



Electronic Supplementary Material Fig. 1. The distribution of Welch p values for all probe sets hybridised with isolated abdominal subcutaneous adipocytes from 20 non-obese and 19 obese Pima Indian subjects. The figure illustrates the frequency of genes (y -axis) with the p value range (x -axis) relative to what would have been expected if the differences in gene expression levels between the two groups were similar to those expected at random

Electronic Supplementary Material Table 1. List of selected 410 genes differentially expressed in adipocytes of non-obese and obese Pima Indians.

Gene	Gene Symbol	Chromosomal location	Change with obesity	Fold change	Probe set
Inflammation/immune response					
apolipoprotein L, 3	<i>APOL3</i>	22q13.1	Up	1.66	50296_i_at
Rho GDP dissociation inhibitor (GDI) beta	<i>ARHGDI2</i>	12p12.3	Up	2.65	1984_s_at
bone marrow stromal cell antigen 1	<i>BST1</i>	4p15	Up	2.07	32675_at
complement component 1, q subcomponent, alpha polypeptide	<i>CIQA</i>	1p36.3-p34.1	Up	2.37	46713_at
complement component 1, q subcomponent, beta polypeptide	<i>CIQB</i>	1p36.3-p34.1	Up	3.55	38796_at
complement component 1, q subcomponent, gamma polypeptide	<i>CIQG</i>	1p36.11	Up	3.51	46705_at
Clq and tumour necrosis factor related protein 5	<i>CIQTNF5</i>	11q23.3	Up	2.08	91279_at
complement component 1, r subcomponent	<i>CIR</i>	12p13	Up	2.85	39409_at
complement component 1, s subcomponent	<i>CIS</i>	12p13	Up	2.36	40496_at
chemokine (C-C motif) ligand 2	<i>CCL2</i>	17q11.2-q21.1	Up	3.73	34375_at
chemokine (C-C motif) ligand 3	<i>CCL3</i>	17q11-q21	Up	3.33	36103_at
chemokine (C-C motif) ligand 4	<i>CCL4</i>	17q12	Up	4.03	36674_at
CD53 antigen	<i>CD53</i>	1p13	Up	2.97	38378_at
CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	<i>CD59</i>	11p13	Up	1.68	39351_at
CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)	<i>CD83</i>	6p23	Up	2.58	89856_at
chemokine-like factor super family 3	<i>CKLFSF3</i>	16q22.1	Up	2.08	46279_at
C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2	<i>CLECSF2</i>	12p13-p12	Up	2.04	40698_at
collectin sub-family member 12	<i>COLEC12</i>	18pter-p11.3	Up	3.09	88197_at
cathepsin S	<i>CTSS</i>	1q21	Up	4.87	65578_at
chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	<i>CXCL1</i>	4q21	Up	3.65	408_at
chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	<i>CXCL12</i>	10q11.1	Up	3.28	32666_at
chemokine (C-X-C motif) ligand 2	<i>CXCL2</i>	4q21	Up	3.36	37187_at
chemokine (C-X-C motif) ligand 3	<i>CXCL3</i>	4q21	Up	2.46	34022_at
Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	<i>EBI2</i>	13q32.3	Up	9.74	931_at
Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	<i>FCGR3A</i>	1q23	Up	2.57	37200_at
interferon, alpha-inducible protein (clone IFI-15K)	<i>GIP2</i>	1p36.33	Up	1.59	1107_s_at
H factor 1 (complement)	<i>HF1</i>	1q32	Up	1.87	32250_at
H factor (complement)-like 1	<i>HFL1</i>	1q32	Up	2.5	32249_at
major histocompatibility complex, class I, A	<i>HLA-A</i>	6p21.3	Up	1.7	41237_at
major histocompatibility complex, class II, DP alpha 1	<i>HLA-DPA1</i>	6p21.3	Up	1.92	38833_at
major histocompatibility complex, class II, DP beta 1	<i>HLA-DPB1</i>	6p21.3	Up	2.6	38095_i_at
major histocompatibility complex, class II, DR alpha	<i>HLA-DRA</i>	6p21.3	Up	2.59	37039_at
interferon, alpha-inducible protein 27	<i>IFI27</i>	14q32	Up	2.0	48864_at
interferon, gamma-inducible protein 30	<i>IFI30</i>	19p13.1	Up	3.34	39728_at
interferon-induced protein 35	<i>IFI35</i>	17q21	Up	1.41	464_s_at
interferon-induced protein with tetratricopeptide repeats 4	<i>IFIT4</i>	10q24	Up	1.79	38584_at
interferon induced transmembrane protein 2 (1-8D)	<i>IFITM2</i>	11p15.5	Up	1.45	411_i_at
immunoglobulin heavy constant gamma 3 (G3m marker)	<i>IGHG3</i>	14q32.33	Up	4.54	37864_s_at
immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	<i>IGJ</i>	4q21	Up	3.99	37006_at
interleukin 1 receptor antagonist	<i>IL1RN</i>	2q14.2	Up	3.37	37603_at
interleukin 8	<i>IL8</i>	4q13-q21	Up	3.95	1369_s_at
interferon regulatory factor 1	<i>IRF1</i>	5q31.1	Up	3.00	669_s_at
integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	<i>ITGB2</i>	21q22.3	Up	5.32	37918_at
leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	<i>LILRB1</i>	19q13.4	Up	7.53	35926_s_at
Myelin basic protein	<i>MBP</i>	18q23	Up	1.69	57954_at
macrophage migration inhibitory factor (glycosylation-inhibiting factor)	<i>MIF</i>	22q11.23	Up	1.67	895_at
myxovirus (influenza virus) resistance 2 (mouse)	<i>MX2</i>	21q22.3	Up	1.49	89899_at
prostaglandin E receptor 4 (subtype EP4)	<i>PTGER4</i>	5p13.1	Up	2.11	50746_at
regulator of G-protein signalling 1	<i>RGS1</i>	1q31	Up	2.30	36575_at
secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	<i>SPP1</i>	4q21-q25	Up	4.87	74815_at
TAP binding protein (tapasin)	<i>TAPBP</i>	6p21.3	Up	1.56	41168_at
Thy-1 cell surface antigen	<i>THY1</i>	11q22.3-q23	Up	1.84	39395_at
amine oxidase, copper containing 3 (vascular adhesion protein 1)	<i>AOC3</i>	17q21	Down	-1.2	33756_at
alpha-2-glycoprotein 1, zinc	<i>AZGP1</i>	7q22.1	Down	-10.46	35834_at

Gene	Symbol	Chromosomal location	Change with obesity	Fold change	Probe set
<u>Signalling</u>					
adrenomedullin	<i>ADM</i>	11p15.4	Up	1.65	34777_at
Rho GTPase activating protein 6	<i>ARHGAP6</i>	Xp22.3	Up	1.88	49901_at
ADP-ribosylation factor-like 4	<i>ARL4</i>	7p21-p15.3	Up	1.51	33796_at
endothelial cell growth factor 1 (platelet-derived)	<i>ECGF1</i>	22q13.33	Up	3.59	36879_at
endothelin receptor type B	<i>EDNRB</i>	13q22	Up	2.07	1198_at
fibroblast growth factor (acidic) intracellular binding protein	<i>FIBP</i>	11q13.1	Up	1.43	57259_at
Duffy blood group	<i>FY</i>	1q21-q22	Up	2.10	33295_at
guanine nucleotide binding protein (G protein), gamma 2	<i>GNG2</i>	14q21	Up	1.58	65575_at
G protein-coupled receptor kinase 5	<i>GPRK5</i>	10q24-qter	Up	1.76	1135_at
granulin	<i>GRN</i>	17q21.32	Up	1.40	41198_at
IQ motif containing GTPase activating protein 1	<i>IQGAP1</i>	15q26.1	Up	1.41	1825_at
myelin protein zero-like 1	<i>MPZL1</i>	1q23.2	Up	1.60	57035_at
membrane-spanning 4-domains, subfamily A, member 6A	<i>MS4A6A</i>	11q12.1	Up	1.94	65730_at
membrane-spanning 4-domains, subfamily A, member 7	<i>MS4A7</i>	11q12	Up	1.70	63360_at
phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	<i>PIK3R1</i>	5q12-q13	Up	1.42	1269_at
protein tyrosine phosphatase, receptor type, C	<i>PTPRC</i>	1q31-q32	Up	3.28	40518_at
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	<i>RAPH1</i>	2q33	Up	1.45	64373_at
regulator of G-protein signalling 2, 24 kD	<i>RGS2</i>	1q31	Up	1.62	37701_at
regulator of G-protein signalling 5	<i>RGS5</i>	1q23.1	Up	2.21	33890_at
ras homologue gene family, member C	<i>RHOC</i>	1p13.1	Up	1.71	74701_at
ribosomal protein S6 kinase, 90 kDa, polypeptide 3	<i>RPS6KA3</i>	Xp22.2-p22.1	Up	1.51	46959_at
T-cell activation GTPase activating protein	<i>TAGAP</i>	6q25.3	Up	2.60	82887_at
Tax interaction protein 1	<i>TIP-1</i>	17p13	Up	1.54	39416_at
WNT1 inducible signalling pathway protein 2	<i>WISP2</i>	20q12-q13.1	Up	2.49	35898_at
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	<i>YWHAH</i>	22q12.3	Up	1.54	1424_s_at
adrenergic, beta, receptor kinase 2	<i>ADRBK2</i>	22q12.1	Down	-1.80	724_at
calcitonin receptor-like	<i>CALCRL</i>	2q32.2	Down	-1.95	34995_at
gamma-aminobutyric acid (GABA) A receptor, epsilon	<i>GABRE</i>	Xq28	Down	-1.58	34280_at
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	<i>GNAI1</i>	7q21	Down	-1.36	33809_at
guanine nucleotide binding protein (G protein), gamma 7	<i>GNG7</i>	19p13.3	Down	-2.05	46622_at
natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	<i>NPR1</i>	1q21-q22	Down	-1.53	32625_at
phosphodiesterase 3B, cGMP-inhibited	<i>PDE3B</i>	11p15.1	Down	-1.73	746_at
phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	<i>PIP5K3</i>	2q34	Down	-1.39	32085_at
protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	<i>PPP1R1B</i>	17q21.1	Down	-1.56	65792_at
protein phosphatase 2, regulatory subunit B (B56), alpha isoform	<i>PPP2R5A</i>	1q41	Down	-1.31	903_at
proline rich membrane anchor 1	<i>PRIMA1</i>	14q32.13	Down	-1.53	46164_at
protein tyrosine phosphatase, non-receptor type 1	<i>PTPN1</i>	20q13.1-q13.2	Down	-1.45	1629_s_at
S100 calcium binding protein A1	<i>SI00A1</i>	1q21	Down	-3.23	34674_at
son of sevenless homologue 2 (<i>Drosophila</i>)	<i>SOS2</i>	14q21	Down	-1.37	32857_at
tensin	<i>TNS</i>	2q35-q36	Down	-1.40	54428_at
thyroid receptor interacting protein 15	<i>TRIP15</i>	15q21.2	Down	-1.41	34323_at
ras-like protein VTS58635	<i>VTS58635</i>	17q12	Down	-1.75	50038_at
<u>Transcription factor/transcription regulation</u>					
AT rich interactive domain 1B (SWII-like)	<i>ARID1B</i>	6q25.1	Up	1.87	44608_g_at
basic helix-loop-helix domain containing, class B, 5	<i>BHLHB5</i>	8q13	Up	5.63	51546_at
cAMP responsive element modulator	<i>CREM</i>	10p12.1-p11.1	Up	1.45	32067_at
early B-cell factor 2	<i>EBF2</i>	8p21.2	Up	1.94	74623_at
ets variant gene 6 (TEL oncogene)	<i>ETV6</i>	12p13	Up	3.02	55594_at
forkhead box C1	<i>FOXC1</i>	6p25	Up	1.35	61298_at
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	<i>ID2</i>	2p25	Up	1.85	64354_f_at
leucine rich repeat (in FLII) interacting protein 1	<i>LRRFIP1</i>	2q37.3	Up	1.56	50309_at
musculin (activated B-cell factor-1)	<i>MSC</i>	8q21	Up	2.13	35992_at
v-myc myelocytomatosis viral oncogene homologue (avian)	<i>MYC</i>	8q24.12-24.13	Up	2.57	37724_at
paired related homeobox 1	<i>PRRX1</i>	1q24	Up	2.61	65573_at
snail homologue 2 (<i>Drosophila</i>)	<i>SNAI2</i>	8q11	Up	2.14	63992_at

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Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	<i>CITED2</i>	6q23.3	Down	-1.46	33113_at
doublesex and mab-3 related transcription factor 2	<i>DMRT2</i>	9p24.3	Down	-2.74	54434_at
E2F transcription factor 4, p107/p130-binding enhancer of zeste homologue 1 (<i>Drosophila</i>)	<i>E2F4</i> <i>EZH1</i>	16q21-q22 17q21.1-q21.3	Down	-1.25 -1.32	38707_r_at 32259_at
forkhead box J3	<i>FOXJ3</i>	1pter-q31.3	Down	-1.27	35163_at
histone deacetylase 5	<i>HDAC5</i>	17q21	Down	-1.27	38810_at
myelodysplasia syndrome 1	<i>MDS1</i>	3q26	Down	-1.42	31532_at
nuclear transcription factor, X-box binding 1	<i>NFX1</i>	9p12	Down	-1.35	34667_at
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	<i>NR3C1</i>	5q31	Down	-1.46	706_at
nuclear receptor interacting protein 1	<i>NRIP1</i>	21q11.2	Down	-1.67	40088_at
PHD finger protein 3	<i>PHF3</i>	6q12	Down	-1.43	37694_at
REST corepressor	<i>RCOR</i>	14q32.33	Down	-1.56	37651_at
special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNAs)	<i>SATB1</i>	3p23	Down	-1.58	36899_at
Sp1 transcription factor	<i>SPI</i>	12q13.1	Down	-1.40	50335_at
transcription factor-like 1	<i>TCFL1</i>	1q21	Down	-1.32	33873_at
transcription factor-like 4	<i>TCFL4</i>	17q21.1	Down	-1.40	32578_at
TEA domain family member 1 (SV40 transcriptional enhancer factor)	<i>TEAD1</i>	11p15.4	Down	-1.27	45777_at
transcription factor Dp-2 (E2F dimerisation partner 2)	<i>TFDP2</i>	3q23	Down	-1.30	633_s_at
twist homologue 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (<i>Drosophila</i>)	<i>TWIST1</i>	7p21.2	Down	-1.77	40328_at
twist homologue 2 (<i>Drosophila</i>)	<i>TWIST2</i>	2q37.3	Down	-1.35	44596_at
Williams Beuren syndrome chromosome region 14	<i>WBSCR14</i>	7q11.23	Down	-1.93	60082_s_at
zinc finger protein 451	<i>ZNF451</i>	6p12.1	Down	-1.49	40811_at
<u>Cell cycle control/cell proliferation</u>					
branched chain aminotransferase 1, cytosolic	<i>BCAT1</i>	12pter-q12	Up	6.17	72960_s_at
calpain, small subunit 1	<i>CAPNS1</i>	19q13.12	Up	1.21	36138_at
cat eye syndrome chromosome region, candidate 1	<i>CECR1</i>	22q11.2	Up	2.43	58410_at
disabled homologue 2, mitogen-responsive phosphoprotein (<i>Drosophila</i>)	<i>DAB2</i>	5p13	Up	1.59	479_at
deleted in liver cancer 1	<i>DLCL1</i>	8p22-p21.3	Up	1.58	37951_at
endothelin 1	<i>EDN1</i>	6p24.1	Up	4.43	1520_s_at
epithelial membrane protein 3	<i>EMP3</i>	19q13.3	Up	3.21	39182_at
fibroblast growth factor 1 (acidic)	<i>FGF1</i>	5q31	Up	2.67	996_at
Fzr1 protein	<i>FZR1</i>	19p13.3	Up	2.19	64274_at
glypican 1	<i>GPC1</i>	2q35-q37	Up	1.40	33929_at
glycoprotein (transmembrane) nmb	<i>GPNMB</i>	7p15	Up	2.99	38379_at
insulin-like growth factor binding protein 4	<i>IGFBP4</i>	17q12-q21.1	Up	1.78	39781_at
pregnancy-induced growth inhibitor	<i>OKL38</i>	16q23.3	Up	1.44	44580_at
oncostatin M receptor	<i>OSMR</i>	5p13.1	Up	1.85	39277_at
platelet-derived growth factor alpha polypeptide	<i>PDGFA</i>	7p22	Up	1.84	35703_at
retinoic acid receptor responder (tazarotene induced) 3	<i>RARRES3</i>	11q23	Up	1.90	33236_at
S100 calcium binding protein A11 (calgizzarin)	<i>S100A11</i>	1q21	Up	1.69	38138_at
S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homologue)	<i>S100A4</i>	1q21	Up	2.61	38087_s_at
SAM and SH3 domain containing 1	<i>SASH1</i>	6q24.3	Up	1.59	41644_at
septin 8	<i>SEPT8</i>	5q31	Up	1.54	38067_at
septin 10	<i>SEPT10</i>	2q13	Up	1.29	38033_at
SH3-domain binding protein 4	<i>SH3BP4</i>	2q37.1-q37.2	Up	1.62	63396_at
transforming growth factor, beta receptor II (70-80 kD)	<i>TGFBR2</i>	3p22	Up	1.43	1814_at
tumour protein p53 (Li-Fraumeni syndrome)	<i>TP53</i>	17p13.1	Up	1.41	1939_at
cyclin G2	<i>CCNG2</i>	4q21.21	Down	-1.61	1913_at
cyclin-dependent kinase inhibitor 1B (p27, Kip1)	<i>CDKN1B</i>	12p13.1-p12	Down	-1.53	33847_s_at
progesterone induced protein	<i>DD5</i>	8q22	Down	-1.37	45514_at
fibroblast growth factor 2 (basic)	<i>FGF2</i>	4q26-q27	Down	-1.63	1828_s_at
immunoglobulin superfamily, member 4	<i>IGSF4</i>	11q23.2	Down	-2.00	37929_at
pleckstrin homology domain containing, family C (with FERM domain) member 1	<i>PLEKHC1</i>	14q22.1	Down	-1.20	36577_at
retinoblastoma-like 2 (p130)	<i>RBL2</i>	16q12.2	Down	-1.38	32597_at
vascular endothelial growth factor	<i>VEGF</i>	6p12	Down	-1.57	36100_at

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<u>Cell adhesion</u>					
ras homologue gene family, member E	<i>ARHE</i>	2q23.3	Up	2.78	35803_at
CD44 antigen (homing function and Indian blood group system)	<i>CD44</i>	11p13	Up	1.61	40493_at
CD9 antigen (p24)	<i>CD9</i>	12p13.3	Up	2.08	39389_at
collagen, type XI, alpha 1	<i>COL11A1</i>	1p21	Up	3.35	37892_at
collagen, type XVI, alpha 1	<i>COL16A1</i>	1p35-p34	Up	2.25	35168_f_at
collagen, type VI, alpha 1	<i>COL6A1</i>	21q22.3	Up	1.86	38722_at
collagen, type VI, alpha 2	<i>COL6A2</i>	21q22.3	Up	3.35	34802_at
endoglin (Osler-Rendu-Weber syndrome 1)	<i>ENG</i>	9q33-q34.1	Up	1.75	32562_at
filamin-binding LIM protein-1	<i>FBLP-1</i>	1p36.13	Up	1.50	44793_s_at
fasciculation and elongation protein zeta 1 (zygin I)	<i>FEZ1</i>	11q24.2	Up	2.99	37743_at
fibronectin 1	<i>FN1</i>	2q34	Up	6.56	31719_at
intercellular adhesion molecule 2	<i>ICAM2</i>	17q23-q25	Up	1.46	590_at
immunoglobulin superfamily containing leucine-rich repeat	<i>ISLR</i>	15q23-q24	Up	1.45	38636_at
integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	<i>ITGA5</i>	12q11-q13	Up	2.48	39753_at
integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	<i>ITGAV</i>	2q31-q32	Up	1.67	39071_at
integrin, beta 5	<i>ITGB5</i>	3q21.2	Up	1.88	39754_at
milk fat globule-EGF factor 8 protein	<i>MFGE8</i>	15q25	Up	2.19	34403_at
nidogen (enactin)	<i>NID</i>	1q43	Up	1.53	35366_at
neuropilin 2	<i>NRP2</i>	2q33.3	Up	1.51	43463_at
osteoblast specific factor 2 (fasciclin I-like)	<i>OSF-2</i>	13q13.2	Up	2.35	1451_s_at
sarcoglycan, epsilon	<i>SGCE</i>	7q21-q22	Up	1.47	41449_at
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)	<i>SPOCK</i>	5q31	Up	1.76	78788_at
transforming growth factor, beta-induced, 68kD	<i>TGFBI</i>	5q31	Up	3.96	1385_at
tenascin C (hexabrachion)	<i>TNC</i>	9q33	Up	3.21	32818_at
upregulated in colorectal cancer gene 1	<i>UCC1</i>	7p14.1	Up	1.88	64397_at
extracellular link domain containing 1	<i>XLKD1</i>	11p15	Up	3.34	65731_at
protocadherin 18	<i>PCDH18</i>	4q31	Down	-1.81	59623_at
TYRO3 protein tyrosine kinase	<i>TYRO3</i>	15q15.1-q21.1	Down	-1.47	35246_at
<u>Structural protein/cytoskeleton organization</u>					
actin, alpha 2, smooth muscle, aorta	<i>ACTA2</i>	10q23.3	Up	3.13	32755_at
actin, gamma 1	<i>ACTG1</i>	17q25	Up	1.56	43831_s_at
actin related protein 2/3 complex, subunit 1B (41 kD)	<i>ARPC1B</i>	7q22.1	Up	1.90	39043_at
cofilin 1 (non-muscle)	<i>CFL1</i>	11q13	Up	1.23	33659_at
collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	<i>COL3A1</i>	2q31	Up	2.17	32488_at
collagen, type V, alpha 2	<i>COL5A2</i>	2q14-q32	Up	1.98	65797_at
FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	<i>FARP1</i>	13q32.2	Up	1.43	32148_at
fibrillin 1 (Marfan syndrome)	<i>FBN1</i>	15q21.1	Up	1.73	32535_at
filamin A, alpha (actin binding protein 280)	<i>FLNA</i>	Xq28	Up	1.69	89945_s_at
lamin A/C	<i>LMNA</i>	1q21.2-q21.3	Up	1.46	37377_i_at
lumican	<i>LUM</i>	12q21.3-q22	Up	2.41	38038_at
Microfibril-associated glycoprotein-2	<i>MAGP2</i>	12p13.1-p12.3	Up	4.65	36513_at
myosin IB	<i>MYO1B</i>	2q12-q34	Up	1.96	41439_at
protein kinase C and casein kinase substrate in neurons 2	<i>PACSN2</i>	22q13.2-q13.33	Up	1.24	57086_at
TPM1: tropomyosin 1 (alpha)	<i>TPM1</i>	15q22.1	Up	1.62	36790_at
tropomyosin 2 (beta)	<i>TPM2</i>	9p13.2-p13.1	Up	2.20	32313_at
tropomyosin 3	<i>TPM3</i>	1q21.2	Up	1.72	57840_at
tropomyosin 4	<i>TPM4</i>	19p13.1	Up	2.47	33866_at
tubulin, alpha 3	<i>TUBA3</i>	12q12-q14.3	Up	1.93	40567_at
tubulin, beta, 4	<i>TUBB4</i>	16q24.3	Up	1.38	471_f_at
villin 2 (ezrin)	<i>VIL2</i>	6q25.2-q26	Up	1.41	40103_at
erythrocyte membrane protein band 4.1 like 4B	<i>EPB41LAB</i>	9q31	Down	-2.00	64833_at
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	<i>MYL6</i>	12q13.13	Down	-1.34	33993_at
<u>Transport/carrier</u>					
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	<i>ABCC3</i>	17q22	Up	4.54	38261_at

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adaptor-related protein complex 1, sigma 2 subunit	<i>AP1S2</i>	Xp22.22	Up	1.88	56267_at
adaptor-related protein complex 2, mu 1 subunit	<i>AP2M1</i>	3q28	Up	1.29	39795_at
aquaporin 3	<i>AQP3</i>	9p13	Up	2.99	39248_at
Rho GTPase activating protein 17	<i>ARHGAP17</i>	16p12.2	Up	1.43	57053_s_at
ATP1A1: ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	<i>ATP1A1</i>	1p13	Up	1.48	87941_r_at
ATPase, Ca ²⁺ transporting, plasma membrane 1	<i>ATP2B1</i>	12q21-q23	Up	2.20	61289_at
epimorphin	<i>EPIM</i>	12q24.33	Up	1.38	41864_at
potassium channel tetramerisation domain containing 12	<i>KCTD12</i>	13q22.1	Up	2.09	38972_at
proteolipid protein 2 (colonic epithelium-enriched)	<i>PLP2</i>	Xp11.23	Up	1.42	37326_at
prostaglandin D2 synthase 21 kDa (brain)	<i>PTGDS</i>	9q34.2-q34.3	Up	6.62	38407_r_at
ribosome binding protein 1 homologue 180 kDa (dog)	<i>RRBP1</i>	20p12	Up	1.62	33212_at
solute carrier family 15, member 3	<i>SLC15A3</i>	11q12.1	Up	1.92	61277_at
solute carrier family 39 (zinc transporter), member 7	<i>SLC39A7</i>	6p21.3	Up	1.49	40329_at
transferrin receptor (p90, CD71)	<i>TFRC</i>	3q26.2-qter	Up	1.99	37324_at
cargo selection protein (mannose 6 phosphate receptor binding protein)	<i>TIP47</i>	19p13.3	Up	2.51	51002_s_at
translocation associated membrane protein 2	<i>TRAM2</i>	6p21.1-p12	Up	2.07	40051_at
transient receptor potential cation channel, subfamily V, member 2	<i>TRPV2</i>	17p11.2	Up	2.26	90306_at
apolipoprotein B (including Ag(x) antigen)	<i>APOB</i>	2p24-p23	Down	-2.74	261_s_at
aquaporin 7	<i>AQP7</i>	9p13	Down	-1.35	39568_g_at
hypothetical protein FLJ10618	<i>FLJ10618</i>	3q23	Down	-1.37	34804_at
glioblastoma amplified sequence	<i>GBAS</i>	7p12	Down	-1.42	39793_at
SEC24 related gene family, member B (<i>S. cerevisiae</i>)	<i>SEC24B</i>	4q25	Down	-1.39	35845_at
solute carrier family 16 (monocarboxylic acid transporters), member 7	<i>SLC16A7</i>	12q13	Down	-1.72	35547_at
solute carrier family 19, member 3	<i>SLC19A3</i>	2q37	Down	-1.78	86499_at
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	<i>SLC25A6</i>	Xp22.32 and Yp	Down	-1.28	40436_g_at
solute carrier family 4, sodium bicarbonate cotransporter, member 4	<i>SLC4A4</i>	4q21	Down	-1.64	35285_at
solute carrier family 5 (sodium-dependent vitamin transporter), member 6	<i>SLC5A6</i>	2p23	Down	-1.35	35256_at
syntaxin binding protein 1	<i>STXBP1</i>	9q34.1	Down	-1.43	33942_s_at
translocated promoter region (to activated MET oncogene)	<i>TPR</i>	1q25	Down	-1.24	421_at
vesicle docking protein p115	<i>VDP</i>	4q21.1	Down	-1.25	45396_at
vacuolar protein sorting 11 (yeast)	<i>VPS11</i>	11q23	Down	-1.29	32823_at
Apoptosis					
amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	<i>APP</i>	21q21.3	Up	2.49	64309_f_at
BCL2-associated athanogene 3	<i>BAG3</i>	10q25.2-q26.2	Up	1.57	48971_at
baculoviral IAP repeat-containing 3	<i>BIRC3</i>	11q22	Up	2.33	63769_at
CD14 antigen	<i>CD14</i>	5q31.1	Up	2.54	36661_s_at
Fas (TNFRSF6)-associated via death domain	<i>FADD</i>	11q13.3	Up	1.44	38755_at
immediate early response 3	<i>IER3</i>	6p21.3	Up	2.53	1237_at
interleukin 1, beta	<i>IL1B</i>	2q14	Up	2.25	39402_at
phosphoprotein enriched in astrocytes 15	<i>PEA15</i>	1q21.1	Up	1.51	32260_at
pleckstrin homology-like domain, family A, member 2	<i>PHLDA2</i>	11p15.5	Up	3.04	40237_at
thymosin, beta 10	<i>TMSB10</i>	2p11.2	Up	1.34	31481_s_at
tumour necrosis factor, alpha-induced protein 3	<i>TNFAIP3</i>	6q23	Up	2.22	595_at
tumour necrosis factor receptor superfamily, member 12A	<i>TNFRSF12A</i>	16p13.3	Up	5.03	48013_at
tumour necrosis factor receptor superfamily, member 1A	<i>TNFRSF1A</i>	12p13.2	Up	1.26	1563_s_at
tumour necrosis factor receptor superfamily, member 1B	<i>TNFRSF1B</i>	1p36.3-p36.2	Up	1.35	1583_at
B-cell CLL/lymphoma 2	<i>BCL2</i>	18q21.3	Down	-1.52	1909_at
BCL2/adenovirus E1B 19kD interacting protein 3	<i>BNIP3</i>	14q11.2-q12	Down	-1.35	38010_at
death-associated protein kinase 2	<i>DAPK2</i>	15q22.1	Down	-1.62	34912_at
RAD21 homologue (<i>S. pombe</i>)	<i>RAD21</i>	8q24	Down	-1.46	38114_at
sirtuin silent mating type information regulation 2 homologue 1 (<i>S. cerevisiae</i>)	<i>SIRT1</i>	10q22.1	Down	-1.87	64265_s_at
SON DNA binding protein	<i>SON</i>	21q22.11	Down	-1.23	39097_at
Protein biosynthesis					
DnaI (Hsp40) homologue, subfamily C, member 10	<i>DNAJC10</i>	2q32.1	Up	1.31	48849_i_at
eukaryotic translation initiation factor 2 alpha kinase 4	<i>EIF2AK4</i>	15q14	Up	1.51	76067_at

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FK506 binding protein 14, 22 kDa	<i>FKBP14</i>	7p15.1	Up	1.64	62807_at
FK506 binding protein 9 (63 kD)	<i>FKBP9</i>	7p11.1	Up	1.37	38761_s_at
glycyl-tRNA synthetase	<i>GARS</i>	7p15	Up	1.35	36581_at
seryl-tRNA synthetase 2	<i>SARS2</i>	19q13.13	Up	1.50	75337_s_at
eukaryotic translation initiation factor 4A, isoform 2	<i>EIF4A2</i>	3q28	Down	-1.53	1420_s_at
eukaryotic translation initiation factor 4B	<i>EIF4B</i>	12q13.13	Down	-1.24	39110_at
eukaryotic translation initiation factor 4E binding protein 1	<i>EIF4EBP1</i>	8p12	Down	-1.57	54152_at
KIAA0256 gene product	<i>KIAA0256</i>	15q15.2	Down	-1.34	41634_at
PABP-interacting protein 2	<i>PAIP2</i>	5q31.3	Down	-1.25	43855_at
peptidylprolyl isomerase E (cyclophilin E)	<i>PPIE</i>	1p32	Down	-1.38	34366_g_at
pumilio homologue 2 (<i>Drosophila</i>)	<i>PUM2</i>	2p22-p21	Down	-1.21	35359_at
ribosomal protein L23	<i>RPL23</i>	17q	Down	-1.28	32394_s_at
ribosomal protein L30	<i>RPL30</i>	8q22	Down	-1.27	31708_at
suppression of tumourigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	<i>ST13</i>	22q13.2	Down	-1.31	1640_at
translational inhibitor protein p14.5	<i>UK114</i>	8q22	Down	-1.43	32173_at
<u>Carbohydrate metabolism</u>					
aldo-keto reductase family 1, member B1 (aldose reductase)	<i>AKR1B1</i>	7q35	Up	1.33	36589_at
galactosidase, beta 1	<i>GLB1</i>	3p21.33	Up	1.77	37742_at
glucose phosphate isomerase	<i>GPI</i>	19q13.1	Up	1.47	88482_at
lactate dehydrogenase B	<i>LDHB</i>	12p12.2-p12.1	Up	1.33	33820_g_at
sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	<i>SMPD1</i>	11p15.4-p15.1	Up	1.31	32574_at
sulfatase modifying factor 1	<i>SUMF1</i>	3p26.2	Up	1.31	52973_at
amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	<i>AGL</i>	1p21	Down	-1.53	38253_at
dicarbonyl/L-xylulose reductase	<i>DCXR</i>	17q25.3	Down	-1.41	57729_at
genethonin 1	<i>GENX-3414</i>	4q24-q25	Down	-1.60	38975_at
insulin receptor substrate 2	<i>IRS2</i>	13q34	Down	-1.79	56338_at
KIAA0089 protein	<i>KIAA0089</i>	3p22.3	Down	-2.16	38394_at
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A	<i>MGAT4A</i>	2q12	Down	-1.32	43444_at
pyruvate carboxylase	<i>PC</i>	11q13.4-q13.5	Down	-1.77	38000_at
pyruvate dehydrogenase kinase, isoenzyme 2	<i>PKD2</i>	17q21.32	Down	-2.00	38844_at
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	<i>PFKFB1</i>	Xp11.21	Down	-1.93	33980_at
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	<i>PFKFB3</i>	10p14-p15	Down	-2.02	56246_at
TDP-glucose 4,6-dehydratase	<i>TGDS</i>	13q32.1	Down	-1.31	41667_s_at
<u>Energy pathway/electron transport</u>					
ATPase, H ⁺ transporting, lysosomal 42 kDa, V1 subunit C isoform 2	<i>ATP6VIC2</i>	2	Up	1.46	74808_s_at
NAD(P)H dehydrogenase, quinone 1	<i>NQO1</i>	16q22.1	Up	1.93	38066_at
UDP-glucose dehydrogenase	<i>UGDH</i>	4p15.1	Up	1.52	35214_at
acyl-Coenzyme A dehydrogenase, long chain	<i>ACADL</i>	2q34-q35	Down	-2.01	37523_at
acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	<i>ACADM</i>	1p31	Down	-1.91	37532_at
acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	<i>ACADS</i>	12q22-qter	Down	-1.33	39408_at
acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	<i>ACAT1</i>	11q22.3-q23.1	Down	-1.44	39678_at
biliverdin reductase B (flavin reductase (NADPH))	<i>BLVRB</i>	19q13.1-q13.2	Down	-1.49	37002_at
citrate synthase	<i>CS</i>	12p11-qter	Down	-1.38	41314_at
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	<i>ECHS1</i>	10q26.2-q26.3	Down	-1.43	37016_at
glutaryl-Coenzyme A dehydrogenase	<i>GCDH</i>	19p13.2	Down	-1.51	33314_at
monoamine oxidase A	<i>MAOA</i>	Xp11.4-p11.3	Down	-1.42	41770_at
monoamine oxidase B	<i>MAOB</i>	Xp11.4-p11.3	Down	-1.52	37628_at
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	<i>NDUFA10</i>	2q37.3	Down	-1.28	65759_at
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	<i>NDUFB2</i>	7q34	Down	-1.43	55694_at
NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	<i>NDUFS1</i>	2q33-q34	Down	-1.47	38395_at
oxidase (cytochrome c) assembly 1-like	<i>OXAIL</i>	14q11.2	Down	-1.30	39774_at
<u>Protein modification</u>					
KIAA0537 gene product	<i>ARK5</i>	12q24.11	Up	1.45	33787_at
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2)	<i>GALNT2</i>	1q41-q42	Up	1.59	65953_at

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indolethylamine <i>N</i> -methyltransferase	<i>INMT</i>	7p15.3-p15.2	Up	1.89	63798_at
NEDD8-conjugating enzyme	<i>NCE2</i>	2q37.3	Up	1.35	49057_g_at
<i>N</i> -myristoyltransferase 2	<i>NMT2</i>	10p13	Up	1.72	41656_at
palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	<i>PPT1</i>	1p32	Up	1.40	34774_at
protein tyrosine phosphatase, non-receptor type 12	<i>PTPN12</i>	7q11.23	Up	1.34	1463_at
serine/threonine kinase 38	<i>STK38</i>	6p21	Up	1.52	78801_at
likely ortholog of mouse myocytic induction/differentiation originator	<i>MIDORI</i>	15q25.2	Down	-1.99	52816_at
<i>O</i> -linked <i>N</i> -acetylglucosamine (GlcNAc)	<i>OGT</i>	Xq13	Down	-1.82	38614_s_at
protein kinase, cAMP-dependent, regulatory, type II, beta	<i>PRKAR2B</i>	7q22-q31.1	Down	-1.47	37221_at
protein tyrosine phosphatase, non-receptor type 3	<i>PTPN3</i>	9q31	Down	-1.42	1458_at
Rab geranylgeranyltransferase, beta subunit	<i>RABGGTB</i>	1p31	Down	-1.31	781_at
sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	<i>SIAT10</i>	3q12.2	Down	-2.36	39298_at
SNF1-like kinase 2	<i>SNF1LK2</i>	11q23.2	Down	-1.71	35999_r_at
<u>Nucleic acid metabolism</u>					
dihydropyrimidinase-like 2	<i>DPYSL2</i>	8p22-p21	Up	1.75	40607_at
ectonucleoside triphosphate diphosphohydrolase 2	<i>ENTPD2</i>	9q34	Up	1.40	82049_at
heterogeneous nuclear ribonucleoprotein A/B	<i>HNRPAB</i>	5q35.3	Up	1.46	38094_at
nicotinamide <i>N</i> -methyltransferase	<i>NNMT</i>	11q23.1	Up	2.12	37032_at
3'-phosphoadenosine 5'-phosphosulfate synthase 2	<i>PAPSS2</i>	10q23-q24	Up	1.81	60873_at
phosphoribosyl transferase domain containing 1	<i>PRTFDC1</i>	10p12.31	Up	4.40	49126_at
ribonuclease/angiogenin inhibitor	<i>RNH</i>	11p15.5	Up	1.21	90021_s_at
uridine phosphorylase 1	<i>UPP1</i>	7p12.3	Up	1.88	37351_at
adenylosuccinate synthase like 1	<i>ADSSLI</i>	14q32.33	Down	-2.02	48086_at
angiogenin, ribonuclease, RNase A family, 5	<i>ANG</i>	14q11.1-q11.2	Down	-1.84	1103_at
AU RNA binding protein/enoyl-Coenzyme A hydratase	<i>AUH</i>	9q22.31	Down	-1.43	37616_at
excision repair cross-complementing rodent repair deficiency, complementation group 5	<i>ERCC5</i>	13q33.3	Down	-1.42	2064_g_at
MYST histone acetyltransferase 1	<i>MYST1</i>	16p11.2	Down	-1.33	35988_i_at
ribonuclease, RNase A family, 4	<i>RNASE4</i>	14q11.1	Down	-1.56	32664_at
<u>Proteolysis/peptidolysis</u>					
a disintegrin and metalloproteinase domain 12 (meltrin alpha)	<i>ADAM12</i>	10q26.3	Up	2.08	55567_at
a disintegrin and metalloproteinase domain 9 (meltrin gamma)	<i>ADAM9</i>	8p11.21	Up	1.80	34761_r_at
a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 5	<i>ADAMTS5</i>	21q21.3	Up	1.78	47321_at
calpain 2, (m/II) large subunit	<i>CAPN2</i>	1q41-q42	Up	1.41	37001_at
cathepsin K (pyncnodysostosis)	<i>CTSK</i>	1q21	Up	2.32	38466_at
legumain	<i>LGMN</i>	14q32.1	Up	1.54	51728_at
matrix metalloproteinase 2 (gelatinase A, 72 kDa gelatinase, 72 kDa type IV collagenase)	<i>MMP2</i>	16q13-q21	Up	1.87	56572_at
phosphatidylinositol glycan, class K	<i>PIGK</i>	1p31.1	Up	1.37	57713_at
protease, serine, 23	<i>SPUVE</i>	11q14.1	Up	4.92	40078_at
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	<i>TIMP1</i>	Xp11.3-p11.23	Up	10.20	1693_s_at
ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	<i>UCHL1</i>	4p14	Up	2.03	36990_at
carboxypeptidase M	<i>CPM</i>	12q15	Down	-1.78	36708_at
aminopeptidase puromycin sensitive	<i>NPEPPS</i>	17q21	Down	-1.30	39431_at
<u>Lipid metabolism</u>					
aldehyde dehydrogenase 1 family, member A3	<i>ALDH1A3</i>	15q26	Up	3.65	36686_at
angiopoietin-like 4	<i>ANGPTL4</i>	19p13.3	Up	2.01	48753_at
apolipoprotein L, 1	<i>APOLI</i>	22q13.1	Up	2.68	49459_at
2-hydroxyphytanoyl-CoA lyase	<i>HPCL2</i>	3p25.1	Up	1.43	53979_at
phospholipid transfer protein	<i>PLTP</i>	20q12-q13.1	Up	1.57	40081_at
acetyl-Coenzyme A synthetase 2 (ADP forming)	<i>ACAS2</i>	20q11.21	Down	-1.37	57033_at
1-acylglycerol-3-phosphate <i>O</i> -acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	<i>AGPAT2</i>	9q34.3	Down	-1.37	32837_at
choline/ethanolaminephosphotransferase	<i>CEPT1</i>	1p13.1	Down	-1.56	84454_at
oxysterol binding protein-like 1A	<i>OSBPL1A</i>	18q11.1	Down	-1.38	36689_at
phosphodiesterase 3A, cGMP-inhibited	<i>PDE3A</i>	12p12	Down	-1.81	61343_at

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sterol-C5-desaturase (ERG3 delta-5-desaturase homologue, fungal)-like	<i>SC5DL</i>	11q23.3	Down	-1.64	33421_s_at
transmembrane 7 superfamily, member 2	<i>TM7SF2</i>	11q13	Down	-1.53	35628_at
<u>Amino acid metabolism</u>					
catechol- <i>O</i> -methyltransferase	<i>COMT</i>	22q11.21	Up	1.30	34651_at
glutaminase	<i>GLS</i>	2q32-q34	Up	1.76	43839_f_at
methionine adenosyltransferase II, alpha	<i>MAT2A</i>	2p11.2	Up	1.37	80415_at
ornithine decarboxylase 1	<i>ODC1</i>	2p25	Up	1.37	1081_at
aldehyde dehydrogenase 6 family, member A1	<i>ALDH6A1</i>	14q24.2	Down	-2.27	32676_at
branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)	<i>BCKDHA</i>	19q13.1-q13.2	Down	-1.56	37704_at
glutamate-ammonia ligase (glutamine synthase)	<i>GLUL</i>	1q31	Down	-2.30	40522_at
glutamic pyruvate transaminase (alanine aminotransferase) 2	<i>GPT2</i>	16q12.1	Down	-1.64	54066_at
methylenetetrahydrofolate dehydrogenase (NADP ⁺ dependent), methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	<i>MTHFD1</i>	14q24	Down	-1.41	673_at
serine hydroxymethyltransferase 1 (soluble)	<i>SHMT1</i>	17p11.2	Down	-1.97	34738_at
<u>Response to stress</u>					
superoxide dismutase 2, mitochondrial	<i>SOD2</i>	6q25.3	Up	1.42	45237_at
serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	<i>SERPINH1</i>	11q13.5	Up	1.38	39166_s_at
heat shock 70 kD protein 5 (glucose-regulated protein, 78kD)	<i>HSPA5</i>	9q33-q34.1	Up	1.44	36614_at
hypoxia up-regulated 1	<i>HYOU1</i>	11q23.1-q23.3	Up	1.24	33863_at
PDZ and LIM domain 1 (elfin)	<i>PDLIM1</i>	10q22-q26.3	Up	1.79	36937_s_at
thioredoxin reductase 1	<i>TXNRD1</i>	12q23-q24.1	Up	1.51	39425_at
peroxiredoxin 6	<i>PRDX6</i>	1q23.3	Down	-1.31	39354_at
serine/threonine kinase 25 (STE20 homologue, yeast)	<i>STK25</i>	2q37.3	Down	-1.21	40104_at
cold inducible RNA binding protein	<i>CIRBP</i>	19p13.3	Down	-1.36	39864_at
<u>Cell growth and maintenance</u>					
CDC42 effector protein (Rho GTPase binding) 4	<i>CDC42EP4</i>	17q24-q25	Up	1.66	34776_at
connective tissue growth factor	<i>CTGF</i>	6q23.1	Up	4.67	36638_at
exostoses (multiple) 1	<i>EXT1</i>	8q24.11-q24.13	Up	1.23	222_at
FYN oncogene related to SRC, FGR, YES	<i>FYN</i>	6q21	Up	1.67	2039_s_at
procollagen C-endopeptidase enhancer	<i>PCOLCE</i>	7q22	Up	1.48	31609_s_at
protease, serine, 11 (IGF binding)	<i>PRSS11</i>	10q26.3	Up	1.74	48727_at
hepatic leukemia factor	<i>HLF</i>	17q22	Down	-2.05	38627_at
<u>Fatty acid metabolism</u>					
caritine palmitoyltransferase I, liver	<i>CPT1A</i>	11q13.1-q13.2	Up	1.95	74870_at
acetyl-Coenzyme A carboxylase beta	<i>ACACB</i>	12q24.1	Down	-1.66	38529_at
acyl-CoA synthetase long-chain family member 1	<i>ACSL1</i>	4q34-q35	Down	-1.53	40082_at
dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	<i>DCI</i>	16p13.3	Down	-1.42	37982_at
fatty acid synthase	<i>FASN</i>	17q25	Down	-1.84	38429_at
L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	<i>HADHSC</i>	4q22-q26	Down	-1.86	38768_at
propionyl Coenzyme A carboxylase, alpha polypeptide	<i>PCCA</i>	13q32	Down	-1.57	1348_s_at
PCCB: propionyl Coenzyme A carboxylase, beta polypeptide	<i>PCCB</i>	3q21-q22	Down	-1.48	36561_at
<u>Blood coagulation</u>					
plasminogen activator, urokinase	<i>PLAU</i>	10q24	Up	1.65	37310_at
plasminogen activator, urokinase receptor	<i>PLAUR</i>	19q13	Up	3.65	189_s_at
protein S (alpha)	<i>PROS1</i>	3p11-q11.2	Up	1.78	35752_s_at
serine (or cysteine) proteinase inhibitor, clade E(nexin, plasminogen activator inhibitor type 1), member 1	<i>SERPINE1</i>	7q21.3-q22	Up	2.61	38125_at
coagulation factor XIII, A1 polypeptide	<i>F13A1</i>	6p25.3-p24.3	Up	3.63	38052_at
von Willebrand factor	<i>VWF</i>	12p13.3	Up	2.34	48871_at