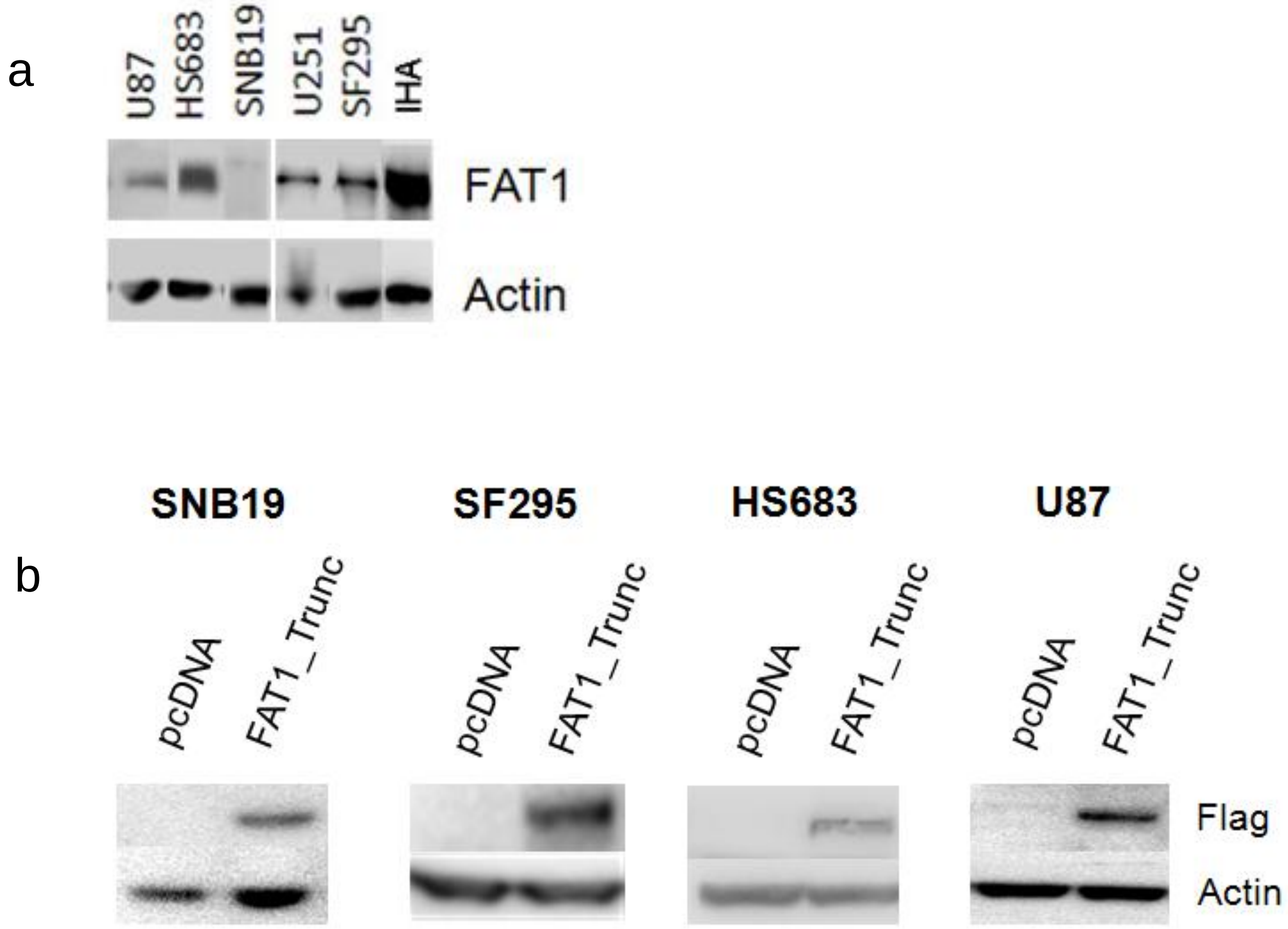
Morris et al. Supplementary Figure 1



Supplementary Figure 1. Copy number alterations and somatic mutations in *FAT1*.

(a)Array CGH segmentation map showing deletions on chromosome 4q35 in the Tumorscape dataset (genomic coordinates at top). A 4,310 kilobase peak region of deletion (highlighted at top in red) encompasses 14 genes. For convenience of viewing, tumors have been sorted by extent of deletion in this peak region (color legend, bottom right), and top 600 (20%) tumors shown. Genes in this region, and surrounding genes, are indicated with blue arrows.

(b)Sequencing traces of representative tumors (top row) with *FAT1* mutations, and verified matched normal samples (bottom row). Vertical lines designate mutation sites. (Although the Arg1268QGln mutation is annotated in dbSNP (rs113970444), a somatic mutation was identified in tumor, but not matching normal tissue).

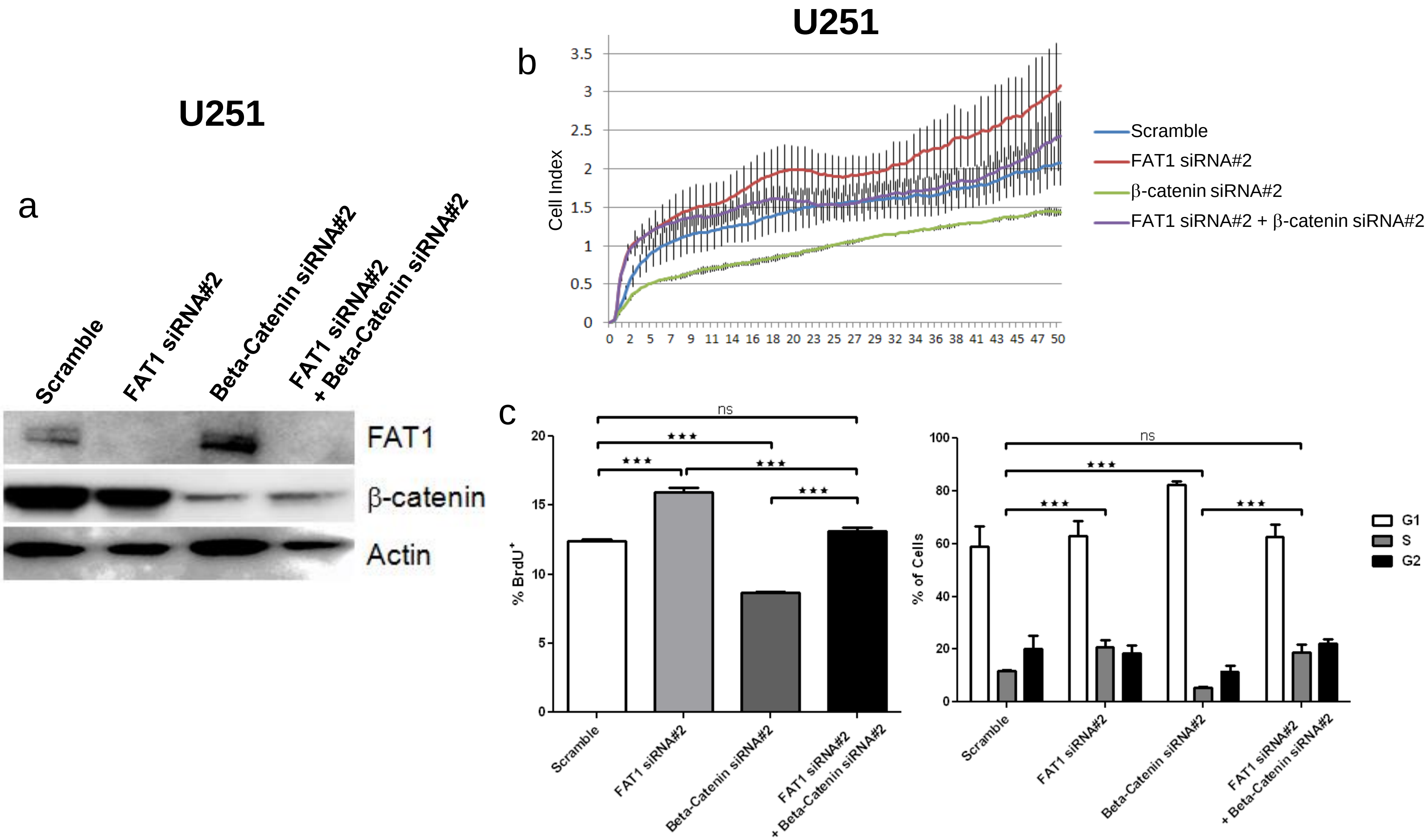


Supplementary Figure 2. Endogenous FAT1 and transfected FAT1_Trunc protein expression.

(a) FAT1 protein expression levels across glioma and immortalized human astrocyte cell lines. Western blot analysis of cell lines using FAT1 antibody, and actin as loading control. Equal amounts of protein (60μg) were loaded in each lane. IHA, immortalized human astrocytes.

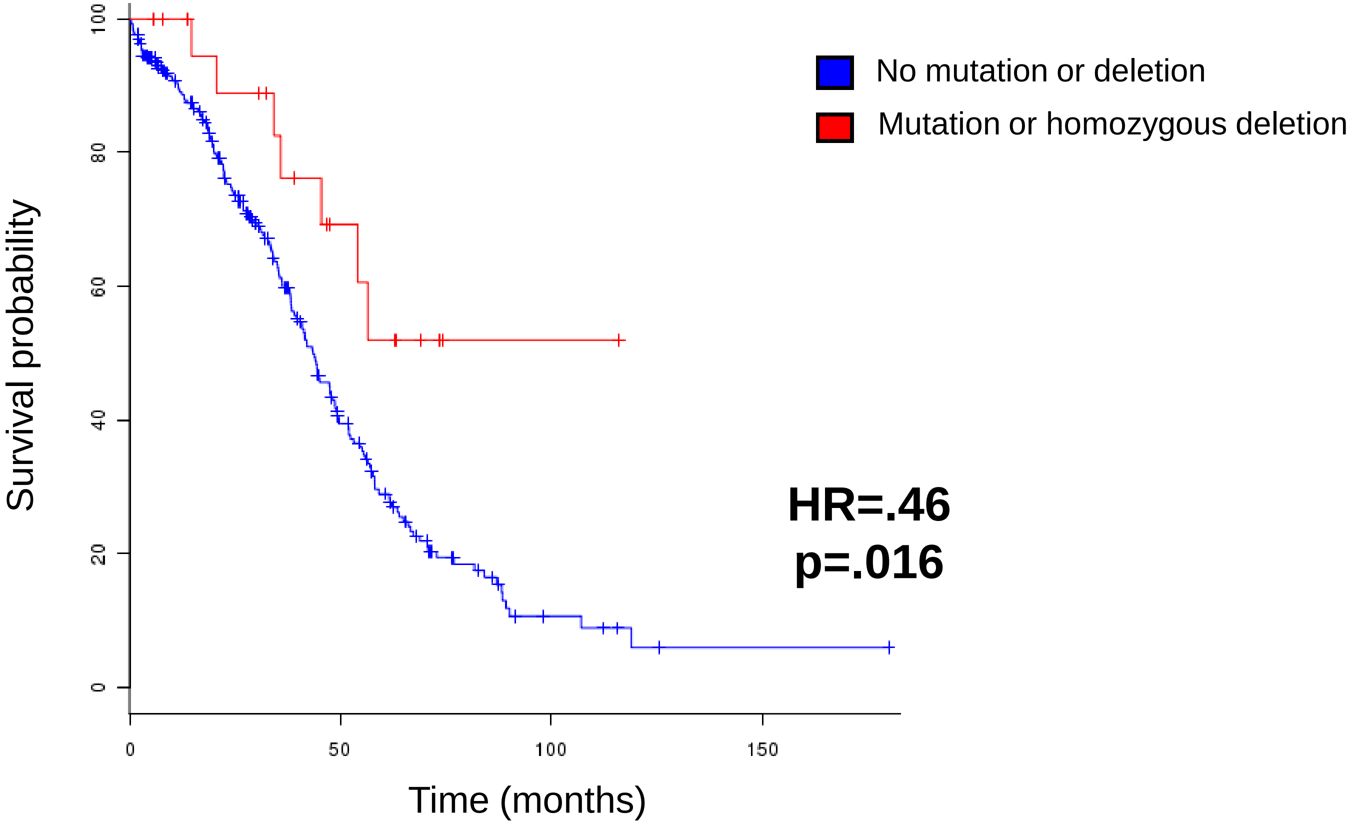
(b) Western Blots of expression of FAT1_Trunc, after transient transfection in cell lines indicated.

Morris et al. Supplementary Figure 3

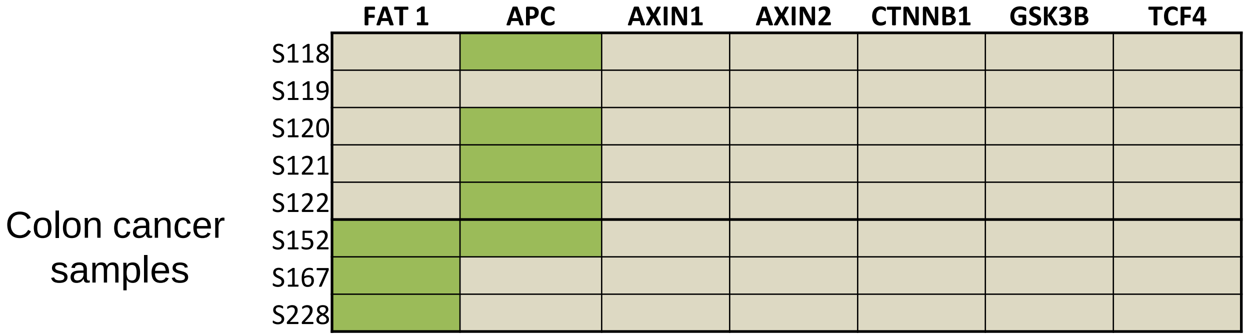


Supplementary Figure 3. Effects on cell growth after depletion of FAT1, β-catenin, or both. (a) Western blot showing co-transfection of siRNAs targeting FAT1 and β-catenin, in U251 glioma cells, using siRNAs distinct from those in Figs. 6d-f. **(b)** Growth curve demonstrating accelerated growth after FAT1 knockdown, reversed by concurrent knockdown of β-catenin. Experiments performed in quadruplicate, using the xCELLigence system. **(c)** BrdU and cell cycle assays demonstrate enhancement in DNA synthesis and cells in S phase, after FAT1 knockdown, repressed with concurrent β-catenin knockdown. ***p<.001; ns, nonsignificant.

Morris et al. Supplementary Figure 4



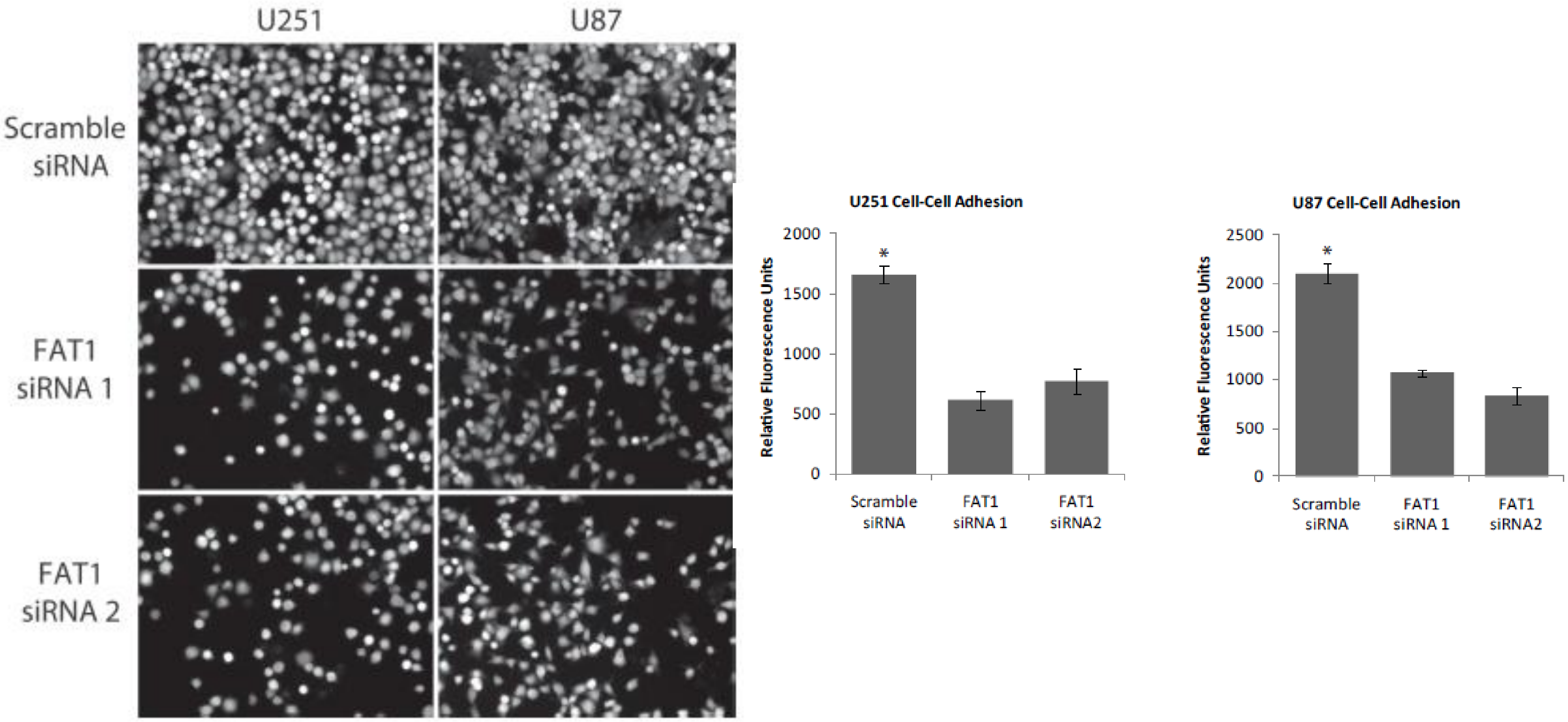
Supplementary Figure 4. Impact of FAT1 homozygous deletion or mutation on survival, among patients in The Cancer Genome Atlas ovarian cancer dataset. Patients with tumors harboring FAT1 mutated or deleted tumors experienced significantly longer survival.



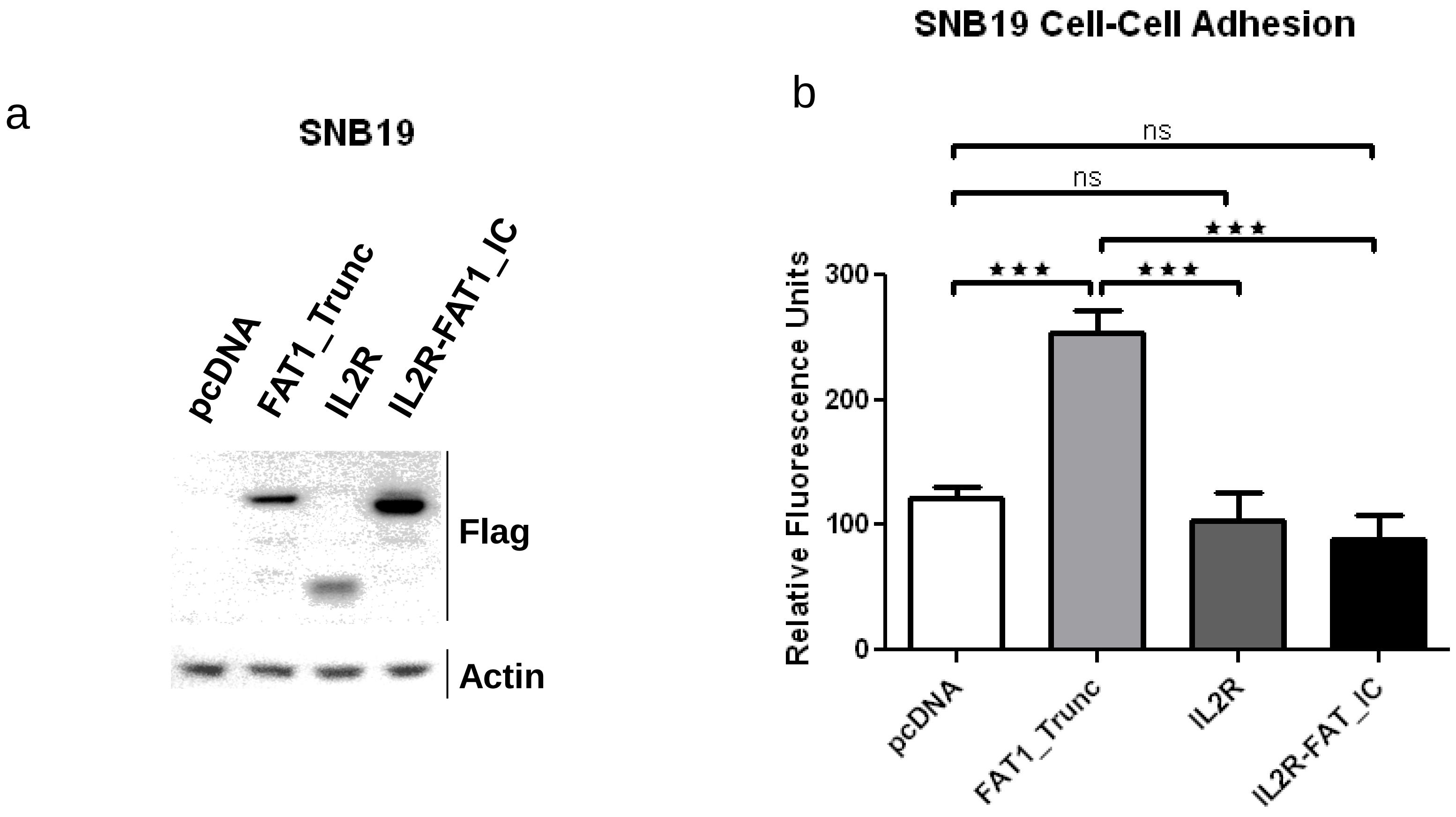
Colon cancer samples

	FAT 1	APC	AXIN1	AXIN2	CTNNB1	GSK3B	TCF4
S118	⬜	🟩	⬜	⬜	⬜	⬜	⬜
S119	⬜	⬜	⬜	⬜	⬜	⬜	⬜
S120	⬜	🟩	⬜	⬜	⬜	⬜	⬜
S121	⬜	🟩	⬜	⬜	⬜	⬜	⬜
S122	⬜	🟩	⬜	⬜	⬜	⬜	⬜
S152	🟩	🟩	⬜	⬜	⬜	⬜	⬜
S167	🟩	⬜	⬜	⬜	⬜	⬜	⬜
S228	🟩	⬜	⬜	⬜	⬜	⬜	⬜

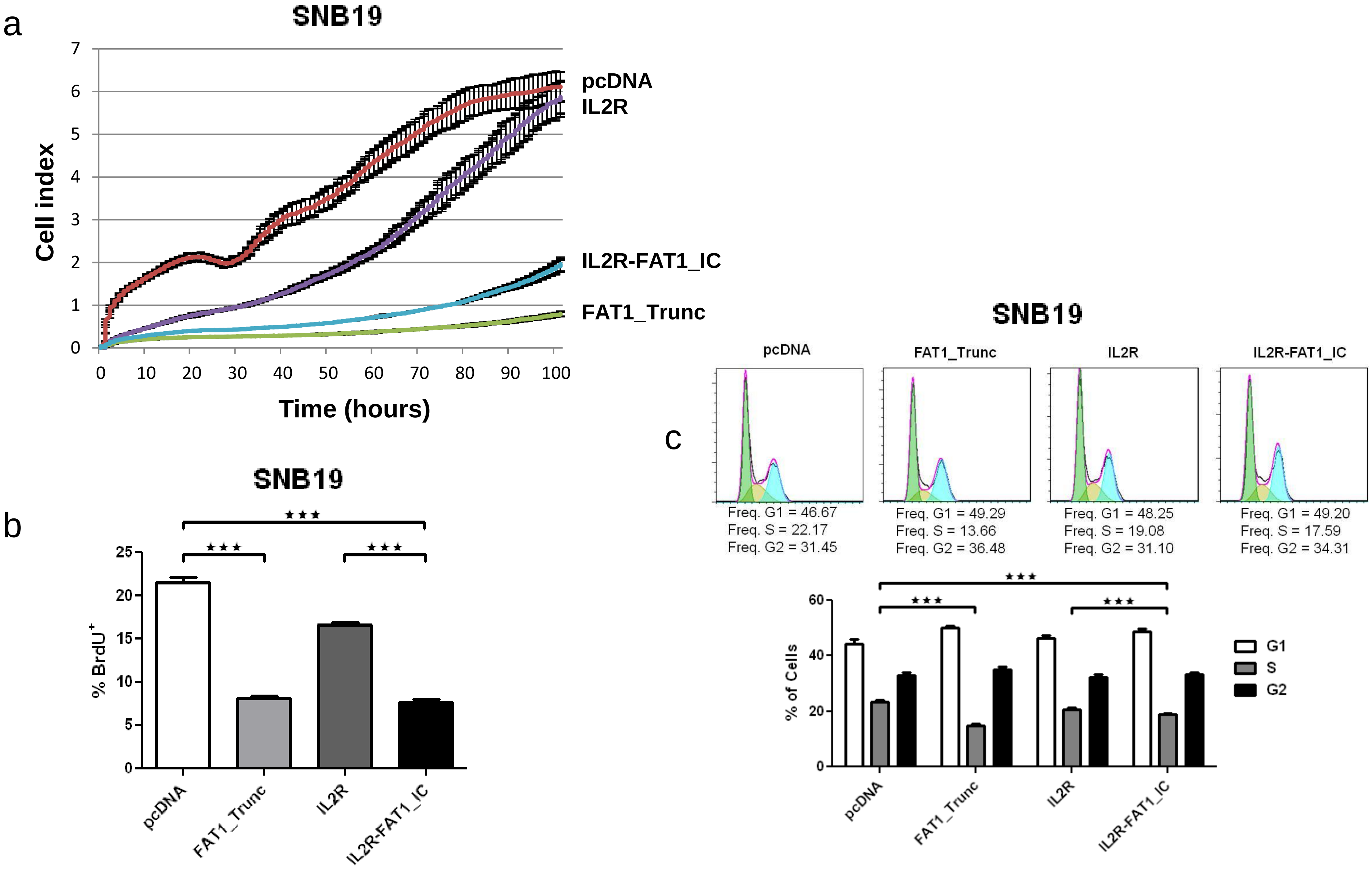
Supplementary Figure 5. Mutational profile of Wnt/β-catenin pathway genes in colorectal tumors harboring wild-type or mutated *FAT1*. Green, mutated; gray, wild-type. Sequencing was done on the colorectal tumors as listed in Table 1 using Sanger sequencing.



Supplementary Figure 6. Knockdown of FAT1 in GBM cell lines impairs cell-cell adhesion. Representative images on the left, and fluorescence-based quantification on the right. Error bars represent standard deviation, comparisons made with ANOVA. * $p<0.05$.



Supplementary Figure 7. Adhesion effects of a non-adhesive FAT1 construct. (a) A non-adhesive FAT1 protein was created by fusing the extracellular and transmembrane portions of the IL2 receptor to the intracytoplasmic tail of FAT1, denoted “IL2R-FAT1_IC.” The IL2Rα receptor was used as an additional control, “IL2R.” **(b)** Cell-cell adhesion was measured using the fluorescence-based assay in SNB19 glioma cells. Expression of FAT1_Trunc increased cell-cell adhesion, compared to pcDNA empty vector. There was no increase in cell-cell adhesion seen with IL2R, or IL2R-FAT_IC. *** p<.001



Supplementary Figure 8. The intracytoplasmic region of FAT1 is sufficient to suppress glioma cell growth in an adhesion-independent manner. (a) Growth curve, (b) BrdU and (c) cell cycle assays, of SNB19 glioma cells transfected with FAT1_Trunc, non-adhesive IL2R-FAT1_Trunc, and empty vector and IL2R controls, demonstrate consistent suppression of growth with both FAT1 proteins. ***p<.001

Supplementary Table 1.

Frequency of deletion at 4q35.2, by cancer subset, in Tumorscape dataset

Cancer Subset	# genes in peak	Q-value	Frequency of Deletion		
			Overall	Focal	High-level
All cancers	14	5.08E-56	0.2664	0.0744	0.0093
All epithelial cancers	14	2.64E-42	0.3602	0.0916	0.0114
All lung cancers	41	1.78E-15	0.3527	0.1047	0.0039
Lung (non-small cell)	41	4.79E-15	0.337	0.1064	0.0027
Melanoma	20	1.91E-06	0.4865	0.1081	0.045
Hepatocellular	41	0.00335	0.3223	0.0579	0.0165
Colorectal	36	0.00371	0.3416	0.0683	0
All hematologic cancers	60	0.00858	0.0386	0.02	0
Prostate	90	0.00996	0.2391	0.1087	0.0217
Renal	120	0.0183	0.2778	0.0476	0.0079
Medulloblastoma	177	0.0912	0.0938	0.0469	0
All neural cancers	102	0.202	0.1429	0.0369	0
Esophageal squamous	56	0.271	0.4318	0.1136	0.0227
Acute lymphoblastic leukemia		3.01E-05	0.0588	0.0332	0
Breast		1.53E-04	0.3251	0.1029	0.0165
Lung (small cell)		0.525	0.65	0.075	0.025
Ovarian		0.542	0.3689	0.068	0
Myeloproliferative disorder		1	0.0047	0	0

Q-value is the false discovery rate-adjusted likelihood of the identified deletion occurring by chance.

URL for Tumorscape dataset portal: http://www.broadinstitute.org/tumorscape/

Reference: Beroukhim et al, "The landscape of somatic copy-number alteration across human cancers" (2010), Nature, 18:899-905.

Supplementary Table 2.

Genes located within peak region of deletion at 4q35.2

Gene ID	**Gene name**
CYP4V2	cytochrome P450, family 4, subfamily V, polypeptide 2
F11	coagulation factor XI
FAM149A	family with sequence similarity 149, member A
FAT1	FAT tumor suppressor homolog 1 (Drosophila)
FRG1	FSHD region gene 1
FRG2	FSHD region gene 2
KLKB1	kallikrein B, plasma (Fletcher factor) 1
MTNR1A	melatonin receptor 1A
SORBS2	sorbin and SH3 domain containing 2
TLR3	toll-like receptor 3
TRIML1	tripartite motif family-like 1
TRIML2	tripartite motif family-like 2
TUBB4Q	tubulin, beta polypeptide 4, member Q, pseudogene
ZFP42	zinc finger protein 42 homolog (mouse)

URL for Tumorscape dataset portal: http://www.broadinstitute.org/tumorscape/

Reference: Beroukhim et al, "The landscape of somatic copy-number alteration across human cancers" (2010), Nature, 18:899-905.

Supplementary Table 3.

Prediction of FAT1 mutation consequences by Polpyhen-2.

GENE	POSITION	WILD-TYPE AMINO ACID	MUTANT AMINO ACID	WILD-TYPE NUCLEOTIDE	MUTANT NUCLEOTIDE	POLYPHEN CLASSIFICATION	PROBABILITY	FDR
FAT1	4511	Thr	Ile	C	T	neutral	0.054	0.191
FAT1	4419	Ala	Ser	G	T	neutral	0.005	0.267
FAT1	4310	Pro	Leu	C	T	**deleterious**	**1**	**0.0109**
FAT1	4309	Pro	Ala	C	G	**deleterious**	**1**	**0.0109**
FAT1	3860	Arg	Lys	G	A	**deleterious**	**0.65**	**0.121**
FAT1	3310	Gly	Gly	G	A	**deleterious**	**1**	**0.0109**
FAT1	3124	Glu	Lys	G	A	neutral	0.025	0.213
FAT1	2496	Glu	Lys	G	A	**deleterious**	**0.984**	**0.065**
FAT1	2004	Ile	Met	T	G	**deleterious**	**0.539**	**0.128**
FAT1	1268	Arg	Gln	G	A	**deleterious**	**1**	**0.0109**
FAT1	809	His	Arg	A	G	neutral	0.036	0.202
FAT1	636	Ala	Thr	G	A	neutral	0.002	0.452
FAT1	313	Lys	Asn	G	C	**deleterious**	**0.822**	**0.101**
FAT1	306	Val	Met	G	A	neutral	0.03	0.206
FAT1	146	Arg	Met	C	Deletion	**deleterious**	**1**	**0.0109**

SOURCES:
PolyPhen-2 v2.2.2r394

URL: http://genetics.bwh.harvard.edu/pph2/
Reference: Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P, Kondrashov AS, Sunyaev SR. Nature Methods **7**(4):248-249 (2010).

Sequences: UniProtKB/UniRef100 Release 2011_12 (14-Dec-2011)

Structures: PDB/DSSP Snapshot 03-Jan-2012 (78304 Structures)

Genes: UCSC MultiZ46Way GRCh37/hg19 (08-Oct-2009)

Supplementary Table 4.
FAT1 mutational status in cancer cell lines.

Cell line	Origin	FAT1 Mutation(s)
COLO320	colon adenocarcinoma	-
DLD1	colon adenocarcinoma	Ala1480Asp (Heterozygous)
HCT116	colon adenocarcinoma	-
HT29	colon adenocarcinoma	-
RKO	colon adenocarcinoma	Leu3199Arg/Lys3200Asn frameshift
HS683	glioma	-
SF268	glioma	-
SF295	glioma	-
SF539	glioma	-
SKMG3	glioma	-
SNB19	glioma	-
U118	glioma	-
U251	glioma	-
U87[1]	glioma	-
MDA-1586	head and neck squamous cell cancer	-
OSCC3	head and neck squamous cell cancer	Arg1268Gln (Homozygous)[2]
SCC25	head and neck squamous cell cancer	-

1. The U87 cell line genome has been sequenced, with no FAT1 mutations identified.
(Clark et al, PLoS Genetics 2010:e1000832; PMID 20126413)

2. The Arg1268Gln mutation was also identified as a somatic mutation in tumor GBM_37;
it is also listed as a polymorphism in dbSNP (rs113970444).

Supplementary Table 6.
Results of pathway analyses, based on genes differentially expressed after FAT1 knockdown.

1. INGENUITY PATHWAY ANALYSIS

Canonical Pathway	p value	-log(p)	Ratio	Pathway components
Molecular Mechanisms of Cancer	3.3E-05	4.48	0.12	RAP2B,RALA,SMAD3,LRP6,KRAS,PSEN2,MAPK13,FZD1,JAK2,TGFBR2,E2F6,LAMTOR3,CASP9 (includes EG:100140945),RHOB,BBC3,ARHGEF2,HIPK2,RHOF,CASP8,PRKD3,PRKDC,CDC25C,PMAIP1,CCNE2,NRAS,PAK2,GNAS,ARHGEF12,PIK3C2A, DVL1,GNAQ,AURKA,TCF3,APC,GNAI3,FZD8,CCND3,PRKCI,RRAS2,PTPN11,RND3,PRKCD,E2F1,CFLAR
Polyamine Regulation in Colon Cancer	0.00048	3.32	0.24	PSME1,AZIN1,PSME2,PSME4,OAZ2,KRAS,APC
Breast Cancer Regulation by Stathmin1	0.001	3.16	0.13	PPP1CC,PPP1CB,KRAS,PPP1R14B,ROCK2,E2F6,STMN1,ARHGEF2,PRKD3,CCNE2,NRAS,ARHGEF12,GNAS,PIK3C2A,PPP2R5C,ITPR2,PPP2R5D,GNAQ,CDK1,PPP2CB,GNAI3,PRKCI,RRAS2,PRKCD,E2F1,PPP2R1B
Telomerase Signaling	0.003	2.52	0.15	NRAS,HDAC4,PIK3C2A,PPP2R5C,PPP2R5D,TERF2IP,KRAS,ELF1,PPP2CB,HSP90B1,RRAS2,E2F1,HSP90AA1,PPP2R1B,EGFR
p53 Signaling	0.004	2.36	0.15	PRKDC,PMAIP1,PLAGL1,PIK3C2A,MED1 (includes EG:19014),BIRC5,SCO2 (includes EG:606683),GADD45A,STAG1,BBC3,E2F1,HIPK2,PIDD,PML
Glioma Invasiveness Signaling	0.005	2.30	0.17	NRAS,RRAS2,RND3,PIK3C2A,RHOB,HMMR,ITGAV,PLAUR,KRAS,RHOF
Colorectal Cancer Metastasis Signaling	0.007	2.15	0.11	TLR1,MSH3 (includes EG:17686),SMAD3,LRP6,MMP13,KRAS,JAK2,FZD1,BIRC5,TGFBR2,CASP9 (includes EG:100140945),RHOB,TLR3,STAT1,RHOF,PTGER4,EGFR,NRAS,GNAS,PIK3C2A,DVL1,VEGFC,TCF3,APC,FZD8,RRAS2,RND3
Role of Tissue Factor in Cancer	0.008	2.12	0.13	NRAS,PIK3C2A,GNAQ,PLAUR,MMP13,VEGFC,HBEGF,KRAS,MAPK13,JAK2,EIF4E,RRAS2,PTPN11,ITGAV,EGFR
Hypoxia Signaling in the Cardiovascular Sys	0.011	1.94	0.15	HSP90B1,UBE2Q1,UBE2N,NQO1,HSP90AA1,UBE2E3,UBE2S,UBE2L6,UBE2D1,ATF2
Hereditary Breast Cancer Signaling	0.012	1.92	0.12	NPM1,CDC25C,NRAS,HDAC4,PIK3C2A,KRAS,SMARCA4,CDK1,CCNB1,RRAS2,POLR2C,GADD45A,POLR2E,E2F1,FANCA
Pancreatic Adenocarcinoma Signaling	0.013	1.87	0.12	RALA,PIK3C2A,SMAD3,VEGFC,HBEGF,KRAS,JAK2,BIRC5,TGFBR2,E2F6,CASP9 (includes EG:100140945),E2F1,STAT1,EGFR
Telomere Extension by Telomerase	0.016	1.79	0.24	TNKS,XRCC6,TERF2IP,XRCC5
Prostate Cancer Signaling	0.022	1.65	0.11	CCNE2,HSP90B1,NRAS,RRAS2,CASP9 (includes EG:100140945),PIK3C2A,E2F1,NKX3-1,HSP90AA1,KRAS,ATF2
Chronic Myeloid Leukemia Signaling	0.025	1.60	0.12	CTBP1,TGFBR2,IKBKB,E2F6,NRAS,RRAS2,HDAC4,PTPN11,PIK3C2A,SMAD3,E2F1,KRAS
Glioblastoma Multiforme Signaling	0.029	1.54	0.10	NRAS,PIK3C2A,ITPR2,GNAQ,KRAS,FZD1,TCF3,APC,FZD8,E2F6,RRAS2,RHOB,RND3,PRKCD,E2F1,RHOF,EGFR
PI3K/AKT Signaling	0.032	1.50	0.10	NRAS,YWHAE,PPP2R5C,PPP2R5D,KRAS,JAK2,EIF4E,PPP2CB,IKBKB,HSP90B1,RRAS2,HSP90AA1,PPP2R1B,MCL1
HER-2 Signaling in Breast Cancer	0.035	1.46	0.13	CCNE2,PRKCI,NRAS,RRAS2,CASP9 (includes EG:100140945),PIK3C2A,PRKCD,KRAS,PRKD3,EGFR
ERK/MAPK Signaling	0.049	1.31	0.09	PPP1CC,PAK2,NRAS,PIK3C2A,PPP2R5C,PPP2R5D,PPP1CB,KRAS,PPP1R14B,EIF4E,ATF2,ELF1,PPP2CB,LAMTOR3,PRKCI,RRAS2,PRKCD,STAT1,PPP2R1B
Role of BRCA1 in DNA Damage Response	0.051	1.29	0.12	E2F6,GADD45A,E2F1,PLK1,BRCC3,STAT1,FANCA,SMARCA4
Thyroid Cancer Signaling	0.054	1.27	0.14	CXCL10,NRAS,RRAS2,KRAS,NGF,TCF3
Glioma Signaling	0.060	1.22	0.10	E2F6,PRKCI,NRAS,RRAS2,PIK3C2A,PRKCD,E2F1,KRAS,PRKD3,IGF2R,EGFR
Wnt/b-catenin Signaling	**0.069**	**1.16**	**0.10**	**APPL2,PPP2R5C,PPP2R5D,MARK2,DVL1,LRP6,GNAQ,FZD1,TCF3,APC,TGFBR2,CSNK1E,PPP2CB,FZD8,CSNK2A1,DKK2,PPP2R1B**
Non-Small Cell Lung Cancer Signaling	0.076	1.12	0.10	NRAS,RRAS2,CASP9 (includes EG:100140945),PIK3C2A,ITPR2,E2F1,KRAS,EGFR
Renal Cell Carcinoma Signaling	0.106	0.97	0.11	MET,PAK2,NRAS,RRAS2,PTPN11,PIK3C2A,KRAS,FH
Small Cell Lung Cancer Signaling	0.113	0.95	0.09	TRAF6,IKBKB,CCNE2,CASP9 (includes EG:100140945),PIK3C2A,E2F1,SKP2 (includes EG:27401),TRAF1
Estrogen-Dependent Breast Cancer Signali	0.116	0.94	0.10	NRAS,RRAS2,PIK3C2A,KRAS,HSD17B4,EGFR,ATF2
Ovarian Cancer Signaling	0.121	0.92	0.09	NRAS,PIK3C2A,DVL1,PTGS1,VEGFC,KRAS,FZD1,TCF3,APC,FZD8,RRAS2,E2F1,EGFR
Melanoma Signaling	0.159	0.80	0.11	NRAS,RRAS2,PIK3C2A,E2F1,KRAS
PTEN Signaling	0.240	0.62	0.08	MAST2,TGFBR2,IKBKB,NRAS,RRAS2,CASP9 (includes EG:100140945),CSNK2A1,KRAS,IGF2R,EGFR
FAK Signaling	0.247	0.61	0.08	ARHGAP26,PAK2,NRAS,RRAS2,PIK3C2A,HMMR,KRAS,EGFR
Endometrial Cancer Signaling	0.285	0.55	0.09	NRAS,RRAS2,CASP9 (includes EG:100140945),PIK3C2A,KRAS
Bladder Cancer Signaling	0.401	0.40	0.08	NRAS,RRAS2,E2F1,MMP13,VEGFC,KRAS,EGFR
Acute Myeloid Leukemia Signaling	0.437	0.36	0.07	NRAS,RRAS2,PIK3C2A,KRAS,PML,TCF3
Basal Cell Carcinoma Signaling	0.531	0.28	0.07	FZD8,DVL1,FZD1,TCF3,APC

2. Biocarta PATHWAY ANALYSIS

Canonical Pathway	p value	-log(p)	Fold Enrichment	Pathway components

Role of Ran in mitotic spindle regulatio	0.01514	1.819807	3.665816327	NUMA1, RAN, TPX2, RANBP1, AURKA, KPNB1
Telomeres, Cellular Aging, and Immor	0.02553	1.59293	2.851190476	EGFR, XRCC5, HSP90AA1, KRAS, XRCC6, TNKS, CDKL3
WNT Signaling Pathway	**0.04048**	**1.39**	2.370309278	**CSNK1A1, CTBP1, CSNK2A1, BTRC, FZD1, CDKL3, DVL1, APC**

3. KEGG PATHWAY ANALYSIS

Canonical Pathway	p value	-log(p)	Fold Enrichment	Pathway components
hsa03010:Ribosome	1.99E-04	3.701147	2.390078195	RPL14, RPL13, RPL15, RPLP0P6, RPL21P28, RPL7, RPL6, RPS3A, RPLP0, RPL8, RPL3, RPL11, RPL4, RPS21, RPS23, RPL36AL, RPS10P7, RPSA, RPS9, RPL24, RPS7, RPL23, RPS16, RPL21, RPS10
hsa04142:Lysosome	0.00439	2.357375	1.858021161	ARSB, AGA, SGSH, HYAL1, NAGLU, CLTB, AP3S2, ACP2, CTSS, CLTC, CD164, CTSL1, GNS, DNASE2, CD68, LAMP3, AP3M2, GNPTAB, IGF2R, ARSA, ENTPD4, GGA2, CTSG
hsa04114:Oocyte meiosis	0.00443	2.353551	1.890334572	PPP2R1B, CDK1, BTRC, PPP2R5D, PPP2R5C, AURKA, PTTG2, PTTG1, PPP1CC, CDC25C, PPP1CB, CDC27, YWHAE, ITPR2, CCNE2, CCNB1, REC8, CCNB2, PLK1, PPP2CB, BUB1, SMC1A, FBXW11
hsa04110:Cell cycle	0.00977	2.010202	1.739107807	E2F1, CDK1, CDC14A, SKP2, SMAD3, PRKDC, PTTG2, CDK7, PTTG1, CDC25C, CDC27, YWHAE, MCM4, MCM6, CCNE2, CCNB1, CCNB2, CCND3, PLK1, BUB1, SMC1A, CCNA2, GADD45A, STAG1
hsa04115:p53 signaling pathway	0.02238	1.650165	1.945932648	CDK1, LRDD, PMAIP1, GTSE1, CCNB1, CCNE2, EI24, CCNB2, CCND3, CASP9, BBC3, RRM2, CASP8, GADD45A
hsa04612:Antigen processing and pres	0.02398	1.6202	1.822009226	HLA-DQB1, HSP90AA1, HLA-A, IFI30, HLA-C, CTSS, NFYA, HLA-B, HLA-E, CANX, CTSL1, HLA-G, B2M, HLA-F, PSME1, PSME2, TAP1
hsa00100:Steroid biosynthesis	0.0264	1.578336	3.33588454	CYP51A1, SQLE, DHCR7, LSS, FDFT1, SC4MOL
hsa05210:Colorectal cancer	0.02648	1.577037	1.912838555	EGFR, FZD8, MSH3, APC2, MET, TGFBR2, FZD1, SMAD3, RAF1, BIRC5, RALGDS, DVL1, KRAS, CASP9, SOS2, APC
hsa04120:Ubiquitin mediated proteolys	0.02668	1.573773	1.586777196	BTRC, UBE4B, UBA7, SKP2, PML, UBE2L6, HERC4, UBE3C, MID1, CDC27, UBE2Q1, UBE2N, CUL3, UBE2E3, HUWE1, UBR5, DET1, SMURF2, SMURF1, UBE2D1, TRAF6, UBE2S, FBXW11
hsa05322:Systemic lupus erythematos	0.02694	1.569541	1.718485975	HLA-DQB1, HIST2H2AA3, HIST1H2AC, HIST2H2AA4, HIST1H2AD, HIST2H4A, HIST2H4B, TROVE2, HIST1H2BK, FCGR1C, H2AFV, FCGR1A, HIST1H2BI, H2AFZ, HIST1H4C, HIST3H2A, HIST1H4H, HIST1H2BD, HIST1H2BE, HIST1H2BG, ACTN2, TRIM21, HIST1H2AI, HIST1H3D, HIST1H2AJ, CTSG
hsa04621:NOD-like receptor signaling	0.05499	1.259712	1.829356038	CASP5, NOD2, HSP90B1, NOD1, HSP90AA1, MAPK13, CASP8, RIPK2, TRAF6, IKBKB, CCL5, NLRP1
hsa04623:Cytosolic DNA-sensing path	0.05692	1.244725	1.890334572	DDX58, POLR3G, IFNB1, TBK1, TREX1, IKBKB, POLR3C, CCL5, ZBP1, POLR3D, CXCL10
hsa04310:Wnt signaling pathway	**0.06769**	**1.169444**	**1.603784743**	**CSNK1A1, PPP2R1B, FZD8, TBL1XR1, CTBP1, APC2, ROCK2, BTRC, PPP2R5D, PPP2R5C, FZD1, SMAD3, DVL1, DKK2, CSNK2A1, CCND3, CSNK1E, PPP2CB, CACYBP, LRP6, WNT6, FBXW11, APC**
hsa05215:Prostate cancer	0.0781	1.107325	1.699177144	E2F1, EGFR, FGFR2, HSP90AA1, MAP2K2, RAF1, , CCNE2, NRAS, HSP90B1, KRAS, CASP9, SOS2, NKX3-1, MTOR, IKBKB

4. REACTOME PATHWAY ANALYSIS

Canonical Pathway	p value	-log(p)	Fold Enrichment	Pathway components
REACT_11061:Signalling by NGF	0.04466	1.35	1.433928141	PPP2R5D, CLTC, KRAS, MYD88, CASP9, SQSTM1, PPP2CB, RALA, TRAF6, PPP2R1B, IRAK1, MAP2K2, PRKCI, NR4A1, RAF1, YWHAE, PRKCD, RALGDS, ITPR2, NRAS, DUSP3, MAPK13, PSEN2, RIPK2, RIT1, MTOR, IKBKB, NGF
REACT_152:Cell Cycle, Mitotic	1.61E-07	6.79	1.897528968	E2F1, CDC14A, BTRC, PPP2R5D, PPP2R5C, PTTG2, AURKA, PTTG1, CCNE2, INCENP, PSMD1, PSMD2, RANBP2, CCNA2, STAG1, PPP2R1B, CDK1, HSP90AA1, SKP2, CDK7, PPP1CC, MCM4, MCM6, REC8, PSME1, CCND3, PSME2, RRM2, FGFR1OP, PSMB10, NUP98, NEK2, POLA1, TYMS, SPC25, NUMA1, CENPA, PPP2CB, BUB1, PAFAH1B1, CLASP1, UBE2D1, CENPN, CENPM, GINS4, ALMS1, CENPF, BIRC5, NDC80, CENPE, CDC25C, CDC27, MLF1IP, YWHAE, PSMB9, CCNB1, CCNB2, DHFR, PSMD12, CSNK1E, PSMC3, PLK1, POLD2, SMC1A, KIF20A
REACT_6167:Influenza Infection	4.35E-07	6.36	2.296372637	NCBP2, FUS, POLR2E, RPL14, RPL13, RPL15, RPLP0P6, POLR2C, YBX1, RPL21P28, HNRNPL, HNRNPA3, HNRNPK, RPL7, CD2BP2, RPL6, RPS3A, RPLP0, RPL8, HNRNPD, U2AF1, RPL3, RPL11, RPL4, RPS21, KPNB1, RPS23, RPS10P7, RPSA, RAN, PTBP1, RPS9, RPL24, HNRNPA1, HNRNPA0, RPS7, RPL23, RPS16, HNRNPUL1, RPL21, RPS10, LOC728643, HNRNPH1, SMC1A

REACT_71:Gene Expression	1.44E-06	5.84	1.751148162	NCBP2, TARS2, RPL14, RPL13, RPL15, RPLP0P6, YBX1, WARS, GTF2E2, GTF2H2D, GTF2H2C, RPS3A, RPLP0, EIF1AX, CLP1, U2AF1, RPL11, CARS, TAF4B, PTBP1, CDK7, SARS2, GTF2H2, GTF2H2B, MED15, RPS16, SNRNP200, HARS, EEF1G, RPS10, EEF1D, MED1, FUS, POLR2E, EEF1B2, NHP2L1, WARS2, POLR2C, SF3B3, RPL21P28, HNRNPA3, HNRNPL, EIF3A, HNRNPK, RPL7, RPL6, CD2BP2, EIF3F, CDC40, RPL8, RPL3, HNRNPD, PABPC1, RPL4, RPS21, RPS23, RPS10P7, RPSA, SSRP1, AIMP1, RPS9, RPL24, HNRNPA1, HNRNPA0, RPS7, EIF4B, NOTCH2, PAPOLA, EIF4E, RPL23, HNRNPUL1, RPL21, LOC728643, HNRNPH1, SMC1A
REACT_1762:3' -UTR-mediated transl	7.17E-05	4.14	2.25331565	RPL14, RPL13, RPL15, RPLP0P6, RPL21P28, EIF3A, RPL7, RPS3A, RPL6, EIF1AX, RPLP0, EIF3F, RPL8, RPL3, RPL11, RPL4, PABPC1, RPS21, RPS23, RPS10P7, RPSA, RPS9, RPL24, RPS7, EIF4B, EIF4E, RPL23, RPS16, RPL21, RPS10
REACT_17015:Metabolism of proteins	0.00108	2.97	1.661430894	EEF1B2, RPL14, RPL13, RPL15, RPLP0P6, VBP1, CCT2, RPL21P28, EIF3A, RPL7, RPL6, RPS3A, RPLP0, EIF1AX, EIF3F, RPL8, RPL3, PIGC, RPL11, PABPC1, RPL4, RPS21, TUBA1B, RPS23, RPS10P7, RPSA, F10, RPS9, RPL24, PLAUR, RPS7, PIGN, CCT7, EIF4B, CCT5, EIF4E, RPL23, RPS16, TBCD, RPL21, EEF1G, RPS10, EEF1D
REACT_125:Processing of Capped Int	0.00158	2.80	1.966530022	NCBP2, FUS, POLR2E, NHP2L1, POLR2C, SF3B3, YBX1, HNRNPL, HNRNPA3, HNRNPK, CD2BP2, CLP1, CDC40, U2AF1, HNRNPD, PTBP1, HNRNPA1, HNRNPA0, PAPOLA, EIF4E, HNRNPUL1, SNRNP200, LOC728643, SMC1A, HNRNPH1
REACT_6185:HIV Infection	0.00514	2.29	1.616509053	XRCC5, PSMB10, NCBP2, NUP98, POLR2E, BTRC, XRCC6, APOBEC3G, POLR2C, APOBEC3F, B2M, AP2B1, GTF2H2D, GTF2E2, GTF2H2C, PAK2, NUP50, PSMD1, NPM1, PSMD2, RANBP1, RANBP2, KPNB1, SSRP1, SLC25A4, RAN, TAF4B, HLA-A, CDK7, GTF2H2, PSMB9, GTF2H2B, PSME1, PSMD12, PSME2, PSMC3
REACT_11045:Signaling by Wnt	**0.00541**	**2.27**	**2.222270666**	**PPP2R1B, PSMB10, CSNK1A1, BTRC, PPP2R5D, PPP2R5C, PSMB9, PSME1, PSMD12, PSMC3, PSME2, PSMD1, PPP2CB, PSMD2, APC**
REACT_7970:Telomere Maintenance	0.00656	2.18	2.25331565	HIST1H2AC, HIST2H2AA3, HIST2H2AA4, HIST1H2BD, HIST1H2BE, HIST1H2BG, HIST1H2AD, POLA1, TERF2IP, HIST2H4A, HIST2H4B, H2BFS, HIST1H2BK, HIST1H2BI, POLD2, HIST1H2AI, H2AFZ, HIST1H4C, HIST1H3D, HIST1H2AJ, HIST1H4H
REACT_6844:Signaling by TGF beta	0.01875	1.73	3.60530504	ZFYVE9, TGFBR2, SMAD3, SMURF2, SMURF1, UBE2D1

Supplementary Table 7. Genes differentially expressed in GBMs with low FAT1 expression (TCGA dataset).

Wnt/β-catenin Signaling Components: APC2, CDH2, CDH5, EP300, FZD3, FZD5, FZD7, JUN, LEF1, LRP1, PPP2R3A, RARA, SOX9, TCF3, TCF4, TLE1, TP53, WIF1

Probeset	Fold Change (FAT1low/FAT1nl)	q value		Gene Description
201579_at	*-2.6076*	*0*	*FAT1*	FAT tumor suppressor homolog 1 (Drosophila)
				**FAT1 NOT INCLUDED IN PATHWAY ANALYSIS*
201150_s_at	-1.66768	3.21E-09	TIMP3	TIMP metallopeptidase inhibitor 3
201148_s_at	-1.60469	4.68E-09	TIMP3	TIMP metallopeptidase inhibitor 3
221958_s_at	-1.38267	4.35E-08	WLS	wntless homolog (Drosophila)
203215_s_at	-1.37958	4.35E-08	MYO6	myosin VI
213395_at	-1.69129	4.82E-08	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1
201149_s_at	-1.61473	4.82E-08	TIMP3	TIMP metallopeptidase inhibitor 3
203216_s_at	-1.40165	6.38E-08	MYO6	myosin VI
218247_s_at	-1.30421	1.11E-07	MEX3C	mex-3 homolog C (C. elegans)
201147_s_at	-1.65801	1.30E-07	TIMP3	TIMP metallopeptidase inhibitor 3
201145_at	1.25152	1.30E-07	HAX1	HCLS1 associated protein X-1
206185_at	1.21465	1.57E-07	CRYBB1	crystallin, beta B1
218938_at	1.24676	1.57E-07	FBXL15	F-box and leucine-rich repeat protein 15
218718_at	-1.50037	1.57E-07	PDGFC	platelet derived growth factor C
202197_at	-1.28326	1.86E-07	MTMR3	myotubularin related protein 3
218678_at	-1.5805	2.01E-07	NES	nestin
203440_at	-1.33064	2.20E-07	CDH2	cadherin 2, type 1, N-cadherin (neuronal)
219926_at	1.67157	2.36E-07	POPDC3	popeye domain containing 3
203989_x_at	-1.48149	2.45E-07	F2R	coagulation factor II (thrombin) receptor
218977_s_at	1.2707	2.45E-07	TRNAU1AP	tRNA selenocysteine 1 associated protein 1
210473_s_at	-1.41504	2.45E-07	GPR125	G protein-coupled receptor 125
205559_s_at	-1.69931	2.51E-07	PCSK5	proprotein convertase subtilisin/kexin type 5
203149_at	-1.26205	3.80E-07	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)
212132_at	-1.20368	3.80E-07	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)
219061_s_at	1.30263	4.98E-07	LAGE3	L antigen family, member 3
217814_at	-1.21587	4.98E-07	CCDC47	coiled-coil domain containing 47
211964_at	-1.63789	5.34E-07	COL4A2	collagen, type IV, alpha 2
202077_at	1.21346	5.74E-07	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
200075_s_at	1.26686	6.51E-07	GUK1	guanylate kinase 1
221452_s_at	1.34609	8.22E-07	TMEM14B	transmembrane protein 14B
213298_at	-1.34737	9.15E-07	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)
221885_at	-1.42488	1.22E-06	DENND2A	DENN/MADD domain containing 2A
204422_s_at	-1.34473	1.30E-06	FGF2	fibroblast growth factor 2 (basic)
218609_s_at	1.38189	1.43E-06	NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2
202279_at	1.33127	1.44E-06	C14orf2	chromosome 14 open reading frame 2
211966_at	-1.6098	1.44E-06	COL4A2	collagen, type IV, alpha 2

213201_s_at	1.24988	1.44E-06	TNNT1	troponin T type 1 (skeletal, slow)
205417_s_at	-1.26658	1.51E-06	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)
217499_x_at	1.43686	1.51E-06	OR7E37P	olfactory receptor, family 7, subfamily E, member 37 pseudogene
208890_s_at	-1.32316	1.67E-06	PLXNB2	plexin B2
219683_at	-1.42408	1.74E-06	FZD3	frizzled homolog 3 (Drosophila)
200665_s_at	-1.20811	1.74E-06	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)
200078_s_at	1.25126	1.82E-06	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b
36612_at	-1.29462	1.82E-06	FAM168A	family with sequence similarity 168, member A
220140_s_at	1.21341	1.84E-06	SNX11	sorting nexin 11
40560_at	-1.32412	1.94E-06	TBX2	T-box 2
218775_s_at	-1.22217	1.94E-06	WWC2	WW and C2 domain containing 2
212610_at	-1.23761	2.03E-06	PTPN11	protein tyrosine phosphatase, non-receptor type 11
214803_at	-1.59247	2.03E-06	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
218495_at	1.24745	2.04E-06	UXT	ubiquitously-expressed transcript
206375_s_at	1.30068	2.06E-06	HSPB3	heat shock 27kDa protein 3
53991_at	-1.43062	2.07E-06	DENND2A	DENN/MADD domain containing 2A
209184_s_at	-1.43467	2.07E-06	IRS2	insulin receptor substrate 2
214626_s_at	-1.20573	2.10E-06	GANAB	glucosidase, alpha; neutral AB
213421_x_at	1.26365	2.11E-06	PRSS3	protease, serine, 3
212412_at	-1.28181	2.37E-06	PDLIM5	PDZ and LIM domain 5
1007_s_at	-1.28236	2.50E-06	DDR1	discoidin domain receptor tyrosine kinase 1
58780_s_at	-1.26653	2.61E-06	ARHGEF40	Rho guanine nucleotide exchange factor (GEF) 40
41220_at	-1.24594	2.87E-06	SEPT9	septin 9
210232_at	1.47046	2.89E-06	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)
201651_s_at	-1.23721	2.89E-06	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
213652_at	-1.42987	2.89E-06	PCSK5	proprotein convertase subtilisin/kexin type 5
205560_at	-1.42085	2.97E-06	PCSK5	proprotein convertase subtilisin/kexin type 5
209249_s_at	1.22925	3.95E-06	GHITM	growth hormone inducible transmembrane protein
207463_x_at	1.24206	4.09E-06	PRSS3	protease, serine, 3
213712_at	-2.06582	4.09E-06	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
219896_at	1.29551	4.09E-06	CALY	calcyon neuron-specific vesicular protein
209023_s_at	-1.27142	4.09E-06	STAG2	stromal antigen 2
202391_at	1.6994	4.09E-06	BASP1	brain abundant, membrane attached signal protein 1
203441_s_at	-1.35956	4.22E-06	CDH2	cadherin 2, type 1, N-cadherin (neuronal)
214778_at	-1.25997	4.32E-06	MEGF8	multiple EGF-like-domains 8
200989_at	-1.20608	4.47E-06	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription
202744_at	-1.31178	4.47E-06	SLC20A2	solute carrier family 20 (phosphate transporter), member 2
200601_at	-1.22984	4.61E-06	ACTN4	actinin, alpha 4
202551_s_at	-1.38621	4.74E-06	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
202211_at	-1.2038	4.74E-06	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3
218773_s_at	1.2577	4.80E-06	MSRB2	methionine sulfoxide reductase B2
220326_s_at	-1.25784	5.09E-06	ARHGEF40	Rho guanine nucleotide exchange factor (GEF) 40
201226_at	1.25644	5.14E-06	NDUFB8 /// SEC31B	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa /// SEC31 homolog B
211737_x_at	-1.30446	5.26E-06	PTN	pleiotrophin
215146_s_at	-1.31476	5.29E-06	TTC28	tetratricopeptide repeat domain 28
209859_at	-1.48805	5.29E-06	TRIM9	tripartite motif-containing 9

218950_at	-1.54355	5.42E-06	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3
203031_s_at	1.32119	5.94E-06	UROS	uroporphyrinogen III synthase
202336_s_at	-1.28084	5.94E-06	PAM	peptidylglycine alpha-amidating monooxygenase
213417_at	-1.31904	6.29E-06	TBX2	T-box 2
217941_s_at	-1.22634	6.54E-06	ERBB2IP	erbb2 interacting protein
202478_at	-1.5535	7.32E-06	TRIB2	tribbles homolog 2 (Drosophila)
204246_s_at	1.2921	7.53E-06	DCTN3	dynactin 3 (p22)
214721_x_at	-1.39259	7.53E-06	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
219746_at	-1.32677	7.53E-06	DPF3	D4, zinc and double PHD fingers, family 3
208862_s_at	-1.211	7.68E-06	CTNND1	catenin (cadherin-associated protein), delta 1
211980_at	-1.56118	7.72E-06	COL4A1	collagen, type IV, alpha 1
201734_at	-1.22397	8.13E-06	CLCN3	chloride channel 3
202168_at	1.21255	8.13E-06	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
209465_x_at	-1.36076	8.46E-06	PTN	pleiotrophin
201733_at	-1.27174	8.48E-06	CLCN3	chloride channel 3
204478_s_at	1.23647	8.70E-06	RABIF	RAB interacting factor
209233_at	1.27017	8.87E-06	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)
209765_at	-1.46286	8.87E-06	ADAM19	ADAM metallopeptidase domain 19
203549_s_at	-1.65233	8.87E-06	LPL	lipoprotein lipase
219522_at	-1.46024	8.87E-06	FJX1	four jointed box 1 (Drosophila)
209466_x_at	-1.33292	8.87E-06	PTN	pleiotrophin
201662_s_at	-1.33437	9.07E-06	ACSL3	acyl-CoA synthetase long-chain family member 3
214290_s_at	1.50482	9.07E-06	HIST2H2AA3 /// HIST2	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4
212027_at	-1.30894	9.23E-06	RBM25	RNA binding motif protein 25
220454_s_at	-1.33496	9.23E-06	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
222101_s_at	-1.35673	9.71E-06	DCHS1	dachsous 1 (Drosophila)
212958_x_at	-1.25363	9.71E-06	PAM	peptidylglycine alpha-amidating monooxygenase
214006_s_at	1.23923	9.71E-06	GGCX	gamma-glutamyl carboxylase
202815_s_at	-1.2225	9.71E-06	HEXIM1	hexamethylene bis-acetamide inducible 1
215836_s_at	-1.28394	1.00E-05	##################	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// p
207827_x_at	1.3552	1.01E-05	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
218813_s_at	1.21543	1.01E-05	SH3GLB2	SH3-domain GRB2-like endophilin B2
221886_at	-1.48821	1.01E-05	DENND2A	DENN/MADD domain containing 2A
45297_at	-1.3922	1.03E-05	EHD2	EH-domain containing 2
204273_at	-1.63994	1.07E-05	EDNRB	endothelin receptor type B
208779_x_at	-1.29849	1.07E-05	DDR1	discoidin domain receptor tyrosine kinase 1
207169_x_at	-1.30101	1.07E-05	DDR1	discoidin domain receptor tyrosine kinase 1
214212_x_at	-1.26927	1.10E-05	FERMT2	fermitin family member 2
32099_at	-1.21585	1.12E-05	SAFB2	scaffold attachment factor B2
202304_at	-1.2358	1.16E-05	FNDC3A	fibronectin type III domain containing 3A
202694_at	-1.31859	1.20E-05	STK17A	serine/threonine kinase 17a
212670_at	-1.53696	1.24E-05	ELN	elastin
219312_s_at	-1.26289	1.24E-05	ZBTB10	zinc finger and BTB domain containing 10
211959_at	-1.40869	1.27E-05	IGFBP5	insulin-like growth factor binding protein 5
204736_s_at	-1.34726	1.28E-05	CSPG4	chondroitin sulfate proteoglycan 4
202933_s_at	-1.21316	1.29E-05	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1

203548_s_at	-1.65787	1.31E-05	LPL	lipoprotein lipase
205717_x_at	-1.28369	1.31E-05	##################	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// p
202660_at	-1.3428	1.33E-05	ITPR2	inositol 1,4,5-triphosphate receptor, type 2
218131_s_at	-1.21677	1.33E-05	GATAD2A	GATA zinc finger domain containing 2A
212507_at	-1.22176	1.34E-05	TMEM131	transmembrane protein 131
215005_at	1.25275	1.36E-05	NECAB2	N-terminal EF-hand calcium binding protein 2
213262_at	-1.33768	1.36E-05	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)
213194_at	-1.34427	1.36E-05	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)
221870_at	-1.3545	1.37E-05	EHD2	EH-domain containing 2
202221_s_at	-1.22808	1.38E-05	EP300	E1A binding protein p300
212764_at	-1.27651	1.40E-05	ZEB1	zinc finger E-box binding homeobox 1
209210_s_at	-1.26641	1.41E-05	FERMT2	fermitin family member 2
218280_x_at	1.48418	1.46E-05	HIST2H2AA3 /// HIST2	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4
201534_s_at	-1.21131	1.46E-05	UBL3	ubiquitin-like 3
200771_at	-1.30552	1.46E-05	LAMC1	laminin, gamma 1 (formerly LAMB2)
211981_at	-1.58824	1.47E-05	COL4A1	collagen, type IV, alpha 1
201206_s_at	-1.34052	1.47E-05	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)
214230_at	1.45166	1.47E-05	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)
201910_at	-1.28052	1.48E-05	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
200952_s_at	-1.54819	1.55E-05	CCND2	cyclin D2
209185_s_at	-1.32578	1.56E-05	IRS2	insulin receptor substrate 2
55583_at	-1.21387	1.68E-05	DOCK6	dedicator of cytokinesis 6
213273_at	-1.45306	1.68E-05	ODZ4	odz, odd Oz/ten-m homolog 4 (Drosophila)
214044_at	1.28094	1.68E-05	RYR2	ryanodine receptor 2 (cardiac)
204247_s_at	1.23097	1.68E-05	CDK5	cyclin-dependent kinase 5
220301_at	-1.4061	1.73E-05	CCDC102B	coiled-coil domain containing 102B
217848_s_at	1.22333	1.73E-05	PPA1	pyrophosphatase (inorganic) 1
205880_at	-1.29751	1.74E-05	PRKD1	protein kinase D1
202822_at	-1.27227	1.75E-05	LPP	LIM domain containing preferred translocation partner in lipoma
203342_at	1.21498	1.75E-05	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)
206118_at	1.26402	1.80E-05	STAT4	signal transducer and activator of transcription 4
206384_at	1.29198	1.80E-05	CACNG3	calcium channel, voltage-dependent, gamma subunit 3
205546_s_at	-1.2219	1.83E-05	TYK2	tyrosine kinase 2
204228_at	1.2296	1.83E-05	PPIH	peptidylprolyl isomerase H (cyclophilin H)
211958_at	-1.56317	1.91E-05	IGFBP5	insulin-like growth factor binding protein 5
216264_s_at	-1.31674	1.91E-05	LAMB2	laminin, beta 2 (laminin S)
206376_at	1.26607	1.92E-05	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15
221689_s_at	1.22489	1.97E-05	PIGP	phosphatidylinositol glycan anchor biosynthesis, class P
208320_at	1.21972	1.97E-05	CABP1	calcium binding protein 1
201470_at	1.27834	2.12E-05	GSTO1	glutathione S-transferase omega 1
211136_s_at	-1.26215	2.14E-05	CLPTM1	cleft lip and palate associated transmembrane protein 1
201911_s_at	-1.26175	2.15E-05	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
210315_at	1.20071	2.26E-05	SYN2	synapsin II
214023_x_at	-1.26513	2.26E-05	TUBB2B	tubulin, beta 2B
203243_s_at	-1.32225	2.27E-05	PDLIM5	PDZ and LIM domain 5
208657_s_at	-1.25155	2.30E-05	41161	septin 9

203274_at	1.23111	2.30E-05	F8A1 /// F8A2 /// F8A	coagulation factor VIII-associated (intronic transcript) 1 /// coagulation facto
210749_x_at	-1.28277	2.32E-05	DDR1	discoidin domain receptor tyrosine kinase 1
201661_s_at	-1.29909	2.32E-05	ACSL3	acyl-CoA synthetase long-chain family member 3
211066_x_at	-1.25407	2.36E-05	##################	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// p
203044_at	-1.25201	2.36E-05	CHSY1	chondroitin sulfate synthase 1
200785_s_at	-1.34051	2.36E-05	LRP1	low density lipoprotein receptor-related protein 1
205523_at	-1.53152	2.39E-05	HAPLN1	hyaluronan and proteoglycan link protein 1
212544_at	1.23403	2.43E-05	ZNHIT3	zinc finger, HIT-type containing 3
201307_at	-1.20908	2.46E-05	41163	septin 11
212099_at	-1.25581	2.48E-05	RHOB	ras homolog gene family, member B
209079_x_at	-1.27304	2.48E-05	##################	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// p
202350_s_at	-1.56167	2.54E-05	MATN2	matrilin 2
202427_s_at	1.22003	2.57E-05	BRP44	brain protein 44
222010_at	1.21662	2.64E-05	TCP1	t-complex 1
221270_s_at	-1.21624	2.64E-05	QTRT1	queuine tRNA-ribosyltransferase 1
203238_s_at	-1.26493	2.64E-05	NOTCH3	notch 3
201962_s_at	1.29021	2.65E-05	RNF41	ring finger protein 41
218354_at	1.22505	2.71E-05	TRAPPC2L	trafficking protein particle complex 2-like
201203_s_at	-1.21197	2.76E-05	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)
214620_x_at	-1.22965	2.76E-05	PAM	peptidylglycine alpha-amidating monooxygenase
219594_at	1.41317	2.76E-05	NINJ2	ninjurin 2
203616_at	1.24277	2.79E-05	POLB	polymerase (DNA directed), beta
212357_at	-1.28314	2.79E-05	FAM168A	family with sequence similarity 168, member A
219557_s_at	1.45952	2.79E-05	NRIP3	nuclear receptor interacting protein 3
220617_s_at	-1.30542	2.79E-05	ZNF532	zinc finger protein 532
202202_s_at	-1.45791	2.86E-05	LAMA4	laminin, alpha 4
212242_at	1.3645	2.97E-05	TUBA4A	tubulin, alpha 4a
213787_s_at	1.2962	2.99E-05	EBP	emopamil binding protein (sterol isomerase)
201660_at	-1.27094	3.00E-05	ACSL3	acyl-CoA synthetase long-chain family member 3
209064_x_at	1.39525	3.10E-05	PAIP1	poly(A) binding protein interacting protein 1
37408_at	-1.45265	3.10E-05	MRC2	mannose receptor, C type 2
202552_s_at	-1.29479	3.20E-05	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
205893_at	-1.34386	3.23E-05	NLGN1	neuroligin 1
208813_at	1.25527	3.37E-05	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
221729_at	-1.55717	3.45E-05	COL5A2	collagen, type V, alpha 2
219416_at	-1.31295	3.46E-05	SCARA3	scavenger receptor class A, member 3
214075_at	1.23297	3.47E-05	NENF	neuron derived neurotrophic factor
202561_at	-1.25748	3.57E-05	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
205888_s_at	-1.24733	3.82E-05	JAKMIP2	janus kinase and microtubule interacting protein 2
213158_at	-1.33502	3.86E-05	---	---
202066_at	-1.21639	3.91E-05	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting
205532_s_at	-1.39975	3.93E-05	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
207358_x_at	-1.21652	3.93E-05	MACF1	microtubule-actin crosslinking factor 1
207671_s_at	1.24846	3.96E-05	BEST1	bestrophin 1
202065_s_at	-1.23034	4.00E-05	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting
213058_at	-1.31489	4.01E-05	TTC28	tetratricopeptide repeat domain 28

211616_s_at	1.27978	4.01E-05	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A
222237_s_at	-1.27633	4.01E-05	ZFP112	zinc finger protein 112 homolog (mouse)
205562_at	1.2032	4.03E-05	RPP38	ribonuclease P/MRP 38kDa subunit
215416_s_at	1.2515	4.20E-05	STOML2	stomatin (EPB72)-like 2
202935_s_at	-1.38747	4.22E-05	SOX9	SRY (sex determining region Y)-box 9
204078_at	-1.23159	4.26E-05	LEPREL4	leprecan-like 4
209651_at	-1.33096	4.35E-05	TGFB1I1	transforming growth factor beta 1 induced transcript 1
206888_s_at	1.25704	4.35E-05	ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma
200953_s_at	-1.46206	4.38E-05	CCND2	cyclin D2
218062_x_at	-1.34248	4.45E-05	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
209507_at	1.27655	4.46E-05	RPA3	replication protein A3, 14kDa
207760_s_at	-1.23922	4.53E-05	NCOR2	nuclear receptor corepressor 2
205428_s_at	1.38263	4.62E-05	CALB2	calbindin 2
205227_at	-1.54715	4.68E-05	IL1RAP	interleukin 1 receptor accessory protein
204521_at	1.23732	4.80E-05	C12orf24	chromosome 12 open reading frame 24
204363_at	-1.41925	4.84E-05	F3	coagulation factor III (thromboplastin, tissue factor)
204675_at	1.3128	5.17E-05	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-de
219737_s_at	-1.44979	5.21E-05	PCDH9	protocadherin 9
203426_s_at	-1.34796	5.22E-05	IGFBP5	insulin-like growth factor binding protein 5
219831_at	1.21118	5.24E-05	CDKL3	cyclin-dependent kinase-like 3
208828_at	1.2484	5.25E-05	POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit)
204311_at	-1.48212	5.25E-05	ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide
204591_at	-1.65838	5.25E-05	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)
218656_s_at	-1.30489	5.26E-05	LHFP	lipoma HMGIC fusion partner
214198_s_at	-1.2186	5.26E-05	DGCR2	DiGeorge syndrome critical region gene 2
215241_at	1.29254	5.26E-05	ANO3	anoctamin 3
204836_at	-1.43838	5.57E-05	GLDC	glycine dehydrogenase (decarboxylating)
216804_s_at	-1.36723	5.57E-05	PDLIM5	PDZ and LIM domain 5
209282_at	-1.2057	5.57E-05	PRKD2	protein kinase D2
219714_s_at	1.2991	5.57E-05	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3
202479_s_at	-1.48944	5.64E-05	TRIB2	tribbles homolog 2 (Drosophila)
212295_s_at	-1.24112	5.71E-05	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
208321_s_at	1.26934	5.71E-05	CABP1	calcium binding protein 1
210852_s_at	-1.22254	5.77E-05	AASS	aminoadipate-semialdehyde synthase
213051_at	-1.22403	5.77E-05	ZC3HAV1	zinc finger CCCH-type, antiviral 1
209529_at	1.23976	5.77E-05	PPAP2C	phosphatidic acid phosphatase type 2C
205645_at	1.2296	6.00E-05	REPS2	RALBP1 associated Eps domain containing 2
219477_s_at	-1.29045	6.21E-05	THSD1 /// THSD1P1	thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain c
205196_s_at	1.2645	6.31E-05	AP1S1	adaptor-related protein complex 1, sigma 1 subunit
210150_s_at	-1.26766	6.44E-05	LAMA5	laminin, alpha 5
212285_s_at	-1.22486	6.49E-05	AGRN	agrin
203221_at	-1.29461	6.53E-05	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
220994_s_at	1.26051	6.78E-05	STXBP6	syntaxin binding protein 6 (amisyn)
219933_at	1.20876	6.82E-05	GLRX2	glutaredoxin 2
220029_at	-1.5429	6.83E-05	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
202381_at	-1.26318	6.85E-05	ADAM9	ADAM metallopeptidase domain 9

205899_at	1.31254	6.85E-05	CCNA1	cyclin A1
208643_s_at	1.2066	6.95E-05	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-s
206013_s_at	1.38688	7.20E-05	ACTL6B	actin-like 6B
221974_at	-1.34034	7.21E-05	IPW	imprinted in Prader-Willi syndrome (non-protein coding)
202936_s_at	-1.33413	7.25E-05	SOX9	SRY (sex determining region Y)-box 9
213746_s_at	-1.32316	7.39E-05	FLNA	filamin A, alpha
200811_at	-1.22283	7.47E-05	CIRBP	cold inducible RNA binding protein
209711_at	-1.25679	7.93E-05	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual tra
214436_at	1.3254	7.93E-05	FBXL2	F-box and leucine-rich repeat protein 2
203222_s_at	-1.31106	8.04E-05	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
201324_at	-1.38561	8.12E-05	EMP1	epithelial membrane protein 1
213428_s_at	-1.43059	8.21E-05	COL6A1	collagen, type VI, alpha 1
201645_at	-1.4561	8.39E-05	TNC	tenascin C
219143_s_at	1.20261	8.46E-05	RPP25	ribonuclease P/MRP 25kDa subunit
208407_s_at	-1.25697	8.46E-05	CTNND1	catenin (cadherin-associated protein), delta 1
564_at	-1.20108	8.46E-05	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
205572_at	-1.49953	8.46E-05	ANGPT2	angiopoietin 2
204541_at	-1.28608	8.47E-05	SEC14L2	SEC14-like 2 (S. cerevisiae)
202084_s_at	-1.30138	8.49E-05	SEC14L1	SEC14-like 1 (S. cerevisiae)
200050_at	-1.22214	8.49E-05	ZNF146	zinc finger protein 146
43544_at	-1.21699	8.50E-05	MED16	mediator complex subunit 16
217427_s_at	-1.22176	8.72E-05	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)
202082_s_at	-1.28298	8.72E-05	SEC14L1	SEC14-like 1 (S. cerevisiae)
200784_s_at	-1.28281	8.72E-05	LRP1	low density lipoprotein receptor-related protein 1
205437_at	-1.28731	8.76E-05	ZNF211	zinc finger protein 211
204867_at	1.24047	8.80E-05	GCHFR	GTP cyclohydrolase I feedback regulator
201204_s_at	-1.28203	8.80E-05	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)
200907_s_at	-1.22365	8.96E-05	PALLD	palladin, cytoskeletal associated protein
202854_at	1.30609	8.99E-05	HPRT1	hypoxanthine phosphoribosyltransferase 1
213744_at	1.26554	8.99E-05	ATRNL1	attractin-like 1
208398_s_at	1.27824	8.99E-05	TBPL1	TBP-like 1
204218_at	1.22609	9.12E-05	C11orf51	chromosome 11 open reading frame 51
205733_at	-1.37615	9.20E-05	BLM	Bloom syndrome, RecQ helicase-like
219249_s_at	-1.24623	9.20E-05	FKBP10	FK506 binding protein 10, 65 kDa
209449_at	1.23823	9.29E-05	LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)
217419_x_at	-1.20986	9.40E-05	AGRN	agrin
218394_at	1.2536	9.40E-05	ROGDI	rogdi homolog (Drosophila)
203474_at	-1.33085	9.59E-05	IQGAP2	IQ motif containing GTPase activating protein 2
213169_at	-1.42429	9.92E-05	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembran
204944_at	-1.27	9.92E-05	PTPRG	protein tyrosine phosphatase, receptor type, G
209022_at	-1.22091	9.94E-05	STAG2	stromal antigen 2
201655_s_at	-1.2873	0.000101478	HSPG2	heparan sulfate proteoglycan 2
213155_at	-1.55448	0.000101478	WSCD1	WSC domain containing 1
212813_at	-1.20131	0.000102475	JAM3	junctional adhesion molecule 3
213795_s_at	-1.21229	0.000104554	PTPRA	protein tyrosine phosphatase, receptor type, A
213618_at	-1.39487	0.000104874	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2

204557_s_at	-1.29943	0.000106275	DZIP1	DAZ interacting protein 1
217297_s_at	-1.21156	0.000107422	MYO9B	myosin IXB
211494_s_at	-1.56545	0.000107422	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
90265_at	1.27862	0.000107422	ADAP1	ArfGAP with dual PH domains 1
209099_x_at	-1.31486	0.00010874	JAG1	jagged 1
219212_at	1.22346	0.000112215	HSPA14	heat shock 70kDa protein 14
215259_s_at	-1.2672	0.000112215	CADM4	cell adhesion molecule 4
213469_at	-1.31556	0.000112215	PGAP1	post-GPI attachment to proteins 1
41577_at	1.37797	0.000113812	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B
210292_s_at	1.59467	0.000114556	PCDH11X /// PCDH11	protocadherin 11 X-linked /// protocadherin 11 Y-linked
204467_s_at	1.41863	0.000117433	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
210408_s_at	1.20212	0.000117666	CPNE6	copine VI (neuronal)
216268_s_at	-1.33082	0.000118327	JAG1	jagged 1
208741_at	-1.21501	0.000121481	SAP18	Sin3A-associated protein, 18kDa
202506_at	-1.2211	0.000123801	SSFA2	sperm specific antigen 2
219671_at	1.50453	0.000125586	HPCAL4	hippocalcin like 4
201412_at	-1.22562	0.000126658	LRP10	low density lipoprotein receptor-related protein 10
202647_s_at	1.26894	0.000127064	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog
214752_x_at	-1.28462	0.000127064	FLNA	filamin A, alpha
211934_x_at	-1.20667	0.00012788	GANAB	glucosidase, alpha; neutral AB
214297_at	-1.37921	0.000129435	CSPG4	chondroitin sulfate proteoglycan 4
220316_at	-1.39701	0.000130374	NPAS3	neuronal PAS domain protein 3
209202_s_at	-1.2242	0.000131005	EXTL3	exostoses (multiple)-like 3
205334_at	1.43284	0.000131005	S100A1	S100 calcium binding protein A1
202175_at	-1.21613	0.000134735	CHPF	chondroitin polymerizing factor
208612_at	-1.20839	0.000134735	PDIA3	protein disulfide isomerase family A, member 3
209633_at	1.21862	0.000137291	PPP2R3A	protein phosphatase 2, regulatory subunit B'', alpha
205827_at	1.62691	0.00013836	CCK	cholecystokinin
210809_s_at	-2.63317	0.000138732	POSTN	periostin, osteoblast specific factor
202756_s_at	-1.3478	0.000138759	GPC1	glypican 1
219162_s_at	1.20357	0.000139242	MRPL11	mitochondrial ribosomal protein L11
218069_at	1.21555	0.000139936	DCTPP1	dCTP pyrophosphatase 1
211836_s_at	1.61529	0.00014085	MOG	myelin oligodendrocyte glycoprotein
202223_at	-1.20142	0.000144948	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae
214098_at	1.39929	0.000144948	KIAA1107	KIAA1107
218064_s_at	-1.22091	0.000145312	AKAP8L	A kinase (PRKA) anchor protein 8-like
203143_s_at	-1.32268	0.000146674	KIAA0040	KIAA0040
212909_at	-1.43333	0.000147373	LYPD1	LY6/PLAUR domain containing 1
202007_at	-1.38657	0.000147609	NID1	nidogen 1
212165_at	1.22036	0.000147909	TMEM183A /// TMEM	transmembrane protein 183A /// transmembrane protein 183B
203749_s_at	-1.20985	0.000148271	RARA	retinoic acid receptor, alpha
208051_s_at	1.36721	0.000149881	PAIP1	poly(A) binding protein interacting protein 1
218048_at	1.20822	0.000150234	COMMD3	COMM domain containing 3
213938_at	1.42835	0.000152296	ERC2	ELKS/RAB6-interacting/CAST family member 2
219888_at	1.38337	0.000152296	SPAG4	sperm associated antigen 4
208986_at	-1.21452	0.000152422	TCF12	transcription factor 12

203897_at	1.21646	0.000152422	LYRM1	LYR motif containing 1
202898_at	-1.31628	0.000152422	SDC3	syndecan 3
221893_s_at	1.21932	0.000152898	ADCK2	aarF domain containing kinase 2
222266_at	-1.23484	0.000154435	C19orf2	Chromosome 19 open reading frame 2
221245_s_at	-1.39981	0.000154675	FZD5	frizzled homolog 5 (Drosophila)
200859_x_at	-1.29502	0.000156648	FLNA	filamin A, alpha
207107_at	-1.48464	0.000163302	RPE65	retinal pigment epithelium-specific protein 65kDa
204844_at	-1.29669	0.000163407	ENPEP	glutamyl aminopeptidase (aminopeptidase A)
215028_at	-1.42147	0.000167039	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
215127_s_at	-1.27851	0.000168885	RBMS1	RNA binding motif, single stranded interacting protein 1
206929_s_at	-1.26732	0.000168885	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)
218686_s_at	-1.26896	0.000168885	RHBDF1	rhomboid 5 homolog 1 (Drosophila)
213904_at	1.57834	0.000169619	---	---
201578_at	-1.27312	0.000169619	PODXL	podocalyxin-like
218469_at	1.34575	0.000169619	GREM1	gremlin 1
204520_x_at	-1.20385	0.000169619	BRD1	bromodomain containing 1
205116_at	-1.34785	0.00017053	LAMA2	laminin, alpha 2
208704_x_at	-1.20252	0.000173647	APLP2	amyloid beta (A4) precursor-like protein 2
209080_x_at	1.26326	0.000179689	GLRX3	glutaredoxin 3
214428_x_at	-1.41224	0.00018292	C4A /// C4B /// LOC10	complement component 4A (Rodgers blood group) /// complement component 4B (Chido
221794_at	-1.21527	0.00018292	DOCK6	dedicator of cytokinesis 6
210480_s_at	-1.26606	0.000188114	MYO6	myosin VI
200951_s_at	-1.51185	0.000188261	CCND2	cyclin D2
214469_at	1.25774	0.000188261	HIST1H2AE	histone cluster 1, H2ae
204729_s_at	1.23099	0.000189033	STX1A	syntaxin 1A (brain)
201013_s_at	-1.20054	0.000194643	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinoca
218087_s_at	-1.29523	0.000195947	SORBS1	sorbin and SH3 domain containing 1
205348_s_at	1.52843	0.000199703	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1
218093_s_at	-1.27362	0.000201059	ANKRD10	ankyrin repeat domain 10
208998_at	1.34505	0.000205122	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
201785_at	1.50198	0.000205433	RNASE1	ribonuclease, RNase A family, 1 (pancreatic)
213519_s_at	-1.43575	0.000207186	LAMA2	laminin, alpha 2
204730_at	1.45267	0.000209077	RIMS3	regulating synaptic membrane exocytosis 3
206039_at	1.57863	0.000209927	RAB33A	RAB33A, member RAS oncogene family
205454_at	1.37935	0.000210401	HPCA	hippocalcin
214574_x_at	1.34258	0.000210401	LST1	leukocyte specific transcript 1
204466_s_at	1.4847	0.000210401	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
204204_at	1.38148	0.000211272	SLC31A2	solute carrier family 31 (copper transporters), member 2
210762_s_at	-1.41313	0.000211743	DLC1	deleted in liver cancer 1
203801_at	-1.22666	0.000216067	MRPS14	mitochondrial ribosomal protein S14
212567_s_at	-1.21927	0.000216067	MAP4	microtubule-associated protein 4
202315_s_at	-1.30758	0.000216451	BCR	breakpoint cluster region
204270_at	-1.2142	0.000222072	SKI	v-ski sarcoma viral oncogene homolog (avian)
219373_at	1.2701	0.000222304	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3
210629_x_at	1.30764	0.000227185	LST1	leukocyte specific transcript 1
209012_at	-1.33881	0.000227454	TRIO	triple functional domain (PTPRF interacting)

205325_at	1.28171	0.000227454	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein
214703_s_at	-1.22925	0.000227663	MAN2B2	mannosidase, alpha, class 2B, member 2
213435_at	-1.28758	0.000231155	SATB2	SATB homeobox 2
216867_s_at	-1.4028	0.000232388	PDGFA	platelet-derived growth factor alpha polypeptide
210115_at	1.39353	0.000234834	RPL39L	ribosomal protein L39-like
209692_at	-1.3377	0.000236352	EYA2	eyes absent homolog 2 (Drosophila)
205989_s_at	1.67899	0.000236352	MOG	myelin oligodendrocyte glycoprotein
203960_s_at	1.2065	0.000240867	HSPB11	heat shock protein family B (small), member 11
201847_at	1.25576	0.000240867	LIPA	lipase A, lysosomal acid, cholesterol esterase
205433_at	-1.46668	0.000240867	BCHE	butyrylcholinesterase
206465_at	-1.55679	0.000241242	ACSBG1	acyl-CoA synthetase bubblegum family member 1
219628_at	-1.30373	0.000243514	ZMAT3	zinc finger, matrin-type 3
205923_at	1.30675	0.000245146	RELN	reelin
209695_at	-1.2985	0.000245581	PTP4A3	protein tyrosine phosphatase type IVA, member 3
204950_at	-1.21306	0.000253213	CARD8	caspase recruitment domain family, member 8
204201_s_at	-1.20663	0.000253213	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated
209684_at	1.21108	0.00025357	RIN2	Ras and Rab interactor 2
211563_s_at	-1.23163	0.000253801	C19orf2	chromosome 19 open reading frame 2
222344_at	-1.24207	0.00025483	---	---
210739_x_at	-1.37801	0.000254979	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
219378_at	-1.21686	0.000258677	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit
205637_s_at	1.60595	0.000259015	SH3GL3	SH3-domain GRB2-like 3
219365_s_at	1.24559	0.000259034	CAMKV	CaM kinase-like vesicle-associated
47550_at	-1.33414	0.000259746	LZTS1	leucine zipper, putative tumor suppressor 1
219032_x_at	1.27011	0.000260721	OPN3	opsin 3
205917_at	-1.31784	0.000266009	ZNF264	zinc finger protein 264
202255_s_at	-1.26655	0.000268526	SIPA1L1	signal-induced proliferation-associated 1 like 1
209149_s_at	-1.2432	0.000270516	TM9SF1	transmembrane 9 superfamily member 1
210263_at	-1.46323	0.000272824	KCNF1	potassium voltage-gated channel, subfamily F, member 1
219538_at	1.21076	0.000273076	WDR5B	WD repeat domain 5B
209806_at	1.30874	0.000273076	HIST1H2BK	histone cluster 1, H2bk
206772_at	1.21157	0.000273587	PTH2R	parathyroid hormone 2 receptor
218330_s_at	-1.25043	0.000273925	NAV2	neuron navigator 2
211890_x_at	1.44827	0.000273925	CAPN3	calpain 3, (p94)
214650_x_at	1.75859	0.00027599	MOG	myelin oligodendrocyte glycoprotein
214181_x_at	1.349	0.00027599	LST1	leukocyte specific transcript 1
203908_at	-1.52422	0.000280318	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
204412_s_at	1.28364	0.000284056	NEFH	neurofilament, heavy polypeptide
213436_at	-1.57755	0.000284085	CNR1	cannabinoid receptor 1 (brain)
205816_at	-1.32479	0.000286865	ITGB8	integrin, beta 8
204840_s_at	-1.21291	0.000289937	EEA1	early endosome antigen 1
205656_at	-1.27573	0.000289937	PCDH17	protocadherin 17
222005_s_at	1.54667	0.000292768	GNG3	guanine nucleotide binding protein (G protein), gamma 3
219042_at	-1.23613	0.000293393	LZTS1	leucine zipper, putative tumor suppressor 1
33850_at	-1.2083	0.000293393	MAP4	microtubule-associated protein 4
208212_s_at	-1.35678	0.000293393	ALK	anaplastic lymphoma receptor tyrosine kinase

204997_at	1.21635	0.000295314	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)
218211_s_at	1.29723	0.000295314	MLPH	melanophilin
206280_at	1.26501	0.000296467	CDH18	cadherin 18, type 2
213225_at	-1.22263	0.000296692	PPM1B	protein phosphatase, Mg2+/Mn2+ dependent, 1B
206014_at	1.43691	0.000296692	ACTL6B	actin-like 6B
201079_at	1.29501	0.000296829	SYNGR2	synaptogyrin 2
213156_at	-1.31013	0.000297138	---	---
210519_s_at	1.35604	0.000298855	NQO1	NAD(P)H dehydrogenase, quinone 1
219429_at	1.50358	0.000309575	FA2H	fatty acid 2-hydroxylase
205383_s_at	-1.25459	0.000315715	ZBTB20	zinc finger and BTB domain containing 20
211581_x_at	1.29792	0.000315715	LST1	leukocyte specific transcript 1
204465_s_at	1.61175	0.000315715	INA	internexin neuronal intermediate filament protein, alpha
210650_s_at	1.21099	0.000315715	PCLO	piccolo (presynaptic cytomatrix protein)
216450_x_at	-1.23345	0.000316565	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1
207012_at	-1.50333	0.000317698	MMP16	matrix metallopeptidase 16 (membrane-inserted)
208934_s_at	1.27323	0.000326494	LGALS8	lectin, galactoside-binding, soluble, 8
208703_s_at	-1.22859	0.000327734	APLP2	amyloid beta (A4) precursor-like protein 2
213789_at	1.23085	0.000328593	---	---
213093_at	-1.22167	0.000328788	PRKCA	protein kinase C, alpha
213558_at	1.40523	0.000329401	PCLO	piccolo (presynaptic cytomatrix protein)
210169_at	1.279	0.000331768	SEC14L5	SEC14-like 5 (S. cerevisiae)
212558_at	-1.40144	0.000331768	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
210253_at	1.35767	0.000337558	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa
209896_s_at	-1.24441	0.000337558	PTPN11	protein tyrosine phosphatase, non-receptor type 11
204271_s_at	-1.3744	0.000340161	EDNRB	endothelin receptor type B
209911_x_at	1.37154	0.000340161	HIST1H2BD	histone cluster 1, H2bd
211582_x_at	1.34385	0.000345271	LST1	leukocyte specific transcript 1
209098_s_at	-1.39304	0.000347106	JAG1	jagged 1
203395_s_at	-1.22419	0.000352935	HES1	hairy and enhancer of split 1, (Drosophila)
219922_s_at	-1.23847	0.000352935	LTBP3	latent transforming growth factor beta binding protein 3
216836_s_at	-1.317	0.000353918	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma de
202695_s_at	-1.29325	0.000355336	STK17A	serine/threonine kinase 17a
218631_at	1.20332	0.000355575	AVPI1	arginine vasopressin-induced 1
208451_s_at	-1.42691	0.000357751	C4A /// C4B /// LOC10	complement component 4A (Rodgers blood group) /// complement component 4B (Chido
214722_at	-1.24771	0.000357751	NOTCH2NL	notch 2 N-terminal like
219140_s_at	1.23605	0.000358263	RBP4	retinol binding protein 4, plasma
207030_s_at	-1.29491	0.000361151	CSRP2	cysteine and glycine-rich protein 2
216840_s_at	-1.40158	0.000361289	LAMA2	laminin, alpha 2
207853_s_at	1.30322	0.000361634	SNCB	synuclein, beta
212951_at	-1.27495	0.000361634	GPR116	G protein-coupled receptor 116
211031_s_at	-1.29308	0.000361634	CLIP2	CAP-GLY domain containing linker protein 2
219643_at	-1.34252	0.000370246	LRP1B	low density lipoprotein receptor-related protein 1B
33767_at	1.4155	0.000371208	NEFH	neurofilament, heavy polypeptide
206773_at	1.50334	0.000374509	LY6H	lymphocyte antigen 6 complex, locus H
204774_at	1.41478	0.00037664	EVI2A	ecotropic viral integration site 2A
212926_at	-1.21216	0.000383406	SMC5	structural maintenance of chromosomes 5

210993_s_at	-1.20853	0.000383406	SMAD1	SMAD family member 1
200672_x_at	-1.20829	0.000383406	SPTBN1	spectrin, beta, non-erythrocytic 1
203604_at	-1.21328	0.000383406	ZNF516	zinc finger protein 516
221868_at	1.26704	0.000387943	PAIP2B	poly(A) binding protein interacting protein 2B
215248_at	-1.36021	0.000388286	GRB10	growth factor receptor-bound protein 10
222028_at	-1.20354	0.000389671	ZNF45	zinc finger protein 45
221730_at	-1.50578	0.000389674	COL5A2	collagen, type V, alpha 2
201369_s_at	-1.29898	0.000391261	ZFP36L2	zinc finger protein 36, C3H type-like 2
202507_s_at	1.63665	0.000399563	SNAP25	synaptosomal-associated protein, 25kDa
202145_at	1.24781	0.000399733	LY6E	lymphocyte antigen 6 complex, locus E
220305_at	-1.20457	0.000400039	MAVS	mitochondrial antiviral signaling protein
208997_s_at	1.27656	0.000400156	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
218806_s_at	-1.27246	0.000402824	VAV3	vav 3 guanine nucleotide exchange factor
205691_at	1.3664	0.000404342	SYNGR3	synaptogyrin 3
212667_at	-1.24632	0.0004056	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)
53071_s_at	-1.20906	0.000409442	C17orf101	chromosome 17 open reading frame 101
201897_s_at	1.28602	0.000415915	CKS1B	CDC28 protein kinase regulatory subunit 1B
220359_s_at	1.3722	0.000424044	ARPP21	cAMP-regulated phosphoprotein, 21kDa
201117_s_at	-1.29071	0.000427071	CPE	carboxypeptidase E
212750_at	1.34647	0.000427214	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B
211596_s_at	-1.26937	0.000435317	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1
215071_s_at	1.35993	0.000435868	HIST1H2AC	histone cluster 1, H2ac
204160_s_at	1.51953	0.000435868	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)
205933_at	-1.25318	0.000435868	SETBP1	SET binding protein 1
208579_x_at	1.33675	0.000435868	H2BFS	H2B histone family, member S
205320_at	-1.28064	0.000435868	APC2	adenomatosis polyposis coli 2
63825_at	-1.262	0.000436576	ABHD2	abhydrolase domain containing 2
203543_s_at	-1.33336	0.000444334	KLF9	Kruppel-like factor 9
207180_s_at	1.26298	0.000444334	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa
215633_x_at	1.31582	0.000445146	LST1	leukocyte specific transcript 1
213238_at	-1.21376	0.000445703	ATP10D	ATPase, class V, type 10D
221486_at	1.20364	0.000445703	ENSA	endosulfine alpha
202668_at	-1.28899	0.000449378	EFNB2	ephrin-B2
210136_at	1.36447	0.000450844	MBP	myelin basic protein
202083_s_at	-1.26255	0.000451297	SEC14L1	SEC14-like 1 (S. cerevisiae)
218468_s_at	1.20478	0.000451297	GREM1	gremlin 1
205366_s_at	1.24983	0.000462117	HOXB6	homeobox B6
221556_at	-1.20531	0.000464446	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
221605_s_at	-1.50384	0.00046509	PIPOX	pipecolic acid oxidase
211932_at	-1.20225	0.00046509	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
222326_at	-1.26867	0.00047205	---	---
219992_at	1.46671	0.00047205	TAC3	tachykinin 3
204428_s_at	-1.24714	0.000476029	LCAT	lecithin-cholesterol acyltransferase
211148_s_at	-1.36705	0.000477715	ANGPT2	angiopoietin 2
214314_s_at	-1.22058	0.000477715	EIF5B	eukaryotic translation initiation factor 5B
209445_x_at	1.22162	0.00047805	C7orf44	chromosome 7 open reading frame 44

208892_s_at	-1.30694	0.000487958	DUSP6	dual specificity phosphatase 6
212070_at	-1.28166	0.000491326	GPR56	G protein-coupled receptor 56
202133_at	-1.31254	0.000497484	WWTR1	WW domain containing transcription regulator 1
209870_s_at	-1.23237	0.000506908	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2
213779_at	-1.2333	0.000506908	EMID1	EMI domain containing 1
214829_at	-1.21742	0.000514013	AASS	aminoadipate-semialdehyde synthase
91816_f_at	-1.27257	0.000515651	MEX3D	mex-3 homolog D (C. elegans)
203498_at	1.61896	0.000518377	RCAN2	regulator of calcineurin 2
213543_at	1.25023	0.000524555	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
203080_s_at	-1.22342	0.000530383	BAZ2B	bromodomain adjacent to zinc finger domain, 2B
214052_x_at	-1.21124	0.000532072	BAT2L2	HLA-B associated transcript 2-like 2
204118_at	1.36213	0.000536459	CD48	CD48 molecule
206928_at	1.25146	0.000536865	ZNF124	zinc finger protein 124
209153_s_at	-1.2303	0.000546573	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
204378_at	1.54452	0.000566907	BCAS1	breast carcinoma amplified sequence 1
212458_at	-1.26748	0.000568929	SPRED2	sprouty-related, EVH1 domain containing 2
209020_at	1.21467	0.000584676	C20orf111	chromosome 20 open reading frame 111
203934_at	-1.21067	0.000584676	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)
219225_at	1.28496	0.000584676	PGBD5	piggyBac transposable element derived 5
212758_s_at	-1.25194	0.000584676	ZEB1	zinc finger E-box binding homeobox 1
221217_s_at	1.2451	0.000584676	RBFOX1	RNA binding protein, fox-1 homolog (C. elegans) 1
202759_s_at	-1.35248	0.000584676	AKAP2 /// PALM2-AKA	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrough
202962_at	-1.22902	0.000584676	KIF13B	kinesin family member 13B
203424_s_at	-1.43719	0.00058901	IGFBP5	insulin-like growth factor binding protein 5
202254_at	-1.27431	0.00058901	SIPA1L1	Signal-induced proliferation-associated 1 like 1
207714_s_at	-1.32161	0.00058901	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen
219616_at	-1.44316	0.000596553	ACSS3	acyl-CoA synthetase short-chain family member 3
202760_s_at	-1.36722	0.000597426	AKAP2 /// PALM2-AKA	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrough
200878_at	-1.23104	0.000597426	EPAS1	endothelial PAS domain protein 1
222243_s_at	-1.2202	0.000597426	TOB2	transducer of ERBB2, 2
211493_x_at	-1.23008	0.000597426	DTNA	dystrobrevin, alpha
202149_at	-1.26375	0.000603326	NEDD9	neural precursor cell expressed, developmentally down-regulated 9
209895_at	-1.2355	0.000607763	PTPN11	protein tyrosine phosphatase, non-receptor type 11
221480_at	-1.20211	0.000607784	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1
206448_at	1.33226	0.000608141	ZNF365	zinc finger protein 365
219161_s_at	1.21491	0.000610192	CKLF	chemokine-like factor
203725_at	-1.26266	0.000610661	GADD45A	growth arrest and DNA-damage-inducible, alpha
218859_s_at	-1.22273	0.000613135	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
215215_s_at	1.20745	0.000613135	LOC81691	exonuclease NEF-sp
200808_s_at	-1.26849	0.000616593	ZYX	zyxin
201465_s_at	-1.2428	0.00061964	JUN	jun proto-oncogene
202554_s_at	1.30485	0.000626762	GSTM3	glutathione S-transferase mu 3 (brain)
204697_s_at	1.35978	0.000633464	CHGA	chromogranin A (parathyroid secretory protein 1)
205489_at	1.52663	0.0006399	CRYM	crystallin, mu
220131_at	1.44955	0.000642437	FXYD7	FXYD domain containing ion transport regulator 7
208891_at	-1.30154	0.000648707	DUSP6	dual specificity phosphatase 6

202921_s_at	-1.27354	0.000669749	ANK2	ankyrin 2, neuronal
207135_at	1.28481	0.000682093	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A
203542_s_at	-1.29764	0.000687823	KLF9	Kruppel-like factor 9
206456_at	1.24608	0.00068803	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5
219578_s_at	1.24399	0.000692263	CPEB1	cytoplasmic polyadenylation element binding protein 1
207983_s_at	-1.21251	0.000692263	STAG2	stromal antigen 2
218438_s_at	1.23239	0.000698297	MED28	mediator complex subunit 28
212486_s_at	-1.26855	0.000698297	FYN	FYN oncogene related to SRC, FGR, YES
204345_at	-1.33093	0.000705218	COL16A1	collagen, type XVI, alpha 1
205379_at	1.21796	0.000710373	CBR3	carbonyl reductase 3
221645_s_at	-1.23205	0.000718908	ZNF83	zinc finger protein 83
202661_at	-1.201	0.000718908	ITPR2	inositol 1,4,5-triphosphate receptor, type 2
202724_s_at	-1.26122	0.000719579	FOXO1	forkhead box O1
215228_at	1.34183	0.000719579	NHLH2	nescient helix loop helix 2
206408_at	-1.43737	0.000724294	LRRTM2	leucine rich repeat transmembrane neuronal 2
219973_at	-1.3761	0.000731733	ARSJ	arylsulfatase family, member J
209841_s_at	-1.3041	0.000731733	LRRN3	leucine rich repeat neuronal 3
201732_s_at	-1.20755	0.00073332	CLCN3	chloride channel 3
222121_at	-1.22846	0.000741556	ARHGEF26	Rho guanine nucleotide exchange factor (GEF) 26
201200_at	1.25297	0.000749694	CREG1	cellular repressor of E1A-stimulated genes 1
219265_at	1.22563	0.000749694	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)
209663_s_at	-1.3432	0.000749694	ITGA7	integrin, alpha 7
206196_s_at	1.48287	0.000749694	RUNDC3A	RUN domain containing 3A
214956_at	1.21284	0.000753113	AAK1	AP2 associated kinase 1
212950_at	-1.23578	0.000753411	GPR116	G protein-coupled receptor 116
204823_at	1.42484	0.000753411	NAV3	neuron navigator 3
213998_s_at	-1.28092	0.000782026	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
212775_at	-1.20977	0.000789532	OBSL1	obscurin-like 1
201505_at	-1.45136	0.000793895	LAMB1	laminin, beta 1
219738_s_at	-1.3305	0.000795004	PCDH9	protocadherin 9
203705_s_at	-1.4177	0.000803824	FZD7	frizzled homolog 7 (Drosophila)
202920_at	-1.22309	0.000807524	ANK2	ankyrin 2, neuronal
201116_s_at	-1.29266	0.000824055	CPE	carboxypeptidase E
212845_at	-1.24199	0.000829795	SAMD4A	sterile alpha motif domain containing 4A
209295_at	-1.27661	0.000832351	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b
204014_at	-1.47822	0.000836093	DUSP4	dual specificity phosphatase 4
206678_at	1.43378	0.000838431	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1
203890_s_at	-1.2193	0.000847577	DAPK3	death-associated protein kinase 3
209094_at	-1.20641	0.000858195	DDAH1	dimethylarginine dimethylaminohydrolase 1
205524_s_at	-1.32028	0.000869725	HAPLN1	hyaluronan and proteoglycan link protein 1
210372_s_at	1.34242	0.000870152	TPD52L1	tumor protein D52-like 1
213910_at	-1.20774	0.000874207	IGFBP7	insulin-like growth factor binding protein 7
203471_s_at	1.28828	0.000891429	PLEK	pleckstrin
219308_s_at	1.35722	0.00090849	AK5	adenylate kinase 5
214475_x_at	1.48028	0.00090849	CAPN3	calpain 3, (p94)
209793_at	-1.58971	0.00090849	GRIA1	glutamate receptor, ionotropic, AMPA 1

212776_s_at	-1.23538	0.00092033	OBSL1	obscurin-like 1
203946_s_at	1.30364	0.000929508	ARG2	arginase, type II
203425_s_at	-1.25537	0.000942094	IGFBP5	insulin-like growth factor binding protein 5
213069_at	-1.22555	0.00094972	HEG1	HEG homolog 1 (zebrafish)
209292_at	-1.4511	0.00094972	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
205463_s_at	-1.38689	0.000952239	PDGFA	platelet-derived growth factor alpha polypeptide
220287_at	-1.22125	0.000953744	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9
203497_at	-1.22026	0.000958136	MED1	mediator complex subunit 1
220551_at	1.34969	0.000971802	SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), m
219574_at	1.27984	0.000974268	40969	membrane-associated ring finger (C3HC4) 1
218623_at	1.47098	0.000980134	HMP19	HMP19 protein
216456_at	-1.25792	0.000988342	---	---
212268_at	1.33787	0.00100474	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
205404_at	1.20998	0.00100796	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1
218456_at	-1.21877	0.00101905	CAPRIN2	caprin family member 2
201069_at	-1.31939	0.00101905	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collage
203153_at	1.49247	0.00101925	IFIT1	interferon-induced protein with tetratricopeptide repeats 1
214806_at	-1.21996	0.00102474	BICD1	bicaudal D homolog 1 (Drosophila)
221527_s_at	-1.21823	0.00102844	PARD3	par-3 partitioning defective 3 homolog (C. elegans)
210729_at	-1.33043	0.00103364	NPY2R	neuropeptide Y receptor Y2
220574_at	-1.20526	0.00103364	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
203185_at	-1.27301	0.00104875	RASSF2	Ras association (RalGDS/AF-6) domain family member 2
31874_at	-1.22103	0.00105147	GAS2L1	growth arrest-specific 2 like 1
210721_s_at	1.30432	0.00105686	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7
213157_s_at	-1.27314	0.00105928	WSCD1	WSC domain containing 1
204916_at	-1.31931	0.00106181	RAMP1	receptor (G protein-coupled) activity modifying protein 1
206825_at	-1.53204	0.00106998	OXTR	oxytocin receptor
208121_s_at	1.27412	0.00107758	PTPRO	protein tyrosine phosphatase, receptor type, O
210715_s_at	1.20734	0.00108023	SPINT2	serine peptidase inhibitor, Kunitz type, 2
203242_s_at	-1.25933	0.00109004	PDLIM5	PDZ and LIM domain 5
207659_s_at	1.66515	0.00110029	MOBP	myelin-associated oligodendrocyte basic protein
212012_at	-1.34702	0.00110094	PXDN	peroxidasin homolog (Drosophila)
203400_s_at	1.68483	0.0011159	TF	transferrin
221933_at	-1.21418	0.00112135	NLGN4X	neuroligin 4, X-linked
213666_at	1.25689	0.00113095	41158	septin 6
221748_s_at	-1.25224	0.001142	TNS1	tensin 1
205859_at	1.36572	0.00114464	LY86	lymphocyte antigen 86
212091_s_at	-1.32503	0.00115069	COL6A1	collagen, type VI, alpha 1
207076_s_at	1.42434	0.00116474	ASS1	argininosuccinate synthase 1
217388_s_at	1.31962	0.00117388	KYNU	kynureninase (L-kynurenine hydrolase)
213341_at	-1.20618	0.00117391	FEM1C	fem-1 homolog c (C. elegans)
220543_at	-1.4626	0.00119056	C21orf62	chromosome 21 open reading frame 62
214157_at	1.3497	0.00120348	GNAS	GNAS complex locus
208789_at	-1.2893	0.00120881	PTRF	polymerase I and transcript release factor
208961_s_at	-1.22916	0.00121031	KLF6	Kruppel-like factor 6
204122_at	1.31857	0.00121031	TYROBP	TYRO protein tyrosine kinase binding protein

204249_s_at	-1.28588	0.00121031	LMO2	LIM domain only 2 (rhombotin-like 1)
210066_s_at	-1.48199	0.00121171	AQP4	aquaporin 4
209840_s_at	-1.29389	0.00121563	LRRN3	leucine rich repeat neuronal 3
205121_at	-1.22148	0.00122744	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
220975_s_at	-1.25855	0.00123195	C1QTNF1	C1q and tumor necrosis factor related protein 1
204073_s_at	1.44794	0.00123506	C11orf9	chromosome 11 open reading frame 9
209431_s_at	-1.20466	0.00125031	PATZ1	POZ (BTB) and AT hook containing zinc finger 1
210040_at	1.37606	0.00125362	SLC12A5	solute carrier family 12 (potassium/chloride transporter), member 5
204042_at	-1.29345	0.0012662	WASF3	WAS protein family, member 3
201617_x_at	-1.25136	0.00126638	CALD1	caldesmon 1
221919_at	-1.2123	0.0012685	LOC100506653	hypothetical LOC100506653
221489_s_at	-1.44305	0.00128144	SPRY4	sprouty homolog 4 (Drosophila)
203636_at	-1.20554	0.00128144	MID1	midline 1 (Opitz/BBB syndrome)
209883_at	-1.31851	0.00130468	GLT25D2	glycosyltransferase 25 domain containing 2
214433_s_at	1.32894	0.0013064	SELENBP1	selenium binding protein 1
206001_at	1.58719	0.00131495	NPY	neuropeptide Y
210235_s_at	-1.20951	0.00132884	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting
202508_s_at	1.63164	0.00133432	SNAP25	synaptosomal-associated protein, 25kDa
210247_at	1.25714	0.00133761	SYN2	synapsin II
204469_at	-1.26609	0.00134655	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
211663_x_at	1.53162	0.00136642	PTGDS	prostaglandin D2 synthase 21kDa (brain)
209398_at	1.35179	0.00136876	HIST1H1C	histone cluster 1, H1c
208719_s_at	-1.27776	0.00136876	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
213439_x_at	1.2245	0.00137336	RUNDC3A	RUN domain containing 3A
207173_x_at	-1.20824	0.00137888	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)
213108_at	1.28857	0.00140821	CAMK2A	calcium/calmodulin-dependent protein kinase II alpha
213638_at	1.27101	0.00143158	PHACTR1	phosphatase and actin regulator 1
219403_s_at	1.25858	0.00143833	HPSE	heparanase
215017_s_at	-1.21742	0.00144191	FNBP1L	formin binding protein 1-like
213830_at	-1.71482	0.00144761	TRD@	T cell receptor delta locus
221815_at	-1.24887	0.00145298	ABHD2	abhydrolase domain containing 2
202112_at	-1.26922	0.00151236	VWF	von Willebrand factor
203786_s_at	1.44447	0.00151236	TPD52L1	tumor protein D52-like 1
219064_at	-1.2172	0.00153453	ITIH5	inter-alpha (globulin) inhibitor H5
211067_s_at	-1.27723	0.00154674	GAS7	growth arrest-specific 7
212985_at	-1.22509	0.00156947	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2
205257_s_at	1.37406	0.00157359	AMPH	amphiphysin
219763_at	1.2686	0.00158365	DENND1A	DENN/MADD domain containing 1A
202718_at	-1.46494	0.00159258	IGFBP2	insulin-like growth factor binding protein 2, 36kDa
204869_at	1.30995	0.00160257	PCSK2	proprotein convertase subtilisin/kexin type 2
204224_s_at	1.27256	0.00161008	GCH1	GTP cyclohydrolase 1
213990_s_at	1.24046	0.00162515	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7
202284_s_at	-1.27215	0.00162515	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
212646_at	-1.27527	0.00162515	RFTN1	raftlin, lipid raft linker 1
204733_at	1.47843	0.00163229	KLK6	kallikrein-related peptidase 6
210193_at	1.42502	0.00163285	MOBP	myelin-associated oligodendrocyte basic protein

202546_at	1.33152	0.00163557	VAMP8	vesicle-associated membrane protein 8 (endobrevin)
219728_at	1.37165	0.00163557	MYOT	myotilin
212187_x_at	1.56898	0.00163663	PTGDS	prostaglandin D2 synthase 21kDa (brain)
212387_at	-1.20176	0.00165812	TCF4	transcription factor 4
202421_at	-1.28964	0.00165812	IGSF3	immunoglobulin superfamily, member 3
208636_at	-1.2627	0.0016904	ACTN1	actinin, alpha 1
204678_s_at	1.31433	0.00169356	KCNK1	potassium channel, subfamily K, member 1
210016_at	1.49468	0.00169458	MYT1L	myelin transcription factor 1-like
210944_s_at	1.47033	0.00169458	CAPN3	calpain 3, (p94)
204214_s_at	1.30626	0.00169955	RAB32	RAB32, member RAS oncogene family
205613_at	-1.21373	0.00169955	SYT17	synaptotagmin XVII
221496_s_at	-1.2383	0.00169955	TOB2	transducer of ERBB2, 2
218975_at	-1.22618	0.00170981	COL5A3	collagen, type V, alpha 3
207172_s_at	-1.24439	0.00171958	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)
206306_at	-1.50625	0.00173141	RYR3	ryanodine receptor 3
204069_at	-1.30127	0.00173544	MEIS1	Meis homeobox 1
214913_at	-1.46628	0.00173544	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif, 3
211748_x_at	1.53848	0.00173652	PTGDS	prostaglandin D2 synthase 21kDa (brain)
204319_s_at	1.29102	0.00173712	RGS10	regulator of G-protein signaling 10
204561_x_at	1.35796	0.00174065	APOC2	apolipoprotein C-II
206715_at	1.23638	0.00174696	TFEC	transcription factor EC
214063_s_at	1.64466	0.00175591	TF	transferrin
204161_s_at	1.3156	0.00175591	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)
219304_s_at	-1.45808	0.00177451	PDGFD	platelet derived growth factor D
215706_x_at	-1.22222	0.00178111	ZYX	zyxin
204103_at	1.48475	0.00178851	CCL4	chemokine (C-C motif) ligand 4
210609_s_at	-1.24896	0.00179177	TP53I3	tumor protein p53 inducible protein 3
219726_at	-1.22326	0.00179177	NLGN3	neuroligin 3
202016_at	-1.33187	0.00179177	MEST	mesoderm specific transcript homolog (mouse)
205626_s_at	1.36054	0.00180799	CALB1	calbindin 1, 28kDa
205590_at	-1.40319	0.00181441	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
203798_s_at	1.54713	0.00181553	VSNL1	visinin-like 1
216307_at	1.31024	0.00181553	DGKB	diacylglycerol kinase, beta 90kDa
218404_at	1.43417	0.0018227	SNX10	sorting nexin 10
207643_s_at	-1.21402	0.0018227	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A
203706_s_at	-1.36894	0.00183353	FZD7	frizzled homolog 7 (Drosophila)
210445_at	1.22383	0.00183671	FABP6	fatty acid binding protein 6, ileal
222067_x_at	1.20415	0.00186208	HIST1H2BD	histone cluster 1, H2bd
207677_s_at	1.21496	0.00186208	NCF4	neutrophil cytosolic factor 4, 40kDa
214735_at	1.22647	0.00186208	IPCEF1	interaction protein for cytohesin exchange factors 1
203708_at	-1.22849	0.00188069	PDE4B	phosphodiesterase 4B, cAMP-specific
221666_s_at	1.2985	0.00188167	PYCARD	PYD and CARD domain containing
209933_s_at	1.27277	0.00188746	CD300A	CD300a molecule
204547_at	1.23799	0.0018889	RAB40B	RAB40B, member RAS oncogene family
208464_at	-1.20004	0.0018889	GRIA4	glutamate receptor, ionotrophic, AMPA 4
208782_at	-1.22925	0.0018889	FSTL1	follistatin-like 1

204324_s_at	-1.2033	0.00193952	GOLIM4	golgi integral membrane protein 4
221031_s_at	-1.22765	0.00194034	APOLD1	apolipoprotein L domain containing 1
221899_at	-1.23119	0.00194604	N4BP2L2	NEDD4 binding protein 2-like 2
211651_s_at	-1.3945	0.00194604	LAMB1	laminin, beta 1
203637_s_at	-1.2014	0.00198883	MID1	midline 1 (Opitz/BBB syndrome)
208107_s_at	1.2433	0.00199022	LOC81691	exonuclease NEF-sp
204679_at	1.46772	0.0019921	KCNK1	potassium channel, subfamily K, member 1
205695_at	1.2034	0.00202603	SDS	serine dehydratase
204677_at	-1.25396	0.00203479	CDH5	cadherin 5, type 2 (vascular endothelium)
217811_at	1.21596	0.00203869	SELT	selenoprotein T
202723_s_at	-1.24458	0.00203869	FOXO1	forkhead box O1
219073_s_at	-1.30657	0.00204501	OSBPL10	oxysterol binding protein-like 10
219635_at	-1.21456	0.00204501	ZNF606	zinc finger protein 606
213359_at	-1.26023	0.00205941	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1
219478_at	1.25481	0.00206395	WFDC1	WAP four-disulfide core domain 1
204712_at	1.39527	0.00207007	WIF1	WNT inhibitory factor 1
221261_x_at	-1.22494	0.00207664	MAGED4 /// MAGED4	melanoma antigen family D, 4 /// melanoma antigen family D, 4B
204724_s_at	-1.51259	0.00208984	COL9A3	collagen, type IX, alpha 3
218807_at	-1.36226	0.00210132	VAV3	vav 3 guanine nucleotide exchange factor
205551_at	1.37169	0.00211214	SV2B	synaptic vesicle glycoprotein 2B
216222_s_at	-1.27443	0.00212441	MYO10	myosin X
210906_x_at	-1.35419	0.00213842	AQP4	aquaporin 4
214120_at	1.25004	0.00221145	RFPL1S	RFPL1 antisense RNA (non-protein coding)
207574_s_at	-1.28465	0.00222227	GADD45B	growth arrest and DNA-damage-inducible, beta
213703_at	-1.23992	0.00222272	LOC150759	hypothetical LOC150759
207323_s_at	1.69615	0.00222485	MBP	myelin basic protein
213338_at	-1.35191	0.00222708	TMEM158	transmembrane protein 158 (gene/pseudogene)
204230_s_at	1.34355	0.00224207	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), m
204680_s_at	1.22187	0.00225813	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5
207084_at	-1.26272	0.00227602	POU3F2	POU class 3 homeobox 2
201746_at	-1.23232	0.00228011	TP53	tumor protein p53
209591_s_at	-1.35433	0.00229287	BMP7	bone morphogenetic protein 7
217143_s_at	-1.58486	0.002304	TRD@	T cell receptor delta locus
210508_s_at	-1.45391	0.00231204	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2
218541_s_at	-1.36068	0.00234872	C8orf4	chromosome 8 open reading frame 4
218856_at	-1.23386	0.00236565	TNFRSF21	tumor necrosis factor receptor superfamily, member 21
218902_at	-1.21927	0.00237749	NOTCH1	notch 1
204057_at	1.23151	0.00238953	IRF8	interferon regulatory factor 8
206701_x_at	-1.31888	0.00238954	EDNRB	endothelin receptor type B
218728_s_at	1.20014	0.0024006	CNIH4	cornichon homolog 4 (Drosophila)
205739_x_at	-1.20238	0.00241583	ZNF107	zinc finger protein 107
204743_at	1.40424	0.002421	TAGLN3	transgelin 3
204457_s_at	-1.38278	0.00243558	GAS1	growth arrest-specific 1
201791_s_at	-1.20217	0.00243558	DHCR7	7-dehydrocholesterol reductase
207957_s_at	1.37232	0.00243558	PRKCB	protein kinase C, beta
201976_s_at	-1.2167	0.00244184	MYO10	myosin X

219700_at	-1.25204	0.00244602	PLXDC1	plexin domain containing 1
203476_at	1.45927	0.00244796	TPBG	trophoblast glycoprotein
208002_s_at	1.2294	0.00247767	ACOT7	acyl-CoA thioesterase 7
202697_at	1.20673	0.00247767	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21
209013_x_at	-1.25803	0.00255526	TRIO	triple functional domain (PTPRF interacting)
207469_s_at	1.35097	0.00255823	PIR	pirin (iron-binding nuclear protein)
212719_at	-1.25675	0.00258587	PHLPP1	PH domain and leucine rich repeat protein phosphatase 1
219646_at	1.20862	0.00260734	DEF8	differentially expressed in FDCP 8 homolog (mouse)
216191_s_at	-1.53344	0.00260766	TRDV3	T cell receptor delta variable 3
209448_at	1.30345	0.00261248	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa
213326_at	1.22672	0.00269868	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)
209072_at	1.93587	0.00270413	MBP	myelin basic protein
207261_at	-1.37332	0.00270912	CNGA3	cyclic nucleotide gated channel alpha 3
212533_at	-1.23512	0.00270912	WEE1	WEE1 homolog (S. pombe)
205580_s_at	-1.28306	0.00274041	HRH1	histamine receptor H1
206167_s_at	-1.24443	0.00275459	ARHGAP6	Rho GTPase activating protein 6
212328_at	-1.21937	0.0027645	LIMCH1	LIM and calponin homology domains 1
207437_at	-1.22307	0.00277051	NOVA1	neuro-oncological ventral antigen 1
FFX-r2-Ec-bioC-3_a	-1.28369	0.00277821	---	---
208893_s_at	-1.26531	0.00280313	DUSP6	dual specificity phosphatase 6
206866_at	-1.28106	0.00280823	CDH4	cadherin 4, type 1, R-cadherin (retinal)
209487_at	-1.28691	0.00281607	RBPMS	RNA binding protein with multiple splicing
214457_at	1.2744	0.00285421	HOXA2	homeobox A2
213212_x_at	-1.23108	0.00289768	GOLGA6L5 /// GOLGA	golgin A6 family-like 5 (pseudogene) /// golgin A6 family-like 9
205579_at	-1.29977	0.00290065	HRH1	histamine receptor H1
205306_x_at	1.20915	0.00292824	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
219833_s_at	-1.21627	0.0029335	EFHC1	EF-hand domain (C-terminal) containing 1
219799_s_at	1.28521	0.00293743	DHRS9	dehydrogenase/reductase (SDR family) member 9
200965_s_at	-1.23647	0.00294239	ABLIM1	actin binding LIM protein 1
220239_at	1.24557	0.00294239	KLHL7	kelch-like 7 (Drosophila)
208018_s_at	1.29984	0.00296585	HCK	hemopoietic cell kinase
219773_at	-1.23851	0.00298166	NOX4	NADPH oxidase 4
219269_at	-1.2132	0.00300482	HMBOX1	homeobox containing 1
221766_s_at	-1.25231	0.00300987	FAM46A	family with sequence similarity 46, member A
206025_s_at	-1.4118	0.00303034	TNFAIP6	tumor necrosis factor, alpha-induced protein 6
209081_s_at	-1.22377	0.00303274	COL18A1	collagen, type XVIII, alpha 1
205425_at	-1.27746	0.00303509	HIP1	huntingtin interacting protein 1
206381_at	1.22013	0.00303509	SCN2A	sodium channel, voltage-gated, type II, alpha subunit
218618_s_at	-1.22465	0.00304627	FNDC3B	fibronectin type III domain containing 3B
202203_s_at	-1.24178	0.0030473	AMFR	autocrine motility factor receptor
214808_at	-1.21579	0.00306941	---	---
204955_at	-1.40937	0.00308509	SRPX	sushi-repeat-containing protein, X-linked
209590_at	-1.28743	0.0030871	BMP7	bone morphogenetic protein 7
208370_s_at	-1.28264	0.00313806	RCAN1	regulator of calcineurin 1
207789_s_at	-1.34127	0.00314464	DPP6	dipeptidyl-peptidase 6
205499_at	-1.41708	0.00314999	SRPX2	sushi-repeat-containing protein, X-linked 2

218901_at	-1.2431	0.00315339	PLSCR4	phospholipid scramblase 4
204379_s_at	-1.53082	0.00322534	FGFR3	fibroblast growth factor receptor 3
215399_s_at	-1.26981	0.00323833	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin
206201_s_at	-1.64381	0.00324229	MEOX2	mesenchyme homeobox 2
52940_at	1.20436	0.00326529	LOC100294402 /// SIG	single Ig IL-1-related receptor-like /// single immunoglobulin and toll-interleu
203413_at	-1.38638	0.00326879	NELL2	NEL-like 2 (chicken)
213059_at	-1.27121	0.00329403	CREB3L1	cAMP responsive element binding protein 3-like 1
221577_x_at	-1.36321	0.00330672	GDF15	growth differentiation factor 15
214564_s_at	-1.21875	0.00330837	PCDHGC3	protocadherin gamma subfamily C, 3
205110_s_at	1.47278	0.00332707	FGF13	fibroblast growth factor 13
204777_s_at	1.45357	0.00333572	MAL	mal, T-cell differentiation protein
213790_at	-1.27171	0.00334743	ADAM12	ADAM metallopeptidase domain 12
209626_s_at	-1.25517	0.00336315	OSBPL3	oxysterol binding protein-like 3
216563_at	-1.21507	0.00336315	ANKRD12	Ankyrin repeat domain 12
208960_s_at	-1.21747	0.00337013	KLF6	Kruppel-like factor 6
202662_s_at	-1.24442	0.00337013	ITPR2	inositol 1,4,5-triphosphate receptor, type 2
206089_at	1.3009	0.00337013	NELL1	NEL-like 1 (chicken)
201468_s_at	1.24274	0.00337013	NQO1	NAD(P)H dehydrogenase, quinone 1
205403_at	1.40917	0.00337013	IL1R2	interleukin 1 receptor, type II
204442_x_at	-1.22798	0.00339941	LTBP4	latent transforming growth factor beta binding protein 4
AFFX-BioC-5_at	-1.29479	0.00343086	---	---
213524_s_at	1.28024	0.00343086	G0S2	G0/G1switch 2
204337_at	1.49578	0.00344955	RGS4	regulator of G-protein signaling 4
205481_at	-1.2652	0.00344955	ADORA1	adenosine A1 receptor
204081_at	1.40633	0.00346209	NRGN	neurogranin (protein kinase C substrate, RC3)
206710_s_at	1.35813	0.00348148	EPB41L3	erythrocyte membrane protein band 4.1-like 3
AFFX-BioC-3_at	-1.29031	0.00348148	---	---
209866_s_at	-1.30501	0.00349926	LPHN3	latrophilin 3
205472_s_at	1.20145	0.00351282	DACH1	dachshund homolog 1 (Drosophila)
214607_at	1.33815	0.00351403	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3
215714_s_at	-1.25302	0.00352166	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf
209071_s_at	-1.26227	0.00352166	RGS5	regulator of G-protein signaling 5
201430_s_at	-1.23733	0.00354072	DPYSL3	dihydropyrimidinase-like 3
204979_s_at	1.29139	0.00357269	SH3BGR	SH3 domain binding glutamic acid-rich protein
204338_s_at	1.27861	0.00358032	RGS4	regulator of G-protein signaling 4
211776_s_at	1.31605	0.00358032	EPB41L3	erythrocyte membrane protein band 4.1-like 3
201615_x_at	-1.23765	0.00358151	CALD1	caldesmon 1
212664_at	1.46373	0.00358151	TUBB4	tubulin, beta 4
221914_at	1.31584	0.00359377	SYN1	synapsin I
213107_at	-1.22151	0.0036054	TNIK	TRAF2 and NCK interacting kinase
214591_at	-1.35966	0.00366952	KLHL4	kelch-like 4 (Drosophila)
218418_s_at	-1.20996	0.0036855	KANK2	KN motif and ankyrin repeat domains 2
205471_s_at	1.22331	0.00371695	DACH1	dachshund homolog 1 (Drosophila)
201325_s_at	-1.26865	0.00371909	EMP1	epithelial membrane protein 1
205363_at	-1.37423	0.00371909	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxyla
205681_at	1.33616	0.00371909	BCL2A1	BCL2-related protein A1

210611_s_at	-1.36267	0.00371909	DTNA	dystrobrevin, alpha
210135_s_at	-1.36335	0.00373189	SHOX2	short stature homeobox 2
209685_s_at	1.30408	0.00373189	PRKCB	protein kinase C, beta
209291_at	-1.26794	0.0037515	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
203932_at	1.27774	0.0038098	HLA-DMB	major histocompatibility complex, class II, DM beta
219725_at	1.29175	0.00387977	TREM2	triggering receptor expressed on myeloid cells 2
216617_s_at	1.34071	0.00389558	MAG	myelin associated glycoprotein
211126_s_at	-1.2389	0.00395371	CSRP2	cysteine and glycine-rich protein 2
213482_at	1.20364	0.00397225	DOCK3	dedicator of cytokinesis 3
210736_x_at	-1.20913	0.00409027	DTNA	dystrobrevin, alpha
205128_x_at	-1.29745	0.00410698	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxyge
202286_s_at	1.21217	0.00413317	TACSTD2	tumor-associated calcium signal transducer 2
208430_s_at	-1.24808	0.00413317	DTNA	dystrobrevin, alpha
201971_s_at	1.23763	0.00414756	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
218847_at	-1.35203	0.00417389	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2
208396_s_at	1.21908	0.00424004	PDE1A	phosphodiesterase 1A, calmodulin-dependent
209789_at	-1.21466	0.00424004	CORO2B	coronin, actin binding protein, 2B
213241_at	1.20166	0.00426001	PLXNC1	plexin C1
202073_at	1.21516	0.00426706	OPTN	optineurin
203416_at	1.2748	0.00428195	CD53	CD53 molecule
206404_at	1.27736	0.0042936	FGF9	fibroblast growth factor 9 (glia-activating factor)
FFX-r2-Ec-bioC-5_a	-1.26989	0.00431311	---	---
204232_at	1.29218	0.00433271	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
206893_at	-1.21081	0.00433271	SALL1	sal-like 1 (Drosophila)
210139_s_at	-1.20131	0.00433271	PMP22	peripheral myelin protein 22
202669_s_at	-1.26836	0.00434029	EFNB2	ephrin-B2
202712_s_at	1.23107	0.00438196	CKMT1A /// CKMT1B	creatine kinase, mitochondrial 1A /// creatine kinase, mitochondrial 1B
219415_at	-1.3503	0.00444304	TTYH1	tweety homolog 1 (Drosophila)
219779_at	-1.24156	0.00444535	ZFHX4	zinc finger homeobox 4
213197_at	-1.26006	0.00453242	ASTN1	astrotactin 1
215870_s_at	-1.53613	0.00454626	PLA2G5	phospholipase A2, group V
215695_s_at	-1.25803	0.00454626	GYG2	glycogenin 2
202688_at	1.30836	0.00454626	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
205405_at	-1.27713	0.00454626	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembran
208443_x_at	-1.23222	0.00459263	SHOX2	short stature homeobox 2
206777_s_at	-1.28162	0.00466177	CRYBB2 /// CRYBB2P1	crystallin, beta B2 /// crystallin, beta B2 pseudogene 1
222379_at	-1.27811	0.00466177	KCNE4	potassium voltage-gated channel, Isk-related family, member 4
205364_at	-1.23864	0.004685	ACOX2	acyl-CoA oxidase 2, branched chain
210091_s_at	-1.28613	0.00471122	DTNA	dystrobrevin, alpha
215123_at	-1.2389	0.00477727	NPIPL3	nuclear pore complex interacting protein-like 3
214753_at	-1.22455	0.00478083	N4BP2L2	NEDD4 binding protein 2-like 2
216331_at	-1.24254	0.00478083	ITGA7	integrin, alpha 7
203797_at	1.61094	0.00490112	VSNL1	visinin-like 1
205053_at	1.2223	0.00490546	PRIM1	primase, DNA, polypeptide 1 (49kDa)
211161_s_at	-1.50607	0.0049067	COL3A1	collagen, type III, alpha 1
202178_at	1.3139	0.00492173	PRKCZ	protein kinase C, zeta

210875_s_at	-1.265	0.00493817	ZEB1	zinc finger E-box binding homeobox 1
202132_at	-1.24966	0.00500183	WWTR1	WW domain containing transcription regulator 1
205445_at	1.20196	0.00506264	PRL	prolactin
205568_at	1.29497	0.00509691	AQP9	aquaporin 9
220227_at	-1.31582	0.00509691	CDH4	cadherin 4, type 1, R-cadherin (retinal)
205794_s_at	-1.20801	0.00510141	NOVA1	neuro-oncological ventral antigen 1
201261_x_at	-1.23397	0.00520718	BGN	biglycan
201043_s_at	-1.22045	0.00524033	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
203445_s_at	-1.21253	0.00525084	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas
209011_at	-1.22589	0.00527944	TRIO	triple functional domain (PTPRF interacting)
222218_s_at	1.20081	0.00530088	PILRA	paired immunoglobin-like type 2 receptor alpha
216452_at	-1.29485	0.00530186	TRPM3	transient receptor potential cation channel, subfamily M, member 3
217995_at	1.24766	0.00533406	SQRDL	sulfide quinone reductase-like (yeast)
219545_at	-1.23008	0.00533522	KCTD14	potassium channel tetramerisation domain containing 14
213676_at	1.20159	0.00534785	TMEM151B	transmembrane protein 151B
209209_s_at	-1.22193	0.00542081	FERMT2	fermitin family member 2
206026_s_at	-1.38092	0.00543648	TNFAIP6	tumor necrosis factor, alpha-induced protein 6
205931_s_at	-1.21145	0.00543648	CREB5	cAMP responsive element binding protein 5
204463_s_at	-1.27272	0.00546414	EDNRA	endothelin receptor type A
206953_s_at	-1.2715	0.00552623	LPHN2	latrophilin 2
205259_at	-1.2492	0.00552623	NR3C2	nuclear receptor subfamily 3, group C, member 2
205814_at	1.30672	0.00554812	GRM3	glutamate receptor, metabotropic 3
213593_s_at	-1.21327	0.00555489	TRA2A	transformer 2 alpha homolog (Drosophila)
211372_s_at	1.23756	0.00559639	IL1R2	interleukin 1 receptor, type II
209459_s_at	-1.26207	0.00560912	ABAT	4-aminobutyrate aminotransferase
210512_s_at	-1.30632	0.00561487	VEGFA	vascular endothelial growth factor A
221590_s_at	-1.20975	0.00561891	ALDH6A1	Aldehyde dehydrogenase 6 family, member A1
218826_at	-1.20569	0.00568948	SLC35F2	solute carrier family 35, member F2
36711_at	-1.27512	0.00577187	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
222024_s_at	-1.20629	0.00581066	AKAP13	A kinase (PRKA) anchor protein 13
206397_x_at	-1.26399	0.00581554	GDF1 /// LASS1	growth differentiation factor 1 /// LAG1 homolog, ceramide synthase 1
213109_at	-1.23702	0.00581554	TNIK	TRAF2 and NCK interacting kinase
202260_s_at	1.2326	0.00581554	STXBP1	syntaxin binding protein 1
221558_s_at	-1.24023	0.00581554	LEF1	lymphoid enhancer-binding factor 1
213451_x_at	-1.22642	0.00581554	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB
206574_s_at	-1.20355	0.00581554	PTP4A3	protein tyrosine phosphatase type IVA, member 3
203159_at	1.21649	0.00583526	GLS	glutaminase
205751_at	1.47623	0.00589703	SH3GL2	SH3-domain GRB2-like 2
205479_s_at	-1.3112	0.00595748	PLAU	plasminogen activator, urokinase
200770_s_at	-1.20441	0.00596532	LAMC1	laminin, gamma 1 (formerly LAMB2)
37005_at	1.20267	0.00600844	NBL1	neuroblastoma, suppression of tumorigenicity 1
204829_s_at	1.30448	0.00607379	FOLR2	folate receptor 2 (fetal)
219697_at	1.23764	0.00608866	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2
209293_x_at	-1.28515	0.00608932	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
204170_s_at	1.25652	0.00611315	CKS2	CDC28 protein kinase regulatory subunit 2
203178_at	-1.23299	0.00622515	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)

206018_at	-1.33632	0.00625848	FOXG1	forkhead box G1
213566_at	1.27109	0.00630127	RNASE6	ribonuclease, RNase A family, k6
204220_at	1.22407	0.00636805	GMFG	glia maturation factor, gamma
218353_at	-1.25037	0.00638661	RGS5	regulator of G-protein signaling 5
209372_x_at	-1.23878	0.00646126	TUBB2A /// TUBB2B	tubulin, beta 2A /// tubulin, beta 2B
205549_at	1.41063	0.00648646	PCP4	Purkinje cell protein 4
205266_at	-1.28886	0.00654782	LIF	leukemia inhibitory factor (cholinergic differentiation factor)
211302_s_at	-1.25913	0.00660579	PDE4B	phosphodiesterase 4B, cAMP-specific
200884_at	-1.23465	0.00662849	CKB	creatine kinase, brain
200714_x_at	-1.20624	0.00670728	OS9	osteosarcoma amplified 9, endoplasmic reticulum lectin
219305_x_at	1.21061	0.00672112	FBXO2	F-box protein 2
208358_s_at	1.46037	0.00677835	UGT8	UDP glycosyltransferase 8
202369_s_at	-1.20271	0.00681868	TRAM2	translocation associated membrane protein 2
203000_at	1.6491	0.00683576	STMN2	stathmin-like 2
220115_s_at	-1.3722	0.00685316	CDH10	cadherin 10, type 2 (T2-cadherin)
205358_at	-1.4158	0.00687114	GRIA2	glutamate receptor, ionotropic, AMPA 2
212414_s_at	-1.21485	0.00692109	GLYR1 /// SEPT6	glyoxylate reductase 1 homolog (Arabidopsis) /// septin 6
206395_at	-1.20462	0.0069379	DGKG	diacylglycerol kinase, gamma 90kDa
221911_at	-1.2322	0.0069379	ETV1	ets variant 1
217997_at	-1.22669	0.00702246	PHLDA1	pleckstrin homology-like domain, family A, member 1
206135_at	1.25405	0.00718589	ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)
208790_s_at	-1.22988	0.00723519	PTRF	polymerase I and transcript release factor
208178_x_at	-1.22193	0.00723519	TRIO	triple functional domain (PTPRF interacting)
211668_s_at	-1.29442	0.00725884	PLAU	plasminogen activator, urokinase
210738_s_at	-1.21922	0.00726439	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
205483_s_at	1.32696	0.00731426	ISG15	ISG15 ubiquitin-like modifier
216005_at	-1.28186	0.00733044	TNC	Tenascin C
209993_at	-1.20642	0.00737521	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1
206580_s_at	-1.2515	0.00737521	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2
205660_at	1.22895	0.00741325	OASL	2'-5'-oligoadenylate synthetase-like
201850_at	1.22638	0.00743906	CAPG	capping protein (actin filament), gelsolin-like
206645_s_at	1.3849	0.00743906	NR0B1	nuclear receptor subfamily 0, group B, member 1
219147_s_at	1.22365	0.00746613	C9orf95	chromosome 9 open reading frame 95

Supplementary Table 8. Genes differentially expressed in ovarian cancers with low FAT1 expression (TCGA dataset).

Wnt/β-catenin Signaling Components: SFRP4, GJA1, MMP7, PPP2R2B, AKT3, FZD1

Probeset	Fold Change (FAT1low/FAT1nl)	q value	Gene Symbol	Gene Description
201579_at	-2.00071	0	*FAT1*	FAT tumor suppressor homolog 1 (Drosophila)
				**FAT1 NOT INCLUDED IN PATHWAY ANALYSIS*
213169_at	-1.2663	3.63E-16	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembran
215446_s_at	-1.4214	7.82E-16	LOX	lysyl oxidase
211675_s_at	-1.29655	8.16E-15	MDFIC	MyoD family inhibitor domain containing
212473_s_at	-1.27752	1.09E-14	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2
37892_at	-1.78029	1.66E-14	COL11A1	collagen, type XI, alpha 1
212472_at	-1.24938	2.62E-14	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2
201150_s_at	-1.3895	4.34E-14	TIMP3	TIMP metallopeptidase inhibitor 3
204451_at	-1.22743	4.34E-14	FZD1	frizzled homolog 1 (Drosophila)
210809_s_at	-1.79821	5.55E-14	POSTN	periostin, osteoblast specific factor
221730_at	-1.47623	7.32E-14	COL5A2	collagen, type V, alpha 2
221729_at	-1.45438	9.18E-14	COL5A2	collagen, type V, alpha 2
204620_s_at	-1.47759	1.32E-13	VCAN	versican
221731_x_at	-1.48918	1.70E-13	VCAN	versican
203083_at	-1.47658	2.68E-13	THBS2	thrombospondin 2
209487_at	-1.27634	3.17E-13	RBPMS	RNA binding protein with multiple splicing
212488_at	-1.4479	3.54E-13	COL5A1	collagen, type V, alpha 1
204320_at	-1.65046	3.61E-13	COL11A1	collagen, type XI, alpha 1
212646_at	-1.2351	4.68E-13	RFTN1	raftlin, lipid raft linker 1
202202_s_at	-1.24353	4.79E-13	LAMA4	laminin, alpha 4
221541_at	-1.33323	1.00E-12	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2
221760_at	-1.28787	1.22E-12	MAN1A1	mannosidase, alpha, class 1A, member 1
212489_at	-1.38674	1.43E-12	COL5A1	collagen, type V, alpha 1
205479_s_at	-1.30764	1.65E-12	PLAU	plasminogen activator, urokinase
204619_s_at	-1.38137	1.87E-12	VCAN	versican
213429_at	-1.24224	1.94E-12	BICC1	bicaudal C homolog 1 (Drosophila)
219087_at	-1.42718	2.22E-12	ASPN	asporin
201939_at	-1.27444	2.56E-12	PLK2	polo-like kinase 2
210511_s_at	-1.34325	4.54E-12	INHBA	inhibin, beta A
221942_s_at	-1.28869	5.19E-12	GUCY1A3	guanylate cyclase 1, soluble, alpha 3
213338_at	-1.32374	6.78E-12	TMEM158	transmembrane protein 158 (gene/pseudogene)
221911_at	-1.22414	7.59E-12	ETV1	ets variant 1
209955_s_at	-1.34276	8.11E-12	FAP	fibroblast activation protein, alpha
203325_s_at	-1.3449	8.68E-12	COL5A1	collagen, type V, alpha 1

201963_at	-1.22546	8.78E-12	ACSL1	acyl-CoA synthetase long-chain family member 1
213194_at	-1.24577	1.20E-11	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)
211571_s_at	-1.34181	1.60E-11	VCAN	versican
204083_s_at	-1.23401	1.63E-11	TPM2	tropomyosin 2 (beta)
201645_at	-1.32015	1.68E-11	TNC	tenascin C
202311_s_at	-1.37863	2.11E-11	COL1A1	collagen, type I, alpha 1
215646_s_at	-1.37715	2.17E-11	VCAN	versican
203878_s_at	-1.36959	2.29E-11	MMP11	matrix metallopeptidase 11 (stromelysin 3)
210503_at	1.36722	2.51E-11	MAGEA11	melanoma antigen family A, 11
202952_s_at	-1.23428	2.79E-11	ADAM12	ADAM metallopeptidase domain 12
201438_at	-1.3024	3.11E-11	COL6A3	collagen, type VI, alpha 3
202310_s_at	-1.32813	3.46E-11	COL1A1	collagen, type I, alpha 1
201069_at	-1.30566	3.61E-11	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collage
211668_s_at	-1.31096	4.40E-11	PLAU	plasminogen activator, urokinase
215076_s_at	-1.28982	4.47E-11	COL3A1	collagen, type III, alpha 1
213139_at	-1.29518	4.51E-11	SNAI2	snail homolog 2 (Drosophila)
212667_at	-1.26141	5.41E-11	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)
211161_s_at	-1.32879	5.76E-11	COL3A1	collagen, type III, alpha 1
203476_at	-1.2876	5.86E-11	TPBG	trophoblast glycoprotein
202465_at	-1.26479	6.13E-11	PCOLCE	procollagen C-endopeptidase enhancer
209047_at	-1.21224	7.32E-11	AQP1	aquaporin 1 (Colton blood group)
209156_s_at	-1.29953	8.73E-11	COL6A2	collagen, type VI, alpha 2
201852_x_at	-1.35396	9.54E-11	COL3A1	collagen, type III, alpha 1
204464_s_at	-1.23321	1.01E-10	EDNRA	endothelin receptor type A
200974_at	-1.29221	1.34E-10	ACTA2	actin, alpha 2, smooth muscle, aorta
210495_x_at	-1.26586	1.44E-10	FN1	fibronectin 1
209488_s_at	-1.24676	1.45E-10	RBPMS	RNA binding protein with multiple splicing
202007_at	-1.21084	1.50E-10	NID1	nidogen 1
209651_at	-1.20703	1.86E-10	TGFB1I1	transforming growth factor beta 1 induced transcript 1
212464_s_at	-1.29908	2.09E-10	FN1	fibronectin 1
202620_s_at	-1.21291	2.45E-10	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
216442_x_at	-1.26431	2.70E-10	FN1	fibronectin 1
202391_at	-1.30175	2.70E-10	BASP1	brain abundant, membrane attached signal protein 1
209781_s_at	-1.25791	2.73E-10	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3
202450_s_at	-1.35409	3.14E-10	CTSK	cathepsin K
213790_at	-1.21562	3.16E-10	ADAM12	ADAM metallopeptidase domain 12
202998_s_at	-1.22681	3.35E-10	LOXL2	lysyl oxidase-like 2
209621_s_at	-1.24411	3.38E-10	PDLIM3	PDZ and LIM domain 3
211719_x_at	-1.24504	3.64E-10	FN1	fibronectin 1
204457_s_at	-1.28262	4.38E-10	GAS1	growth arrest-specific 1
204463_s_at	-1.2064	5.13E-10	EDNRA	endothelin receptor type A
201108_s_at	-1.21567	5.22E-10	THBS1	thrombospondin 1
212607_at	-1.21429	5.49E-10	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)

203180_at	-1.23335	5.90E-10	ALDH1A3	aldehyde dehydrogenase 1 family, member A3
201983_s_at	-1.23791	6.00E-10	EGFR	epidermal growth factor receptor
201148_s_at	-1.24077	6.21E-10	TIMP3	TIMP metallopeptidase inhibitor 3
204114_at	-1.25251	8.09E-10	NID2	nidogen 2 (osteonidogen)
201792_at	-1.28747	8.20E-10	AEBP1	AE binding protein 1
208322_s_at	-1.2092	9.57E-10	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
209365_s_at	-1.20558	1.04E-09	ECM1	extracellular matrix protein 1
202619_s_at	-1.21652	1.23E-09	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
213909_at	-1.33116	1.26E-09	LRRC15	leucine rich repeat containing 15
201615_x_at	-1.20199	1.32E-09	CALD1	caldesmon 1
202766_s_at	-1.29329	1.46E-09	FBN1	fibrillin 1
213428_s_at	-1.22084	1.72E-09	COL6A1	collagen, type VI, alpha 1
210764_s_at	-1.26501	1.75E-09	CYR61	cysteine-rich, angiogenic inducer, 61
213943_at	-1.28027	1.81E-09	TWIST1	twist homolog 1 (Drosophila)
201149_s_at	-1.2584	1.87E-09	TIMP3	TIMP metallopeptidase inhibitor 3
201505_at	-1.23228	2.38E-09	LAMB1	laminin, beta 1
209309_at	1.22635	2.40E-09	AZGP1	alpha-2-glycoprotein 1, zinc-binding
203868_s_at	-1.32	2.71E-09	VCAM1	vascular cell adhesion molecule 1
208131_s_at	-1.28465	3.00E-09	PTGIS	prostaglandin I2 (prostacyclin) synthase
201215_at	-1.22351	5.10E-09	PLS3	plastin 3
205941_s_at	-1.35155	5.28E-09	COL10A1	collagen, type X, alpha 1
203876_s_at	-1.24581	5.53E-09	MMP11	matrix metallopeptidase 11 (stromelysin 3)
201289_at	-1.22704	5.61E-09	CYR61	cysteine-rich, angiogenic inducer, 61
202157_s_at	-1.20561	5.86E-09	CELF2	CUGBP, Elav-like family member 2
202404_s_at	-1.2356	5.91E-09	COL1A2	collagen, type I, alpha 2
217428_s_at	-1.33874	6.96E-09	COL10A1	collagen, type X, alpha 1
201109_s_at	-1.21689	8.52E-09	THBS1	thrombospondin 1
212353_at	-1.36876	8.89E-09	SULF1	sulfatase 1
219304_s_at	-1.2168	9.17E-09	PDGFD	platelet derived growth factor D
210394_x_at	1.29296	1.09E-08	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B
209596_at	-1.23317	1.30E-08	MXRA5	matrix-remodelling associated 5
204298_s_at	-1.21455	1.31E-08	LOX	lysyl oxidase
204135_at	-1.21797	1.43E-08	FILIP1L	filamin A interacting protein 1-like
213764_s_at	-1.33648	1.46E-08	MFAP5	microfibrillar associated protein 5
211651_s_at	-1.20771	1.70E-08	LAMB1	laminin, beta 1
207172_s_at	-1.25803	1.72E-08	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)
211425_x_at	1.25948	1.90E-08	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B
37005_at	-1.20589	1.96E-08	NBL1	neuroblastoma, suppression of tumorigenicity 1
201744_s_at	-1.34908	1.99E-08	LUM	lumican
201147_s_at	-1.29012	2.08E-08	TIMP3	TIMP metallopeptidase inhibitor 3
217430_x_at	-1.23753	2.13E-08	COL1A1	collagen, type I, alpha 1
212354_at	-1.32937	3.84E-08	SULF1	sulfatase 1
207808_s_at	-1.20639	5.22E-08	PROS1	protein S (alpha)

213765_at	-1.26406	5.73E-08	MFAP5	microfibrillar associated protein 5
215388_s_at	-1.20341	8.50E-08	CFH /// CFHR1	complement factor H /// complement factor H-related 1
201667_at	-1.21631	1.13E-07	GJA1	gap junction protein, alpha 1, 43kDa
201110_s_at	-1.23083	1.17E-07	THBS1	thrombospondin 1
203939_at	-1.22621	1.24E-07	NT5E	5'-nucleotidase, ecto (CD73)
204646_at	-1.22757	1.36E-07	DPYD	dihydropyrimidine dehydrogenase
202068_s_at	-1.20973	1.72E-07	LDLR	low density lipoprotein receptor
203963_at	-1.26475	1.98E-07	CA12	carbonic anhydrase XII
201431_s_at	-1.20748	2.26E-07	DPYSL3	dihydropyrimidinase-like 3
209335_at	-1.25988	2.63E-07	DCN	decorin
202283_at	-1.27131	2.76E-07	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium der
207173_x_at	-1.273	2.84E-07	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)
204955_at	-1.22527	2.99E-07	SRPX	sushi-repeat-containing protein, X-linked
205943_at	-1.29207	3.02E-07	TDO2	tryptophan 2,3-dioxygenase
215867_x_at	-1.26498	4.68E-07	CA12	carbonic anhydrase XII
201952_at	-1.20673	5.09E-07	ALCAM	activated leukocyte cell adhesion molecule
204415_at	1.23289	5.43E-07	IFI6	interferon, alpha-inducible protein 6
201694_s_at	-1.20124	5.69E-07	EGR1	early growth response 1
206439_at	-1.29816	6.69E-07	EPYC	epiphycan
202274_at	-1.24481	6.79E-07	ACTG2	actin, gamma 2, smooth muscle, enteric
201430_s_at	-1.20212	1.41E-06	DPYSL3	dihydropyrimidinase-like 3
205547_s_at	-1.25028	1.57E-06	TAGLN	transgelin
214164_x_at	-1.23245	1.59E-06	CA12	carbonic anhydrase XII
203153_at	1.25322	1.76E-06	IFIT1	interferon-induced protein with tetratricopeptide repeats 1
221019_s_at	-1.20268	1.99E-06	COLEC12	collectin sub-family member 12
202436_s_at	-1.23243	2.82E-06	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
206772_at	1.30334	2.93E-06	PTH2R	parathyroid hormone 2 receptor
205206_at	-1.22032	3.27E-06	KAL1	Kallmann syndrome 1 sequence
219778_at	-1.21267	3.69E-06	ZFPM2	zinc finger protein, multitype 2
219873_at	1.26066	4.08E-06	COLEC11	collectin sub-family member 11
213800_at	-1.20375	4.93E-06	CFH	complement factor H
211896_s_at	-1.2615	4.97E-06	DCN	decorin
212344_at	-1.22528	5.16E-06	SULF1	sulfatase 1
204052_s_at	-1.20718	5.64E-06	SFRP4	secreted frizzled-related protein 4
211813_x_at	-1.23517	5.66E-06	DCN	decorin
213849_s_at	-1.21304	6.14E-06	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta
202437_s_at	-1.23629	6.34E-06	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
201893_x_at	-1.229	6.83E-06	DCN	decorin
207739_s_at	1.35739	7.48E-06	2B /// GAGE2C /// GAG	G antigen 1 /// G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen
204051_s_at	-1.24091	7.70E-06	SFRP4	secreted frizzled-related protein 4
206640_x_at	1.35027	8.22E-06	GAGE12H /// GAGE12I	G antigen 12C /// G antigen 12D /// G antigen 12E /// G antigen 12F /// G antige
208155_x_at	1.33323	9.26E-06	AGE12I /// GAGE12J ///	G antigen 1 /// G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen
202238_s_at	-1.26966	1.12E-05	NNMT	nicotinamide N-methyltransferase

203074_at	-1.20186	1.15E-05	A8 /// ANXA8L1 /// ANX	annexin A8 /// annexin A8-like 1 /// annexin A8-like 2
202237_at	-1.29428	1.21E-05	NNMT	nicotinamide N-methyltransferase
207086_x_at	1.32964	1.34E-05	E12I /// GAGE12J /// GA	G antigen 1 /// G antigen 12C /// G antigen 12D /// G antigen 12E /// G antigen
208235_x_at	1.33792	1.49E-05	GE12G /// GAGE12I ///	G antigen 12F /// G antigen 12G /// G antigen 12I /// G antigen 5 /// G antigen
209687_at	-1.22141	1.64E-05	CXCL12	chemokine (C-X-C motif) ligand 12
218002_s_at	-1.2542	2.09E-05	CXCL14	chemokine (C-X-C motif) ligand 14
217073_x_at	1.26517	2.74E-05	APOA1	apolipoprotein A-I
207663_x_at	1.27854	3.43E-05	GAGE3	G antigen 3
204450_x_at	1.24718	4.36E-05	APOA1	apolipoprotein A-I
203824_at	1.26775	4.55E-05	TSPAN8	tetraspanin 8
211737_x_at	-1.25764	6.35E-05	PTN	pleiotrophin
214183_s_at	1.29418	7.49E-05	TKTL1	transketolase-like 1
222242_s_at	-1.26119	8.65E-05	KLK5	kallikrein-related peptidase 5
221872_at	-1.25749	9.94E-05	RARRES1	retinoic acid receptor responder (tazarotene induced) 1
209242_at	1.23322	0.000111587	PEG3	paternally expressed 3
205932_s_at	1.23114	0.000148396	MSX1	msh homeobox 1
220332_at	-1.22083	0.000169388	CLDN16	claudin 16
209466_x_at	-1.23302	0.000169567	PTN	pleiotrophin
204475_at	-1.21194	0.00027477	MMP1	matrix metallopeptidase 1 (interstitial collagenase)
203820_s_at	1.23101	0.000356858	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
33767_at	1.20154	0.000637607	NEFH	neurofilament, heavy polypeptide
203819_s_at	1.25311	0.000677783	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
204259_at	-1.20935	0.000892523	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)
206392_s_at	-1.21697	0.000917595	RARRES1	retinoic acid receptor responder (tazarotene induced) 1
205328_at	-1.21865	0.00104182	CLDN10	claudin 10
213880_at	1.21055	0.00590003	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5

Supplementary Table 9. Sequencing primers and siRNA sequences.

FAT1 SEQUENCING PRIMERS

gene	target pos	primer name	seq	primer pos	size
FAT1	chr4:187746691-187747070	FAT_481804_L_14563820_chr4_187746593_20	ACAGCCGATGAAAACCTCAC	chr4:187746542-187746562	712
FAT1	chr4:187746691-187747070	FAT_481804_R_14563821_chr4_187747976_20	CGCCATCGATACGGACTATT	chr4:187747234-187747254	712
FAT1	chr4:187747071-187747368	FAT_481805_L_12913012_chr4_187746779_20	ATCATGACCTCGGACTCCAC	chr4:187746825-187746845	705
FAT1	chr4:187747071-187747368	FAT_481805_R_12913013_chr4_187748148_20	GGGGATGTCTTCAAAGCAAA	chr4:187747510-187747530	705
FAT1	chr4:187753836-187753974	FAT_481800_L_12212434_chr4_187753676_20	CAGTTTGGCTATTTTCCCCA	chr4:187753656-187753676	411
FAT1	chr4:187753836-187753974	FAT_481800_R_12212435_chr4_187754457_20	ATCGTTGGGTAATGCATGGT	chr4:187754047-187754067	411
FAT1	chr4:187754687-187755067	FAT_481796_L_chr4_187754606	cacacattttgactggacaga		
FAT1	chr4:187754687-187755067	FAT_481796_R_chr4_187755148	ggaaggaattggaatcgttg		
FAT1	chr4:187755068-187755379	FAT_481797_L_12115704_chr4_187754788_20	AAAGTGCTGAATTCGGGATG	chr4:187754828-187754848	691
FAT1	chr4:187755068-187755379	FAT_481797_R_12115705_chr4_187756129_20	TGCGATCACATGATTGGTTT	chr4:187755499-187755519	691
FAT1	chr4:187755829-187755940	FAT_481795_L_14754562_chr4_187755387_20	ATGTGATCGCATGCTTTTGA	chr4:187755508-187755528	746
FAT1	chr4:187755829-187755940	FAT_481795_R_14754563_chr4_187756838_20	GCCTTGTACATAGGGACCCA	chr4:187756234-187756254	746
FAT1	chr4:187756119-187756273	FAT_481794_L_13605292_chr4_187755617_20	TCTGCCAGTCAATATGACGC	chr4:187755768-187755788	670
FAT1	chr4:187756119-187756273	FAT_481794_R_13605293_chr4_187756916_20	GCAGTGGAAGGCTTGTTGAT	chr4:187756418-187756438	670
FAT1	chr4:187758045-187758425	FAT_481792_L_13757780_chr4_187757573_20	AAGGGCTAAGCGGTACGAAT	chr4:187757709-187757729	1012
FAT1	chr4:187758045-187758425	FAT_481792_R_13757781_chr4_187759556_20	TGCTTTGTGGATGTGCATTT	chr4:187758701-187758721	1012
FAT1	chr4:187758426-187758508	FAT_481793_L_12036490_chr4_187758154_20	GCTCCTGCCCATTCAAATAA	chr4:187758190-187758210	410
FAT1	chr4:187758426-187758508	FAT_481793_R_12036491_chr4_187758933_20	CTCCCTAAGCCCTCTCCTGT	chr4:187758580-187758600	410
FAT1	chr4:187759416-187759574	FAT_481791_L_14963680_chr4_187759130_20	TGGGGCATCACCTAGAGTTT	chr4:187759173-187759193	576
FAT1	chr4:187759416-187759574	FAT_481791_R_14963681_chr4_187760241_20	GTCATGCTGGGCTTTTCATT	chr4:187759729-187759749	576
FAT1	chr4:187761050-187761182	FAT_481790_L_chr4_187760906	tgtcattctttattcatctccaca		
FAT1	chr4:187761050-187761182	FAT_481790_R_chr4_187761299	tcggtgtcacagatggtttc		
FAT1	chr4:187761323-187761703	FAT_481787_L_12578482_chr4_187761221_20	GCACCTTCCCTCTTCATTCA	chr4:187761172-187761192	714
FAT1	chr4:187761323-187761703	FAT_481787_R_12578483_chr4_187762608_20	GGCAAGCTGATAGCACACAA	chr4:187761866-187761886	714
FAT1	chr4:187761704-187762083	FAT_481788_L_12704592_chr4_187761698_20	ATGTGGGTGAGGTTCAGAGG	chr4:187761601-187761621	784
FAT1	chr4:187761704-187762083	FAT_481788_R_12704593_chr4_187763225_20	ACCTTCCATTTTTATCCCGC	chr4:187762365-187762385	784
FAT1	chr4:187762084-187762125	FAT_481789_L_13369146_chr4_187761848_20	TTGTGTGCTATCAGCTTGCC	chr4:187761866-187761886	519
FAT1	chr4:187762084-187762125	FAT_481789_R_13369147_chr4_187762845_20	ACCTTCCATTTTTATCCCGC	chr4:187762365-187762385	519
FAT1	chr4:187762524-187762722	FAT_481786_L_14904920_chr4_187762406_20	GCGGGATAAAAATGGAAGGT	chr4:187762365-187762385	412
FAT1	chr4:187762524-187762722	FAT_481786_R_14904921_chr4_187763189_20	AGATTTGGCTGTGTTCCAGG	chr4:187762757-187762777	412
FAT1	chr4:187764217-187764361	FAT_481785_L_12880222_chr4_187764017_20	ATCAAAGCACGGAAAGGAAA	chr4:187764017-187764037	417
FAT1	chr4:187764217-187764361	FAT_481785_R_12880223_chr4_187764810_20	GGAGGACACTCCTCATTGGA	chr4:187764414-187764434	417
FAT1	chr4:187767330-187767468	FAT_481784_L_13647052_chr4_187767282_20	TGTTGCCGTCAGTTCTTGAG	chr4:187767206-187767226	612
FAT1	chr4:187767330-187767468	FAT_481784_R_13647053_chr4_187768465_20	AGGCCAACTGATTGCTGACT	chr4:187767798-187767818	612
FAT1	chr4:187767948-187768163	FAT_481783_L_14614084_chr4_187767848_20	AGTCAGCAATCAGTTGGCCT	chr4:187767798-187767818	557
FAT1	chr4:187767948-187768163	FAT_481783_R_14614085_chr4_187768921_20	ATAAAGATCCAGGGATGGGC	chr4:187768335-187768355	557
FAT1	chr4:187769533-187769913	FAT_481781_L_12162112_chr4_187769381_20	CTGAAGCCTTCCAAACAACA	chr4:187769357-187769377	578
FAT1	chr4:187769533-187769913	FAT_481781_R_12162113_chr4_187770492_22	TGTCTTCATAGGATTAAATCGG	chr4:187769913-187769935	578
FAT1	chr4:187771256-187771490	FAT_481780_L_13111142_chr4_187771064_20	ACTGGGCACAACTTTGGAAC	chr4:187771060-187771080	613
FAT1	chr4:187771256-187771490	FAT_481780_R_13111143_chr4_187772249_20	TTGGAGACCTGGAGCTCACT	chr4:187771653-187771673	613
FAT1	chr4:187772338-187772492	FAT_481779_L_chr4_187772280	cccacatatatgatactgttggaat		
FAT1	chr4:187772338-187772492	FAT_481779_R_chr4_187772546	tttgtgctgcctgttaatgc		
FAT1	chr4:187775152-187775349	FAT_481778_L_12435872_chr4_187774694_20	TGTTTCCCGTCAGATCCTTC	chr4:187774823-187774843	702
FAT1	chr4:187775152-187775349	FAT_481778_R_12435873_chr4_187776057_20	AATGCTGCCCTTGTTTTTGT	chr4:187775505-187775525	702
FAT1	chr4:187775855-187776235	FAT_481767_L_15342952_chr4_187775355_20	ACAAAAACAAGGGCAGCATT	chr4:187775505-187775525	1029
FAT1	chr4:187775855-187776235	FAT_481767_R_15342953_chr4_187777372_20	TTTACAGCCTGGTCAAAGGG	chr4:187776514-187776534	1029
FAT1	chr4:187776236-187776615	FAT_481768_L_14806600_chr4_187776076_20	CCATGATCTGATGCAACCAC	chr4:187776056-187776076	733
FAT1	chr4:187776236-187776615	FAT_481768_R_14806601_chr4_187777501_20	ACAAACTGTCCGGCGTAATC	chr4:187776769-187776789	733
FAT1	chr4:187776616-187776995	FAT_481769_L_13101536_chr4_187776110_20	CCTGGCAGGTTTTCAACAAT	chr4:187776263-187776283	756
FAT1	chr4:187776616-187776995	FAT_481769_R_13101537_chr4_187777581_20	TGCTGGAGGAAAAGTTGCTT	chr4:187776999-187777019	756
FAT1	chr4:187776996-187777375	FAT_481770_L_13605352_chr4_187776738_20	GTGATTACGCCGGACAGTTT	chr4:187776767-187776787	862
FAT1	chr4:187776996-187777375	FAT_481770_R_13605353_chr4_187778421_20	CGCTGAGCAGTGATGTGATT	chr4:187777609-187777629	862
FAT1	chr4:187777376-187777755	FAT_481771_L_14401410_chr4_187777332_20	GAAGGAAAGCAGGACTGTGC	chr4:187777254-187777274	623
FAT1	chr4:187777376-187777755	FAT_481771_R_14401411_chr4_187778537_20	GTCTTATGCGGTGACCCTGT	chr4:187777857-187777877	623
FAT1	chr4:187777756-187778135	FAT_481772_L_chr4_187777703	agtgagatgaggccagtgct		
FAT1	chr4:187777756-187778135	FAT_481772_R_chr4_187778204	aagccatgcctgtgtttga		
FAT1	chr4:187778136-187778515	FAT_481773_L_13377906_chr4_187777778_20	ACAGGGTCACCGCATAAGAC	chr4:187777857-187777877	804
FAT1	chr4:187778136-187778515	FAT_481773_R_13377907_chr4_187779345_20	TAAGCCGCACTTCAGGAGTT	chr4:187778641-187778661	804
FAT1	chr4:187778516-187778895	FAT_481774_L_14022840_chr4_187777972_20	ACCTGGATGCTCTCTGCAAT	chr4:187778144-187778164	793
FAT1	chr4:187778516-187778895	FAT_481774_R_14022841_chr4_187779517_20	CTGGTGCTCTCACTGTCCAA	chr4:187778917-187778937	793
FAT1	chr4:187778896-187779275	FAT_481775_L_11897100_chr4_187778586_20	AACTCCTGAAGTGCGGCTTA	chr4:187778641-187778661	751
FAT1	chr4:187778896-187779275	FAT_481775_R_11897101_chr4_187780047_20	CAGCGTGGTCCTAACAGACA	chr4:187779372-187779392	751
FAT1	chr4:187779276-187779655	FAT_481776_L_14833420_chr4_187778758_20	TTGGACAGTGAGAGCACCAG	chr4:187778917-187778937	780
FAT1	chr4:187779276-187779655	FAT_481776_R_14833421_chr4_187780277_20	GTCAGCATTGGGAGTTTCGT	chr4:187779677-187779697	780
FAT1	chr4:187779656-187779923	FAT_481777_L_13644340_chr4_187779288_20	TGTCTGTTAGGACCACGCTG	chr4:187779372-187779392	909
FAT1	chr4:187779656-187779923	FAT_481777_R_13644341_chr4_187781065_20	TGAGGGACTCCTGGAAAGTG	chr4:187780261-187780281	909
FAT1	chr4:187786301-187786512	FAT_481766_L_chr4_187786212	tgcttcaatacccagaactga		
FAT1	chr4:187786301-187786512	FAT_481766_R_chr4_187786601	gtcctgaggcctttgtgtgt		
FAT1	chr4:187786635-187786911	FAT_481765_L_13640742_chr4_187786233_20	TTCCCTTTGTCCTTGTCCAG	chr4:187786334-187786354	894
FAT1	chr4:187786635-187786911	FAT_481765_R_13640743_chr4_187787980_20	TACCTTCTCTGTGGAGGCGT	chr4:187787208-187787228	894
FAT1	chr4:187791831-187791971	FAT_481764_L_13285988_chr4_187791815_20	TTTAGACCCTCACAGGGCAG	chr4:187791723-187791743	386
FAT1	chr4:187791831-187791971	FAT_481764_R_13285989_chr4_187792546_20	TTCAAAATGCTCCTCCTTGG	chr4:187792089-187792109	386
FAT1	chr4:187794172-187794383	FAT_481763_L_14714880_chr4_187794208_20	TTGTGCCCAAAACTCATCAA	chr4:187794090-187794110	499
FAT1	chr4:187794172-187794383	FAT_481763_R_14714881_chr4_187795165_20	ACGTTTGAGAATCAGGGTGC	chr4:187794569-187794589	499
FAT1	chr4:187794732-187795062	FAT_481762_L_15403118_chr4_187794360_20	TGAAGCACAGACTGGTTTGG	chr4:187794446-187794466	790

FAT1	chr4:187794732-187795062	FAT_481762_R_15403119_chr4_187795899_20	CTGCCTCACCTCCTTACAGC	chr4:187795216-187795236	790
FAT1	chr4:187797869-187797931	FAT_481761_L_11997672_chr4_187797689_20	GGGATAAAGGGGACAAGAGC	chr4:187797679-187797699	337
FAT1	chr4:187797869-187797931	FAT_481761_R_11997673_chr4_187798322_20	cctggccAAGAGTGTGATTT	chr4:187797996-187798016	337
FAT1	chr4:187821446-187821761	FAT_481760_L_13740372_chr4_187821300_20	tgtgcccggTTATGCTAAAT	chr4:187821273-187821293	527
FAT1	chr4:187821446-187821761	FAT_481760_R_13740373_chr4_187822313_20	TTGATGTGCTGCTTTACGCT	chr4:187821780-187821800	527
FAT1	chr4:187864710-187865090	FAT_481751_L_chr4_187864677	gggcatcaaatgagagcaat		
FAT1	chr4:187864710-187865090	FAT_481751_R_chr4_187865159	tcttccagaaggaaccgtca		
FAT1	chr4:187865091-187865470	FAT_481752_L_14537140_chr4_187864587_20	AACGCCAGAGCCATCTCTAA	chr4:187864739-187864759	784
FAT1	chr4:187865091-187865470	FAT_481752_R_14537141_chr4_187866114_20	TCCACCCGAGTTTTTACAGG	chr4:187865503-187865523	784
FAT1	chr4:187865471-187865850	FAT_481753_L_14256200_chr4_187865001_20	ATGATGACGGTTCCTTCTGG	chr4:187865136-187865156	784
FAT1	chr4:187865471-187865850	FAT_481753_R_14256201_chr4_187866528_20	AGCTCCTGCAGGCAAATAAA	chr4:187865900-187865920	784
FAT1	chr4:187865851-187866230	FAT_481754_L_13285980_chr4_187865497_20	TGGGGTATCCCAAGGTCATA	chr4:187865574-187865594	681
FAT1	chr4:187865851-187866230	FAT_481754_R_13285981_chr4_187866818_20	TGAAGGGACAATTCCCAGAG	chr4:187866235-187866255	681
FAT1	chr4:187866231-187866610	FAT_481755_L_13174894_chr4_187866113_20	CCTAAGCCATCCATTAGCGA	chr4:187866072-187866092	771
FAT1	chr4:187866231-187866610	FAT_481755_R_13174895_chr4_187867614_20	ATTTGCTCCTCCCAACACAC	chr4:187866823-187866843	771
FAT1	chr4:187866611-187866990	FAT_481756_L_14034424_chr4_187866059_20	CTCTGGGAATTGTCCCTTCA	chr4:187866235-187866255	1064
FAT1	chr4:187866611-187866990	FAT_481756_R_14034425_chr4_187868146_20	CCGTGGCATGAAGTTGTATG	chr4:187867279-187867299	1064
FAT1	chr4:187866991-187867370	FAT_481757_L_13316796_chr4_187866855_20	GTGTGTTGGGAGGAGCAAAT	chr4:187866823-187866843	929
FAT1	chr4:187866991-187867370	FAT_481757_R_13316797_chr4_187868672_20	TTCCGGAGACAGTGAAAACC	chr4:187867732-187867752	929
FAT1	chr4:187867371-187867750	FAT_481758_L_13006022_chr4_187867387_20	CATACAACTTCATGCCACGG	chr4:187867279-187867299	629
FAT1	chr4:187867371-187867750	FAT_481758_R_13006023_chr4_187868604_20	CAGCCAACGACTTGAACAGA	chr4:187867888-187867908	629
FAT1	chr4:187867751-187867993	FAT_481759_L_11986922_chr4_187867185_20	ACACCACTGGTTGGGTGAAT	chr4:187867368-187867388	662
FAT1	chr4:187867751-187867993	FAT_481759_R_11986923_chr4_187868468_20	TCCCCAAGGTAACGATTCTG	chr4:187868010-187868030	662

AXIN1 SEQUENCING PRIMERS

AXIN1	chr16:277821-278200	AXIN1_391591_L_13151152_chr16_277407_20	TCGCATGAAAAACAGACTCG	chr16:277514-277534	714
AXIN1	chr16:277821-278200	AXIN1_391591_R_13151153_chr16_278794_20	GACGAGTTTGACTGTGGGGT	chr16:278208-278228	714
AXIN1	chr16:278201-278249	AXIN1_391592_L_14698552_chr16_277945_20	CCTGCCTCTAGACACGGGTA	chr16:277973-277993	653
AXIN1	chr16:278201-278249	AXIN1_391592_R_14698553_chr16_279210_20	ACTGCAGATGTGGTGCTGAG	chr16:278606-278626	653
AXIN1	chr16:279440-279608	AXIN1_391588_L_13185032_chr16_278850_20	AGGGACATGAGCTGAAATGG	chr16:279045-279065	863
AXIN1	chr16:279440-279608	AXIN1_391588_R_13185033_chr16_280535_20	CATCCTAGAGGTGGGAGCTG	chr16:279888-279908	863
AXIN1	chr16:281190-281298	AXIN1_391587_L_13193442_chr16_281018_20	TGATGGAGACAGGAGAAGGC	chr16:281004-281024	638
AXIN1	chr16:281190-281298	AXIN1_391587_R_13193443_chr16_282253_20	CTGAAGGACAGACTCTCGGG	chr16:281622-281642	638
AXIN1	chr16:283488-283719	AXIN1_391585_L_12593270_chr16_283490_20	CGTTTTTCCCCTGAAGACCT	chr16:283389-283409	435
AXIN1	chr16:283488-283719	AXIN1_391585_R_12593271_chr16_284319_20	TCCTATCCCTCAAGGAGGCT	chr16:283804-283824	435
AXIN1	chr16:287056-287227	AXIN1_L_chr16_286959	actcgccacacacactgaag		
AXIN1	chr16:287056-287227	AXIN1_R_chr16_287324	gagccttacagatgccagga		
AXIN1	chr16:287722-288102	AXIN1_391579_L_13811030_chr16_287442_20	CTGAAGACTGAGGGCCAGAG	chr16:287482-287502	813
AXIN1	chr16:287722-288102	AXIN1_391579_R_13811031_chr16_289027_20	AGCTGGTGCTGAGAGGTGAT	chr16:288275-288295	813
AXIN1	chr16:288103-288252	AXIN1_391580_L_15482688_chr16_287987_20	CCTGACTTGGGTACGTGCTT	chr16:287945-287965	350
AXIN1	chr16:288103-288252	AXIN1_391580_R_15482689_chr16_288646_20	AGCTGGTGCTGAGAGGTGAT	chr16:288275-288295	350
AXIN1	chr16:294304-294442	AXIN1_391577_L_15388808_chr16_293936_20	GATCAGGTACACAGCAGGCA	chr16:294020-294040	499
AXIN1	chr16:294304-294442	AXIN1_391577_R_15388809_chr16_294893_20	CGCTCTTTCCCTTCACAAAG	chr16:294499-294519	499
AXIN1	chr16:299973-300070	AXIN1_391575_L_13900960_chr16_299585_20	ATCCACCTTCACAAGGCAAG	chr16:299679-299699	600
AXIN1	chr16:299973-300070	AXIN1_391575_R_13900961_chr16_300744_20	CCATCACGTGTGAACCTTTG	chr16:300259-300279	600
AXIN1	chr16:304543-304684	AXIN1_391573_L_12009682_chr16_304537_20	CTGGGGCAGGACTTACACAT	chr16:304440-304460	409
AXIN1	chr16:304543-304684	AXIN1_391573_R_12009683_chr16_305314_20	AGGACAGGTGGAGATGTTGG	chr16:304829-304849	409
AXIN1	chr16:336148-336528	AXIN1_391567_L_14279324_chr16_335586_20	AAACGTCCACTCCTCCCTTT	chr16:335767-335787	914
AXIN1	chr16:336148-336528	AXIN1_391567_R_14279325_chr16_337373_20	ACTTCTGGTTTGCCTGCACT	chr16:336661-336681	914
AXIN1	chr16:336529-336908	AXIN1_391568_L_13692222_chr16_336551_20	TTTTCCTCCATAGTGGCCTG	chr16:336440-336460	601
AXIN1	chr16:336529-336908	AXIN1_391568_R_13692223_chr16_337712_20	CGCAGAGTCCCAAAATGAAT	chr16:337021-337041	601
AXIN1	chr16:336909-337107	AXIN1_391569_L_13518716_chr16_336811_20	CAGTGACTCAGCCCACTTCA	chr16:336760-336780	582
AXIN1	chr16:336909-337107	AXIN1_391569_R_13518717_chr16_337934_20	GGCATCCCTTCTTAGCATGA	chr16:337322-337342	582

AXIN2 SEQUENCING PRIMERS

AXIN2	chr17:60956285-60956664	AXIN2_391627_L_14079610_chr17_60956025_20	GAAACCATGAACGCACTCCT	chr17:60956055-60956075	715
AXIN2	chr17:60956285-60956664	AXIN2_391627_R_14079611_chr17_60957414_20	CCTCAGTCCTCCATGTTGGT	chr17:60956750-60956770	715
AXIN2	chr17:60956665-60956682	AXIN2_391628_L_12513642_chr17_60956367_20	CACTGGCCGATTCTTCCTTA	chr17:60956416-60956436	354
AXIN2	chr17:60956665-60956682	AXIN2_391628_R_12513643_chr17_60957034_20	CCTCAGTCCTCCATGTTGGT	chr17:60956750-60956770	354
AXIN2	chr17:60960491-60960659	AXIN2_391622_L_12304952_chr17_60959893_20	AATCAGTGTGCCTGTCCCTC	chr17:60960092-60960112	958
AXIN2	chr17:60960491-60960659	AXIN2_391622_R_12304953_chr17_60961768_20	TCTCCAATCCAGGTGAGACC	chr17:60961030-60961050	958
AXIN2	chr17:60962205-60962301	AXIN2_391620_L_15193568_chr17_60961739_20	GCTCAGGGGTGACAAATGTT	chr17:60961872-60961892	569
AXIN2	chr17:60962205-60962301	AXIN2_391620_R_15193569_chr17_60962836_20	GTCTTGGTTGGGTCTCCGTA	chr17:60962421-60962441	569
AXIN2	chr17:60962899-60963133	AXIN2_391618_L_chr17_60962780	tcttctcatgggagggtttg		
AXIN2	chr17:60962899-60963133	AXIN2_391618_R_chr17_60963279	gcactgacccctgttcatgt		
AXIN2	chr17:60963448-60963643	AXIN2_391617_L_13858280_chr17_60963482_20	ACTGCAAAAACAGCCATTCC	chr17:60963365-60963385	445
AXIN2	chr17:60963448-60963643	AXIN2_391617_R_13858281_chr17_60964331_20	TAGTTTCTAAGAGGGCGGCA	chr17:60963790-60963810	445
AXIN2	chr17:60963903-60964283	AXIN2_391613_L_12301702_chr17_60963877_20	TGCCGCCCTCTTAGAAACTA	chr17:60963790-60963810	671
AXIN2	chr17:60963903-60964283	AXIN2_391613_R_12301703_chr17_60965178_20	TTCTGCTTCCTGGGTCACTT	chr17:60964441-60964461	671
AXIN2	chr17:60964284-60964415	AXIN2_391614_L_13046272_chr17_60964274_20	GGAGTGGTACTGCGAATGGT	chr17:60964179-60964199	595
AXIN2	chr17:60964284-60964415	AXIN2_391614_R_13046273_chr17_60965423_20	CCTAGGCCTTCTTCCTGCTT	chr17:60964754-60964774	595
AXIN2	chr17:60964782-60964923	AXIN2_391611_L_14001240_chr17_60964300_20	AAGTGACCCAGGAAGCAGAA	chr17:60964441-60964461	602
AXIN2	chr17:60964782-60964923	AXIN2_391611_R_14001241_chr17_60965463_20	ACTCTACACCCGAACATGGG	chr17:60965023-60965043	602
AXIN2	chr17:60968034-60968137	AXIN2_391609_L_14191482_chr17_60968058_20	ATACCTCTCCCCATTCCACC	chr17:60967946-60967966	236
AXIN2	chr17:60968034-60968137	AXIN2_391609_R_14191483_chr17_60968489_20	ACATCCTCGTAAGCCTGTGG	chr17:60968162-60968182	236
AXIN2	chr17:60976099-60976240	AXIN2_391607_L_13173636_chr17_60976125_20	CAGCTGAGGATGACAGACGA	chr17:60976012-60976032	285
AXIN2	chr17:60976099-60976240	AXIN2_391607_R_13173637_chr17_60976654_20	TACCTGGGTTTCTGGTGAGG	chr17:60976277-60976297	285
AXIN2	chr17:60984385-60984765	AXIN2_391598_L_13335216_chr17_60984135_20	TGCCACTGTTTGAAGTCAGC	chr17:60984160-60984180	742

AXIN2	chr17:60984385-60984765	AXIN2_391598_R_13335217_chr17_60985578_20	GAGGGAGAAATGCGTGGATA	chr17:60984882-60984902	742
AXIN2	chr17:60984766-60985145	AXIN2_391599_L_13999190_chr17_60984236_20	ACAGTTTCCGTGGACCTCAC	chr17:60984401-60984421	829
AXIN2	chr17:60984766-60985145	AXIN2_391599_R_13999191_chr17_60985853_20	CCAGACTCAGTGGGAAGAGC	chr17:60985210-60985230	829
AXIN2	chr17:60985146-60985316	AXIN2_391600_L_13290816_chr17_60984818_20	TATCCACGCATTTCTCCCTC	chr17:60984882-60984902	641
AXIN2	chr17:60985146-60985316	AXIN2_391600_R_13290817_chr17_60986059_20	AGTGTGCAGGGAGCTCAGAT	chr17:60985503-60985523	641

CTNNB1 SEQUENCING PRIMERS

CTNNB1	chr3:41240515-41240576	CTNNB1_91704_L_8102522_chr3_41240153_20	GATGGAGCTGTGGTTGAGGT	chr3:41240334-41240354	400
CTNNB1	chr3:41240515-41240576	CTNNB1_91704_R_8102523_chr3_41240912_20	TTCACCAAGCCATTAGGAGG	chr3:41240714-41240734	400
CTNNB1	chr3:41241020-41241248	CTNNB1_91709_L_9805086_chr3_41240700_20	TCACTGAGCTAACCCTGGCT	chr3:41240860-41240880	561
CTNNB1	chr3:41241020-41241248	CTNNB1_91709_R_9805087_chr3_41241779_21	TCCACAGTTCAGCATTTACCT	chr3:41241400-41241421	561
CTNNB1	chr3:41241448-41241702	CTNNB1_91710_L_11145498_chr3_41241110_24	AAAGTCAGAATGCAGTTTTGAGAA	chr3:41241279-41241303	623
CTNNB1	chr3:41241448-41241702	CTNNB1_91710_R_11145499_chr3_41242315_20	GCATGATAGCGTGTCTGGAA	chr3:41241882-41241902	623
CTNNB1	chr3:41241828-41242067	CTNNB1_91715_L_10891970_chr3_41241492_20	TGCAATCCCTGAACTGACAA	chr3:41241660-41241680	588
CTNNB1	chr3:41241828-41242067	CTNNB1_91715_R_10891971_chr3_41242627_20	GCTAAACGCACTGCCATTTT	chr3:41242228-41242248	588
CTNNB1	chr3:41242154-41242356	CTNNB1_91718_L_10735170_chr3_41241830_20	ACCTTTCCCATCATCGTGAG	chr3:41241992-41242012	531
CTNNB1	chr3:41242154-41242356	CTNNB1_91718_R_10735171_chr3_41242851_20	TGGAATGGTGTCATCCAGAA	chr3:41242503-41242523	531
CTNNB1	chr3:41243702-41243847	CTNNB1_91721_L_8205858_chr3_41243358_20	GTTGGATAGGGCCCCAGTAT	chr3:41243530-41243550	445
CTNNB1	chr3:41243702-41243847	CTNNB1_91721_R_8205859_chr3_41244207_20	TGGCTGCAAACTGAATAGGA	chr3:41243955-41243975	445
CTNNB1	chr3:41249835-41249939	CTNNB1_91722_L_8039532_chr3_41249459_20	TGAGGTGAACTGGCAAAGTG	chr3:41249647-41249667	405
CTNNB1	chr3:41249835-41249939	CTNNB1_91722_R_8039533_chr3_41250228_20	GAGTCCCAAGGAGACCTTCC	chr3:41250032-41250052	405
CTNNB1	chr3:41250023-41250362	CTNNB1_91727_L_10823690_chr3_41249881_20	TAAACTGGTGCCATGGGAAT	chr3:41249952-41249972	550
CTNNB1	chr3:41250023-41250362	CTNNB1_91727_R_10823691_chr3_41250940_20	CCTATCGCAGCCATACTTCC	chr3:41250482-41250502	550
CTNNB1	chr3:41250633-41250792	CTNNB1_91730_L_11680246_chr3_41250339_20	GTATGGCTGCGATAGGGGTA	chr3:41250486-41250506	420
CTNNB1	chr3:41250633-41250792	CTNNB1_91730_R_11680247_chr3_41251138_20	GCTCTTCAGGAAGACGGATG	chr3:41250886-41250906	420
CTNNB1	chr3:41252166-41252338	CTNNB1_91731_L_10433136_chr3_41251924_20	CAGGAGGCCTCTTTTCAGTG	chr3:41252045-41252065	469
CTNNB1	chr3:41252166-41252338	CTNNB1_91731_R_10433137_chr3_41252817_22	CCTCCCTCTTCTCAAGTCTCAA	chr3:41252492-41252514	469
CTNNB1	chr3:41252843-41253223	CTNNB1_91741_L_11445368_chr3_41252631_20	TGTGAATGCCTCTTGCACTC	chr3:41252737-41252757	585
CTNNB1	chr3:41252843-41253223	CTNNB1_91741_R_11445369_chr3_41253760_20	CAAGCCAGGGAAACATCAAT	chr3:41253302-41253322	585
CTNNB1	chr3:41254510-41254571	CTNNB1_91746_L_10460176_chr3_41254174_22	TCTTTGAGGTGTGGAGTTTTGA	chr3:41254342-41254364	413
CTNNB1	chr3:41254510-41254571	CTNNB1_91746_R_10460177_chr3_41254959_20	GCTCTGAATTCCCTGTGCTC	chr3:41254735-41254755	413
CTNNB1	chr3:41255628-41256008	CTNNB1_91755_L_10104496_chr3_41255406_20	TTGCTGCTGAACTTTGGATG	chr3:41255517-41255537	684
CTNNB1	chr3:41255628-41256008	CTNNB1_91755_R_10104497_chr3_41256733_20	TCAGCAACTCTACAGGCCAA	chr3:41256181-41256201	684

GSK3B SEQUENCING PRIMERS

GSK3B	chr3:121028235-121028392	GSK3B_505030_L_13942666_chr3_121028177_20	CCTGGATCTCCCTCAAAGTG	chr3:121028106-121028126	387
GSK3B	chr3:121028235-121028392	GSK3B_505030_R_13942667_chr3_121028910_20	AGGCCATACAGTTCACAGCC	chr3:121028473-121028493	387
GSK3B	chr3:121044791-121044890	GSK3B_505028_L_chr3_121044758	atgtttttatagaagagacttagaacg		
GSK3B	chr3:121044791-121044890	GSK3B_505028_R_chr3_121044980	gcagaatcttattttcactcttacca		
GSK3B	chr3:121064955-121065142	GSK3B_505025_L_14303778_chr3_121064949_20	ATGTCCGTTTTTGTCCTCCA	chr3:121064852-121064872	597
GSK3B	chr3:121064955-121065142	GSK3B_505025_R_14303779_chr3_121066102_20	CTAGTTGTGCTTGCCACCAG	chr3:121065429-121065449	597
GSK3B	chr3:121068126-121068165	GSK3B_505024_L_15196428_chr3_121067636_20	TCCGCTGTCACTTCTTTCCT	chr3:121067781-121067801	437
GSK3B	chr3:121068126-121068165	GSK3B_505024_R_15196429_chr3_121068469_20	TTTTGGATTGACTTCCCCTG	chr3:121068198-121068218	437
GSK3B	chr3:121077949-121078045	GSK3B_505022_L_14345070_chr3_121077689_20	ACTGCCCTTACCTTGCAAAT	chr3:121077719-121077739	409
GSK3B	chr3:121077949-121078045	GSK3B_505022_R_14345071_chr3_121078466_20	CAGTGAATCCAATGCCTGAA	chr3:121078108-121078128	409
GSK3B	chr3:121107291-121107389	GSK3B_505020_L_chr3_121107170	acgtgaccttggattgcttc		
GSK3B	chr3:121107291-121107389	GSK3B_505020_R_chr3_121107531	tgactttttctctgttttggattg		
GSK3B	chr3:121114240-121114347	GSK3B_505018_L_13875080_chr3_121114130_23	tgcctATACATGTTTGCATCTCA	chr3:121114085-121114108	594
GSK3B	chr3:121114240-121114347	GSK3B_505018_R_13875081_chr3_121115277_20	TTCTGCCCTTGCTTCTTTGT	chr3:121114659-121114679	594
GSK3B	chr3:121117580-121117711	GSK3B_505016_L_12998752_chr3_121117602_20	GGCTGATATTGCAAAAGGAA	chr3:121117491-121117511	359
GSK3B	chr3:121117580-121117711	GSK3B_505016_R_12998753_chr3_121118277_21	TGAAAGGAAGATTGAGTGCCA	chr3:121117829-121117850	359
GSK3B	chr3:121124909-121125020	GSK3B_505014_L_13377940_chr3_121124451_20	CGCTCCTATTTTGGTTTGTG	chr3:121124580-121124600	811
GSK3B	chr3:121124909-121125020	GSK3B_505014_R_13377941_chr3_121126032_20	ccctgccaccacGATACTTA	chr3:121125371-121125391	811
GSK3B	chr3:121148804-121148888	GSK3B_505012_L_13663626_chr3_121148740_20	GTATTGCTGGGGCAAGTGTT	chr3:121148672-121148692	320
GSK3B	chr3:121148804-121148888	GSK3B_505012_R_13663627_chr3_121149331_24	GCTTGCTAATTTTAGTGCTTAATG	chr3:121148968-121148992	320
GSK3B	chr3:121203582-121203776	GSK3B_505010_L_14971080_chr3_121203534_20	TTGAGCTGAACAAAAATGCG	chr3:121203458-121203478	364
GSK3B	chr3:121203582-121203776	GSK3B_505010_R_14971081_chr3_121204215_23	TTCCTTACAGTTCTCGTGAAAAA	chr3:121203799-121203822	364
GSK3B	chr3:121294883-121295203	GSK3B_505008_L_12163942_chr3_121294739_20	GGGGGTATGGGAGGAGTAAA	chr3:121294711-121294731	702
GSK3B	chr3:121294883-121295203	GSK3B_505008_R_12163943_chr3_121296102_20	AGCGTGAGACTCGTGATCCT	chr3:121295393-121295413	702

TCF4 SEQUENCING PRIMERS

TCF4	chr18:51046445-51046590	TCF4_663877_L_12645832_chr18_51045987_20	CTTGCGTCTGCGATTCATAA	chr18:51046116-51046136	558
TCF4	chr18:51046445-51046590	TCF4_663877_R_12645833_chr18_51047062_20	CAGACACGCAAGAAGAGTGC	chr18:51046654-51046674	558
TCF4	chr18:51047075-51047305	TCF4_663870_L_13729952_chr18_51047091_20	TGTCTGCCACTGCTCAAGAC	chr18:51046983-51047003	449
TCF4	chr18:51047075-51047305	TCF4_663870_R_13729953_chr18_51047948_20	AATTCTGCCAAAAACATGGC	chr18:51047412-51047432	449
TCF4	chr18:51050737-51050900	TCF4_663867_L_13647522_chr18_51050497_20	AGCATTGGGTCCAGATTCAT	chr18:51050517-51050537	569
TCF4	chr18:51050737-51050900	TCF4_663867_R_13647523_chr18_51051594_20	CCAATGCAGGGAAAACTTGT	chr18:51051066-51051086	569
TCF4	chr18:51052776-51052912	TCF4_663860_L_14769660_chr18_51052638_20	TTAGCGGGCGAAGTTCTAAA	chr18:51052607-51052627	339
TCF4	chr18:51052776-51052912	TCF4_663860_R_14769661_chr18_51053275_20	TGCTCACCTCTCTGGTTCCT	chr18:51052926-51052946	339
TCF4	chr18:51072725-51072929	TCF4_663853_L_chr18_51072650	acagcaacaatagtatctatatctgaaa		
TCF4	chr18:51072725-51072929	TCF4_663853_R_chr18_51072983	tttaggcaccccttttgaac		
TCF4	chr18:51075543-51075620	TCF4_663846_L_13461626_chr18_51075375_20	TGGGTTCCCATCTCCAAATA	chr18:51075359-51075379	654
TCF4	chr18:51075543-51075620	TCF4_663846_R_13461627_chr18_51076642_20	CTGGTGCGAGAATTTTGGTT	chr18:51075993-51076013	654
TCF4	chr18:51078177-51078256	TCF4_663839_L_chr18_51078082	ggggaagtgagtttccacct		
TCF4	chr18:51078177-51078256	TCF4_663839_R_chr18_51078343	gaattgcgttgacaacttcg		
TCF4	chr18:51079694-51079762	TCF4_663832_L_13851154_chr18_51079252_20	CTGGTCAATGTGCACCCATA	chr18:51079373-51079393	437
TCF4	chr18:51079694-51079762	TCF4_663832_R_13851155_chr18_51080085_20	AGACGTCTCACTGCCTGGTT	chr18:51079790-51079810	437
TCF4	chr18:51087773-51088152	TCF4_663830_L_11914532_chr18_51087389_20	AATTTCTGGCCAACTGATGC	chr18:51087481-51087501	743

TCF4	chr18:51087773-51088152	TCF4_663830_R_11914533_chr18_51088834_20	TATGGCCACCTTTTTCTGCT	chr18:51088204-51088224	743
TCF4	chr18:51088153-51088192	TCF4_663831_L_13826410_chr18_51088177_20	ATACTGTCTGTCCCGTTGGC	chr18:51088065-51088085	159
TCF4	chr18:51088153-51088192	TCF4_663831_R_13826411_chr18_51088454_20	TATGGCCACCTTTTTCTGCT	chr18:51088204-51088224	159
TCF4	chr18:51093847-51093981	TCF4_663809_L_14378700_chr18_51093807_20	AATGGGTGTGTGCCATTTTT	chr18:51093727-51093747	301
TCF4	chr18:51093847-51093981	TCF4_663809_R_14378701_chr18_51094368_20	AAGGCTGAATGCCTCAGAAA	chr18:51094008-51094028	301
TCF4	chr18:51097779-51097885	TCF4_663801_L_14334270_chr18_51097455_20	ACCATCATAAGCATCGGCTC	chr18:51097517-51097537	713
TCF4	chr18:51097779-51097885	TCF4_663801_R_14334271_chr18_51098840_20	GCTTATGGGCCATCTGTGTT	chr18:51098210-51098230	713
TCF4	chr18:51168587-51168637	TCF4_663794_L_11950202_chr18_51168057_20	TTCGCATGCAAATCCATAAA	chr18:51168222-51168242	450
TCF4	chr18:51168587-51168637	TCF4_663794_R_11950203_chr18_51168916_20	TTTGGGAGCTGAAAGCATCT	chr18:51168652-51168672	450
TCF4	chr18:51169102-51169232	TCF4_663789_L_15251678_chr18_51169034_20	GGCTGACAACTGAGCCAAAT	chr18:51168968-51168988	337
TCF4	chr18:51169102-51169232	TCF4_663789_R_15251679_chr18_51169667_20	AACAATCAGTTGGGAGGTGG	chr18:51169285-51169305	337
TCF4	chr18:51221682-51221747	TCF4_663784_L_12045086_chr18_51221084_20	ATTTAGGGCAATAGCCACCC	chr18:51221283-51221303	563
TCF4	chr18:51221682-51221747	TCF4_663784_R_12045087_chr18_51222169_20	GTAAACATCGGGGAAGAGCA	chr18:51221826-51221846	563
TCF4	chr18:51279247-51279344	TCF4_663779_L_14635190_chr18_51278881_20	CATTGAAACTGTGGTCCGTG	chr18:51278964-51278984	771
TCF4	chr18:51279247-51279344	TCF4_663779_R_14635191_chr18_51280382_20	TGCCTAATTTTCCCTTGTGG	chr18:51279715-51279735	771
TCF4	chr18:51282304-51282366	TCF4_663775_L_chr18_51282257	acatatgtgggatgtctggtt		
TCF4	chr18:51282304-51282366	TCF4_663775_R_chr18_51282488	ccggtgcctggttcttaat		
TCF4	chr18:51403508-51403581	TCF4_663772_L_13830730_chr18_51403414_20	ACCACTGATGGGTAATGCAA	chr18:51403361-51403381	400
TCF4	chr18:51403508-51403581	TCF4_663772_R_13830731_chr18_51404173_20	TGGGGTGGGATCTGTAATGT	chr18:51403741-51403761	400
TCF4	chr18:51405273-51405365	TCF4_663770_L_12805532_chr18_51404923_20	TTTCCACTGGGGTGAGATTC	chr18:51404998-51405018	422
TCF4	chr18:51405273-51405365	TCF4_663770_R_12805533_chr18_51405726_20	TTCTCCAAGGATTGGGACTG	chr18:51405400-51405420	422

FAT1 siRNA SEQUENCES

FAT1 si#1	Qiagen Hs_FAT_7 (Catalog# SI02664417) Sequence: CCC UAC UAC GCC GUU GUU AAA
FAT1 si#2	Ambion Silencer Select (Catalog #S5033) Sequence: GGACCGAAAUUCCUUCGAAtt
b-catenin #1	Santa Cruz Biotech (Catalog #sc29209) Sequence: AGCUGAUAUUGAUGGACAGTT
b-catenin #2	Thermo Scientific Dharmacon (Catalog #L-003482-00) Pooled siRNA sequences: GAUCCUAGCUAUCGUUCUU UAAUGAGGACCUAUACUUA GCGUUUGGCUGAACCAUCA CGUACGAGCUGCUAUGUUC

SUPPLEMENTARY NOTE ON CLINICAL SAMPLES

Tumor samples were obtained at the time of surgery at Memorial Sloan-Kettering Cancer Center and University of California, Los Angeles. Matched normal tissue or peripheral blood was also obtained for each patient. All patients provided informed consent as part of institutional review board-approved protocols at the treating institution, Memorial Sloan-Kettering Cancer Center or University of California, Los Angeles.