Supplemental Table 1. Basic patients characteristics of the cohort used for serum HGF measurements.

SAMPLE	DIAGNOSIS	DISEASE STATUS	GENDER	RACE	AGE	FUNCTIONAL STATUS*
1	Healthy Control	No Cancer	F	W		N/A
2	Healthy Control	No Cancer	F	W		N/A
3	Healthy Control	No Cancer	M	H		N/A
4	Healthy Control	No Cancer	M	W		N/A
5	Healthy Control	No Cancer	M	H		N/A
6	Healthy Control	No Cancer	F	H		N/A
7	Healthy Control	No Cancer	F	H		N/A
8	ACC	DM	F	W		1,3
9	ACC	DM	M	H		0
10	ACC	Preop	F	W		1
11	ACC	DM	F	W		1
12	ACC	DM	M	H		1
13	ACC	DM	M	W		0
14	ACC	DM	M	W		0
15	ACC	DM	F	W		0
16	ACC	DM	F	W		1
17	ACC	DM	F	W		1,3
18	ACC	DM	M	H		0
19	ACC	DM	F	W		1,3
20	ACC	DM	M	W		2
21	ACC	DM	M	A		0
22	ACC	DM	F	W		1
23	ACC	DM	F	W		3
24	ACC	DM	F	W		1,3
25	ACC	DM	M	W		0
26	ACC	DM	F	W		0
27	ACC	DM	F	W		1,3
28	ACC	DM	M	H		1
29	ACC	DM	F	B		3

* Functional Status (0: Non functioning, 1: Cortisol, 2 Aldosterone, 3, Androgens), DM: Distal metastasis

Supplemental Table 2. Basic patients characteristics of second TMA.

SAMPLE	DIAGNOSIS	GENDER	AGE AT DIAGNOSIS	HORMONAL STATUS	FIRST SURGERY	TUMOR SIZE	STAGE	WEISS SCORE	RESECTION MARGIN	ADJUVANT MITOTANE	STATUS AT FOLLOW-UP
1	Adenoma	F	49	NF	lap	2.2	NA	0	NA	NA	Alive
2	Adenoma	M	72	FC	lap	2.5	NA	0	NA	NA	Alive
3	Adenoma	F	35	FC	lap	4	NA	0	NA	NA	Alive
4	Adenoma	M	55	NF	open	9	NA	0	NA	NA	Alive
5	Adenoma	M	50	NF	open	4.4	NA	0	NA	NA	Alive
6	Adenoma	M	51	NF	lap	2.2	NA	0	NA	NA	Alive
7	Adenoma	F	48	NF	lap	3	NA	0	NA	NA	Alive
8	Adenoma	M	51	NF	lap	2.5	NA	0	NA	NA	Alive
9	Adenoma	F	51	NF	lap	3	NA	0	NA	NA	Alive
10	Adenoma	M	47	NF	lap	2.1	NA	0	NA	NA	Alive
11	Adenoma	M	69	NF	lap	2.2	NA	0	NA	NA	Alive
12	Adenoma	M	49	NF	open	6	NA	0	NA	NA	Alive
13	Adenoma	F	82	NF	lap	4.2	NA	0	NA	NA	Alive
14	Adenoma	F	49	NF	lap	3.2	NA	0	NA	NA	Alive
15	Adenoma	M	33	NF	open	4	NA	0	NA	NA	Alive
1	ACC-Naive	F	56	FC	open	8	2	5	R0	No	Alive
2	ACC-Naive	F	53	FC	open	6.5	2	8	Rx	Yes	Dead
3	ACC-Naive	F	51	FS	open	10	2	8	Rx	Yes	Alive
4	ACC-Naive	M	79	FA	open	9	2	6	R0	No	Dead
5	ACC-Naive	F	28	FC, FS	open	26	4	6	R1	Yes	Dead
6	ACC-Naive	M	74	FC, FS	open	10.8	3	7	R0	No	Dead
7	ACC-Naive	F	58	FC	open	11	2	8	R0	No	Alive
8	ACC-Naive	F	50	FC	open	10	3	8	R0	No	Alive
9	ACC-Naive	F	55	FC,FS	open	12.5	2	7	R0	No	Dead
10	ACC-Naive	M	75	NF	open	13	2	4	R0	Yes	Alive
11	ACC-Naive	M	86	NF	open	15	3	9	R0	No	Dead
12	ACC-Naive	F	48	FA, FS	open	9	3	8	R0	Yes	Dead
13	ACC-Naive	F	61	NF	open	13	2	7	R0	Yes	Alive
14	ACC-Naive	F	30	FC,FS	open	9	2	6	R0	Yes	Alive
15	ACC-Naive	M	38	NF	open	15	4	5	R0	Yes	Alive
16	ACC-Naive	F	45	FC	open	8.2	3	7	R1	Yes	Alive
17	ACC-Naive	M	43	NF	open	23	3	6	R0	No	Dead
18	ACC-Naive	F	33	NF	open	13.5	3	4	Rx	Yes	Alive
19	ACC-Naive	M	51	FC	open	19	3	9	R0	Yes	Dead
20	ACC-Naive	M	59	NF	open	12.5	2	6	R0	No	Alive
21	ACC-Naive	M	38	FC	open	9	3	4	R0	Yes	Alive
22	ACC-Naive	F	66	NF	open	8	4	7	RX	No	Dead
23	ACC-Naive	F	76	NF	open	15	3	9	R0	Yes	Dead

24	ACC-Naive	M	44	NF	open	25	3	9	R1	Yes	Dead
25	ACC-Naive	F	53	NF	open	12	3	8	R0	Yes	Alive
26	ACC-Naive	F	28	FC	open	7	3	7	R0	Yes	Alive
27	ACC-Naive	M	60	FC	open	15	2	8	R0	No	Dead
28	ACC-Naive	M	55	NF	open	4.5	1	6	R0	No	Alive

NF: nonfunctioning, FC: cortisol producing, FA: Aldosterone producing, FS: Androgens producing, R0: Complete surgical resection, R1: microscopically positive resection margins. Lap: laparoscopic resection, Open: open adrenalectomy
Tumor size (cm). Age at diagnosis (year)

Supplemental Table 3. Genes with significantly (*P* ≤ 0.05, absolute value of log ratio > 0.1) changed expression in tumors from ACC patients (dataset GSE10927) relative to expression in normal adrenocortical tissues.

PROBE	GENE SYMBOL	GENE TITLE	LOG RATIO (LOG10)	*P*- VALUE *
1007_s_at	DDR1	discoidin domain receptor family; member 1	0.9648	0.0022
1053_at	RFC2	replication factor C (activator 1) 2; 40kDa	0.7519	0.0051
1552272_a_at	MGC24975	hypothetical protein MGC24975	0.375	0.0051
1552277_a_at	C9orf30	chromosome 9 open reading frame 30	1.0681	0.0045
1552287_s_at	AFG3L1	AFG3 ATPase family gene 3-like 1 (S. cerevisiae)	0.8205	0.0055
1552304_at	ALG10	asparagine-linked glycosylation 10 homolog (yeast; alpha-1;2-glucosyltransferase)	0.3158	0.0194
1552306_at	ALG10	asparagine-linked glycosylation 10 homolog (yeast; alpha-1;2-glucosyltransferase)	0.5368	0.0132
1552312_a_at	MFAP3	microfibrillar-associated protein 3	0.8599	0.0038
1552325_at	CCDC11	coiled-coil domain containing 11	0.1137	0.0464
1552330_at	MGC16385	hypothetical protein MGC16385	1.4018	0.0011
1552343_s_at	PDE7A	phosphodiesterase 7A	0.2148	0.0378
1552347_at	CRYZL1	crystallin; zeta (quinone reductase)-like 1	0.8002	0.0072
1552399_a_at	BRF1	BRF1 homolog; subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	0.1308	0.0345
1552400_a_at	C15orf27	chromosome 15 open reading frame 27	0.8214	0.0068
1552417_a_at	NEDD1	neural precursor cell expressed; developmentally down-regulated 1	0.8595	0.0027
1552427_at	ZNF485	zinc finger protein 485	0.248	0.0433
1552470_a_at	ABHD11	abhydrolase domain containing 11	0.3619	0.038
1552472_a_at	CENTB2	centaurin; beta 2	0.4121	0.008
1552518_s_at	MTBP	Mdm2; transformed 3T3 cell double minute 2; p53 binding protein (mouse) binding protein; 104kDa	0.2453	0.0026
1552546_a_at	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	0.1949	0.0114
1552563_a_at	C8orf6	chromosome 8 open reading frame 6	0.3558	0.0385
1552612_at	CDC42SE2	CDC42 small effector 2	1.0065	0.0004
1552613_s_at	CDC42SE2	CDC42 small effector 2	1.17	0
1552618_at	STX6	syntaxin 6	0.664	0.0133
1552619_a_at	ANLN	anillin; actin binding protein	3.11	0
1552621_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related, RPB11b2 protein	2.238	0

1552622_s_at	LOC441259	DNA directed RNA polymerase II polypeptide J-related, PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like, RPB11b2 protein, similar to postmeiotic segregation increased 2-like 2	2.1935	0
1552627_a_at	ARHGAP5	Rho GTPase activating protein 5	1.0846	0.0116
1552628_a_at	HERPUD2	HERPUD family member 2	0.3847	0.0163
1552634_a_at	ZNF101	zinc finger protein 101	0.4719	0.042
1552648_a_at	TNFRSF10A	tumor necrosis factor receptor superfamily; member 10a	0.4232	0.0464
1552656_s_at	UHMK1	U2AF homology motif (UHM) kinase 1	0.4209	0.0341
1552660_a_at	C5orf22	chromosome 5 open reading frame 22	1.353	0.0074
1552670_a_at	LOC286044	hypothetical protein LOC286044	1.2667	0.0098
1552678_a_at	USP28	ubiquitin specific peptidase 28	0.4335	0.0471
1552680_a_at	CASC5	cancer susceptibility candidate 5	0.5356	0.0038
1552682_a_at	CASC5	cancer susceptibility candidate 5	0.2743	0.0077
1552689_at	CASKIN1	CASK interacting protein 1	0.3168	0.0058
1552695_a_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	0.7187	0.0341
1552705_at	DUSP19	dual specificity phosphatase 19	0.3936	0.0398
1552708_a_at	DUSP19	dual specificity phosphatase 19	0.1964	0.0261
1552716_at	FLJ23577	KPL2 protein	0.7467	0.0005
1552729_at	SNHG7	small nucleolar RNA host gene (non-protein coding) 7	0.2819	0.006
1552735_at	PCDHGA4	protocadherin gamma subfamily A; 4	1.6657	0.0106
1552740_at	C2orf15	chromosome 2 open reading frame 15	0.2168	0.0076
1552765_x_at	TMEM67	transmembrane protein 67	0.2931	0.0002
1552770_s_at	ZNF563	zinc finger protein 563	0.5457	0.0022
1552774_a_at	SLC25A27	solute carrier family 25; member 27	0.756	0.0105
1552782_at	SLC44A5	solute carrier family 44; member 5	0.6179	0.0091
1552783_at	ZNF417	zinc finger protein 417	0.3104	0.0001
1552792_at	SOCS4	suppressor of cytokine signaling 4	0.2315	0.0326
1552793_at	C8orf31	chromosome 8 open reading frame 31	1.3836	0.0207
1552812_a_at	SENP1	SUMO1/sentrin specific peptidase 1	0.4322	0.0061
1552816_at	NXNL2	nucleoredoxin-like 2	0.1118	0.035
1552845_at	CLDN15	claudin 15	0.4397	0.0001
1552914_a_at	CD276	CD276 molecule	0.4261	0.0216
1552921_a_at	FIGNL1	fidgetin-like 1	1.0777	0.0051
1552927_at	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	0.2526	0.0157
1552928_s_at	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	0.4702	0.0056
1552937_s_at	ATRIP	ATR interacting protein, three prime repair exonuclease 1	0.2337	0.0268
1552946_at	ZNF114	zinc finger protein 114	0.7847	0.0149

1552947_x_at	ZNF114	zinc finger protein 114	0.5909	0.0155
1552978_a_at	SCAMP1	secretory carrier membrane protein 1	1.4371	0.0032
1553015_a_at	RECQL4	RecQ protein-like 4	0.4043	0.0168
1553099_at	TIGD1	tigger transposable element derived 1	1.8474	0
1553106_at	C5orf24	chromosome 5 open reading frame 24	0.9766	0.0094
1553107_s_at	C5orf24	chromosome 5 open reading frame 24	0.6234	0.047
1553108_at	C5orf24	chromosome 5 open reading frame 24	0.7137	0.0078
1553112_s_at	CDK8	cyclin-dependent kinase 8	1.3157	0.0134
1553117_a_at	STK38	serine/threonine kinase 38	0.9321	0.0135
1553122_s_at	RBAK	RB-associated KRAB zinc finger	0.7681	0.0028
1553145_at	FLJ39653	hypothetical FLJ39653	1.2383	0.0018
1553148_a_at	SNX13	sorting nexin 13	0.8032	0.0075
1553158_at	C3orf34	chromosome 3 open reading frame 34	0.3219	0.0378
1553159_at	DNAH11	dynein; axonemal; heavy chain 11	1.3521	0.0447
1553162_x_at	C19orf55	chromosome 19 open reading frame 55	0.3884	0.0011
1553167_a_at	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.275	0.0476
1553172_at	ZNF777	zinc finger protein 777	0.4541	0.0038
1553185_at	RASEF	RAS and EF-hand domain containing	1.2088	0.0003
1553186_x_at	RASEF	RAS and EF-hand domain containing	1.4138	0.0001
1553192_at	ZNF441	zinc finger protein 441	0.5464	0.005
1553193_at	ZNF441	zinc finger protein 441	0.5759	0.005
1553216_at	ZNF41	zinc finger protein 41	0.2711	0.0215
1553217_s_at	ZNF41	zinc finger protein 41	0.4608	0.0056
1553225_s_at	ZNF75	zinc finger protein 75 (D8C6)	1.127	0.002
1553227_s_at	BRWD1	bromodomain and WD repeat domain containing 1	0.5544	0.0485
1553229_at	ZNF572	zinc finger protein 572	0.2494	0.0183
1553244_at	FANCB	Fanconi anemia; complementation group B	0.165	0.0196
1553247_a_at	ZNF709	zinc finger protein 709	0.2313	0.0096
1553252_a_at	BRWD3	bromodomain and WD repeat domain containing 3	0.5739	0.0259
1553271_at	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0.5305	0.0065
1553274_a_at	C6orf151	chromosome 6 open reading frame 151	0.715	0.0165
1553286_at	ZNF555	zinc finger protein 555	0.8484	0.002
1553299_at	RP4-621O15.2	hypothetical protein FLJ31401	0.388	0.0335
1553300_a_at	DGKH	diacylglycerol kinase; eta	0.1537	0.0024
1553301_a_at	TMEM182	transmembrane protein 182	0.1412	0.0336
1553336_a_at	MIER3	mesoderm induction early response 1; family member 3	0.2286	0.007

1553349_at	ARID2	AT rich interactive domain 2 (ARID; RFX-like)	1.6355	0.0001
1553387_at	ATM	ataxia telangiectasia mutated	0.1777	0.0235
1553423_a_at	SLFN13	schlafen family member 13	0.7257	0.0069
1553459_at	FLJ39660	hypothetical protein FLJ39660	0.1993	0.0114
1553508_at	MDS2	myelodysplastic syndrome 2 translocation associated	0.1236	0.0179
1553528_a_at	TAF5	TAF5 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 100kDa	0.788	0.0086
1553542_at	CCDC125	coiled-coil domain containing 125	0.303	0.0057
1553625_at	FAM98B	family with sequence similarity 98; member B	0.2638	0.0005
1553651_at	C18orf54	chromosome 18 open reading frame 54	0.1384	0.0108
1553675_at	KLC4	kinesin light chain 4	0.1517	0.0206
1553677_a_at	TIPRL	TIP41; TOR signaling pathway regulator-like (S. cerevisiae)	0.5755	0.026
1553679_s_at	VKORC1L1	vitamin K epoxide reductase complex; subunit 1-like 1	0.3831	0.0234
1553685_s_at	SP1	Sp1 transcription factor	0.8136	0.0081
1553691_at	B3GALNT2	beta-1;3-N-acetylgalactosaminyltransferase 2	0.4995	0.0384
1553693_s_at	CBR4	carbonyl reductase 4	0.8991	0.0005
1553696_s_at	ZNF569	zinc finger protein 569	0.6621	0.0242
1553697_at	C1orf96	chromosome 1 open reading frame 96	0.2456	0.013
1553698_a_at	C1orf96	chromosome 1 open reading frame 96	0.3637	0.0298
1553703_at	ZNF791	zinc finger protein 791	0.8554	0
1553704_x_at	ZNF791	zinc finger protein 791	0.8549	0.0001
1553710_at	C4orf39	chromosome 4 open reading frame 39	0.4611	0.0306
1553711_a_at	C4orf39	chromosome 4 open reading frame 39	0.3447	0.0159
1553717_at	KCTD7	potassium channel tetramerisation domain containing 7	0.2889	0.0014
1553732_s_at	CCDC123	coiled-coil domain containing 123	0.6076	0.0004
1553750_a_at	FAM76B	family with sequence similarity 76; member B	0.4087	0.0462
1553764_a_at	JUB	jub; ajuba homolog (Xenopus laevis)	1.2362	0.0114
1553781_at	ZC3HAV1L	zinc finger CCCH-type; antiviral 1-like	0.2033	0.017
1553798_a_at	FBXL13	F-box and leucine-rich repeat protein 13	1.5057	0.0027
1553810_a_at	KIAA1524	KIAA1524	0.4442	0.0005
1553815_a_at			0.3342	0.042
1553852_at	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	0.3125	0.0226
1553868_a_at	C5orf36	chromosome 5 open reading frame 36	0.2433	0.0083
1553885_x_at	ZNF99	zinc finger protein 99	0.2329	0.0449
1553901_x_at	ZNF486	zinc finger protein 486	0.2112	0.0223

1553909_x_at	C10orf6	chromosome 10 open reading frame 6	0.7169	0.0067
1553957_at	ZNF564	zinc finger protein 564	0.8486	0.0004
1553976_a_at	RP11-529I10.4	deleted in a mouse model of primary ciliary dyskinesia	1.3594	0.0006
1553987_at	C12orf47	chromosome 12 open reading frame 47	0.7792	0.007
1553990_at	C16orf79	chromosome 16 open reading frame 79	0.6161	0.0001
1553992_s_at	NBR2	neighbor of BRCA1 gene 2	0.7669	0.0395
1553993_s_at	MED25	mediator complex subunit 25	0.4788	0.0146
1553997_a_at	ASPHD1	aspartate beta-hydroxylase domain containing 1	1.1626	0.0197
1554006_a_at	LLGL2	lethal giant larvae homolog 2 (Drosophila)	0.188	0.0472
1554019_s_at	C6orf182	chromosome 6 open reading frame 182	0.3704	0.0015
1554020_at	BICD1	bicaudal D homolog 1 (Drosophila)	0.7578	0.0132
1554021_a_at	ZNF12	zinc finger protein 12	1.0387	0
1554026_a_at	MYO10	myosin X	0.5995	0.0348
1554029_a_at	KIAA0372	KIAA0372	1.2766	0.002
1554052_at	CNOT1	CCR4-NOT transcription complex; subunit 1	0.5238	0.003
1554057_at	LOC645676	hypothetical LOC645676	0.6006	0.0287
1554077_a_at	TMEM53	transmembrane protein 53	0.8538	0.0495
1554079_at	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	1.7385	0.0004
1554095_at	RBM33	RNA binding motif protein 33	0.3507	0.0298
1554098_at	SPIN3	spindlin family; member 3	0.1662	0.0241
1554101_a_at	TMTC4	transmembrane and tetratricopeptide repeat containing 4	0.2532	0.018
1554102_a_at	TMTC4	transmembrane and tetratricopeptide repeat containing 4	0.3492	0.0279
1554113_a_at	SLC4A8	solute carrier family 4; sodium bicarbonate cotransporter; member 8	0.5411	0.0034
1554119_at	C16orf57	chromosome 16 open reading frame 57	0.146	0.0436
1554127_s_at	MSRB3	methionine sulfoxide reductase B3	1.6199	0.0046
1554152_a_at	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0.6538	0.045
1554154_at	GDAP2	ganglioside induced differentiation associated protein 2	0.4415	0.0355
1554160_a_at	ZNF446	zinc finger protein 446	0.3306	0.0003
1554168_a_at	SH3KBP1	SH3-domain kinase binding protein 1	0.8027	0.0032
1554178_a_at	FAM126B	family with sequence similarity 126; member B	0.8849	0.0051
1554193_s_at	MANEA	mannosidase; endo-alpha	0.2381	0.0397
1554216_at	CCDC132	coiled-coil domain containing 132	0.2004	0.0099
1554217_a_at	CCDC132	coiled-coil domain containing 132	0.6301	0.0012
1554229_at	LOC153222	adult retina protein	0.643	0.005

1554249_a_at	ZNF638	zinc finger protein 638	0.5013	0.0417
1554250_s_at	TRIM73	tripartite motif-containing 73	0.867	0.0052
1554260_a_at	FRYL	FRY-like	1.0652	0.0005
1554264_at	CKAP2	cytoskeleton associated protein 2	0.1981	0.0067
1554271_a_at	CENPL	centromere protein L	1.2677	0.0013
1554277_s_at	FANCM	Fanconi anemia; complementation group M	0.3091	0.0004
1554287_at	TRIM4	tripartite motif-containing 4	0.4646	0.0025
1554290_at	HERC3	hect domain and RLD 3	0.282	0.0234
1554292_a_at	KIAA0701	KIAA0701 protein	0.2663	0.0277
1554294_s_at	TTBK2	tau tubulin kinase 2	0.1837	0.0071
1554298_a_at	WDR49	WD repeat domain 49	0.1045	0.0333
1554310_a_at	EIF4G3	eukaryotic translation initiation factor 4 gamma; 3	0.2307	0.0264
1554316_at	PGLS	6-phosphogluconolactonase	0.3009	0.0053
1554321_a_at	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	1.0244	0.0471
1554324_s_at	DYNC2LI1	dynein; cytoplasmic 2; light intermediate chain 1	0.4186	0.0002
1554327_a_at	CANT1	calcium activated nucleotidase 1	0.3613	0.0262
1554345_a_at	GIN1	gypsy retrotransposon integrase 1	0.6006	0.0193
1554348_s_at	CDKN2AIPNL	CDKN2A interacting protein N-terminal like	0.2963	0.0083
1554390_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.137	0.0105
1554408_a_at	TK1	thymidine kinase 1; soluble	1.0537	0.0064
1554414_a_at	OSGIN2	oxidative stress induced growth inhibitor family member 2	0.938	0.0308
1554424_at	FIP1L1	FIP1 like 1 (S. cerevisiae)	0.2466	0.0347
1554433_a_at	ZNF146	zinc finger protein 146	1.3485	0.0084
1554447_at	LOC554203	hypothetical LOC554203	0.7564	0.0386
1554448_at	LOC554203	hypothetical LOC554203	0.2112	0.0414
1554449_at	MIER3	mesoderm induction early response 1; family member 3	0.4655	0.0064
1554450_s_at	MIER3	mesoderm induction early response 1; family member 3	0.878	0.0057
1554451_s_at	CIP29	DnaJ (Hsp40) homolog; subfamily C; member 14, cytokine induced protein 29 kDa	0.7922	0.0156
1554452_a_at	HIG2	hypoxia-inducible protein 2	2.2394	0.0005
1554455_at	LINS1	lines homolog 1 (Drosophila)	0.6276	0.0377
1554456_a_at	LINS1	lines homolog 1 (Drosophila)	1.0125	0.0033
1554465_s_at	ZNF673	zinc finger protein 673, zinc finger protein 674	0.4093	0.0453
1554472_a_at	PHF20L1	PHD finger protein 20-like 1	0.6935	0.0102
1554478_a_at	HEATR3	HEAT repeat containing 3	0.4793	0.0418
1554487_a_at	CREBL1	cAMP responsive element binding protein-like 1	0.2608	0.0246
1554501_at	TSC22D4	TSC22 domain family; member 4	1.1582	0.0011
1554512_a_at	CCDC123	coiled-coil domain containing 123	0.4573	0.0009

1554513_s_at	CCDC123	coiled-coil domain containing 123	0.7337	0.0003
1554539_a_at	RHOF	ras homolog gene family; member F (in filopodia)	1.2286	0.0025
1554553_s_at	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	1.4627	0
1554555_a_at	SETD6	SET domain containing 6	0.5424	0.0061
1554572_a_at	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.9507	0.0055
1554577_a_at	PSMD10	proteasome (prosome; macropain) 26S subunit; non-ATPase; 10	0.8939	0.0189
1554588_a_at	TTC30B	tetratricopeptide repeat domain 30B	1.1072	0
1554614_a_at	PTBP2	polypyrimidine tract binding protein 2	0.6384	0.0336
1554618_at	HRBL	HIV-1 Rev binding protein-like	0.3355	0.0038
1554619_at	LOC153364	similar to metallo-beta-lactamase superfamily protein	0.3394	0.0025
1554628_at	ZNF57	zinc finger protein 57	1.7436	0.0001
1554637_a_at	CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	0.7486	0.0013
1554638_at	ZFYVE16	zinc finger; FYVE domain containing 16	0.9933	0.0189
1554696_s_at	TYMS	thymidylate synthetase	2.3347	0.0006
1554697_at	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif; 9	0.4274	0.0463
1554704_at	ATP8B3	ATPase; Class I; type 8B; member 3	1.311	0.0027
1554723_x_at			0.1008	0.0103
1554726_at	ZNF655	zinc finger protein 655	1.1302	0.0051
1554740_a_at	IPP	intracisternal A particle-promoted polypeptide	0.6963	0.0156
1554761_a_at	HEATR2	HEAT repeat containing 2	0.5912	0.0089
1554762_a_at	WWC2	WW and C2 domain containing 2	0.3031	0.0277
1554767_s_at	CRYZL1	crystallin; zeta (quinone reductase)-like 1	0.5838	0.0461
1554768_a_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	3.1648	0
1554769_at	ZNF785	zinc finger protein 785	1.0149	0.0007
1554770_x_at	ZNF785	zinc finger protein 785	1.0614	0.0013
1554771_at		CDNA clone IMAGE:4300887	0.5365	0.0053
1554780_a_at	PHTF2	putative homeodomain transcription factor 2	0.4238	0.003
1554789_a_at	PDE8B	phosphodiesterase 8B	2.6635	0.0002
1554794_a_at	UBE3C	ubiquitin protein ligase E3C	0.6854	0.0057
1554808_at	ACP1	acid phosphatase 1; soluble	0.1206	0.0177
1554810_at	PLA2G4C	phospholipase A2; group IVC (cytosolic; calcium-independent)	0.4347	0.01
1554822_at	PHTF2	putative homeodomain transcription factor 2	0.3471	0.0047
1554873_at	CSPP1	centrosome and spindle pole associated protein 1	0.2541	0.0087
1554878_a_at	ABCD3	ATP-binding cassette; sub-family D (ALD); member 3	1.0523	0.02

1554883_a_at	ERCC8	excision repair cross-complementing rodent repair deficiency; complementation group 8	0.9533	0.0065
1554885_a_at	PRIM2	primase; DNA; polypeptide 2 (58kDa)	0.7212	0.0044
1554889_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	0.4018	0.003
1554890_a_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	0.6569	0.0233
1554933_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.3925	0.0119
1554946_at		CDNA FLJ39613 fis; clone SKNSH2009357	0.258	0.045
1554958_at	ZNF641	zinc finger protein 641	0.6297	0.0356
1554962_a_at	FGFR4	fibroblast growth factor receptor 4	0.291	0.0327
1554988_at	SLC9A11	solute carrier family 9; member 11	0.1282	0.0294
1555004_a_at	RBL1	retinoblastoma-like 1 (p107)	0.2824	0.0258
1555014_x_at		OK/SW-cl.92	1.4522	0.0019
1555015_a_at	ZNF398	zinc finger protein 398	0.3589	0.0106
1555039_a_at	ABCC4	ATP-binding cassette; sub-family C (CFTR/MRP); member 4	0.2657	0.0157
1555057_at	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4; 18kDa (NADH-coenzyme Q reductase)	0.3912	0.0026
1555106_a_at	CTDSPL2	CTD (carboxy-terminal domain; RNA polymerase II; polypeptide A) small phosphatase like 2	1.0225	0.0136
1555107_a_at	KIAA1530	KIAA1530 protein	0.1443	0.0136
1555110_a_at	KLHL3	kelch-like 3 (Drosophila)	0.151	0.0489
1555125_at	C21orf66	chromosome 21 open reading frame 66	0.7845	0.004
1555146_at	ATF2	activating transcription factor 2	0.3705	0.0036
1555153_s_at	FCHO2	FCH domain only 2	0.1478	0.0174
1555192_at	ZNF277P	zinc finger protein 277 pseudogene	0.3303	0.0041
1555193_a_at	ZNF277P	zinc finger protein 277 pseudogene	0.7723	0.0161
1555227_a_at	MANEA	mannosidase; endo-alpha	0.1314	0.0045
1555243_x_at	C8orf59	chromosome 8 open reading frame 59	0.3546	0.04
1555247_a_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	1.7908	0
1555259_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	0.6597	0.0123
1555262_a_at	MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	0.3056	0.0001
1555274_a_at	SELI	selenoprotein I	1.1645	0.0033
1555303_at			0.6865	0.0057
1555307_at	TTF2	transcription termination factor; RNA polymerase II	0.2201	0.0154
1555325_s_at	ZNF26	zinc finger protein 26	0.534	0.01
1555326_a_at	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	1.3521	0.0397
1555330_at	GCLC	glutamate-cysteine ligase; catalytic subunit	0.2035	0.0085

1555334_s_at	SLC30A5	solute carrier family 30 (zinc transporter); member 5	0.8814	0.0388
1555337_a_at	ZNF317	zinc finger protein 317	0.5591	0.0104
1555347_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.2867	0.0097
1555350_at	PPHLN1	periphilin 1	0.317	0.002
1555358_a_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	0.3215	0.0183
1555370_a_at	CAMTA1	calmodulin binding transcription activator 1	1.3313	0.0302
1555373_at	C21orf114	chromosome 21 open reading frame 114	0.3892	0.0007
1555391_a_at	ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 8	0.1471	0.0178
1555408_at	BAGE2	B melanoma antigen family; member 2, B melanoma antigen family; member 4	0.4428	0.0328
1555409_a_at	BAGE2	B melanoma antigen family; member 2, B melanoma antigen family; member 3, B melanoma antigen family; member 5, myeloid/lymphoid or mixed-lineage leukemia 3	0.4191	0.0211
1555412_at	FBXL21	F-box and leucine-rich repeat protein 21	1.0621	0.0496
1555448_at	C14orf108	chromosome 14 open reading frame 108	0.3295	0.012
1555460_a_at	SLC39A6	solute carrier family 39 (zinc transporter); member 6	1.5544	0.0015
1555464_at	IFIH1	interferon induced with helicase C domain 1	0.1812	0.0481
1555469_a_at	CLASP2	cytoplasmic linker associated protein 2	0.3681	0.0203
1555476_at	IREB2	iron-responsive element binding protein 2	0.6659	0.0007
1555487_a_at	ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	0.4694	0.0101
1555495_a_at	SDCCAG10	serologically defined colon cancer antigen 10	0.6628	0.0065
1555500_s_at	SLC2A4RG	SLC2A4 regulator	0.8094	0.0059
1555501_s_at	RSRC1	arginine/serine-rich coiled-coil 1	0.9166	0.0027
1555514_a_at	PIAS2	protein inhibitor of activated STAT; 2	0.6404	0.0181
1555547_at		BPA-1 mRNA for brain peptide A1	0.3105	0.0086
1555555_at	BBS9	Bardet-Biedl syndrome 9	0.1062	0.0276
1555560_at	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	0.1208	0.0077
1555562_a_at	ZCCHC7	zinc finger; CCHC domain containing 7	0.3985	0.0253
1555571_at	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.4186	0.0418
1555573_at	C10orf93	chromosome 10 open reading frame 93	0.339	0.0372
1555575_a_at	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	0.583	0
1555594_a_at	MBNL1	muscleblind-like (Drosophila)	0.77	0.0085

1555608_at	CAPRIN2	caprin family member 2	0.2081	0.0059
1555618_s_at	SAE1	SUMO1 activating enzyme subunit 1	1.4009	0.0027
1555677_s_at	SMC1A	structural maintenance of chromosomes 1A	0.3005	0.002
1555751_a_at	GEMIN7	gem (nuclear organelle) associated protein 7	1.3165	0.0001
1555758_a_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	4.3841	0
1555772_a_at	CDC25A	cell division cycle 25 homolog A (S. pombe)	0.8808	0.0006
1555778_a_at	POSTN	periostin; osteoblast specific factor	2.2679	0.0137
1555785_a_at	XRN1	5'-3' exoribonuclease 1	0.2756	0.0489
1555793_a_at	ZNF545	zinc finger protein 545	1.0275	0.0326
1555826_at	EPR1	Effector cell peptidase receptor 1	0.4516	0.0038
1555841_at			0.9481	0.008
1555842_at	LOC284356	hypothetical protein LOC284356	2.3316	0
1555843_at	HNRPM	Heterogeneous nuclear ribonucleoprotein M	0.56	0.0238
1555882_at	SPIN3	spindlin family; member 3	1.0131	0.0228
1555894_s_at	ABBA-1	actin-bundling protein with BAIAP2 homology	0.713	0.0106
1555895_at	DNM2	dynamin 2	0.4418	0.0041
1555898_at	LOC150759	Hypothetical protein LOC150759	0.2867	0.007
1555900_at		CDNA clone IMAGE:5284820	0.8142	0.0064
1555907_at		Homo sapiens; clone IMAGE:5247320; mRNA	1.3185	0.0155
1555910_at	PTCD2	pentatricopeptide repeat domain 2	0.7526	0.0031
1555920_at	CBX3	Chromobox homolog 3 (HP1 gamma homolog; Drosophila)	1.1362	0.0101
1555932_at		CDNA FLJ36889 fis; clone BNGH42009021	0.1016	0.0409
1555938_x_at	VIM	vimentin	1.2195	0.0277
1555944_at	FAM120A	family with sequence similarity 120A	0.132	0.0184
1555960_at	HINT1	Histidine triad nucleotide binding protein 1	0.9533	0
1555996_s_at	EIF4A2	eukaryotic translation initiation factor 4A; isoform 2	1.3548	0.0097
1556009_at	PEX13	peroxisome biogenesis factor 13	0.5943	0.0136
1556015_a_at	MESP2	mesoderm posterior 2 homolog (mouse)	0.1946	0.0136
1556033_at		CDNA FLJ38785 fis; clone LIVER2001329	0.543	0.0083
1556049_at	RTN4	reticulon 4	1.0091	0.0134
1556051_a_at	BICD1	bicaudal D homolog 1 (Drosophila)	1.4401	0.0018
1556054_at		Full length insert cDNA clone ZD45C02	0.7204	0.025
1556061_at	LOC283012	hypothetical protein LOC283012, ribonuclease P/MRP 30kDa subunit	0.8723	0.0008
1556064_at	LOC284926	Hypothetical protein LOC284926	0.4828	0.0466
1556088_at	OR5T2	olfactory receptor; family 5; subfamily T; member 2	0.473	0.0443

1556097_at		MRNA; cDNA DKFZp686A11113 (from clone DKFZp686A11113)	1.0048	0.0043
1556103_at		CDNA FLJ30565 fis; clone BRAWH2005008	0.5848	0.0037
1556117_at		CDNA FLJ33523 fis; clone BRAMY2006411	0.1194	0.0256
1556121_at		CDNA FLJ11689 fis; clone HEMBA1004977	0.7368	0.0322
1556125_at	GPATCH2	G patch domain containing 2	0.2811	0.0084
1556144_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	0.3002	0.0011
1556175_at	ABBA-1	actin-bundling protein with BAIAP2 homology	0.1323	0.0071
1556180_at	LOC729678	hypothetical protein LOC729678	0.9673	0.0127
1556187_at		Clone 23822 mRNA sequence	0.2114	0.0081
1556202_at	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	0.2784	0.0458
1556204_a_at	ZNF814	Zinc finger protein 814	0.2781	0.0017
1556211_a_at		CDNA FLJ38810 fis; clone LIVER2006251	0.6249	0.0213
1556212_x_at		CDNA FLJ38810 fis; clone LIVER2006251	0.2669	0.044
1556277_a_at	PAPD4	PAP associated domain containing 4	1.3442	0.0004
1556282_at	FGFR1OP2	FGFR1 oncogene partner 2	0.251	0.0311
1556301_at		CDNA clone IMAGE:5288145	0.6764	0.0001
1556306_at		Chromosome 7 unknown mRNA	0.803	0.0166
1556318_s_at		Full length insert cDNA YQ07B06	0.7486	0.0228
1556322_a_at		Full length insert cDNA clone YU27F12	0.2966	0.0183
1556331_a_at		CDNA clone IMAGE:5259142	0.6612	0.0323
1556336_at	RBMX	RNA binding motif protein; X-linked	0.5184	0.0425
1556338_at		CDNA FLJ39845 fis; clone SPLEN2014452	1.0081	0.0021
1556339_a_at		CDNA FLJ39845 fis; clone SPLEN2014452	0.6995	0.0061
1556345_s_at		Full length insert cDNA clone ZE07C03	0.575	0.0017
1556347_at		Full length insert cDNA clone ZD70G04	0.7396	0.0058
1556357_s_at	ERICH1	glutamate-rich 1	0.1702	0.0458
1556373_a_at	MGC35361	Hypothetical MGC35361	0.5666	0.0412
1556404_a_at	LOC441208	hypothetical gene supported by AK094370	0.1853	0.0009
1556416_s_at		Full length insert cDNA clone ZD37D10	1.0698	0.0045
1556423_at	VASH1	Vasohibin 1	0.5645	0.017
1556429_a_at	WDR67	WD repeat domain 67	0.2359	0.0395
1556432_at		CDNA FLJ35329 fis; clone PROST2013873	0.2602	0.0172
1556434_at		CDNA FLJ25798 fis; clone TST07050	0.2248	0.0148
1556527_a_at		CDNA clone IMAGE:4402168	1.2137	0.0021
1556543_at		Full length insert cDNA clone YW18F01	1.0659	0.0044

1556551_s_at	SLC39A6	solute carrier family 39 (zinc transporter); member 6	1.3011	0.0028
1556629_a_at	SNAP25	Synaptosomal-associated protein; 25kDa	2.1811	0.0015
1556646_at			1.3989	0.0001
1556657_at		CDNA FLJ36459 fis; clone THYMU2014762	0.3444	0.0369
1556658_a_at		CDNA FLJ36459 fis; clone THYMU2014762	0.633	0.0247
1556659_at		CDNA FLJ33647 fis; clone BRAMY2024374	0.4686	0.0172
1556678_a_at		Full length insert cDNA clone ZD41C11	0.4775	0.0255
1556682_s_at		Full length insert cDNA clone ZD73H04	0.3172	0.0206
1556715_at	PRPSAP1	Phosphoribosyl pyrophosphate synthetase-associated protein 1	0.5874	0.0066
1556743_at	ZNF654	zinc finger protein 654	0.5756	0.0041
1556744_a_at	ZNF654	zinc finger protein 654	1.4473	0.0003
1556781_at		I.M.A.G.E. clone 120151; mRNA sequence	0.1682	0.0075
1556783_a_at		Full length insert cDNA clone YY49D02	0.5785	0.0003
1556794_at		CDNA FLJ33615 fis; clone BRAMY2018396	0.3702	0.0052
1556804_s_at	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	0.243	0.0156
1556815_at		Full length insert cDNA clone ZB72E12	0.2977	0.0014
1556820_a_at	DLEU2	deleted in lymphocytic leukemia; 2	0.8055	0.011
1556821_x_at	DLEU2	deleted in lymphocytic leukemia; 2	0.8255	0.0201
1556828_at		CDNA FLJ36457 fis; clone THYMU2014500	0.3089	0.0018
1556831_at	DYNC1H1	Dynein; cytoplasmic 1; heavy chain 1	0.1883	0.0003
1556834_at		CDNA clone IMAGE:5296106	0.1255	0.026
1556849_at		CDNA FLJ11909 fis; clone HEMBB1000099	0.3185	0.0491
1556911_at		Homo sapiens; clone IMAGE:5493056; mRNA	0.338	0.0394
1556925_at	SMC3	Structural maintenance of chromosomes 3	0.3152	0.0053
1556938_a_at		CDNA FLJ38433 fis; clone FEBRA2014578	0.3871	0.0018
1556984_at		Full length insert cDNA clone YU27A09	0.2489	0.0131
1557012_a_at		CDNA clone IMAGE:4816709	0.5652	0.0002
1557036_at	ZBTB1	Zinc finger and BTB domain containing 1	0.3109	0.0008
1557044_at		CDNA clone IMAGE:5301514	0.1533	0.0495
1557046_x_at		CDNA clone IMAGE:5301514	0.231	0.0096
1557062_at		Full-length cDNA clone CS0DF025YH20 of Fetal brain of Homo sapiens (human)	0.3708	0.0376
1557066_at	LUC7L	LUC7-like (S. cerevisiae)	0.6883	0.0029
1557071_s_at	NUB1	negative regulator of ubiquitin-like proteins 1	0.5414	0.0028

1557073_s_at	TTBK2	Tau tubulin kinase 2	1.1851	0.0011
1557091_at	FLJ36070	likely ortholog of MEF2-activating SAP transcriptional regulator	1.9742	0.0002
1557098_s_at	HAR1A	highly accelerated region 1A (non-protein-coding RNA)	0.9549	0.0124
1557129_a_at	FAM111B	family with sequence similarity 111; member B	0.2392	0.024
1557139_at		CDNA FLJ39041 fis; clone NT2RP7010109	0.1728	0.0132
1557158_s_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.5255	0.0019
1557164_a_at		Full length insert cDNA clone ZD68D12	1.196	0.0001
1557166_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	0.6397	0.006
1557174_a_at		CDNA FLJ39542 fis; clone PUAEN2008815	0.516	0.0095
1557189_at	DNASE1	deoxyribonuclease I	0.1978	0.0028
1557196_a_at		MRNA; cDNA DKFZp547B198 (from clone DKFZp547B198)	0.3227	0.0064
1557218_s_at	FANCB	Fanconi anemia; complementation group B	0.263	0.0028
1557224_at		CDNA FLJ30981 fis; clone HHDPC2000258	0.8331	0.0072
1557227_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.7069	0.0364
1557239_at		Full length insert cDNA clone YW25E05	1.3779	0.0019
1557240_a_at		Full length insert cDNA clone YW25E05	1.3273	0.0125
1557242_at		MRNA expressed in skin fibroblast	1.2932	0.0003
1557267_s_at	LOC284952	hypothetical protein LOC284952	0.4193	0.0038
1557270_at		CDNA FLJ36375 fis; clone THYMU2008226	2.0298	0.0002
1557278_s_at	TNPO1	Transportin 1	0.3058	0.0028
1557283_a_at	ZNF519	zinc finger protein 519	0.3859	0.0435
1557289_s_at	GTF2IRD2	GTF2I repeat domain containing 2	0.1921	0.0262
1557290_at	DPY19L2	dpy-19-like 2 (C. elegans), dpy-19-like 2 pseudogene 1 (C. elegans), dpy-19-like 2 pseudogene 2 (C. elegans), dpy-19-like 2 pseudogene 4 (C. elegans)	0.2779	0.0008
1557300_s_at		CDNA FLJ34138 fis; clone FCBBF3011003	1.2732	0.0011
1557301_a_at		CDNA FLJ33905 fis; clone CTONG2008405	0.1689	0.0163
1557302_at		CDNA FLJ33255 fis; clone ASTRO2005553	0.7481	0.0247
1557311_at		CDNA FLJ40469 fis; clone TESTI2042473	0.3921	0.0249
1557314_at		CDNA clone IMAGE:5303069	0.1555	0.0344
1557322_at	ZNF230	zinc finger protein 230	0.6354	0.0234
1557350_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	0.6949	0.0214
1557352_at	SQLE	Squalene epoxidase	1.7743	0.0085
1557363_a_at	PHIP	pleckstrin homology domain interacting protein	0.3201	0.0019

1557366_at	CCDC144B	coiled-coil domain containing 144B	0.4775	0.0273
1557385_at	FLJ13305	hypothetical protein FLJ13305	0.6373	0.008
1557409_at		CDNA FLJ45930 fis; clone PLACE7000707	0.6397	0.0033
1557415_s_at	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	0.2851	0.0108
1557430_at	LOC147670	hypothetical protein LOC147670	0.627	0.002
1557438_at		CDNA clone IMAGE:5285425	0.2081	0.0394
1557466_at	FLJ31104	Hypothetical gene supported by AK055666; BC039324	0.1101	0.0292
1557478_at		CDNA FLJ25058 fis; clone CBL04608	0.9881	0.0094
1557504_at		Full length insert cDNA YQ11E04	0.5222	0.0161
1557505_a_at		Full length insert cDNA YQ11E04	0.927	0.0068
1557512_at		Full length insert cDNA YQ02G04	0.4929	0.0061
1557521_a_at		CDNA clone IMAGE:5311184	0.447	0.0209
1557543_at		MRNA; cDNA DKFZp313P2412 (from clone DKFZp313P2412)	0.7655	0.0039
1557555_at		CDNA FLJ12016 fis; clone HEMBB1001707	0.1843	0.016
1557558_s_at	MATN1	Matrilin 1; cartilage matrix protein	0.3915	0.0056
1557562_at	GRIPAP1	GRIP1 associated protein 1	0.2443	0.0051
1557571_at	VPS13D	Vacuolar protein sorting 13 homolog D (S. cerevisiae)	0.1211	0.0318
1557580_at		CDNA clone IMAGE:3923254	0.4603	0.0066
1557581_x_at		CDNA clone IMAGE:3923254	0.2563	0.0173
1557585_at	ATP6V1H	ATPase; H+ transporting; lysosomal 50/57kDa; V1 subunit H	0.3653	0.0081
1557586_s_at	ATP6V1H	ATPase; H+ transporting; lysosomal 50/57kDa; V1 subunit H	0.6499	0.0044
1557637_at		CDNA clone IMAGE:5267718	0.2529	0.0139
1557638_at		CDNA clone IMAGE:4793048	0.1063	0.0477
1557644_at		CDNA FLJ30692 fis; clone FCBBF2000677	0.3998	0.0035
1557685_at	C4orf38	chromosome 4 open reading frame 38	0.433	0.018
1557692_a_at		CDNA clone IMAGE:5298801	0.1361	0.0083
1557698_at		Homo sapiens; clone IMAGE:4043992; mRNA	0.3768	0.0025
1557699_x_at		Homo sapiens; clone IMAGE:4043992; mRNA	0.4026	0.0105
1557701_s_at	POLH	polymerase (DNA directed); eta	0.3111	0.0088
1557737_s_at	NKTR	natural killer-tumor recognition sequence	0.6299	0.0043
1557744_at		CDNA FLJ25841 fis; clone TST08665	0.388	0.035
1557765_at	LOC643401	hypothetical protein LOC643401	1.037	0.0206
1557772_at		CDNA clone IMAGE:4826031	0.3169	0.0338
1557780_at		MRNA; cDNA DKFZp564C1072 (from clone DKFZp564C1072)	0.1697	0.0321
1557798_at	TMEM4	Transmembrane protein 4	0.1665	0.0048
1557805_at		Full length insert cDNA clone YT85B06	0.467	0.0229

1557809_a_at		Full length insert cDNA clone YF46C08	0.162	0.0453
1557813_at		Full length insert cDNA clone YB34C04	2.1534	0.0002
1557814_a_at		Full length insert cDNA clone YB34C04	1.1014	0.0034
1557828_a_at	LOC646916	hypothetical protein LOC646916	2.2934	0
1557830_at		CDNA FLJ10112 fis; clone HEMBA1002750	0.7803	0.012
1557835_at		CDNA FLJ31592 fis; clone NT2RI2002447	0.8018	0.0181
1557883_a_at		CDNA FLJ30446 fis; clone BRACE2009255	0.1444	0.0134
1557889_at		CDNA clone IMAGE:4138742	0.202	0.0349
1557891_s_at	LOC729178	hypothetical protein LOC729178	0.1753	0.0214
1557895_at	FLJ35934	FLJ35934 protein	0.4404	0.0094
1557918_s_at	SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	1.1497	0.0089
1557984_s_at	RPAP3	RNA polymerase II associated protein 3	0.9154	0.005
1557985_s_at	CEP78	centrosomal protein 78kDa	0.4385	0.0163
1557987_at	LOC641298	PI-3-kinase-related kinase SMG-1 - like locus	1.5314	0.0001
1557991_at	METTL6	methyltransferase like 6	0.2913	0.0001
1557996_at			1.5357	0
1558014_s_at	MLSTD2	male sterility domain containing 2	0.6031	0.0401
1558015_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.1072	0.0164
1558027_s_at	PRKAB2	protein kinase; AMP-activated; beta 2 non-catalytic subunit	2.0154	0.0001
1558028_x_at	LOC647979	hypothetical protein LOC647979	0.8459	0.009
1558044_s_at	EXOSC6	Exosome component 6	0.621	0.0114
1558075_at	LOC399491	LOC399491 protein	0.4489	0.0181
1558076_at	ANKRD32	ankyrin repeat domain 32	0.3371	0.0011
1558078_at		Homo sapiens; clone IMAGE:3925788; mRNA	1.3521	0
1558088_a_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog; yeast)	0.4641	0.0066
1558093_s_at	LOC727839	matrin 3, similar to Matrin-3 (Nuclear scaffold protein P130/MAT3)	1.293	0.0096
1558111_at	MBNL1	muscleblind-like (Drosophila)	0.6618	0.0263
1558115_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	0.2566	0.026
1558117_s_at	USP31	ubiquitin specific peptidase 31	0.4652	0.0383
1558122_s_at		CDNA FLJ39178 fis; clone OCBBF2004104	0.4574	0.029
1558123_at	FLJ35390	hypothetical protein FLJ35390	0.2861	0.0304
1558139_at	FLJ39632	hypothetical LOC642477	1.175	0.0013
1558163_at	PEX13	Peroxisome biogenesis factor 13	0.2724	0.0152
1558164_s_at	PEX13	Peroxisome biogenesis factor 13	0.7924	0.0102
1558184_s_at	ZNF17	zinc finger protein 17	0.7147	0.0044
1558217_at	SLFN13	schlafen family member 13	1.5892	0.0032

1558249_s_at	STX16	syntaxin 16	0.7379	0.0073
1558251_a_at	ZNF587	zinc finger protein 587	0.3326	0.0196
1558253_x_at	ZNF587	zinc finger protein 587	0.4764	0.0016
1558254_s_at	SRPK2	SFRS protein kinase 2	1.4704	0.0007
1558256_at	LOC148189	hypothetical protein LOC148189	0.5923	0.0013
1558280_s_at	ARHGAP29	Rho GTPase activating protein 29	0.1917	0.0263
1558310_s_at	FLJ90723	hypothetical protein FLJ90723	0.2418	0.0432
1558331_at	SIRT2	Sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	1.2982	0.0001
1558346_at	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.8521	0
1558354_s_at		CDNA clone IMAGE:5260583	0.1635	0.0023
1558365_at	PGK1	phosphoglycerate kinase 1	1.8608	0.0013
1558369_at	MPHOSPH9	M-phase phosphoprotein 9	1.3209	0.0004
1558381_a_at		Homo sapiens; clone IMAGE:3830652; mRNA	0.2146	0.0089
1558385_at			0.4096	0.0326
1558391_s_at	ZNF599	zinc finger protein 599	0.2933	0.0002
1558394_s_at	KRT7	keratin 7	0.1919	0.0377
1558401_at		CDNA FLJ37332 fis; clone BRAMY2019710	0.6324	0.0445
1558426_x_at	ORAI2	ORAI calcium release-activated calcium modulator 2	0.8232	0.0029
1558444_at		CDNA FLJ35140 fis; clone PLACE6009524	1.2556	0.0101
1558466_at		Clone IMAGE:125405; mRNA sequence	0.3595	0.0495
1558474_at		CDNA FLJ38034 fis; clone CTONG2013393	0.3419	0.0269
1558486_at	ZNF493	zinc finger protein 493	1.0355	0.0271
1558504_at		Full length insert cDNA clone ZE14C04	0.2234	0.0356
1558515_at		CDNA clone IMAGE:4328048	1.3805	0.0082
1558518_at	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	0.181	0.016
1558519_at	FLJ23861	Hypothetical protein FLJ23861, Ribulose-5-phosphate-3-epimerase	0.1546	0.0049
1558522_at		Homo sapiens; clone IMAGE:3459334; mRNA	0.7879	0.043
1558523_at	C6orf60	chromosome 6 open reading frame 60	0.2656	0.0152
1558603_at	PLGLB2	plasminogen-like B2	0.1417	0.0134
1558604_a_at		MRNA; clone CD 43T7	0.9697	0.015
1558605_at		CDNA clone IMAGE:4819775	0.7072	0.0334
1558606_s_at		CDNA clone IMAGE:4819775	0.163	0.0162
1558620_at	ZNF621	zinc finger protein 621	0.5456	0.0243
1558622_a_at	ZNF548	zinc finger protein 548	0.3727	0.0047
1558626_at		CDNA clone IMAGE:3628701	0.4687	0.0483
1558651_at		CDNA FLJ35273 fis; clone PROST2006020	0.2452	0.0126

1558673_s_at	ZNF77	zinc finger protein 77	0.3839	0.0064
1558695_at		Full length insert cDNA clone YR58H12	1.8088	0.0019
1558699_a_at	HERPUD2	HERPUD family member 2	0.5242	0.0102
1558700_s_at	ZNF260	zinc finger protein 260	0.9136	0.0049
1558719_s_at		CDNA FLJ30490 fis; clone BRAWH2000169	0.3524	0.0391
1558738_at	NOL3	Nucleolar protein 3 (apoptosis repressor with CARD domain)	1.0402	0.0323
1558747_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	0.8238	0.0245
1558748_at		MRNA; cDNA DKFZp686E1027 (from clone DKFZp686E1027)	1.0765	0.003
1558750_a_at		CDNA FLJ34964 fis; clone NTONG2004095	0.7771	0.0038
1558755_x_at	ZNF763	zinc finger protein 763	0.6927	0.0093
1558801_at		Homo sapiens; clone IMAGE:2900205; mRNA	1.1382	0.0008
1558809_s_at	LOC284408	hypothetical protein LOC284408	0.7098	0.0024
1558816_at	ZNF664	zinc finger protein 664	0.4774	0.002
1558831_x_at		CDNA FLJ34403 fis; clone HCHON2001607	0.3072	0.0007
1558841_at	SDCCAG10	serologically defined colon cancer antigen 10	0.1581	0.0459
1558854_a_at		MRNA; cDNA DKFZp667D0824 (from clone DKFZp667D0824)	0.6236	0.0272
1558859_at	LOC222159	hypothetical protein LOC222159	0.2147	0.0348
1558922_at		Full length insert cDNA clone YF43G08	0.9083	0.0059
1558937_s_at		MRNA (fetal brain cDNA b2_2g)	1.1431	0.0001
1558943_x_at	ZNF765	zinc finger protein 765	0.5726	0.049
1558953_s_at	CEP164	centrosomal protein 164kDa	0.9014	0.0145
1558959_at		CDNA FLJ37917 fis; clone CTONG1000137	0.2932	0.0324
1558996_at	FOXP1	forkhead box P1	0.3165	0.0164
1558999_x_at	LOC283922	hypothetical protein LOC283922, pyruvate dehydrogenase phosphatase regulatory subunit, similar to pyruvate dehydrogenase phosphatase regulatory subunit	0.3994	0.0017
1559006_at		CDNA clone IMAGE:4304686	1.0721	0.0004
1559007_s_at		CDNA clone IMAGE:4304686	0.648	0.0058
1559042_at	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 6; 17kDa	0.367	0.0002
1559044_at	EXOSC1	exosome component 1	0.1601	0.0246
1559045_at		CDNA FLJ37541 fis; clone BRCAN2026340	0.3534	0.0012
1559054_a_at		Homo sapiens; clone IMAGE:5199859; mRNA	0.3124	0.0001
1559059_s_at	ZNF611	Zinc finger protein 611	0.2162	0.0028
1559078_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	0.6948	0.0423
1559102_at		CDNA clone IMAGE:4791593	0.4687	0.0016

1559103_s_at		CDNA clone IMAGE:4791593	0.3782	0.0187
1559109_a_at		CDNA FLJ32270 fis; clone PROST1000527	0.1314	0.0062
1559128_at	HSDL2	hydroxysteroid dehydrogenase like 2	0.5057	0.036
1559132_at			0.188	0.0274
1559154_at		CDNA FLJ40682 fis; clone THYMU2023264	0.4927	0.0225
1559161_at		CDNA FLJ38294 fis; clone FCBBF3010211	0.4495	0.0068
1559171_at	LOC147080	hypothetical protein LOC147080	0.228	0.0198
1559180_at	HOMER2	Homer homolog 2 (Drosophila)	0.2123	0.0075
1559190_s_at	RDH13	MRNA; cDNA DKFZp313H0740 (from clone DKFZp313H0740), Retinol dehydrogenase 13 (all-trans/9-cis)	1.1046	0.0081
1559203_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.3589	0.0004
1559214_at		MRNA full length insert cDNA clone EUROIMAGE 839551	0.9474	0.001
1559222_at		CDNA FLJ30725 fis; clone FCBBF4000415	0.327	0.0028
1559259_at		Clone IMAGE:418054; mRNA sequence	0.469	0.0034
1559270_at	ZFHX4	zinc finger homeobox 4	0.1974	0.0009
1559307_s_at	RBL1	retinoblastoma-like 1 (p107)	0.1945	0.0037
1559331_x_at		CDNA FLJ25030 fis; clone CBL02631	0.1642	0.0089
1559369_at	FLJ13611	hypothetical protein FLJ13611	0.1976	0.0093
1559384_at		Transcribed locus	0.1102	0.0249
1559406_at	ANKRD18A	ankyrin repeat domain 18A	0.2343	0.0016
1559410_at		Transcribed locus	0.9892	0.0485
1559413_at	TCP11L2	t-complex 11 (mouse)-like 2	0.5908	0.0471
1559444_at		MRNA; cDNA DKFZp666H208 (from clone DKFZp666H208)	0.1706	0.0279
1559449_a_at	ZNF254	Zinc finger protein 254	0.2812	0.0321
1559455_at		CDNA FLJ34603 fis; clone KIDNE2013388	0.6563	0.0005
1559462_at		Homo sapiens; clone IMAGE:6155889; mRNA	1.7909	0.0182
1559491_at		MRNA; cDNA DKFZp761L149 (from clone DKFZp761L149)	0.5288	0.0232
1559494_at		CDNA FLJ38710 fis; clone KIDNE2002980	0.1372	0.0175
1559496_at	PPA2	Pyrophosphatase (inorganic) 2	1.6805	0.0002
1559500_at	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	0.5001	0.0003
1559513_a_at	FANCC	Fanconi anemia; complementation group C	0.1498	0.0008
1559523_at		CDNA clone IMAGE:4821044	0.2582	0.0001
1559524_at		MRNA; cDNA DKFZp566N0924 (from clone DKFZp566N0924)	0.4653	0.0009
1559528_at	PCGF3	Polycomb group ring finger 3	0.1665	0.0187
1559529_at	PTK2	PTK2 protein tyrosine kinase 2	1.0478	0.0044

1559532_at	LOC646450	hypothetical LOC646450	0.2021	0.0486
1559534_at		Homo sapiens; clone IMAGE:5743779; mRNA	0.5053	0.0016
1559535_s_at		Homo sapiens; clone IMAGE:5743779; mRNA	0.6123	0.0022
1559565_x_at		MRNA; cDNA DKFZp686K1037 (from clone DKFZp686K1037)	0.1378	0.0415
1559585_at	FLJ31033	hypothetical protein FLJ31033	0.1303	0.0175
1559589_a_at		CDNA FLJ37400 fis; clone BRAMY2027714	0.1953	0.0047
1559598_at		CDNA FLJ38424 fis; clone FEBRA2012090	0.6336	0.0005
1559600_at		MRNA; cDNA DKFZp547G2314 (from clone DKFZp547G2314)	0.2517	0.0446
1559606_at	GBP6	Guanylate binding protein family; member 6	0.1083	0.0414
1559691_at		CDNA clone IMAGE:3869664	0.5243	0.0116
1559707_at		MRNA; cDNA DKFZp434J0927 (from clone DKFZp434J0927)	0.2317	0.0034
1559820_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	0.5311	0.0192
1559876_at		Homo sapiens; clone IMAGE:4347394; mRNA	0.2853	0.0025
1559881_s_at	ZNF12	zinc finger protein 12	1.9694	0
1559890_a_at	ABI1	abl-interactor 1	0.1171	0.0076
1559893_at	CCDC75	coiled-coil domain containing 75	0.263	0.0443
1559932_at		Full length insert cDNA clone YR28G06	0.3905	0.0001
1559954_s_at	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	0.9078	0.0447
1559964_at	FLJ38717	FLJ38717 protein	0.7935	0.0009
1560006_a_at	LOC646762	hypothetical protein LOC646762	0.2213	0.032
1560013_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.5025	0.0078
1560017_at	TMTC3	transmembrane and tetratricopeptide repeat containing 3	0.4976	0.0002
1560020_at	DNAJC13	DnaJ (Hsp40) homolog; subfamily C; member 13	0.1504	0.0091
1560033_at	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.2889	0.0025
1560034_a_at		MRNA; cDNA DKFZp313E1515 (from clone DKFZp313E1515)	0.1366	0.0227
1560089_at	LOC286208	hypothetical protein LOC286208	0.6142	0.0213
1560116_a_at	NEDD1	neural precursor cell expressed; developmentally down-regulated 1	1.2771	0
1560145_at	MKLN1	Muskelin 1; intracellular mediator containing kelch motifs	0.8792	0.0106
1560171_at		CDNA FLJ32354 fis; clone PROST2007818	0.4659	0.0194
1560172_at	INTS10	integrator complex subunit 10	0.2421	0.0067
1560201_at	ZNF713	zinc finger protein 713	0.3674	0.003
1560222_at		CDNA clone IMAGE:3846805	0.3555	0.0039
1560224_at	AHCTF1	AT hook containing transcription factor 1	0.3515	0.006
1560258_a_at		Homo sapiens; clone IMAGE:5590287; mRNA	0.5169	0.0404

1560290_at		Homo sapiens; clone IMAGE:5480271; mRNA	0.344	0.0011
1560297_at		Homo sapiens; clone IMAGE:4043205; mRNA	0.3921	0.0168
1560316_s_at	GLCCI1	glucocorticoid induced transcript 1	0.2209	0.0257
1560318_at	ARHGAP29	Rho GTPase activating protein 29	0.1381	0.0155
1560332_at		MRNA; cDNA DKFZp451C0318 (from clone DKFZp451C0318)	0.2923	0.0194
1560339_s_at	NAP1L4	nucleosome assembly protein 1-like 4	0.7127	0.0105
1560340_s_at	LOC441212	retinitis pigmentosa 9 pseudogene	0.155	0.0183
1560354_at	CCDC127	Coiled-coil domain containing 127	0.3408	0.0305
1560358_at	PHKA2	phosphorylase kinase; alpha 2 (liver)	1.0451	0.0288
1560372_at		CDNA FLJ34680 fis; clone LIVER2003524	0.1292	0.0376
1560385_x_at		CDNA FLJ38270 fis; clone FCBBF3002592	0.1335	0.0163
1560386_at		Homo sapiens; clone IMAGE:5740472; mRNA	1.0435	0.0004
1560422_at		CDNA clone IMAGE:4155541	0.3293	0.0257
1560433_at		CDNA FLJ31398 fis; clone NT2NE1000175	1.0432	0.0066
1560434_x_at	CLTA	clathrin; light chain (Lca)	0.9302	0.0054
1560443_at		CDNA clone IMAGE:3937917	0.3874	0.0329
1560445_x_at	ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	0.4135	0.0014
1560474_at		Homo sapiens; clone IMAGE:4294221; mRNA	0.3566	0
1560475_at		CDNA FLJ34815 fis; clone NT2NE2007786	0.3138	0.0104
1560492_at		CDNA clone IMAGE:4578339	0.9518	0.0052
1560498_at		Homo sapiens; clone IMAGE:4539309; mRNA	0.6912	0.041
1560500_at		CDNA clone IMAGE:5299346	1.025	0.0301
1560509_at		MRNA; cDNA DKFZp547H194 (from clone DKFZp547H194)	0.181	0.0414
1560526_at	PR47	platelet receptor for type III collagen; 47 kDa	0.6264	0.0464
1560556_a_at	PLEKHA8	Pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 8	0.3098	0.0086
1560599_a_at	CCDC123	coiled-coil domain containing 123	0.3606	0.005
1560654_at	FLJ37201	hypothetical protein FLJ37201	0.2735	0.0023
1560659_at			0.7355	0.0008
1560661_x_at			0.6772	0.0012
1560665_at	SCPEP1	serine carboxypeptidase 1	0.2221	0.0291
1560680_at	LOC732014	Similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP)	0.5168	0.0027
1560689_s_at	AKT2	V-akt murine thymoma viral oncogene homolog 2	0.5089	0.014

1560712_at	TMPRSS11B	transmembrane protease; serine 11B	0.1528	0.0042
1560739_a_at		CDNA clone IMAGE:5300703	0.4338	0.0354
1560775_at		CDNA FLJ25185 fis; clone CBR09429	0.3886	0
1560814_a_at	CCDC32	coiled-coil domain containing 32	1.2195	0.0066
1560827_at		CDNA clone IMAGE:4820845	0.1503	0.0477
1560926_at		Full length insert cDNA clone YR43G06	0.4668	0.041
1560982_at		Full length insert cDNA clone ZD81C11	0.7005	0.0004
1560986_a_at		Full length insert cDNA clone YW21C01	0.3876	0.0267
1560992_at	LOC400590	hypothetical LOC400590	0.1844	0.029
1561042_at	ITGB1	integrin; beta 1 (fibronectin receptor; beta polypeptide; antigen CD29 includes MDF2; MSK12)	0.1898	0.0243
1561079_at	ANKRD28	ankyrin repeat domain 28	0.9432	0.003
1561121_at		Full length insert cDNA clone ZD64C04	0.1666	0.0319
1561130_at	C12orf51	Chromosome 12 open reading frame 51	0.3069	0.0239
1561149_at		Full length insert cDNA clone ZD75C06	0.1672	0.0037
1561152_a_at		Full length insert cDNA clone ZC66G12	0.1865	0.0002
1561154_at		Full length insert cDNA YU78B07	0.1429	0.017
1561155_at		Full length insert cDNA clone ZD60E09	0.4142	0.0159
1561177_at		CDNA FLJ14141 fis; clone MAMMA1002868	0.2183	0.0027
1561180_at		CDNA FLJ11745 fis; clone HEMBA1005526	0.8558	0.0328
1561190_at	CDKL3	cyclin-dependent kinase-like 3	0.6735	0
1561198_at	LOC387790	hypothetical LOC387790	0.2036	0.0016
1561206_at	KLHL8	kelch-like 8 (Drosophila)	0.4499	0.0211
1561219_x_at		CDNA clone IMAGE:4837157	0.1102	0.0396
1561238_at	PXMP3	Peroxisomal membrane protein 3; 35kDa (Zellweger syndrome)	0.347	0.001
1561346_at		CDNA FLJ32691 fis; clone TESTI2000221	0.6057	0.001
1561578_s_at	MCART6	mitochondrial carrier triple repeat 6	0.1177	0.0102
1561604_at		CDNA clone IMAGE:4796102	0.1291	0.0324
1561609_at		Homo sapiens; clone IMAGE:5392784; mRNA	0.1394	0.0269
1561690_at		CDNA clone IMAGE:5303966	1.0918	0.0092
1561749_at		Full length insert cDNA clone ZD97H10	0.473	0.0001
1561754_at		Full length insert cDNA clone ZA88B06	1.5025	0.0069
1561762_s_at		Full length insert cDNA clone ZD67D03	0.5034	0.0001
1561884_at	CEPT1	choline/ethanolamine phosphotransferase 1	0.2764	0.0197
1561886_a_at		CDNA FLJ39506 fis; clone PROST2017612	0.8737	0.0139

1561893_at		CDNA clone IMAGE:4096047	0.524	0.0264
1561896_at		CDNA FLJ30156 fis; clone BRACE2000487	0.1642	0.0351
1561906_at		Homo sapiens; clone IMAGE:3626122	0.1769	0.0169
1561924_at		Full length insert cDNA clone YU27B01	0.1873	0.022
1561965_at	SNRPB2	Small nuclear ribonucleoprotein polypeptide B''	0.2448	0.0144
1561973_at	SMARCC2	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 2	0.4327	0.0036
1562022_s_at	RAD9A	RAD9 homolog A (S. pombe)	0.443	0.0009
1562095_at		Homo sapiens; clone IMAGE:4663772; mRNA	0.181	0.0025
1562208_a_at		MRNA; cDNA DKFZp761E11121 (from clone DKFZp761E11121)	0.4446	0.0016
1562209_at	WDR21B	WD repeat domain 21B	0.1104	0.0174
1562230_at		Full length insert cDNA clone YI60C11	0.2034	0.0253
1562236_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.2288	0.0272
1562281_at		MRNA; cDNA DKFZp313A0310 (from clone DKFZp313A0310)	0.1394	0.0471
1562386_s_at	ZNF501	zinc finger protein 501	0.4822	0.0003
1562387_at	FLJ13231	hypothetical protein FLJ13231	0.2622	0.0015
1562396_at	PP8961	hypothetical protein LOC650662	0.1007	0.0347
1562412_at		CDNA clone IMAGE:3847423	0.1522	0.0185
1562440_at	MAP3K13	Mitogen-activated protein kinase kinase kinase 13	0.3129	0.04
1562442_a_at	SSBP1	single-stranded DNA binding protein 1	0.3176	0.0085
1562458_at	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	0.1213	0.017
1562477_at	EBF2	early B-cell factor 2	0.1168	0.0127
1562497_at		CDNA FLJ38224 fis; clone FCBBF2003395	1.2147	0.0014
1562505_at		Homo sapiens; clone IMAGE:5550275; mRNA	0.4962	0.0435
1562516_at	WDR60	WD repeat domain 60	0.5297	0.0025
1562677_at		Homo sapiens; Similar to v-myb avian myeloblastosis viral oncogene homolog; clone IMAGE:3535159; mRNA	0.3183	0
1562718_at		Homo sapiens; clone IMAGE:5171428; mRNA	0.1762	0.0327
1562738_a_at		Homo sapiens; clone IMAGE:4132913; mRNA	0.2787	0.0485
1562775_at	NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	0.3337	0.0025
1562789_at	ZNF229	zinc finger protein 229	0.2933	0.01
1562849_at		CDNA FLJ37115 fis; clone BRACE2022158	0.1452	0.0285
1562876_s_at	LOC541471	Homo sapiens; clone IMAGE:4337889; mRNA, Hypothetical LOC541471	0.1996	0.0008

1562938_at	LOC729234	Similar to fumarylacetoacetate hydrolase domain containing 2A	0.4132	0.0016
1562940_at		CDNA clone IMAGE:5301683	0.2816	0.0051
1562946_at		Homo sapiens; clone IMAGE:3503939; mRNA	0.2748	0.0418
1563012_x_at		CDNA clone IMAGE:5302718	0.3243	0.0059
1563016_at		Homo sapiens; clone IMAGE:4295692; mRNA	0.1278	0.0435
1563051_at	OSBP	oxysterol binding protein	0.4163	0.0187
1563075_s_at		Clone IMAGE:110987 mRNA sequence	0.7337	0.0049
1563076_x_at		Clone IMAGE:110987 mRNA sequence	0.3127	0.0043
1563104_at		CDNA clone IMAGE:4155841	0.3655	0.02
1563129_at		MRNA full length insert cDNA clone EUROIMAGE 626063	0.3423	0.0018
1563130_a_at		MRNA full length insert cDNA clone EUROIMAGE 626063	0.8045	0.0011
1563147_at		CDNA clone IMAGE:3632505	0.1319	0.0207
1563173_at		MRNA; cDNA DKFZp667P1917 (from clone DKFZp667P1917)	0.1457	0.0301
1563209_a_at	MACROD2	MACRO domain containing 2	1.3365	0.0365
1563210_at		Homo sapiens; clone IMAGE:5785570; mRNA	0.1664	0.0229
1563303_at		Full length insert cDNA clone ZD88D08	0.1355	0.0027
1563321_s_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 10	0.747	0.0264
1563364_at		Homo sapiens; clone IMAGE:4272847; mRNA	0.8315	0.0139
1563396_x_at		Homo sapiens; clone IMAGE:4281761; mRNA	0.1393	0.0176
1563452_at		MRNA; cDNA DKFZp686G0344 (from clone DKFZp686G0344)	0.5191	0.0015
1563468_at		MRNA; cDNA DKFZp451O249 (from clone DKFZp451O249)	0.4322	0.0011
1563471_at	KIAA1632	KIAA1632	0.2824	0.0037
1563482_at		MRNA; cDNA DKFZp451M0319 (from clone DKFZp451M0319)	0.1362	0.046
1563483_at	FAM91A2	family with sequence similarity 91; member A2	0.3609	0.0033
1563620_at	BTRC	beta-transducin repeat containing	0.1078	0.0217
1563646_a_at	TMEM67	transmembrane protein 67	0.3812	0.0203
1563687_a_at	FRYL	FRY-like	0.3016	0.0217
1563776_at		CDNA clone IMAGE:4837134	0.2299	0.0032
1563781_at	LOC285949	hypothetical protein LOC285949	0.9443	0.0008
1563881_at		MRNA; cDNA DKFZp547O108 (from clone DKFZp547O108)	0.6586	0.0182
1563947_a_at	ERC1	ELKS/RAB6-interacting/CAST family member 1	0.6539	0.0188
1564015_at	C18orf58	chromosome 18 open reading frame 58	0.1217	0.0101
1564070_s_at		CDNA FLJ36668 fis; clone UTERU2003926	0.1977	0.0092
1564166_s_at	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	0.3106	0.0208

1564220_a_at		CDNA FLJ39613 fis; clone SKNSH2009357	3.2161	0
1564227_at		CDNA: FLJ21299 fis; clone COL02041	0.3667	0.0025
1564231_at	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	0.1492	0.0179
1564240_at		CDNA FLJ38408 fis; clone FEBRA2009029	0.2584	0.0064
1564467_at	FLJ13305	hypothetical protein FLJ13305	0.6417	0.007
1564474_at	LOC728723	hypothetical protein LOC728723	0.1833	0.0015
1564475_s_at	LOC728723	hypothetical protein LOC728723	0.252	0.0488
1564547_x_at		Homo sapiens; clone IMAGE:3138608; mRNA	0.1479	0.0381
1564665_at		CDNA: FLJ22725 fis; clone HSI14917	0.2095	0.0177
1564699_at		CDNA clone IMAGE:4297077	0.5503	0.006
1564773_x_at		CDNA clone IMAGE:4715948	0.4689	0.024
1564776_at	LENG10	leukocyte receptor cluster (LRC) member 10	0.2317	0.0384
1564798_at		CDNA FLJ20804 fis; clone ADSE02063	0.3235	0.0031
1564820_at		MRNA; cDNA DKFZp564E012 (from clone DKFZp564E012)	0.1787	0.0201
1564906_at	SNHG4	small nucleolar RNA host gene (non-protein coding) 4	0.2461	0.0072
1564962_at	ZNF92	zinc finger protein 92	0.2414	0.0372
1564963_x_at	ZNF92	zinc finger protein 92	0.2326	0.0429
1564970_at	SETDB2	SET domain; bifurcated 2	0.3714	0.0002
1564972_x_at	SETDB2	SET domain; bifurcated 2	0.2542	0.0006
1565149_at	DYNC2H1	dynein; cytoplasmic 2; heavy chain 1	0.9528	0.0002
1565557_at		FLJ00399 protein	0.1458	0.0198
1565566_a_at		Full length insert cDNA YN68A11	0.3927	0.0321
1565620_at	CTGLF1	Centaurin; gamma-like family; member 1	0.7138	0.0013
1565692_at		CDNA FLJ40647 fis; clone THYMU2017522	0.5025	0.0122
1565696_at		CDNA FLJ11794 fis; clone HEMBA1006138	0.1033	0.0422
1565705_x_at		CDNA: FLJ21395 fis; clone COL03557	0.2247	0.0131
1565717_s_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	2.8167	0
1565743_at		CDNA FLJ37648 fis; clone BRHIP2000532	0.6514	0.0353
1565786_x_at	FLJ45482	hypothetical LOC645566	0.4656	0.0023
1565799_at	RAB3IP	RAB3A interacting protein (rabin3)	0.1575	0.0475
1565800_x_at	RAB3IP	RAB3A interacting protein (rabin3)	0.1767	0.0032
1565810_at		CDNA clone IMAGE:5278245	0.214	0.04
1565811_at		CDNA clone IMAGE:5278245	0.2584	0.0193
1565867_a_at	ZC3H11A	zinc finger CCCH-type containing 11A	0.3067	0.0352
1565873_at		Full length insert cDNA clone YP75C01	0.1356	0.0099

1565881_at		CDNA FLJ12064 fis; clone HEMBB1002232	0.3616	0.0068
1565886_at		Full length insert cDNA clone ZB94A08	1.1917	0.0002
1565887_at	TRPM7	Transient receptor potential cation channel; subfamily M; member 7	0.1952	0.0039
1565889_at		Full length insert cDNA YQ03C01	0.4884	0.0072
1565913_at		Full length insert cDNA clone YR04D03	0.2922	0.0242
1565935_at	LOC91431	prematurely terminated mRNA decay factor-like	0.365	0.0012
1565951_s_at	CHML	choroideremia-like (Rab escort protein 2)	1.0341	0.0001
1565976_at		Full length insert cDNA YU76C01	0.4859	0.0299
1566084_at	LOC644215	Hypothetical LOC644215	0.4157	0.0279
1566102_at	TTLL5	tubulin tyrosine ligase-like family; member 5	0.248	0.0035
1566142_at		CDNA FLJ37949 fis; clone CTONG2009156	0.3564	0.0069
1566166_at		MRNA; cDNA DKFZp313H2139 (from clone DKFZp313H2139)	0.4744	0.0375
1566191_at	SUZ12	Suppressor of zeste 12 homolog (Drosophila)	0.7653	0.0063
1566207_at	TCEA1	transcription elongation factor A (SII); 1	0.4641	0.0029
1566243_at		MRNA; cDNA DKFZp547L144 (from clone DKFZp547L144)	0.292	0.0121
1566403_at	SNORA68	small nucleolar RNA; H/ACA box 68	0.1998	0.0142
1566465_at	LOC728987	Similar to potassium channel; subfamily K; member 1	0.2039	0.0462
1566482_at		MRNA; cDNA DKFZp313L2229 (from clone DKFZp313L2229)	1.0491	0.0106
1566515_at	CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	0.1323	0.0361
1566518_at			0.1427	0.0077
1566539_at		MRNA; cDNA DKFZp586G081 (from clone DKFZp586G081)	0.5233	0.0172
1566597_at		MRNA; cDNA DKFZp761O2417 (from clone DKFZp761O2417)	0.4397	0.0388
1566606_a_at	TEX9	testis expressed 9	0.1663	0.005
1566673_at		CDNA FLJ36337 fis; clone THYMU2006324	0.2161	0.0009
1566860_at	LOC145663	hypothetical protein LOC145663	0.1396	0.0382
1566862_at		CDNA clone IMAGE:5310996	0.1022	0.011
1566889_at	THADA	Thyroid adenoma associated	0.1391	0.022
1566980_at		Full length insert cDNA clone YQ07A04	0.171	0.0417
1567032_s_at	ZNF160	zinc finger protein 160	1.0097	0.0428
1567044_s_at		Full length insert cDNA clone YN86A01	0.4483	0.0269
1567107_s_at	TPM4	tropomyosin 4	1.2623	0.0085
1567575_at		Trapped 3' terminal exon; clone C2C4	0.2081	0.0342
1567862_at	DNAH14	dynein; axonemal; heavy chain 14, hypothetical protein LOC127602	0.2094	0.0312

1568574_x_at	SPP1	Secreted phosphoprotein 1 (osteopontin; bone sialoprotein I; early T-lymphocyte activation 1)	0.2321	0.0179
1568594_s_at	TRIM52	tripartite motif-containing 52	1.8964	0
1568596_a_at	TROAP	trophinin associated protein (tastin)	0.8921	0.0027
1568597_at	LOC646762	hypothetical protein LOC646762	1.7376	0
1568605_at	JRK	jerky homolog (mouse)	0.3773	0.0324
1568611_at		Homo sapiens; clone IMAGE:3892140; mRNA	1.2554	0.0019
1568617_a_at	KIAA1543	KIAA1543	0.8145	0.0095
1568620_at	CSAD	cysteine sulfinic acid decarboxylase	0.332	0.0469
1568623_a_at	SLC35E4	solute carrier family 35; member E4	0.4764	0.0031
1568627_at	SMEK2	SMEK homolog 2; suppressor of mek1 (Dictyostelium)	0.5149	0.0178
1568634_a_at	LOC339977	similar to hypothetical protein MGC38937	0.3032	0.004
1568661_at		CDNA clone IMAGE:5303305	0.1599	0.0075
1568717_a_at	FKBP15	FK506 binding protein 15; 133kDa	0.1661	0.0318
1568720_at	ZNF506	zinc finger protein 506	0.5604	0.0481
1568763_s_at	LOC728613	programmed cell death 6, programmed cell death protein 6-like	1.0817	0.0041
1568781_at		CDNA clone IMAGE:4389310	0.4795	0.0384
1568783_at	SFRS12	Splicing factor; arginine/serine-rich 12	0.4012	0.0043
1568799_at		CDNA clone IMAGE:4798168	0.2474	0.0001
1568801_at	C15orf44	chromosome 15 open reading frame 44	0.2018	0.0152
1568813_at		CDNA clone IMAGE:4620359	0.3156	0.0123
1568822_at	GTPBP5	GTP binding protein 5 (putative)	0.24	0.0073
1568834_s_at	CCDC90B	coiled-coil domain containing 90B	0.8619	0.0378
1568836_at	CLK4	CDC-like kinase 4	0.2328	0.0479
1568838_at		CDNA clone IMAGE:5261280	0.7421	0.0347
1568840_at	WDSOF1	WD repeats and SOF1 domain containing	0.1864	0.0323
1568856_at	NBR2	Neighbor of BRCA1 gene 2	0.2182	0.0024
1568857_a_at	NBR2	Neighbor of BRCA1 gene 2	0.4286	0.0097
1568865_at	FNTB	Farnesyltransferase; CAAX box; beta	0.999	0.0097
1568866_at		CDNA clone IMAGE:5450715	0.1531	0.0467
1568873_at	ZNF519	zinc finger protein 519	0.5244	0.0029
1568877_a_at	ACBD5	acyl-Coenzyme A binding domain containing 5	0.831	0.0111
1568883_at		Homo sapiens; Similar to KIAA1503 protein; clone IMAGE:5505326; mRNA	0.182	0.0025
1568891_x_at	FANCD2	Fanconi anemia; complementation group D2	0.1032	0.0486
1568915_at		CDNA clone IMAGE:4822684	0.255	0.0007
1568983_a_at		CDNA clone IMAGE:5261717	1.3736	0.0061
1568987_at	MGC57346	hypothetical LOC401884	0.2952	0.0054

1569053_at	AP3M2	adaptor-related protein complex 3; mu 2 subunit	0.4291	0.004
1569108_a_at	ZNF589	zinc finger protein 589	0.4511	0.0002
1569112_at	SLC44A5	solute carrier family 44; member 5	1.0363	0.0356
1569139_s_at	FAM53A	family with sequence similarity 53; member A	0.2148	0.0183
1569142_at	TRIM13	tripartite motif-containing 13	0.4383	0.0135
1569147_at		CDNA clone IMAGE:5298846	0.2876	0.0029
1569167_at		Homo sapiens; clone IMAGE:3867502; mRNA	0.529	0.0118
1569180_at		Homo sapiens; clone IMAGE:4250282; mRNA	0.7881	0.0431
1569181_x_at		Homo sapiens; clone IMAGE:4250282; mRNA	0.7377	0.0244
1569183_a_at	CHM	choroideremia (Rab escort protein 1)	0.6369	0.0011
1569189_at	TTC9C	tetratricopeptide repeat domain 9C	0.4508	0.0022
1569194_at	ZNF789	zinc finger protein 789	0.2851	0.0043
1569241_a_at	ZNF93	zinc finger protein 93	0.5522	0.0067
1569250_at	ZNF333	zinc finger protein 333	0.1413	0.026
1569277_at	ZNF91	Zinc finger protein 91	0.1883	0.007
1569291_at	CROCCL1	ciliary rootlet coiled-coil; rootletin-like 1	0.1314	0.0091
1569296_a_at		CDNA clone IMAGE:4722553	0.3079	0.0262
1569302_at	KIAA1731	KIAA1731	0.4727	0.0054
1569311_at		Homo sapiens; clone IMAGE:5557598; mRNA	0.8735	0.0131
1569312_at		CDNA clone IMAGE:4067166	1.1977	0.004
1569318_at	MGC39821	hypothetical protein MGC39821	0.1921	0.008
1569320_at	GPBP1L1	GC-rich promoter binding protein 1-like 1	1.3974	0.001
1569353_at	CP110	CP110 protein	0.3422	0.013
1569368_at	LOC648921	Similar to Actin; cytoplasmic 2 (Gamma-actin)	0.1559	0.0166
1569377_at	TMEM67	transmembrane protein 67	0.8594	0.0015
1569392_at	GPSN2	glycoprotein; synaptic 2	0.2774	0.0115
1569500_at		Homo sapiens; clone IMAGE:4183247; mRNA	0.3477	0.0011
1569503_at	HEATR5B	HEAT repeat containing 5B	0.1968	0.0392
1569519_at	KIAA1245	CLIP-190-like, KIAA1245, hypothetical protein LOC728895, neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 8, neuroblastoma breakpoint family; member 9	0.367	0.0407
1569538_at		Clone FLB8310 PRO2225	0.3608	0.021
1569557_at	ZNF248	zinc finger protein 248	0.1961	0.0105

1569569_x_at		Homo sapiens; Similar to neuronal thread protein; clone IMAGE:3932744; mRNA	0.1139	0.006
1569600_at	DLEU2	Deleted in lymphocytic leukemia; 2	0.3157	0.0395
1569607_s_at	ANKRD20A1	ankyrin repeat domain 20 family; member A1, ankyrin repeat domain 20 family; member A2, ankyrin repeat domain 20 family; member A3, ankyrin repeat domain 20 family; member A4, chromosome 21 open reading frame 81, similar to ankyrin repeat domain 20 family; member A2, similar to ankyrin repeat domain 20A	2.0949	0.0071
1569608_x_at	LOC643187	Similar to ankyrin repeat domain 20A	0.9645	0.0313
1569611_a_at	IQCH	IQ motif containing H	0.1379	0.0134
1569652_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 3	1.2121	0.0208
1569665_at		Homo sapiens; clone IMAGE:5581630; mRNA	0.2457	0.004
1569666_s_at		Homo sapiens; clone IMAGE:5581630; mRNA	0.7012	0.0017
1569677_a_at	C8orf45	chromosome 8 open reading frame 45	0.1665	0.0032
1569685_at		Homo sapiens; clone IMAGE:4428229; mRNA	0.1423	0.0241
1569693_at	BTBD8	BTB (POZ) domain containing 8	0.1145	0.0129
1569701_at	PER3	Period homolog 3 (Drosophila)	0.4642	0.003
1569703_a_at		Homo sapiens; clone IMAGE:4043297; mRNA	0.1996	0.0023
1569813_at	STRN	striatin; calmodulin binding protein	0.2032	0.0065
1569815_x_at	STRN	striatin; calmodulin binding protein	0.3034	0.0054
1569852_at	C7orf53	chromosome 7 open reading frame 53	0.1662	0.0231
1569867_at	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.4334	0.0378
1569868_s_at	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.6978	0.0148
1569930_at		CDNA clone IMAGE:4850172	0.5238	0.0217
1569940_at	SLC6A16	Solute carrier family 6; member 16	0.8087	0.0348
1569948_at		CDNA clone IMAGE:5275301	0.1468	0.004
1569952_x_at		CDNA clone IMAGE:4814292	0.5352	0.0327
1569958_at		Homo sapiens; clone IMAGE:4064953; mRNA	0.1279	0.0408
1569973_at		Homo sapiens; clone IMAGE:4849828; mRNA	0.5246	0.001
1569974_x_at		Homo sapiens; clone IMAGE:4849828; mRNA	0.3879	0.0064
1569999_at		CDNA clone IMAGE:4837159	0.3646	0.003
1570001_at	CASP8AP2	CASP8 associated protein 2	0.1664	0.0243
1570039_at	MGC39900	hypothetical protein MGC39900	0.2534	0.0097
1570042_a_at	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	0.1847	0.0399

1570048_at	DPH4	DPH4; JJJ3 homolog (S. cerevisiae)	0.2002	0.031
1570084_at		CDNA clone IMAGE:4824356	0.1324	0.005
1570120_at		CDNA clone IMAGE:4824334	2.5427	0.0005
1570125_at		Homo sapiens; clone IMAGE:5229457; mRNA	0.2138	0.014
1570130_at	SPATS2	spermatogenesis associated; serine-rich 2	0.4173	0.0003
1570135_at	ZNF230	zinc finger protein 230	0.4308	0.0019
1570143_at		Homo sapiens; clone IMAGE:3932570; mRNA	1.219	0.0001
1570165_at		CDNA clone IMAGE:3895112	0.2787	0.0453
1570166_a_at		CDNA clone IMAGE:4719554	0.217	0.0348
1570173_at	INTS7	integrator complex subunit 7	0.2563	0.0318
1570200_at	HELB	helicase (DNA) B	0.2821	0.0004
1570227_at		CDNA clone IMAGE:4857625; with apparent retained intron	0.339	0.0004
1570253_a_at	RHEBL1	Ras homolog enriched in brain like 1	0.3488	0.0045
1570255_s_at	ANKRD20A1	ankyrin repeat domain 20 family; member A1, ankyrin repeat domain 20 family; member A2, ankyrin repeat domain 20 family; member A3, ankyrin repeat domain 20 family; member A4, ankyrin repeat domain 20B, similar to ankyrin repeat domain 20A	0.6627	0.0388
1570329_at		Homo sapiens; clone IMAGE:4853422; mRNA	0.2271	0.0366
1570351_at	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif; 6	0.2803	0.0156
1570384_at	TAS2R48	taste receptor; type 2; member 48	0.242	0.0014
1570397_x_at	FAM66C	family with sequence similarity 66; member C	0.124	0.0282
1570441_at	NAPB	N-ethylmaleimide-sensitive factor attachment protein; beta	1.0601	0.0012
1570496_at		CDNA clone IMAGE:4616837	0.3585	0.0003
1570507_at	SFRS2IP	Splicing factor; arginine/serine-rich 2; interacting protein	1.0193	0.0002
1570523_s_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	0.7274	0.0386
1570571_at	CCDC91	Coiled-coil domain containing 91	1.67	0
1570572_at	LOC729291	hypothetical protein LOC729291	0.1618	0.0235
1570578_at		CDNA clone IMAGE:5274593	0.197	0.0168
1570579_at		CDNA clone IMAGE:5274593	0.1449	0.0218
1570623_at			0.1683	0.0078
1570629_at		Homo sapiens; clone IMAGE:4401081; mRNA	0.2074	0.0189
200011_s_at	ARF3	ADP-ribosylation factor 3	0.4312	0.0064

200016_x_at	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1, similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)	0.1652	0.0041
200037_s_at	CBX3	chromobox homolog 3 (HP1 gamma homolog; Drosophila), similar to chromobox homolog 3	0.3535	0.0022
200044_at	SFRS9	splicing factor; arginine/serine-rich 9	0.4687	0.0002
200050_at	ZNF146	zinc finger protein 146	0.4552	0.0089
200060_s_at	RNPS1	RNA binding protein S1; serine-rich domain	0.338	0.0017
200063_s_at	LOC399804	nucleophosmin (nucleolar phosphoprotein B23; numatrin), similar to nucleophosmin 1 isoform 1	0.1999	0.0102
200064_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic); class B member 1	0.2778	0.0286
200068_s_at	CANX	calnexin	0.2512	0.0377
200069_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	1.3022	0
200079_s_at	KARS	lysyl-tRNA synthetase	0.296	0.0398
200098_s_at	ANAPC5	anaphase promoting complex subunit 5	0.2919	0.0137
200616_s_at	KIAA0152	KIAA0152	0.6512	0.0259
200623_s_at	CALM3	calmodulin 3 (phosphorylase kinase; delta)	1.3468	0
200627_at	PTGES3	prostaglandin E synthase 3 (cytosolic)	0.3958	0.0005
200635_s_at	PTPRF	protein tyrosine phosphatase; receptor type; F	0.9653	0.0143
200637_s_at	PTPRF	protein tyrosine phosphatase; receptor type; F	1.1867	0.007
200646_s_at	NUCB1	nucleobindin 1	0.9728	0.0038
200649_at	NUCB1	nucleobindin 1	0.7658	0.0005
200663_at	CD63	CD63 molecule	0.2959	0.0009
200664_s_at	DNAJB1	DnaJ (Hsp40) homolog; subfamily B; member 1	0.7206	0.0153
200665_s_at	SPARC	secreted protein; acidic; cysteine-rich (osteonectin)	0.6071	0.0015
200666_s_at	DNAJB1	DnaJ (Hsp40) homolog; subfamily B; member 1	0.6109	0.004
200687_s_at	SF3B3	splicing factor 3b; subunit 3; 130kDa	0.8797	0.0001
200688_at	SF3B3	splicing factor 3b; subunit 3; 130kDa	0.719	0.0044
200697_at	HK1	hexokinase 1	1.1865	0.0001
200700_s_at	KDELR2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	0.6222	0.0168
200701_at	NPC2	Niemann-Pick disease; type C2	0.3065	0.0283
200703_at	DYNLL1	dynein; light chain; LC8-type 1, similar to dynein; cytoplasmic; light peptide	0.496	0

200707_at	PRKCSH	protein kinase C substrate 80K-H	1.012	0
200708_at	GOT2	glutamic-oxaloacetic transaminase 2; mitochondrial (aspartate aminotransferase 2)	0.5607	0.0089
200712_s_at	MAPRE1	microtubule-associated protein; RP/EB family; member 1	0.827	0.0052
200713_s_at	MAPRE1	microtubule-associated protein; RP/EB family; member 1	0.6198	0
200726_at	PPP1CC	protein phosphatase 1; catalytic subunit; gamma isoform	0.334	0.0017
200727_s_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	1.0523	0.0111
200737_at	PGK1	phosphoglycerate kinase 1	0.9135	0.0014
200738_s_at	PGK1	phosphoglycerate kinase 1	0.4124	0.0003
200739_s_at	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	0.8138	0.0362
200740_s_at	SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	0.3539	0.0166
200749_at	RAN	RAN; member RAS oncogene family	0.8218	0.0007
200750_s_at	RAN	RAN; member RAS oncogene family	0.7123	0.0023
200755_s_at	CALU	calumenin	1.4715	0
200756_x_at	CALU	calumenin	2.2672	0.0001
200757_s_at	CALU	calumenin	1.1033	0
200770_s_at	LAMC1	laminin; gamma 1 (formerly LAMB2)	0.6504	0.0126
200778_s_at	2-Sep	septin 2	0.5428	0.0299
200783_s_at	STMN1	stathmin 1/oncoprotein 18	1.7885	0.0002
200794_x_at	DAZAP2	DAZ associated protein 2	0.1982	0.0231
200801_x_at	ACTB	actin; beta	0.1081	0.0119
200803_s_at	TEGT	testis enhanced gene transcript (BAX inhibitor 1)	0.5449	0.0038
200805_at	LMAN2	lectin; mannose-binding 2	0.421	0.0285
200820_at	PSMD8	proteasome (prosome; macropain) 26S subunit; non-ATPase; 8	0.6651	0.0006
200822_x_at	TPI1	triosephosphate isomerase 1	0.4131	0.0005
200827_at	PLOD1	procollagen-lysine 1; 2-oxoglutarate 5-dioxygenase 1	0.4775	0.0348
200833_s_at	RAP1B	RAP1B; member of RAS oncogene family	0.2851	0.0414
200837_at	BCAP31	B-cell receptor-associated protein 31	0.3114	0.0376
200841_s_at	EPRS	glutamyl-prolyl-tRNA synthetase	1.2062	0.0058
200842_s_at	EPRS	glutamyl-prolyl-tRNA synthetase	0.9812	0.0002
200851_s_at	KIAA0174	KIAA0174	0.4226	0.0016
200853_at	H2AFZ	H2A histone family; member Z	1.2408	0
200867_at	ZNF313	zinc finger protein 313	0.5972	0.001
200868_s_at	ZNF313	zinc finger protein 313	0.8147	0.0045
200895_s_at	FKBP4	FK506 binding protein 4; 59kDa	0.5933	0.0191
200898_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.9176	0
200899_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	0.9717	0

200900_s_at	M6PR	mannose-6-phosphate receptor (cation dependent)	1.0835	0.0019
200903_s_at	AHCY	S-adenosylhomocysteine hydrolase	0.602	0.0062
200922_at	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	1.1775	0
200925_at	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	0.2368	0.0146
200931_s_at	VCL	vinculin	0.5964	0.0033
200932_s_at	DCTN2	dynactin 2 (p50)	0.4925	0.0046
200942_s_at	HSBP1	heat shock factor binding protein 1	0.3807	0.0358
200943_at	HMGN1	high-mobility group nucleosome binding domain 1	0.4717	0.0047
200944_s_at	HMGN1	high-mobility group nucleosome binding domain 1	0.4832	0.0002
200948_at	MLF2	myeloid leukemia factor 2	0.2817	0.0376
200959_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	0.9772	0
200961_at	SEPHS2	selenophosphate synthetase 2	0.5957	0.0129
200966_x_at	ALDOA	aldolase A; fructose-bisphosphate	0.4213	0.0002
200988_s_at	PSME3	proteasome (prosome; macropain) activator subunit 3 (PA28 gamma; Ki)	0.3357	0.0357
200990_at	TRIM28	tripartite motif-containing 28	0.6655	0.0005
200998_s_at	CKAP4	cytoskeleton-associated protein 4	1.2655	0.0003
200999_s_at	CKAP4	cytoskeleton-associated protein 4	0.895	0.0016
201000_at	AARS	alanyl-tRNA synthetase	0.5898	0.006
201001_s_at	Kua-UEV	ubiquitin-conjugating enzyme E2 variant 1	0.6248	0.0078
201023_at	TAF7	TAF7 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 55kDa	0.3477	0.0227
201037_at	PFKP	phosphofructokinase; platelet	2.4263	0.0017
201039_s_at	RAD23A	RAD23 homolog A (S. cerevisiae)	0.6018	0.0071
201043_s_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family; member A	1.1563	0.0022
201046_s_at	RAD23A	RAD23 homolog A (S. cerevisiae)	0.4039	0.0019
201050_at	PLD3	phospholipase D family; member 3	0.8764	0.0001
201051_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family; member A	0.9236	0.0002
201052_s_at	PSMF1	proteasome (prosome; macropain) inhibitor subunit 1 (PI31)	0.5959	0.0088
201060_x_at	STOM	stomatin	0.4963	0.015
201065_s_at	GTF2I	general transcription factor II; i, general transcription factor II; i; pseudogene, general transcription factor II; i; pseudogene 1, similar to general transcription factor II; i isoform 1	0.2786	0.0415
201068_s_at	PSMC2	proteasome (prosome; macropain) 26S subunit; ATPase; 2	0.2543	0.0227

201072_s_at	SMARCC1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 1	0.7266	0.0063
201073_s_at	SMARCC1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 1	0.8293	0.0006
201074_at	SMARCC1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 1	0.6648	0.0004
201075_s_at	SMARCC1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 1	1.0004	0.001
201085_s_at	SON	SON DNA binding protein	0.7399	0.0297
201090_x_at	TUBA1B	tubulin; alpha 1b	0.522	0
201101_s_at	BCLAF1	BCL2-associated transcription factor 1	0.8223	0.0264
201102_s_at	PFKL	phosphofructokinase; liver	0.5804	0.003
201111_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.366	0.0415
201112_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.4649	0.0123
201115_at	POLD2	polymerase (DNA directed); delta 2; regulatory subunit 50kDa	0.4229	0.0181
201177_s_at	SAE2	SUMO1 activating enzyme subunit 2	0.3532	0.0363
201181_at	GNAI3	guanine nucleotide binding protein (G protein); alpha inhibiting activity polypeptide 3	0.6712	0.0065
201183_s_at	CHD4	chromodomain helicase DNA binding protein 4	0.752	0.0006
201184_s_at	CHD4	chromodomain helicase DNA binding protein 4	0.3288	0.0132
201194_at	SEPW1	selenoprotein W; 1	0.6211	0.0282
201202_at	PCNA	proliferating cell nuclear antigen	0.6319	0.0027
201203_s_at	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	0.7947	0.0239
201231_s_at	ENO1	enolase 1; (alpha)	0.7885	0.0009
201249_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter); member 1	0.2769	0.0133
201250_s_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter); member 1	2.1504	0.0001
201251_at	PKM2	pyruvate kinase; muscle	0.421	0.008
201264_at	COPE	coatomer protein complex; subunit epsilon	0.4374	0.0062
201270_x_at	NUDCD3	NudC domain containing 3	0.9776	0.0012
201271_s_at	RALY	RNA binding protein; autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	0.6604	0.0041
201276_at	RAB5B	RAB5B; member RAS oncogene family	0.3996	0.0022
201281_at	ADRM1	adhesion regulating molecule 1	0.4079	0.0245
201286_at	SDC1	syndecan 1	1.039	0.0458
201287_s_at	SDC1	syndecan 1	1.6023	0.0152

201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	3.5569	0
201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	4.5628	0
201293_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.1917	0.0002
201299_s_at	MOBKL1B	MOB1; Mps One Binder kinase activator-like 1B (yeast)	0.6662	0.028
201305_x_at	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family; member B	0.3974	0.0163
201306_s_at	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family; member B	0.4902	0.002
201307_at	11-Sep	septin 11	0.6372	0.0303
201308_s_at	11-Sep	septin 11	0.6212	0.0066
201309_x_at	C5orf13	chromosome 5 open reading frame 13	1.2319	0.0237
201313_at	ENO2	enolase 2 (gamma; neuronal)	1.8114	0.0184
201326_at	CCT6A	chaperonin containing TCP1; subunit 6A (zeta 1)	0.7081	0.0001
201340_s_at	ENC1	ectodermal-neural cortex (with BTB-like domain)	2.4643	0.0016
201341_at	ENC1	ectodermal-neural cortex (with BTB-like domain)	3.986	0
201342_at	SNRPC	small nuclear ribonucleoprotein polypeptide C	0.3998	0.0436
201353_s_at	BAZ2A	bromodomain adjacent to zinc finger domain; 2A	0.8919	0
201354_s_at	BAZ2A	bromodomain adjacent to zinc finger domain; 2A	0.3896	0.0154
201379_s_at	TPD52L2	tumor protein D52-like 2	0.5094	0.0286
201381_x_at	CACYBP	calcyclin binding protein	0.3414	0.0312
201386_s_at	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	0.4626	0.0154
201392_s_at	IGF2R	insulin-like growth factor 2 receptor	0.8569	0.0022
201396_s_at	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing; alpha	0.4046	0.0005
201397_at	PHGDH	phosphoglycerate dehydrogenase	1.1205	0.0383
201426_s_at	VIM	vimentin	0.3945	0.0276
201430_s_at	DPYSL3	dihydropyrimidinase-like 3	0.5813	0.0239
201431_s_at	DPYSL3	dihydropyrimidinase-like 3	1.5727	0.0034
201439_at	GBF1	golgi-specific brefeldin A resistance factor 1	0.7409	0.0066
201440_at	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	0.5815	0.0016
201446_s_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	0.8548	0.0398
201456_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	1.878	0
201458_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	1.0436	0
201475_x_at	MARS	methionyl-tRNA synthetase	0.9791	0
201476_s_at	RRM1	ribonucleotide reductase M1 polypeptide	1.1283	0.0241
201478_s_at	DKC1	dyskeratosis congenita 1; dyskerin	0.6145	0.0284

201480_s_at	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	0.6248	0.0012
201485_s_at	RCN2	reticulocalbin 2; EF-hand calcium binding domain	0.7821	0.0179
201488_x_at	KHDRBS1	KH domain containing; RNA binding; signal transduction associated 1	0.4761	0.0006
201514_s_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	0.7483	0.0283
201526_at	ARF5	ADP-ribosylation factor 5	0.6037	0.0002
201527_at	ATP6V1F	ATPase; H+ transporting; lysosomal 14kDa; V1 subunit F	0.5362	0.0007
201544_x_at	PABPN1	poly(A) binding protein; nuclear 1	0.2924	0.0243
201549_x_at	JARID1B	jumonji; AT rich interactive domain 1B	0.776	0.043
201555_at	MCM3	minichromosome maintenance complex component 3	1.5579	0.0001
201558_at	RAE1	RAE1 RNA export 1 homolog (S. pombe)	0.8097	0.001
201564_s_at	FSCN1	fascin homolog 1; actin-bundling protein (Strongylocentrotus purpuratus)	1.8871	0.0013
201576_s_at	GLB1	galactosidase; beta 1	0.4923	0.0216
201579_at	FAT	FAT tumor suppressor homolog 1 (Drosophila)	2.5862	0.0005
201584_s_at	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1.2912	0
201589_at	SMC1A	structural maintenance of chromosomes 1A	0.8647	0
201602_s_at	PPP1R12A	protein phosphatase 1; regulatory (inhibitor) subunit 12A	1.0361	0.0034
201603_at	PPP1R12A	protein phosphatase 1; regulatory (inhibitor) subunit 12A	0.3955	0.0126
201604_s_at	PPP1R12A	protein phosphatase 1; regulatory (inhibitor) subunit 12A	1.0079	0.0016
201606_s_at	PWP1	PWP1 homolog (S. cerevisiae)	0.6225	0
201607_at	PWP1	PWP1 homolog (S. cerevisiae)	0.5745	0.0138
201608_s_at	PWP1	PWP1 homolog (S. cerevisiae)	0.6787	0.0001
201613_s_at	AP1G2	adaptor-related protein complex 1; gamma 2 subunit	0.7098	0.0211
201622_at	SND1	staphylococcal nuclease and tudor domain containing 1	0.2396	0.0308
201639_s_at	CPSF1	cleavage and polyadenylation specific factor 1; 160kDa	0.7449	0.0051
201643_x_at	JMJD1B	jumonji domain containing 1B	0.5619	0.0046
201646_at	SCARB2	scavenger receptor class B; member 2	1.0742	0.0024
201647_s_at	SCARB2	scavenger receptor class B; member 2	1.3642	0.001
201656_at	ITGA6	integrin; alpha 6	0.5915	0.0294
201657_at	ARL1	ADP-ribosylation factor-like 1	0.8427	0.0062
201658_at	ARL1	ADP-ribosylation factor-like 1	0.4066	0.0461
201663_s_at	SMC4	structural maintenance of chromosomes 4	3.3714	0
201664_at	SMC4	structural maintenance of chromosomes 4	2.4966	0
201668_x_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	0.8021	0.0132

201673_s_at	GYS1	glycogen synthase 1 (muscle)	0.859	0.0309
201683_x_at	TOX4	TOX high mobility group box family member 4	0.5394	0.0371
201688_s_at	TPD52	tumor protein D52	1.3088	0.0233
201689_s_at	TPD52	tumor protein D52	1.5718	0.0156
201690_s_at	TPD52	tumor protein D52	1.519	0.0355
201692_at	OPRS1	opioid receptor; sigma 1	0.5049	0.0119
201697_s_at	DNMT1	DNA (cytosine-5-)-methyltransferase 1	1.1904	0
201698_s_at	SFRS9	splicing factor; arginine/serine-rich 9	0.4476	0.0013
201705_at	PSMD7	proteasome (prosome; macropain) 26S subunit; non-ATPase; 7	0.275	0.0356
201710_at	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0.4771	0.0376
201727_s_at	ELAVL1	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 1 (Hu antigen R)	0.7019	0.0135
201736_s_at	6-Mar	membrane-associated ring finger (C3HC4) 6	0.8285	0.0003
201737_s_at	6-Mar	membrane-associated ring finger (C3HC4) 6	0.6085	0.001
201745_at	TWF1	twinfilin; actin-binding protein; homolog 1 (Drosophila)	0.4071	0.0046
201747_s_at	SAFB	scaffold attachment factor B	0.5123	0.004
201748_s_at	SAFB	scaffold attachment factor B	0.525	0
201754_at	COX6C	cytochrome c oxidase subunit VIc	0.2115	0.0201
201755_at	MCM5	minichromosome maintenance complex component 5	1.0942	0.0084
201761_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2; methenyltetrahydrofolate cyclohydrolase	1.8331	0
201764_at	TMEM106C	transmembrane protein 106C	1.5481	0
201768_s_at	CLINT1	clathrin interactor 1	0.854	0.0061
201773_at	ADNP	activity-dependent neuroprotector homeobox	0.4494	0.003
201774_s_at	NCAPD2	non-SMC condensin I complex; subunit D2	1.7827	0.0005
201794_s_at	SMG7	Smg-7 homolog; nonsense mediated mRNA decay factor (C. elegans)	0.6476	0.011
201803_at	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B; 140kDa	0.3128	0.0244
201804_x_at	TBCB	tubulin folding cofactor B	0.4284	0.0023
201817_at	UBE3C	ubiquitin protein ligase E3C	0.7277	0.0153
201823_s_at	RNF14	ring finger protein 14	0.9284	0.0237
201834_at	PRKAB1	protein kinase; AMP-activated; beta 1 non-catalytic subunit	0.789	0.0119
201835_s_at	PRKAB1	protein kinase; AMP-activated; beta 1 non-catalytic subunit	1.2286	0.0142
201841_s_at	HSPB1	heat shock 27kDa protein 1	1.1239	0.0001
201844_s_at	RYBP	RING1 and YY1 binding protein	1.0906	0
201846_s_at	RYBP	RING1 and YY1 binding protein	1.0737	0.0007

201848_s_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	1.5029	0.0038
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	0.9047	0.0013
201851_at	SH3GL1	SH3-domain GRB2-like 1	0.5049	0.0204
201853_s_at	CDC25B	cell division cycle 25 homolog B (S. pombe)	2.6884	0
201854_s_at	ASCIZ	ATM/ATR-Substrate Chk2-Interacting Zn2+-finger protein	0.5538	0.0412
201863_at	FAM32A	family with sequence similarity 32; member A	0.6627	0.0056
201864_at	GDI1	GDP dissociation inhibitor 1	0.5732	0.0011
201868_s_at	TBL1X	transducin (beta)-like 1X-linked	0.5007	0.0248
201870_at	TOMM34	translocase of outer mitochondrial membrane 34	0.8777	0.0021
201890_at	RRM2	ribonucleotide reductase M2 polypeptide	4.6936	0
201896_s_at	PSRC1	proline/serine-rich coiled-coil 1	1.6969	0.0017
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	0.9681	0.0297
201898_s_at	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.4047	0.0327
201899_s_at	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.3692	0.0286
201917_s_at	SLC25A36	solute carrier family 25; member 36	0.8867	0.0018
201918_at	SLC25A36	Solute carrier family 25; member 36	0.943	0.0002
201920_at	SLC20A1	solute carrier family 20 (phosphate transporter); member 1	1.04	0.0016
201929_s_at	PKP4	plakophilin 4	0.7563	0.0373
201930_at	MCM6	minichromosome maintenance complex component 6	1.6906	0
201933_at	CHMP1A	chromatin modifying protein 1A	0.7139	0.0002
201939_at	PLK2	polo-like kinase 2 (Drosophila)	1.2733	0.0066
201940_at	CPD	carboxypeptidase D	0.9822	0.0005
201942_s_at	CPD	carboxypeptidase D	1.0914	0.0024
201943_s_at	CPD	carboxypeptidase D	0.9323	0.003
201944_at	HEXB	hexosaminidase B (beta polypeptide)	0.4575	0.0007
201970_s_at	NASP	nuclear autoantigenic sperm protein (histone-binding)	0.6521	0.0466
201979_s_at	PPP5C	protein phosphatase 5; catalytic subunit	1.1959	0.0005
201991_s_at	KIF5B	kinesin family member 5B	0.4037	0.0053
201992_s_at	KIF5B	kinesin family member 5B	0.5666	0.0413
202015_x_at			0.3633	0.0032
202019_s_at	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	0.5104	0.0176
202022_at	ALDOC	aldolase C; fructose-bisphosphate	2.1555	0.0025
202031_s_at	WIPI2	WD repeat domain; phosphoinositide interacting 2	0.3016	0.0276
202045_s_at	GRLF1	glucocorticoid receptor DNA binding factor 1	0.4646	0.0036
202046_s_at	GRLF1	glucocorticoid receptor DNA binding factor 1	0.3351	0.0245

202062_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	0.5368	0.0096
202064_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	0.4623	0.0247
202088_at	SLC39A6	solute carrier family 39 (zinc transporter); member 6	0.5094	0.0001
202089_s_at	SLC39A6	solute carrier family 39 (zinc transporter); member 6	1.0241	0.0006
202092_s_at	ARL2BP	ADP-ribosylation factor-like 2 binding protein	1.0784	0.0022
202094_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	1.062	0.0055
202095_s_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	3.1563	0
202098_s_at	PRMT2	protein arginine methyltransferase 2	1.3919	0.0001
202102_s_at	BRD4	bromodomain containing 4	0.952	0.0006
202107_s_at	MCM2	minichromosome maintenance complex component 2	2.7147	0
202112_at	VWF	von Willebrand factor	3.3763	0
202120_x_at	AP2S1	adaptor-related protein complex 2; sigma 1 subunit	0.3312	0.0082
202122_s_at	M6PRBP1	mannose-6-phosphate receptor binding protein 1	1.0851	0.0027
202128_at	KIAA0317	KIAA0317	0.8999	0.0181
202129_s_at	RIOK3	RIO kinase 3 (yeast)	1.058	0.0354
202141_s_at	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	0.2266	0.0365
202148_s_at	PYCR1	pyrroline-5-carboxylate reductase 1	0.8183	0.0044
202153_s_at	NUP62	nucleoporin 62kDa	0.5691	0.0055
202159_at	FARSA	phenylalanyl-tRNA synthetase; alpha subunit	0.5992	0.0046
202161_at	PKN1	protein kinase N1	0.6898	0.003
202162_s_at	CNOT8	CCR4-NOT transcription complex; subunit 8	0.6646	0.0307
202163_s_at	CNOT8	CCR4-NOT transcription complex; subunit 8	0.4105	0.0171
202164_s_at	CNOT8	CCR4-NOT transcription complex; subunit 8	0.5879	0.0377
202167_s_at	MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)	0.6195	0.0269
202175_at	CHPF	chondroitin polymerizing factor	0.9083	0.0097
202183_s_at	KIF22	kinesin family member 22, kinesin-like DNA-binding protein pseudogene	1.3365	0
202185_at	PLOD3	procollagen-lysine; 2-oxoglutarate 5-dioxygenase 3	1.2094	0
202187_s_at	PPP2R5A	protein phosphatase 2; regulatory subunit B'; alpha isoform	0.5166	0.0131
202188_at	NUP93	nucleoporin 93kDa	0.9994	0.0001
202189_x_at	PTBP1	polypyrimidine tract binding protein 1	0.4289	0.0005
202190_at	CSTF1	cleavage stimulation factor; 3' pre-RNA; subunit 1; 50kDa	0.5992	0.0296
202199_s_at	SRPK1	SFRS protein kinase 1	0.4936	0.0152
202200_s_at	SRPK1	SFRS protein kinase 1	1.0199	0.0011

202213_s_at	CUL4B	cullin 4B	0.8235	0.0135
202227_s_at	BRD8	bromodomain containing 8	0.9024	0.0002
202230_s_at	CHERP	calcium homeostasis endoplasmic reticulum protein	0.3821	0.0136
202234_s_at	SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	1.071	0.0126
202236_s_at	SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	1.219	0.0004
202240_at	PLK1	polo-like kinase 1 (Drosophila)	0.794	0.0137
202246_s_at	CDK4	cyclin-dependent kinase 4	0.7712	0.002
202253_s_at	DNM2	dynamin 2	0.7576	0
202260_s_at	STXBP1	syntaxin binding protein 1	0.8143	0.0108
202268_s_at	APPBP1	amyloid beta precursor protein binding protein 1	0.4696	0.0001
202289_s_at	TACC2	transforming; acidic coiled-coil containing protein 2	0.6539	0.0433
202301_s_at	RSRC2	arginine/serine-rich coiled-coil 2	1.0462	0.0051
202302_s_at	RSRC2	arginine/serine-rich coiled-coil 2	0.4689	0.0018
202310_s_at	COL1A1	collagen; type I; alpha 1	2.1334	0.0081
202311_s_at	COL1A1	collagen; type I; alpha 1	1.9429	0.0022
202320_at	GTF3C1	general transcription factor IIIC; polypeptide 1; alpha 220kDa	0.5505	0.0021
202323_s_at	ACBD3	acyl-Coenzyme A binding domain containing 3	1.3928	0.0011
202329_at	CSK	c-src tyrosine kinase	0.4658	0.019
202338_at	TK1	thymidine kinase 1; soluble	1.0574	0.0044
202339_at	SYMPK	symplekin	0.3815	0.0015
202345_s_at	FABP5	fatty acid binding protein 5 (psoriasis-associated), similar to Fatty acid-binding protein; epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	2.6295	0
202346_at	HIP2	huntingtin interacting protein 2	0.746	0.0008
202347_s_at	HIP2	huntingtin interacting protein 2	0.4094	0.0082
202356_s_at	GTF2F1	general transcription factor IIF; polypeptide 1; 74kDa	0.6343	0.0282
202360_at	MAML1	mastermind-like 1 (Drosophila)	0.3296	0.0219
202369_s_at	TRAM2	translocation associated membrane protein 2	0.8487	0.0437
202376_at	SERPINA3	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 3	2.0854	0.0315
202379_s_at	NKTR	natural killer-tumor recognition sequence	0.8449	0.0019
202380_s_at	NKTR	natural killer-tumor recognition sequence	0.5752	0.0104
202383_at	JARID1C	jumonji; AT rich interactive domain 1C	0.3952	0.0443
202384_s_at	TCOF1	Treacher Collins-Franceschetti syndrome 1	0.7001	0
202385_s_at	TCOF1	Treacher Collins-Franceschetti syndrome 1	0.6796	0.0003
202396_at	TCERG1	transcription elongation regulator 1	0.4929	0.0005

202397_at	NUTF2	nuclear transport factor 2	0.8143	0.0001
202405_at	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	1.0304	0.0001
202406_s_at	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	0.6373	0.0058
202407_s_at	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	1.1257	0.0027
202408_s_at	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	0.6036	0.0002
202409_at	IGF2	insulin- insulin-like growth factor 2, insulin-like growth factor 2 (somatomedin A)	2.0537	0.0132
202410_x_at	IGF2	insulin- insulin-like growth factor 2, insulin-like growth factor 2 (somatomedin A)	5.8377	0
202412_s_at	USP1	ubiquitin specific peptidase 1	1.0469	0.0079
202415_s_at	HSPBP1	hsp70-interacting protein	0.3669	0.0229
202417_at	KEAP1	kelch-like ECH-associated protein 1	1.1081	0
202421_at	IGSF3	immunoglobulin superfamily; member 3	0.7564	0.0285
202439_s_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	0.9787	0.027
202441_at	ERLIN1	ER lipid raft associated 1	0.5363	0.0184
202442_at	AP3S1	adaptor-related protein complex 3; sigma 1 subunit	0.4229	0.0026
202444_s_at	ERLIN1	ER lipid raft associated 1	1.111	0.0106
202458_at	PRSS23	protease; serine; 23	1.3998	0.0001
202462_s_at	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.5549	0.0048
202466_at	POLS	polymerase (DNA directed) sigma	0.7886	0.001
202470_s_at	CPSF6	cleavage and polyadenylation specific factor 6; 68kDa	1.0181	0.0003
202496_at	EDC4	enhancer of mRNA decapping 4	0.8747	0.0033
202503_s_at	KIAA0101	KIAA0101	5.7452	0
202507_s_at	SNAP25	synaptosomal-associated protein; 25kDa	1.7028	0.0041
202508_s_at	SNAP25	synaptosomal-associated protein; 25kDa	2.5423	0.0022
202516_s_at	DLG1	discs; large homolog 1 (Drosophila)	1.0927	0.0108
202519_at	MLXIP	MLX interacting protein	0.793	0.0128
202521_at	CTCF	CCCTC-binding factor (zinc finger protein)	0.6775	0
202532_s_at	DHFR	dihydrofolate reductase	2.3731	0
202533_s_at	DHFR	dihydrofolate reductase, similar to Dihydrofolate reductase	1.4768	0.0001
202534_x_at	DHFR	dihydrofolate reductase	2.4759	0
202556_s_at	MCRS1	microspherule protein 1	0.5038	0.0204
202558_s_at	STCH	stress 70 protein chaperone; microsome-associated; 60kDa	0.9456	0.0031
202560_s_at	C1orf77	chromosome 1 open reading frame 77	0.3564	0.0232
202570_s_at	DLGAP4	discs; large (Drosophila) homolog-associated protein 4	0.9162	0.0027
202573_at	CSNK1G2	casein kinase 1; gamma 2	0.4386	0.0001

202574_s_at	CSNK1G2	casein kinase 1; gamma 2	0.7235	0.0012
202576_s_at	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A, DEAD (Asp-Glu-Ala-As) box polypeptide 19B	0.5631	0.0008
202577_s_at	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	0.5282	0.0001
202578_s_at	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	0.8573	0.0055
202580_x_at	FOXM1	forkhead box M1	2.2412	0.0003
202589_at	TYMS	thymidylate synthetase	4.6693	0
202600_s_at	NRIP1	nuclear receptor interacting protein 1	0.5087	0.0379
202603_at		Clone MO-30 mRNA sequence	0.5321	0.0015
202604_x_at	ADAM10	ADAM metallopeptidase domain 10	1.0259	0.0069
202605_at	GUSB	glucuronidase; beta	0.8788	0.0003
202606_s_at	TLK1	tousled-like kinase 1	0.3531	0.0384
202610_s_at	MED14	mediator complex subunit 14	0.3426	0.0433
202621_at	IRF3	interferon regulatory factor 3	0.4074	0.0109
202622_s_at	ATXN2	ataxin 2	0.3652	0.0254
202633_at	TOPBP1	topoisomerase (DNA) II binding protein 1	0.9967	0
202642_s_at	TRRAP	transformation/transcription domain-associated protein	0.7847	0
202676_x_at	FASTK	Fas-activated serine/threonine kinase	0.7356	0.0001
202677_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.5986	0.0059
202683_s_at	RNMT	RNA (guanine-7-) methyltransferase	0.4318	0.0094
202694_at	STK17A	serine/threonine kinase 17a	0.687	0.0235
202695_s_at	STK17A	serine/threonine kinase 17a	1.2804	0.0211
202705_at	CCNB2	cyclin B2	4.476	0
202719_s_at	TES	testis derived transcript (3 LIM domains)	1.1025	0.0082
202726_at	LIG1	ligase I; DNA; ATP-dependent	1.9378	0.0001
202730_s_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	1.2925	0.0002
202731_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	2.3113	0
202733_at	P4HA2	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide II	3.3201	0
202744_at	SLC20A2	solute carrier family 20 (phosphate transporter); member 2	0.3041	0.0217
202754_at	R3HDM1	R3H domain containing 1	0.5682	0.0201
202755_s_at	GPC1	glypican 1	0.434	0.0405
202757_at	RP13-122B23.3	cofactor of BRCA1	0.5444	0.0088
202758_s_at	RFXANK	regulatory factor X-associated ankyrin-containing protein	0.8429	0.0001
202761_s_at	SYNE2	spectrin repeat containing; nuclear envelope 2	0.7601	0.0033
202763_at	CASP3	caspase 3; apoptosis-related cysteine peptidase	0.8699	0.0107
202765_s_at	FBN1	fibrillin 1	0.9024	0.0312

202769_at	CCNG2	cyclin G2	0.8102	0.0028
202770_s_at	CCNG2	cyclin G2	1.3177	0.0013
202773_s_at	SFRS8	splicing factor; arginine/serine-rich 8 (suppressor-of-white-apricot homolog; Drosophila)	0.7612	0.0019
202774_s_at	SFRS8	splicing factor; arginine/serine-rich 8 (suppressor-of-white-apricot homolog; Drosophila)	0.9586	0.0003
202775_s_at	SFRS8	splicing factor; arginine/serine-rich 8 (suppressor-of-white-apricot homolog; Drosophila)	0.7989	0.0008
202779_s_at	LOC731049	similar to Ubiquitin-conjugating enzyme E2S (Ubiquitin-conjugating enzyme E2-24 kDa) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-EPF5), ubiquitin-conjugating enzyme E2S	2.1205	0
202783_at	NNT	nicotinamide nucleotide transhydrogenase	0.9541	0.0022
202784_s_at	NNT	nicotinamide nucleotide transhydrogenase	1.6729	0.0008
202789_at	PLCG1	phospholipase C; gamma 1	0.8182	0.0003
202804_at	ABCC1	ATP-binding cassette; sub-family C (CFTR/MRP); member 1	0.6789	0.0049
202805_s_at	ABCC1	ATP-binding cassette; sub-family C (CFTR/MRP); member 1	1.0203	0.0006
202823_at	TCEB1	transcription elongation factor B (SIII); polypeptide 1 (15kDa; elongin C)	0.3668	0.0239
202837_at	TRAFD1	TRAF-type zinc finger domain containing 1	0.5609	0
202844_s_at	RALBP1	ralA binding protein 1	0.6721	0.0333
202852_s_at	FLJ11506	hypothetical protein FLJ11506	0.8521	0
202854_at	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	0.7173	0.0022
202868_s_at	POP4	processing of precursor 4; ribonuclease P/MRP subunit (S. cerevisiae)	0.4018	0.0207
202870_s_at	CDC20	cell division cycle 20 homolog (S. cerevisiae)	2.6433	0.0006
202873_at	ATP6V1C1	ATPase; H+ transporting; lysosomal 42kDa; V1 subunit C1	0.6848	0.0316
202892_at	CDC23	cell division cycle 23 homolog (S. cerevisiae)	1.5882	0
2028_s_at	E2F1	E2F transcription factor 1	0.4803	0.0038
202903_at	LSM5	LSM5 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.7872	0.0046
202905_x_at	NBN	nibrin	1.1108	0.0003
202906_s_at	NBN	nibrin	0.6157	0.002
202925_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	0.6313	0.0054
202934_at	HK2	hexokinase 2	1.9179	0.0027
202940_at	WNK1	WNK lysine deficient protein kinase 1	0.5141	0.0007
202951_at	STK38	serine/threonine kinase 38	0.7192	0.0203
202952_s_at	ADAM12	ADAM metallopeptidase domain 12 (meltrin alpha)	0.5798	0.0263

202954_at	UBE2C	ubiquitin-conjugating enzyme E2C	4.3808	0
202955_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	1.1725	0.0002
202956_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	0.5059	0.0012
202968_s_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	2.236	0
202969_at		MRNA; cDNA DKFZp667B0924 (from clone DKFZp667B0924)	2.1275	0
202970_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0.9912	0.006
202971_s_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	2.783	0
202998_s_at	LOXL2	lysyl oxidase-like 2	2.0748	0
203016_s_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	1.0048	0.02
203018_s_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.5004	0.0283
203019_x_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.3191	0.0475
203022_at	RNASEH2A	ribonuclease H2; subunit A	2.7082	0
203046_s_at	TIMELESS	timeless homolog (Drosophila)	1.9373	0
203047_at	STK10	serine/threonine kinase 10	0.5001	0.0421
203050_at	TP53BP1	tumor protein p53 binding protein 1	0.8491	0.0023
203062_s_at	MDC1	mediator of DNA damage checkpoint 1	0.646	0.0237
203065_s_at	CAV1	caveolin 1; caveolae protein; 22kDa	1.1843	0.0116
203072_at	LOC390588	myosin IE, similar to CDK105 protein	0.3969	0.0482
203078_at	CUL2	cullin 2	1.0809	0.0001
203079_s_at	CUL2	cullin 2	1.047	0
203082_at	BMS1	BMS1 homolog; ribosome assembly protein (yeast)	0.6063	0.0254
203086_at	KIF2A	Kinesin heavy chain member 2A	1.111	0.0006
203087_s_at	KIF2A	kinesin heavy chain member 2A	2.071	0
203092_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	0.3993	0.0028
203093_s_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	0.664	0.0006
203097_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.4593	0.023
203098_at	CDYL	chromodomain protein; Y-like	0.7307	0.0116
203105_s_at	DNM1L	dynamin 1-like	1.0713	0.0011
203109_at	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog; yeast)	0.7773	0.0012
203112_s_at	WHSC2	Wolf-Hirschhorn syndrome candidate 2	0.472	0.0025
203117_s_at	USP52	ubiquitin specific peptidase 52	0.8157	0.0203
203123_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	0.9261	0.0286
203125_x_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	0.628	0.0438

203141_s_at	AP3B1	adaptor-related protein complex 3; beta 1 subunit	0.4175	0.0457
203145_at	SPAG5	sperm associated antigen 5	2.0096	0.0003
203154_s_at	PAK4	p21(CDKN1A)-activated kinase 4	0.8679	0.0006
203163_at	KATNB1	katanin p80 (WD repeat containing) subunit B 1	0.79	0.0023
203176_s_at	TFAM	transcription factor A; mitochondrial	0.5484	0.0262
203181_x_at	SRPK2	SFRS protein kinase 2	1.134	0
203182_s_at	SRPK2	SFRS protein kinase 2	0.729	0
203192_at	ABCB6	ATP-binding cassette; sub-family B (MDR/TAP); member 6	1.1232	0.0441
203196_at	ABCC4	ATP-binding cassette; sub-family C (CFTR/MRP); member 4	0.7714	0.0131
203198_at	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	0.8875	0.011
203202_at	KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	0.9016	0.0068
203203_s_at	KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	0.5633	0.0402
203204_s_at	JMJD2A	jumonji domain containing 2A	0.5626	0.0296
203209_at	RFC5	replication factor C (activator 1) 5; 36.5kDa	2.0024	0
203210_s_at	RFC5	replication factor C (activator 1) 5; 36.5kDa	1.2016	0.0006
203213_at	CDC2	cell division cycle 2; G1 to S and G2 to M	4.7724	0
203214_x_at	CDC2	cell division cycle 2; G1 to S and G2 to M	3.4001	0
203228_at	PAFAH1B3	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit 29kDa	1.5873	0.0002
203235_at	THOP1	thimet oligopeptidase 1	0.5134	0.0016
203238_s_at	NOTCH3	Notch homolog 3 (Drosophila)	1.0293	0.0041
203253_s_at	HISPPD1	histidine acid phosphatase domain containing 1	0.4683	0.0165
203263_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	1.2228	0.0013
203270_at	DTYMK	deoxythymidylate kinase (thymidylate kinase), similar to deoxythymidylate kinase (thymidylate kinase)	0.6118	0.027
203276_at	LMNB1	lamin B1	1.8554	0.0001
203277_at	DFFA	DNA fragmentation factor; 45kDa; alpha polypeptide	0.6675	0.0275
203286_at	RNF44	ring finger protein 44	0.9443	0.0009
203288_at	KIAA0355	KIAA0355	0.6578	0.0247
203301_s_at	DMTF1	cyclin D binding myb-like transcription factor 1	0.4131	0.0008
203318_s_at	ZNF148	zinc finger protein 148	0.5467	0.0112
203319_s_at	ZNF148	zinc finger protein 148	1.0227	0.0003
203321_s_at	ADNP2	ADNP homeobox 2	0.7351	0.003
203325_s_at	COL5A1	collagen; type V; alpha 1	1.5371	0.0183

203340_s_at	SLC25A12	solute carrier family 25 (mitochondrial carrier; Aralar); member 12	0.5263	0.0408
203345_s_at	MTF2	metal response element binding transcription factor 2	0.8077	0.0414
203346_s_at	MTF2	metal response element binding transcription factor 2	1.2006	0.0033
203350_at	AP1G1	adaptor-related protein complex 1; gamma 1 subunit	0.8762	0.0012
203358_s_at	EZH2	enhancer of zeste homolog 2 (Drosophila)	2.8257	0
203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	4.0223	0
203377_s_at	CDC40	cell division cycle 40 homolog (S. cerevisiae)	0.8136	0.0214
203383_s_at	GOLGA1	golgi autoantigen; golgin subfamily a; 1	0.5135	0.0416
203396_at	PSMA4	proteasome (prosome; macropain) subunit; alpha type; 4	0.2587	0.0291
203410_at	AP3M2	adaptor-related protein complex 3; mu 2 subunit	1.7977	0
203415_at	PDCD6	programmed cell death 6	0.5622	0.0248
203418_at	CCNA2	cyclin A2	2.2331	0.0002
203419_at	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	1.4029	0
203422_at	POLD1	polymerase (DNA directed); delta 1; catalytic subunit 125kDa	1.0888	0.0011
203432_at	TMPO	thymopoietin	2.78	0
203438_at	STC2	stanniocalcin 2	1.2349	0.0305
203439_s_at	STC2	stanniocalcin 2	0.2896	0.0416
203451_at	LDB1	LIM domain binding 1	0.6456	0.0475
203459_s_at	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	0.7695	0.0005
203462_x_at	EIF3B	eukaryotic translation initiation factor 3; subunit B	0.4175	0.0128
203476_at	TPBG	trophoblast glycoprotein	2.0753	0.0146
203481_at	C10orf6	chromosome 10 open reading frame 6	0.7763	0.0234
203484_at	SEC61G	Sec61 gamma subunit	0.4117	0.0034
203490_at	ELF4	E74-like factor 4 (ets domain transcription factor)	1.1521	0
203495_at	LRRC14	leucine rich repeat containing 14	0.4561	0.0003
203510_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	1.3322	0.0307
203519_s_at	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	0.6804	0.0153
203521_s_at	ZNF318	zinc finger protein 318	0.6653	0.0026
203525_s_at	APC	adenomatosis polyposis coli	1.3339	0
203526_s_at	APC	adenomatosis polyposis coli	1.7394	0.0001
203527_s_at	APC	adenomatosis polyposis coli	0.4552	0.0345
203538_at	CAMLG	calcium modulating ligand	0.3754	0.05
203550_s_at	C1orf2	chromosome 1 open reading frame 2	0.8765	0.0105
203553_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	0.9798	0.0342

203554_x_at	PTTG1	pituitary tumor-transforming 1	5.08	0
203560_at	GGH	gamma-glutamyl hydrolase (conjugase; folylpolygammaglutamyl hydrolase)	3.2897	0
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	2.0964	0.0025
203564_at	FANCG	Fanconi anemia; complementation group G	1.5828	0
203569_s_at	OFD1	oral-facial-digital syndrome 1	0.5174	0.0352
203575_at	CSNK2A2	casein kinase 2; alpha prime polypeptide	1.1316	0.0003
203578_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter; y+ system); member 6	0.6381	0.0411
203579_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter; y+ system); member 6	1.1416	0.0064
203580_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter; y+ system); member 6	0.8609	0.0332
203590_at	DYNC1LI2	dynein; cytoplasmic 1; light intermediate chain 2	0.7954	0.0003
203600_s_at	C4orf8	chromosome 4 open reading frame 8	0.5578	0.0262
203625_x_at	SKP2	S-phase kinase-associated protein 2 (p45)	2.3142	0
203626_s_at	SKP2	S-phase kinase-associated protein 2 (p45)	0.7501	0.0291
203629_s_at	COG5	component of oligomeric golgi complex 5	0.7715	0.0001
203630_s_at	COG5	component of oligomeric golgi complex 5	1.1793	0
203636_at	MID1	midline 1 (Opitz/BBB syndrome)	0.724	0.0299
203637_s_at	MID1	midline 1 (Opitz/BBB syndrome)	0.8052	0.0109
203643_at	ERF	Ets2 repressor factor	0.6275	0.0215
203644_s_at	MON1B	MON1 homolog B (yeast)	0.6163	0.0027
203653_s_at	COIL	coilin	0.7434	0.0085
203654_s_at	COIL	coilin	0.7082	0.0061
203655_at	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	0.6251	0.0002
203664_s_at	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	0.9583	0.0044
203676_at	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	1.3728	0.0072
203677_s_at	TARBP2	TAR (HIV-1) RNA binding protein 2	1.4847	0
203695_s_at	DFNA5	deafness; autosomal dominant 5	2.2185	0.0156
203696_s_at	RFC2	replication factor C (activator 1) 2; 40kDa	1.1526	0.0017
203701_s_at	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	0.5016	0.0256
203702_s_at	TTLL4	tubulin tyrosine ligase-like family; member 4	0.93	0.0091
203709_at	PHKG2	phosphorylase kinase; gamma 2 (testis)	0.4598	0.0129
203716_s_at	DPP4	dipeptidyl-peptidase 4 (CD26; adenosine deaminase complexing protein 2)	1.3958	0.04

203717_at	DPP4	dipeptidyl-peptidase 4 (CD26; adenosine deaminase complexing protein 2)	1.2531	0.0376
203725_at	GADD45A	growth arrest and DNA-damage-inducible; alpha	1.3172	0.0021
203726_s_at	LAMA3	laminin; alpha 3	0.6072	0.0226
203730_s_at	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	1.198	0
203731_s_at	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	0.4722	0.0002
203734_at	FOXJ2	forkhead box J2	0.7173	0.0038
203736_s_at	PPFIBP1	PTPRF interacting protein; binding protein 1 (liprin beta 1)	0.7706	0.044
203738_at	C5orf22	chromosome 5 open reading frame 22	1.0909	0.0002
203744_at	HMGB3	high-mobility group box 3	1.6877	0
203746_s_at	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	0.6523	0.0486
203755_at	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	3.6796	0
203764_at	DLG7	discs; large homolog 7 (Drosophila)	2.2849	0.0002
203785_s_at	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0.6013	0.0437
203787_at	SSBP2	single-stranded DNA binding protein 2	1.0567	0.05
203795_s_at	BCL7A	B-cell CLL/lymphoma 7A	1.1843	0.0002
203796_s_at	BCL7A	B-cell CLL/lymphoma 7A	0.7247	0.0001
203802_x_at	NSUN5	NOL1/NOP2/Sun domain family; member 5	0.9155	0.0001
203805_s_at	FANCA	Fanconi anemia; complementation group A	0.9784	0.0042
203806_s_at	FANCA	Fanconi anemia; complementation group A	0.3072	0.0476
203819_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	1.5489	0.0474
203820_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	1.6969	0.0404
203823_at	RGS3	regulator of G-protein signaling 3	1.3378	0.0006
203825_at	BRD3	bromodomain containing 3	0.6346	0.0356
203828_s_at	IL32	interleukin 32	1.6462	0.0218
203830_at	C17orf75	chromosome 17 open reading frame 75	0.3988	0.0467
203832_at	SNRPF	small nuclear ribonucleoprotein polypeptide F	0.6271	0.0007
203841_x_at	MAPRE3	microtubule-associated protein; RP/EB family; member 3	0.4697	0.018
203847_s_at	AKAP8	A kinase (PRKA) anchor protein 8	0.5794	0.0008
203852_s_at	SMN1	survival of motor neuron 1; telomeric, survival of motor neuron 2; centromeric	0.5756	0.0456
203856_at	VRK1	vaccinia related kinase 1	1.0011	0.0101
203883_s_at	RAB11FIP2	RAB11 family interacting protein 2 (class I)	0.7578	0.0016
203890_s_at	DAPK3	death-associated protein kinase 3	1.0653	0.0005
203891_s_at	DAPK3	death-associated protein kinase 3	0.5082	0.0002

203899_s_at	RCP9	calcitonin gene-related peptide-receptor component protein	0.3773	0.0205
203904_x_at	CD82	CD82 molecule	0.5871	0.0032
203909_at	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger); member 6	0.4688	0.0411
203936_s_at	MMP9	matrix metallopeptidase 9 (gelatinase B; 92kDa gelatinase; 92kDa type IV collagenase)	1.1349	0.028
203937_s_at	TAF1C	TATA box binding protein (TBP)-associated factor; RNA polymerase I; C; 110kDa	0.3403	0.0261
203938_s_at	TAF1C	TATA box binding protein (TBP)-associated factor; RNA polymerase I; C; 110kDa	0.5959	0.0069
203956_at	MORC2	MORC family CW-type zinc finger 2	0.5876	0.0049
203957_at	E2F6	E2F transcription factor 6	0.6099	0.0142
203963_at	CA12	carbonic anhydrase XII	1.1432	0.025
203967_at	CDC6	cell division cycle 6 homolog (S. cerevisiae)	1.4837	0.0004
203968_s_at	CDC6	cell division cycle 6 homolog (S. cerevisiae)	1.2077	0.0013
203974_at	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	1.3661	0.001
203975_s_at	CHAF1A	chromatin assembly factor 1; subunit A (p150)	0.8412	0.0018
203976_s_at	CHAF1A	chromatin assembly factor 1; subunit A (p150)	1.0019	0.0006
203977_at	TAZ	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.284	0.0188
203985_at	ZNF212	zinc finger protein 212	0.4934	0.0102
203986_at	STBD1	starch binding domain 1	2.0252	0.0001
203990_s_at	UTX	ubiquitously transcribed tetratricopeptide repeat; X chromosome	0.8333	0.0024
203991_s_at	UTX	ubiquitously transcribed tetratricopeptide repeat; X chromosome	0.6162	0.0445
203992_s_at	UTX	ubiquitously transcribed tetratricopeptide repeat; X chromosome	0.8139	0.0353
203997_at	PTPN3	protein tyrosine phosphatase; non-receptor type 3	1.288	0.0126
204003_s_at	NUPL2	nucleoporin like 2	0.8079	0
204009_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.421	0.0086
204013_s_at	LCMT2	leucine carboxyl methyltransferase 2	0.347	0.007
204023_at	RFC4	replication factor C (activator 1) 4; 37kDa	2.3327	0
204024_at	OSGIN2	oxidative stress induced growth inhibitor family member 2	0.5231	0.032
204026_s_at	ZWINT	ZW10 interactor	3.78	0
204028_s_at	RABGAP1	RAB GTPase activating protein 1	0.5181	0.0099
204033_at	TRIP13	thyroid hormone receptor interactor 13	2.6232	0.0003
204055_s_at	CTAGE5	CTAGE family; member 5	0.6307	0.0206

204065_at	CHST10	carbohydrate sulfotransferase 10	0.8439	0.0375
204066_s_at	CENTG2	centaurin; gamma 2	1.1457	0.007
204072_s_at	FRY	furry homolog (Drosophila)	1.8229	0.0007
204076_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	0.7386	0.0001
204077_x_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	0.2787	0.0222
204092_s_at	AURKA	aurora kinase A	2.2287	0
204107_at	NFYA	nuclear transcription factor Y; alpha	0.598	0.0305
204126_s_at	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	0.8132	0.0022
204129_at	BCL9	B-cell CLL/lymphoma 9	0.3393	0.0231
204138_s_at	MZF1	myeloid zinc finger 1	0.153	0.0352
204139_x_at	MZF1	myeloid zinc finger 1	0.8856	0.0038
204146_at	RAD51AP1	RAD51 associated protein 1	3.0786	0
204148_s_at	POMZP3	POM (POM121 homolog; rat) and ZP3 fusion, zona pellucida glycoprotein 3 (sperm receptor)	1.143	0.0268
204162_at	NDC80	NDC80 homolog; kinetochore complex component (S. cerevisiae)	2.7827	0
204165_at	WASF1	WAS protein family; member 1	1.3667	0.0001
204169_at	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	0.4966	0.0129
204170_s_at	CKS2	CDC28 protein kinase regulatory subunit 2	0.7987	0.0007
204172_at	CPOX	coproporphyrinogen oxidase	0.6954	0.0251
204180_s_at	ZBTB43	zinc finger and BTB domain containing 43	0.822	0.0212
204181_s_at	ZBTB43	zinc finger and BTB domain containing 43	0.6957	0.0357
204182_s_at	ZBTB43	zinc finger and BTB domain containing 43	0.7054	0.0485
204185_x_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	0.3364	0.0327
204186_s_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	0.9428	0.0014
204195_s_at	PKNOX1	PBX/knotted 1 homeobox 1	0.2444	0.016
204199_at	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	1.2545	0.009
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP); gamma	1.3985	0.0005
204211_x_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.255	0.0439
204228_at	PPIH	peptidylprolyl isomerase H (cyclophilin H)	0.6768	0.039
204240_s_at	SMC2	structural maintenance of chromosomes 2	1.9958	0.0002
204244_s_at	DBF4	DBF4 homolog (S. cerevisiae)	2.3014	0
204245_s_at	RPP14	ribonuclease P/MRP 14kDa subunit	0.5175	0.0268
204247_s_at	CDK5	cyclin-dependent kinase 5	0.802	0.0055
204250_s_at	CEP164	centrosomal protein 164kDa	0.19	0.0269
204251_s_at	CEP164	centrosomal protein 164kDa	0.4626	0.0243
204252_at	CDK2	cyclin-dependent kinase 2	1.7388	0

204267_x_at	PKMYT1	protein kinase; membrane associated tyrosine/threonine 1	0.7834	0.0011
204275_at	SOLH	small optic lobes homolog (Drosophila)	0.48	0.0055
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.3442	0.0021
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.0803	0.0042
204291_at	ZNF518	zinc finger protein 518	0.8358	0.0127
204299_at	FUSIP1	FUS interacting protein (serine/arginine-rich) 1, similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein...	0.6166	0.0033
204302_s_at	KIAA0427	KIAA0427	0.308	0.0174
204303_s_at	KIAA0427	KIAA0427	0.9866	0.0017
204315_s_at	GTSE1	G-2 and S-phase expressed 1	1.1378	0.0028
204318_s_at	GTSE1	G-2 and S-phase expressed 1	2.0597	0.0003
204320_at	COL11A1	collagen; type XI; alpha 1	3.0856	0.0064
204325_s_at	NF1	neurofibromin 1 (neurofibromatosis; von Recklinghausen disease; Watson disease)	0.3755	0.0116
204329_s_at	ZNF202	zinc finger protein 202	0.244	0.0293
204330_s_at	MRPS12	mitochondrial ribosomal protein S12	0.3254	0.0072
204331_s_at	MRPS12	mitochondrial ribosomal protein S12	0.5358	0.0231
204347_at	AK3L2	adenylate kinase 3-like 2	1.641	0.0043
204348_s_at	AK3L1	adenylate kinase 3-like 1, adenylate kinase 3-like 2, similar to Adenylate kinase isoenzyme 4; mitochondrial (ATP-AMP transphosphorylase)	2.8316	0.0005
204352_at	TRAF5	TNF receptor-associated factor 5	1.2546	0.0316
204353_s_at	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	1.0758	0.0023
204354_at	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	0.6915	0.0004
204372_s_at	KHSRP	KH-type splicing regulatory protein (FUSE binding protein 2)	0.4802	0.0013
204375_at	CLSTN3	calsyntenin 3	0.5818	0.0151
204384_at	GOLGA2	golgi autoantigen; golgin subfamily a; 2	0.8426	0.0112
204403_x_at	FAM115A	family with sequence similarity 115; member A	0.5391	0.0034
204413_at	TRAF2	TNF receptor-associated factor 2	0.1941	0.0056
204432_at	SOX12	SRY (sex determining region Y)-box 12	0.9318	0
204434_at	SPATA2	spermatogenesis associated 2	0.6623	0.0373
204441_s_at	POLA2	polymerase (DNA directed); alpha 2 (70kD subunit)	0.6256	0.0121
204444_at	KIF11	kinesin family member 11	3.0331	0
204447_at	ProSAPiP1	ProSAPiP1 protein	0.5922	0.0417

204448_s_at	PDCL	phosducin-like	0.5305	0.0154
204449_at	PDCL	phosducin-like	0.7585	0.0007
204453_at	ZNF84	zinc finger protein 84	1.281	0
204458_at	LYPLA3	lysophospholipase 3 (lysosomal phospholipase A2)	0.521	0.0403
204461_x_at	RAD1	RAD1 homolog (S. pombe)	0.5936	0.0056
204475_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	0.3665	0.0335
204483_at	ENO3	enolase 3 (beta; muscle)	0.6102	0.0176
204491_at	PDE4D	phosphodiesterase 4D; cAMP-specific (phosphodiesterase E3 dunce homolog; Drosophila)	1.6112	0.0081
204492_at	ARHGAP11A	Rho GTPase activating protein 11A	0.3183	0.0041
204494_s_at	C15orf39	chromosome 15 open reading frame 39	1.1881	0.0003
204495_s_at	C15orf39	chromosome 15 open reading frame 39	0.5705	0.0061
204504_s_at	HIRIP3	HIRA interacting protein 3	0.7366	0.0097
204508_s_at	CA12	carbonic anhydrase XII	0.3158	0.0496
204510_at	CDC7	cell division cycle 7 homolog (S. cerevisiae)	1.9137	0.0009
204512_at	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	0.9667	0.0016
204521_at	C12orf24	chromosome 12 open reading frame 24	1.0836	0.0008
204525_at	PHF14	PHD finger protein 14	0.6912	0.0014
204526_s_at	TBC1D8	TBC1 domain family; member 8 (with GRAM domain)	1.5062	0.0134
204531_s_at	BRCA1	breast cancer 1; early onset	0.9675	0.0009
204538_x_at	LOC339047	hypothetical protein LOC339047, nuclear pore complex interacting protein, similar to nuclear pore complex interacting protein	0.6869	0.0016
204555_s_at	PPP1R3D	protein phosphatase 1; regulatory (inhibitor) subunit 3D	0.2308	0.0212
204557_s_at	DZIP1	DAZ interacting protein 1	1.2712	0.0466
204558_at	RAD54L	RAD54-like (S. cerevisiae)	0.7271	0.0067
204559_s_at	LSM7	LSM7 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.6241	0.0014
204579_at	FGFR4	fibroblast growth factor receptor 4	1.7115	0.0172
204586_at	BSN	bassoon (presynaptic cytomatrix protein)	0.4198	0.0347
204595_s_at	STC1	stanniocalcin 1	4.0226	0
204596_s_at	STC1	stanniocalcin 1	1.7396	0.0031
204597_x_at	STC1	stanniocalcin 1	2.9383	0
204601_at	N4BP1	Nedd4 binding protein 1	0.5634	0.0005
204603_at	EXO1	exonuclease 1	0.9358	0.0012
204608_at	ASL	argininosuccinate lyase	0.7599	0.0078
204617_s_at	ACD	adrenocortical dysplasia homolog (mouse)	0.7469	0.0202
204641_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2	2.4532	0.0001
204649_at	TROAP	trophinin associated protein (tastin)	1.2317	0.0005

204651_at	NRF1	nuclear respiratory factor 1	0.302	0.0371
204652_s_at	NRF1	nuclear respiratory factor 1	0.1665	0.0405
204662_at	CP110	CP110 protein	1.0807	0
204666_s_at	SIKE	suppressor of IKK epsilon	0.583	0.0202
204675_at	SRD5A1	steroid-5-alpha-reductase; alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	2.3358	0.0001
204678_s_at	KCNK1	potassium channel; subfamily K; member 1	1.3529	0.0181
204679_at	KCNK1	potassium channel; subfamily K; member 1	1.4929	0.0323
204685_s_at	ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	2.1613	0.0092
204695_at	CDC25A	cell division cycle 25 homolog A (S. pombe)	1.4316	0.0007
204698_at	ISG20	interferon stimulated exonuclease gene 20kDa	1.0884	0.0496
204699_s_at	C1orf107	chromosome 1 open reading frame 107	0.4823	0.0481
204709_s_at	KIF23	kinesin family member 23	1.9101	0.0007
204710_s_at	WIPI2	WD repeat domain; phosphoinositide interacting 2	0.7663	0
204726_at	CDH13	cadherin 13; H-cadherin (heart)	0.551	0.0001
204727_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.6913	0.0002
204728_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.7762	0.0097
204732_s_at	TRIM23	tripartite motif-containing 23	0.7604	0.0094
204741_at	BICD1	bicaudal D homolog 1 (Drosophila)	0.4748	0.0103
204742_s_at	PDS5B	PDS5; regulator of cohesion maintenance; homolog B (S. cerevisiae)	0.8042	0.0105
204744_s_at	IARS	isoleucyl-tRNA synthetase	0.3421	0.0099
204752_x_at	PARP2	poly (ADP-ribose) polymerase family; member 2	0.7361	0.0062
204760_s_at	NR1D1	nuclear receptor subfamily 1; group D; member 1, thyroid hormone receptor; alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog; avian)	1.8773	0.0001
204766_s_at	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	1.0139	0.0011
204767_s_at	FEN1	flap structure-specific endonuclease 1	0.7129	0.0394
204768_s_at	FEN1	flap structure-specific endonuclease 1	1.384	0.0019
204771_s_at	TTF1	transcription termination factor; RNA polymerase I	0.5014	0.032
204775_at	CHAF1B	chromatin assembly factor 1; subunit B (p60)	0.3485	0.0042
204776_at	THBS4	thrombospondin 4	1.3602	0.0024
204783_at	MLF1	myeloid leukemia factor 1	1.5907	0.0002
204784_s_at	MLF1	myeloid leukemia factor 1	1.6568	0.0001
204791_at	NR2C1	nuclear receptor subfamily 2; group C; member 1	0.638	0.0059
204795_at	PRR3	proline rich 3	0.684	0.0276

204797_s_at	EML1	echinoderm microtubule associated protein like 1	1.1569	0.0375
204805_s_at	H1FX	H1 histone family; member X	0.6679	0.0104
204817_at	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	1.0522	0.001
204822_at	TTK	TTK protein kinase	3.2606	0
204825_at	MELK	maternal embryonic leucine zipper kinase	3.3022	0
204826_at	CCNF	cyclin F	0.5103	0.0002
204827_s_at	CCNF	cyclin F	0.2651	0.0047
204828_at	RAD9A	RAD9 homolog A (S. pombe)	0.7703	0.002
204831_at	CDK8	cyclin-dependent kinase 8	0.9052	0.0135
204833_at	ATG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	0.6902	0.0174
204835_at	POLA1	polymerase (DNA directed); alpha 1	1.217	0.0012
204840_s_at	EEA1	early endosome antigen 1	0.8366	0.0013
204842_x_at	PRKAR2A	protein kinase; cAMP-dependent; regulatory; type II; alpha	0.3333	0.0136
204849_at	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	1.2282	0.0049
204853_at	ORC2L	origin recognition complex; subunit 2-like (yeast)	0.9816	0.0104
204859_s_at	APAF1	apoptotic peptidase activating factor 1	1.4709	0
204871_at	MTERF	mitochondrial transcription termination factor	0.6879	0.0113
204873_at	PEX1	peroxisome biogenesis factor 1	0.4451	0.0283
204884_s_at	HUS1	HUS1 checkpoint homolog (S. pombe)	0.3287	0.0282
204886_at	PLK4	polo-like kinase 4 (Drosophila)	1.5189	0.0001
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	1.6667	0.0001
204899_s_at	SAP30	Sin3A-associated protein; 30kDa	0.527	0.0202
204900_x_at	SAP30	Sin3A-associated protein; 30kDa	0.9154	0.0011
204903_x_at	ATG4B	ATG4 autophagy related 4 homolog B (S. cerevisiae)	0.3472	0.0338
204946_s_at	TOP3A	topoisomerase (DNA) III alpha	0.3353	0.0005
204947_at	E2F1	E2F transcription factor 1	0.585	0
204950_at	CARD8	caspase recruitment domain family; member 8	1.4421	0.0006
204957_at	ORC5L	origin recognition complex; subunit 5-like (yeast)	1.7204	0
204962_s_at	CENPA	centromere protein A	2.2264	0.0003
204967_at	SHROOM2	shroom family member 2	1.444	0.0314
204975_at	EMP2	epithelial membrane protein 2	1.6209	0.0109
204978_at	SFRS16	splicing factor; arginine/serine-rich 16	0.6746	0.0089
204982_at	GIT2	G protein-coupled receptor kinase interactor 2	0.5304	0.0379
204992_s_at	PFN2	profilin 2	0.6835	0.0184
204995_at	CDK5R1	cyclin-dependent kinase 5; regulatory subunit 1 (p35)	0.7646	0.0013
205005_s_at	NMT2	N-myristoyltransferase 2	0.8311	0.0287

205010_at	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	1.1985	0.013
205023_at	RAD51	RAD51 homolog (RecA homolog; E. coli) (S. cerevisiae)	0.1827	0.0038
205024_s_at	RAD51	RAD51 homolog (RecA homolog; E. coli) (S. cerevisiae)	0.9888	0.0005
205034_at	CCNE2	cyclin E2	1.7452	0.0013
205046_at	CENPE	centromere protein E; 312kDa	1.4917	0.0002
205047_s_at	ASNS	asparagine synthetase	1.9357	0
205051_s_at	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	2.3871	0.0003
205053_at	PRIM1	primase; DNA; polypeptide 1 (49kDa)	1.7435	0.0001
205060_at	LOC727726	poly (ADP-ribose) glycohydrolase, similar to poly (ADP-ribose) glycohydrolase	0.3662	0.0066
205061_s_at	EXOSC9	exosome component 9	0.3284	0.0478
205062_x_at	ARID4A	AT rich interactive domain 4A (RBP1-like)	0.826	0.0015
205063_at	SIP1	survival of motor neuron protein interacting protein 1	0.7002	0.0087
205070_at	ING3	inhibitor of growth family; member 3	0.9115	0.0033
205071_x_at	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.6804	0.0065
205072_s_at	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.6685	0.0004
205088_at	CXorf6	chromosome X open reading frame 6	1.5572	0.0103
205089_at	ZNF7	zinc finger protein 7	0.7324	0.0012
205090_s_at	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	1.166	0.0005
205091_x_at	RECQL	RecQ protein-like (DNA helicase Q1-like)	0.5568	0.0163
205095_s_at	ATP6V0A1	ATPase; H+ transporting; lysosomal V0 subunit a1	0.6802	0.0338
205106_at	MTCP1	mature T-cell proliferation 1	0.4921	0.0087
205107_s_at	EFNA4	ephrin-A4	0.6021	0.0494
205111_s_at	PLCE1	phospholipase C; epsilon 1	1.3435	0.0201
205112_at	PLCE1	phospholipase C; epsilon 1	1.1755	0.0302
205113_at	NEFM	neurofilament; medium polypeptide 150kDa	1.975	0.019
205115_s_at	RBM19	RNA binding motif protein 19	1.3259	0.0018
205122_at	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	1.4779	0.0002
205123_s_at	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	0.5041	0.0113
205146_x_at	APBA3	amyloid beta (A4) precursor protein-binding; family A; member 3 (X11-like 2)	0.36	0.0129
205148_s_at	CLCN4	chloride channel 4	0.7966	0.0019
205149_s_at	CLCN4	chloride channel 4	0.3525	0.0232

205162_at	ERCC8	excision repair cross-complementing rodent repair deficiency; complementation group 8	0.6317	0.0304
205167_s_at	CDC25C	cell division cycle 25 homolog C (S. pombe)	1.5021	0.0003
205176_s_at	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	0.9312	0.0054
205178_s_at	RBBP6	retinoblastoma binding protein 6	0.8452	0.0022
205181_at	ZNF193	zinc finger protein 193	0.8976	0.0088
205182_s_at	ZNF324	zinc finger protein 324	0.6012	0.0118
205187_at	SMAD5	SMAD family member 5	1.1093	0.0023
205188_s_at	SMAD5	SMAD family member 5	0.9348	0.0129
205194_at	PSPH	phosphoserine phosphatase	1.4069	0.0003
205195_at	AP1S1	adaptor-related protein complex 1; sigma 1 subunit	2.0717	0.0001
205196_s_at	AP1S1	adaptor-related protein complex 1; sigma 1 subunit	2.2679	0.0002
205209_at	ACVR1B	activin A receptor; type IB	0.3824	0.0156
205218_at	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F; 39 kDa	0.5124	0.0299
205222_at	EHHADH	enoyl-Coenzyme A; hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	0.8054	0.0155
205228_at	RBMS2	RNA binding motif; single stranded interacting protein 2	0.2982	0.0143
205232_s_at	PAFAH2	platelet-activating factor acetylhydrolase 2; 40kDa	0.5606	0.0182
205233_s_at	PAFAH2	platelet-activating factor acetylhydrolase 2; 40kDa	0.4416	0.0322
205235_s_at	MPHOSPH1	M-phase phosphoprotein 1	1.8257	0
205238_at	CXorf34	chromosome X open reading frame 34	1.0693	0.0098
205240_at	GPSM2	G-protein signaling modulator 2 (AGS3-like; C. elegans)	1.0342	0.0141
205244_s_at	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter); member 3	0.7271	0.0454
205250_s_at	CEP290	centrosomal protein 290kDa	0.983	0.0001
205252_at	ZNF174	zinc finger protein 174	0.6975	0
205256_at	ZBTB39	zinc finger and BTB domain containing 39	0.5029	0.0006
205262_at	KCNH2	potassium voltage-gated channel; subfamily H (eag-related); member 2	1.8411	0.0042
205264_at	CD3EAP	CD3e molecule; epsilon associated protein	0.6344	0.0266
205278_at	GAD1	glutamate decarboxylase 1 (brain; 67kDa)	2.5168	0.0008
205296_at	RBL1	retinoblastoma-like 1 (p107)	1.3511	0
205300_s_at	U1SNRNPBP	U11/U12 snRNP 35K	0.435	0.0301
205308_at	C8orf70	chromosome 8 open reading frame 70	1.4545	0
205310_at	FBXO46	F-box protein 46	0.4345	0.0415

205315_s_at	SNTB2	syntrophin; beta 2 (dystrophin-associated protein A1; 59kDa; basic component 2)	1.2658	0.0009
205339_at	STIL	SCL/TAL1 interrupting locus	2.0041	0.0001
205340_at	ZBTB24	zinc finger and BTB domain containing 24	0.6359	0.0111
205345_at	BARD1	BRCA1 associated RING domain 1	2.6194	0
205346_at	ST3GAL2	ST3 beta-galactoside alpha-2;3-sialyltransferase 2	0.4169	0.0037
205347_s_at	TMSL8	thymosin-like 8	1.6408	0.0265
205348_s_at	DYNC1I1	dynein; cytoplasmic 1; intermediate chain 1	1.8168	0.0093
205367_at	SH2B2	SH2B adaptor protein 2	0.6258	0.0041
205386_s_at	MDM2	Mdm2; transformed 3T3 cell double minute 2; p53 binding protein (mouse)	0.7488	0.0038
205393_s_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	1.211	0.003
205394_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	1.6307	0.0006
205396_at	SMAD3	SMAD family member 3	0.2546	0.0155
205397_x_at	SMAD3	SMAD family member 3	0.2361	0.0225
205398_s_at	SMAD3	SMAD family member 3	0.625	0.0011
205401_at	AGPS	alkylglycerone phosphate synthase	1.0527	0.0123
205408_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 10	0.9294	0.0132
205425_at	HIP1	huntingtin interacting protein 1	1.5275	0.0005
205426_s_at	HIP1	huntingtin interacting protein 1	0.3822	0.0166
205427_at	ZNF354A	zinc finger protein 354A	0.831	0.0173
205429_s_at	MPP6	membrane protein; palmitoylated 6 (MAGUK p55 subfamily member 6)	1.1443	0.039
205437_at	ZNF211	zinc finger protein 211	0.5335	0.0392
205447_s_at	MAP3K12	mitogen-activated protein kinase kinase kinase 12	0.5285	0.0319
205449_at	SAC3D1	SAC3 domain containing 1	0.724	0.0231
205457_at	C6orf106	chromosome 6 open reading frame 106	0.3004	0.0411
205458_at	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	0.7946	0.0012
205461_at	RAB35	RAB35; member RAS oncogene family	0.5932	0.009
205493_s_at	DPYSL4	dihydropyrimidinase-like 4	1.8365	0.0154
205494_at	LOC55565	hypothetical protein LOC55565	0.1566	0.0249
205497_at	ZNF175	zinc finger protein 175	0.5537	0.008
205511_at	FLJ10038	hypothetical protein FLJ10038	0.2446	0.0472
205519_at	WDR76	WD repeat domain 76	0.3723	0.0036
205546_s_at	TYK2	tyrosine kinase 2	0.6971	0
205548_s_at	BTG3	BTG family; member 3	0.7929	0.0054
205567_at	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	1.3976	0.0245

205569_at	LAMP3	lysosomal-associated membrane protein 3	1.0574	0.0151
205572_at	ANGPT2	angiopoietin 2	3.2439	0
205586_x_at	VGF	VGF nerve growth factor inducible	0.723	0.0265
205598_at	TRAIP	TRAF interacting protein	0.4279	0
205604_at	HOXD9	homeobox D9	0.9017	0.0045
205606_at	LRP6	low density lipoprotein receptor-related protein 6	0.9291	0.0002
205625_s_at	CALB1	calbindin 1; 28kDa	3.7776	0.0044
205626_s_at	CALB1	calbindin 1; 28kDa	3.6207	0.0046
205628_at	PRIM2	primase; DNA; polypeptide 2 (58kDa)	0.8309	0.0002
205642_at	CEP110	centrosomal protein 110kDa	0.5222	0.0287
205647_at	RAD52	RAD52 homolog (S. cerevisiae)	0.5351	0.0267
205655_at	MDM4	Mdm4; transformed 3T3 cell double minute 4; p53 binding protein (mouse)	0.2459	0.0433
205658_s_at	SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	0.5732	0.0068
205687_at	UBFD1	ubiquitin family domain containing 1	1.3949	0.0002
205690_s_at	BUD31	BUD31 homolog (S. cerevisiae)	0.4136	0.021
205700_at	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	1.5506	0.0446
205701_at	IPO8	importin 8	0.5157	0.0139
205704_s_at	ATP6V0A2	ATPase; H+ transporting; lysosomal V0 subunit a2	1.0943	0.0077
205705_at	ANKRD26	ankyrin repeat domain 26	0.2746	0.0083
205706_s_at	ANKRD26	ankyrin repeat domain 26	0.4236	0.0101
205716_at	SLC25A40	solute carrier family 25; member 40	0.8278	0.0072
205731_s_at	NCOA2	nuclear receptor coactivator 2	0.4812	0.0303
205732_s_at	NCOA2	nuclear receptor coactivator 2	0.8121	0.034
205733_at	BLM	Bloom syndrome	0.788	0.0465
205740_s_at	RBM42	RNA binding motif protein 42	0.5114	0.0029
205761_s_at	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	0.9976	0.0019
205762_s_at	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	0.5528	0.0012
205770_at	GSR	glutathione reductase	0.9882	0.0282
205787_x_at	ZC3H11A	zinc finger CCCH-type containing 11A	0.6716	0.0355
205791_x_at	ZNF230	zinc finger protein 230	0.3769	0.0232
205802_at	TRPC1	transient receptor potential cation channel; subfamily C; member 1	1.1937	0.0134
205803_s_at	TRPC1	transient receptor potential cation channel; subfamily C; member 1	1.8001	0.0008
205807_s_at	TUFT1	tuftelin 1	1.2708	0.0021
205809_s_at	WASL	Wiskott-Aldrich syndrome-like	1.42	0.0001
205810_s_at	WASL	Wiskott-Aldrich syndrome-like	0.3771	0.0135
205811_at	POLG2	polymerase (DNA directed); gamma 2; accessory subunit	0.7267	0.006

205812_s_at	TMED9	transmembrane emp24 protein transport domain containing 9	0.4365	0.0229
205813_s_at	MAT1A	methionine adenosyltransferase I; alpha	0.5202	0.0395
205822_s_at	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.9259	0.04
205830_at	CLGN	calmegin	2.3124	0.0027
205851_at	NME6	non-metastatic cells 6; protein expressed in (nucleoside-diphosphate kinase)	0.8725	0.0001
205854_at	TULP3	tubby like protein 3	0.9966	0.0029
205855_at	ZNF197	zinc finger protein 197	0.1804	0.0154
205860_x_at	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	1.2216	0.0031
205865_at	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	0.4789	0.0248
205867_at	PTPN11	protein tyrosine phosphatase; non-receptor type 11 (Noonan syndrome 1)	0.2472	0.0255
205881_at	ZNF74	zinc finger protein 74	0.3911	0.027
205882_x_at	ADD3	adducin 3 (gamma)	0.6856	0.0273
205887_x_at	MSH3	mutS homolog 3 (E. coli)	0.2144	0.0332
205888_s_at	JAKMIP2	janus kinase and microtubule interacting protein 2	2.0682	0
205889_s_at	JAKMIP2	janus kinase and microtubule interacting protein 2	1.5124	0.0006
205904_at	MICA	MHC class I polypeptide-related sequence A	1.0424	0.0046
205905_s_at	MICA	MHC class I polypeptide-related sequence A, MHC class I polypeptide-related sequence B	1.5227	0.0025
205909_at	POLE2	polymerase (DNA directed); epsilon 2 (p59 subunit)	1.6303	0.0006
205917_at	ZNF264	zinc finger protein 264	1.4159	0.0004
205928_at	ZNF443	zinc finger protein 443	0.955	0.0031
205931_s_at	CREB5	cAMP responsive element binding protein 5	0.6986	0.0089
205932_s_at	MSX1	msh homeobox 1	1.4215	0.002
205942_s_at	ACSM3	acyl-CoA synthetase medium-chain family member 3	1.726	0.0092
205956_x_at	PSMC3IP	PSMC3 interacting protein	0.3306	0.0079
205961_s_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.8206	0.0164
205967_at	HIST1H4C	histone cluster 1; H4c	0.3801	0.0324
205970_at	MT3	metallothionein 3	1.9411	0.0211
205990_s_at	WNT5A	wingless-type MMTV integration site family; member 5A	1.911	0.0153
205995_x_at	IQCB1	IQ motif containing B1	0.6416	0.0032
206003_at	CEP135	centrosomal protein 135kDa	0.8325	0.0001
206015_s_at	FOXJ3	forkhead box J3	0.3967	0.029
206016_at	CCDC22	coiled-coil domain containing 22	0.5783	0.0375
206021_at	SCAND2	SCAN domain containing 2	0.1643	0.0036
206022_at	NDP	Norrie disease (pseudoglioma)	1.6475	0.013

206031_s_at	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	0.5917	0.0008
206038_s_at	NR2C2	nuclear receptor subfamily 2; group C; member 2	0.2347	0.0261
206044_s_at	BRAF	v-raf murine sarcoma viral oncogene homolog B1	0.3152	0.0365
206046_at	ADAM23	ADAM metallopeptidase domain 23	0.6219	0.0157
206052_s_at	SLBP	stem-loop (histone) binding protein	0.5885	0.0012
206053_at	ZNF510	zinc finger protein 510	0.8459	0.005
206061_s_at	DICER1	Dicer1; Dcr-1 homolog (Drosophila)	1.4703	0
206070_s_at	EPHA3	EPH receptor A3	1.6549	0.0335
206075_s_at	CSNK2A1	casein kinase 2; alpha 1 polypeptide	0.7599	0.0173
206079_at	CHML	choroideremia-like (Rab escort protein 2)	0.1861	0.0011
206088_at	LRRC37A2	leucine rich repeat containing 37; member A2	0.5318	0.007
206091_at	MATN3	matrilin 3	0.9557	0.0388
206098_at	ZBTB6	zinc finger and BTB domain containing 6	0.5472	0.0223
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	4.1945	0
206110_at	HIST1H3H	histone cluster 1; H3h	1.166	0.0293
206114_at	EPHA4	EPH receptor A4	0.904	0.0414
206132_at	MCC	mutated in colorectal cancers	0.3617	0.0345
206135_at	ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	0.221	0.0461
206140_at	LHX2	LIM homeobox 2	1.0075	0.0316
206141_at	MOCS3	molybdenum cofactor synthesis 3	0.5593	0.023
206144_at	MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	0.6963	0.0077
206172_at	IL13RA2	interleukin 13 receptor; alpha 2	2.6241	0.0173
206188_at			1.0909	0.0005
206205_at	MPHOSPH9	M-phase phosphoprotein 9	1.4314	0.0001
206217_at	EDA	ectodysplasin A	0.7729	0.0137
206236_at	GPR4	G protein-coupled receptor 4	0.9441	0.0477
206240_s_at	ZNF136	zinc finger protein 136	1.205	0.0004
206245_s_at	IVNS1ABP	influenza virus NS1A binding protein	0.5825	0.0249
206247_at	MICB	MHC class I polypeptide-related sequence B	1.6803	0.0172
206308_at	TRDMT1	tRNA aspartic acid methyltransferase 1	0.557	0.0044
206311_s_at	PLA2G1B	phospholipase A2; group IB (pancreas)	2.9313	0.0005
206316_s_at	KNTC1	kinetochore associated 1	2.3598	0
206342_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	1.0383	0.0372
206347_at	PDK3	pyruvate dehydrogenase kinase; isozyme 3	0.1824	0.009
206348_s_at	PDK3	pyruvate dehydrogenase kinase; isozyme 3	0.7734	0.0006

206364_at	KIF14	kinesin family member 14	1.7557	0.0006
206367_at	REN	renin	1.8399	0.0424
206383_s_at	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	0.827	0.0099
206445_s_at	PRMT1	protein arginine methyltransferase 1	0.5617	0.0196
206463_s_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	1.2874	0.0378
206467_x_at	RTEL1	regulator of telomere elongation helicase 1, tumor necrosis factor receptor superfamily; member 6b; decoy	0.5468	0.0023
206470_at	PLXNC1	plexin C1	1.513	0.0044
206471_s_at	PLXNC1	plexin C1	1.7458	0.0005
206472_s_at	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog; Drosophila)	0.4841	0.0473
206474_at	PCTK2	PCTAIRE protein kinase 2	0.5006	0.0054
206487_at	UNC84A	unc-84 homolog A (C. elegans)	0.4157	0.0028
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	2.7908	0.0001
206497_at	C7orf44	chromosome 7 open reading frame 44	0.3202	0.0039
206499_s_at	RCC1	regulator of chromosome condensation 1	0.8653	0.0124
206500_s_at	C14orf106	chromosome 14 open reading frame 106	0.7889	0.0021
206507_at	ZSCAN12	zinc finger and SCAN domain containing 12	0.7753	0.0003
206516_at	AMH	anti-Mullerian hormone	0.3528	0.0478
206527_at	ABAT	4-aminobutyrate aminotransferase	1.1191	0.0354
206533_at	CHRNA5	cholinergic receptor; nicotinic; alpha 5	0.4458	0.0165
206536_s_at	BIRC4	baculoviral IAP repeat-containing 4	0.5119	0.0362
206550_s_at	NUP155	nucleoporin 155kDa	1.3479	0.0005
206551_x_at	KLHL24	kelch-like 24 (Drosophila)	0.4853	0.0207
206555_s_at	THUMPD1	THUMP domain containing 1	0.4956	0.0202
206562_s_at	CSNK1A1	casein kinase 1; alpha 1	0.4485	0.0151
206565_x_at	SMA4	glucuronidase; beta pseudogene	0.4211	0.0121
206574_s_at	PTP4A3	protein tyrosine phosphatase type IVA; member 3	1.8072	0.0004
206579_at	ZNF192	zinc finger protein 192	0.1903	0.0355
206591_at	RAG1	recombination activating gene 1	0.1655	0.0214
206592_s_at	AP3D1	adaptor-related protein complex 3; delta 1 subunit	0.3054	0.0082
206601_s_at	HOXD3	homeobox D3	1.071	0.0015
206613_s_at	TAF1A	TATA box binding protein (TBP)-associated factor; RNA polymerase I; A; 48kDa	0.8214	0.0168
206621_s_at	EIF4H	eukaryotic translation initiation factor 4H	0.2436	0.0248
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 3B	4.4753	0
206652_at	ZMYM5	zinc finger; MYM-type 5	0.6619	0.04

206656_s_at	C20orf3	chromosome 20 open reading frame 3	0.5321	0.0013
206659_at	FLJ14082	hypothetical protein FLJ14082	0.4445	0.0118
206665_s_at	BCL2L1	BCL2-like 1	0.601	0.0259
206667_s_at	SCAMP1	secretory carrier membrane protein 1	1.2299	0.0022
206668_s_at	SCAMP1	secretory carrier membrane protein 1	1.4722	0.0008
206669_at	GAD1	glutamate decarboxylase 1 (brain; 67kDa)	0.3603	0.0235
206670_s_at	GAD1	glutamate decarboxylase 1 (brain; 67kDa)	0.5799	0.0158
206685_at	HCG4	HLA complex group 4	0.9122	0.0469
206688_s_at	CPSF4	cleavage and polyadenylation specific factor 4; 30kDa	0.5252	0.0041
206695_x_at	ZNF43	zinc finger protein 43	1.2894	0.0083
206704_at	CLCN5	chloride channel 5 (nephrolithiasis 2; X-linked; Dent disease)	0.6751	0.0043
206752_s_at	DFFB	DNA fragmentation factor; 40kDa; beta polypeptide (caspase-activated DNase)	0.4186	0.004
206765_at	KCNJ2	potassium inwardly-rectifying channel; subfamily J; member 2	1.6005	0.0001
206788_s_at	CBFB	core-binding factor; beta subunit	1.1359	0.0143
206792_x_at	PDE4C	phosphodiesterase 4C; cAMP-specific (phosphodiesterase E1 dunce homolog; Drosophila)	0.5307	0.0005
206822_s_at	L3MBTL	l(3)mbt-like (Drosophila)	0.3306	0.0034
206829_x_at	ZNF430	zinc finger protein 430	1.6279	0.0007
206832_s_at	SEMA3F	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3F	0.2094	0.0219
206845_s_at	RNF40	ring finger protein 40	0.7979	0.0027
206854_s_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	0.5107	0.0192
206860_s_at	FLJ20323	hypothetical protein FLJ20323	0.5287	0.0233
206875_s_at	SLK	STE20-like kinase (yeast)	0.5826	0.0069
206892_at	AMHR2	anti-Mullerian hormone receptor; type II	1.388	0.0196
206900_x_at	ZNF253	zinc finger protein 253	0.5054	0.0241
206918_s_at	CPNE1	copine I	1.0328	0.0014
206942_s_at	PMCH	pro-melanin-concentrating hormone	0.2037	0.0459
206951_at	HIST1H4E	histone cluster 1; H4e	0.2291	0.0332
206976_s_at	HSPH1	heat shock 105kDa/110kDa protein 1	0.5098	0.0193
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	2.4939	0
207031_at	NKX3-2	NK3 homeobox 2	0.5092	0.0242
207034_s_at	GLI2	GLI-Kruppel family member GLI2	0.6141	0.0268
207039_at	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma; p16; inhibits CDK4)	1.8374	0.0003
207050_at	CACNA2D1	calcium channel; voltage-dependent; alpha 2/delta subunit 1	0.4379	0.0057

207056_s_at	SLC4A8	solute carrier family 4; sodium bicarbonate cotransporter; member 8	1.0812	0.0078
207068_at	ZFP37	zinc finger protein 37 homolog (mouse)	0.9324	0.0021
207078_at	MED6	mediator complex subunit 6	1.5008	0.0002
207079_s_at	MED6	mediator complex subunit 6	0.8954	0.0034
207090_x_at	ZFP30	zinc finger protein 30 homolog (mouse)	0.7024	0.0072
207091_at	P2RX7	purinergic receptor P2X; ligand-gated ion channel; 7	0.3186	0.041
207099_s_at	CHM	choroideremia (Rab escort protein 1)	0.4848	0.0439
207108_s_at	NIPBL	Nipped-B homolog (Drosophila)	1.209	0.0042
207120_at	ZNF667	zinc finger protein 667	1.4287	0.0072
207121_s_at	MAPK6	mitogen-activated protein kinase 6	0.9182	0.0002
207130_at	ZMYND8	zinc finger; MYND-type containing 8	1.0487	0.0001
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	3.9849	0
207168_s_at	H2AFY	H2A histone family; member Y	0.4002	0.0002
207169_x_at	DDR1	discoidin domain receptor family; member 1	0.9389	0.0043
207178_s_at	FRK	fyn-related kinase	0.51	0.019
207193_at	AGRP	agouti related protein homolog (mouse)	1.8185	0.0271
207219_at	ZNF643	zinc finger protein 643	0.2655	0.0182
207223_s_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	0.4153	0.0067
207229_at	KLRA1	killer cell lectin-like receptor subfamily A; member 1	0.2569	0.0012
207236_at	ZNF345	zinc finger protein 345	0.2982	0.0103
207253_s_at	UBN1	ubinuclein 1	0.4627	0.0004
207263_x_at	VEZT	vezatin; adherens junctions transmembrane protein	0.4152	0.0075
207265_s_at	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	0.9454	0.0262
207268_x_at	ABI2	abl interactor 2	0.8207	0.0107
207286_at	CEP135	centrosomal protein 135kDa	0.2614	0.0013
207300_s_at	F7	coagulation factor VII (serum prothrombin conversion accelerator)	0.2385	0.0164
207304_at	ZNF45	zinc finger protein 45	0.6029	0.0083
207318_s_at	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	0.6044	0.0005
207319_s_at	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	0.6837	0.0043
207331_at			0.1567	0.02
207338_s_at	ZNF200	zinc finger protein 200	0.7684	0.001
207346_at	STX2	syntaxin 2	0.4362	0.001

207347_at	ERCC6	excision repair cross-complementing rodent repair deficiency; complementation group 6	0.1994	0.0159
207357_s_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	1.017	0.0363
207365_x_at	USP34	ubiquitin specific peptidase 34	0.7845	0.0029
207373_at	HOXD10	homeobox D10	0.5378	0.0288
207393_at	HCRTR2	hypocretin (orexin) receptor 2	1.4307	0.0238
207394_at	ZNF137	zinc finger protein 137	0.6914	0.0013
207405_s_at	RAD17	RAD17 homolog (S. pombe)	0.4411	0.0046
207414_s_at	PCSK6	proprotein convertase subtilisin/kexin type 6	2.6994	0.0026
207417_s_at	ZNF177	zinc finger protein 177	1.3185	0.0001
207437_at	NOVA1	neuro-oncological ventral antigen 1	0.6605	0.0301
207439_s_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter); member A2	0.5862	0.0379
207467_x_at	CAST	calpastatin	0.4681	0.0086
207483_s_at	CAND1	cullin-associated and neddylation-dissociated 1	0.5436	0.0065
207489_at	FLJ12331	ribosomal protein S2 pseudogene	0.1115	0.0229
207499_x_at	UNC45A	unc-45 homolog A (C. elegans)	0.378	0
207522_s_at	ATP2A3	ATPase; Ca++ transporting; ubiquitous	1.412	0.0313
207525_s_at	GIPC1	GIPC PDZ domain containing family; member 1	0.6095	0.0001
207543_s_at	P4HA1	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide I	0.8915	0.0021
207559_s_at	ZMYM3	zinc finger; MYM-type 3	0.7358	0.0075
207561_s_at	ACCN3	amiloride-sensitive cation channel 3	0.2813	0.0031
207583_at	ABCD2	ATP-binding cassette; sub-family D (ALD); member 2	0.3391	0.0227
207590_s_at	CENPI	centromere protein I	0.6038	0.0052
207594_s_at	SYNJ1	synaptojanin 1	0.3579	0.0038
207598_x_at	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	0.5061	0.0017
207605_x_at	ZNF117	zinc finger protein 117	0.8859	0.0488
207606_s_at	ARHGAP12	Rho GTPase activating protein 12	0.8581	0.0069
207614_s_at	CUL1	cullin 1	0.8588	0.0001
207620_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	1.2101	0.0003
207625_s_at	CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	0.5756	0.0098
207627_s_at	TFCP2	transcription factor CP2	1.2351	0.0011
207628_s_at	WBSCR22	Williams Beuren syndrome chromosome region 22	0.5013	0.0088
207657_x_at	TNPO1	transportin 1	0.9273	0

207686_s_at	CASP8	caspase 8; apoptosis-related cysteine peptidase	0.4998	0.0231
207702_s_at	MAGI2	membrane associated guanylate kinase; WW and PDZ domain containing 2	0.9652	0.0167
207714_s_at	SERPINH1	serpin peptidase inhibitor; clade H (heat shock protein 47); member 1; (collagen binding protein 1)	1.1936	0.0005
207728_at	ATF7IP	activating transcription factor 7 interacting protein	0.446	0.0008
207730_x_at			0.4019	0.0083
207740_s_at	NUP62	nucleoporin 62kDa	0.9616	0.0034
207746_at	POLQ	polymerase (DNA directed); theta	0.9717	0.0005
207797_s_at	LRP2BP	LRP2 binding protein	0.8472	0.0056
207809_s_at	ATP6AP1	ATPase; H+ transporting; lysosomal accessory protein 1	0.7069	0.0004
207822_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	0.4678	0.0103
207824_s_at	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	0.8157	0.0004
207828_s_at	CENPF	centromere protein F; 350/400ka (mitosin)	3.1324	0
207833_s_at	HLCS	holocarboxylase synthetase (biotin-(proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)) ligase)	0.5775	0.0121
207839_s_at	C9orf127	chromosome 9 open reading frame 127	0.6293	0.0461
207856_s_at	FLJ41352	FLJ41352 protein, sphingomyelin phosphodiesterase 4; neutral membrane (neutral sphingomyelinase-3)	0.6719	0.0027
207877_s_at	NVL	nuclear VCP-like	0.5685	0.0415
207879_at			0.1205	0.0309
207891_s_at	TREX2	UCHL5 interacting protein, three prime repair exonuclease 2	0.9958	0.0034
207904_s_at	LNPEP	leucyl/cystinyl aminopeptidase	0.3094	0.0122
207937_x_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	0.3963	0.0175
207939_x_at	RNPS1	RNA binding protein S1; serine-rich domain	0.3335	0.0096
207941_s_at	RBM39	RNA binding motif protein 39	0.3549	0.0018
207953_at	RP5-886K2.1	neuronal thread protein AD7c-NTP	0.2343	0.0284
207966_s_at	GLG1	golgi apparatus protein 1	0.8849	0
207971_s_at	CEP68	centrosomal protein 68kDa	0.379	0.0021
207983_s_at	STAG2	stromal antigen 2	0.677	0.0214
207987_s_at	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	0.1954	0.0195
208002_s_at	ACOT7	acyl-CoA thioesterase 7	1.5912	0.0021
208015_at	SMAD1	SMAD family member 1	0.6852	0.001
208025_s_at	HMGA2	high mobility group AT-hook 2	2.2416	0.0083
208042_at	AGGF1	angiogenic factor with G patch and FHA domains 1	0.6315	0.0025

208050_s_at	CASP2	caspase 2; apoptosis-related cysteine peptidase (neural precursor cell expressed; developmentally down-regulated 2)	0.3739	0.012
208051_s_at	PAIP1	poly(A) binding protein interacting protein 1	0.6135	0.0046
208074_s_at	AP2S1	adaptor-related protein complex 2; sigma 1 subunit	0.3527	0.0245
208079_s_at	AURKA	aurora kinase A	3.0726	0
208082_x_at			0.2455	0.0034
208107_s_at	LOC81691	exonuclease NEF-sp	1.2799	0.0002
208113_x_at	PABPC3	poly(A) binding protein; cytoplasmic 3	0.1846	0.0287
208118_x_at	IMAA	PI-3-kinase-related kinase SMG-1 - like locus, PI-3-kinase-related kinase SMG-1 pseudogene, SLC7A5 pseudogene, hypothetical protein LOC440345, similar to PI-3-kinase-related kinase SMG-1, solute carrier family 7 (cationic amino acid transporter; y+ system); member 5 pseudogene 1	0.4798	0.0039
208119_s_at	ZNF93	zinc finger protein 93	1.2516	0.0039
208120_x_at	FKSG49	FKSG49, hypothetical protein LOC730444	0.7436	0
208137_x_at	LOC731901	similar to zinc finger protein 160, zinc finger protein 137, zinc finger protein 600, zinc finger protein 611	0.793	0
208144_s_at			0.1591	0.0422
208149_x_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog; S. cerevisiae)	1.1426	0.0003
208159_x_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog; S. cerevisiae)	0.779	0.0011
208174_x_at	ZRSR2	zinc finger (CCCH type); RNA-binding motif and serine/arginine rich 2	0.8318	0.0238
208184_s_at	TMEM1	transmembrane protein 1	0.3798	0.0413
208200_at	IL1A	interleukin 1; alpha	0.598	0.0013
208238_x_at			0.2741	0.003
208246_x_at		CDNA FLJ20006 fis; clone ADKA02694	0.3477	0.0076
208308_s_at	GPI	glucose phosphate isomerase	0.5865	0.0009
208309_s_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.4591	0.0209
208336_s_at	GPSN2	glycoprotein; synaptic 2	0.463	0.0289
208363_s_at	INPP4A	inositol polyphosphate-4-phosphatase; type I; 107kDa	0.2886	0.0317
208368_s_at	BRCA2	breast cancer 2; early onset	1.3495	0.0003
208393_s_at	RAD50	RAD50 homolog (S. cerevisiae)	0.8054	0.007
208394_x_at	ESM1	endothelial cell-specific molecule 1	1.9764	0
208424_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.7018	0.0078
208425_s_at	TANC2	tetratricopeptide repeat; ankyrin repeat and coiled-coil containing 2	0.2783	0.0053

208445_s_at	BAZ1B	bromodomain adjacent to zinc finger domain; 1B	0.6775	0.0007
208447_s_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	1.4305	0.0043
208453_s_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1; soluble	1.0646	0.0009
208459_s_at	XPO7	exportin 7	1.2565	0.0029
208478_s_at	BAX	BCL2-associated X protein	1.0448	0.0007
208490_x_at	HIST1H2BF	histone cluster 1; H2bf	0.7929	0.0462
208493_at	HOXA11	homeobox A11	0.2552	0.0169
208502_s_at	PITX1	paired-like homeodomain 1	0.7769	0.0296
208503_s_at	GATAD1	GATA zinc finger domain containing 1	1.0175	0.0004
208511_at	PTTG3	pituitary tumor-transforming 3	0.6873	0.0001
208546_x_at	HIST1H2BH	histone cluster 1; H2bh	1.1216	0.0227
208640_at	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family; small GTP binding protein Rac1)	0.2109	0.0007
208641_s_at	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family; small GTP binding protein Rac1)	0.1909	0.0169
208653_s_at	CD164	CD164 molecule; sialomucin	0.7577	0.0487
208658_at	PDIA4	protein disulfide isomerase family A; member 4	0.6219	0.0302
208660_at	CS	citrate synthase	0.3553	0.0139
208676_s_at	PA2G4	proliferation-associated 2G4; 38kDa	0.3652	0.0136
208682_s_at	MAGED2	melanoma antigen family D; 2	1.3688	0.0011
208688_x_at	EIF3B	eukaryotic translation initiation factor 3; subunit B	0.4003	0.0113
208689_s_at	RPN2	ribophorin II	0.3515	0.0057
208693_s_at	GARS	glycyl-tRNA synthetase	0.9392	0
208698_s_at	NONO	non-POU domain containing; octamer-binding	0.6687	0.0316
208702_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	0.9016	0.0034
208709_s_at	NRD1	nardilysin (N-arginine dibasic convertase)	0.2614	0.0493
208710_s_at	AP3D1	adaptor-related protein complex 3; delta 1 subunit	1.0408	0.0122
208720_s_at	RBM39	RNA binding motif protein 39	0.3291	0.0053
208721_s_at	ANAPC5	anaphase promoting complex subunit 5	0.9254	0.0202
208722_s_at	ANAPC5	anaphase promoting complex subunit 5	0.4969	0.001
208723_at	USP11	ubiquitin specific peptidase 11	1.0756	0.0001
208725_at	EIF2S2	eukaryotic translation initiation factor 2; subunit 2 beta; 38kDa	0.686	0.016
208726_s_at	EIF2S2	eukaryotic translation initiation factor 2; subunit 2 beta; 38kDa	0.3891	0.0324
208744_x_at	HSPH1	heat shock 105kDa/110kDa protein 1	1.1719	0.0081
208757_at	TMED9	transmembrane emp24 protein transport domain containing 9	0.5098	0.0263

208772_at	ANKHD1	MASK-4E-BP3 alternate reading frame gene, ankyrin repeat and KH domain containing 1	0.4638	0.0348
208773_s_at	ANKHD1	MASK-4E-BP3 alternate reading frame gene, ankyrin repeat and KH domain containing 1	0.3347	0.0393
208775_at	XPO1	exportin 1 (CRM1 homolog; yeast)	0.6359	0
208777_s_at	PSMD11	proteasome (prosome; macropain) 26S subunit; non-ATPase; 11	0.5497	0.0189
208779_x_at	DDR1	discoidin domain receptor family; member 1	0.8032	0.007
208795_s_at	MCM7	minichromosome maintenance complex component 7	1.325	0.0005
208796_s_at	CCNG1	cyclin G1	0.4175	0.0355
208797_s_at	GOLGA8B	golgi autoantigen; golgin subfamily a; 8B	0.4142	0.0082
208798_x_at	GOLGA8A	golgi autoantigen; golgin subfamily a; 8A	0.8257	0.0213
208808_s_at	HMGB2	high-mobility group box 2	1.4362	0
208815_x_at	HSPA4	heat shock 70kDa protein 4	0.5553	0.0098
208819_at	RAB8A	RAB8A; member RAS oncogene family	0.6084	0.0007
208821_at	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	0.6985	0.0006
208823_s_at	PCTK1	PCTAIRE protein kinase 1	0.599	0.0054
208837_at	TMED3	transmembrane emp24 protein transport domain containing 3	1.4621	0
208838_at	CAND1	cullin-associated and neddylation-dissociated 1	0.8113	0.0045
208839_s_at	CAND1	cullin-associated and neddylation-dissociated 1	1.0363	0
208840_s_at	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	0.6208	0.0323
208845_at	VDAC3	voltage-dependent anion channel 3	0.1869	0.0313
208846_s_at	VDAC3	voltage-dependent anion channel 3	0.4342	0.0216
208850_s_at	THY1	Thy-1 cell surface antigen	1.6165	0.0013
208851_s_at	THY1	Thy-1 cell surface antigen	1.0012	0.0122
208853_s_at	CANX	calnexin	0.9664	0.027
208879_x_at	PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	0.4961	0.0451
208882_s_at	UBR5	ubiquitin protein ligase E3 component n-recognin 5	1.19	0
208883_at	UBR5	ubiquitin protein ligase E3 component n-recognin 5	0.9977	0.0012
208884_s_at	LOC730429	similar to E3 ubiquitin protein ligase; HECT domain containing; 1, ubiquitin protein ligase E3 component n-recognin 5	0.8802	0.0001
208913_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	0.6822	0.0012
208914_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	0.9111	0.0051
208915_s_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	1.2808	0.0004

208926_at	NEU1	sialidase 1 (lysosomal sialidase)	0.884	0.0052
208930_s_at	ILF3	interleukin enhancer binding factor 3; 90kDa	1.4695	0
208931_s_at	ILF3	interleukin enhancer binding factor 3; 90kDa	0.6195	0.0238
208932_at	PPP4C	protein phosphatase 4 (formerly X); catalytic subunit	0.9434	0.0001
208947_s_at	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	0.4981	0.0081
208957_at	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	0.8893	0.011
208974_x_at	KPNB1	karyopherin (importin) beta 1	0.5198	0.001
208979_at	NCOA6	nuclear receptor coactivator 6	1.2867	0
208980_s_at	UBC	ubiquitin C	0.3704	0.0002
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	0.9788	0.0169
208986_at	TCF12	transcription factor 12 (HTF4; helix-loop-helix transcription factors 4)	0.3106	0.0086
208999_at	8-Sep	septin 8	1.175	0.0002
209000_s_at	8-Sep	septin 8	0.7919	0.0121
209012_at	TRIO	triple functional domain (PTPRF interacting)	0.3965	0.0464
209020_at	C20orf111	chromosome 20 open reading frame 111	0.6735	0.0056
209027_s_at	ABI1	abl-interactor 1	0.5583	0.0171
209032_s_at	CADM1	cell adhesion molecule 1	1.1941	0.0398
209041_s_at	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog; yeast)	0.7594	0.0183
209043_at	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.8242	0.0098
209045_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1; soluble	0.3984	0.0049
209048_s_at	ZMYND8	zinc finger; MYND-type containing 8	1.023	0.0004
209049_s_at	ZMYND8	zinc finger; MYND-type containing 8	0.6053	0.004
209052_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.4835	0.0202
209053_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	1.2939	0.001
209054_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.822	0.0014
209060_x_at	NCOA3	nuclear receptor coactivator 3	1.0138	0.0048
209062_x_at	NCOA3	nuclear receptor coactivator 3	0.3178	0.0322
209064_x_at	PAIP1	poly(A) binding protein interacting protein 1	0.6012	0.0103
209068_at	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	0.9067	0.0076
209088_s_at	UBN1	ubinuclein 1	0.8723	0.002
209098_s_at	JAG1	jagged 1 (Alagille syndrome)	2.8434	0.0003
209099_x_at	JAG1	jagged 1 (Alagille syndrome)	1.7204	0.0001
209113_s_at	HMG20B	high-mobility group 20B	0.6109	0.0093
209118_s_at	TUBA1A	tubulin; alpha 1a	0.5177	0.0095
209127_s_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	1.5973	0.0002

209128_s_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	0.4899	0
209136_s_at	USP10	ubiquitin specific peptidase 10	1.3208	0.003
209137_s_at	USP10	ubiquitin specific peptidase 10	0.5537	0.0013
209144_s_at	CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	0.2456	0.0325
209145_s_at	CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	0.3662	0.0002
209152_s_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.85	0.0028
209153_s_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.2758	0.0016
209172_s_at	CENPF	centromere protein F; 350/400ka (mitosin)	1.349	0.0002
209178_at	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	0.5037	0.0185
209190_s_at	DIAPH1	diaphanous homolog 1 (Drosophila)	0.7299	0.0061
209203_s_at	BICD2	bicaudal D homolog 2 (Drosophila)	0.6981	0.0451
209222_s_at	OSBPL2	oxysterol binding protein-like 2	0.8948	0
209225_x_at	TNPO1	transportin 1	0.7974	0
209226_s_at	TNPO1	transportin 1	0.8935	0
209231_s_at	DCTN5	dynactin 5 (p25)	1.1364	0.0015
209232_s_at	DCTN5	dynactin 5 (p25)	0.7312	0.0003
209251_x_at	TUBA1C	tubulin; alpha 1c	0.5492	0
209254_at	KIAA0265	KIAA0265 protein	0.6167	0.0215
209257_s_at	SMC3	structural maintenance of chromosomes 3	1.9967	0.0005
209258_s_at	SMC3	structural maintenance of chromosomes 3	1.3704	0.0007
209259_s_at	SMC3	structural maintenance of chromosomes 3	0.5546	0.0232
209262_s_at	NR2F6	nuclear receptor subfamily 2; group F; member 6	1.0015	0.0001
209267_s_at	SLC39A8	solute carrier family 39 (zinc transporter); member 8	2.4313	0
209281_s_at	ATP2B1	ATPase; Ca++ transporting; plasma membrane 1	1.4286	0.0001
209282_at	PRKD2	protein kinase D2	0.7985	0.0003
209284_s_at	C3orf63	chromosome 3 open reading frame 63	0.7664	0.0041
209338_at	TFCP2	transcription factor CP2	0.7719	0.0076
209344_at	TPM4	tropomyosin 4	0.8073	0.0127
209349_at	RAD50	RAD50 homolog (S. cerevisiae)	1.0898	0.0009
209367_at	STXBP2	syntaxin binding protein 2	0.8778	0.0374
209376_x_at	SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	0.8635	0.0057
209380_s_at	ABCC5	ATP-binding cassette; sub-family C (CFTR/MRP); member 5	1.1468	0.0001
209381_x_at	SF3A2	splicing factor 3a; subunit 2; 66kDa	0.4788	0.0172
209383_at	DDIT3	DNA-damage-inducible transcript 3	1.2062	0.0045

209391_at	DPM2	dolichyl-phosphate mannosyltransferase polypeptide 2; regulatory subunit	0.8454	0.0017
209404_s_at	TMED7	transmembrane emp24 protein transport domain containing 7	0.2659	0.0483
209408_at	KIF2C	kinesin family member 2C	2.1291	0.0014
209412_at	TMEM1	transmembrane protein 1	0.4018	0.0201
209440_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.6433	0.016
209446_s_at	C7orf44	chromosome 7 open reading frame 44	2.6235	0
209456_s_at	FBXW11	F-box and WD repeat domain containing 11	0.7647	0.0103
209461_x_at	WDR18	WD repeat domain 18	1.3264	0.0047
209464_at	AURKB	aurora kinase B	1.0702	0.0055
209471_s_at	FNTA	farnesyltransferase; CAAX box; alpha	0.5167	0.0161
209482_at	POP7	processing of precursor 7; ribonuclease P/MRP subunit (S. cerevisiae)	0.726	0.0002
209495_at	CEP250	centrosomal protein 250kDa	0.4692	0.0016
209507_at	RPA3	replication protein A3; 14kDa	0.6662	0.0055
209518_at	SMARCD1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily d; member 1	0.3311	0.0418
209519_at	NCBP1	nuclear cap binding protein subunit 1; 80kDa	0.5772	0.0019
209520_s_at	NCBP1	nuclear cap binding protein subunit 1; 80kDa	0.9141	0.0174
209527_at	EXOSC2	exosome component 2	0.6621	0.0069
209528_s_at	TELO2	TEL2; telomere maintenance 2; homolog (S. cerevisiae)	0.398	0.0235
209535_s_at			0.4468	0.0225
209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	0.7494	0.015
209547_s_at	SF4	splicing factor 4	0.2946	0.0076
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	2.7987	0.0008
209565_at	RNF113A	ring finger protein 113A	0.8899	0.0027
209566_at	INSIG2	insulin induced gene 2	1.2855	0.0019
209572_s_at	EED	embryonic ectoderm development	0.8433	0.0022
209575_at	IL10RB	interleukin 10 receptor; beta	0.5749	0.0437
209593_s_at	TOR1B	torsin family 1; member B (torsin B)	0.6776	0.0219
209621_s_at	PDLIM3	PDZ and LIM domain 3	0.8831	0.0474
209624_s_at	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.7646	0.0353
209626_s_at	OSBPL3	oxysterol binding protein-like 3	0.9674	0.0042
209627_s_at	OSBPL3	oxysterol binding protein-like 3	1.0149	0.0175
209628_at	NXT2	nuclear transport factor 2-like export factor 2	1.6954	0.0003
209629_s_at	NXT2	nuclear transport factor 2-like export factor 2	2.0911	0.0006

209635_at	AP1S1	adaptor-related protein complex 1; sigma 1 subunit	1.9583	0
209637_s_at	RGS12	regulator of G-protein signaling 12	0.1775	0.0386
209642_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	3.0216	0
209644_x_at	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma; p16; inhibits CDK4)	1.2395	0.0022
209653_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	1.2282	0.0054
209662_at	CETN3	centrin; EF-hand protein; 3 (CDC31 homolog; yeast)	0.4576	0.0126
209678_s_at	PRKCI	protein kinase C; iota	0.4839	0.032
209680_s_at	KIFC1	kinesin family member C1	0.6677	0.0177
209695_at	PTP4A3	protein tyrosine phosphatase type IVA; member 3	1.2152	0.0007
209709_s_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	2.6587	0
209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	3.9511	0
209715_at	CBX5	chromobox homolog 5 (HP1 alpha homolog; Drosophila)	0.9406	0.0004
209721_s_at	HOM-TES-103	hypothetical protein LOC25900	1.2599	0.0002
209725_at	LOC653877	UTP20; small subunit (SSU) processome component; homolog (yeast), similar to Down-regulated in metastasis protein (Key-1A6 protein) (Novel nucleolar protein 73) (NNP73)	0.8753	0.0021
209743_s_at	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	0.9842	0.0009
209744_x_at	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	1.219	0.0009
209750_at	NR1D2	nuclear receptor subfamily 1; group D; member 2	1.8864	0.0001
209753_s_at	TMPO	thymopoietin	1.8009	0.0001
209754_s_at	TMPO	thymopoietin	2.8766	0
209760_at	KIAA0922	KIAA0922	1.1851	0.0003
209766_at	PRDX3	peroxiredoxin 3	0.3396	0.0288
209773_s_at	RRM2	ribonucleotide reductase M2 polypeptide	4.4587	0
209780_at	PHTF2	putative homeodomain transcription factor 2	1.5697	0
209782_s_at	DBP	D site of albumin promoter (albumin D-box) binding protein	1.8434	0
209790_s_at	CASP6	caspase 6; apoptosis-related cysteine peptidase	1.3247	0.0005
209797_at	TMEM4	transmembrane protein 4	0.5834	0.0347
209799_at	PRKAA1	protein kinase; AMP-activated; alpha 1 catalytic subunit	0.5576	0.0498
209804_at	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog; S. cerevisiae)	0.8853	0
209805_at	PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae), PMS2-C terminal-like	0.7034	0.0013

209811_at	CASP2	caspase 2; apoptosis-related cysteine peptidase (neural precursor cell expressed; developmentally down-regulated 2)	0.711	0.0005
209812_x_at	CASP2	caspase 2; apoptosis-related cysteine peptidase (neural precursor cell expressed; developmentally down-regulated 2)	0.208	0.0144
209814_at	ZNF330	zinc finger protein 330	0.4637	0.0402
209832_s_at	CDT1	chromatin licensing and DNA replication factor 1	1.0482	0.0013
209833_at	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	0.7248	0.0405
209844_at	HOXB13	homeobox B13	0.1624	0.0352
209845_at	MKRN1	makorin; ring finger protein; 1	0.639	0.0038
209856_x_at	ABI2	abl interactor 2	0.593	0.039
209862_s_at	CEP57	centrosomal protein 57kDa	0.6305	0.0435
209869_at	ADRA2A	adrenergic; alpha-2A-; receptor	1.7852	0.0126
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin; bone sialoprotein I; early T-lymphocyte activation 1)	4.8771	0
209890_at	TSPAN5	tetraspanin 5	1.1887	0.0049
209891_at	SPC25	SPC25; NDC80 kinetochore complex component; homolog (S. cerevisiae)	1.4566	0.0019
209895_at	PTPN11	protein tyrosine phosphatase; non-receptor type 11 (Noonan syndrome 1)	0.9654	0.0094
209896_s_at	PTPN11	protein tyrosine phosphatase; non-receptor type 11 (Noonan syndrome 1)	1.11	0.0042
209900_s_at	SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	0.7151	0.009
209913_x_at	KIAA0415	KIAA0415	0.4779	0.0046
209921_at	SLC7A11	solute carrier family 7; (cationic amino acid transporter; y+ system) member 11	1.3524	0.0215
209922_at	BRAP	BRCA1 associated protein	0.4617	0.0278
209932_s_at	DUT	dUTP pyrophosphatase	0.4462	0.0035
209936_at	RBM5	RNA binding motif protein 5	0.5188	0.0334
209953_s_at	CDC37	cell division cycle 37 homolog (S. cerevisiae)	0.6151	0.0007
209955_s_at	FAP	fibroblast activation protein; alpha	1.8635	0.0019
209974_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	0.4305	0.0237
210008_s_at	MRPS12	mitochondrial ribosomal protein S12	0.3799	0.0119
210018_x_at	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.3281	0.0463
210021_s_at	CCNO	cyclin O	0.2604	0.0467
210022_at	PCGF1	polycomb group ring finger 1	0.7894	0.007
210023_s_at	PCGF1	polycomb group ring finger 1	0.6942	0.0098
210029_at	INDO	indoleamine-pyrrole 2;3 dioxygenase	1.0082	0.0287

210036_s_at	KCNH2	potassium voltage-gated channel; subfamily H (eag-related); member 2	2.3132	0.0043
210040_at	SLC12A5	solute carrier family 12; (potassium-chloride transporter) member 5	1.3189	0.0094
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+); mitochondrial	1.0403	0.0487
210050_at	TPI1	triosephosphate isomerase 1	0.3958	0.0046
210052_s_at	TPX2	TPX2; microtubule-associated; homolog (Xenopus laevis)	4.0424	0
210053_at	TAF5	TAF5 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 100kDa	1.0079	0.0042
210054_at	C4orf15	chromosome 4 open reading frame 15	0.8977	0.0003
210057_at	SMG1	PI-3-kinase-related kinase SMG-1	0.5343	0.0048
210074_at	CTSL2	cathepsin L2	1.1514	0.0155
210095_s_at	IGFBP3	insulin-like growth factor binding protein 3	2.7459	0
210115_at	RPL39L	ribosomal protein L39-like	1.1659	0.0019
210117_at	SPAG1	sperm associated antigen 1	0.5379	0.0152
210124_x_at	SEMA4F	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4F	0.3461	0.0121
210128_s_at	LTB4R	leukotriene B4 receptor	0.6388	0.0219
210132_at	EFNA3	ephrin-A3	0.8618	0.0472
210135_s_at	SHOX2	short stature homeobox 2	1.0153	0.0399
210188_at	GABPA	GA binding protein transcription factor; alpha subunit 60kDa	0.7626	0.0028
210203_at	CNOT4	CCR4-NOT transcription complex; subunit 4	0.8036	0.0004
210206_s_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog; S. cerevisiae)	0.5217	0.0059
210212_x_at	MTCP1	mature T-cell proliferation 1	0.6934	0.0208
210215_at	TFR2	transferrin receptor 2	0.8236	0.027
210220_at	FZD2	frizzled homolog 2 (Drosophila)	0.9297	0.0097
210240_s_at	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19; inhibits CDK4)	1.1177	0
210242_x_at	ST20	suppressor of tumorigenicity 20	0.354	0.0078
210257_x_at	CUL4B	cullin 4B	0.9549	0.019
210286_s_at	SLC4A7	solute carrier family 4; sodium bicarbonate cotransporter; member 7	0.3218	0.0057
210287_s_at	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	0.401	0.0136
210306_at	L3MBTL	l(3)mbt-like (Drosophila)	0.8986	0.0015
210334_x_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	0.9515	0.002
210336_x_at	MZF1	myeloid zinc finger 1	0.9851	0.0013
210341_at	MYT1	myelin transcription factor 1	0.5758	0.0101

210346_s_at	CLK4	CDC-like kinase 4	0.5129	0.016
210361_s_at	ELF2	E74-like factor 2 (ets domain transcription factor)	0.3479	0.0318
210368_at	PCDHGA8	protocadherin gamma subfamily A; 8, protocadherin gamma subfamily B; 4	0.5616	0.0108
210377_at	ACSM3	acyl-CoA synthetase medium-chain family member 3	2.0374	0.0084
210379_s_at	TLK1	tousled-like kinase 1	1.0807	0.0063
210400_at	GRIN2C	glutamate receptor; ionotropic; N-methyl D-aspartate 2C	0.6307	0.002
210407_at	PPM1A	protein phosphatase 1A (formerly 2C); magnesium-dependent; alpha isoform	1.127	0.0003
210410_s_at	MSH5	mutS homolog 5 (E. coli)	0.7634	0.0398
210424_s_at	GOLGA8A	golgi autoantigen; golgin subfamily a; 8A, golgi autoantigen; golgin subfamily a; 8B	0.8816	0.0037
210425_x_at	GOLGA8B	golgi autoantigen; golgin subfamily a; 8B	1.4165	0.0012
210449_x_at	MAPK14	mitogen-activated protein kinase 14	0.8891	0.0403
210455_at	C10orf28	chromosome 10 open reading frame 28	0.3194	0.0167
210463_x_at	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	0.7151	0.0047
210470_x_at	NONO	non-POU domain containing; octamer-binding	0.547	0.0286
210495_x_at	FN1	fibronectin 1	1.9731	0
210510_s_at	NRP1	neuropilin 1	0.8338	0.023
210525_x_at	C14orf143	chromosome 14 open reading frame 143	0.1012	0.0484
210527_x_at	TUBA3C	tubulin; alpha 3c	0.2317	0.011
210529_s_at	FAM115A	family with sequence similarity 115; member A, family with sequence similarity 115; member B	1.2726	0.0207
210530_s_at	NR2C1	nuclear receptor subfamily 2; group C; member 1	0.6377	0.0105
210531_at	NR2C1	nuclear receptor subfamily 2; group C; member 1	0.3573	0.019
210537_s_at	TADA2L	transcriptional adaptor 2 (ADA2 homolog; yeast)-like	0.1912	0.0259
210540_s_at	B4GALT4	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 4	0.8437	0.0031
210543_s_at	PRKDC	protein kinase; DNA-activated; catalytic polypeptide	0.9708	0.0441
210553_x_at	PCSK6	proprotein convertase subtilisin/kexin type 6	0.4431	0.0106
210555_s_at	NFATC3	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 3	0.9174	0.0007
210556_at	NFATC3	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 3	0.4516	0.047
210559_s_at	CDC2	cell division cycle 2; G1 to S and G2 to M	4.1926	0
210567_s_at	SKP2	S-phase kinase-associated protein 2 (p45)	1.3228	0.0051
210568_s_at	RECQL	RecQ protein-like (DNA helicase Q1-like)	0.7355	0.015

210585_s_at	TNPO2	transportin 2 (importin 3; karyopherin beta 2b)	0.3206	0.0051
210595_at	ZNF235	zinc finger protein 235	0.1876	0.0036
210598_at			0.5624	0.0363
210621_s_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.7563	0.0243
210627_s_at	GCS1	glucosidase I	0.5287	0.0216
210630_s_at	RAD52	RAD52 homolog (S. cerevisiae)	0.5397	0.01
210649_s_at	ARID1A	AT rich interactive domain 1A (SWI-like)	0.7481	0.0094
210650_s_at	PCLO	piccolo (presynaptic cytomatrix protein)	1.5	0.0113
210656_at	EED	embryonic ectoderm development	1.1536	0.0055
210658_s_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	1.1094	0.0002
210671_x_at	MAPK8	mitogen-activated protein kinase 8	0.2229	0.0164
210672_s_at	C16orf35	chromosome 16 open reading frame 35	0.6856	0.008
210674_s_at	PCDHA1	protocadherin alpha 1, protocadherin alpha 10, protocadherin alpha 11, protocadherin alpha 12, protocadherin alpha 13, protocadherin alpha 2, protocadherin alpha 3, protocadherin alpha 4, protocadherin alpha 5, protocadherin alpha 6, protocadherin alpha 7, protocadherin alpha 8, protocadherin alpha 9, protocadherin alpha subfamily C; 1, protocadherin alpha subfamily C; 2	2.15	0.0179
210679_x_at			0.5703	0.0037
210686_x_at	SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen); member 16	0.6295	0
210693_at	SPPL2B	signal peptide peptidase-like 2B	0.2249	0.0404
210694_s_at			0.8006	0.0077
210698_at		Clone HQ0117 PRO0117	0.1007	0.0122
210701_at	CFDP1	craniofacial development protein 1	1.3208	0.0023
210703_at			0.1568	0.009
210706_s_at	RNF24	ring finger protein 24	0.7223	0.0363
210707_x_at	PMS2L11	postmeiotic segregation increased 2-like 11	0.7363	0.0002
210717_at		PRO1412	0.4371	0.0039
210719_s_at	HMG20B	high-mobility group 20B	0.4026	0.0301
210732_s_at	LGALS8	lectin; galactoside-binding; soluble; 8 (galectin 8)	1.0324	0.0464
210743_s_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0.1721	0.0179
210749_x_at	DDR1	discoidin domain receptor family; member 1	0.999	0.0033

210758_at	PSIP1	PC4 and SFRS1 interacting protein 1	0.3729	0.0337
210760_x_at	TRIP11	thyroid hormone receptor interactor 11	0.1569	0.0017
210765_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.3798	0.0046
210766_s_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.4106	0.0273
210776_x_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.901	0.0002
210787_s_at	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2; beta	0.5414	0.0063
210800_at	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	0.3644	0.0073
210811_s_at	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	0.6295	0.0015
210813_s_at	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.7171	0.0038
210820_x_at	COQ7	coenzyme Q7 homolog; ubiquinone (yeast)	0.6655	0.0297
210821_x_at	CENPA	centromere protein A	0.5313	0.0215
210822_at	LOC283345	RPL13-2 pseudogene	0.6434	0.0318
210826_x_at	RAD17	RAD17 homolog (S. pombe)	0.9029	0.0036
210829_s_at	SSBP2	single-stranded DNA binding protein 2	1.5787	0.0043
210849_s_at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	1.1051	0
210871_x_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.3978	0.0243
210878_s_at	JMJD1B	jumonji domain containing 1B	0.5134	0.0085
210881_s_at	IGF2	insulin- insulin-like growth factor 2, insulin-like growth factor 2 (somatomedin A)	6.2195	0
210892_s_at	GTF2I	general transcription factor II; i	1.2031	0.0027
210910_s_at	POMZP3	POM (POM121 homolog; rat) and ZP3 fusion	0.9931	0.0347
210920_x_at		CDNA clone IMAGE:3609012	0.1795	0.0209
210933_s_at	FSCN1	fascin homolog 1; actin-bundling protein (Strongylocentrotus purpuratus)	1.081	0.0067
210947_s_at	MSH3	mutS homolog 3 (E. coli)	0.842	0.0012
210959_s_at	SRD5A1	steroid-5-alpha-reductase; alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.3058	0.0014
210965_x_at	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	0.3762	0
210966_x_at	LARP1	La ribonucleoprotein domain family; member 1	0.5769	0.0225
210969_at	PKN2	protein kinase N2	0.411	0.0016
210973_s_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	2.6342	0
210974_s_at	AP3D1	adaptor-related protein complex 3; delta 1 subunit	0.6911	0.0067
210975_x_at	FASTK	Fas-activated serine/threonine kinase	0.6641	0.0001

210983_s_at	MCM7	minichromosome maintenance complex component 7	1.9115	0.0005
210993_s_at	SMAD1	SMAD family member 1	1.0072	0.0034
210994_x_at	TRIM23	tripartite motif-containing 23	0.6371	0.0211
210995_s_at	TRIM23	tripartite motif-containing 23	0.9301	0.0044
211015_s_at	HSPA4	heat shock 70kDa protein 4	1.0963	0.0036
211016_x_at	HSPA4	heat shock 70kDa protein 4	1.6331	0.0018
211022_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	0.3793	0.0338
211027_s_at	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase beta	0.2412	0.0482
211034_s_at	FLJ30092	AF-1 specific protein phosphatase	0.8724	0.001
211036_x_at	ANAPC5	anaphase promoting complex subunit 5	0.4482	0.0004
211040_x_at	GTSE1	G-2 and S-phase expressed 1	0.7739	0
211042_x_at	MCAM	melanoma cell adhesion molecule	1.5492	0
211047_x_at	AP2S1	adaptor-related protein complex 2; sigma 1 subunit	0.3893	0.0048
211056_s_at	SRD5A1	steroid-5-alpha-reductase; alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.2662	0.0006
211058_x_at	TUBA1B	tubulin; alpha 1b	0.4978	0
211065_x_at	PFKL	phosphofructokinase; liver	0.8151	0.0019
211072_x_at	TUBA1B	tubulin; alpha 1b	0.4929	0
211078_s_at	STK3	serine/threonine kinase 3 (STE20 homolog; yeast)	0.3309	0.0347
211080_s_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2	0.8707	0.018
211081_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	0.588	0.0066
211085_s_at	STK4	serine/threonine kinase 4	0.5563	0.0152
211087_x_at	MAPK14	mitogen-activated protein kinase 14	0.4495	0.0167
211088_s_at	PLK4	polo-like kinase 4 (Drosophila)	0.2552	0.0249
211089_s_at	NEK3	NIMA (never in mitosis gene a)-related kinase 3	0.2891	0.035
211124_s_at	KITLG	KIT ligand	0.1771	0.043
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	2.0382	0.0002
211127_x_at	EDA	ectodysplasin A	0.7473	0.0005
211128_at	EDA	ectodysplasin A	0.2633	0.0072
211129_x_at	EDA	ectodysplasin A	0.6603	0.0002
211130_x_at	EDA	ectodysplasin A	0.9135	0.0008
211137_s_at	ATP2C1	ATPase; Ca++ transporting; type 2C; member 1	0.7218	0.0113
211148_s_at	ANGPT2	angiopoietin 2	1.9214	0.0001
211165_x_at	EPHB2	EPH receptor B2	0.4993	0.0417
211168_s_at	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	0.4085	0.0063
211202_s_at	JARID1B	jumonji; AT rich interactive domain 1B	0.6936	0.0495

211205_x_at	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase; type I; alpha	0.7503	0.0402
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.5983	0.0025
211212_s_at	ORC5L	origin recognition complex; subunit 5-like (yeast)	1.3196	0.0005
211228_s_at	RAD17	RAD17 homolog (S. pombe)	0.8694	0.0013
211237_s_at	FGFR4	fibroblast growth factor receptor 4	1.4338	0.0158
211270_x_at	PTBP1	polypyrimidine tract binding protein 1	0.4174	0.0003
211271_x_at	PTBP1	polypyrimidine tract binding protein 1	0.4106	0.0008
211277_x_at	APP	amyloid beta (A4) precursor protein (peptidase nexin-II; Alzheimer disease)	0.3972	0.0167
211296_x_at	UBC	ubiquitin C	0.1842	0.0009
211297_s_at	CDK7	cyclin-dependent kinase 7 (MO15 homolog; Xenopus laevis; cdk-activating kinase)	1.2323	0
211300_s_at	TP53	tumor protein p53 (Li-Fraumeni syndrome)	0.623	0.0274
211303_x_at	PSMAL	growth-inhibiting protein 26	0.5318	0.0181
211318_s_at	RAE1	RAE1 RNA export 1 homolog (S. pombe)	1.3486	0.0003
211352_s_at	NCOA3	nuclear receptor coactivator 3	0.8519	0.005
211374_x_at		PRO2829	0.2342	0.0042
211375_s_at	ILF3	interleukin enhancer binding factor 3; 90kDa	0.7524	0.0003
211378_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.2045	0.0001
211379_x_at	B3GALNT1	beta-1;3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	1.0983	0.0093
211382_s_at	TACC2	transforming; acidic coiled-coil containing protein 2	0.7664	0.0178
211404_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	0.6756	0.006
211411_at		LDLR-FUT fusion protein (LDLR-FUT)	0.148	0.0493
211422_at	TRPM3	transient receptor potential cation channel; subfamily M; member 3	0.2938	0.0465
211424_x_at	METTL7A	methyltransferase like 7A	0.3059	0.0257
211454_x_at	FKSG49	FKSG49	0.7222	0.0001
211459_at			0.1661	0.0075
211464_x_at	CASP6	caspase 6; apoptosis-related cysteine peptidase	0.549	0.01
211466_at	NFIB	nuclear factor I/B	0.3868	0.0168
211471_s_at	RAB36	RAB36; member RAS oncogene family	0.3346	0.0434
211478_s_at	DPP4	dipeptidyl-peptidase 4 (CD26; adenosine deaminase complexing protein 2)	1.6858	0.0243
211502_s_at	PFTK1	PFTAIRE protein kinase 1	0.2091	0.0045
211518_s_at	BMP4	bone morphogenetic protein 4	1.597	0.0143
211519_s_at	KIF2C	kinesin family member 2C	1.0431	0.0276

211522_s_at	GNRHR	gonadotropin-releasing hormone receptor	1.5292	0.0313
211526_s_at	RTEL1	regulator of telomere elongation helicase 1	0.2083	0.0059
211535_s_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	2.1148	0
211536_x_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	1.067	0.0043
211537_x_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	0.9071	0.0332
211543_s_at	GRK6	G protein-coupled receptor kinase 6	0.3439	0.0206
211547_s_at	PAFAH1B1	platelet-activating factor acetylhydrolase; isoform Ib; alpha subunit 45kDa	0.9249	0.0177
211553_x_at	APAF1	apoptotic peptidase activating factor 1	0.118	0.0136
211554_s_at	APAF1	apoptotic peptidase activating factor 1	0.2701	0.0001
211555_s_at	GUCY1B3	guanylate cyclase 1; soluble; beta 3	0.4241	0.0103
211559_s_at	CCNG2	cyclin G2	1.6908	0.0025
211561_x_at	MAPK14	mitogen-activated protein kinase 14	1.0118	0.0273
211565_at	SH3GL3	SH3-domain GRB2-like 3	0.2076	0.0287
211602_s_at	TRPC1	transient receptor potential cation channel; subfamily C; member 1	1.0378	0.002
211651_s_at	LAMB1	laminin; beta 1	1.1427	0.0413
211671_s_at	NR3C1	nuclear receptor subfamily 3; group C; member 1 (glucocorticoid receptor)	0.8075	0.0131
211678_s_at	ZNF313	zinc finger protein 313	0.3045	0.0163
211707_s_at	IQCB1	IQ motif containing B1	0.5474	0.0215
211708_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	1.8124	0.0283
211713_x_at	KIAA0101	KIAA0101	0.8302	0.0005
211719_x_at	FN1	fibronectin 1	1.6998	0.0001
211721_s_at	ZNF551	zinc finger protein 551	1.2018	0.0011
211750_x_at	TUBA1C	tubulin; alpha 1c	0.5755	0
211759_x_at	TBCB	tubulin folding cofactor B	0.4674	0.0022
211762_s_at	KPNA2	karyopherin alpha 2 (RAG cohort 1; importin alpha 1)	0.8129	0.0107
211765_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.2002	0.0001
211766_s_at	PNLIPRP2	pancreatic lipase-related protein 2	0.5363	0.0408
211767_at	GINS4	GINS complex subunit 4 (Sld5 homolog)	0.8169	0.0045
211789_s_at	MLXIP	MLX interacting protein	0.5467	0.0031
211793_s_at	ABI2	abl interactor 2	0.9129	0.0108
211804_s_at	CDK2	cyclin-dependent kinase 2	0.9507	0.0134
211812_s_at	B3GALNT1	beta-1;3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	0.8761	0.0063
211814_s_at	CCNE2	cyclin E2	0.608	0.021
211828_s_at	TNIK	TRAF2 and NCK interacting kinase	1.9247	0.0031

211833_s_at	BAX	BCL2-associated X protein	1.8962	0
211851_x_at	BRCA1	breast cancer 1; early onset	0.3677	0.0119
211855_s_at	SLC25A14	solute carrier family 25 (mitochondrial carrier; brain); member 14	0.6119	0.038
211865_s_at	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.3034	0.039
211874_s_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.58	0.0116
211875_x_at	PCDHGA10	protocadherin gamma subfamily A; 10	0.5085	0.0252
211923_s_at	ZNF471	zinc finger protein 471	0.1509	0.044
211928_at	DYNC1H1	dynein; cytoplasmic 1; heavy chain 1	0.3215	0.0461
211935_at	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	0.2794	0.0071
211947_s_at	BAT2D1	BAT2 domain containing 1	0.6941	0.0251
211948_x_at	BAT2D1	BAT2 domain containing 1	0.738	0.0228
211968_s_at	HSP90AA1	heat shock protein 90kDa alpha (cytosolic); class A member 1	0.3327	0.037
211969_at	HSP90AA1	heat shock protein 90kDa alpha (cytosolic); class A member 1	0.2526	0.0245
211977_at	GPR107	G protein-coupled receptor 107	0.718	0.0296
211978_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.213	0
211980_at	COL4A1	collagen; type IV; alpha 1	0.8157	0.0011
211981_at	COL4A1	collagen; type IV; alpha 1	1.4477	0.0029
211982_x_at	XPO6	exportin 6	0.8572	0
211992_at	WNK1	WNK lysine deficient protein kinase 1	0.4709	0.0082
211994_at	WNK1	WNK lysine deficient protein kinase 1	0.4977	0.0093
211996_s_at	DKFZp547E087	KIAA0220-like protein, hypothetical gene LOC283846, hypothetical protein LOC440345, nuclear pore complex interacting protein pseudogene, similar to Protein KIAA0220	0.4563	0.0108
212000_at	SFRS14	splicing factor; arginine/serine-rich 14	1.0501	0
212001_at	SFRS14	splicing factor; arginine/serine-rich 14	0.7479	0.0001
212007_at	UBXD2	UBX domain containing 2	0.4566	0.0151
212008_at	UBXD2	UBX domain containing 2	1.1925	0.0018
212009_s_at	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	1.2424	0.0239
212015_x_at	PTBP1	polypyrimidine tract binding protein 1	0.4245	0.0008
212016_s_at	PTBP1	polypyrimidine tract binding protein 1	0.6567	0.0085
212020_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	1.1359	0.0048
212021_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	2.1302	0.0015
212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	2.0319	0.001

212023_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	1.289	0.0036
212028_at	RBM25	RNA binding motif protein 25	0.5741	0.0277
212030_at	RBM25	RNA binding motif protein 25	0.5476	0.0341
212038_s_at	VDAC1	voltage-dependent anion channel 1	0.3917	0.0243
212045_at	GLG1	golgi apparatus protein 1	0.8229	0.0009
212053_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.4936	0.0065
212058_at	SR140	U2-associated SR140 protein	0.4128	0.0217
212060_at	SR140	U2-associated SR140 protein	0.5697	0.0021
212064_x_at	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	0.6455	0.0003
212072_s_at	CSNK2A1	casein kinase 2; alpha 1 polypeptide	0.6063	0.0043
212073_at	CSNK2A1	casein kinase 2; alpha 1 polypeptide, casein kinase 2; alpha 1 polypeptide pseudogene	0.6325	0.0111
212074_at	UNC84A	unc-84 homolog A (C. elegans)	0.3319	0.0243
212075_s_at	CSNK2A1	casein kinase 2; alpha 1 polypeptide	1.4618	0.0002
212079_s_at	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila)	0.6133	0.0123
212082_s_at	MYL6	myosin; light chain 6; alkali; smooth muscle and non-muscle	0.1587	0.0194
212097_at	CAV1	caveolin 1; caveolae protein; 22kDa	1.1133	0.0104
212098_at	LOC151162	hypothetical protein LOC151162	0.4515	0.0433
212104_s_at	RBM9	RNA binding motif protein 9	0.8892	0.0082
212105_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.4715	0.0456
212107_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.8366	0.0385
212113_at	LOC552889	hypothetical LOC552889	0.85	0.0001
212114_at	LOC552889	hypothetical LOC552889	0.4881	0.0069
212115_at	HN1L	hematological and neurological expressed 1-like	0.4717	0.025
212126_at		CDNA clone IMAGE:4842353	1.3814	0
212132_at	LSM14A	LSM14A; SCD6 homolog A (S. cerevisiae)	0.5226	0.0134
212137_at	LARP1	La ribonucleoprotein domain family; member 1	0.2652	0.0047
212138_at	PDS5A	PDS5; regulator of cohesion maintenance; homolog A (S. cerevisiae)	0.4911	0.0001
212141_at	MCM4	minichromosome maintenance complex component 4	1.6416	0.0001
212142_at	MCM4	minichromosome maintenance complex component 4	0.7422	0.003
212143_s_at	IGFBP3	insulin-like growth factor binding protein 3	3.8834	0
212152_x_at	ARID1A	AT rich interactive domain 1A (SWI-like)	0.4961	0.0089
212154_at	SDC2	syndecan 2	2.318	0.0002
212157_at	SDC2	syndecan 2	1.3819	0.0163
212158_at	SDC2	syndecan 2	1.7044	0.002

212160_at	XPOT	exportin; tRNA (nuclear export receptor for tRNAs)	0.8775	0
212162_at	KIDINS220	kinase D-interacting substrate of 220 kDa	0.4464	0.0184
212178_s_at	LOC100101267	POM121 membrane glycoprotein (rat), POM121 membrane glycoprotein (rat) pseudogene, POM121 membrane glycoprotein (rat)-like	0.6591	0.0226
212189_s_at	COG4	component of oligomeric golgi complex 4	0.3038	0.0364
212190_at	SERPINE2	serpin peptidase inhibitor; clade E (nexin; plasminogen activator inhibitor type 1); member 2	1.7573	0.0367
212193_s_at	LARP1	La ribonucleoprotein domain family; member 1	0.7449	0.0053
212194_s_at	TM9SF4	transmembrane 9 superfamily protein member 4	1.8922	0
212198_s_at	TM9SF4	transmembrane 9 superfamily protein member 4	1.0873	0.0001
212202_s_at	TMEM87A	transmembrane protein 87A	0.4577	0.0135
212207_at	MED13L	mediator complex subunit 13-like	0.4994	0.0391
212208_at	MED13L	mediator complex subunit 13-like	0.7554	0.0117
212220_at	PSME4	proteasome (prosome; macropain) activator subunit 4	0.8546	0.0419
212234_at	ASXL1	additional sex combs like 1 (Drosophila)	0.5301	0.0162
212238_at	ASXL1	additional sex combs like 1 (Drosophila)	0.91	0.0024
212247_at	NUP205	nucleoporin 205kDa	0.9583	0
212252_at	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2; beta	0.6521	0.0172
212272_at	LPIN1	lipin 1	1.0745	0.0054
212274_at	LPIN1	lipin 1	1.1413	0.0003
212276_at	LPIN1	lipin 1	0.8593	0.0071
212303_x_at			0.4546	0.0034
212307_s_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	1.0114	0.0285
212317_at	TNPO3	transportin 3	0.7333	0.0002
212318_at	TNPO3	transportin 3	0.8048	0
212320_at	TUBB	tubulin; beta	0.341	0.0379
212322_at	SGPL1	sphingosine-1-phosphate lyase 1	0.6765	0.0041
212332_at	RBL2	retinoblastoma-like 2 (p130)	0.8444	0.0258
212337_at	TI-227H	hypothetical protein TI-227H, taurine upregulated gene 1	0.9442	0.0047
212340_at	YIPF6	Yip1 domain family; member 6	0.7408	0.026
212349_at	POFUT1	protein O-fucosyltransferase 1	0.5073	0.0024
212350_at	TBC1D1	TBC1 (tre-2/USP6; BUB2; cdc16) domain family; member 1	0.8768	0.0388
212356_at	KIAA0323	KIAA0323	0.762	0.0243
212365_at	MYO1B	myosin IB	0.9778	0.0313
212366_at	ZNF292	zinc finger protein 292	0.7127	0.0028

212367_at	FEM1B	fem-1 homolog b (C. elegans)	0.4873	0.0061
212368_at	ZNF292	zinc finger protein 292	0.763	0.005
212369_at	ZNF384	zinc finger protein 384	0.3898	0.0454
212375_at	EP400	E1A binding protein p400	0.7611	0.015
212376_s_at	EP400	E1A binding protein p400	1.1012	0.003
212379_at	GART	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	1.0349	0.0147
212384_at	BAT1	HLA-B associated transcript 1	0.5852	0.0243
212392_s_at	LOC652526	phosphodiesterase 4D interacting protein (myomegalin), similar to phosphodiesterase 4D interacting protein isoform 2	0.2078	0.0475
212403_at	UBE3B	ubiquitin protein ligase E3B	0.3684	0.0297
212404_s_at	UBE3B	ubiquitin protein ligase E3B	0.719	0.0014
212416_at	SCAMP1	secretory carrier membrane protein 1	0.5568	0.0002
212417_at	SCAMP1	secretory carrier membrane protein 1	1.1749	0.0005
212425_at	SCAMP1	secretory carrier membrane protein 1	0.648	0.0287
212426_s_at	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; theta polypeptide	0.2232	0.0266
212430_at	RBM38	RNA binding motif protein 38	0.944	0.0035
212436_at	TRIM33	tripartite motif-containing 33	0.5702	0.0363
212452_x_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.477	0.0134
212463_at	CD59	CD59 molecule; complement regulatory protein	0.6708	0.0475
212464_s_at	FN1	fibronectin 1	1.9447	0.0001
212469_at	NIPBL	Nipped-B homolog (Drosophila)	1.2499	0.0002
212474_at	KIAA0241	KIAA0241	0.7557	0.0014
212475_at	KIAA0241	KIAA0241	0.8297	0
212481_s_at	TPM4	tropomyosin 4	1.0648	0.0053
212483_at	NIPBL	Nipped-B homolog (Drosophila)	0.8522	0.0009
212485_at	GPATCH8	G patch domain containing 8	0.3402	0.0256
212487_at	GPATCH8	G patch domain containing 8	0.8797	0.0046
212488_at	COL5A1	collagen; type V; alpha 1	1.8151	0.0129
212489_at	COL5A1	collagen; type V; alpha 1	1.475	0.0102
212505_s_at	KIAA0892	KIAA0892	0.8965	0.0002
212520_s_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	1.157	0.0001
212529_at	LSM12	LSM12 homolog (S. cerevisiae)	0.4657	0.0348
212533_at	WEE1	WEE1 homolog (S. pombe)	1.1231	0

212540_at	CDC34	cell division cycle 34 homolog (S. cerevisiae)	1.0051	0.0001
212542_s_at	PHIP	pleckstrin homology domain interacting protein	1.1734	0.0001
212546_s_at	FRYL	FRY-like	0.6223	0.002
212571_at	CHD8	chromodomain helicase DNA binding protein 8	0.6568	0.0036
212572_at	STK38L	serine/threonine kinase 38 like	0.6785	0.0368
212574_x_at	C19orf6	chromosome 19 open reading frame 6	1.5685	0.0001
212575_at	C19orf6	chromosome 19 open reading frame 6	0.5335	0.0111
212576_at	MGRN1	mahogunin; ring finger 1	0.6041	0.0089
212577_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	1.1894	0.0123
212581_x_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.5494	0
212582_at	OSBPL8	oxysterol binding protein-like 8	0.587	0.0007
212593_s_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	1.0049	0
212594_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	1.2971	0.0001
212599_at	AUTS2	autism susceptibility candidate 2	1.5825	0.0024
212619_at	KIAA0286	KIAA0286 protein	1.4474	0.0008
212621_at	KIAA0286	KIAA0286 protein	2.3027	0
212624_s_at	CHN1	chimerin (chimaerin) 1	1.4485	0.0013
212635_at	TNPO1	transportin 1	0.6173	0.0001
212639_x_at	TUBA1B	tubulin; alpha 1b	0.518	0
212655_at	ZCCHC14	zinc finger; CCHC domain containing 14	0.8164	0.001
212661_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.1988	0
212669_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	0.5127	0.0146
212673_at	METAP1	methionyl aminopeptidase 1	0.6845	0.0106
212684_at	ZNF3	zinc finger protein 3	1.0061	0.0002
212686_at	PPM1H	protein phosphatase 1H (PP2C domain containing)	0.8847	0.0288
212689_s_at	JMJD1A	jumonji domain containing 1A	0.9292	0.0018
212699_at	SCAMP5	secretory carrier membrane protein 5	0.8968	0.0392
212721_at	SFRS12	splicing factor; arginine/serine-rich 12	0.6792	0
212727_at	DLG3	discs; large homolog 3 (neuroendocrine-dlg; Drosophila)	0.4014	0.0419
212729_at	DLG3	discs; large homolog 3 (neuroendocrine-dlg; Drosophila)	0.8569	0.0068
212743_at	RCHY1	ring finger and CHY zinc finger domain containing 1	0.2045	0.0342
212746_s_at	CEP170	centrosomal protein 170kDa	0.7313	0.0478
212751_at	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog; yeast)	0.3951	0.0289
212754_s_at	MON2	MON2 homolog (S. cerevisiae)	0.6267	0.0036

212757_s_at	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	0.3832	0.0308
212771_at	C10orf38	chromosome 10 open reading frame 38	2.698	0.0001
212777_at	SOS1	son of sevenless homolog 1 (Drosophila)	0.5531	0.0066
212781_at	RBBP6	retinoblastoma binding protein 6	0.4446	0.0439
212783_at	RBBP6	retinoblastoma binding protein 6	0.8162	0.0019
212784_at	CIC	capicua homolog (Drosophila)	0.6241	0.0005
212789_at	NCAPD3	non-SMC condensin II complex; subunit D3	0.4986	0.0398
212794_s_at	KIAA1033	KIAA1033	1.1848	0.0001
212795_at	KIAA1033	KIAA1033	0.4048	0.003
212797_at	SORT1	sortilin 1	0.4072	0.0438
212798_s_at	ANKMY2	ankyrin repeat and MYND domain containing 2	0.7011	0.0066
212800_at	STX6	syntaxin 6	0.7256	0.0048
212804_s_at	GAPVD1	GTPase activating protein and VPS9 domains 1	0.9824	0.0083
212806_at	PRUNE2	prune homolog 2 (Drosophila)	1.1061	0.0303
212808_at	NFATC2IP	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 2 interacting protein	0.4729	0.0418
212809_at	NFATC2IP	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 2 interacting protein	0.646	0.0012
212814_at	KIAA0828	adenosylhomocysteinase 3	0.6463	0.0162
212815_at	ASCC3	activating signal cointegrator 1 complex subunit 3	0.7192	0.0108
212825_at	PAXIP1	PAX interacting (with transcription-activation domain) protein 1	1.3891	0
212836_at	POLD3	polymerase (DNA-directed); delta 3; accessory subunit	1.0502	0.0064
212840_at	UBXD7	UBX domain containing 7	0.7583	0.0135
212851_at	DCUN1D4	DCN1; defective in cullin neddylation 1; domain containing 4 (S. cerevisiae)	0.7272	0.0091
212853_at	DCUN1D4	DCN1; defective in cullin neddylation 1; domain containing 4 (S. cerevisiae)	0.6959	0.0173
212858_at	PAQR4	progestin and adipoQ receptor family member IV	0.9479	0.0042
212861_at	MFSD5	major facilitator superfamily domain containing 5	0.9531	0.0006
212879_x_at	PIAS4	protein inhibitor of activated STAT; 4	0.7033	0.0017
212881_at	PIAS4	protein inhibitor of activated STAT; 4	1.2022	0
212888_at	DICER1	Dicer1; Dcr-1 homolog (Drosophila)	0.6336	0.0038
212892_at	LOC731863	similar to zinc finger protein 282, zinc finger protein 282	0.6627	0.0021
212897_at	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	1.2926	0.0001
212898_at	KIAA0406	KIAA0406	0.7573	0.0001
212899_at	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	1.3875	0.0005

212910_at	THAP11	THAP domain containing 11	0.6028	0.0098
212913_at	C6orf26	chromosome 6 open reading frame 26, mutS homolog 5 (E. coli)	0.6301	0.0155
212916_at	LOC731069	PHD finger protein 8, similar to PHD finger protein 8	0.4384	0.0226
212917_x_at	RECQL	RecQ protein-like (DNA helicase Q1-like)	0.526	0.0146
212919_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	0.6091	0.0246
212921_at	SMYD2	SET and MYND domain containing 2	1.3875	0.0059
212922_s_at	SMYD2	SET and MYND domain containing 2	1.1901	0.0008
212926_at	SMC5	structural maintenance of chromosomes 5	0.8612	0.0066
212930_at	ATP2B1	ATPase; Ca++ transporting; plasma membrane 1	1.6522	0.0001
212949_at	NCAPH	non-SMC condensin I complex; subunit H	1.1738	0.0036
212957_s_at	LOC92249	hypothetical protein LOC92249	0.7122	0.0315
212960_at	TBC1D9	TBC1 domain family; member 9 (with GRAM domain)	0.3166	0.0167
212977_at	CXCR7	chemokine (C-X-C motif) receptor 7	3.2504	0.0001
212982_at	ZDHHC17	zinc finger; DHHC-type containing 17	0.4918	0.0033
212994_at	THOC2	THO complex 2	0.8296	0.0186
213001_at	ANGPTL2	angiopoietin-like 2	1.6911	0.0008
213004_at	ANGPTL2	angiopoietin-like 2	1.7729	0.0001
213007_at	FANCI	Fanconi anemia; complementation group I	3.0935	0
213008_at	FANCI	Fanconi anemia; complementation group I	2.6423	0
213011_s_at	TPI1	triosephosphate isomerase 1	0.2893	0.0022
213017_at	ABHD3	abhydrolase domain containing 3	0.7037	0.008
213018_at	GATAD1	GATA zinc finger domain containing 1	0.9374	0.0002
213026_at	ATG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	0.814	0
213054_at	KIAA0841	KIAA0841	0.9595	0.0001
213072_at	CYHR1	cysteine/histidine-rich 1	0.3336	0.0331
213074_at		Full-length cDNA clone CS0DF025YM09 of Fetal brain of Homo sapiens (human)	0.5809	0.0094
213078_x_at	AGPAT7	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase; eta)	0.6072	0.0026
213082_s_at	SLC35D2	solute carrier family 35; member D2	0.7612	0.0001
213083_at	SLC35D2	solute carrier family 35; member D2	0.711	0.0005
213088_s_at	DNAJC9	DnaJ (Hsp40) homolog; subfamily C; member 9	1.7971	0
213089_at	GUSBP1	glucuronidase; beta pseudogene 1	1.6819	0.0001
213090_s_at	TAF4	TAF4 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 135kDa	1.272	0
213092_x_at	DNAJC9	DnaJ (Hsp40) homolog; subfamily C; member 9	1.5509	0

213097_s_at	ZRF1	zuotin related factor 1	0.5455	0.0047
213107_at	TNIK	TRAF2 and NCK interacting kinase	1.2262	0.0386
213109_at	TNIK	TRAF2 and NCK interacting kinase	0.919	0.0133
213116_at	NEK3	NIMA (never in mitosis gene a)-related kinase 3	0.5593	0.0486
213119_at	SLC36A1	solute carrier family 36 (proton/amino acid symporter); member 1	0.9525	0.0001
213120_at	KIAA0701	KIAA0701 protein	0.3727	0.0008
213124_at	ZNF473	zinc finger protein 473	1.421	0.0004
213130_at	ZNF473	zinc finger protein 473	0.5735	0.0057
213134_x_at	BTG3	BTG family; member 3	0.7277	0.0024
213140_s_at	SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	0.4854	0.0409
213153_at	SETD1B	SET domain containing 1B	0.4651	0.0045
213175_s_at	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	0.6457	0.0009
213178_s_at	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	0.5564	0.0065
213190_at	COG7	component of oligomeric golgi complex 7	0.7154	0.0091
213196_at	ZNF629	zinc finger protein 629	0.5196	0.0213
213198_at	ACVR1B	activin A receptor; type IB	0.8384	0.0034
213200_at	SYP	synaptophysin	1.5134	0.0157
213202_at	SETD1A	SET domain containing 1A	0.3302	0.0483
213213_at	DIDO1	death inducer-obliterator 1	0.692	0.0239
213218_at	ZNF187	zinc finger protein 187	0.6864	0.0384
213226_at	CCNA2	cyclin A2	2.793	0
213228_at	PDE8B	phosphodiesterase 8B	3.2634	0
213229_at	DICER1	Dicer1; Dcr-1 homolog (Drosophila)	0.6366	0.0012
213231_at	DMWD	dystrophia myotonica; WD repeat containing	0.3312	0.0053
213234_at	KIAA1467	KIAA1467	0.9695	0.0151
213237_at	LOC400506	similar to TSG118.1	0.9858	0.0001
213241_at	PLXNC1	plexin C1	1.7987	0
213244_at	SCAMP4	secretory carrier membrane protein 4	0.6518	0.0075
213253_at	SMC2	structural maintenance of chromosomes 2	1.38	0
213266_at	76P	Gamma tubulin ring complex protein (76p gene)	0.9399	0.0048
213267_at	DOPEY1	dopey family member 1	0.3156	0.0097
213286_at	ZFR	zinc finger RNA binding protein	0.6032	0.0248
213292_s_at	SNX13	sorting nexin 13	0.9393	0.0004
213298_at	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	0.4864	0.0419
213303_x_at	ZBTB7A	zinc finger and BTB domain containing 7A	0.2682	0.0318
213313_at	RABGAP1	RAB GTPase activating protein 1	0.4534	0.025

213314_at	C6orf162	chromosome 6 open reading frame 162	0.3741	0.025
213325_at	PVRL3	poliovirus receptor-related 3	1.8203	0.0035
213330_s_at	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	0.4468	0.0035
213334_x_at	UCHL5IP	UCHL5 interacting protein	0.8945	0.0069
213346_at	C13orf27	chromosome 13 open reading frame 27	0.7218	0.0202
213356_x_at	hCG_2023776	hCG2023776, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A1 pseudogene, heterogeneous nuclear ribonucleoprotein A1 pseudogene 4, heterogeneous nuclear ribonucleoprotein A1 pseudogene 5, heterogeneous nuclear ribonucleoprotein A1-like, hypothetical LOC642817, similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP), similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)	0.1695	0.003
213358_at	KIAA0802	KIAA0802	0.4795	0.0385
213360_s_at	LOC100101267	POM121 membrane glycoprotein (rat), POM121 membrane glycoprotein (rat) pseudogene, POM121 membrane glycoprotein (rat)-like	0.3982	0.0081
213361_at	TDRD7	tudor domain containing 7	0.6735	0.0171
213368_x_at	PPFIA3	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 3	0.996	0.0001
213370_s_at	SFMBT1	Scm-like with four mbt domains 1	0.7044	0.0087
213372_at	PAQR3	progestin and adipoQ receptor family member III	1.1002	0.0022
213376_at	ZBTB1	zinc finger and BTB domain containing 1	0.5299	0.0144
213378_s_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog; S. cerevisiae), DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11-like, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog; S. cerevisiae)	1.3427	0.0004
213387_at	ATAD2B	ATPase family; AAA domain containing 2B	0.7289	0.0368
213388_at	LOC727942	similar to phosphodiesterase 4D interacting protein isoform 2	1.2071	0.0026
213390_at	C19orf7	chromosome 19 open reading frame 7	0.3677	0.031

213391_at	DPY19L4	dpy-19-like 4 (C. elegans)	0.5376	0.0404
213399_x_at	RPN2	ribophorin II	0.2537	0.0057
213402_at	ZNF787	zinc finger protein 787	0.3909	0.0257
213406_at	WSB1	WD repeat and SOCS box-containing 1	0.2223	0.0063
213410_at	C10orf137	chromosome 10 open reading frame 137	0.8598	0.0012
213434_at	STX2	syntaxin 2	1.7364	0
213444_at	LOC643641	hypothetical protein LOC643641	0.5625	0.0076
213445_at	ZC3H3	zinc finger CCCH-type containing 3	1.2286	0
213446_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	0.7066	0.0181
213452_at	ZNF184	zinc finger protein 184	0.6943	0.0064
213453_x_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.6502	0
213460_x_at	NSUN5C	NOL1/NOP2/Sun domain family; member 5C	0.9276	0.0044
213461_at	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.9946	0.0138
213470_s_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	0.9915	0.0118
213472_at	HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	0.6267	0.0025
213476_x_at	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor), tubulin; beta 3	0.7912	0.017
213479_at	NPTX2	neuronal pentraxin II	2.337	0
213483_at	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	0.9552	0.0005
213491_x_at	RPN2	ribophorin II	0.2749	0.0039
213505_s_at	SFRS14	splicing factor; arginine/serine-rich 14	0.4222	0.0005
213507_s_at	KPNB1	karyopherin (importin) beta 1	0.3749	0.0399
213511_s_at	MTMR1	myotubularin related protein 1	0.895	0.0007
213514_s_at	DIAPH1	diaphanous homolog 1 (Drosophila)	0.459	0.0051
213517_at	PCBP2	poly(rC) binding protein 2	1.3837	0
213523_at	CCNE1	cyclin E1	3.0763	0
213530_at	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	0.58	0.0058
213534_s_at	PASK	PAS domain containing serine/threonine kinase	0.5423	0.0014
213535_s_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog; yeast)	0.3329	0.0357
213570_at	EIF4E2	eukaryotic translation initiation factor 4E family member 2	0.7076	0.0021
213577_at	SQLE	squalene epoxidase	1.8738	0.0145

213594_x_at	FUSIP1	FUS interacting protein (serine/arginine-rich) 1, similar to FUS interacting protein (serine-arginine rich) 1, similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein...	0.6598	0.0235
213598_at	KIF2A	Kinesin heavy chain member 2A	1.5707	0
213599_at	OIP5	Opa interacting protein 5	1.8382	0.0012
213605_s_at	LOC728411	Similar to Beta-glucuronidase precursor	2.0855	0
213610_s_at	KLHL23	kelch-like 23 (Drosophila)	0.5441	0.0315
213623_at	KIF3A	kinesin family member 3A	2.2788	0
213625_at	ZKSCAN4	zinc finger with KRAB and SCAN domains 4	0.667	0.0321
213627_at	MAGED2	melanoma antigen family D; 2	0.8051	0.0065
213638_at	PHACTR1	phosphatase and actin regulator 1	0.4155	0.0101
213639_s_at	ZNF500	zinc finger protein 500	0.9771	0
213641_at	ZNF500	zinc finger protein 500	0.5369	0
213646_x_at	TUBA1B	tubulin; alpha 1b	0.5347	0
213647_at	DNA2L	DNA2 DNA replication helicase 2-like (yeast)	1.0269	0.0003
213650_at	GOLGA8A	golgi autoantigen; golgin subfamily a; 8A, golgi autoantigen; golgin subfamily a; 8B	0.794	0.0044
213653_at	METTL3	methyltransferase like 3	0.9216	0.0056
213654_at	TAF5L	TAF5-like RNA polymerase II; p300/CBP-associated factor (PCAF)-associated factor; 65kDa	0.4197	0.0253
213659_at	ZNF75	zinc finger protein 75 (D8C6)	0.6001	0.0325
213664_at	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter; system Xag); member 1	1.5982	0.0128
213670_x_at	NSUN5B	NOL1/NOP2/Sun domain family; member 5B	0.7401	0.0229
213671_s_at	MARS	methionyl-tRNA synthetase	0.6745	0.0003
213672_at	MARS	methionyl-tRNA synthetase	0.7196	0.0087
213679_at	TTC30A	tetratricopeptide repeat domain 30A	0.7047	0.0012
213688_at	CALM1	calmodulin 1 (phosphorylase kinase; delta)	0.5413	0.0174
213689_x_at	FAM69A	family with sequence similarity 69; member A	1.2798	0.0036
213700_s_at		Transcribed locus	1.4541	0.0001
213703_at	LOC150759	hypothetical protein LOC150759	1.4939	0.0002
213729_at	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.5006	0.0059
213730_x_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.7928	0.0001

213747_at			0.1541	0.0361
213758_at	COX4I1	cytochrome c oxidase subunit IV isoform 1	1.1638	0.0001
213761_at	MDM1	Mdm4; transformed 3T3 cell double minute 1; p53 binding protein (mouse)	1.6577	0.0001
213772_s_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	0.887	0.0005
213773_x_at	NSUN5	NOL1/NOP2/Sun domain family; member 5	0.9433	0.0001
213784_at	RABL4	RAB; member of RAS oncogene family-like 4	0.3381	0.019
213793_s_at	HOMER1	homer homolog 1 (Drosophila)	2.3585	0.0001
213795_s_at	PTPRA	protein tyrosine phosphatase; receptor type; A	0.636	0.0158
213799_s_at	PTPRA	protein tyrosine phosphatase; receptor type; A	0.7126	0.0103
213808_at		Clone 23688 mRNA sequence	1.1553	0.0166
213811_x_at	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.9712	0.0007
213815_x_at	C19orf29	chromosome 19 open reading frame 29	0.4455	0.0011
213822_s_at	UBE3B	ubiquitin protein ligase E3B	1.186	0.0017
213823_at	HOXA11	homeobox A11	1.0213	0.001
213827_at	SNX26	sorting nexin 26	0.6714	0.0034
213835_x_at	GTPBP3	GTP binding protein 3 (mitochondrial)	0.4209	0.0006
213839_at	KIAA0500	KIAA0500 protein	0.8902	0.0243
213842_x_at	NSUN5C	NOL1/NOP2/Sun domain family; member 5C	0.6811	0.0102
213850_s_at	SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	0.8158	0.0157
213856_at	CD47	CD47 molecule	0.2632	0.0242
213858_at	ZNF250	zinc finger protein 250	0.517	0.0096
213869_x_at	THY1	Thy-1 cell surface antigen	1.0066	0.0223
213876_x_at	ZRSR2	zinc finger (CCCH type); RNA-binding motif and serine/arginine rich 2	0.7846	0.0299
213893_x_at	LOC441259	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like, postmeiotic segregation increased 2-like 5, similar to postmeiotic segregation increased 2-like 2	0.5548	0.0174
213894_at	THSD7A	thrombospondin; type I; domain containing 7A	1.3008	0.0169
213901_x_at	RBM9	RNA binding motif protein 9	0.9704	0.013
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	4.291	0
213911_s_at	H2AFZ	H2A histone family; member Z	1.0089	0
213916_at	ZNF20	zinc finger protein 20	0.7271	0.0029
213922_at	TTBK2	tau tubulin kinase 2	1.0819	0.0004
213927_at	MAP3K9	mitogen-activated protein kinase kinase kinase 9	1.3259	0.0011

213934_s_at	ZNF19	zinc finger protein 19, zinc finger protein 23 (KOX 16)	1.0122	0.0014
213943_at	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)	2.3927	0
213951_s_at	PSMC3IP	PSMC3 interacting protein	0.555	0.0125
213954_at	KIAA0888	KIAA0888 protein	1.3275	0.0242
213959_s_at	RPGRIP1L	RPGRIP1-like	0.9636	0.0015
213971_s_at	SUZ12	suppressor of zeste 12 homolog (Drosophila), suppressor of zeste 12 homolog pseudogene	0.8674	0.0024
213973_at	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	0.27	0.0311
213986_s_at	C19orf6	chromosome 19 open reading frame 6	1.8613	0.0001
213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0.9418	0.0202
214007_s_at	TWF1	twinfilin; actin-binding protein; homolog 1 (Drosophila)	1.5667	0.0045
214017_s_at	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	0.3842	0.0117
214035_x_at	LOC399491	LOC399491 protein	0.6568	0.0008
214051_at	MGC39900	hypothetical protein MGC39900	1.6577	0.0015
214055_x_at	BAT2D1	BAT2 domain containing 1	0.8212	0.027
214060_at	SSBP1	single-stranded DNA binding protein 1	1.0575	0.0006
214061_at	WDR67	WD repeat domain 67	1.3156	0.0002
214079_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	2.846	0.0021
214080_x_at	PRKCSH	protein kinase C substrate 80K-H	0.7233	0.0002
214086_s_at	PARP2	poly (ADP-ribose) polymerase family; member 2	0.8696	0.004
214092_x_at	SFRS14	splicing factor; arginine/serine-rich 14	0.487	0.0008
214094_at	FUBP1	far upstream element (FUSE) binding protein 1	0.3846	0.0112
214095_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.6625	0.0008
214096_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.1776	0.0002
214099_s_at	LOC727927	phosphodiesterase 4D interacting protein (myomegalin), similar to phosphodiesterase 4D interacting protein isoform 2	0.2854	0.0061
214100_x_at	NSUN5B	NOL1/NOP2/Sun domain family; member 5B	0.7755	0.0083
214114_x_at	FASTK	Fas-activated serine/threonine kinase	0.6437	0.0002
214129_at	LOC727942	similar to phosphodiesterase 4D interacting protein isoform 2	0.9809	0.0045
214130_s_at	LOC727942	phosphodiesterase 4D interacting protein (myomegalin), similar to phosphodiesterase 4D interacting protein isoform 2	0.7687	0.0024
214132_at	ATP5C1	ATP synthase; H+ transporting; mitochondrial F1 complex; gamma polypeptide 1	2.0047	0
214148_at		Clone 23641 mRNA sequence	0.4051	0.0017

214156_at	MYRIP	myosin VIIA and Rab interacting protein	1.1488	0.0183
214163_at	C1orf41	chromosome 1 open reading frame 41	0.9133	0.0039
214164_x_at	CA12	carbonic anhydrase XII	0.9267	0.0308
214190_x_at	GGA2	golgi associated; gamma adaptin ear containing; ARF binding protein 2	0.9614	0.0034
214193_s_at	C1orf107	chromosome 1 open reading frame 107	0.5609	0.029
214209_s_at	ABCB9	ATP-binding cassette; sub-family B (MDR/TAP); member 9	0.651	0.01
214221_at	ALMS1	Alstrom syndrome 1	0.5408	0.0368
214225_at			0.375	0.0148
214226_at	POL3S	polyserase 3	0.5463	0.0126
214235_at	CYP3A5	cytochrome P450; family 3; subfamily A; polypeptide 5	1.9819	0.0244
214241_at	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 8; 19kDa	0.8385	0.006
214245_at	RPS14	ribosomal protein S14	0.5039	0.0002
214249_at	TRIM2	tripartite motif-containing 2	0.2747	0.0094
214250_at	NUMA1	nuclear mitotic apparatus protein 1	0.5179	0.0074
214260_at	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	0.3369	0.01
214264_s_at	C14orf143	chromosome 14 open reading frame 143	0.8135	0.0067
214270_s_at	MAPRE3	microtubule-associated protein; RP/EB family; member 3	0.4631	0.0484
214280_x_at	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	0.5804	0.0015
214297_at	CSPG4	chondroitin sulfate proteoglycan 4	0.201	0.0472
214299_at	TOP3A	topoisomerase (DNA) III alpha	0.1881	0.0289
214318_s_at	FRY	furry homolog (Drosophila)	0.3559	0.0082
214319_at	FRY	furry homolog (Drosophila)	0.3585	0.007
214335_at	RPL18	ribosomal protein L18	0.2598	0.0298
214336_s_at	COPA	coatomer protein complex; subunit alpha	0.6989	0.0403
214352_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1.1923	0
214374_s_at	PPFIBP1	PTPRF interacting protein; binding protein 1 (liprin beta 1)	0.8277	0.0265
214375_at	LOC729222	PTPRF interacting protein; binding protein 1 (liprin beta 1), similar to PTPRF interacting protein binding protein 1 isoform 1	1.1001	0.0377
214389_at		MRNA; cDNA DKFZp564G223 (from clone DKFZp564G223)	0.1027	0.0232
214415_at	PLGLB1	plasminogen-like B1, plasminogen-like B2	0.3707	0.0267
214426_x_at	CHAF1A	chromatin assembly factor 1; subunit A (p150)	1.1386	0
214430_at	GLA	galactosidase; alpha	0.536	0.0307
214436_at	FBXL2	F-box and leucine-rich repeat protein 2	0.6398	0.0474

214437_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	1.709	0.0003
214473_x_at	PMS2L3	postmeiotic segregation increased 2-like 3	0.6747	0.0013
214474_at	PRKAB2	protein kinase; AMP-activated; beta 2 non-catalytic subunit	0.8349	0.017
214483_s_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	0.83	0.015
214484_s_at	OPRS1	opioid receptor; sigma 1	0.5678	0.0254
214496_x_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	0.6302	0.0048
214500_at	H2AFY	H2A histone family; member Y	1.3954	0.0057
214501_s_at	H2AFY	H2A histone family; member Y	0.6444	0.0023
214507_s_at	EXOSC2	exosome component 2	0.7678	0.0262
214526_x_at	PMS2L1	postmeiotic segregation increased 2-like 1	0.4609	0.0336
214550_s_at	TNPO3	transportin 3	1.235	0.0003
214563_at	PCDHGC3	protocadherin gamma subfamily C; 3	0.1179	0.0299
214577_at	MAP1B	microtubule-associated protein 1B	1.1396	0.0078
214588_s_at	MFAP3	Microfibrillar-associated protein 3	0.3033	0.0179
214594_x_at	ATP8B1	ATPase; Class I; type 8B; member 1	0.574	0.0108
214605_x_at	GPR1	G protein-coupled receptor 1	0.6473	0.0246
214631_at	ZBTB33	zinc finger and BTB domain containing 33	0.2207	0.0042
214650_x_at	MOG	myelin oligodendrocyte glycoprotein	0.1232	0.01
214668_at	C13orf1	chromosome 13 open reading frame 1	0.7248	0.0072
214686_at	ZNF266	zinc finger protein 266	1.0108	0.0003
214687_x_at	ALDOA	aldolase A; fructose-bisphosphate	0.3565	0.0003
214691_x_at	FAM63B	family with sequence similarity 63; member B	0.5197	0.0257
214692_s_at	JRK	jerky homolog (mouse)	0.4291	0.0122
214693_x_at	KIAA1245	KIAA1245, hypothetical protein LOC728980, hypothetical protein LOC730476, neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 14, neuroblastoma breakpoint family; member 15, neuroblastoma breakpoint family; member 16, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 8, neuroblastoma breakpoint family; member 9	0.6856	0.0265
214697_s_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	1.2131	0.0014
214699_x_at	WIPI2	WD repeat domain; phosphoinositide interacting 2	0.1586	0.046
214700_x_at	RIF1	RAP1 interacting factor homolog (yeast)	0.7013	0.0223

214707_x_at	ALMS1	Alstrom syndrome 1	0.4895	0.0012
214710_s_at	CCNB1	cyclin B1	4.5789	0
214711_at	15E1.2	hypothetical protein LOC283459	1.0647	0.028
214718_at	GATAD1	GATA zinc finger domain containing 1	0.6271	0.0129
214722_at	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	0.7927	0.0124
214723_x_at	KIAA1641	KIAA1641	1.0407	0.0011
214727_at	BRCA2	breast cancer 2; early onset	0.9579	0.0025
214730_s_at	GLG1	golgi apparatus protein 1	1.0545	0
214731_at	CTTNBP2NL	CTTNBP2 N-terminal like	0.728	0.0317
214732_at	SP1	Sp1 transcription factor	0.1911	0.0498
214734_at	EXPH5	exophilin 5	0.4459	0.0341
214738_s_at	NEK9	NIMA (never in mitosis gene a)- related kinase 9	0.4648	0.0332
214743_at	CUTL1	cut-like 1; CCAAT displacement protein (Drosophila)	0.5654	0.035
214753_at	PFAAP5	Phosphonoformate immuno-associated protein 5	0.6795	0.0468
214755_at	UAP1L1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	1.1343	0.0072
214757_at		CDNA clone IMAGE:3456494	0.5414	0.0006
214760_at	ZNF337	zinc finger protein 337	1.2189	0
214761_at	ZNF423	zinc finger protein 423	1.3457	0.0319
214769_at	CLCN4	chloride channel 4	1.9361	0.0002
214772_at	C11orf41	chromosome 11 open reading frame 41	0.404	0.0346
214773_x_at	TIPRL	TIP41; TOR signaling pathway regulator-like (S. cerevisiae)	0.4505	0.0017
214780_s_at	MYO9B	myosin IXB	0.4929	0.0076
214782_at	CTTN	cortactin	0.7553	0.0155
214784_x_at	XPO6	exportin 6	0.5408	0
214795_at	ZMYND8	zinc finger; MYND-type containing 8	0.5155	0.0086
214804_at			1.2936	0.0036
214806_at	BICD1	bicaudal D homolog 1 (Drosophila)	0.7635	0.0049
214813_at	ZNF75	zinc finger protein 75 (D8C6)	0.6714	0.021
214815_at	TRIM33	Tripartite motif-containing 33	0.3941	0.0092
214816_x_at	C19orf40	chromosome 19 open reading frame 40	0.512	0.0003
214820_at	BRWD1	bromodomain and WD repeat domain containing 1	0.7874	0.0379
214831_at	ELK4	ELK4; ETS-domain protein (SRF accessory protein 1)	0.3329	0.0011
214845_s_at	CALU	calumenin	2.1771	0.0002
214850_at	SMA4	Glucuronidase; beta pseudogene	1.2493	0.0009
214861_at	JMJD2C	jumonji domain containing 2C	0.7161	0.0093
214862_x_at		MRNA; cDNA DKFZp564G1162 (from clone DKFZp564G1162)	0.3882	0.0443
214869_x_at	GAPVD1	GTPase activating protein and VPS9 domains 1	1.1409	0.0069

214870_x_at	LOC339047	hypothetical protein LOC339047, nuclear pore complex interacting protein, similar to nuclear pore complex interacting protein	0.6335	0.0016
214871_x_at		CDNA clone IMAGE:3347954	0.2287	0.0144
214875_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	1.0101	0.0013
214878_at	ZNF37A	zinc finger protein 37A, zinc finger protein 37B	0.4509	0.0181
214887_at	CG018	Hypothetical gene CG018	0.1293	0.0028
214895_s_at	ADAM10	ADAM metallopeptidase domain 10	1.3076	0.0051
214899_at	ZNF780B	zinc finger protein 780B	0.1672	0.0042
214900_at	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	0.4447	0.009
214902_x_at		MRNA; cDNA DKFZp586A061 (from clone DKFZp586A061)	0.3063	0.0445
214904_at	ZNF41	zinc finger protein 41	0.1616	0.0499
214908_s_at	TRRAP	transformation/transcription domain-associated protein	1.3906	0.0005
214913_at	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif; 3	1.5569	0.0034
214920_at	THSD7A	thrombospondin; type I; domain containing 7A	1.2722	0.0128
214925_s_at	SPTAN1	spectrin; alpha; non-erythrocytic 1 (alpha-fodrin)	0.5905	0.0409
214931_s_at	SRPK2	SFRS protein kinase 2	0.6956	0.0036
214948_s_at	TMF1	TATA element modulatory factor 1	0.8836	0.015
214949_at		CDNA FLJ31919 fis; clone NT2RP7004964	1.0894	0.001
214962_s_at	NUP160	nucleoporin 160kDa	0.3617	0.0177
214968_at	DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	0.1764	0.0333
214972_at	MGEA5	Meningioma expressed antigen 5 (hyaluronidase)	0.5175	0.0007
214975_s_at	MTMR1	myotubularin related protein 1	1.0661	0.0049
214984_at	DKFZp547E087	PI-3-kinase-related kinase SMG-1, PI-3-kinase-related kinase SMG-1 pseudogene, hypothetical gene LOC283846, hypothetical protein LOC440345, similar to PI-3-kinase-related kinase SMG-1	0.2751	0.0008
214989_x_at		CDNA FLJ11875 fis; clone HEMBA1007078	0.293	0.02
215004_s_at	SF4	splicing factor 4	0.8514	0.0019
215006_at		CDNA FLJ13754 fis; clone PLACE3000362	0.6703	0
215009_s_at	SEC31A	SEC31 homolog A (S. cerevisiae)	0.5735	0.0404
215011_at	SNHG3	small nucleolar RNA host gene (non-protein coding) 3	0.5156	0.0428
215017_s_at	FNBP1L	formin binding protein 1-like	1.1401	0.0003
215018_at	KIAA1731	KIAA1731	0.2961	0.0006
215023_s_at	PEX1	peroxisome biogenesis factor 1	0.9755	0.0046

215024_at	ASNS	MGC72080 pseudogene, asparagine synthetase, chromosome 7 open reading frame 28A, chromosome 7 open reading frame 28B, similar to CG14980-PB	0.4657	0.0356
215029_at			0.6486	0.0215
215031_x_at	RNF126	ring finger protein 126	0.3995	0.0015
215037_s_at	BCL2L1	BCL2-like 1	0.7478	0.0058
215043_s_at	SMA4	glucuronidase; beta pseudogene	0.7571	0.0043
215063_x_at	LRRC40	leucine rich repeat containing 40	0.2459	0.0009
215066_at	PTPRF	protein tyrosine phosphatase; receptor type; F	0.2582	0.0191
215069_at	NMT2	N-myristoyltransferase 2	0.3039	0.0227
215070_x_at	RABGAP1	RAB GTPase activating protein 1	0.3861	0.0061
215072_x_at	C10orf137	chromosome 10 open reading frame 137	0.1554	0.0316
215083_at		MRNA; cDNA DKFZp564F133 (from clone DKFZp564F133)	0.8889	0.0049
215092_s_at	NFAT5	nuclear factor of activated T-cells 5; tonicity-responsive	0.8947	0.0179
215095_at	ESD	Esterase D/formylglutathione hydrolase	0.7673	0.0047
215102_at	DPY19L1P1	dpy-19-like 1 pseudogene 1 (C. elegans)	0.1984	0.003
215123_at	LOC23117	KIAA0220-like protein, hypothetical protein LOC339047, similar to Protein KIAA0220, similar to nuclear pore complex interacting protein	1.981	0
215124_at	ZNF550	zinc finger protein 550	0.2463	0.0045
215143_at	DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	2.7312	0
215148_s_at	APBA3	amyloid beta (A4) precursor protein-binding; family A; member 3 (X11-like 2)	0.767	0.0004
215155_at	HEXA	Hexosaminidase A (alpha polypeptide)	0.4003	0.0145
215156_at	WDR61	WD repeat domain 61	0.5836	0.017
215157_x_at	PABPC1	poly(A) binding protein; cytoplasmic 1	0.2455	0.0085
215170_s_at	CEP152	centrosomal protein 152kDa	0.5384	0.0315
215177_s_at	ITGA6	integrin; alpha 6	0.8507	0.0167
215179_x_at	PGF	Placental growth factor; vascular endothelial growth factor-related protein	0.4083	0.0024
215197_at		CDNA FLJ13776 fis; clone PLACE4000387	0.1281	0.0374
215201_at	REPS1	RALBP1 associated Eps domain containing 1	0.5501	0.0169
215203_at	GOLGA4	golgi autoantigen; golgin subfamily a; 4	1.0816	0.0156
215208_x_at	RPL35A	Ribosomal protein L35a	0.2205	0.0178
215215_s_at	LOC81691	exonuclease NEF-sp	0.8772	0.0026
215218_s_at	WDR62	WD repeat domain 62	0.1487	0.0359
215236_s_at	PICALM	phosphatidylinositol binding clathrin assembly protein	0.9433	0.0336

215239_x_at	ZNF273	zinc finger protein 273	1.1445	0.0042
215249_at	RPL35A	ribosomal protein L35a	0.2943	0.0081
215252_at		CDNA: FLJ21350 fis; clone COL02751	0.3673	0.0396
215262_at		Clone 24629 mRNA sequence	0.262	0.0008
215280_s_at	PPFIA3	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 3	0.6618	0
215282_at	ANAPC13	anaphase promoting complex subunit 13	0.1355	0.0082
215286_s_at	PHTF2	putative homeodomain transcription factor 2	0.8481	0.0004
215310_at	APC	adenomatosis polyposis coli	0.7441	0.0007
215316_at		MRNA; cDNA DKFZp434M091 (from clone DKFZp434M091)	0.534	0.0482
215318_at	CG012	hypothetical gene CG012	0.5882	0.0057
215338_s_at	NKTR	natural killer-tumor recognition sequence	0.9163	0.0015
215339_at	NKTR	natural killer-tumor recognition sequence	0.2865	0.0058
215351_at	RTCD1	RNA terminal phosphate cyclase domain 1	0.4025	0.0047
215356_at	ECAT8	ES cell associated transcript 8	1.5191	0.0495
215363_x_at	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	1.3702	0.0034
215366_at	SNX13	sorting nexin 13	0.1853	0.008
215371_at	MED27	mediator complex subunit 27	0.2313	0.0137
215372_x_at		CDNA FLJ12002 fis; clone HEMBB1001536	0.2857	0.0134
215373_x_at	FLJ12151	hypothetical protein FLJ12151	0.3885	0.0118
215376_at		CDNA FLJ12295 fis; clone MAMMA1001818	0.3995	0.0005
215378_at		CDNA FLJ14151 fis; clone MAMMA1003031	0.2451	0.0398
215380_s_at	C7orf24	chromosome 7 open reading frame 24	0.5164	0.0034
215387_x_at		CDNA FLJ11917 fis; clone HEMBB1000218	0.4423	0.0271
215404_x_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	0.3614	0.005
215412_x_at	PMS2L2	postmeiotic segregation increased 2-like 2	0.7198	0.0002
215434_x_at	NBPF1	neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10	0.8959	0.045
215435_at		CDNA FLJ11921 fis; clone HEMBB1000318	0.7212	0.0397
215437_x_at	BAZ2A	bromodomain adjacent to zinc finger domain; 2A	0.2138	0
215441_at	LOC730453	hypothetical protein LOC730453	0.894	0.0343
215457_at		Clone 24438 mRNA sequence	0.2183	0.0198
215467_x_at	LOC647070	hypothetical LOC647070	0.3385	0.0002
215470_at	DKFZP686M0199	general transcription factor IIH; polypeptide 2; 44kDa-like	2.5384	0

215474_at		CDNA FLJ12032 fis; clone HEMBB1001880	0.3013	0.0008
215483_at	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	1.1577	0.0023
215501_s_at	DUSP10	dual specificity phosphatase 10	0.5752	0.0429
215504_x_at		Clone 25061 mRNA sequence	0.3847	0.0007
215508_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	0.4075	0.0025
215509_s_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	1.1981	0.0063
215512_at	6-Mar	membrane-associated ring finger (C3HC4) 6	0.5932	0.0118
215521_at	PHC3	polyhomeotic homolog 3 (Drosophila)	0.5149	0.0026
215529_x_at	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	0.3664	0.02
215532_x_at	ZNF492	zinc finger protein 492	0.3204	0.0226
215544_s_at	UBOX5	U-box domain containing 5	0.5219	0.0188
215553_x_at		CDNA FLJ14253 fis; clone OVARC1001376	0.4044	0.0009
215558_at	UBR2	Ubiquitin protein ligase E3 component n-recognin 2	0.4103	0.0083
215567_at	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0.5746	0.0316
215570_s_at	ZNF780A	zinc finger protein 780A, zinc finger protein 780B	0.6836	0.0223
215578_at		CDNA FLJ11662 fis; clone HEMBA1004629	0.479	0.0312
215581_s_at	MCM3AP	minichromosome maintenance complex component 3 associated protein	0.4331	0.0083
215586_at		CDNA FLJ14111 fis; clone MAMMA1001630	0.7104	0.0029
215587_x_at		CDNA FLJ13829 fis; clone THYRO1000625	0.2409	0.0386
215591_at	SATB2	SATB homeobox 2	0.2479	0.0031
215595_x_at		CDNA FLJ13856 fis; clone THYRO1000988	0.1542	0.0354
215597_x_at		CDNA FLJ11353 fis; clone HEMBA1000042	0.1855	0.0475
215599_at	LOC730390	glucuronidase; beta pseudogene, similar to SMA4	1.9289	0
215600_x_at	FBXW12	F-box and WD repeat domain containing 12	0.4906	0.006
215604_x_at		CDNA FLJ13721 fis; clone PLACE2000450	0.2956	0.0299
215605_at	NCOA2	Nuclear receptor coactivator 2	0.7605	0.0096
215611_at	TCF12	transcription factor 12 (HTF4; helix-loop-helix transcription factors 4)	0.3669	0.041
215615_x_at		CDNA FLJ14152 fis; clone MAMMA1003089	0.2071	0.0018
215623_x_at	SMC4	structural maintenance of chromosomes 4	0.4498	0.0035
215627_at		CDNA FLJ13453 fis; clone PLACE1003205	0.1507	0.0005
215628_x_at		MRNA; cDNA DKFZp564M193 (from clone DKFZp564M193)	0.2388	0.0316

215629_s_at	DLEU2	deleted in lymphocytic leukemia 2-like, deleted in lymphocytic leukemia; 2	1.9049	0
215648_at		CDNA FLJ11461 fis; clone HEMBA1001570	0.5832	0
215650_at		CDNA FLJ11552 fis; clone HEMBA1003021	0.1322	0.0368
215655_at	GRIK2	Glutamate receptor; ionotropic; kainate 2	0.1132	0.0056
215667_x_at	LOC441259	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like, similar to postmeiotic segregation increased 2-like 2	0.7719	0.0008
215672_s_at	KIAA0828	adenosylhomocysteinase 3	0.6213	0.0022
215674_at	KIAA1659	KIAA1659 protein	0.1292	0.0243
215694_at	SPATA5L1	spermatogenesis associated 5-like 1	0.31	0.0122
215708_s_at	PRIM2	primase; DNA; polypeptide 2 (58kDa)	0.8661	0.0062
215711_s_at	WEE1	WEE1 homolog (S. pombe)	0.7244	0.018
215716_s_at	ATP2B1	ATPase; Ca++ transporting; plasma membrane 1	1.1505	0.0001
215728_s_at	ACOT7	acyl-CoA thioesterase 7	0.5698	0.046
215731_s_at	MPHOSPH9	M-phase phosphoprotein 9	1.156	0.0096
215743_at	NMT2	N-myristoyltransferase 2	0.462	0.0076
215747_s_at	RCC1	regulator of chromosome condensation 1	0.2976	0.0178
215758_x_at	ZNF93	zinc finger protein 93	1.1828	0.0006
215761_at	DMXL2	Dmx-like 2	0.3983	0.0187
215766_at	GSTA1	Glutathione S-transferase A1	0.3139	0.0137
215773_x_at	PARP2	poly (ADP-ribose) polymerase family; member 2	0.7643	0.0066
215786_at		CDNA FLJ12108 fis; clone MAMMA1000009	0.8153	0.0254
215791_at		Chromosome 21q22.1 anonymous mRNA sequence	0.6094	0.0448
215812_s_at	LOC653562	similar to Sodium- and chloride-dependent creatine transporter 1 (CT1) (Creatine transporter 1) (Solute carrier family 6 member 8), solute carrier family 6 (neurotransmitter transporter; creatine); member 10 (pseudogene), solute carrier family 6 (neurotransmitter transporter; creatine); member 8	1.1314	0.0363
215820_x_at	SNX13	sorting nexin 13	0.5227	0.0038
215823_x_at	LOC341315	hypothetical LOC341315, poly(A) binding protein; cytoplasmic 1, poly(A) binding protein; cytoplasmic 3, similar to Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1)	0.254	0.0058
215832_x_at	PICALM	phosphatidylinositol binding clathrin assembly protein	0.4643	0.0258
215833_s_at	SPPL2B	signal peptide peptidase-like 2B	0.438	0.0133

215850_s_at	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5; 13kDa	0.9749	0.0023
215854_at		CDNA FLJ11844 fis; clone HEMBA1006665	0.3867	0.0096
215861_at	RP4-724E16.2	hypothetical protein FLJ14031	0.1802	0.0015
215866_at		CDNA: FLJ21285 fis; clone COL01912	0.2572	0.0042
215867_x_at	CA12	carbonic anhydrase XII	1.0248	0.013
215873_x_at	ABCC10	ATP-binding cassette; sub-family C (CFTR/MRP); member 10	0.4093	0.0335
215882_at	CEP152	Centrosomal protein 152kDa	0.3589	0.0323
215887_at	ZNF277P	zinc finger protein 277 pseudogene	0.3305	0.0425
215888_at	PDS5B	Androgen-induced proliferation inhibitor	1.1762	0.0098
215891_s_at	GM2A	GM2 ganglioside activator	1.2282	0.019
215895_x_at	ADFP	Adipose differentiation-related protein	0.1943	0.0018
215897_at	MED25	mediator complex subunit 25	0.4378	0.0119
215898_at	TTLL5	tubulin tyrosine ligase-like family; member 5	0.6703	0.0042
215910_s_at	FNDC3A	fibronectin type III domain containing 3A	0.6407	0.0418
215919_s_at	MRPS11	mitochondrial ribosomal protein S11	0.9356	0.0007
215920_s_at	LOC388237	pyridoxal-dependent decarboxylase domain containing 2, similar to kidney-specific protein (KS), similar to nuclear pore complex interacting protein	0.7397	0.0006
215921_at	LOC388237	similar to kidney-specific protein (KS), similar to nuclear pore complex interacting protein	0.9949	0.0001
215926_x_at	SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	0.4186	0.0029
215936_s_at	KIAA1033	KIAA1033	1.5404	0
215942_s_at	GTSE1	G-2 and S-phase expressed 1	0.9545	0.0015
215945_s_at	TRIM2	tripartite motif-containing 2	0.389	0.0429
215954_s_at	C19orf29	chromosome 19 open reading frame 29	0.5844	0.0044
215968_at		Clone 24442 mRNA sequence	0.3278	0.008
215978_x_at	LOC152719	hypothetical protein LOC152719	0.4384	0.0141
215992_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.7059	0.006
215997_s_at	CUL4B	cullin 4B	0.8144	0.0123
216002_at		CDNA FLJ12105 fis; clone HEMBB1002699	0.1594	0.0272
216022_at		Transcribed locus	0.7387	0.0023
216026_s_at	POLE	polymerase (DNA directed); epsilon	0.5187	0.0034
216044_x_at	FAM69A	family with sequence similarity 69; member A	1.1704	0.0042
216048_s_at	RHOBTB3	Rho-related BTB domain containing 3	1.6373	0.0063
216049_at	RHOBTB3	Rho-related BTB domain containing 3	0.3711	0.0029
216068_at		MRNA; cDNA DKFZp434N021 (from clone DKFZp434N021)	0.1009	0.0352

216069_at		CDNA FLJ31388 fis; clone NT2NE1000023	0.2995	0.0003
216086_at	SV2C	synaptic vesicle glycoprotein 2C	1.6609	0.0147
216091_s_at	BTRC	beta-transducin repeat containing	0.6045	0.0007
216094_at		CDNA: FLJ21670 fis; clone COL09010	0.4545	0.0048
216095_x_at	MTMR1	myotubularin related protein 1	0.6783	0.0022
216101_at		Full length insert cDNA clone YR67C11	0.2693	0.0113
216109_at	THRAP2	Thyroid hormone receptor associated protein 2	1.4599	0.0005
216111_x_at	PMS2L3	postmeiotic segregation increased 2-like 3	0.831	0.0001
216113_at	ABI2	Abl interactor 2	0.2845	0.0157
216115_at	NF1	Neurofibromin 1 (neurofibromatosis; von Recklinghausen disease; Watson disease)	0.6188	0.0263
216120_s_at	ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	1.3238	0.0259
216144_at		MRNA; cDNA DKFZp434K1126 (from clone DKFZp434K1126)	0.175	0.0086
216155_at		CDNA: FLJ20890 fis; clone ADKA03323	0.2653	0.0239
216170_at		CDNA: FLJ21618 fis; clone COL07487	0.5633	0
216173_at		CDNA: FLJ21707 fis; clone COL09953	0.8005	0.001
216187_x_at		Alu repeat (LNX1) mRNA sequence	0.3657	0.0066
216189_at		Homo sapiens; clone IMAGE:3344506	0.5027	0.0003
216194_s_at	TBCB	tubulin folding cofactor B	0.4421	0.007
216197_at	ATF7IP	activating transcription factor 7 interacting protein	1.662	0
216198_at	ATF7IP	activating transcription factor 7 interacting protein	0.2519	0.0011
216211_at		MRNA; cDNA DKFZp564A023 (from clone DKFZp564A023)	0.649	0.0275
216222_s_at	MYO10	myosin X	0.4766	0.0401
216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.7861	0.0085
216232_s_at	GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	0.5201	0.0214
216234_s_at	LOC730418	protein kinase; cAMP-dependent; catalytic; alpha, similar to protein kinase; cAMP-dependent; catalytic; gamma	0.5416	0.0036
216236_s_at	SLC2A14	solute carrier family 2 (facilitated glucose transporter); member 14, solute carrier family 2 (facilitated glucose transporter); member 3	1.141	0.0121
216237_s_at	MCM5	minichromosome maintenance complex component 5	2.091	0.0011
216242_x_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related, RPB11b2 protein, polymerase (RNA) II (DNA directed) polypeptide J; 13.3kDa pseudogene	0.6108	0.004
216263_s_at	NGDN	neuroguidin; EIF4E binding protein	0.2293	0.0072

216266_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	1.3608	0
216268_s_at	JAG1	jagged 1 (Alagille syndrome)	1.9825	0
216297_at		MRNA; cDNA DKFZp564C156 (from clone DKFZp564C156)	0.1933	0.0024
216306_x_at	PTBP1	polypyrimidine tract binding protein 1	0.3578	0.001
216309_x_at	JRK	jerky homolog (mouse)	0.6535	0.0119
216315_x_at	Kua-UEV	similar to ubiquitin-conjugating enzyme E2 variant 1 isoform d, ubiquitin-conjugating enzyme E2 variant 1	0.1825	0.0316
216347_s_at	PPP1R13B	protein phosphatase 1; regulatory (inhibitor) subunit 13B	0.8488	0.0236
216388_s_at	LTB4R	leukotriene B4 receptor	0.5995	0.0456
216442_x_at	FN1	fibronectin 1	1.8888	0.0001
216459_x_at	TIGD1L	tigger transposable element derived 1-like	0.2479	0.003
216468_s_at	ZNF682	zinc finger protein 682	0.5313	0.0054
216497_at	hCG_2023776	hCG2023776, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A1 pseudogene, heterogeneous nuclear ribonucleoprotein A1 pseudogene 4, heterogeneous nuclear ribonucleoprotein A1 pseudogene 5, heterogeneous nuclear ribonucleoprotein A1-like, hypothetical LOC642817, similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP), similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)	0.1692	0.0465
216506_x_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 10	0.2686	0.0314
216509_x_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 10	0.1862	0.0135
216525_x_at	PMS2L3	postmeiotic segregation increased 2-like 3	0.6832	0.0009
216527_at		CDNA FLJ46556 fis; clone THYMU3039807	0.3059	0.035
216531_at	YY2	YY2 transcription factor	0.1511	0.0281
216538_at		MRNA; cDNA DKFZp566C093 (from clone DKFZp566C093)	0.365	0.0057
216548_x_at	HMG4L	high-mobility group (nonhistone chromosomal) protein 4-like	0.6861	0.014
216550_x_at	ANKRD12	ankyrin repeat domain 12	0.4594	0.0129

216551_x_at	PLCG1	phospholipase C; gamma 1	0.2742	0.0292
216563_at	ANKRD12	Ankyrin repeat domain 12	0.4157	0.0242
216602_s_at	FARSA	phenylalanyl-tRNA synthetase; alpha subunit	0.7873	0.0022
216614_at		MRNA; cDNA DKFZp564F212 (from clone DKFZp564F212)	0.7279	0.0382
216677_at	ZNF154	zinc finger protein 154	0.1227	0.0081
216697_at	TRIO	Triple functional domain (PTPRF interacting)	0.2546	0.0296
216702_x_at		Unknown protein	0.1578	0.0136
216713_at	KRIT1	KRIT1; ankyrin repeat containing	0.465	0.003
216755_at	OSBPL10	oxysterol binding protein-like 10	0.1412	0.0384
216766_at		CDNA: FLJ21499 fis; clone COL05634	0.3554	0.0475
216843_x_at	LOC732139	postmeiotic segregation increased 2-like 1, similar to postmeiotic segregation increased 2-like 2	0.6343	0.0078
216858_x_at			0.6408	0.0016
216859_x_at			0.3259	0.0067
216863_s_at	MORC2	MORC family CW-type zinc finger 2	0.8432	0.0021
216870_x_at	DLEU2	deleted in lymphocytic leukemia; 2	1.2076	0.0001
216902_s_at	LOC653390	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae), RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	1.0222	0.0146
216908_x_at	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	1.2482	0.0004
216915_s_at	PTPN12	protein tyrosine phosphatase; non-receptor type 12	0.8399	0.0177
216926_s_at	KIAA0892	KIAA0892	0.2156	0.0251
216933_x_at	APC	adenomatosis polyposis coli	1.2428	0
216945_x_at	PASK	PAS domain containing serine/threonine kinase	0.5001	0.001
216952_s_at	LMNB2	lamin B2	1.094	0.0026
216957_at	USP22	ubiquitin specific peptidase 22	0.2825	0.0014
216960_s_at	ZNF133	zinc finger protein 133	1.299	0
216969_s_at	KIF22	kinesin family member 22, kinesin-like DNA-binding protein pseudogene	0.4081	0.0045
216977_x_at	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	0.4594	0.0401
216983_s_at	ZNF224	zinc finger protein 224	0.7624	0.0001
217010_s_at	CDC25C	cell division cycle 25 homolog C (S. pombe)	0.3028	0.0386
217016_x_at	FLJ23172	hypothetical LOC389177	0.1695	0.0397
217027_x_at	KPNB1	karyopherin (importin) beta 1	0.3603	0.0254
217042_at	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	0.8292	0.0003
217049_x_at	PCDH11Y	protocadherin 11 Y-linked	0.1293	0.0343
217076_s_at			0.202	0.0085

217094_s_at	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	1.0373	0.0006
217097_s_at	PHTF2	putative homeodomain transcription factor 2	0.9004	0.0008
217100_s_at	UBXD7	UBX domain containing 7	0.8356	0.0125
217104_at	ST20	suppressor of tumorigenicity 20	0.5439	0.0004
217123_x_at	PMCHL1	pro-melanin-concentrating hormone-like 1	0.1109	0.0478
217124_at	IQCE	IQ motif containing E	0.6734	0.0058
217140_s_at	VDAC1	voltage-dependent anion channel 1	0.8794	0.0025
217152_at		CDNA FLJ14074 fis; clone HEMBB1001869	0.3707	0.0093
217164_at			1.1971	0.0003
217176_s_at	ZFX	zinc finger protein; X-linked	0.2392	0.0156
217189_s_at	SMG7	Smg-7 homolog; nonsense mediated mRNA decay factor (C. elegans)	0.39	0.0012
217208_s_at	DLG1	discs; large homolog 1 (Drosophila)	1.075	0.0063
217225_x_at	NOMO2	NODAL modulator 2	0.7734	0
217226_s_at	SFXN3	sideroflexin 3	1.089	0.0088
217246_s_at	DIAPH2	diaphanous homolog 2 (Drosophila)	0.2389	0.0075
217294_s_at	ENO1	enolase 1; (alpha)	1.332	0.0094
217297_s_at	MYO9B	myosin IXB	1.2878	0.001
217299_s_at	NBN	nibrin	0.8813	0.0017
217300_at			0.1162	0.0464
217310_s_at	FOXJ3	forkhead box J3	0.5087	0.0035
217353_at	hCG_2023776	hCG2023776, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A1 pseudogene, heterogeneous nuclear ribonucleoprotein A1 pseudogene 4, heterogeneous nuclear ribonucleoprotein A1 pseudogene 5, heterogeneous nuclear ribonucleoprotein A1-like, hypothetical LOC642817, similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP), similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-1) (Topoisomerase-inhibitor suppressed)	0.326	0.0055
217356_s_at	PGK1	phosphoglycerate kinase 1	0.8016	0.0036
217370_x_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	1.2242	0
217373_x_at	MDM2	Mdm2; transformed 3T3 cell double minute 2; p53 binding protein (mouse)	0.7486	0.0185

217398_x_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.5555	0
217403_s_at	ZNF227	zinc finger protein 227	1.1128	0.002
217432_s_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	0.5107	0.0174
217440_at		MRNA; cDNA DKFZp566A193 (from clone DKFZp566A193)	0.1104	0.018
217445_s_at	GART	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	0.4894	0.0245
217446_x_at		MRNA; cDNA DKFZp434M054 (from clone DKFZp434M054)	0.2631	0.0084
217448_s_at	LOC285412	TOX high mobility group box family member 4, similar to Epidermal Langerhans cell protein LCP1	0.4331	0.0391
217485_x_at	LOC732139	postmeiotic segregation increased 2-like 1, similar to postmeiotic segregation increased 2-like 2	0.3991	0.0472
217486_s_at	ZDHHC17	zinc finger; DHHC-type containing 17	0.819	0.0011
217506_at	LOC400642	Hypothetical gene supported by BC041875; BX648984	0.8911	0.0497
217536_x_at		Transcribed locus	0.2597	0.0292
217539_at	C18orf25	chromosome 18 open reading frame 25	0.2091	0.0355
217540_at		Transcribed locus	0.6054	0.0056
217547_x_at	ZNF675	zinc finger protein 675	0.6659	0.0305
217556_at	CLCN4	chloride channel 4	0.4392	0.0042
217586_x_at			0.5999	0.0038
217588_at	CATSPER2	cation channel; sperm associated 2, cation channel; sperm associated 2 pseudogene 1	0.2503	0.0483
217602_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.2194	0.018
217605_at	USP27X	ubiquitin specific peptidase 27; X-linked	0.2223	0.0247
217608_at	P18SRP	P18SRP protein	0.6944	0.0277
217610_at		CDNA FLJ38765 fis; clone KIDNE2014489	0.7425	0.0047
217612_at	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	0.2538	0.0364
217620_s_at	PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	0.1999	0.0493
217624_at	PDAP1	PDGFA associated protein 1	0.2832	0.0005
217627_at	ZNF573	zinc finger protein 573	0.9501	0.0071
217640_x_at	C18orf24	chromosome 18 open reading frame 24	1.1533	0.0017
217643_x_at			0.7009	0
217644_s_at	SOS2	son of sevenless homolog 2 (Drosophila)	0.4561	0.0111
217650_x_at	ST3GAL2	ST3 beta-galactoside alpha-2;3-sialyltransferase 2	0.3006	0.0133
217653_x_at			0.795	0.0017

217656_at		Transcribed locus	0.1344	0.0225
217662_x_at		Transcribed locus	0.3361	0.0026
217665_at		CDNA FLJ25947 fis; clone JTH14708	0.3402	0.0483
217671_at		Transcribed locus	0.5454	0.02
217678_at	SLC7A11	solute carrier family 7; (cationic amino acid transporter; y+ system) member 11	1.1832	0.0292
217679_x_at			0.4211	0.0311
217701_x_at			0.5882	0.016
217704_x_at	SUZ12P	Suppressor of zeste 12 homolog pseudogene	0.5633	0.0046
217713_x_at			0.2276	0.0286
217714_x_at	STMN1	stathmin 1/oncoprotein 18	0.5501	0.0001
217715_x_at			0.3063	0.0028
217718_s_at	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; beta polypeptide	0.1658	0.0207
217727_x_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.5462	0.0001
217736_s_at	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	0.5126	0.0011
217765_at	NRBP1	nuclear receptor binding protein 1	0.4558	0.0127
217775_s_at	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	0.5165	0.0276
217784_at	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	0.8299	0.0106
217785_s_at	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	0.9446	0.041
217791_s_at	ALDH18A1	aldehyde dehydrogenase 18 family; member A1	0.8827	0.0015
217794_at	PRR13	proline rich 13	0.3408	0.0041
217802_s_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.372	0.0037
217805_at	ILF3	interleukin enhancer binding factor 3; 90kDa	0.6778	0.0017
217815_at	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.5708	0.0187
217819_at	GOLGA7	golgi autoantigen; golgin subfamily a; 7	0.3096	0.0161
217835_x_at	C20orf24	chromosome 20 open reading frame 24	0.3954	0.0201
217840_at	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	1.013	0.0001
217842_at	LUC7L2	LUC7-like 2 (S. cerevisiae)	0.5286	0.001
217859_s_at	SLC39A9	solute carrier family 39 (zinc transporter); member 9	0.8841	0.0098
217871_s_at	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	0.3494	0.0016
217878_s_at	CDC27	cell division cycle 27 homolog (S. cerevisiae)	0.5708	0.0227
217888_s_at	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	0.8256	0.0027
217891_at	C16orf58	chromosome 16 open reading frame 58	0.6679	0.0216

217926_at	C19orf53	chromosome 19 open reading frame 53	0.3941	0.0016
217941_s_at	ERBB2IP	erbb2 interacting protein	0.4292	0.0015
217946_s_at	SAE1	SUMO1 activating enzyme subunit 1	1.2456	0
217948_at	FAM127B	family with sequence similarity 127; member B	0.6748	0.0005
217949_s_at	VKORC1	vitamin K epoxide reductase complex; subunit 1	0.663	0.0098
217956_s_at	ENOPH1	enolase-phosphatase 1	0.3093	0.0184
217957_at	C16orf80	chromosome 16 open reading frame 80	0.8825	0.0001
217970_s_at	CNOT6	CCR4-NOT transcription complex; subunit 6	0.6122	0.0332
217972_at	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	0.3716	0.0399
218008_at	C7orf42	chromosome 7 open reading frame 42	0.574	0.0001
218009_s_at	PRC1	protein regulator of cytokinesis 1	5.0663	0
218010_x_at	C20orf149	chromosome 20 open reading frame 149	0.8147	0.0055
218013_x_at	DCTN4	dynactin 4 (p62)	0.9005	0.0401
218023_s_at	FAM53C	family with sequence similarity 53; member C	0.7612	0.0023
218036_x_at	NMD3	NMD3 homolog (S. cerevisiae)	0.7694	0.0476
218039_at	NUSAP1	nucleolar and spindle associated protein 1	1.0908	0.0016
218045_x_at	PTMS	parathymosin	1.0095	0.0008
218048_at	COMMD3	COMM domain containing 3	0.3444	0.0298
218052_s_at	ATP13A1	ATPase type 13A1	1.0396	0
218055_s_at	WDR41	WD repeat domain 41	1.6181	0
218056_at	BFAR	bifunctional apoptosis regulator	1.2137	0
218057_x_at	COX4NB	COX4 neighbor	0.4394	0.0069
218064_s_at	AKAP8L	A kinase (PRKA) anchor protein 8-like	1.4531	0
218069_at	XTP3TPA	XTP3-transactivated protein A	0.5877	0.0167
218075_at	AAAS	achalasia; adrenocortical insufficiency; alacrimia (Allgrove; triple-A)	0.3757	0.0211
218088_s_at	RRAGC	Ras-related GTP binding C	0.5434	0.036
218089_at	C20orf4	chromosome 20 open reading frame 4	0.5708	0.002
218110_at	XAB2	XPA binding protein 2	0.3394	0.0025
218115_at	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	2.4878	0.0002
218131_s_at	GATAD2A	GATA zinc finger domain containing 2A	0.6553	0.0064
218134_s_at	RBM22	RNA binding motif protein 22	0.5564	0.0003
218135_at	ERGIC2	ERGIC and golgi 2	0.8626	0
218137_s_at	SMAP1	stromal membrane-associated protein 1	0.4843	0.0055
218138_at	MKKS	McKusick-Kaufman syndrome	0.7124	0.0205
218145_at	TRIB3	tribbles homolog 3 (Drosophila)	1.9204	0.0007

218146_at	GLT8D1	glycosyltransferase 8 domain containing 1	0.4665	0.0027
218147_s_at	GLT8D1	glycosyltransferase 8 domain containing 1	0.5082	0.0077
218148_at	CENPT	centromere protein T	0.6361	0.0257
218149_s_at	ZNF395	zinc finger protein 395	0.7458	0.026
218152_at	HMG20A	high-mobility group 20A	0.4894	0.0165
218173_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	0.2812	0.0174
218183_at	C16orf5	chromosome 16 open reading frame 5	0.6217	0.0208
218185_s_at	ARMC1	armadillo repeat containing 1	0.6368	0.0003
218188_s_at	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	0.3953	0.0249
218189_s_at	NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	1.4211	0.0001
218198_at	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	0.778	0.0064
218240_at	NKIRAS2	NFKB inhibitor interacting Ras-like 2	0.7039	0.0002
218244_at	NOL8	nucleolar protein 8	0.4954	0.0089
218250_s_at	CNOT7	CCR4-NOT transcription complex; subunit 7	0.4166	0.0035
218252_at	CKAP2	cytoskeleton associated protein 2	1.7243	0
218260_at	C19orf58	chromosome 19 open reading frame 58	0.5196	0.0083
218269_at	RNASEN	ribonuclease III; nuclear	0.7263	0.0047
218274_s_at	ANKZF1	ankyrin repeat and zinc finger domain containing 1	0.6661	0.0074
218284_at	SMAD3	SMAD family member 3	0.8594	0.0069
218290_at	PLEKHJ1	pleckstrin homology domain containing; family J member 1	0.523	0.01
218300_at	C16orf53	chromosome 16 open reading frame 53	0.7234	0.0111
218302_at	PSENEN	presenilin enhancer 2 homolog (C. elegans)	0.8733	0.0012
218308_at	TACC3	transforming; acidic coiled-coil containing protein 3	1.4475	0.0006
218317_x_at	GIYD1	GIY-YIG domain containing 1, GIY-YIG domain containing 2	0.9459	0.0025
218324_s_at	SPATS2	spermatogenesis associated; serine-rich 2	2.2252	0
218329_at	PRDM4	PR domain containing 4	1.2311	0.0004
218337_at	RAI16	retinoic acid induced 16	0.4332	0.0064
218340_s_at	UBE1L2	ubiquitin-activating enzyme E1-like 2	1.6021	0.001
218343_s_at	GTF3C3	general transcription factor IIIC; polypeptide 3; 102kDa	0.5399	0.0368
218344_s_at	RCOR3	REST corepressor 3	1.3314	0.0016
218348_s_at	ZC3H7A	zinc finger CCCH-type containing 7A	0.5673	0.0017
218349_s_at	ZWILCH	Zwilch; kinetochore associated; homolog (Drosophila)	2.4367	0
218350_s_at	GMNN	geminin; DNA replication inhibitor	2.6377	0
218355_at	KIF4A	kinesin family member 4A	2.49	0.0001

218366_x_at	METT11D1	methyltransferase 11 domain containing 1	0.4535	0.0038
218368_s_at	TNFRSF12A	tumor necrosis factor receptor superfamily; member 12A	1.6369	0.003
218374_s_at	C12orf4	chromosome 12 open reading frame 4	1.0767	0.0016
218381_s_at	U2AF2	U2 small nuclear RNA auxiliary factor 2	0.3222	0.0351
218392_x_at	SFXN1	sideroflexin 1	0.9646	0.0077
218395_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	0.6596	0.0007
218398_at	MRPS30	mitochondrial ribosomal protein S30	0.658	0.0358
218399_s_at	CDCA4	cell division cycle associated 4	2.0459	0
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3; 100kDa	1.4171	0.0237
218403_at	TRIAP1	TP53 regulated inhibitor of apoptosis 1	0.4227	0.0192
218404_at	SNX10	sorting nexin 10	0.8925	0.0057
218409_s_at	DNAJC1	DnaJ (Hsp40) homolog; subfamily C; member 1	0.7269	0.0034
218412_s_at	GTF2IRD1	GTF2I repeat domain containing 1	0.7441	0.006
218414_s_at	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	0.4814	0.0073
218415_at	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	0.7045	0.0071
218425_at	TRIAD3	TRIAD3 protein	0.6938	0.004
218426_s_at	TRIAD3	TRIAD3 protein	0.8856	0.0004
218427_at	SDCCAG3	serologically defined colon cancer antigen 3	0.5798	0.001
218430_s_at	RFXDC2	regulatory factor X domain containing 2	0.538	0.0257
218434_s_at	AACS	acetoacetyl-CoA synthetase	1.4499	0.0004
218445_at	H2AFY2	H2A histone family; member Y2	0.8967	0.0014
218447_at	C16orf61	chromosome 16 open reading frame 61	0.52	0.0042
218448_at	C20orf11	chromosome 20 open reading frame 11	0.9232	0.0001
218456_at	CAPRIN2	caprin family member 2	0.9895	0.0001
218457_s_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.7555	0.0096
218458_at	GMCL1	germ cell-less homolog 1 (Drosophila)	1.1498	0
218460_at	HEATR2	HEAT repeat containing 2	0.7698	0.0021
218464_s_at	C17orf63	chromosome 17 open reading frame 63	0.5676	0.0003
218465_at	TMEM33	transmembrane protein 33	0.6808	0.02
218473_s_at	GLT25D1	glycosyltransferase 25 domain containing 1	0.4669	0.0111
218474_s_at	KCTD5	potassium channel tetramerisation domain containing 5	0.6663	0.0083
218478_s_at	ZCCHC8	zinc finger; CCHC domain containing 8	0.5599	0.0023
218484_at	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 4-like 2	0.9129	0.0057
218490_s_at	ZNF302	zinc finger protein 302	0.7608	0.0071
218494_s_at	SLC2A4RG	SLC2A4 regulator	1.2442	0.0026

218498_s_at	ERO1L	ERO1-like (S. cerevisiae)	1.5733	0.0001
218507_at	HIG2	hypoxia-inducible protein 2	1.8454	0.0018
218515_at	C21orf66	chromosome 21 open reading frame 66	1.1968	0.0002
218520_at	TBK1	TANK-binding kinase 1	0.7069	0.0055
218521_s_at	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	1.098	0.0011
218522_s_at	MAP1S	microtubule-associated protein 1S	0.5712	0.0054
218524_at	E4F1	E4F transcription factor 1	0.5923	0.0002
218529_at	CD320	CD320 molecule	0.8384	0.0069
218542_at	CEP55	centrosomal protein 55kDa	3.2032	0
218546_at	C1orf115	chromosome 1 open reading frame 115	1.5721	0.0326
218547_at	DHDDS	dehydrodolichyl diphosphate synthase	0.5275	0.0367
218564_at	RFWD3	ring finger and WD repeat domain 3	1.7199	0
218567_x_at	DPP3	dipeptidyl-peptidase 3	0.6963	0.0141
218579_s_at	DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	0.6457	0.0014
218581_at	ABHD4	abhydrolase domain containing 4	0.961	0.0008
218585_s_at	DTL	denticleless homolog (Drosophila)	4.1604	0
218586_at	C20orf20	chromosome 20 open reading frame 20	1.1164	0
218593_at	RBM28	RNA binding motif protein 28	0.5691	0.027
218597_s_at	CISD1	CDGSH iron sulfur domain 1	0.4942	0.0493
218598_at	RINT1	RAD50 interactor 1	1.0588	0.0001
218602_s_at	FAM29A	family with sequence similarity 29; member A	0.4795	0.0231
218604_at	LEMD3	LEM domain containing 3	0.7912	0
218610_s_at	FLJ11151	hypothetical protein FLJ11151	0.76	0.0125
218614_at	C12orf35	chromosome 12 open reading frame 35	0.7541	0.0178
218616_at	INTS12	integrator complex subunit 12	0.5613	0.0014
218619_s_at	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.7696	0.0018
218622_at	NUP37	nucleoporin 37kDa	1.3189	0.0002
218624_s_at	MGC2752	hypothetical protein MGC2752	0.778	0.0016
218625_at	NRN1	neuritin 1	2.4864	0.0062
218636_s_at	MAN1B1	mannosidase; alpha; class 1B; member 1	0.5317	0.0289
218640_s_at	PLEKHF2	pleckstrin homology domain containing; family F (with FYVE domain) member 2	0.6663	0.0291
218653_at	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	1.4361	0.0032
218658_s_at	ACTR8	ARP8 actin-related protein 8 homolog (yeast)	0.2711	0.0424
218662_s_at	NCAPG	non-SMC condensin I complex; subunit G	2.2167	0
218663_at	NCAPG	non-SMC condensin I complex; subunit G	2.1819	0.0001

218667_at	PJA1	praja 1	0.9816	0.0007
218668_s_at	RAP2C	RAP2C; member of RAS oncogene family	0.4278	0.0157
218669_at	RAP2C	RAP2C; member of RAS oncogene family	0.5142	0.0041
218670_at	PUS1	pseudouridylate synthase 1	0.44	0.0444
218674_at	FLJ13611	hypothetical protein FLJ13611	0.7213	0.0153
218676_s_at	PCTP	phosphatidylcholine transfer protein	0.7161	0.0324
218685_s_at	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	1.0286	0.0002
218705_s_at	SNX24	sorting nexin 24	0.5922	0.0173
218709_s_at	IFT52	intraflagellar transport 52 homolog (Chlamydomonas)	0.6615	0.0069
218714_at	PRR14	proline rich 14	0.5461	0.0131
218719_s_at	GINS3	GINS complex subunit 3 (Psf3 homolog)	1.1363	0.0015
218720_x_at	SEZ6L2	seizure related 6 homolog (mouse)-like 2	1.1901	0.0087
218725_at	SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate); member 22	0.5189	0.0456
218726_at	DKFZp762E1312	hypothetical protein DKFZp762E1312	1.1607	0.0042
218727_at	FLJ10815	amino acid transporter	1.3862	0.0001
218734_at	NAT11	N-acetyltransferase 11	1.0023	0.003
218741_at	CENPM	centromere protein M	1.721	0.0008
218745_x_at	TMEM161A	transmembrane protein 161A	0.3035	0.0482
218748_s_at	EXOC5	exocyst complex component 5	1.517	0.0051
218751_s_at	FBXW7	F-box and WD repeat domain containing 7	1.1471	0.0108
218753_at	XKR8	XK; Kell blood group complex subunit-related family; member 8	0.2746	0.0274
218755_at	KIF20A	kinesin family member 20A	2.6086	0.0001
218757_s_at	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	1.688	0
218761_at	RNF111	ring finger protein 111	0.4486	0.0153
218762_at	ZNF574	zinc finger protein 574	0.5605	0.0015
218767_at	REXO4	REX4; RNA exonuclease 4 homolog (S. cerevisiae)	0.3903	0.0078
218768_at	NUP107	nucleoporin 107kDa	0.9418	0.0062
218769_s_at	ANKRA2	ankyrin repeat; family A (RFXANK-like); 2	0.5413	0.022
218775_s_at	WWC2	WW and C2 domain containing 2	0.6964	0.0176
218777_at	REEP4	receptor accessory protein 4	1.1736	0
218780_at	HOOK2	hook homolog 2 (Drosophila)	0.2992	0.0312
218781_at	SMC6	structural maintenance of chromosomes 6	1.3725	0.0001
218782_s_at	ATAD2	ATPase family; AAA domain containing 2	1.9752	0.0012
218794_s_at	TXNL4B	thioredoxin-like 4B	1.1766	0
218798_at	KRI1	KRI1 homolog (S. cerevisiae)	0.4124	0.0029

218803_at	CHFR	checkpoint with forkhead and ring finger domains	0.9713	0.0017
218817_at	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0.6574	0.0084
218823_s_at	KCTD9	potassium channel tetramerisation domain containing 9	0.7433	0.0158
218824_at	FLJ10781	hypothetical protein FLJ10781	0.7089	0.0021
218834_s_at	TMEM132A	transmembrane protein 132A	2.3573	0
218838_s_at	TTC31	tetratricopeptide repeat domain 31	0.7058	0.0172
218839_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	1.0718	0.0354
218842_at	RPAP3	RNA polymerase II associated protein 3	0.8734	0.0171
218848_at	THOC6	THO complex 6 homolog (Drosophila)	0.7319	0.0016
218867_s_at	C12orf49	chromosome 12 open reading frame 49	1.2509	0.0004
218868_at	ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	0.4928	0.0263
218875_s_at	FBXO5	F-box protein 5	1.4267	0.0024
218883_s_at	MLF1IP	MLF1 interacting protein	3.7611	0
218884_s_at	GUF1	GUF1 GTPase homolog (S. cerevisiae)	0.5623	0.0369
218888_s_at	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	2.6291	0
218893_at	ISOC2	isochorismatase domain containing 2	0.7178	0.0069
218894_s_at	FLJ10292	mago-nashi homolog 2	0.6814	0.0144
218898_at	FAM57A	family with sequence similarity 57; member A	1.5387	0.0111
218904_s_at	C9orf40	chromosome 9 open reading frame 40	1.1288	0.0008
218905_at	INTS8	integrator complex subunit 8	1.1354	0
218908_at	ASPSCR1	alveolar soft part sarcoma chromosome region; candidate 1	0.6623	0.0117
218911_at	YEATS4	YEATS domain containing 4	1.0014	0.0057
218916_at	ZNF768	zinc finger protein 768	0.5716	0.0003
218920_at	FLJ10404	hypothetical protein FLJ10404	1.0005	0.0002
218926_at	MYNN	myoneurin	0.4798	0.0072
218942_at	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase; type II; gamma	0.9502	0.0003
218944_at	PYCRL	pyrroline-5-carboxylate reductase-like	0.3331	0.0359
218945_at	C16orf68	chromosome 16 open reading frame 68	0.6496	0.006
218947_s_at	PAPD1	PAP associated domain containing 1	0.6014	0.0295
218951_s_at	PLCXD1	phosphatidylinositol-specific phospholipase C; X domain containing 1	1.1859	0.016
218953_s_at	PCYOX1L	prenylcysteine oxidase 1 like	1.9904	0
218954_s_at	BRF2	BRF2; subunit of RNA polymerase III transcription initiation factor; BRF1-like	1.1046	0.002
218955_at	BRF2	BRF2; subunit of RNA polymerase III transcription initiation factor; BRF1-like	1.0751	0.0009

218956_s_at	PTCD1	pentatricopeptide repeat domain 1	0.6038	0.0029
218958_at	C19orf60	chromosome 19 open reading frame 60	0.441	0.0376
218959_at	HOXC10	homeobox C10	1.4038	0.0361
218968_s_at	ZFP64	zinc finger protein 64 homolog (mouse)	0.7432	0.0096
218971_s_at	WDR91	WD repeat domain 91	0.6045	0.0278
218978_s_at	SLC25A37	solute carrier family 25; member 37	0.5863	0.0356
218979_at	RMI1	RMI1; RecQ mediated genome instability 1; homolog (S. cerevisiae)	1.0605	0.0026
218984_at	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	0.9871	0.0038
218987_at	ATF7IP	activating transcription factor 7 interacting protein	1.0426	0.0026
218988_at	SLC35E3	solute carrier family 35; member E3	0.8091	0.0039
218994_s_at	FLJ13195	stromal antigen 3-like	0.5342	0.0193
218996_at	TFPT	TCF3 (E2A) fusion partner (in childhood Leukemia)	0.8149	0.0022
219000_s_at	DCC1	defective in sister chromatid cohesion homolog 1 (S. cerevisiae)	1.4983	0.0003
219003_s_at	MANEA	mannosidase; endo-alpha	0.5803	0.0475
219004_s_at	C21orf45	chromosome 21 open reading frame 45	1.359	0.0009
219007_at	NUP43	nucleoporin 43kDa	0.5569	0.0002
219009_at	C14orf93	chromosome 14 open reading frame 93	0.2416	0.0333
219022_at	C12orf43	chromosome 12 open reading frame 43	0.5925	0.0067
219024_at	PLEKHA1	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 1	1.6553	0
219026_s_at	RASAL2	RAS protein activator like 2	0.4451	0.0243
219027_s_at	MYO9A	myosin IXA	0.702	0.0006
219029_at	C5orf28	chromosome 5 open reading frame 28	1.4338	0
219034_at	PARP16	poly (ADP-ribose) polymerase family; member 16	0.6748	0.0275
219035_s_at	RNF34	ring finger protein 34	1.778	0
219045_at	RHOF	ras homolog gene family; member F (in filopodia)	0.8229	0.0327
219047_s_at	ZNF668	zinc finger protein 668	0.4234	0.0065
219075_at	YIPF2	Yip1 domain family; member 2	0.3491	0.0014
219088_s_at	ZNF576	zinc finger protein 576	0.6107	0.0126
219105_x_at	ORC6L	origin recognition complex; subunit 6 like (yeast)	2.0352	0
219111_s_at	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	0.4723	0.0192
219112_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	1.1122	0
219119_at	LSM8	LSM8 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.3335	0.0417
219120_at	C2orf44	chromosome 2 open reading frame 44	0.4978	0.0204
219122_s_at	THG1L	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	0.8574	0.035

219123_at	ZNF232	zinc finger protein 232	0.5543	0.0321
219124_at	C8orf41	chromosome 8 open reading frame 41	0.5825	0.0058
219136_s_at	TMEM112	transmembrane protein 112	0.6424	0.0213
219145_at	LPHN1	latrophilin 1	0.5253	0.0192
219148_at	PBK	PDZ binding kinase	5.1616	0
219149_x_at	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	0.3489	0.0306
219158_s_at	NARG1	NMDA receptor regulated 1	0.64	0.0468
219161_s_at	CKLF	chemokine-like factor	0.5957	0.0405
219163_at	ZNF562	zinc finger protein 562	0.6784	0.0013
219175_s_at	SLC41A3	solute carrier family 41; member 3	0.9979	0.0216
219178_at	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	0.7334	0.0005
219182_at	FLJ22167	hypothetical protein FLJ22167	1.2105	0.0017
219193_at	WDR70	WD repeat domain 70	0.5732	0.0163
219201_s_at	TWSG1	twisted gastrulation homolog 1 (Drosophila)	1.3342	0.0175
219212_at	HSPA14	heat shock 70kDa protein 14	0.7691	0.0186
219230_at	TMEM100	transmembrane protein 100	1.8688	0.0099
219231_at	TGS1	trimethylguanosine synthase homolog (S. cerevisiae)	0.3206	0.024
219233_s_at	GSDML	gasdermin-like	0.2347	0.0399
219235_s_at	PHACTR4	phosphatase and actin regulator 4	1.2261	0
219236_at	PAQR6	progestin and adipoQ receptor family member VI	0.2813	0.0101
219237_s_at	DNAJB14	DnaJ (Hsp40) homolog; subfamily B; member 14	0.5122	0.0224
219239_s_at	ZNF654	zinc finger protein 654	0.7528	0.0228
219240_s_at	C10orf88	chromosome 10 open reading frame 88	0.7668	0.0004
219245_s_at	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.8347	0.0003
219246_s_at	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.5489	0.0094
219249_s_at	FKBP10	FK506 binding protein 10; 65 kDa	0.6316	0.0338
219251_s_at	WDR60	WD repeat domain 60	0.664	0.0002
219261_at	C7orf26	chromosome 7 open reading frame 26	0.3418	0.0173
219264_s_at	PPP2R3B	protein phosphatase 2 (formerly 2A); regulatory subunit B''; beta	0.6399	0.008
219268_at	ETNK2	ethanolamine kinase 2	1.7267	0.0048
219275_at	PDCD5	programmed cell death 5	0.5627	0.018
219277_s_at	OGDHL	oxoglutarate dehydrogenase-like	1.3701	0.0244
219280_at	BRWD1	bromodomain and WD repeat domain containing 1	0.4933	0.0177
219296_at	ZDHHC13	zinc finger; DHHC-type containing 13	1.2796	0
219303_at	C13orf7	chromosome 13 open reading frame 7	0.5355	0.045
219306_at	KIF15	kinesin family member 15	1.5872	0.0007

219328_at	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	0.2894	0.0414
219346_at	LRFN3	leucine rich repeat and fibronectin type III domain containing 3	0.4485	0.0091
219350_s_at	DIABLO	diablo homolog (Drosophila)	0.646	0
219351_at	TRAPPC2	trafficking protein particle complex 2	0.7094	0.0342
219355_at	CXorf57	chromosome X open reading frame 57	1.0247	0.0486
219369_s_at	OTUB2	OTU domain; ubiquitin aldehyde binding 2	0.2221	0.0255
219372_at	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	1.1673	0.0005
219376_at	ZNF322B	zinc finger protein 322B	0.596	0.0198
219380_x_at	POLH	polymerase (DNA directed); eta	0.241	0.0442
219381_at	FLJ13231	hypothetical protein FLJ13231	0.5678	0.0312
219384_s_at	ADAT1	adenosine deaminase; tRNA-specific 1	1.0087	0.0004
219387_at	CCDC88A	coiled-coil domain containing 88A	0.6746	0.0407
219390_at	FKBP14	FK506 binding protein 14; 22 kDa	1.4319	0.0009
219392_x_at	PRR11	proline rich 11	0.5948	0.0001
219402_s_at	DERL1	Der1-like domain family; member 1	0.5042	0.0241
219421_at	TTC33	tetratricopeptide repeat domain 33	0.5108	0.0295
219428_s_at	PXMP4	peroxisomal membrane protein 4; 24kDa	0.9536	0.016
219430_at	GPR137	G protein-coupled receptor 137	0.1956	0.0439
219437_s_at	ANKRD11	ankyrin repeat domain 11	0.9561	0.0028
219439_at	C1GALT1	core 1 synthase; glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase; 1	1.5021	0.0006
219445_at	GLTSCR1	glioma tumor suppressor candidate region gene 1	0.2916	0.0437
219446_at	RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	0.6445	0.001
219447_s_at	SLC35C2	solute carrier family 35; member C2	0.6099	0.0165
219453_at	C16orf44	chromosome 16 open reading frame 44	0.4243	0.0103
219467_at	GIN1	gypsy retrotransposon integrase 1	0.6813	0.0348
219479_at	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	1.2886	0.0009
219481_at	TTC13	tetratricopeptide repeat domain 13	0.6646	0.0092
219482_at	SETD4	SET domain containing 4	0.7394	0.0026
219485_s_at	PSMD10	proteasome (prosome; macropain) 26S subunit; non-ATPase; 10	0.5063	0.0028
219490_s_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog; S. cerevisiae)	0.3565	0.0049
219493_at	SHCBP1	SHC SH2-domain binding protein 1	3.5071	0
219494_at	RAD54B	RAD54 homolog B (S. cerevisiae)	1.846	0.0002
219495_s_at	ZNF180	zinc finger protein 180	0.7177	0.0024
219499_at	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	0.7014	0.0005
219502_at	NEIL3	nei endonuclease VIII-like 3 (E. coli)	0.6486	0.0153

219507_at	RSRC1	arginine/serine-rich coiled-coil 1	1.5105	0.0001
219510_at	POLQ	polymerase (DNA directed); theta	1.2031	0.0006
219514_at	ANGPTL2	angiopoietin-like 2	0.5953	0.008
219515_at	PRDM10	PR domain containing 10	0.4985	0.0082
219530_at	PALB2	partner and localizer of BRCA2	1.4582	0
219531_at	CEP72	centrosomal protein 72kDa	0.751	0.0135
219532_at	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2; SUR4/Elo3; yeast)-like 4	2.0176	0.0009
219540_at	ZNF267	zinc finger protein 267	0.735	0.0436
219544_at	C13orf34	chromosome 13 open reading frame 34	1.066	0.0042
219548_at	ZNF16	zinc finger protein 16	0.5768	0.0001
219555_s_at	CENPN	centromere protein N	1.6133	0.0038
219556_at	C16orf59	chromosome 16 open reading frame 59	0.3488	0.0005
219558_at	ATP13A3	ATPase type 13A3	0.7167	0.0312
219567_s_at	C1orf176	chromosome 1 open reading frame 176	0.3269	0.0015
219571_s_at	ZNF12	zinc finger protein 12	1.1095	0
219577_s_at	ABCA7	ATP-binding cassette; sub-family A (ABC1); member 7	0.343	0.0213
219588_s_at	NCAPG2	non-SMC condensin II complex; subunit G2	2.4622	0
219595_at	ZNF26	zinc finger protein 26	0.8151	0.0043
219596_at	THAP10	THAP domain containing 10	1.7376	0.0004
219608_s_at	FBXO38	F-box protein 38	0.778	0.0105
219611_s_at	CCDC21	coiled-coil domain containing 21	0.7819	0.0026
219618_at	IRAK4	interleukin-1 receptor-associated kinase 4	0.6098	0.0101
219623_at	ACTR5	ARP5 actin-related protein 5 homolog (yeast)	0.5992	0.0063
219624_at	BAG4	BCL2-associated athanogene 4	0.4453	0.0292
219625_s_at	COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	1	0
219627_at	ZNF767	zinc finger family member 767	0.6396	0.0066
219631_at	LRP12	low density lipoprotein-related protein 12	0.9513	0.0264
219635_at	ZNF606	zinc finger protein 606	1.2064	0.0006
219640_at	CLDN15	claudin 15	0.7041	0.0003
219644_at	CCDC41	coiled-coil domain containing 41	1.4092	0.0004
219650_at	ERCC6L	excision repair cross-complementing rodent repair deficiency; complementation group 6-like	0.6844	0.01
219653_at	LSM14B	LSM14B; SCD6 homolog B (S. cerevisiae)	0.4483	0.0021
219658_at	PTCD2	pentatricopeptide repeat domain 2	0.8744	0.0002
219678_x_at	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog; S. cerevisiae)	1.0147	0
219690_at	TMEM149	transmembrane protein 149	0.528	0.027

219691_at	SAMD9	sterile alpha motif domain containing 9	0.7877	0.0358
219693_at	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase; delta)	0.6357	0.0453
219698_s_at	METTL4	methyltransferase like 4	0.4764	0.0237
219703_at	MNS1	meiosis-specific nuclear structural 1	0.8785	0.0042
219715_s_at	TDP1	tyrosyl-DNA phosphodiesterase 1	0.7222	0.0009
219717_at	C4orf30	chromosome 4 open reading frame 30	1.2653	0.0047
219719_at	HIGD1B	HIG1 domain family; member 1B	0.6289	0.0023
219720_s_at	C14orf118	chromosome 14 open reading frame 118	0.218	0.0486
219736_at	TRIM36	tripartite motif-containing 36	1.2831	0.0099
219742_at	PRR7	proline rich 7 (synaptic)	0.8138	0.0069
219753_at	STAG3	stromal antigen 3	1.1137	0.0026
219754_at	RBM41	RNA binding motif protein 41	0.7977	0.046
219757_s_at	C14orf101	chromosome 14 open reading frame 101	0.8881	0.0011
219758_at	TTC26	tetratricopeptide repeat domain 26	0.4854	0.01
219760_at	LIN7B	lin-7 homolog B (C. elegans)	0.6289	0.0022
219763_at	DENND1A	DENN/MADD domain containing 1A	0.5706	0.0419
219786_at	MTL5	metallothionein-like 5; testis-specific (tesmin)	0.2197	0.0054
219787_s_at	ECT2	epithelial cell transforming sequence 2 oncogene	3.2749	0
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	1.5682	0.0181
219793_at	SNX16	sorting nexin 16	0.6137	0.0292
219801_at	ZNF34	zinc finger protein 34	0.5951	0.0002
219817_at	C12orf47	chromosome 12 open reading frame 47	0.8577	0.0004
219818_s_at	GPATCH1	G patch domain containing 1	1.3536	0
219826_at	ZNF419	zinc finger protein 419	1.1028	0
219828_at	C9orf86	chromosome 9 open reading frame 86	0.4034	0.0058
219831_at	CDKL3	cyclin-dependent kinase-like 3	0.3456	0.0339
219832_s_at	HOXC13	homeobox C13	0.5477	0.019
219843_at	IPP	intracisternal A particle-promoted polypeptide	1.1019	0.0003
219844_at	C10orf118	chromosome 10 open reading frame 118	0.3261	0.0021
219846_at	GON4L	gon-4-like (C. elegans)	0.3206	0.0397
219854_at	ZNF14	zinc finger protein 14	0.7791	0.0269
219862_s_at	NARF	nuclear prelamin A recognition factor	0.6551	0.0369
219869_s_at	SLC39A8	solute carrier family 39 (zinc transporter); member 8	1.3259	0.0024
219880_at			1.2915	0
219881_s_at			0.5226	0.0001
219884_at	LHX6	LIM homeobox 6	0.5125	0.0017

219886_at	LRRIQ2	leucine-rich repeats and IQ motif containing 2	0.3659	0.0012
219894_at	MAGEL2	MAGE-like 2	2.0793	0.0082
219900_s_at	ZNF446	zinc finger protein 446	0.2721	0.0149
219917_at	ZCCHC4	zinc finger; CCHC domain containing 4	0.2811	0.0488
219918_s_at	ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	4.1799	0
219925_at	ZMYM6	zinc finger; MYM-type 6	0.395	0.0332
219931_s_at	KLHL12	kelch-like 12 (Drosophila)	0.84	0.0074
219935_at	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif; 5 (aggrecanase-2)	1.1778	0.036
219941_at	TMEM19	transmembrane protein 19	0.2187	0.0152
219951_s_at	C20orf12	chromosome 20 open reading frame 12	1.7072	0.0049
219958_at	C20orf46	chromosome 20 open reading frame 46	1.1918	0.0081
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	1.6042	0.0023
219980_at	C4orf29	chromosome 4 open reading frame 29	0.5189	0.0171
219981_x_at	ZNF587	zinc finger protein 587	0.9283	0
219983_at	HRASLS	HRAS-like suppressor	1.2041	0.0079
219984_s_at	HRASLS	HRAS-like suppressor	0.859	0.0248
219990_at	E2F8	E2F transcription factor 8	1.155	0.0007
219997_s_at	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	0.3984	0.0498
220011_at	C1orf135	chromosome 1 open reading frame 135	0.6399	0.0155
220019_s_at	ZNF224	zinc finger protein 224	0.7766	0.0004
220022_at	ZNF334	zinc finger protein 334	0.9986	0.0296
220032_at	FLJ21986	hypothetical protein FLJ21986	0.5725	0.0471
220036_s_at	LMBR1L	limb region 1 homolog (mouse)-like	1.1342	0.0002
220047_at	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	0.5964	0.0106
220055_at	ZNF287	zinc finger protein 287	0.2095	0.0395
220056_at	IL22RA1	interleukin 22 receptor; alpha 1	0.3482	0.0263
220060_s_at	C12orf48	chromosome 12 open reading frame 48	1.4626	0.0001
220063_at	GSTCD	glutathione S-transferase; C-terminal domain containing	0.3863	0
220071_x_at	CEP27	centrosomal protein 27kDa	0.3051	0.0072
220072_at	CSPP1	centrosome and spindle pole associated protein 1	0.6443	0.0009
220085_at	HELLS	helicase; lymphoid-specific	2.2126	0.0002
220089_at	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.4956	0
220091_at	SLC2A6	solute carrier family 2 (facilitated glucose transporter); member 6	1.1197	0.0382
220099_s_at	LUC7L2	LUC7-like 2 (S. cerevisiae)	0.3425	0.0104

220113_x_at	POLR1B	polymerase (RNA) I polypeptide B; 128kDa	0.6264	0.0008
220121_at	LINS1	lines homolog 1 (Drosophila)	0.5237	0.0079
220127_s_at	FBXL12	F-box and leucine-rich repeat protein 12	0.4739	0.0112
220144_s_at	ANKRD5	ankyrin repeat domain 5	0.7067	0.0023
220155_s_at	BRD9	bromodomain containing 9	0.8804	0.0111
220172_at	C2orf37	chromosome 2 open reading frame 37	0.5042	0.0392
220178_at	C19orf28	chromosome 19 open reading frame 28	0.577	0.026
220200_s_at	LOC647597	SET domain containing (lysine methyltransferase) 8, similar to Histone-lysine N-methyltransferase; H4 lysine-20 specific (Histone H4-K20 methyltransferase) (H4-K20-HMTase) (SET domain-containing protein 8) (PR/SET domain-containing protein 07) (PR/SET07) (PR-Set7)	0.7663	0.0012
220202_s_at	RC3H2	ring finger and CCCH-type zinc finger domains 2	1.146	0.0003
220215_at	ZNF669	zinc finger protein 669	0.3249	0.0181
220216_at	C8orf44	chromosome 8 open reading frame 44	0.2615	0.0195
220219_s_at	LOC728863	hypothetical protein LOC728863, leucine rich repeat containing 37; member A2, leucine rich repeat containing 37; member A3, leucine rich repeat containing 37; member A4 (pseudogene), leucine rich repeat containing 37A	0.2578	0.0343
220221_at	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	0.3839	0.0349
220232_at	SCD5	stearoyl-CoA desaturase 5	0.4723	0.0068
220235_s_at	C1orf103	chromosome 1 open reading frame 103	1.2965	0
220236_at	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	0.268	0.0054
220238_s_at	KLHL7	kelch-like 7 (Drosophila)	1.1939	0.0058
220239_at	KLHL7	kelch-like 7 (Drosophila)	1.2219	0.0028
220242_x_at	ZNF701	zinc finger protein 701	0.2887	0.004
220250_at	ZNF286A	zinc finger protein 286A	0.1575	0.0435
220252_x_at	CXorf21	chromosome X open reading frame 21	0.2192	0.0496
220253_s_at	LRP12	low density lipoprotein-related protein 12	0.9518	0.043
220278_at	JMJD2D	jumonji domain containing 2D	0.1962	0.0029
220285_at	FAM108B1	family with sequence similarity 108; member B1	0.7606	0.0134
220295_x_at	DEPDC1	DEP domain containing 1, similar to DEP domain containing 1	1.2933	0.0145
220305_at	MGC3260	hypothetical protein MGC3260	0.7669	0.0023
220336_s_at	GP6	glycoprotein VI (platelet)	0.2175	0.0016
220338_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	0.3989	0.024

220340_at	KIAA1772	KIAA1772	1.0324	0.0166
220352_x_at			0.3685	0.0099
220360_at	THAP9	THAP domain containing 9	0.2334	0.0356
220361_at	IQCH	IQ motif containing H	0.3748	0.0009
220371_s_at	SLC12A9	solute carrier family 12 (potassium/chloride transporters); member 9	0.2498	0.0447
220401_at	FLJ21369	hypothetical protein FLJ21369	0.2647	0.0117
220410_s_at	CAMSAP1	calmodulin regulated spectrin-associated protein 1	0.2203	0.0186
220411_x_at	PODNL1	podocan-like 1	0.1772	0.0153
220434_at	ADCK4	aarF domain containing kinase 4	0.2952	0.0005
220435_at	SLC30A10	solute carrier family 30; member 10	3.3101	0.001
220451_s_at	BIRC7	baculoviral IAP repeat-containing 7 (livin)	1.792	0.0093
220456_at	SPTLC3	serine palmitoyltransferase; long chain base subunit 3	0.3094	0.0078
220458_at	FLJ10246	FLJ10246	0.3561	0.0084
220459_at	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	1.0503	0.0332
220466_at	CCDC15	coiled-coil domain containing 15	0.2671	0.0074
220467_at	FLJ21272	hypothetical protein FLJ21272	1.0434	0.0232
220512_at	DLC1	deleted in liver cancer 1	1.3634	0.0063
220549_at	RAD54B	RAD54 homolog B (S. cerevisiae)	0.2626	0.0395
220561_at	IGF2AS	insulin-like growth factor 2 antisense	0.5601	0.0027
220572_at	DKFZp547G183	hypothetical protein DKFZp547G183	0.3101	0.0054
220574_at	SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	0.203	0.0163
220586_at	CHD9	chromodomain helicase DNA binding protein 9	0.531	0.004
220613_s_at	SYTL2	synaptotagmin-like 2	1.0817	0.0491
220619_at	CHD7	chromodomain helicase DNA binding protein 7	0.1058	0.0161
220632_s_at	POMT2	protein-O-mannosyltransferase 2	0.3209	0.006
220642_x_at	GPR89A	G protein-coupled receptor 89A, G protein-coupled receptor 89B, G protein-coupled receptor 89C	0.6512	0.0039
220651_s_at	MCM10	minichromosome maintenance complex component 10	1.1309	0.008
220652_at	KIF24	kinesin family member 24	0.1533	0.022
220661_s_at	ZNF692	zinc finger protein 692	1.0093	0.0022
220666_at			0.6199	0.0267
220668_s_at	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	0.436	0.0003
220674_at	FLJ22814	hypothetical protein FLJ22814	0.1528	0.0408
220691_at		Clone HQ0097 PRO0097	0.156	0.0465
220702_at			0.8625	0.0009

220707_s_at	FOXRED2	FAD-dependent oxidoreductase domain containing 2	0.5706	0.0376
220710_at	C15orf28	chromosome 15 open reading frame 28	0.2263	0.0429
220711_at			0.3169	0.029
220715_at	FLJ12547	hypothetical protein FLJ12547	0.2793	0.0019
220716_at	FLJ12595	guanine nucleotide binding protein-like 3 (nucleolar)-like pseudogene	0.297	0.0005
220720_x_at	FAM128B	family with sequence similarity 128; member B	0.5059	0.0087
220728_at			0.5398	0.0119
220735_s_at	SENP7	SUMO1/sentrin specific peptidase 7	0.5685	0.0156
220746_s_at	UIMC1	ubiquitin interaction motif containing 1	0.6188	0.0089
220750_s_at	LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	1.0903	0.0025
220760_x_at	ZNF665	zinc finger protein 665	0.7347	0.0037
220761_s_at	TAOK3	TAO kinase 3	0.5458	0.0112
220768_s_at	CSNK1G3	casein kinase 1; gamma 3	0.5396	0.0372
220770_s_at	LOC63920	transposon-derived Buster3 transposase-like	2.3204	0
220789_s_at	TBRG4	transforming growth factor beta regulator 4	0.7279	0
220796_x_at	SLC35E1	solute carrier family 35; member E1	0.548	0.0022
220800_s_at	TMOD3	tropomodulin 3 (ubiquitous)	0.9702	0.0112
220803_at	STAMBPL1	STAM binding protein-like 1	0.2221	0.02
220828_s_at	FLJ11292	hypothetical protein FLJ11292	0.1999	0.0112
220838_at	FLJ20433	hypothetical protein FLJ20433	0.1474	0.0283
220840_s_at	C1orf112	chromosome 1 open reading frame 112	0.6732	0.0042
220855_at		Clone HQ0456 PRO0456	0.262	0.0413
220864_s_at	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 13	0.2798	0.0163
220865_s_at	PDSS1	prenyl (decaprenyl) diphosphate synthase; subunit 1	0.7398	0.0147
220878_at			0.1042	0.0153
220890_s_at	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	0.3436	0.0124
220900_at	FLJ12078	hypothetical protein FLJ12078	0.1812	0.0275
220905_at			0.2657	0.0092
220925_at	MAK10	MAK10 homolog; amino-acid N-acetyltransferase subunit; (S. cerevisiae)	0.739	0.0035
220935_s_at	CDK5RAP2	CDK5 regulatory subunit associated protein 2	0.5644	0.0325
220940_at	KIAA1641	KIAA1641	2.4313	0
220954_s_at	PILRB	paired immunoglobin-like type 2 receptor beta	1.0119	0.0032
220955_x_at	RAB23	RAB23; member RAS oncogene family	1.0805	0.0047
220967_s_at	ZNF696	zinc finger protein 696	0.3261	0.0012
220969_s_at			0.7215	0.0095
220974_x_at	SFXN3	sideroflexin 3	1.414	0.0024

220980_s_at	ADPGK	ADP-dependent glucokinase	0.436	0.0042
220985_s_at	RNF170	ring finger protein 170	0.6251	0.005
220986_s_at	TIGD6	tigger transposable element derived 6	0.2681	0.0286
220987_s_at	C11orf17	NUAK family; SNF1-like kinase; 2, chromosome 11 open reading frame 17	0.5897	0.0438
220991_s_at	RNF32	ring finger protein 32	0.2356	0.0373
221004_s_at	ITM2C	integral membrane protein 2C	0.894	0.0389
221006_s_at	SNX27	sorting nexin family member 27	0.5549	0.0417
221007_s_at	FIP1L1	FIP1 like 1 (S. cerevisiae)	0.634	0.002
221011_s_at	LBH	limb bud and heart development homolog (mouse)	1.2253	0.0188
221021_s_at	CTNNBL1	catenin; beta like 1	0.5003	0.0003
221025_x_at	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	0.5271	0.0161
221027_s_at	PLA2G12A	phospholipase A2; group XIIA	0.6518	0.037
221030_s_at	ARHGAP24	Rho GTPase activating protein 24	0.4952	0.0387
221039_s_at	DDEF1	development and differentiation enhancing factor 1	1.0408	0.0005
221041_s_at	SLC17A5	solute carrier family 17 (anion/sugar transporter); member 5	1.4563	0.0041
221050_s_at	GTPBP2	GTP binding protein 2	0.9457	0.0027
221058_s_at	CKLF	chemokine-like factor	0.6279	0.0024
221064_s_at	C16orf28	chromosome 16 open reading frame 28	0.6136	0.0472
221071_at			0.191	0.0194
221094_s_at	ELP3	elongation protein 3 homolog (S. cerevisiae)	0.6544	0.0128
221123_x_at	ZNF395	zinc finger protein 395	1.2978	0.0021
221125_s_at	KCNMB3	potassium large conductance calcium-activated channel; subfamily M beta member 3	0.3652	0
221135_s_at	ASTE1	asteroid homolog 1 (Drosophila)	0.6868	0.043
221139_s_at	CSAD	cysteine sulfinic acid decarboxylase	0.8931	0.0013
221191_at	DKFZP434A0131	DKFZp434A0131 protein	0.5292	0.0009
221192_x_at	MFSD11	major facilitator superfamily domain containing 11	0.2732	0.0056
221201_s_at	ZNF155	zinc finger protein 155	0.2886	0.0476
221203_s_at	YEATS2	YEATS domain containing 2	0.9338	0.0001
221206_at	PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	1.0457	0
221220_s_at	SCYL2	SCY1-like 2 (S. cerevisiae)	1.8327	0.0001
221248_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	0.1936	0.0154
221258_s_at	KIF18A	kinesin family member 18A	1.6283	0.0001
221260_s_at	FAM130A1	family with sequence similarity 130; member A1	1.2976	0
221262_s_at	SLC2A11	solute carrier family 2 (facilitated glucose transporter); member 11	0.2482	0.0359
221268_s_at	SGPP1	sphingosine-1-phosphate phosphatase 1	1.2501	0.0312

221270_s_at	QTRT1	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)	0.3817	0.0352
221274_s_at	LMAN2L	lectin; mannose-binding 2-like	0.4507	0.0294
221275_s_at			0.2494	0.0002
221290_s_at	MUM1	melanoma associated antigen (mutated) 1	0.8159	0.0062
221291_at	ULBP2	UL16 binding protein 2	0.736	0.0209
221335_x_at	C19orf61	chromosome 19 open reading frame 61	1.1894	0
221406_s_at	C6orf26	chromosome 6 open reading frame 26, mutS homolog 5 (E. coli)	0.1837	0.025
221412_at	VN1R1	vomeronasal 1 receptor 1	0.2632	0.0046
221419_s_at			0.2739	0.0329
221423_s_at	YIPF5	Yip1 domain family; member 5	1.3473	0.0065
221436_s_at	CDCA3	cell division cycle associated 3	1.4962	0.0077
221480_at	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1; 37kDa)	1.1692	0.0011
221501_x_at	LOC339047	hypothetical protein LOC339047	0.6771	0.0007
221506_s_at	TNPO2	transportin 2 (importin 3; karyopherin beta 2b)	0.6892	0.0001
221507_at	TNPO2	transportin 2 (importin 3; karyopherin beta 2b)	0.5359	0.0019
221509_at	DENR	density-regulated protein	0.5931	0
221520_s_at	CDCA8	cell division cycle associated 8	1.6215	0.0006
221521_s_at	GINS2	GINS complex subunit 2 (Psf2 homolog)	2.4972	0
221522_at	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	1.0308	0.0001
221529_s_at	PLVAP	plasmalemma vesicle associated protein	0.8373	0.03
221539_at	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	1.7392	0.0002
221540_x_at	DKFZP686M0199	general transcription factor IIH; polypeptide 2; 44kDa, general transcription factor IIH; polypeptide 2; 44kDa-like	0.698	0.0001
221545_x_at	MED16	mediator complex subunit 16	0.6783	0.0001
221560_at	MARK4	MAP/microtubule affinity-regulating kinase 4	0.4213	0.0187
221572_s_at	SLC26A6	solute carrier family 26; member 6	0.9144	0.0069
221573_at	C7orf25	chromosome 7 open reading frame 25	0.664	0.0037
221583_s_at	KCNMA1	potassium large conductance calcium-activated channel; subfamily M; alpha member 1	0.4443	0.0456
221591_s_at	FAM64A	family with sequence similarity 64; member A	1.4027	0.0021
221592_at	TBC1D8	TBC1 domain family; member 8 (with GRAM domain)	0.1702	0.0139
221595_at			0.5937	0.0021
221597_s_at	HSPC171	HSPC171 protein	0.494	0.0223
221598_s_at	MED27	mediator complex subunit 27	0.7028	0.0056

221625_at		CDNA FLJ46609 fis; clone TKIDN2010200	0.3003	0.0008
221628_s_at	N-PAC	cytokine-like nuclear factor n-pac	0.5563	0.0087
221638_s_at	STX16	syntaxin 16	0.5099	0.0155
221645_s_at	ZNF83	zinc finger protein 83	0.6865	0.0196
221667_s_at	HSPB8	heat shock 22kDa protein 8	2.6407	0.0058
221673_s_at	CSNK1G1	casein kinase 1; gamma 1	0.2577	0.0051
221676_s_at	CORO1C	coronin; actin binding protein; 1C	1.0178	0.0037
221677_s_at	DONSON	downstream neighbor of SON	2.239	0
221683_s_at	CEP290	centrosomal protein 290kDa	1.1481	0.0011
221685_s_at	CCDC99	coiled-coil domain containing 99	1.8861	0
221691_x_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23; numatrin)	0.5996	0.0066
221695_s_at	MAP3K2	mitogen-activated protein kinase kinase kinase 2	0.6276	0.0084
221703_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.6278	0.0015
221705_s_at	SIKE	suppressor of IKK epsilon	1.1995	0.0004
221728_x_at	XIST	X (inactive)-specific transcript	2.7532	0.0489
221729_at	COL5A2	collagen; type V; alpha 2	1.8911	0.0069
221730_at	COL5A2	collagen; type V; alpha 2	1.8432	0.005
221734_at	PRRC1	proline-rich coiled-coil 1	1.3737	0.0008
221736_at	KIAA1219	KIAA1219	0.5411	0.0094
221738_at	KIAA1219	KIAA1219	1.1061	0
221741_s_at	YTHDF1	YTH domain family; member 1	0.5946	0.0001
221744_at	WDR68	WD repeat domain 68	1.0066	0
221745_at	WDR68	WD repeat domain 68	1.5511	0.0001
221753_at	SSH1	slingshot homolog 1 (Drosophila)	0.5086	0.0236
221762_s_at	C20orf67	chromosome 20 open reading frame 67	1.1733	0.0059
221764_at	C19orf22	chromosome 19 open reading frame 22	0.5764	0.0129
221783_at	WIZ	widely interspaced zinc finger motifs	0.5335	0.0046
221785_at	WIZ	widely interspaced zinc finger motifs	0.3241	0.0128
221789_x_at	RHOT2	ras homolog gene family; member T2	0.4461	0.0191
221799_at	CSGlcA-T	chondroitin sulfate glucuronyltransferase	0.4337	0.0375
221801_x_at	NEFL	neurofilament; light polypeptide 68kDa	1.2668	0.0164
221805_at	NEFL	neurofilament; light polypeptide 68kDa	3.7288	0.0003
221812_at	FBXO42	F-box protein 42	0.4786	0.0375
221819_at	RAB35	RAB35; member RAS oncogene family	0.4546	0.0017
221821_s_at	C12orf41	chromosome 12 open reading frame 41	0.613	0.0016
221823_at	C5orf30	chromosome 5 open reading frame 30	1.9598	0
221829_s_at	TNPO1	transportin 1	0.6783	0

221842_s_at	ZNF131	zinc finger protein 131	0.3413	0.0236
221843_s_at	KIAA1609	KIAA1609	1.3175	0
221849_s_at	LOC90379	hypothetical protein BC002926	1.1457	0
221850_x_at	CTGLF1	KIAA1975 protein similar to MRIP2, centaurin; gamma-like family; member 1, centaurin; gamma-like family; member 3, centaurin; gamma-like family; member 4, centaurin; gamma-like family; member 5, centaurin; gamma-like family; member 9 pseudogene	0.7666	0.0009
221851_at	LOC90379	hypothetical protein BC002926	0.6679	0.0012
221853_s_at	NOMO1	NODAL modulator 1, NODAL modulator 2, NODAL modulator 3	0.8732	0
221855_at	LOC644096	hypothetical protein LOC644096	0.5088	0.0083
221860_at	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.7361	0.0226
221864_at	ORAI3	ORAI calcium release-activated calcium modulator 3	1.2658	0.0107
221865_at	C9orf91	chromosome 9 open reading frame 91	1.0551	0.0103
221869_at	ZNF512B	zinc finger protein 512B	0.4046	0.0003
221873_at	ZNF143	zinc finger protein 143	0.2996	0.0242
221876_at	ZNF783	zinc finger protein 783	0.4307	0.0402
221882_s_at	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	1.3871	0
221884_at	EVI1	ecotropic viral integration site 1	1.0443	0.0003
221888_at	CC2D1A	coiled-coil and C2 domain containing 1A	0.2691	0.032
221889_at	KCTD13	potassium channel tetramerisation domain containing 13	0.6684	0.0035
221893_s_at	ADCK2	aarF domain containing kinase 2	1.0592	0.0021
221895_at	MOSPD2	motile sperm domain containing 2	0.8789	0.0002
221897_at	TRIM52	tripartite motif-containing 52	1.1616	0.0001
221909_at	TMEM118	transmembrane protein 118	1.9249	0
221916_at	NEFL	neurofilament; light polypeptide 68kDa	3.0366	0.0023
221919_at	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1, hypothetical protein LOC728844	0.8601	0.0033
221922_at	GPSM2	G-protein signaling modulator 2 (AGS3-like; C. elegans)	1.1387	0.0101
221923_s_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23; numatrin)	0.6157	0.004
221925_s_at	CSPP1	centrosome and spindle pole associated protein 1	0.5056	0.0115
221938_x_at	MED16	mediator complex subunit 16	0.3552	0.0164
221939_at	YIPF2	Yip1 domain family; member 2	0.717	0.0123
221940_at	RPUSD2	RNA pseudouridylate synthase domain containing 2	0.2861	0.0291
221954_at	C20orf111	Chromosome 20 open reading frame 111	0.8523	0.003
221957_at	PDK3	pyruvate dehydrogenase kinase; isozyme 3	1.1414	0.0006

221962_s_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog; yeast)	0.8111	0.0462
221965_at	MPHOSPH9	M-phase phosphoprotein 9	1.4154	0.0007
221971_x_at	CTGLF1	centaurin; gamma-like family; member 1, centaurin; gamma-like family; member 2, centaurin; gamma-like family; member 6, centaurin; gamma-like family; member 7, centaurin; gamma-like family; member 9 pseudogene	0.9179	0.0004
221973_at		CDNA clone IMAGE:5217021; with apparent retained intron	1.6002	0
221986_s_at	KLHL24	kelch-like 24 (Drosophila)	0.9752	0.0205
221988_at	CRSP7	Cofactor required for Sp1 transcriptional activation; subunit 7; 70kDa	1.118	0.0004
221999_at	VRK3	vaccinia related kinase 3	0.7373	0.0019
222018_at	NACA	NACA family member 3 pseudogene, nascent polypeptide-associated complex alpha subunit, nascent polypeptide-associated complex alpha subunit 2, nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	1.5173	0.0001
222019_at	PFDN6	prefoldin subunit 6	0.245	0.0417
222034_at	GNB2L1	Guanine nucleotide binding protein (G protein); beta polypeptide 2-like 1	1.0216	0.0065
222036_s_at	MCM4	minichromosome maintenance complex component 4	1.4103	0
222037_at	MCM4	minichromosome maintenance complex component 4	1.1531	0.0011
222039_at	LOC146909	hypothetical protein LOC146909	1.5248	0.0004
222052_at	C19orf54	chromosome 19 open reading frame 54	0.5521	0.0044
222058_at			0.3792	0.0093
222060_at	KRT8P12	keratin 8 pseudogene 12	0.3629	0.002
222074_at	UROD	uroporphyrinogen decarboxylase	0.4647	0.0001
222077_s_at	RACGAP1	Rac GTPase activating protein 1	4.0823	0
222088_s_at	SLC2A14	solute carrier family 2 (facilitated glucose transporter); member 14, solute carrier family 2 (facilitated glucose transporter); member 3	1.1681	0.0124
222094_at	SULT1A3	sulfotransferase family; cytosolic; 1A; phenol-preferring; member 3, sulfotransferase family; cytosolic; 1A; phenol-preferring; member 4	0.2851	0.03
222104_x_at	GTF2H3	general transcription factor IIH; polypeptide 3; 34kDa	0.5632	0.001
222105_s_at	NKIRAS2	NFKB inhibitor interacting Ras-like 2	0.5201	0.0025
222112_at	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	0.1009	0.0114
222113_s_at	EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	0.6425	0.0224
222122_s_at	THOC2	THO complex 2	0.9874	0.0012
222128_at	NSUN6	NOL1/NOP2/Sun domain family; member 6	0.6004	0.0382

222130_s_at	FTSJ2	FtsJ homolog 2 (E. coli)	0.4608	0.0151
222131_x_at	RHOT2	ras homolog gene family; member T2	0.2613	0.0184
222132_s_at	AGK	acylglycerol kinase	0.4416	0.0432
222133_s_at	PHF20L1	PHD finger protein 20-like 1	0.7857	0.0139
222139_at	KIAA1466	KIAA1466 gene	0.6532	0.0343
222140_s_at	GPR89A	G protein-coupled receptor 89A, G protein-coupled receptor 89B, G protein-coupled receptor 89C	0.4515	0.0151
222141_at	KLHL22	kelch-like 22 (Drosophila)	0.1757	0.0397
222147_s_at	ACTR5	ARP5 actin-related protein 5 homolog (yeast)	0.3978	0.0123
222164_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	0.7648	0.0178
222167_at		CDNA FLJ11774 fis; clone HEMBA1005884	0.6598	0.0137
222169_x_at	SH2D3A	SH2 domain containing 3A	0.1385	0.0001
222174_at		CDNA FLJ14025 fis; clone HEMBA1003667	0.1408	0.0104
222182_s_at	CNOT2	CCR4-NOT transcription complex; subunit 2	0.5744	0.012
222190_s_at	C16orf58	chromosome 16 open reading frame 58	0.2637	0.0287
222201_s_at	CASP8AP2	CASP8 associated protein 2	0.7707	0.0213
222206_s_at	NCLN	nicalin homolog (zebrafish)	0.8424	0.0346
222207_x_at	LOC389517	Williams Beuren syndrome chromosome region 19 pseudogene	0.1809	0.007
222208_s_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J; 13.3kDa pseudogene	0.3113	0.0001
222214_at		CDNA: FLJ21335 fis; clone COL02546	1.0201	0.0046
222233_s_at	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog; S. cerevisiae)	1.3643	0
222237_s_at	ZNF228	zinc finger protein 228	1.0236	0.0041
222238_s_at	POLM	polymerase (DNA directed); mu	0.3146	0.0096
222244_s_at	TUG1	taurine upregulated gene 1	0.3912	0.013
222248_s_at	SIRT4	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	0.5252	0.0139
222249_at		KIAA1651 protein	0.1398	0.0211
222250_s_at	INTS7	integrator complex subunit 7	1.4108	0.0004
222263_at	SLC35E1	solute carrier family 35; member E1	0.9518	0
222266_at	C19orf2	Chromosome 19 open reading frame 2	0.6756	0.0123
222272_x_at	SCIN	scinderin	0.1619	0.004
222282_at		Transcribed locus	1.219	0.0034
222283_at	ZNF480	zinc finger protein 480	0.327	0.001
222307_at	LOC282997	hypothetical protein LOC282997	0.5384	0.0058
222313_at		Transcribed locus	1.4747	0.0092
222335_at		Transcribed locus	0.4347	0.0014
222341_x_at		Transcribed locus	0.2498	0.0001

222344_at		Transcribed locus	1.3086	0.0135
222345_at		Transcribed locus	0.1979	0.0378
222361_at	LOC643224	similar to tubulin; beta 8	1.1399	0.0201
222368_at		CDNA FLJ37098 fis; clone BRACE2019004	0.8821	0.0016
222372_at		Transcribed locus	1.3822	0.0013
222376_at		Transcribed locus	1.2859	0.0076
222379_at		Transcribed locus	1.336	0.0442
222380_s_at	PDCD6	Programmed cell death 6	1.7712	0.0001
222382_x_at	NUP205	nucleoporin 205kDa	0.2992	0.0163
222387_s_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	1.9777	0.0004
222388_s_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.4885	0.0044
222398_s_at	EFTUD2	elongation factor Tu GTP binding domain containing 2	0.3827	0.0114
222413_s_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	1.7152	0
222414_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.7278	0
222415_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.5487	0.0002
222416_at	ALDH18A1	aldehyde dehydrogenase 18 family; member A1	0.4103	0.0434
222424_s_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.5148	0.0482
222427_s_at	LARS	leucyl-tRNA synthetase	0.4566	0.0153
222451_s_at	ZDHHC9	zinc finger; DHHC-type containing 9	1.1905	0.0006
222460_s_at	NIP30	NEFA-interacting nuclear protein NIP30	0.9364	0
222463_s_at	BACE1	beta-site APP-cleaving enzyme 1	0.8493	0.0208
222466_s_at	MRPL42	mitochondrial ribosomal protein L42	0.5282	0.0357
222473_s_at	ERBB2IP	erbb2 interacting protein	0.9803	0
222499_at	MRPS16	mitochondrial ribosomal protein S16	0.4166	0.0114
222501_s_at	REPIN1	replication initiator 1	0.5372	0.0196
222503_s_at	WDR41	WD repeat domain 41	1.2013	0
222505_at	LMBR1	limb region 1 homolog (mouse)	0.5591	0.0221
222510_s_at	MKRN2	makorin; ring finger protein; 2	0.8645	0.0029
222527_s_at	RBM22	RNA binding motif protein 22	1.2374	0.0003
222530_s_at	MKKS	McKusick-Kaufman syndrome	0.8126	0.0018
222538_s_at	APPL1	adaptor protein; phosphotyrosine interaction; PH domain and leucine zipper containing 1	0.9228	0.0269
222544_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	1.1665	0.0001
222548_s_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	0.4241	0.0446
222550_at	ARMC1	armadillo repeat containing 1	0.3477	0.0168
222593_s_at	SPATS2	spermatogenesis associated; serine-rich 2	2.0055	0
222594_s_at	SPATS2	spermatogenesis associated; serine-rich 2	1.4631	0

222600_s_at	UBE1L2	ubiquitin-activating enzyme E1-like 2	1.3425	0
222601_at	UBE1L2	ubiquitin-activating enzyme E1-like 2	0.8272	0.0003
222605_at	RCOR3	REST corepressor 3	0.8253	0.0012
222606_at	ZWILCH	Zwilch; kinetochore associated; homolog (Drosophila)	2.5038	0
222608_s_at	ANLN	anillin; actin binding protein	5.0946	0
222613_at	C12orf4	chromosome 12 open reading frame 4	1.386	0.0001
222615_s_at	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	0.6698	0.0176
222620_s_at	DNAJC1	DnaJ (Hsp40) homolog; subfamily C; member 1	0.5238	0.0038
222621_at	DNAJC1	DnaJ (Hsp40) homolog; subfamily C; member 1	0.7299	0.0011
222622_at	LOC283871	hypothetical protein LOC283871	0.922	0.0035
222628_s_at	REV1	REV1 homolog (S. cerevisiae)	0.8349	0.0082
222635_s_at	MED28	mediator complex subunit 28	0.4678	0.0109
222636_at	MED28	mediator complex subunit 28	0.6225	0.0174
222640_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.7878	0.0224
222641_s_at	C17orf63	chromosome 17 open reading frame 63	1.0148	0.0005
222644_s_at	GLT25D1	glycosyltransferase 25 domain containing 1	0.5924	0.0042
222645_s_at	KCTD5	potassium channel tetramerisation domain containing 5	0.536	0.0086
222646_s_at	ERO1L	ERO1-like (S. cerevisiae)	1.4779	0.0009
222650_s_at	SLC2A4RG	SLC2A4 regulator	0.6937	0.0056
222652_s_at	N-PAC	cytokine-like nuclear factor n-pac	0.5402	0.0441
222656_at	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	0.4124	0.0473
222661_at	AGGF1	angiogenic factor with G patch and FHA domains 1	0.5123	0.026
222662_at	LOC286044	hypothetical protein LOC286044	1.771	0.0032
222663_at	RIOK2	RIO kinase 2 (yeast)	1.2722	0.0016
222673_x_at	FAM122B	family with sequence similarity 122B, transmembrane protein 57	0.5672	0.0032
222680_s_at	DTL	denticleless homolog (Drosophila)	2.6089	0.0002
222685_at	FAM29A	family with sequence similarity 29; member A	1.243	0.0003
222686_s_at	FLJ11151	hypothetical protein FLJ11151	1.3274	0.0029
222697_s_at	ABHD10	abhydrolase domain containing 10	0.8117	0.0423
222699_s_at	PLEKHF2	pleckstrin homology domain containing; family F (with FYVE domain) member 2	0.8795	0.0384
222705_s_at	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	0.2688	0.0428
222716_s_at	SNX24	sorting nexin 24	0.5884	0.0016
222718_at	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	0.7494	0.0002
222726_s_at	EXOC5	exocyst complex component 5	0.6622	0.0103

222729_at	FBXW7	F-box and WD repeat domain containing 7	0.7398	0.0403
222735_at	TMEM38B	transmembrane protein 38B	0.5577	0.0101
222736_s_at	TMEM38B	transmembrane protein 38B	1.1943	0.0118
222740_at	ATAD2	ATPase family; AAA domain containing 2	1.5597	0.0002
222747_s_at	SCML1	sex comb on midleg-like 1 (Drosophila)	1.204	0.0034
222748_s_at	TXNL4B	thioredoxin-like 4B	0.9309	0.0113
222752_s_at	C1orf75	chromosome 1 open reading frame 75	0.8945	0.0433
222758_s_at	TMEM132A	transmembrane protein 132A	0.3658	0.0021
222760_at	ZNF703	zinc finger protein 703	1.0998	0.0053
222767_s_at	C12orf49	chromosome 12 open reading frame 49	0.8382	0.0042
222768_s_at	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	0.5251	0.0168
222774_s_at	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	2.987	0
222777_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.8132	0.0169
222781_s_at	C9orf40	chromosome 9 open reading frame 40	1.5258	0.0003
222786_at	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	0.5367	0.0041
222792_s_at	CCDC59	coiled-coil domain containing 59	0.4345	0.03
222799_at	WDR91	WD repeat domain 91	0.3759	0.0093
222802_at	EDN1	endothelin 1	0.9241	0.0461
222810_s_at	RASAL2	RAS protein activator like 2	0.6825	0.0148
222812_s_at	RHOF	ras homolog gene family; member F (in filopodia)	0.6654	0.0081
222821_s_at	GEMIN7	gem (nuclear organelle) associated protein 7	1.1581	0.0002
222841_s_at	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	0.5691	0.0366
222843_at	FIGNL1	fidgetin-like 1	1.5503	0
222848_at	CENPK	centromere protein K	3.4383	0
222850_s_at	DNAJB14	DnaJ (Hsp40) homolog; subfamily B; member 14	1.032	0.0002
222852_at	C10orf88	chromosome 10 open reading frame 88	0.3312	0.0272
222873_s_at	EHMT1	euchromatic histone-lysine N-methyltransferase 1	0.6369	0.008
222878_s_at	OTUB2	OTU domain; ubiquitin aldehyde binding 2	0.2153	0.0495
222879_s_at	POLH	polymerase (DNA directed); eta	0.3835	0.003
222884_at	ZNF346	zinc finger protein 346	0.6329	0.0014
222889_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog; S. cerevisiae)	0.8996	0.0016
222890_at	CCDC113	coiled-coil domain containing 113	0.7624	0.0323
222891_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	1.2845	0.0468
222894_x_at	C20orf7	chromosome 20 open reading frame 7	0.5584	0.0342
222906_at	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	1.4272	0.0136

222909_s_at	BAG4	BCL2-associated athanogene 4	0.4763	0.0395
222918_at	RAB9B	RAB9B; member RAS oncogene family	1.4637	0.0215
222929_at	RAI16	retinoic acid induced 16	0.1071	0.0267
222947_at	ZNF224	Zinc finger protein 224	0.6189	0.0218
222951_s_at	ANKRD5	ankyrin repeat domain 5	0.188	0.0361
222958_s_at	DEPDC1	DEP domain containing 1	2.2225	0.001
222962_s_at	MCM10	minichromosome maintenance complex component 10	0.7197	0.0226
222985_at	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; gamma polypeptide	0.2172	0.0269
223016_x_at	ZRANB2	zinc finger; RAN-binding domain containing 2	0.5037	0.0139
223020_at	CLPTM1L	CLPTM1-like	0.4451	0.0469
223024_at	AP1M1	adaptor-related protein complex 1; mu 1 subunit	0.4361	0.0182
223031_s_at	TRAF7	TNF receptor-associated factor 7	0.5747	0.001
223038_s_at	FAM60A	family with sequence similarity 60; member A, similar to Protein FAM60A (Tera protein), similar to teratocarcinoma expressed; serine rich	1.3386	0.0059
223065_s_at	STARD3NL	STARD3 N-terminal like	0.4748	0.0048
223075_s_at	C9orf58	chromosome 9 open reading frame 58	2.4941	0.0046
223078_s_at	TMOD3	tropomodulin 3 (ubiquitous)	0.6605	0.0037
223080_at	GLS	Glutaminase	0.5136	0.0055
223082_at	SH3KBP1	SH3-domain kinase binding protein 1	0.6447	0.0355
223086_x_at	MRPL51	mitochondrial ribosomal protein L51	0.213	0.0364
223098_s_at	LONP2	lon peptidase 2; peroxisomal	0.6312	0.0136
223099_s_at	LONP2	lon peptidase 2; peroxisomal	0.5141	0.0137
223110_at	KIAA1429	KIAA1429	0.961	0.0001
223111_x_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.535	0.0083
223116_at	BCAR1	breast cancer anti-estrogen resistance 1	0.3877	0.0185
223158_s_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	1.636	0.0182
223159_s_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	1.4409	0.0312
223163_s_at	ZC3HC1	zinc finger; C3HC-type containing 1	0.7065	0.0078
223172_s_at	MTP18	mitochondrial protein 18 kDa	1.2071	0.0197
223173_at	SPNS1	spinster homolog 1 (Drosophila)	0.6662	0.0001
223186_at	TMEM189	transmembrane protein 189	0.5383	0.0009
223188_at	C19orf61	chromosome 19 open reading frame 61	0.3186	0.003
223189_x_at	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog; Drosophila)	0.6494	0.0312
223195_s_at	SESN2	sestrin 2	1.6589	0.0001

223196_s_at	SESN2	sestrin 2	0.7944	0.0007
223197_s_at	SMARCAD1	SWI/SNF-related; matrix-associated actin-dependent regulator of chromatin; subfamily a; containing DEAD/H box 1	0.5619	0.0101
223199_at	MKNK2	MAP kinase interacting serine/threonine kinase 2	0.6879	0.0118
223200_s_at	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	0.7153	0.0144
223203_at	TMEM29	transmembrane protein 29, transmembrane protein 29B	1.1203	0.0001
223212_at	ZDHHC16	zinc finger; DHHC-type containing 16	0.9854	0.0015
223216_x_at	FBXO16	F-box protein 16, zinc finger protein 395	1.3712	0.0027
223219_s_at	CNOT10	CCR4-NOT transcription complex; subunit 10	0.6302	0.0313
223229_at	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	3.4965	0
223234_at	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	0.7654	0.0339
223244_s_at	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 12	0.4505	0
223246_s_at	STRBP	spermatid perinuclear RNA binding protein	0.7235	0.0248
223247_at	MED10	mediator complex subunit 10	1.3118	0.0002
223248_at	HSDL1	hydroxysteroid dehydrogenase like 1	1.3342	0.0007
223249_at	CLDN12	claudin 12	0.5641	0.0025
223252_at	HDGF2	hepatoma-derived growth factor-related protein 2	0.4146	0.0008
223254_s_at	KIAA1333	KIAA1333	1.2748	0.0013
223255_at	KIAA1333	KIAA1333	0.8569	0.0004
223256_at	KIAA1333	KIAA1333	1.1218	0.0005
223257_at	KIAA1333	KIAA1333	0.9523	0
223258_s_at	KIAA1333	KIAA1333	1.2968	0.0007
223260_s_at	POLK	polymerase (DNA directed) kappa	1.2532	0.0005
223261_at	POLK	polymerase (DNA directed) kappa	0.3023	0.0468
223271_s_at	CTDSPL2	CTD (carboxy-terminal domain; RNA polymerase II; polypeptide A) small phosphatase like 2	1.2475	0.0043
223274_at	TCF19	transcription factor 19 (SC1)	1.1166	0.0029
223284_at	NAT14	N-acetyltransferase 14	1.743	0.0003
223287_s_at	FOXP1	forkhead box P1	1.0323	0.014
223289_s_at	USP38	ubiquitin specific peptidase 38	0.8249	0.0044
223304_at	SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter); member 3	1.015	0
223307_at	CDCA3	cell division cycle associated 3	2.2494	0.0002
223308_s_at	WDR5	WD repeat domain 5	1.0174	0.0008
223323_x_at	TRPM7	transient receptor potential cation channel; subfamily M; member 7	0.2096	0.0393
223326_s_at	FLJ22795	hypothetical protein FLJ22795, similar to cis-Golgi matrix protein GM130	0.5048	0.0374

223332_x_at	RNF126	ring finger protein 126	0.3924	0.0262
223339_at	ATPIF1	ATPase inhibitory factor 1	1.2801	0.0007
223348_x_at	MUM1	melanoma associated antigen (mutated) 1	0.5487	0.0122
223358_s_at		CDNA FLJ33024 fis; clone THYMU1000532; moderately similar to HIGH-AFFINITY CAMP-SPECIFIC 3';5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)	0.7265	0.0179
223361_at	C6orf115	chromosome 6 open reading frame 115	2.0586	0.0004
223363_at	PSMG3	proteasome (prosome; macropain) assembly chaperone 3	0.7802	0.0001
223373_s_at	PLA2G12A	phospholipase A2; group XIIA	1.1658	0.0058
223374_s_at	B3GALNT1	beta-1;3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	1.088	0.0065
223381_at	NUF2	NUF2; NDC80 kinetochore complex component; homolog (S. cerevisiae)	2.9798	0
223388_s_at	ZFYVE1	zinc finger; FYVE domain containing 1	0.7401	0.0317
223396_at	TMEM60	transmembrane protein 60	0.5595	0.0018
223406_x_at	NIP30	NEFA-interacting nuclear protein NIP30	0.6791	0.0005
223407_at	C16orf48	chromosome 16 open reading frame 48	0.8135	0.0399
223413_s_at	LYAR	Ly1 antibody reactive homolog (mouse)	1.0152	0.0012
223414_s_at	LYAR	Ly1 antibody reactive homolog (mouse)	0.2554	0.0415
223417_at	RAD18	RAD18 homolog (S. cerevisiae)	0.5314	0.0038
223420_at	DNAJC14	DnaJ (Hsp40) homolog; subfamily C; member 14	0.4827	0.0114
223422_s_at	ARHGAP24	Rho GTPase activating protein 24	1.0432	0.0093
223423_at	GPR160	G protein-coupled receptor 160	1.0516	0.0119
223424_s_at	ZSCAN21	zinc finger and SCAN domain containing 21	0.7289	0.0244
223425_at	RAVER1	ribonucleoprotein; PTB-binding 1	0.7205	0.0046
223435_s_at	PCDHA1	protocadherin alpha 1, protocadherin alpha 10, protocadherin alpha 11, protocadherin alpha 12, protocadherin alpha 13, protocadherin alpha 2, protocadherin alpha 3, protocadherin alpha 4, protocadherin alpha 5, protocadherin alpha 6, protocadherin alpha 7, protocadherin alpha 8, protocadherin alpha 9, protocadherin alpha subfamily C; 1, protocadherin alpha subfamily C; 2	2.1229	0.0224
223440_at	C16orf70	chromosome 16 open reading frame 70	0.7094	0.0008
223445_at	DTNBP1	dystrobrevin binding protein 1	0.424	0.0276
223451_s_at	CKLF	chemokine-like factor	0.5745	0.0092

223456_s_at	TCHP	trichoplein; keratin filament binding	0.1587	0.0138
223458_at	SEZ6L2	seizure related 6 homolog (mouse)-like 2	0.9353	0.0255
223461_at	TBC1D7	TBC1 domain family; member 7	0.5335	0.0387
223463_at	RAB23	RAB23; member RAS oncogene family	1.0759	0
223465_at	COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	0.9051	0.0001
223466_x_at	COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	1.0041	0
223470_at	PIGM	phosphatidylinositol glycan anchor biosynthesis; class M	0.5944	0.0346
223472_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.4161	0.0223
223476_s_at	C12orf65	chromosome 12 open reading frame 65	1.0479	0
223477_s_at	C12orf65	chromosome 12 open reading frame 65	0.962	0.0002
223488_s_at	GNB4	guanine nucleotide binding protein (G protein); beta polypeptide 4	0.2818	0.04
223494_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	1.5676	0
223495_at	CCDC8	coiled-coil domain containing 8	1.1728	0.0404
223496_s_at	CCDC8	coiled-coil domain containing 8	0.9473	0.0334
223501_at	TNFSF13B	tumor necrosis factor (ligand) superfamily; member 13b	1.9138	0.0211
223502_s_at	TNFSF13B	tumor necrosis factor (ligand) superfamily; member 13b	1.7838	0.02
223506_at	ZC3H8	zinc finger CCCH-type containing 8	1.2542	0
223513_at	CENPJ	centromere protein J	1.4962	0.0013
223522_at	C9orf45	chromosome 9 open reading frame 45	0.163	0.0181
223528_s_at	LOC731602	methyltransferase 11 domain containing 1, similar to methyltransferase 11 domain containing 1 isoform 2	0.4459	0.0054
223531_x_at	GPR89A	G protein-coupled receptor 89A, G protein-coupled receptor 89B, G protein-coupled receptor 89C	0.4465	0.0086
223538_at	SERF1A	small EDRK-rich factor 1A (telomeric), small EDRK-rich factor 1B (centromeric)	0.6135	0.017
223539_s_at	SERF1A	small EDRK-rich factor 1A (telomeric), small EDRK-rich factor 1B (centromeric)	1.1833	0.0061
223542_at	ANKRD32	ankyrin repeat domain 32	2.2918	0
223545_at	FANCD2	Fanconi anemia; complementation group D2	0.3845	0.0033
223547_at	C14orf100	chromosome 14 open reading frame 100	0.6934	0.0083
223556_at	HELLS	helicase; lymphoid-specific	1.9884	0.0004
223558_at	C9orf80	chromosome 9 open reading frame 80	0.4354	0.0184
223567_at	SEMA6B	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6B	1.0864	0.0181

223570_at	MCM10	minichromosome maintenance complex component 10	0.5531	0.0008
223575_at	KIAA1549	KIAA1549 protein	0.467	0.0247
223584_s_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	1.1663	0.0031
223585_x_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	0.8527	0.0462
223588_at	THAP2	THAP domain containing; apoptosis associated protein 2	0.6006	0.0106
223590_at	ZNF700	zinc finger protein 700	1.3211	0.0001
223596_at	SLC12A6	solute carrier family 12 (potassium/chloride transporters); member 6	0.2784	0.039
223602_at	USP30	ubiquitin specific peptidase 30	0.7517	0.0018
223614_at	C8orf57	chromosome 8 open reading frame 57	2.3641	0.0154
223621_at	PNMA3	paraneoplastic antigen MA3	0.9195	0.0304
223628_at	TMEM191A	transmembrane protein 191A	0.2264	0.0404
223629_at	PCDHB5	protocadherin beta 5	1.4262	0.0382
223630_at	C7orf13	chromosome 7 open reading frame 13	0.451	0.041
223642_at	ZIC2	Zic family member 2 (odd-paired homolog; Drosophila)	1.1076	0.0122
223643_at	CRYGS	Crystallin; gamma S	0.2909	0.0037
223662_x_at	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	0.3165	0.0068
223677_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	0.7807	0.0073
223680_at	ZNF607	zinc finger protein 607	0.6855	0.0086
223684_s_at	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	0.4309	0.031
223697_x_at	C9orf64	chromosome 9 open reading frame 64	0.5713	0.0036
223700_at	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	2.5958	0
223714_at	ZNF256	zinc finger protein 256	0.7039	0.0063
223720_at	SPINK7	serine peptidase inhibitor; Kazal type 7 (putative)	0.2226	0.0104
223724_s_at	DKFZP434A0131	DKFZp434A0131 protein, STAG3-like	0.3979	0.0161
223728_at	MGC16385	hypothetical protein MGC16385	0.5674	0.0135
223730_at	GPC6	glypican 6	0.8281	0.0395
223735_at	ARL6	ADP-ribosylation factor-like 6	0.5148	0.0231
223737_x_at	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	0.1776	0.0253
223742_at	MRPL4	mitochondrial ribosomal protein L4	0.4628	0.0342
223758_s_at	GTF2H2	general transcription factor IIH; polypeptide 2; 44kDa	0.7591	0.0457
223763_at	DTNBP1	dystrobrevin binding protein 1	0.2541	0.0148
223774_at	C1orf79	chromosome 1 open reading frame 79	0.6834	0.0234
223781_x_at	ADH4	alcohol dehydrogenase 4 (class II); pi polypeptide	0.226	0.0455

223785_at	FANCI	Fanconi anemia; complementation group I	0.6627	0.0096
223789_s_at	GTPBP2	GTP binding protein 2	0.3575	0.0169
223798_at	SLC41A2	solute carrier family 41; member 2	0.7466	0.0255
223803_s_at	ZCCHC10	zinc finger; CCHC domain containing 10	0.5413	0.0494
223804_s_at	THUMPD3	THUMP domain containing 3	0.6019	0.0023
223805_at	OSBPL6	oxysterol binding protein-like 6	3.103	0
223815_at	CCDC45	Coiled-coil domain containing 45	0.2122	0.0234
223854_at	PCDHB10	protocadherin beta 10	1.2466	0.0378
223875_s_at	EPC1	enhancer of polycomb homolog 1 (Drosophila)	0.2443	0.0121
223880_x_at	C20orf24	chromosome 20 open reading frame 24	0.3831	0.0275
223888_s_at	LARS	leucyl-tRNA synthetase	0.4849	0.011
223917_s_at	SLC39A3	solute carrier family 39 (zinc transporter); member 3	0.9702	0.0005
223931_s_at	CHFR	checkpoint with forkhead and ring finger domains	0.7146	0.0033
223945_x_at	LOC441212	retinitis pigmentosa 9 pseudogene	0.4962	0.0248
223981_at	NIN	ninein (GSK3B interacting protein)	0.1776	0.0276
223984_s_at	NUPL1	nucleoporin like 1	0.4394	0.0468
223988_x_at	LOC731602	methyltransferase 11 domain containing 1, similar to methyltransferase 11 domain containing 1 isoform 2	0.4403	0.005
223994_s_at	SLC12A9	solute carrier family 12 (potassium/chloride transporters); member 9	0.1635	0.0471
224010_at	ANAPC11	APC11 anaphase promoting complex subunit 11 homolog (yeast)	0.1403	0.0029
224027_at	CCL28	chemokine (C-C motif) ligand 28	1.1141	0.0255
224046_s_at	PDE7A	phosphodiesterase 7A	0.4161	0.0215
224064_s_at	DHDDS	dehydrodolichyl diphosphate synthase	0.3665	0.0488
224068_x_at	RBM22	RNA binding motif protein 22	0.6703	0.0003
224147_at	C12orf48	chromosome 12 open reading frame 48	0.211	0.0036
224159_x_at	TRIM4	tripartite motif-containing 4	0.2942	0.0365
224165_s_at	IQCH	IQ motif containing H	0.3317	0.0072
224173_s_at	MRPL30	mitochondrial ribosomal protein L30	0.9999	0.0129
224176_s_at	AXIN2	axin 2 (conductin; axil)	0.2104	0.049
224185_at		CDNA FLJ39726 fis; clone SMINT2015306	0.6123	0.0251
224188_s_at	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3; putative	0.2613	0.0076
224199_at	DKK2	dickkopf homolog 2 (Xenopus laevis)	0.1694	0.0072
224200_s_at	RAD18	RAD18 homolog (S. cerevisiae)	0.7783	0.0081
224210_s_at	PXMP4	peroxisomal membrane protein 4; 24kDa	0.766	0.0247

224212_s_at	PCDHA1	protocadherin alpha 1, protocadherin alpha 10, protocadherin alpha 11, protocadherin alpha 12, protocadherin alpha 13, protocadherin alpha 2, protocadherin alpha 3, protocadherin alpha 4, protocadherin alpha 5, protocadherin alpha 6, protocadherin alpha 7, protocadherin alpha 8, protocadherin alpha 9, protocadherin alpha subfamily C; 1, protocadherin alpha subfamily C; 2	1.4458	0.0292
224248_x_at	NIP30	NEFA-interacting nuclear protein NIP30	0.4369	0.0066
224254_x_at			0.6959	0.0035
224284_x_at	FKSG49	FKSG49	0.4017	0.0009
224288_x_at	FKSG49	FKSG49	0.7225	0
224311_s_at	CAB39	calcium binding protein 39	0.7126	0.033
224314_s_at	EGLN1	egl nine homolog 1 (C. elegans)	0.9538	0.045
224320_s_at	MCM8	minichromosome maintenance complex component 8	1.7059	0
224322_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.2974	0.0114
224334_s_at	MRPL51	mitochondrial ribosomal protein L51	0.3505	0.0209
224365_s_at	TIGD7	tigger transposable element derived 7	2.3529	0
224369_s_at	FBXO38	F-box protein 38	0.3934	0.0305
224370_s_at	CAPS2	calcyphosine 2	1.602	0.0027
224376_s_at	C20orf24	chromosome 20 open reading frame 24	0.4873	0.0387
224394_at	RNF7	ring finger protein 7	0.2793	0.0029
224400_s_at	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	0.1734	0.0182
224416_s_at	MED28	mediator complex subunit 28	0.6144	0.0008
224428_s_at	CDCA7	cell division cycle associated 7	1.4985	0.0159
224452_s_at	MGC12966	hypothetical protein LOC84792	0.7599	0
224455_s_at	ADPGK	ADP-dependent glucokinase	0.8546	0.0019
224460_s_at	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.5204	0.0014
224468_s_at	C19orf48	chromosome 19 open reading frame 48	2.4779	0
224478_s_at	C7orf50	chromosome 7 open reading frame 50	1.0195	0.0063
224492_s_at	ZNF627	zinc finger protein 627	1.4071	0
224517_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J; 13.3kDa pseudogene	1.1236	0.0001
224518_s_at	ZNF559	zinc finger protein 559	0.7933	0.0011
224521_s_at	CCDC77	coiled-coil domain containing 77	0.798	0.0193
224546_at			0.205	0.0064
224549_x_at			0.9935	0.0004

224568_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0.8821	0.0406
224587_at	SUB1	SUB1 homolog (S. cerevisiae)	0.5019	0.04
224588_at	XIST	X (inactive)-specific transcript	3.2664	0.0367
224589_at	XIST	X (inactive)-specific transcript	2.3995	0.029
224593_at	ZNF664	zinc finger protein 664	0.4025	0.0267
224601_at		CDNA clone IMAGE:3831740	0.5534	0.009
224603_at		CDNA clone IMAGE:3831740	0.5239	0.0049
224609_at	SLC44A2	solute carrier family 44; member 2	1.411	0.0008
224610_at	SNHG1	small nucleolar RNA host gene (non-protein coding) 1	1.1856	0.0032
224614_at	DYNC1LI2	dynein; cytoplasmic 1; light intermediate chain 2	0.6209	0.0002
224616_at	DYNC1LI2	dynein; cytoplasmic 1; light intermediate chain 2	0.3769	0.0002
224618_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	0.5507	0.0097
224623_at	LOC728554	THO complex 3, similar to THO complex 3	2.499	0
224638_at	UNQ1887	signal peptide peptidase 3	0.8048	0.0076
224639_at	UNQ1887	signal peptide peptidase 3	0.8227	0.0001
224640_at	UNQ1887	signal peptide peptidase 3	1.0757	0
224643_at	PRRC1	proline-rich coiled-coil 1	0.7834	0.0004
224656_s_at	MTPN	myotrophin	0.4385	0
224662_at	KIF5B	kinesin family member 5B	0.4573	0.0046
224667_x_at	C10orf104	chromosome 10 open reading frame 104	0.2815	0.0106
224676_at	TMED4	transmembrane emp24 protein transport domain containing 4	0.7151	0.041
224678_at	KIAA1219	KIAA1219	0.6657	0.0002
224682_at	ANKIB1	ankyrin repeat and IBR domain containing 1	0.9113	0
224687_at	ANKIB1	ankyrin repeat and IBR domain containing 1	0.9131	0
224695_at	C2orf29	chromosome 2 open reading frame 29	0.5216	0.0005
224703_at	WDR22	WD repeat domain 22	0.5034	0.0441
224709_s_at	CDC42SE2	CDC42 small effector 2	0.7828	0.0001
224712_x_at	C19orf42	chromosome 19 open reading frame 42	0.3621	0.0396
224724_at	SULF2	sulfatase 2	2.5149	0
224726_at	MIB1	mindbomb homolog 1 (Drosophila)	0.6179	0.047
224727_at	C19orf63	chromosome 19 open reading frame 63	0.8727	0.002
224730_at	WDR68	WD repeat domain 68	1.5154	0.0002
224740_at	DKFZP686E2158	hypothetical protein LOC643155	0.4206	0.0021
224748_at	WDR68	WD repeat domain 68	0.5778	0.0017
224749_at	ITFG3	integrin alpha FG-GAP repeat containing 3	0.4898	0.0453
224753_at	CDCA5	cell division cycle associated 5	2.0313	0.0003

224759_s_at	C12orf23	chromosome 12 open reading frame 23	0.604	0.0005
224765_at	MSL-1	male-specific lethal-1 homolog	0.7539	0.0115
224772_at	NAV1	neuron navigator 1	1.4028	0.0239
224773_at	NAV1	neuron navigator 1	0.8428	0.0103
224774_s_at	NAV1	neuron navigator 1	1.0456	0.017
224779_s_at	FAM96A	family with sequence similarity 96; member A	0.406	0.0094
224790_at	DDEF1	development and differentiation enhancing factor 1	0.7485	0.0097
224796_at	DDEF1	development and differentiation enhancing factor 1	0.4982	0.0169
224813_at	WASL	Wiskott-Aldrich syndrome-like	0.5003	0.0001
224839_s_at	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	0.9961	0.0258
224842_at	SMG1	PI-3-kinase-related kinase SMG-1	0.527	0.0024
224846_at	SHKBP1	SH3KBP1 binding protein 1	0.3946	0.0167
224853_at	SLAIN2	SLAIN motif family; member 2	0.4265	0.0326
224854_s_at	SLAIN2	SLAIN motif family; member 2	0.4419	0.0056
224859_at	CD276	CD276 molecule	0.5127	0.0146
224873_s_at	MRPS25	mitochondrial ribosomal protein S25	0.6025	0.0039
224875_at	C5orf24	chromosome 5 open reading frame 24	0.5486	0.0187
224878_at	UBFD1	ubiquitin family domain containing 1	0.8473	0.0001
224882_at	ACSS1	acyl-CoA synthetase short-chain family member 1	1.3335	0.0039
224896_s_at	TTL	tubulin tyrosine ligase	0.8076	0.0095
224902_at	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	0.955	0.0038
224903_at	CIRH1A	cirrhosis; autosomal recessive 1A (cirhin)	0.4296	0.039
224904_at	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	0.7107	0.022
224908_s_at	TTL	tubulin tyrosine ligase	0.8829	0.0008
224913_s_at	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	0.5837	0.0027
224914_s_at	CIP29	DnaJ (Hsp40) homolog; subfamily C; member 14, cytokine induced protein 29 kDa	0.2624	0.0498
224922_at	CSNK2A2	casein kinase 2; alpha prime polypeptide	0.6555	0.0003
224935_at	EIF2S3	eukaryotic translation initiation factor 2; subunit 3 gamma; 52kDa	0.343	0.0379
224944_at	TMPO	thymopoietin	1.6297	0
224949_at	YIPF5	Yip1 domain family; member 5	0.5143	0.0363
224951_at	LASS5	LAG1 homolog; ceramide synthase 5	0.6657	0.0026
224952_at	TANC2	tetratricopeptide repeat; ankyrin repeat and coiled-coil containing 2	1.4478	0.0049
224953_at	YIPF5	Yip1 domain family; member 5	0.642	0.0236
224960_at	SCYL2	SCY1-like 2 (S. cerevisiae)	0.6846	0.0002
224961_at	SCYL2	SCY1-like 2 (S. cerevisiae)	0.741	0.0001

224962_at	C9orf69	chromosome 9 open reading frame 69	0.9242	0
224993_at	LOC729433	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 1, similar to myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 1	0.3368	0.0232
225017_at	CCDC14	coiled-coil domain containing 14	1.117	0
225024_at	C20orf77	chromosome 20 open reading frame 77	0.5259	0.0063
225031_at	CHD6	chromodomain helicase DNA binding protein 6	0.7237	0.015
225035_x_at	CXYorf1	CXYorf1-related protein, chromosomes X and Y open reading frame 1, family with sequence similarity 39; member B, family with sequence similarity 39; member D pseudogene, family with sequence similarity 39; member E, similar to CXYorf1-related protein	0.4965	0.0175
225038_s_at	SURF6	surfeit 6	1.0677	0.0007
225042_s_at	FAM130A1	family with sequence similarity 130; member A1	0.5299	0.0024
225052_at	MGC14327	hypothetical protein MGC14327	0.3138	0.0389
225053_at	CNOT7	CCR4-NOT transcription complex; subunit 7	0.2844	0.0239
225067_at	ULK3	unc-51-like kinase 3 (C. elegans)	1.2475	0.0042
225068_at	KLHL12	kelch-like 12 (Drosophila)	0.4671	0.024
225075_at	PDRG1	p53 and DNA damage regulated 1	1.5177	0
225079_at	EMP2	epithelial membrane protein 2	1.2019	0.0331
225081_s_at	CDCA7L	cell division cycle associated 7-like	1.6065	0.0005
225084_at	EXOC5	exocyst complex component 5	0.3746	0.0078
225087_at	C16orf63	chromosome 16 open reading frame 63	0.3707	0.004
225088_at	C16orf63	chromosome 16 open reading frame 63	1.2329	0.0026
225091_at	ZCCHC3	zinc finger; CCHC domain containing 3	0.8681	0.0018
225094_at	SETD8	SET domain containing (lysine methyltransferase) 8	0.8655	0.0012
225099_at	FBXO45	F-box protein 45	0.9853	0.0006
225100_at	FBXO45	F-box protein 45	0.7239	0.0006
225104_at	ZNF598	zinc finger protein 598	0.6403	0.0023
225105_at	OCC-1	overexpressed in colon carcinoma-1	1.9417	0.0088
225111_s_at	NAPB	N-ethylmaleimide-sensitive factor attachment protein; beta	0.7325	0.0479
225119_at	CHMP4B	chromatin modifying protein 4B	0.886	0.0391
225120_at	PURB	purine-rich element binding protein B	0.4038	0.0143
225126_at	MRRF	mitochondrial ribosome recycling factor	0.6232	0.0231
225134_at	SPRYD3	SPRY domain containing 3	0.3849	0.0402

225135_at	SIN3A	SIN3 homolog A; transcription regulator (yeast)	0.9194	0.0031
225137_at	RBM35B	RNA binding motif protein 35B	0.467	0.0385
225139_at	RBM35B	RNA binding motif protein 35B	0.6157	0.0244
225141_at	RBM35B	RNA binding motif protein 35B	0.3822	0.0343
225145_at	NCOA5	nuclear receptor coactivator 5	0.4851	0.0493
225146_at	C9orf25	chromosome 9 open reading frame 25	0.7868	0.0097
225157_at	MLXIP	MLX interacting protein	0.7309	0.0131
225170_at	WDR5	WD repeat domain 5	0.6529	0.0321
225178_at	TTC14	tetratricopeptide repeat domain 14	0.6063	0.0298
225187_at	KIAA1967	KIAA1967	0.4717	0.0318
225191_at	CIRBP	cold inducible RNA binding protein	1.1156	0.0002
225208_s_at	FAM103A1	family with sequence similarity 103; member A1	0.8775	0.0055
225210_s_at	FAM103A1	family with sequence similarity 103; member A1	0.6421	0.0044
225219_at	SMAD5	SMAD family member 5	0.6097	0.001
225224_at	C20orf112	chromosome 20 open reading frame 112	1.9166	0
225235_at	TSPAN17	tetraspanin 17	1.2544	0.0014
225246_at	STIM2	stromal interaction molecule 2	0.8217	0.0018
225247_at	C19orf6	chromosome 19 open reading frame 6	0.5545	0
225248_at	SPPL2B	signal peptide peptidase-like 2B	0.4255	0.0084
225249_at	SPPL2B	signal peptide peptidase-like 2B	0.5341	0.0004
225250_at	STIM2	stromal interaction molecule 2	0.3307	0.0105
225251_at	RAB24	RAB24; member RAS oncogene family	0.5566	0.012
225267_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	0.7017	0.0001
225268_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	0.7602	0
225278_at	PRKAB2	protein kinase; AMP-activated; beta 2 non-catalytic subunit	2.1081	0
225288_at	COL27A1	collagen; type XXVII; alpha 1	1.6227	0.025
225292_at	COL27A1	collagen; type XXVII; alpha 1	1.168	0.0126
225296_at	ZNF317	zinc finger protein 317	0.9551	0
225300_at	C15orf23	chromosome 15 open reading frame 23	1.7221	0.0001
225313_at	C20orf177	chromosome 20 open reading frame 177	1.3535	0.0007
225314_at	OCIAD2	OCIA domain containing 2	0.814	0.0244
225320_at	CCDC109A	coiled-coil domain containing 109A	0.5929	0.0024
225321_s_at	PILRB	paired immunoglobin-like type 2 receptor beta	0.8027	0.0008
225326_at	RBM27	RNA binding motif protein 27	0.7568	0.0001
225342_at	AK3L2	adenylate kinase 3-like 2	3.7585	0.0001
225361_x_at	FAM122B	family with sequence similarity 122B	0.6777	0.0013

225362_at	FAM122B	family with sequence similarity 122B	1.3994	0.0001
225364_at	STK4	serine/threonine kinase 4	0.7204	0.0005
225385_s_at	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	0.5053	0.0042
225387_at	TSPAN5	tetraspanin 5	1.4775	0.0095
225388_at	TSPAN5	tetraspanin 5	0.8723	0.0149
225392_at	GFM2	G elongation factor; mitochondrial 2	0.494	0.0056
225425_s_at	MRPL41	mitochondrial ribosomal protein L41	0.4615	0.0031
225434_at	DEDD2	death effector domain containing 2	0.7065	0.0092
225436_at	FAM108C1	family with sequence similarity 108; member C1	1.1458	0.0088
225438_at	NUDCD1	NudC domain containing 1	0.7216	0.0079
225439_at	NUDCD1	NudC domain containing 1	0.6704	0.0338
225444_at	FLJ25778	hypothetical protein FLJ25778	0.8925	0.0015
225445_at	FLJ25778	hypothetical protein FLJ25778	0.762	0.0021
225446_at	BRWD1	bromodomain and WD repeat domain containing 1	0.5911	0.0381
225454_at	CCDC124	coiled-coil domain containing 124	0.7645	0.0001
225457_s_at	LOC25845	hypothetical LOC25845	0.8969	0.0004
225458_at	LOC25845	hypothetical LOC25845	0.917	0.0012
225463_x_at	GPR89A	G protein-coupled receptor 89A	0.5467	0.0049
225465_at	MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	1.0716	0.0001
225467_s_at	RDH13	retinol dehydrogenase 13 (all-trans/9-cis)	1.4943	0.0005
225474_at	MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	1.6436	0.0001
225484_at	TSGA14	testis specific; 14	0.6158	0.0039
225485_at	TSGA14	testis specific; 14	0.7993	0.0177
225490_at	ARID2	AT rich interactive domain 2 (ARID; RFX-like)	0.6869	0.0024
225527_at	CEBPG	CCAAT/enhancer binding protein (C/EBP); gamma	1.3141	0.0001
225529_at	CENTB5	centaurin; beta 5	0.5286	0.0355
225533_at	PHF19	PHD finger protein 19	0.7704	0.0157
225538_at	ZCCHC9	zinc finger; CCHC domain containing 9	1.1164	0.0003
225542_at	CENTB5	centaurin; beta 5	0.3039	0.0118
225543_at	GTF3C4	general transcription factor IIIC; polypeptide 4; 90kDa	1.0779	0.0029
225545_at	EEF2K	eukaryotic elongation factor-2 kinase	0.6271	0.044
225554_s_at	ANAPC7	anaphase promoting complex subunit 7	0.411	0.0012
225584_at	HCG18	HLA complex group 18	0.3363	0.0053
225586_at	WDR85	WD repeat domain 85	0.4864	0.0395
225590_at	SH3RF1	SH3 domain containing ring finger 1	0.4138	0.0154
225592_at	NRM	nurim (nuclear envelope membrane protein)	1.0095	0.0013

225599_s_at	LOC286144	hypothetical protein LOC286144	0.6784	0.021
225600_at	LOC286144	hypothetical protein LOC286144	0.8184	0.0438
225601_at	HMGB3	high-mobility group box 3	1.6507	0.0006
225609_at	GSR	glutathione reductase	0.4619	0.0391
225610_at	UHRF2	ubiquitin-like; containing PHD and RING finger domains; 2	0.5053	0.0132
225617_at	ODF2	outer dense fiber of sperm tails 2	1.1129	0.0023
225620_at	RAB35	RAB35; member RAS oncogene family	0.7181	0.0037
225623_at	KIAA1737	KIAA1737	0.7925	0.0031
225625_at	ALKBH2	alkB; alkylation repair homolog 2 (E. coli)	0.5409	0.0117
225637_at	DEF8	differentially expressed in FDCP 8 homolog (mouse)	0.6566	0.0016
225640_at	LOC401504	hypothetical gene supported by AK091718	0.5447	0.0185
225648_at	STK35	serine/threonine kinase 35	0.5501	0.0404
225649_s_at	STK35	serine/threonine kinase 35	0.4448	0.0243
225650_at	SAMD1	sterile alpha motif domain containing 1	0.4717	0.0193
225654_at	LOC202347	hypothetical protein LOC202347	0.192	0.0267
225655_at	UHRF1	ubiquitin-like; containing PHD and RING finger domains; 1	2.4233	0.0004
225659_at	LOC339745	hypothetical protein LOC339745	0.3542	0.0214
225668_at	LOC134145	hypothetical protein LOC134145	0.5118	0.001
225674_at	BCAP29	B-cell receptor-associated protein 29	0.736	0.0049
225680_at	DKFZp434K1815	hypothetical protein DKFZp434K1815	0.5029	0.0191
225681_at	CTHRC1	collagen triple helix repeat containing 1	2.8396	0.0015
225683_x_at	PHPT1	phosphohistidine phosphatase 1	0.3203	0.0439
225684_at	FAM33A	family with sequence similarity 33; member A	1.0145	0
225686_at	FAM33A	family with sequence similarity 33; member A	1.2635	0.0001
225687_at	FAM83D	family with sequence similarity 83; member D	3.0098	0.0001
225700_at	GLCCI1	glucocorticoid induced transcript 1	0.3542	0.003
225702_at	C8orf76	chromosome 8 open reading frame 76	0.5659	0.0233
225706_at	GLCCI1	glucocorticoid induced transcript 1	1.3487	0
225713_at	STK11IP	serine/threonine kinase 11 interacting protein	0.7991	0.0021
225716_at		Full-length cDNA clone CS0DK008YI09 of HeLa cells Cot 25-normalized of Homo sapiens (human)	1.5251	0.0004
225717_at	KIAA1715	KIAA1715	1.4563	0
225718_at	KIAA1715	KIAA1715	1.0742	0.0153
225723_at	C6orf129	chromosome 6 open reading frame 129	0.8465	0.0053
225730_s_at	THUMPD3	THUMP domain containing 3	0.8316	0.0258
225731_at	ANKRD50	ankyrin repeat domain 50	0.8031	0.006

225735_at	ANKRD50	ankyrin repeat domain 50	1.0989	0.0035
225741_at	THUMPD3	THUMP domain containing 3	0.5257	0.0199
225742_at	MDM4	Mdm4; transformed 3T3 cell double minute 4; p53 binding protein (mouse)	0.9691	0.0054
225743_at	RPUSD3	RNA pseudouridylate synthase domain containing 3	0.6636	0.0359
225745_at	LRP6	low density lipoprotein receptor-related protein 6	1.3194	0.0006
225750_at		CDNA FLJ14162 fis; clone NT2RM4002504	1.8434	0
225761_at	PAPD4	PAP associated domain containing 4	0.5237	0.0086
225765_at	TNPO1	transportin 1	0.6398	0.0016
225766_s_at	TNPO1	transportin 1	1.0306	0.0013
225768_at	NR1D2	nuclear receptor subfamily 1; group D; member 2	0.7591	0.0131
225770_at	RSPRY1	ring finger and SPRY domain containing 1	0.8376	0.0008
225774_at	RSPRY1	ring finger and SPRY domain containing 1	0.9881	0.0028
225777_at	C9orf140	chromosome 9 open reading frame 140	0.6191	0.0026
225784_s_at	KIAA1166	KIAA1166	0.6816	0.0348
225790_at	MSRB3	methionine sulfoxide reductase B3	1.708	0.0037
225806_at	JUB	jub; ajuba homolog (Xenopus laevis)	1.403	0.0132
225821_s_at	FAM44A	family with sequence similarity 44; member A	0.7511	0.005
225827_at	EIF2C2	eukaryotic translation initiation factor 2C; 2	0.9629	0.0207
225834_at	FAM72A	family with sequence similarity 72; member A, family with sequence similarity 72; member B, gastric cancer up-regulated-2	3.1044	0
225836_s_at	C12orf32	chromosome 12 open reading frame 32	1.3283	0.0002
225837_at	C12orf32	chromosome 12 open reading frame 32	1.4393	0.0001
225839_at	RBM33	RNA binding motif protein 33	0.4288	0.0188
225841_at	C1orf59	chromosome 1 open reading frame 59	1.4325	0.0096
225848_at	ZNF746	zinc finger protein 746	0.4473	0.0306
225852_at	ANKRD17	ankyrin repeat domain 17	0.5347	0.0069
225857_s_at	LOC388796	hypothetical LOC388796	0.6872	0.0357
225858_s_at	BIRC4	baculoviral IAP repeat-containing 4	0.5285	0.0339
225859_at	BIRC4	baculoviral IAP repeat-containing 4	0.4728	0.0183
225864_at	FAM84B	family with sequence similarity 84; member B	0.706	0.0492
225868_at	TRIM47	tripartite motif-containing 47	1.5518	0.0028
225879_at	TSEN54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	0.4877	0.0398
225881_at	SLC35B4	solute carrier family 35; member B4	0.6903	0.0015
225885_at	EEA1	early endosome antigen 1	0.5011	0.0048

225888_at	C12orf30	chromosome 12 open reading frame 30	0.9143	0
225891_at	C9orf75	chromosome 9 open reading frame 75	0.7527	0.0004
225898_at	WDR54	WD repeat domain 54	1.8786	0.0009
225899_x_at	FLJ45445	hypothetical LOC399844, hypothetical LOC402483, hypothetical LOC653340, hypothetical protein LOC728797, hypothetical protein LOC729660, similar to FLJ45445 protein	1.3492	0.0003
225903_at	PIGU	phosphatidylinositol glycan anchor biosynthesis; class U	1.0231	0.0014
225904_at	C1orf96	chromosome 1 open reading frame 96	1.2486	0.0004
225912_at	TP53INP1	tumor protein p53 inducible nuclear protein 1	1.0586	0.0016
225917_at		CDNA FLJ43113 fis; clone CTONG2028208	0.5999	0.0026
225921_at	NIN	ninein (GSK3B interacting protein)	0.8294	0.0229
225943_at	NLN	neurolysin (metallopeptidase M3 family)	0.5755	0.0292
225944_at	NLN	neurolysin (metallopeptidase M3 family)	1.4432	0.002
225947_at	MYOHD1	myosin head domain containing 1	0.9418	0.0005
225948_at	C14orf153	chromosome 14 open reading frame 153	0.5156	0.0358
225961_at	KLHDC5	kelch domain containing 5	1.0077	0.0002
225963_at	KLHDC5	kelch domain containing 5	0.9641	0
225964_at	ZXDC	ZXD family zinc finger C	0.6989	0.0007
225965_at	DDHD1	DDHD domain containing 1	0.6035	0.0044
225969_at	ALKBH6	alkB; alkylation repair homolog 6 (E. coli)	0.9171	0.0021
225970_at	DDHD1	DDHD domain containing 1	0.7963	0.0054
225971_at		CDNA FLJ34209 fis; clone FCBBF3020599	0.7505	0.0177
225986_x_at	CPSF2	cleavage and polyadenylation specific factor 2; 100kDa	0.4503	0.0118
226003_at	KIF21A	kinesin family member 21A	0.8456	0.0154
226004_at	CABLES2	Cdk5 and Abl enzyme substrate 2	0.7727	0.0049
226009_at	RP11-529I10.4	deleted in a mouse model of primary ciliary dyskinesia	0.867	0.0026
226015_at	ZNF12	zinc finger protein 12	0.9413	0
226027_at	C9orf119	chromosome 9 open reading frame 119	1.1048	0.0033
226031_at	CCDC132	coiled-coil domain containing 132	0.6036	0.0085
226032_at	CASP2	caspase 2; apoptosis-related cysteine peptidase (neural precursor cell expressed; developmentally down-regulated 2)	1.7098	0
226033_at	USP31	ubiquitin specific peptidase 31	0.5887	0.0083
226035_at	USP31	ubiquitin specific peptidase 31	1.4405	0.0001
226041_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	1.0161	0.013
226042_at	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	0.4985	0.0003

226044_at	TDP1	tyrosyl-DNA phosphodiesterase 1	0.4006	0.0072
226048_at	MAPK8	mitogen-activated protein kinase 8	0.5904	0.0487
226052_at		Transcribed locus	0.4574	0.0009
226054_at	BRD4	bromodomain containing 4	0.9046	0.0001
226062_x_at	FAM63A	family with sequence similarity 63; member A	0.5721	0.003
226070_at	C9orf142	chromosome 9 open reading frame 142	0.4197	0.024
226076_s_at	MBD6	methyl-CpG binding domain protein 6	1.3661	0.0013
226082_s_at	SFRS15	splicing factor; arginine/serine-rich 15	0.5757	0.0226
226085_at		CDNA clone IMAGE:4842353	1.4184	0.0011
226088_at	ZDHHC12	zinc finger; DHHC-type containing 12	0.5176	0.0057
226098_at	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	0.5483	0.0276
226102_at		Full-length cDNA clone CS0DF010YE22 of Fetal brain of Homo sapiens (human)	0.8132	0.0419
226105_at		Full-length cDNA clone CS0DI084YF13 of Placenta Cot 25-normalized of Homo sapiens (human)	0.5859	0.0237
226107_at		CDNA FLJ13495 fis; clone PLACE1004425, Full-length cDNA clone CS0DI084YF13 of Placenta Cot 25-normalized of Homo sapiens (human)	0.7771	0.0011
226108_at	NHN1	conserved nuclear protein NHN1	0.9624	0.0002
226113_at	ZNF436	zinc finger protein 436	0.947	0.0054
226114_at	ZNF436	zinc finger protein 436	0.9682	0.0066
226115_at	AHCTF1	AT hook containing transcription factor 1	0.8026	0.0012
226117_at	TIFA	TRAF-interacting protein with a forkhead-associated domain	1.5093	0.0008
226118_at	CENPO	centromere protein O	0.8079	0.0075
226121_at	DHRS13	dehydrogenase/reductase (SDR family) member 13	1.6163	0.0004
226124_at	ZFP90	zinc finger protein 90 homolog (mouse)	1.0483	0.0033
226125_at		CDNA clone IMAGE:4346813	0.5615	0.034
226132_s_at	MANEAL	mannosidase; endo-alpha-like	1.6177	0.0004
226149_at	C20orf198	chromosome 20 open reading frame 198	0.8272	0.006
226156_at	AKT2	v-akt murine thymoma viral oncogene homolog 2	1.2178	0.0024
226159_at	LOC285636	hypothetical protein LOC285636	0.709	0
226163_at	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat), zinc finger and BTB domain containing 9	0.361	0.0454
226164_x_at	FAM80B	Family with sequence similarity 80; member B	0.9338	0.0277
226176_s_at	USP42	ubiquitin specific peptidase 42	1.1462	0.0001
226201_at		MRNA; cDNA DKFZp586P1823 (from clone DKFZp586P1823)	0.5625	0.0451

226202_at	ZNF398	zinc finger protein 398	0.9871	0.0035
226207_at	FLJ39378	hypothetical protein FLJ39378	0.8709	0.0083
226209_at	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3; 10kDa	0.4775	0.0183
226215_s_at	FBXL10	F-box and leucine-rich repeat protein 10	1.7376	0
226216_at	INSR	insulin receptor	0.9627	0.0378
226221_at	KIAA1432	KIAA1432	0.5926	0.0004
226228_at	AQP4	aquaporin 4	0.127	0.0277
226247_at	PLEKHA1	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 1	1.4406	0
226249_at	SNX30	sorting nexin family member 30	0.6614	0.0273
226255_at	ZBTB33	zinc finger and BTB domain containing 33	0.4687	0.0447
226258_at	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	0.9481	0.01
226263_at	C6orf151	chromosome 6 open reading frame 151	0.4839	0.0333
226270_at	EXOC2	exocyst complex component 2	0.3873	0.0469
226273_at	CLCN5	chloride channel 5 (nephrolithiasis 2; X-linked; Dent disease)	0.9019	0.0054
226274_at	CLCN5	chloride channel 5 (nephrolithiasis 2; X-linked; Dent disease)	1.4701	0.0023
226277_at		CDNA FLJ43397 fis; clone OCBBF2009788	0.3418	0.004
226279_at	PRSS23	protease; serine; 23	1.2143	0.0067
226287_at	CCDC34	coiled-coil domain containing 34	1.0231	0.0018
226289_at	CAPRIN1	cell cycle associated protein 1	0.5491	0.0374
226290_at	BDP1	B double prime 1; subunit of RNA polymerase III transcription initiation factor IIIB	0.6367	0
226291_at	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	0.9642	0.0193
226294_x_at	FAM91A1	family with sequence similarity 91; member A1	0.3198	0.0099
226306_at	C6orf1	chromosome 6 open reading frame 1	0.605	0.0376
226310_at	RICTOR	rapamycin-insensitive companion of mTOR	1.0578	0.001
226312_at	RICTOR	rapamycin-insensitive companion of mTOR	0.6226	0.0052
226313_at	C10orf35	chromosome 10 open reading frame 35	0.6242	0
226327_at	ZNF507	zinc finger protein 507	0.6874	0.0036
226336_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.8729	0.0001
226337_at	SCYL1BP1	SCY1-like 1 binding protein 1	0.783	0.0108
226340_x_at	CXYorf1	CXYorf1-related protein, chromosomes X and Y open reading frame 1, family with sequence similarity 39; member B, family with sequence similarity 39; member D pseudogene, family with sequence similarity 39; member E	0.3513	0.0389

226346_at	MEX3A	mex-3 homolog A (C. elegans)	0.237	0.0208
226347_at			0.8152	0.0167
226348_at			0.9219	0.028
226350_at	CHML	choroideremia-like (Rab escort protein 2)	1.848	0
226355_at	WDR51A	WD repeat domain 51A	0.7982	0.0039
226362_at		Clone HLS_IMAGE_767345 mRNA sequence	0.8142	0.0022
226364_at	HIP1	Huntingtin interacting protein 1	0.7774	0.0103
226365_at		CDNA FLJ40901 fis; clone UTERU2003704, Clone HLS_IMAGE_767345 mRNA sequence	1.3584	0.0003
226368_at	CHST11	Carbohydrate (chondroitin 4) sulfotransferase 11	0.9136	0.0221
226369_at	LOC338799	hypothetical locus LOC338799	0.4497	0.0044
226384_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	0.9262	0.016
226387_at	RSBN1L	round spermatid basic protein 1-like	0.6623	0.0057
226390_at	STARD4	StAR-related lipid transfer (START) domain containing 4	1.4431	0.0103
226391_at		CDNA FLJ36704 fis; clone UTERU2009335	0.6024	0.0289
226397_s_at		Transcribed locus	1.1726	0.0013
226404_at	LOC643167	RNA binding motif protein 39, similar to RNA-binding region-containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1)	0.9427	0.0058
226410_at	LOC348180	hypothetical protein LOC348180	0.5385	0.004
226412_at	SFRS18	splicing factor; arginine/serine-rich 18	1.0481	0.0001
226413_at	LOC400027	hypothetical gene supported by BC047417	0.6348	0.0197
226416_at	THEX1	three prime histone mRNA exonuclease 1	1.0268	0.0013
226418_at	ERGIC2	ERGIC and golgi 2	0.6159	0.0038
226420_at	EVI1	ecotropic viral integration site 1	1.2186	0.0002
226422_at	ERGIC2	ERGIC and golgi 2	0.5747	0
226428_at	TNPO2	transportin 2 (importin 3; karyopherin beta 2b)	0.5502	0.0156
226430_at	RELL1	RELT-like 1	0.6764	0.0312
226432_at	ETNK1	ethanolamine kinase 1	0.8625	0.005
226437_at	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	1.3426	0
226443_at	FAM122A	family with sequence similarity 122A	0.8425	0.0149
226444_at		CDNA FLJ31108 fis; clone IMR322000164	1.2012	0.0006
226456_at	C16orf75	chromosome 16 open reading frame 75	3.3997	0
226458_at		CDNA FLJ30340 fis; clone BRACE2007411	0.8289	0.0225
226463_at	ATP6V1C1	ATPase; H+ transporting; lysosomal 42kDa; V1 subunit C1	0.4658	0.0491

226464_at	C3orf58	chromosome 3 open reading frame 58	0.714	0.0018
226469_s_at	GGTL3	gamma-glutamyltransferase-like 3	0.4316	0.027
226470_at	GGTL3	gamma-glutamyltransferase-like 3	0.9294	0.005
226471_at	GGTL3	gamma-glutamyltransferase-like 3	0.5226	0.0178
226480_at	KIF2A	Kinesin heavy chain member 2A	0.9544	0.0007
226489_at	TMCC3	transmembrane and coiled-coil domain family 3	0.6506	0.0028
226492_at	SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	1.1795	0.0469
226494_at	KIAA1543	KIAA1543	0.3946	0.0285
226497_s_at		CDNA FLJ35153 fis; clone PLACE6010765	1.209	0.0069
226498_at		CDNA FLJ35153 fis; clone PLACE6010765	1.2448	0.0071
226503_at	RIF1	RAP1 interacting factor homolog (yeast)	0.6726	0.0194
226513_at	LOC145758	hypothetical protein LOC145758	0.9335	0.0057
226514_at	ZNF71	zinc finger protein 71	0.3936	0.001
226520_at		Primary neuroblastoma cDNA; clone:Nbla11485	0.9071	0.0046
226531_at	ORAI1	ORAI calcium release-activated calcium modulator 1	0.848	0.0036
226539_s_at			0.3814	0.0061
226546_at		CDNA clone IMAGE:5268696	1.3	0.0006
226548_at	SBK1	SH3-binding domain kinase 1	1.0096	0.0038
226549_at	SBK1	SH3-binding domain kinase 1	0.6034	0.0167
226554_at	ZBTB7A	zinc finger and BTB domain containing 7A	0.7939	0.0013
226562_at	ZSCAN29	zinc finger and SCAN domain containing 29	0.4631	0.028
226569_s_at	CHTF18	CTF18; chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	1.0288	0
226583_at	FLJ40142	FLJ40142 protein	1.705	0
226590_at	ZNF618	zinc finger protein 618	0.7614	0.0197
226592_at	ZNF618	zinc finger protein 618	1.2087	0.0026
226600_at	TMTC3	transmembrane and tetratricopeptide repeat containing 3	1.5942	0
226603_at	SAMD9L	sterile alpha motif domain containing 9-like	1.1329	0.0457
226604_at	TMTC3	transmembrane and tetratricopeptide repeat containing 3	0.6715	0.0143
226608_at	LOC388272	similar to RIKEN cDNA 4921524J17	1.0943	0.0049
226612_at	FLJ25076	similar to CG4502-PA	2.0384	0.0073
226618_at	FLJ25076	similar to CG4502-PA	1.4045	0.007
226619_at	SENP1	SUMO1/sentrin specific peptidase 1	1.1585	0
226628_at	THOC2	THO complex 2	0.9419	0.0009
226630_at	C14orf106	chromosome 14 open reading frame 106	1.4237	0.0002
226639_at	SFT2D3	SFT2 domain containing 3	0.9407	0.0003

226642_s_at	NUDCD2	NudC domain containing 2	0.6969	0.0288
226649_at	PANK1	pantothenate kinase 1	0.7342	0.0183
226651_at	HOMER1	homer homolog 1 (Drosophila)	1.3827	0.0003
226655_at		Full-length cDNA clone CS0DB009YL20 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	0.5591	0.0033
226661_at	CDCA2	cell division cycle associated 2	1.4805	0.0016
226663_at	ANKRD10	ankyrin repeat domain 10	1.7089	0.0004
226666_at		MRNA; cDNA DKFZp564M243 (from clone DKFZp564M243)	0.6837	0.0471
226669_at	USP42	ubiquitin specific peptidase 42	0.9809	0.0009
226698_at	FCHSD1	FCH and double SH3 domains 1	0.3071	0.0187
226699_at	FCHSD1	FCH and double SH3 domains 1	0.1349	0.0467
226705_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	2.3572	0.0001
226720_at	MST101	MSTP101	0.6207	0.0234
226732_at	RBM33	RNA binding motif protein 33	0.4002	0.0289
226747_at	TXNDC16	thioredoxin domain containing 16	0.8771	0.006
226754_at	ZNF251	zinc finger protein 251	0.6284	0.0006
226762_at	PURB	purine-rich element binding protein B	0.9016	0.0041
226764_at	LOC152485	hypothetical protein LOC152485	0.7925	0.0324
226777_at	ADAM12	ADAM metallopeptidase domain 12 (meltrin alpha)	1.3755	0.0125
226779_at		CDNA FLJ37302 fis; clone BRAMY2016009	0.6743	0.0025
226786_at	RFX1	regulatory factor X; 1 (influences HLA class II expression)	0.3834	0.0098
226791_at	KIFC2	kinesin family member C2	1.0919	0.0129
226792_s_at	KIFC2	kinesin family member C2	0.527	0.0319
226807_at	ZFP1	zinc finger protein 1 homolog (mouse)	0.9072	0.0018
226808_at	LOC643641	hypothetical protein LOC643641	1.7922	0
226819_at		CDNA FLJ30735 fis; clone FEBRA2000228	0.3739	0.0108
226823_at	PHACTR4	phosphatase and actin regulator 4	0.6016	0.008
226826_at		CDNA FLJ30735 fis; clone FEBRA2000228	0.9225	0.027
226839_at	TRA16	TR4 orphan receptor associated protein TRA16	0.8702	0
226840_at	H2AFY	H2A histone family; member Y	0.8015	0.0002
226843_s_at	PAPD5	PAP associated domain containing 5	1.863	0
226854_at			0.5578	0.041
226855_at		CDNA FLJ40954 fis; clone UTERU2010525	2.0728	0
226860_at	TMEM19	transmembrane protein 19	1.8861	0
226862_at	MBD1	methyl-CpG binding domain protein 1	0.3028	0.0468
226871_s_at	ATG4D	ATG4 autophagy related 4 homolog D (S. cerevisiae)	0.3378	0.0145

226872_at	RFX2	regulatory factor X; 2 (influences HLA class II expression)	0.345	0.0355
226876_at	FAM101B	family with sequence similarity 101; member B	1.2093	0.0033
226877_at	RPL32P3	ribosomal protein L32 pseudogene 3	0.8209	0.0065
226880_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.3685	0.019
226881_at	GRPEL2	GrpE-like 2; mitochondrial (E. coli)	0.9869	0.0002
226886_at		Clone 114 tumor rejection antigen	0.7975	0.0014
226890_at	WDR35	WD repeat domain 35	0.5224	0.0305
226891_at	C3orf21	chromosome 3 open reading frame 21	0.3566	0.0051
226897_s_at	ZC3H7A	zinc finger CCCH-type containing 7A	1.5094	0.0001
226905_at	FAM101B	family with sequence similarity 101; member B	0.9098	0.0165
226908_at	LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	0.9049	0.002
226912_at	ZDHHC23	zinc finger; DHHC-type containing 23	1.0948	0.0016
226914_at	ARPC5L	actin related protein 2/3 complex; subunit 5-like	0.8571	0.0037
226916_x_at	DPP9	dipeptidyl-peptidase 9	0.3186	0.0475
226927_at	KRTHB5	Keratin; hair; basic; 5	0.4753	0.0208
226936_at	C6orf173	chromosome 6 open reading frame 173	2.85	0
226938_at	WDR21A	WD repeat domain 21A	0.7105	0.0122
226943_at	KRTHB5	Keratin; hair; basic; 5	0.575	0.011
226945_at	RHBDD1	rhomboid domain containing 1	0.7134	0.0051
226947_at	GUSBL2	glucuronidase; beta-like 2	0.5136	0.014
226949_at	GOLGA3	golgi autoantigen; golgin subfamily a; 3	1.1962	0.0004
226961_at	PRR15	proline rich 15	1.3704	0.0176
226964_at		CDNA clone IMAGE:5272626	1.2711	0.0001
226980_at	DEPDC1B	DEP domain containing 1B	2.1631	0.0001
226983_at	ZNF777	zinc finger protein 777	0.3632	0.0029
226986_at	WIPI2	WD repeat domain; phosphoinositide interacting 2	0.926	0.0031
226999_at	RNPC3	RNA-binding region (RNP1; RRM) containing 3	0.5358	0.0025
227004_at		Transcribed locus	1.317	0.0061
227012_at	SLC25A40	solute carrier family 25; member 40	1.0703	0.0015
227016_at	ERICH1	glutamate-rich 1	0.9564	0
227059_at	GPC6	glypican 6	1.432	0.0479
227068_at	PGK1	phosphoglycerate kinase 1	0.6297	0.0039
227069_at		CDNA clone IMAGE:4816860	0.7094	0.019
227072_at	RTTN	rotatin	0.7442	0.0106
227089_at	HBP1	HMG-box transcription factor 1	0.4508	0.0136
227098_at	DUSP18	dual specificity phosphatase 18	0.5308	0.0378
227101_at	ZNF800	zinc finger protein 800	0.6417	0.0091

227102_at	TRIM35	tripartite motif-containing 35	0.5269	0.011
227103_s_at	ECE2	endothelin converting enzyme 2	0.5683	0.0134
227105_at	CSPP1	centrosome and spindle pole associated protein 1	1.4509	0
227106_at	LOC440104	similar to RIKEN cDNA 1110012D08	0.4279	0.0431
227108_at	STARD9	StAR-related lipid transfer (START) domain containing 9	0.2858	0.0184
227117_at		CDNA FLJ40762 fis; clone TRACH2002847	1.1574	0.001
227122_at		Transcribed locus	0.6331	0.0195
227123_at	RAB3B	RAB3B; member RAS oncogene family	1.5488	0.0328
227124_at	LOC221710	Hypothetical protein LOC221710	0.9029	0.0078
227129_x_at	tcag7.907	hypothetical LOC402483	1.3361	0.0003
227133_at	CXorf39	chromosome X open reading frame 39	0.7524	0.0258
227146_at	QSOX2	quiescin Q6 sulfhydryl oxidase 2	1.5737	0.0004
227152_at	C12orf35	chromosome 12 open reading frame 35	0.9442	0.0083
227156_at	TNRC8	trinucleotide repeat containing 8	0.9359	0.0092
227161_at	NOM1	nucleolar protein with MIF4G domain 1	1.0188	0.0007
227162_at	ZBTB26	zinc finger and BTB domain containing 26	0.9642	0.0006
227165_at	C13orf3	chromosome 13 open reading frame 3	0.4473	0.0079
227166_at	DNAJC18	DnaJ (Hsp40) homolog; subfamily C; member 18	0.4769	0.0237
227186_s_at	MRPL41	mitochondrial ribosomal protein L41	0.4688	0.0064
227187_at		Full-length cDNA clone CS0CAP007YE04 of Thymus of Homo sapiens (human)	0.4262	0.0162
227191_at		Transcribed locus	1.1455	0.0057
227196_at	RHPN2	rhophilin; Rho GTPase binding protein 2	0.9265	0.0106
227205_at	TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	0.9323	0.0007
227211_at	PHF19	PHD finger protein 19	1.0472	0.0134
227212_s_at	PHF19	PHD finger protein 19	1.6106	0.0041
227214_at	GOPC	golgi associated PDZ and coiled-coil motif containing	0.566	0.0345
227215_at	GOPC	golgi associated PDZ and coiled-coil motif containing	0.3029	0.0303
227220_at	NFXL1	nuclear transcription factor; X-box binding-like 1	1.2855	0
227223_at	LOC643167	RNA binding motif protein 39, similar to RNA-binding region-containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1)	0.9456	0.0308
227245_at	C12orf30	chromosome 12 open reading frame 30	0.9738	0.0001
227247_at		MRNA; cDNA DKFZp313M1034 (from clone DKFZp313M1034)	2.1064	0
227249_at	NDE1	NudE nuclear distribution gene E homolog 1 (A. nidulans)	1.3187	0

227255_at	PDIK1L	PDLIM1 interacting kinase 1 like	0.5842	0.0131
227256_at	USP31	ubiquitin specific peptidase 31	1.12	0.0006
227257_s_at	C10orf46	chromosome 10 open reading frame 46	0.6883	0.0198
227260_at	ANKRD10	Ankyrin repeat domain 10	1.4752	0.0103
227267_at	C5orf37	chromosome 5 open reading frame 37	2.252	0
227270_at	LOC285550	hypothetical protein LOC285550	0.4759	0.0359
227284_at	ZNF766	zinc finger protein 766	0.5487	0.0028
227285_at	C1orf51	chromosome 1 open reading frame 51	0.8635	0.04
227290_at		CDNA FLJ13598 fis; clone PLACE1009921	1.9072	0.0087
227291_s_at	BOLA3	bolA homolog 3 (E. coli)	0.4287	0.026
227292_at	LOC144097	hypothetical protein BC007540	0.2335	0.0265
227295_at	IKIP	IKK interacting protein	2.2084	0
227301_at	CCT6AP1	chaperonin containing TCP1; subunit 6A (zeta 1) pseudogene 1	1.2114	0
227312_at	SNTB2	syntrophin; beta 2 (dystrophin-associated protein A1; 59kDa; basic component 2)	0.9017	0.0147
227332_at		Full-length cDNA clone CS0DD005YE10 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)	0.2712	0.0184
227348_at	PARS2	prolyl-tRNA synthetase 2; mitochondrial (putative)	0.4555	0.0203
227349_at			0.8343	0.0015
227350_at		CDNA FLJ11381 fis; clone HEMBA1000501	2.4395	0
227363_s_at	COX4NB	COX4 neighbor	0.3704	0.0149
227371_at	BAIAP2L1	BAI1-associated protein 2-like 1	1.28	0.0017
227372_s_at	BAIAP2L1	BAI1-associated protein 2-like 1	1.0113	0.0122
227374_at	EARS2	glutamyl-tRNA synthetase 2; mitochondrial (putative)	0.5897	0.0365
227383_at	LOC727820	hypothetical protein LOC727820	1.3301	0.0018
227384_s_at	LOC727820	hypothetical protein LOC727820	0.9126	0.0324
227402_s_at	C8orf53	chromosome 8 open reading frame 53	0.7452	0.0012
227406_at	GABPB2	GA binding protein transcription factor; beta subunit 2	0.8597	0.0039
227410_at	FAM43A	family with sequence similarity 43; member A	2.1478	0
227415_at	LOC283508	hypothetical protein LOC283508	0.9393	0.0103
227421_at	C21orf57	chromosome 21 open reading frame 57	0.71	0.0091
227426_at		Transcribed locus	0.3633	0.0161
227431_at		CDNA clone IMAGE:4791585	0.6727	0.033
227438_at	ALPK1	alpha-kinase 1	0.6044	0.0202
227445_at	ZNF689	zinc finger protein 689	0.7246	0.0408
227449_at	EPHA4	EPH receptor A4	1.3811	0.0334
227451_s_at	CCDC90A	Coiled-coil domain containing 90A	1.0172	0.0043

227455_at	C6orf136	chromosome 6 open reading frame 136	0.7126	0.0139
227465_at	KIAA0892	KIAA0892	0.451	0.0272
227485_at	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	0.9671	0.0001
227488_at	MGC16121	hypothetical protein MGC16121	3.168	0
227501_at		Transcribed locus	1.3799	0.0087
227504_s_at		MRNA; cDNA DKFZp686F09227 (from clone DKFZp686F09227)	0.6312	0.0042
227505_at		MRNA; cDNA DKFZp686F09227 (from clone DKFZp686F09227)	0.9582	0.0021
227508_at		CDNA FLJ40982 fis; clone UTERU2014601	0.5607	0.0213
227509_x_at		CDNA FLJ40982 fis; clone UTERU2014601	0.5193	0.0129
227510_x_at	PRO1073	PRO1073 protein	1.5037	0.0164
227511_at	SAMD4B	Sterile alpha motif domain containing 4B	0.4972	0.0338
227518_at	SLC35E1	solute carrier family 35; member E1	0.9145	0.0001
227525_at	GLCCI1	glucocorticoid induced transcript 1	1.0131	0.0016
227527_at	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.5917	0.0009
227528_s_at	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.5619	0.0016
227545_at		Transcribed locus	1.8703	0
227551_at	FAM108B1	family with sequence similarity 108; member B1	0.5246	0.0131
227555_s_at	KHSRP	KH-type splicing regulatory protein (FUSE binding protein 2)	0.1839	0.0004
227578_at		CDNA clone IMAGE:5266100	1.0397	0.0003
227580_s_at	DKFZP434B0335	DKFZP434B0335 protein	0.3941	0.0256
227594_at	ZMYM6	zinc finger; MYM-type 6	0.9225	0.0055
227600_at		Full-length cDNA clone CS0DK012YA15 of HeLa cells Cot 25-normalized of Homo sapiens (human)	0.7032	0.0153
227618_at		CDNA FLJ30378 fis; clone BRACE2007953	1.2374	0.035
227628_at	LOC493869	similar to RIKEN cDNA 2310016C16	3.2276	0
227632_at	TBC1D24	TBC1 domain family; member 24	0.5303	0.0089
227637_at	TFCP2	Transcription factor CP2	0.7736	0.0039
227640_s_at	LOC441212	retinitis pigmentosa 9 (autosomal dominant), retinitis pigmentosa 9 pseudogene	0.4913	0.0306
227641_at	FBXL16	F-box and leucine-rich repeat protein 16	2.0999	0.0178
227647_at	KCNE3	potassium voltage-gated channel; Isk-related family; member 3	1.5891	0.0041
227648_at	C22orf32	chromosome 22 open reading frame 32	0.2263	0.0469
227651_at	BTBD14B	BTB (POZ) domain containing 14B	0.6051	0.0072
227663_at		CDNA FLJ40901 fis; clone UTERU2003704	1.1035	0
227670_at	ZNF75A	zinc finger protein 75a	1.3766	0.0001

227671_at	XIST	X (inactive)-specific transcript	2.8202	0.042
227677_at	JAK3	Janus kinase 3 (a protein tyrosine kinase; leukocyte)	1.5745	0.0076
227678_at	XRCC6BP1	XRCC6 binding protein 1	1.2879	0.0043
227687_at	HYLS1	hydrolethalus syndrome 1	1.2166	0.0035
227689_at	ZNF227	zinc finger protein 227	1.2279	0.0009
227698_s_at	RAB40C	RAB40C; member RAS oncogene family	1.0539	0
227706_at	SPIRE2	spire homolog 2 (Drosophila)	0.2093	0.0498
227729_at	ZNF134	Zinc finger protein 134	0.7115	0.0045
227732_at	ATXN7L1	ataxin 7-like 1	0.6888	0.0143
227733_at	TMEM63C	transmembrane protein 63C	1.4182	0.001
227741_at	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member b	0.7996	0.0247
227746_at	ELAVL1	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 1 (Hu antigen R)	0.9662	0.0017
227747_at	MPZL3	myelin protein zero-like 3	0.2918	0.0024
227751_at	PDCD5	Programmed cell death 5	0.6785	0.0225
227754_at		CDNA FLJ10417 fis; clone NT2RP1000112	0.9001	0
227769_at		Transcribed locus	2.1669	0.0064
227796_at	LOC643836	similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3), zinc finger protein 62 homolog (mouse)	1.3887	0.0001
227798_at	SMAD1	SMAD family member 1	0.6457	0.0145
227801_at	TRIM59	tripartite motif-containing 59	2.2493	0
227810_at	ZNF558	zinc finger protein 558	0.6126	0.0114
227815_at		Transcribed locus	0.5809	0.044
227818_at	CCDC21	coiled-coil domain containing 21	1.4844	0.0001
227822_at	ZNF605	zinc finger protein 605	1.3719	0.001
227823_at	RGAG4	retrotransposon gag domain containing 4	1.2235	0.0003
227825_at	C9orf90	chromosome 9 open reading frame 90	0.2515	0.0267
227833_s_at	MBD6	methyl-CpG binding domain protein 6	1.1545	0.0015
227852_at	RP9	retinitis pigmentosa 9 (autosomal dominant)	0.4896	0.0219
227861_at	TMEM161B	transmembrane protein 161B	0.8438	0.0004
227884_at	TAF15	TAF15 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 68kDa	1.5736	0.0008
227891_s_at	TAF15	TAF15 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 68kDa	1.0628	0.0053
227896_at	BCCIP	BRCA2 and CDKN1A interacting protein	1.4235	0.0006
227911_at	ARHGAP28	Rho GTPase activating protein 28	1.092	0.0346
227918_s_at	ZYG11B	zyg-11 homolog B (C. elegans)	0.5834	0.0217
227921_at			3.1053	0

227922_x_at	LOC441124	hypothetical gene supported by AK093729; BX647918	0.498	0.005
227924_at	FLJ20309	hypothetical protein FLJ20309	0.2263	0.0471
227926_s_at	NBPF11	neuroblastoma breakpoint family; member 11	0.7744	0.0361
227927_at		Clone HLS_IMAGE_594438 mRNA sequence	0.5704	0.0166
227928_at	C12orf48	chromosome 12 open reading frame 48	1.4841	0.0002
227936_at	TMEM68	transmembrane protein 68	0.8231	0.0244
227937_at	LOC339344	hypothetical protein LOC339344	0.3178	0.0212
227940_at	LOC339803	Hypothetical protein LOC339803	0.9404	0.0017
227943_at			0.7211	0.0469
227946_at	OSBPL7	oxysterol binding protein-like 7	0.4233	0.0341
227951_s_at	FAM98C	family with sequence similarity 98; member C	0.5122	0.0208
227972_at	TOR2A	torsin family 2; member A	1.334	0.0013
227974_at		Transcribed locus	0.9785	0.0196
227975_at	GPRIN1	G protein regulated inducer of neurite outgrowth 1	0.295	0.0329
227978_s_at	ZADH2	zinc binding alcohol dehydrogenase; domain containing 2	0.4319	0.0254
227980_at	ZNF322A	zinc finger protein 322A	0.3544	0.0126
227982_at		MRNA; cDNA DKFZp434B1417 (from clone DKFZp434B1417)	0.6789	0.0012
227986_at	ZNF343	zinc finger protein 343	0.4361	0.0302
227994_x_at	C20orf149	chromosome 20 open reading frame 149	0.783	0.0036
227999_at	PWWP2	PWWP domain containing 2	0.6581	0.0037
228010_at	PPP2R2C	protein phosphatase 2 (formerly 2A); regulatory subunit B; gamma isoform	2.0088	0.0323
228013_at		MRNA; cDNA DKFZp586F1523 (from clone DKFZp586F1523)	0.7357	0.0141
228014_at	PTRH1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	0.9542	0.011
228026_at	SIKE	suppressor of IKK epsilon	0.531	0.0038
228029_at	ZNF721	zinc finger protein 721	0.8105	0.0037
228033_at	E2F7	E2F transcription factor 7	0.8723	0.003
228047_at	SNORA72	small nucleolar RNA; H/ACA box 72	0.8366	0.0138
228050_at	UTP15	UTP15; U3 small nucleolar ribonucleoprotein; homolog (S. cerevisiae)	0.4323	0.0157
228057_at	DDIT4L	DNA-damage-inducible transcript 4-like	2.0934	0.0143
228058_at	LOC124220	similar to common salivary protein 1	1.8864	0.0119
228061_at	CCDC126	coiled-coil domain containing 126	1.0656	0.0084
228068_at	C10orf132	chromosome 10 open reading frame 132	0.6197	0.0081
228069_at	FAM54A	family with sequence similarity 54; member A	2.4388	0.0001
228073_at	NANP	N-acetylneuraminic acid phosphatase	0.4546	0.0264

228080_at	LAYN	layilin	0.8726	0.0151
228087_at	CCDC126	coiled-coil domain containing 126	0.6988	0.0212
228091_at		Full-length cDNA clone CS0DB009YL20 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	0.6024	0.0429
228099_at	ZNF550	zinc finger protein 550	1.6716	0
228106_at	C4orf30	chromosome 4 open reading frame 30	0.4693	0.0239
228116_at		Clone IMAGE:120162 mRNA sequence	2.2255	0.0003
228122_at	CCDC66	coiled-coil domain containing 66	0.7606	0.0136
228123_s_at	ABHD12	abhydrolase domain containing 12	0.5665	0.0195
228138_at	ZNF498	zinc finger protein 498	0.4964	0.0023
228141_at	LOC493869	Similar to RIKEN cDNA 2310016C16	3.0956	0
228144_at	ZNF300	zinc finger protein 300	1.3344	0.0004
228145_s_at	ZNF398	zinc finger protein 398	0.8688	0.005
228149_at	FLJ31818	hypothetical protein FLJ31818	1.0406	0
228154_at	C19orf44	chromosome 19 open reading frame 44	0.202	0.0216
228156_at		Homo sapiens; clone IMAGE:4346533; mRNA	1.4859	0.0002
228160_at	LOC400642	hypothetical gene supported by BC041875; BX648984	0.4724	0.0281
228168_at	ATP5G3	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit C3 (subunit 9)	0.5922	0.0183
228171_s_at	PLEKHG4	pleckstrin homology domain containing; family G (with RhoGef domain) member 4	2.3704	0.0002
228175_at		CDNA FLJ31660 fis; clone NT2RI2004410	0.6395	0.0342
228189_at	BAG4	BCL2-associated athanogene 4	0.5596	0.0004
228191_at	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	0.959	0.0291
228198_s_at	FAHD2B	Fumarylacetoacetate hydrolase domain containing 2B	0.59	0.0007
228199_at	FAHD2B	Fumarylacetoacetate hydrolase domain containing 2B	0.1936	0.0457
228226_s_at	ZNF775	zinc finger protein 775	0.2111	0.0244
228229_at	ZNF526	zinc finger protein 526	0.2824	0.0155
228235_at	MGC16121	hypothetical protein MGC16121	3.3307	0
228240_at		Full-length cDNA clone CS0DM002YA18 of Fetal liver of Homo sapiens (human)	0.6002	0.0448
228242_at			0.8309	0.0139
228244_at		CDNA clone IMAGE:5736961	0.7659	0.0006
228245_s_at	LOC728715	ovostatin 2, similar to cDNA sequence BC048546	1.5464	0.0032
228250_at	FNIP1	folliculin interacting protein 1	1.376	0.0002
228253_at	LOXL3	lysyl oxidase-like 3	1.1256	0.0281
228257_at	ANKRD52	ankyrin repeat domain 52	0.7708	0.0022

228260_at	ELAVL2	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 2 (Hu antigen B)	1.4591	0.0119
228262_at	MAP7D2	MAP7 domain containing 2	1.5707	0.022
228269_x_at	KCNIP3	Kv channel interacting protein 3; calsenilin	0.7618	0.0051
228273_at		Transcribed locus	3.4724	0
228280_at	ZC3HAV1L	zinc finger CCCH-type; antiviral 1-like	0.8528	0.0406
228281_at	C11orf82	chromosome 11 open reading frame 82	1.2014	0.003
228286_at	FLJ40869	hypothetical protein FLJ40869	1.107	0.0027
228290_at			0.8622	0.0004
228291_s_at	C20orf19	chromosome 20 open reading frame 19	0.4076	0.0413
228295_at	WDR59	WD repeat domain 59	0.2691	0.0303
228305_at	ZNF565	zinc finger protein 565	0.548	0.0432
228308_at	FKBP11	FK506 binding protein 11; 19 kDa	0.6846	0.0043
228318_s_at	CRIPAK	cysteine-rich PAK1 inhibitor	0.8868	0.0269
228320_x_at	CCDC64	coiled-coil domain containing 64	0.926	0.013
228323_at	CASC5	cancer susceptibility candidate 5	2.1756	0.0002
228324_at	C9orf41	chromosome 9 open reading frame 41	0.6572	0.027
228328_at	KLHL28	kelch-like 28 (Drosophila)	0.6195	0.0185
228334_x_at	KIAA1712	KIAA1712	0.8977	0.0008
228336_at	MST101	MSTP101	0.776	0.0032
228337_at	MST101	MSTP101	0.88	0.0003
228346_at		Transcribed locus	1.0392	0.0409
228348_at	LINS1	lines homolog 1 (Drosophila)	0.5785	0.0312
228354_at	C10orf83	chromosome 10 open reading frame 83	0.5626	0.0044
228357_at	UNK	unkempt homolog (Drosophila)	0.8083	0.0158
228358_at	SOX12	SRY (sex determining region Y)-box 12	0.1735	0.0232
228361_at	E2F2	E2F transcription factor 2	0.5155	0.0294
228374_at	C10orf28	chromosome 10 open reading frame 28	0.4253	0.0011
228382_at	FAM105B	family with sequence similarity 105; member B	0.2277	0.038
228392_at	ZNF302	zinc finger protein 302	1.8879	0
228393_s_at	ZNF302	zinc finger protein 302	1.7323	0.0001
228401_at	ATAD2	ATPase family; AAA domain containing 2	1.3772	0.0001
228415_at			1.3404	0.0158
228426_at	CLEC2D	C-type lectin domain family 2; member D	0.1781	0.0393
228427_at	FBXO16	F-box protein 16	0.6243	0.0149
228437_at	CNIH4	cornichon homolog 4 (Drosophila)	0.555	0.029
228443_s_at			0.5068	0.0389

228450_at	PLEKHA7	pleckstrin homology domain containing; family A member 7	0.5057	0.0093
228454_at	LCOR	ligand dependent nuclear receptor corepressor	1.0314	0.0042
228455_at	RBM15	RNA binding motif protein 15	1.1467	0.017
228464_at		Full-length cDNA clone CS0DF007YJ21 of Fetal brain of Homo sapiens (human)	0.8805	0.0038
228468_at	MASTL	microtubule associated serine/threonine kinase-like	1.1793	0.0056
228476_at	KIAA1407	KIAA1407	0.5723	0.0032
228483_s_at	TAF9B	TAF9B RNA polymerase II; TATA box binding protein (TBP)-associated factor; 31kDa	1.7823	0.003
228493_at		Transcribed locus	0.955	0.0031
228495_at	CCDC75	coiled-coil domain containing 75	0.5575	0.013
228499_at	PFKFB4	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 4	2.4497	0.002
228500_at	THAP8	THAP domain containing 8	0.6487	0.0019
228513_at	LOC124446	hypothetical protein BC017488	0.6821	0.0003
228516_at	CDAN1	congenital dyserythropoietic anemia; type I	1.0156	0.002
228519_x_at	CIRBP	cold inducible RNA binding protein	0.4964	0.0089
228522_at	LOC642031	hypothetical protein LOC642031	0.3408	0.0067
228529_at		Transcribed locus	1.5877	0
228537_at	GLI2	GLI-Kruppel family member GLI2	0.4704	0.0271
228539_at		Transcribed locus	0.709	0.0055
228545_at	ZNF148	zinc finger protein 148	0.5058	0.0326
228563_at	GJA7	gap junction protein; alpha 7; 45kDa	0.4253	0.008
228570_at	BTBD11	BTB (POZ) domain containing 11	1.561	0.0368
228571_at	RBAK	RB-associated KRAB zinc finger	0.6967	0.0001
228578_at	RBM45	RNA binding motif protein 45	0.3727	0.0486
228597_at	C21orf45	chromosome 21 open reading frame 45	1.1642	0.001
228613_at	RAB11FIP3	RAB11 family interacting protein 3 (class II)	0.9692	0.018
228619_x_at	TIPRL	TIP41; TOR signaling pathway regulator-like (S. cerevisiae)	0.595	0.0079
228620_at		CDNA FLJ46701 fis; clone TRACH3014063	0.7871	0.0026
228626_at		Transcribed locus	0.2853	0.0269
228630_at	ZNF84	Zinc finger protein 84	0.8711	0.0255
228639_at		Transcribed locus; moderately similar to XP_001372598.1 similar to FYVE; RhoGEF and PH domain containing 1 [Monodelphis domestica]	0.8738	0.0469
228654_at	SPIN4	spindlin family; member 4	1.8451	0
228660_x_at	SEMA4F	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4F	0.3592	0.0307
228663_x_at	FIZ1	FLT3-interacting zinc finger 1	0.1421	0.049

228667_at	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase; delta)	0.4635	0.0203
228680_at	KIF3A	kinesin family member 3A	1.5511	0
228711_at	ZNF37A	zinc finger protein 37A	0.9276	0
228714_at		CDNA FLJ46701 fis; clone TRACH3014063	0.4452	0.0249
228723_at		CDNA FLJ30445 fis; clone BRACE2009238	0.6514	0.032
228725_x_at	PRMT2	protein arginine methyltransferase 2	0.9273	0.0073
228729_at	CCNB1	cyclin B1	3.2148	0
228734_at		CDNA FLJ41934 fis; clone PERIC2005111	0.7274	0.0094
228741_s_at	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	0.6699	0.0035
228745_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing; beta	0.9482	0.0082
228747_at	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)	0.483	0.0112
228748_at	CD59	CD59 molecule; complement regulatory protein	1.2715	0.0158
228751_at	CLK4	CDC-like kinase 4	0.6599	0.034
228755_at	PERQ1	PERQ amino acid rich; with GYF domain 1	0.3414	0.0024
228766_at	CD36	CD36 molecule (thrombospondin receptor)	2.386	0.0007
228768_at	FNIP1	folliculin interacting protein 1	0.352	0.0269
228774_at	CEP78	centrosomal protein 78kDa	0.8623	0.0041
228776_at	GJA7	gap junction protein; alpha 7; 45kDa	3.3547	0
228801_at	ORMDL1	ORM1-like 1 (S. cerevisiae)	0.8317	0.0002
228816_at	LOC92270	hypothetical protein LOC92270	0.7151	0.0334
228835_at		CDNA FLJ33090 fis; clone TRACH2000559	0.7062	0.0147
228841_at	LYRM7	Lyrm7 homolog (mouse)	0.6056	0.0066
228856_at		Transcribed locus	0.7075	0.0123
228859_at	LOC91431	prematurely terminated mRNA decay factor-like	0.9771	0.0005
228864_at	ZNF653	zinc finger protein 653	0.7219	0.0097
228868_x_at	CDT1	Chromatin licensing and DNA replication factor 1	1.9491	0.0008
228899_at	CUL1	Cullin 1	1.1935	0.0001
228906_at	CXXC6	CXXC finger 6	1.1487	0.0097
228907_at		Transcribed locus	0.7269	0.0039
228910_at		Transcribed locus	0.5001	0.0266
228911_at	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif; 7	0.5263	0.0013
228914_at			0.9458	0.005
228919_at			2.1503	0.0063
228920_at	ZNF260	zinc finger protein 260	1.1977	0.0002

228925_at		Transcribed locus; weakly similar to XP_001114229.1 similar to ADAM metallopeptidase domain 30 preproprotein [Macaca mulatta]	1.0361	0.0004
228927_at	ZNF397	zinc finger protein 397	0.8934	0.0024
228929_at	DNASE1	deoxyribonuclease I	0.3657	0.0063
228931_at	COQ4	coenzyme Q4 homolog (S. cerevisiae)	0.8571	0.0263
228935_at	SLC4A8	solute carrier family 4; sodium bicarbonate cotransporter; member 8	1.3193	0.0044
228946_at	INTU	inturned planar cell polarity effector homolog (Drosophila)	0.9427	0.0036
228951_at		Transcribed locus	0.8456	0.002
228958_at	ZNF19	zinc finger protein 19	0.2505	0.0271
228959_at		CDNA clone IMAGE:5262734	1.2645	0.0042
228961_at	MIER3	mesoderm induction early response 1; family member 3	0.3549	0.0209
228962_at		Transcribed locus	0.6762	0.0319
228968_at	ZNF449	zinc finger protein 449	0.5409	0.0057
228982_s_at	USP42	Ubiquitin specific peptidase 42	0.1225	0.003
228986_at	OSBPL8	oxysterol binding protein-like 8	0.9246	0.0074
228991_at		CDNA FLJ27143 fis; clone SPL09242	0.7553	0.0002
228992_at	MED28	Mediator of RNA polymerase II transcription; subunit 28 homolog (S. cerevisiae)	0.5005	0.0217
228993_s_at	LOC92482	hypothetical protein LOC92482	1.0867	0
228999_at	CHD2	chromodomain helicase DNA binding protein 2	0.632	0.024
229000_at	ZNF77	zinc finger protein 77	0.7771	0.0012
229001_at	PPP1R3E	Protein phosphatase 1; regulatory (inhibitor) subunit 3E	1.1414	0.0031
229009_at	SIX5	SIX homeobox 5	0.6666	0.0089
229022_at	ZFX	zinc finger protein; X-linked	0.542	0.0405
229027_at		Transcribed locus	0.7834	0.0027
229033_s_at	MUM1	melanoma associated antigen (mutated) 1	0.8225	0.001
229038_at	CWF19L1	CWF19-like 1; cell cycle control (S. pombe)	0.4843	0.0025
229043_at	PAPD5	PAP associated domain containing 5	0.7307	0.0028
229050_s_at	SNHG7	small nucleolar RNA host gene (non-protein coding) 7	0.8981	0.0047
229052_at	ANKRD23	ankyrin repeat domain 23, ankyrin repeat domain 39	0.3162	0.0141
229061_s_at	SLC25A13	solute carrier family 25; member 13 (citrin)	1.3863	0.0002
229075_at		Transcribed locus	0.6574	0.0002
229081_at	SLC25A13	Solute carrier family 25; member 13 (citrin)	0.2091	0.0267
229082_at	CCDC125	coiled-coil domain containing 125	0.4152	0.0006
229090_at	LOC220930	hypothetical protein LOC220930	1.2445	0.0001
229097_at	DIAPH3	diaphanous homolog 3 (Drosophila)	2.0076	0.0001

229123_at	ZNF225	Zinc finger protein 225	0.8768	0.0012
229126_at	TMEM19	transmembrane protein 19	1.2535	0.0001
229129_at		Transcribed locus	1.2472	0.0013
229133_s_at	ZNF397	zinc finger protein 397	0.2168	0.0425
229139_at	JPH1	junctophilin 1	1.0601	0.0348
229140_at	ZNF579	zinc finger protein 579	0.4416	0.0067
229143_at	CNOT3	CCR4-NOT transcription complex; subunit 3	0.6706	0.0259
229159_at	THSD7A	Thrombospondin; type I; domain containing 7A	0.7303	0.0368
229173_at	KIAA1715	KIAA1715	0.9193	0.0055
229181_s_at	CEP27	centrosomal protein 27kDa	0.5475	0.0263
229206_at		CDNA FLJ13350 fis; clone OVARC1002143	0.9604	0.0007
229220_x_at	NOM1	nucleolar protein with MIF4G domain 1	0.4022	0.0021
229224_x_at	LOC643085	hypothetical LOC643085	0.2155	0.0128
229227_at	FLJ45244	hypothetical locus FLJ45244	0.3086	0.0354
229228_at	CREB5	cAMP responsive element binding protein 5	1.007	0.0097
229231_at	LRRC37B	leucine rich repeat containing 37B	0.7963	0.0027
229243_at		Transcribed locus	0.6573	0.0002
229254_at	MFSD4	major facilitator superfamily domain containing 4	0.534	0.0009
229256_at	PGM2L1	phosphoglucomutase 2-like 1	1.2926	0.0194
229261_at		Transcribed locus	0.5283	0.0178
229268_at	FAM105B	family with sequence similarity 105; member B	1.318	0.0006
229271_x_at	COL11A1	collagen; type XI; alpha 1	1.3434	0.0315
229297_at		Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	0.5766	0.0178
229300_at		CDNA FLJ37366 fis; clone BRAMY2024416	0.9059	0.0422
229304_s_at	MLF1IP	MLF1 interacting protein	0.8684	0.003
229305_at	MLF1IP	MLF1 interacting protein	1.107	0.0061
229315_at		Transcribed locus	0.6969	0.0137
229328_at	ZNF540	Zinc finger protein 540	0.6168	0.021
229336_at	ST3GAL2	ST3 beta-galactoside alpha-2;3-sialyltransferase 2	0.4795	0.0151
229351_at		Chromosome 6 isolate HA_003120 mRNA sequence	0.7336	0.0005
229353_s_at	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.4973	0.0168
229354_at	AHRR	aryl-hydrocarbon receptor repressor	1.1966	0.0235
229357_at	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif; 5 (aggrecanase-2)	0.9761	0.0378
229360_at	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	2.1769	0
229370_at		Transcribed locus	0.6928	0.0404
229388_at		CDNA clone IMAGE:5295564	0.963	0.0004

229394_s_at	GRLF1	glucocorticoid receptor DNA binding factor 1	0.6831	0.0054
229398_at	RAB18	RAB18; member RAS oncogene family	0.8699	0.0161
229399_at	C10orf118	chromosome 10 open reading frame 118	1.0371	0.0027
229400_at	HOXD10	homeobox D10	2.1986	0.0009
229410_at		MRNA; cDNA DKFZp564G0462 (from clone DKFZp564G0462)	0.7685	0.0056
229418_at	C17orf63	chromosome 17 open reading frame 63	0.5603	0.0035
229425_at		Transcribed locus	0.339	0.0061
229434_at		Transcribed locus	0.5755	0.0328
229442_at	C18orf54	chromosome 18 open reading frame 54	1.232	0.001
229455_at		Full length insert cDNA clone YZ04E02	0.753	0.0257
229457_at	ANKHD1	ankyrin repeat and KH domain containing 1	1.0194	0.0003
229467_at	PCBP2	Poly(rC) binding protein 2	1.273	0.0005
229470_at	FAM105B	Family with sequence similarity 105; member B	0.7636	0.0005
229473_at	MAMDC4	MAM domain containing 4	0.8891	0.001
229483_at		CDNA FLJ42331 fis; clone TSTOM2000588	1.8905	0.0002
229490_s_at		Transcribed locus	1.4311	0.001
229504_at		Transcribed locus	0.9835	0.0076
229513_at	STRBP	Spermatid perinuclear RNA binding protein	0.6739	0.0046
229514_at	C14orf118	chromosome 14 open reading frame 118	0.6104	0.0359
229532_at	ZNF502	zinc finger protein 502	0.5362	0.0049
229538_s_at	IQGAP3	IQ motif containing GTPase activating protein 3	1.0429	0.0003
229539_at		Full length insert cDNA clone ZD70D07	0.5853	0.0046
229546_at	LOC653602	hypothetical LOC653602	0.6278	0.0345
229551_x_at	ZNF367	zinc finger protein 367	3.1438	0
229553_at	PGM2L1	phosphoglucomutase 2-like 1	1.5634	0.0072
229558_at		Transcribed locus	0.3777	0.002
229567_at	LOC161247	similar to CG10671-like	1.1536	0.0494
229571_at		Transcribed locus	0.1566	0.0481
229586_at	CHD9	chromodomain helicase DNA binding protein 9	1.0255	0.002
229603_at	BBS12	Bardet-Biedl syndrome 12	0.8118	0.0082
229610_at	CKAP2L	cytoskeleton associated protein 2-like	1.0154	0.0022
229611_at	LMLN	leishmanolysin-like (metallopeptidase M8 family)	0.1893	0.0451
229614_at	ZNF320	zinc finger protein 320	1.012	0.01
229615_at		Transcribed locus	0.8726	0.0025
229618_at	SNX16	sorting nexin 16	1.0982	0.0013
229622_at	FAM132B	family with sequence similarity 132; member B	0.1844	0.0305

229633_at	INTS10	Integrator complex subunit 10	0.5153	0.0189
229656_s_at	FLJ42562	similar to echinoderm microtubule associated protein like 5	1.8072	0.0123
229660_at	C16orf55	chromosome 16 open reading frame 55	0.1654	0.0106
229671_s_at	C21orf45	Chromosome 21 open reading frame 45	0.3125	0.0391
229672_at	C20orf44	Chromosome 20 open reading frame 44	0.7822	0.0252
229673_at		Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	0.5092	0.003
229700_at	ZNF738	zinc finger protein 738	1.6919	0.016
229701_at	DNAJC9	DnaJ (Hsp40) homolog; subfamily C; member 9	0.2975	0.0039
229706_at	TCERG1	transcription elongation regulator 1	0.6594	0.0182
229712_at	SNAPC3	small nuclear RNA activating complex; polypeptide 3; 50kDa	0.5576	0.0305
229751_s_at	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	0.7102	0.0022
229758_at	TIGD5	tigger transposable element derived 5	0.3912	0.0385
229784_at	MGC16121	Hypothetical protein MGC16121	2.0049	0
229785_at	KRIT1	KRIT1; ankyrin repeat containing	0.7158	0.007
229794_at	ZNF585A	zinc finger protein 585A	0.8386	0.0024
229795_at		Transcribed locus	0.7343	0.0026
229800_at	DCLK1	Doublecortin-like kinase 1	0.7787	0.0137
229815_at		CDNA clone IMAGE:4814828	0.7465	0.0496
229829_at	C18orf18	chromosome 18 open reading frame 18	0.4423	0.0221
229855_at	RNF34	ring finger protein 34	0.2381	0.0046
229859_at		MRNA; cDNA DKFZp434E0516 (from clone DKFZp434E0516)	0.2111	0.0318
229869_at		Transcribed locus	0.9784	0.0054
229878_at	KIAA1731	KIAA1731	0.4099	0.0241
229879_at		Transcribed locus	1.5696	0.0065
229882_at	RPS15A	ribosomal protein S15a	0.4	0.0097
229886_at	C5orf34	chromosome 5 open reading frame 34	2.4847	0
229897_at	ZNF641	Zinc finger protein 641	1.1027	0.005
229899_s_at	C20orf199	chromosome 20 open reading frame 199	1.1429	0.0006
229908_s_at	C16orf28	chromosome 16 open reading frame 28	0.5923	0.018
229949_at		Transcribed locus	1.3598	0
229953_x_at	LCA5	Leber congenital amaurosis 5	0.2842	0.038
229962_at	LRRC37A3	leucine rich repeat containing 37; member A3	0.7798	0.0022
229983_at	TIGD2	tigger transposable element derived 2	1.1723	0.0012
230002_at	CLCC1	Chloride channel CLIC-like 1	1.1498	0.0081
230008_at	THSD7A	thrombospondin; type I; domain containing 7A	1.3688	0.0123

230020_at		Transcribed locus	0.4883	0.006
230021_at	C15orf42	chromosome 15 open reading frame 42	0.43	0.0076
230028_at	KIAA0907	KIAA0907	0.4801	0.0274
230047_at	FLJ32810	hypothetical protein FLJ32810	0.7181	0.0222
230058_at	SDCCAG3	serologically defined colon cancer antigen 3	0.5765	0.0043
230063_at	ZNF264	zinc finger protein 264	0.708	0.0144
230064_at		Transcribed locus	0.763	0.012
230069_at	SFXN1	sideroflexin 1	1.4527	0.0011
230075_at	RAB39B	RAB39B; member RAS oncogene family	0.7703	0.0392
230078_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	0.3955	0.0229
230085_at		Transcribed locus	1.3884	0.0042
230091_at		Transcribed locus	0.9694	0.0001
230097_at	GART	Phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	1.2017	0.0117
230106_at	ZXDC	ZXD family zinc finger C	0.5351	0.0007
230108_at	ERCC6	excision repair cross-complementing rodent repair deficiency; complementation group 6	0.2326	0.0148
230141_at	ARID4A	AT rich interactive domain 4A (RBP1-like)	0.83	0.0021
230142_s_at	CIRBP	cold inducible RNA binding protein	1.1213	0.0169
230151_at	C13orf1	chromosome 13 open reading frame 1	0.6226	0.0293
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	2.0353	0.0004
230168_at		Transcribed locus	0.5138	0.0067
230185_at	THAP9	THAP domain containing 9	0.7396	0.0009
230198_at	WDR37	WD repeat domain 37	0.5201	0.0152
230205_at	ZNF561	zinc finger protein 561	0.8768	0.005
230225_x_at		Transcribed locus	0.1212	0.0199
230229_at	DLG1	Discs; large homolog 1 (Drosophila)	1.3619	0.0213
230235_at		Transcribed locus	0.54	0.0017
230255_at	GABRD	gamma-aminobutyric acid (GABA) A receptor; delta	0.2014	0.0065
230256_at	C1orf104	Chromosome 1 open reading frame 104	1.5564	0.0254
230272_at	LOC645323	hypothetical LOC645323	1.8322	0.0084
230277_at			0.5553	0.029
230304_at		CDNA clone IMAGE:30332316	0.9434	0.0031
230312_at		Transcribed locus	1.4021	0.0001
230324_at		Transcribed locus	0.5158	0.0009
230336_at		Transcribed locus	0.5284	0.0017

230337_at	SOS1	son of sevenless homolog 1 (Drosophila)	0.6277	0.0356
230345_at		Transcribed locus	0.8266	0.015
230361_at	KIAA1833	hypothetical protein KIAA1833	0.3131	0.0047
230375_at	SFRS18	splicing factor; arginine/serine-rich 18	0.8587	0.0077
230387_at		Transcribed locus	1.4967	0.0001
230401_at		Transcribed locus	0.3313	0.0061
230402_at	DUSP15	dual specificity phosphatase 15	0.717	0.0179
230404_at			0.3826	0.0253
230411_at		CDNA FLJ41934 fis; clone PERIC2005111	0.643	0.0072
230424_at	C5orf13	chromosome 5 open reading frame 13	2.5785	0
230425_at	EPHB1	EPH receptor B1	1.6701	0.0224
230426_at	DLD	dihydrolipoamide dehydrogenase	0.5486	0.0372
230434_at	PHOSPHO2	phosphatase; orphan 2	0.979	0.0012
230450_at		Transcribed locus; moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]	0.5909	0.0014
230452_at	FLJ42351	hypothetical gene supported by AK124342	0.2662	0.0269
230461_s_at	MUM1	Melanoma associated antigen (mutated) 1	0.5866	0.0062
230462_at	NUMB	numb homolog (Drosophila)	0.6847	0.0025
230483_at		Transcribed locus	0.3339	0.0251
230497_at	BRUNOL5	bruno-like 5; RNA binding protein (Drosophila)	0.4232	0.0041
230516_at	C7orf30	Chromosome 7 open reading frame 30	1.0319	0.0006
230521_at	C9orf100	chromosome 9 open reading frame 100	0.498	0.0165
230522_s_at	C9orf100	chromosome 9 open reading frame 100	0.52	0.0071
230528_s_at	MGC2752	hypothetical protein MGC2752	0.699	0.0074
230533_at	ZMYND8	zinc finger; MYND-type containing 8	0.8547	0.014
230556_at	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.5094	0.0194
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	1.7942	0.0158
230578_at	ZNF471	Zinc finger protein 471	0.8411	0.0272
230579_at	LOC728705	hypothetical protein LOC728705	0.2979	0.0141
230581_at		CDNA FLJ32217 fis; clone PLACE6003771	0.5358	0.0292
230583_s_at	ZNF75	zinc finger protein 75 (D8C6)	0.2368	0.0353
230584_at	ZNF75	zinc finger protein 75 (D8C6)	0.2189	0.0258
230588_s_at	LOC285074	Hypothetical protein LOC285074	0.7069	0.0101
230601_s_at	LRRC46	leucine rich repeat containing 46	0.1932	0.023
230609_at	CLINT1	clathrin interactor 1	0.3697	0.0417
230620_at		Transcribed locus	0.8692	0.012
230629_s_at	EP400	E1A binding protein p400	0.5203	0.0448

230630_at	AK3L2	adenylate kinase 3-like 2	1.7675	0.006
230637_at	SFXN4	Sideroflexin 4	0.6574	0.0125
230647_at	TMEM53	transmembrane protein 53	0.356	0.0123
230651_at		Transcribed locus	1.0175	0.0165
230653_at	LOC728555	hypothetical protein LOC728555, hypothetical protein LOC730391	1.7035	0
230654_at		Transcribed locus	0.4043	0.0139
230664_at	MGC39900	hypothetical protein MGC39900	0.7088	0.0069
230666_at	HOXA11S	homeo box A11; antisense	0.861	0.0307
230676_s_at	TMEM19	transmembrane protein 19	0.417	0.0085
230684_at	GTPBP10	GTP-binding protein 10 (putative)	0.4389	0.0022
230689_at		Transcribed locus	0.4537	0.0162
230696_at		Transcribed locus	0.2048	0.0011
230697_at	BBS5	Bardet-Biedl syndrome 5	0.2612	0.0015
230702_at	C8orf16	chromosome 8 open reading frame 16	0.2844	0.0142
230710_at		CDNA FLJ41489 fis; clone BRTHA2004582	1.5294	0.0088
230725_at			0.1881	0.025
230728_at		Transcribed locus	0.3941	0.0459
230738_at		CDNA clone IMAGE:6342029	0.7947	0.0234
230746_s_at	STC1	Stanniocalcin 1	4.0012	0
230758_at	GEMIN8	gem (nuclear organelle) associated protein 8	0.8586	0.0199
230786_at		Transcribed locus	0.3224	0.0284
230789_at	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	1.8453	0.0001
230792_at	FAAH2	fatty acid amide hydrolase 2	1.1039	0.0087
230803_s_at	ARHGAP24	Rho GTPase activating protein 24	0.4404	0.025
230808_at	FNTA	farnesyltransferase; CAAX box; alpha	0.2071	0.0092
230838_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.3397	0.0071
230843_at		Transcribed locus	0.2646	0.0263
230860_at		Transcribed locus	0.4504	0.0126
230864_at	MGC42105	hypothetical protein MGC42105	1.0451	0.0087
230876_at	LOC169834	hypothetical protein LOC169834	1.0302	0.0122
230882_at	FLJ34048	hypothetical protein FLJ34048	0.729	0.0075
230884_s_at	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	1.4179	0.0008
230885_at	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	0.7957	0.0062
230892_at		Transcribed locus	0.8288	0.0031
230898_at		Transcribed locus	0.1998	0.0295
230904_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	0.7674	0.0047

230906_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	0.7136	0.0221
230920_at	LOC284542	hypothetical protein LOC284542	0.314	0.0401
230927_at		Transcribed locus	0.722	0.0014
230959_at	LOC730453	hypothetical protein LOC730453	1.5772	0.0107
230961_at			1.1958	0.0058
230962_at		Clones 24632 and 24634 mRNA sequence	0.1859	0.0036
230991_at		Transcribed locus	0.7883	0.0051
230998_at		Transcribed locus	1.3018	0.0008
231012_at	TMEM20	transmembrane protein 20	0.2991	0.0342
231024_at	LOC572558	hypothetical locus LOC572558	0.9842	0.0218
231056_at	LOC339352	similar to ATP binding domain 3	0.4643	0.0157
231059_x_at	SCAND1	SCAN domain containing 1	0.3907	0.049
231088_at	LOC340544	Hypothetical protein LOC340544	0.2689	0.0306
231090_s_at	ARID2	AT rich interactive domain 2 (ARID; RFX-like)	0.6665	0.0003
231099_at		MRNA; cDNA DKFZp547C072 (from clone DKFZp547C072)	0.1993	0.0365
231102_at	CROT	carnitine O-octanoyltransferase	0.9199	0.0071
231106_at	BMS1P5	BMS1 pseudogene 5, centaurin; gamma-like family; member 6, centaurin; gamma-like family; member 7	0.9312	0.0013
231108_at	FUS	Fusion (involved in t(12;16) in malignant liposarcoma)	1.0008	0.0195
231115_at		Transcribed locus	0.3005	0.0169
231125_at		CDNA clone IMAGE:4453251	0.2457	0.0069
231131_at	FAM133A	family with sequence similarity 133; member A	1.822	0.0186
231146_at	FAM24B	family with sequence similarity 24; member B	0.6371	0.0003
231149_s_at	ULK4	unc-51-like kinase 4 (C. elegans)	0.4115	0.0033
231152_at	FLJ20309	Hypothetical protein FLJ20309	0.2502	0.0148
231164_at	LOC440331	hypothetical gene supported by AK095200; BC042853	0.7211	0.0308
231165_at		Transcribed locus	0.4175	0.0013
231173_at	LOC642732	pyridine nucleotide-disulphide oxidoreductase domain 1, similar to CG10721-PA	0.3104	0.0285
231175_at	C6orf65	chromosome 6 open reading frame 65	0.4984	0.0324
231183_s_at	JAG1	Jagged 1 (Alagille syndrome)	1.9306	0.0002
231188_at	ZSCAN2	zinc finger and SCAN domain containing 2	0.3418	0.0003
231207_at			1.3591	0.0002
231208_at		CDNA FLJ13245 fis; clone OVARC1000681	0.3016	0.0214
231219_at	CMTM1	CKLF-like MARVEL transmembrane domain containing 1	0.3992	0.0015
231225_at			0.5392	0.0001

231233_at			0.8441	0.03
231235_at	NKTR	natural killer-tumor recognition sequence	0.5058	0.0203
231247_s_at	LOC642441	hypothetical LOC642441, hypothetical protein LOC730256, hypothetical protein LOC730257	0.178	0.0027
231249_at		Transcribed locus; moderately similar to XP_001094962.1 similar to hydroxypyruvate isomerase homolog isoform 5 [Macaca mulatta]	0.3666	0.0161
231282_at	ZCD1	Zinc finger; CDGSH-type domain 1	0.1212	0.0346
231297_at	DOT1L	DOT1-like; histone H3 methyltransferase (S. cerevisiae)	0.4859	0.0231
231316_at		Transcribed locus	0.618	0.0105
231332_at		Transcribed locus	0.6603	0.0001
231374_at		Transcribed locus	0.4182	0.0088
231437_at	SLC35D2	solute carrier family 35; member D2	0.4316	0.0059
231471_at		Transcribed locus	0.2921	0.0174
231487_at	COX8C	cytochrome c oxidase subunit 8C	0.1059	0.0078
231513_at		Transcribed locus	1.4734	0.0018
231560_at			0.1218	0.0341
231569_at	TMEM31	transmembrane protein 31	0.5344	0.0441
231573_at	FATE1	fetal and adult testis expressed 1	2.7019	0.0165
231576_at		Transcribed locus	1.8468	0.001
231609_at	C10orf82	chromosome 10 open reading frame 82	1.96	0.0141
231614_at		Transcribed locus	0.1503	0.0288
231696_x_at	LOC654779	Hypothetical gene LOC654779	0.2124	0.0046
231716_at	RC3H2	ring finger and CCCH-type zinc finger domains 2	0.7478	0.0004
231717_s_at	ZNF226	zinc finger protein 226	0.1238	0.036
231725_at	PCDHB2	protocadherin beta 2	0.8091	0.0269
231726_at	PCDHB14	protocadherin beta 14	0.8694	0.0224
231763_at	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A; 155kDa	0.4511	0.0245
231764_at	CHRAC1	chromatin accessibility complex 1	0.4799	0.0388
231772_x_at	CENPH	centromere protein H	1.7353	0.0001
231775_at	TNFRSF10A	tumor necrosis factor receptor superfamily; member 10a	0.9087	0.0054
231784_s_at	WDSOF1	WD repeats and SOF1 domain containing	0.6318	0.0127
231786_at	HOXA13	homeobox A13	2.5177	0
231787_at	SLC25A27	solute carrier family 25; member 27	0.4227	0.0082
231809_x_at	PDCD7	programmed cell death 7	0.4907	0.0112
231810_at	BRI3BP	BRI3 binding protein	1.1543	0.0007
231819_at		Homo sapiens; clone IMAGE:3885733; mRNA	0.8589	0.0419
231820_x_at	ZNF587	zinc finger protein 587	0.8973	0.001

231821_x_at	FLJ14186	hypothetical LOC402483, hypothetical gene supported by AK024248; AL137733, hypothetical gene supported by AK093729; BX647918, hypothetical protein LOC284701, hypothetical protein LOC728624, hypothetical protein LOC729021, hypothetical protein LOC729033, hypothetical protein LOC731275	0.4738	0.0306
231822_at	CTTNBP2NL	CTTNBP2 N-terminal like	0.4841	0.0371
231825_x_at	ATF7IP	activating transcription factor 7 interacting protein	0.7264	0
231827_at		Full length insert cDNA clone ZE04G11	0.389	0.0136
231829_at	VISA	virus-induced signaling adapter	0.7513	0.0245
231831_at	COX19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.2575	0.0089
231833_at	RBM33	RNA binding motif protein 33	0.1471	0.0316
231837_at	USP28	ubiquitin specific peptidase 28	0.4702	0.0186
231840_x_at	LYRM7	Lyrm7 homolog (mouse)	1.1641	0.0003
231843_at	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	0.8741	0.0021
231844_at	MGC27345	hypothetical protein MGC27345	0.561	0.0004
231845_at	AARS2	alanyl-tRNA synthetase 2; mitochondrial (putative)	0.5977	0.009
231846_at	FOXRED2	FAD-dependent oxidoreductase domain containing 2	0.7066	0.0452
231850_x_at	KIAA1712	KIAA1712	0.517	0.0012
231852_at	THEX1	three prime histone mRNA exonuclease 1	0.5874	0.0033
231855_at	KIAA1524	KIAA1524	1.4145	0.0001
231862_at		CDNA clone IMAGE:4842353	1.7833	0
231866_at	LNPEP	leucyl/cystinyl aminopeptidase	0.5494	0.0349
231869_at	KIAA1586	KIAA1586	0.5855	0.0397
231871_at	GPR180	G protein-coupled receptor 180	0.4347	0.0404
231874_at	FAM126B	family with sequence similarity 126; member B	1.2358	0.0003
231875_at	KIF21A	kinesin family member 21A	0.46	0.0117
231876_at	TRIM56	tripartite motif-containing 56	0.4174	0.026
231878_at	MVP	Major vault protein	0.7428	0.0173
231882_at	FLJ39632	hypothetical LOC642477	3.2448	0
231883_at	FBXW8	F-box and WD repeat domain containing 8	0.6985	0.0009
231886_at	DKFZP434B2016	similar to hypothetical protein LOC284701	0.6869	0.0005
231895_at	SASS6	spindle assembly 6 homolog (C. elegans)	0.621	0.0007
231896_s_at	DENR	density-regulated protein	0.6486	0
231901_at	C19orf52	chromosome 19 open reading frame 52	0.5012	0.0035
231912_s_at	DKFZP434B0335	DKFZP434B0335 protein	0.4277	0.0143
231917_at	GFM2	G elongation factor; mitochondrial 2	0.9861	0.0077

231918_s_at	GFM2	G elongation factor; mitochondrial 2	1.4988	0.0072
231920_s_at	CSNK1G1	casein kinase 1; gamma 1	0.2788	0.0304
231937_at		CDNA FLJ14200 fis; clone NT2RP3002799	0.3961	0.0073
231938_at	SGOL1	Shugoshin-like 1 (S. pombe)	0.4576	0.0024
231939_s_at	BDP1	B double prime 1; subunit of RNA polymerase III transcription initiation factor IIIB	0.4404	0.0004
231954_at	DKFZP434I0714	hypothetical protein DKFZP434I0714	0.4527	0.014
231956_at	KIAA1618	KIAA1618	0.7526	0.0284
231957_s_at	DPP9	dipeptidyl-peptidase 9	0.3814	0.0012
231964_at		MRNA; cDNA DKFZp564H1663 (from clone DKFZp564H1663)	1.2979	0.0061
231965_at	FAM113A	family with sequence similarity 113; member A	0.2082	0.0365
231969_at	STOX2	storkhead box 2	1.2214	0.0195
231972_at		CDNA: FLJ21028 fis; clone CAE07155	0.4291	0.0188
231973_s_at	ANAPC1	anaphase promoting complex subunit 1	1.1043	0.0026
231974_at	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.4144	0.0344
231975_s_at	MIER3	mesoderm induction early response 1; family member 3	0.7815	0.0066
231976_at	LINS1	lines homolog 1 (Drosophila)	0.5522	0.0381
231979_at		CDNA FLJ13266 fis; clone OVARC1000960	0.8343	0.009
231989_s_at	LOC440345	PI-3-kinase-related kinase SMG-1 - like locus, hypothetical protein LOC440345, similar to PI-3-kinase-related kinase SMG-1	1.6678	0
231996_at	N4BP2	Nedd4 binding protein 2	0.5558	0.027
232002_at		MRNA; cDNA DKFZp547I084 (from clone DKFZp547I084)	1.067	0.0082
232012_at	CAPN1	calpain 1; (mu/I) large subunit	0.7285	0.001
232023_at	TMEM67	transmembrane protein 67	0.7933	0.0033
232028_at	ZNF678	Zinc finger protein 678	1.0737	0.0226
232031_s_at	KIAA1632	KIAA1632	0.2938	0.011
232034_at	LOC203274	hypothetical protein LOC203274	0.8526	0.0155
232055_at	LOC732233	hypothetical protein LOC732233, sideroflexin 1	1.43	0
232057_at	SLC7A6OS	solute carrier family 7; member 6 opposite strand	0.4392	0.048
232060_at	ROR1	receptor tyrosine kinase-like orphan receptor 1	1.2247	0.0401
232064_at		CDNA FLJ35001 fis; clone OCBBF2011887	0.7946	0.0291
232065_x_at	CENPL	centromere protein L	1.0983	0.0027
232070_at	LOC644010	hypothetical LOC644010	0.4008	0
232076_at	ZNF707	zinc finger protein 707	0.1736	0.0158
232078_at	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	1.0107	0.0176
232087_at	CXorf23	chromosome X open reading frame 23	0.669	0.0134

232089_at	TIGD7	Tigger transposable element derived 7	0.2178	0.0133
232092_at	MCART1	mitochondrial carrier triple repeat 1	0.2334	0.0155
232094_at		CDNA FLJ11404 fis; clone HEMBA1000749	0.7622	0.0392
232106_s_at	CCDC123	Coiled-coil domain containing 123	0.3502	0.0007
232117_at	ZNF471	zinc finger protein 471	0.3472	0.018
232128_s_at	CLCN5	chloride channel 5 (nephrolithiasis 2; X-linked; Dent disease)	0.1937	0.0138
232135_at	LOC56755	hypothetical protein LOC56755	0.7975	0.0002
232145_at	LOC388969	hypothetical LOC388969	0.9075	0.0054
232146_at	NDUFC1	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 1; 6kDa	0.5169	0.0351
232147_at	BTBD12	BTB (POZ) domain containing 12	0.3769	0.002
232148_at	NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor	0.4876	0.0033
232149_s_at	NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	0.8639	0.0121
232150_at		CDNA clone IMAGE:4792085	1.1973	0
232152_at	C6orf182	chromosome 6 open reading frame 182	0.22	0.0181
232158_x_at	NPAL1	NIPA-like domain containing 1	0.1413	0.0095
232163_at	WDR19	WD repeat domain 19	0.361	0.0136
232167_at	SLC2A11	solute carrier family 2 (facilitated glucose transporter); member 11	0.358	0.045
232168_x_at	MACF1	microtubule-actin crosslinking factor 1	0.26	0.028
232169_x_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8; 23kDa (NADH-coenzyme Q reductase)	0.5707	0.0023
232180_at	UGP2	UDP-glucose pyrophosphorylase 2	1.1404	0.0026
232182_at	LOC286272	hypothetical protein LOC286272	0.8638	0.0021
232194_at	METTL4	methyltransferase like 4	0.438	0.0147
232195_at	GPR158	G protein-coupled receptor 158	1.0378	0.0321
232198_at		CDNA FLJ12676 fis; clone NT2RM4002383	0.2836	0.0316
232204_at	EBF1	early B-cell factor 1	1.3988	0.0252
232215_x_at	PRR11	proline rich 11	0.3579	0.0072
232221_x_at	RSBN1L	round spermatid basic protein 1-like	0.2466	0.0453
232230_at	C10orf75	Chromosome 10 open reading frame 75	0.5715	0.04
232236_at		CDNA: FLJ22146 fis; clone HEP22153	0.3211	0.0003
232238_at	ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	0.8049	0.0042
232247_at	ZNF502	zinc finger protein 502	0.5298	0.0209
232261_at		Homo sapiens; clone IMAGE:5168282; mRNA	0.1308	0.0454
232264_at		CDNA FLJ12142 fis; clone MAMMA1000356	1.0155	0.0075
232266_x_at	CDC2L5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	0.5404	0.0067

232273_at		CDNA: FLJ21850 fis; clone HEP01929	0.4816	0.0122
232278_s_at	DEPDC1	DEP domain containing 1	2.2513	0.0013
232281_at	LOC148189	Hypothetical protein LOC148189	0.2447	0.0199
232288_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.5831	0.0133
232293_at	LCORL	ligand dependent nuclear receptor corepressor-like	0.8033	0.0036
232295_at	GFM1	G elongation factor; mitochondrial 1	0.3217	0.0008
232301_at	UBE3B	ubiquitin protein ligase E3B	0.5562	0
232307_at		CDNA FLJ11492 fis; clone HEMBA1001939	0.8092	0.0238
232315_at	LOC400713	Zinc finger-like	1.3323	0.016
232319_at		CDNA FLJ12360 fis; clone MAMMA1002356	0.3611	0.0093
232327_at	THSD7B	thrombospondin; type I; domain containing 7B	1.0553	0.0105
232338_at		CDNA FLJ11553 fis; clone HEMBA1003034	1.22	0.038
232344_at		CDNA FLJ11750 fis; clone HEMBA1005568	1.6385	0
232346_at		CDNA FLJ13580 fis; clone PLACE1008851	0.2976	0.0485
232347_x_at		CDNA FLJ11379 fis; clone HEMBA1000469	1.0297	0.0003
232351_at		CDNA FLJ12246 fis; clone MAMMA1001343	0.4443	0.0096
232356_at		CDNA FLJ13539 fis; clone PLACE1006640	0.6494	0.0387
232359_at	RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	0.1845	0.0129
232362_at	CCDC18	coiled-coil domain containing 18	0.3515	0.0077
232363_at		CDNA: FLJ20863 fis; clone ADKA01804	0.5379	0.0123
232366_at	KIAA0232	KIAA0232	0.9175	0.0076
232385_x_at		CDNA: FLJ22020 fis; clone HEP08123	0.1504	0.0173
232395_x_at	AGBL3	ATP/GTP binding protein-like 3	0.5665	0.0008
232398_at	FLJ39660	hypothetical protein FLJ39660	0.9699	0.0037
232406_at		CDNA FLJ13731 fis; clone PLACE3000142	1.5408	0.0039
232410_at		MRNA differentially expressed from human RPE cell in differential display experiment	0.313	0.0024
232412_at		CDNA: FLJ21037 fis; clone CAE10055	1.1722	0.0108
232427_at	ZNF224	Zinc finger protein 224	0.6337	0.0009
232431_at		Glucocorticoid receptor alpha mRNA; variant 3' UTR	1.4968	0.0004
232436_at	ZNF274	zinc finger protein 274	0.5665	0.0089
232440_at	ZDHHC13	Zinc finger; DHHC-type containing 13	0.4771	0.0012
232441_at	KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	1.1224	0.0032
232442_at	BCAR1	Breast cancer anti-estrogen resistance 1	0.2314	0.0267

232463_at	CXYorf10	chromosome X and Y open reading frame 10	0.3787	0.003
232469_x_at	C1orf191	Chromosome 1 open reading frame 191	0.2972	0.0009
232478_at		CDNA clone IMAGE:4815026	1.5721	0.0006
232489_at	CCDC76	coiled-coil domain containing 76	0.9883	0.0023
232510_s_at	DPP3	dipeptidyl-peptidase 3	0.5609	0.0417
232523_at	MEGF10	multiple EGF-like-domains 10	2.1382	0.0146
232529_at	SP3	Sp3 transcription factor	0.672	0.0036
232537_x_at	MARK3	MAP/microtubule affinity-regulating kinase 3	0.56	0.0113
232551_at	SLC26A6	solute carrier family 26; member 6	0.525	0.0256
232552_at	DAAM1	Dishevelled associated activator of morphogenesis 1	0.6056	0.0389
232559_at		CDNA FLJ11683 fis; clone HEMBA1004900	0.2064	0.0364
232560_at	UROS	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	0.1594	0.0113
232563_at	ZNF684	zinc finger protein 684	1.1714	0.012
232569_at		CDNA FLJ14193 fis; clone NT2RP3001115	0.7233	0.0006
232579_at		CDNA: FLJ22719 fis; clone HSI14307	0.5416	0.0163
232580_x_at		MRNA; cDNA DKFZp564F1171 (from clone DKFZp564F1171)	0.5022	0.0044
232596_at	DIAPH3	diaphanous homolog 3 (Drosophila)	0.6558	0.0007
232597_x_at	SFRS2IP	Splicing factor; arginine/serine-rich 2; interacting protein	0.6346	0.0334
232599_at	EXOC6	exocyst complex component 6	0.4038	0.0053
232611_at	LOC92497	hypothetical protein LOC92497	0.3097	0.0089
232612_s_at	ATG16L1	ATG16 autophagy related 16-like 1 (S. cerevisiae)	0.2103	0.0359
232615_at		CDNA: FLJ22765 fis; clone KAIA1180	1.3624	0.0015
232627_at		CDNA FLJ11421 fis; clone HEMBA1000991	0.1687	0.0364
232632_at		CDNA FLJ11757 fis; clone HEMBA1005606	0.2348	0.0359
232635_at	C14orf145	chromosome 14 open reading frame 145	0.3504	0.0023
232641_at	ZNF596	zinc finger protein 596	0.7179	0.005
232644_x_at	OCIAD1	OCIA domain containing 1	0.2594	0.0039
232645_at	LOC153684	hypothetical protein LOC153684	0.8621	0.0008
232648_at	PSMA3	proteasome (prosome; macropain) subunit; alpha type; 3	0.2717	0.0013
232661_s_at	DKFZP564O0523	hypothetical protein DKFZp564O0523	0.4413	0.0324
232691_at	SFXN5	sideroflexin 5	0.1771	0.0467
232693_s_at	FBXO16	F-box protein 16, zinc finger protein 395	0.9567	0.0152
232694_at	ZNF395	zinc finger protein 395	0.4902	0.0152
232696_at	LOC648556	uncharacterized gastric protein ZA43P	0.3444	0.0074
232704_s_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	0.3181	0.0316

232710_at		CDNA FLJ11415 fis; clone HEMBA1000942	0.4533	0.001
232740_at	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	0.7004	0.0367
232744_x_at		CDNA FLJ11681 fis; clone HEMBA1004865	0.8234	0.0486
232751_at	RBBP9	retinoblastoma binding protein 9	0.6755	0.0411
232753_at	ZNF346	zinc finger protein 346	0.3377	0.008
232754_at		CDNA FLJ11563 fis; clone HEMBA1003202	0.2814	0
232759_at			0.8584	0.0083
232760_at	TEX15	testis expressed 15	0.7666	0.0463
232768_at	CCNB2	Cyclin B2	0.1685	0.0068
232772_at	LOC221272	hypothetical protein LOC221272	0.1463	0.0458
232773_at		CDNA: FLJ21440 fis; clone COL04389	1.1279	0.0144
232774_x_at	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	0.4278	0.021
232778_at		CDNA: FLJ22383 fis; clone HRC07564	0.5738	0.0043
232779_at		CDNA FLJ20781 fis; clone COL04235	0.1157	0.0494
232784_at		CDNA FLJ12405 fis; clone MAMMA1002838	0.3047	0.0155
232794_at	LOC153682	Hypothetical protein LOC153682	0.5783	0.0002
232796_at		CDNA FLJ11494 fis; clone HEMBA1001942	0.5397	0.0237
232801_at	LOC375748	RAD26L hypothetical protein	0.2698	0.0089
232803_at	FLJ31958	hypothetical protein FLJ31958	0.3176	0.0341
232805_at		CDNA FLJ11973 fis; clone HEMBB1001221	1.6747	0.0179
232814_x_at	C14orf153	Chromosome 14 open reading frame 153	0.3947	0.0081
232816_s_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog; S. cerevisiae), DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11-like, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog; S. cerevisiae)	0.6154	0.0002
232822_x_at	MGC16121	Hypothetical protein MGC16121	0.515	0.0001
232826_at		CDNA FLJ11400 fis; clone HEMBA1000673	0.3576	0.0049
232832_at	DKFZp434J0226	hypothetical gene DKFZp434J0226	0.4064	0.0431
232834_at		CDNA FLJ11994 fis; clone HEMBB1001436	0.6414	0.0005
232859_s_at	MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	0.4959	0.0012
232860_x_at	RBM41	RNA binding motif protein 41	0.5773	0.0153
232861_at	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	1.3263	0.0066
232862_at	ABHD5	Abhydrolase domain containing 5	0.1148	0.0171

232876_at		CDNA: FLJ21881 fis; clone HEP02746	0.639	0.0249
232879_at	CRTC3	CREB regulated transcription coactivator 3	0.6205	0.0285
232885_at	LOC92482	hypothetical protein LOC92482	0.3922	0.0078
232886_at		CDNA FLJ14179 fis; clone NT2RP2003668	0.1171	0.0095
232889_at	GUSBP1	glucuronidase; beta pseudogene 1	1.5256	0
232893_at	LMBRD2	LMBR1 domain containing 2	0.6808	0.0087
232896_at	ERBB2IP	Erbb2 interacting protein	0.4463	0.0005
232910_at	LOC92482	hypothetical protein LOC92482	0.178	0.0103
232911_at	ZFP14	zinc finger protein 14 homolog (mouse)	0.2602	0.0332
232912_at	GPR180	G protein-coupled receptor 180	0.2902	0.0012
232918_at	LOC541471	Hypothetical LOC541471	0.477	0.0015
232931_at	ASCC3L1	activating signal cointegrator 1 complex subunit 3-like 1	0.6858	0.0159
232940_s_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.7455	0.0157
232945_at	CCDC139	Coiled-coil domain containing 139	0.1719	0.0206
232952_at		CDNA FLJ11942 fis; clone HEMBB1000652	0.2778	0.0245
232957_x_at		CDNA FLJ13017 fis; clone NT2RP3000628	0.1674	0.013
232961_at	LOC26010	Viral DNA polymerase-transactivated protein 6	0.1472	0.0284
232962_x_at		CDNA FLJ34323 fis; clone FEBRA2008866	0.1485	0.0321
232964_at	WBSCR19	Williams Beuren syndrome chromosome region 19	0.3852	0.0001
232968_at	FANK1	fibronectin type III and ankyrin repeat domains 1	1.2871	0.0057
232975_at		Homo sapiens; clone IMAGE:6152133; mRNA	0.4757	0.0373
232991_at	ARL17	ADP-ribosylation factor-like 17	0.9839	0.0018
233003_at		CDNA FLJ11942 fis; clone HEMBB1000652	0.6023	0.0052
233013_x_at	LOC220906	hypothetical protein LOC220906	0.4647	0.0021
233014_at		CDNA FLJ12918 fis; clone NT2RP2004580	1.3598	0.0003
233017_x_at		CDNA FLJ12326 fis; clone MAMMA1002132	0.2605	0.0152
233019_at	CNOT7	CCR4-NOT transcription complex; subunit 7	0.9613	0.0005
233024_at		CDNA FLJ11719 fis; clone HEMBA1005275	0.4707	0.0379
233027_at		CDNA FLJ12302 fis; clone MAMMA1001864	0.3642	0.0014
233037_at		Clone FLB2932 mRNA sequence	0.6438	0.0325
233041_x_at		CDNA: FLJ21356 fis; clone COL02831	0.2123	0.0475
233050_at	C6orf174	chromosome 6 open reading frame 174	0.3968	0.0085
233053_at		Transcribed locus	0.2744	0.0157
233056_x_at	DLGAP4	discs; large (Drosophila) homolog-associated protein 4	0.442	0.0315

233057_at	HSPB8	heat shock 22kDa protein 8	0.5872	0.0445
233070_at	ZNF197	zinc finger protein 197	0.4639	0.0053
233080_s_at	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.434	0.0452
233081_at		CDNA FLJ12305 fis; clone MAMMA1001890	0.2824	0.0164
233087_at	FBXL17	F-box and leucine-rich repeat protein 17	0.6814	0.0038
233089_at	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	0.3596	0.041
233090_at		CDNA FLJ11419 fis; clone HEMBA1000985	1.401	0.0378
233097_x_at		CDNA FLJ11133 fis; clone PLACE1006357	0.2472	0.0021
233099_at		MRNA full length insert cDNA clone EUROIMAGE 2005220	0.2051	0.0321
233101_at	MTMR9	myotubularin related protein 9	0.4713	0.0076
233106_at	C14orf82	chromosome 14 open reading frame 82	0.3623	0.0327
233110_s_at	BCL2L12	BCL2-like 12 (proline rich)	1.0034	0.003
233115_at		CDNA FLJ12950 fis; clone NT2RP2005454	0.1594	0.0075
233133_at		Clone 24993 mRNA sequence	0.426	0.0309
233152_x_at		MRNA; cDNA DKFZp564C142 (from clone DKFZp564C142)	0.3483	0.0376
233174_at		CDNA clone IMAGE:5288145	0.2623	0.0037
233182_x_at	ATXN3	Ataxin 3	0.3067	0.0023
233187_s_at		Clone IMAGE:113308 mRNA sequence	0.15	0.0346
233198_at	LOC92497	hypothetical protein LOC92497	1.1011	0.0025
233214_at		CDNA FLJ11900 fis; clone HEMBA1007341	0.7593	0.0022
233219_at		CDNA FLJ13365 fis; clone PLACE1000332	0.5994	0.0167
233224_at		MRNA; cDNA DKFZp586D0924 (from clone DKFZp586D0924)	0.451	0.0243
233229_at	SCFD1	sec1 family domain containing 1	0.1795	0.0202
233230_s_at	SLAIN2	SLAIN motif family; member 2	0.4118	0.0382
233231_at	MCCC2	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0.9441	0.0006
233241_at	C20orf19	chromosome 20 open reading frame 19	0.8059	0.0011
233243_at		CDNA FLJ11533 fis; clone HEMBA1002678	0.4871	0.0013
233251_at	STRBP	Spermatid perinuclear RNA binding protein	0.2251	0.0197
233252_s_at	STRBP	spermatid perinuclear RNA binding protein	0.6206	0.0469
233254_x_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	0.5039	0.037
233263_at		CDNA FLJ12236 fis; clone MAMMA1001244	0.3564	0.0082
233270_x_at		CDNA FLJ12039 fis; clone HEMBB1001930	0.6565	0.0218
233271_at		CDNA FLJ11709 fis; clone HEMBA1005133	0.943	0.0061

233284_at		CDNA FLJ13318 fis; clone OVARC1001600	0.6668	0
233288_at	ATR	ataxia telangiectasia and Rad3 related	0.5141	0.0005
233290_at		CDNA FLJ11451 fis; clone HEMBA1001433	0.4625	0.0015
233292_s_at	ANKHD1	MASK-4E-BP3 alternate reading frame gene, ankyrin repeat and KH domain containing 1	1.3666	0.0013
233295_at		Pheromone receptor (PHRET) pseudogene; partial mRNA sequence	0.1309	0.0034
233300_at		CDNA FLJ11548 fis; clone HEMBA1002944	0.775	0.0366
233313_at		CDNA FLJ14302 fis; clone PLACE2000003	0.3236	0.0434
233319_x_at		CDNA FLJ13845 fis; clone THYRO1000815	0.2629	0.0231
233334_x_at	GIYD1	GIY-YIG domain containing 1, GIY-YIG domain containing 2, sulfotransferase family; cytosolic; 1A; phenol-preferring; member 3, sulfotransferase family; cytosolic; 1A; phenol-preferring; member 4	0.6438	0.0082
233337_s_at	SEZ6L2	seizure related 6 homolog (mouse)-like 2	1.2227	0.0216
233340_at	SPINK5L3	serine PI Kazal type 5-like 3	3.4235	0.0001
233366_at	FBXO4	F-box protein 4	0.2018	0.0015
233369_at		CDNA FLJ11835 fis; clone HEMBA1006595	1.1476	0.0029
233376_at		G protein interaction factor 2-like mRNA sequence	0.2992	0.0091
233399_x_at	LOC441383	Hypothetical gene supported by AF086559; BC065734	0.4046	0.0072
233405_at		CDNA FLJ13333 fis; clone OVARC1001828	0.5291	0.0216
233415_at		Clone IMAGE:246773; mRNA sequence	0.1857	0.0123
233417_at		CDNA FLJ11625 fis; clone HEMBA1004200	0.5918	0.0062
233423_at	KIAA1609	KIAA1609	0.3073	0.0025
233428_at		CDNA: FLJ22144 fis; clone HEP21732	0.2808	0.0001
233431_x_at		Breast cancer estrogen-induced apoptosis 3 mRNA sequence	0.4683	0.003
233436_at	MTBP	Mdm2; transformed 3T3 cell double minute 2; p53 binding protein (mouse) binding protein; 104kDa	0.519	0.0021
233438_at		CDNA FLJ14068 fis; clone HEMBB1001500	0.2464	0.0428
233440_at		CDNA FLJ12367 fis; clone MAMMA1002413	0.6034	0.0123
233445_at		Transcribed locus	0.8018	0.0012
233461_x_at	ZNF226	zinc finger protein 226	1.4072	0
233465_at		CDNA FLJ11300 fis; clone PLACE1009886	0.1317	0.0168
233518_at		CDNA FLJ11493 fis; clone HEMBA1001940	0.7786	0.0013
233532_x_at	IFT52	intraflagellar transport 52 homolog (Chlamydomonas)	0.223	0.0484

233539_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	1.0982	0.0007
233548_at		Clone IMAGE:35115; mRNA sequence	0.2269	0.0053
233555_s_at	SULF2	sulfatase 2	3.4706	0
233557_s_at	MON1B	MON1 homolog B (yeast)	0.7483	0.0015
233571_x_at	C20orf149	chromosome 20 open reading frame 149	0.7293	0.0091
233579_at		CDNA: FLJ22749 fis; clone KAIA0458	0.2224	0.0067
233596_at		Clone FLB2543	0.5475	0.0322
233605_x_at	HNRPM	heterogeneous nuclear ribonucleoprotein M	0.1478	0.0229
233620_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	0.1051	0.0245
233630_at	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.289	0.0152
233635_at		MRNA; cDNA DKFZp564G212 (from clone DKFZp564G212)	0.3109	0.0003
233637_at	WDR42A	WD repeat domain 42A	0.5153	0.0178
233655_s_at	FAM29A	family with sequence similarity 29; member A	0.7559	0.0025
233658_at			0.4083	0.0011
233664_at		CDNA: FLJ22803 fis; clone KAIA2685	0.4162	0.0099
233678_at			0.2807	0.0307
233702_x_at		CDNA: FLJ20946 fis; clone ADSE01819	0.3962	0.005
233713_at		CDNA FLJ12119 fis; clone MAMMA1000092	1.9986	0.0016
233732_at	LOC222159	Hypothetical protein LOC222159	0.3795	0.0119
233742_at	C16orf68	Chromosome 16 open reading frame 68	0.342	0.0017
233750_s_at	C1orf25	chromosome 1 open reading frame 25	0.6397	0.0329
233775_x_at		CDNA FLJ13242 fis; clone OVARC1000578	0.3161	0.0348
233786_at		CDNA FLJ10171 fis; clone HEMBA1003807	0.113	0.0469
233799_at		CDNA FLJ11418 fis; clone HEMBA1000972	0.8605	0.0187
233807_at	ASB7	ankyrin repeat and SOCS box-containing 7	0.1973	0.009
233808_at		CDNA FLJ11984 fis; clone HEMBB1001348	0.205	0.0306
233818_at	ZNF294	zinc finger protein 294	0.1058	0.0229
233819_s_at	ZNF294	zinc finger protein 294	0.8157	0.0303
233827_s_at	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	1.1478	0.0062
233834_at		CDNA: FLJ21392 fis; clone COL03505	0.3627	0.0352
233836_at	TNRC6A	trinucleotide repeat containing 6A	0.3136	0.0061
233841_s_at	SUDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	0.7766	0.0012
233852_at	POLH	polymerase (DNA directed); eta	0.461	0.0139

233864_s_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.4737	0.0009
233869_x_at	DKFZP586B0319	DKFZP586B0319 protein	0.7341	0.0354
233870_at	NAV1	neuron navigator 1	0.2302	0.0379
233873_x_at	PAPD1	PAP associated domain containing 1	0.6141	0.0164
233874_at	SLAIN2	SLAIN motif family; member 2	0.548	0.0082
233882_s_at	SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	0.3622	0.0273
233884_at		Homo sapiens; clone IMAGE:5180231; mRNA	0.344	0.0144
233908_x_at		CDNA FLJ12050 fis; clone HEMBB1002002	0.8016	0.016
233912_x_at		CDNA FLJ11463 fis; clone HEMBA1001608	0.3044	0.0342
233929_x_at	FAM39DP	CXYorf1-related protein, family with sequence similarity 39; member D pseudogene, family with sequence similarity 39; member E, similar to CXYorf1-related protein	0.4728	0.0176
233940_at		CDNA FLJ12739 fis; clone NT2RP2000498	0.4111	0.0403
233945_at	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	0.2067	0.0368
233995_at		Clone HQ0663 PRO0663	1.887	0
233999_s_at	TTC26	tetratricopeptide repeat domain 26	0.8222	0.0006
234001_s_at	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	0.7921	0.0112
234020_x_at		CDNA clone IMAGE:4698949	0.2814	0.0011
234032_at		PRO1550	1.2629	0.0069
234033_at		Clone IMAGE:110218 mRNA sequence	0.3854	0.0304
234040_at	HELLS	helicase; lymphoid-specific	0.2485	0.0016
234042_at	TAS2R45	taste receptor; type 2; member 45	0.4599	0.0168
234059_at		CDNA FLJ12093 fis; clone HEMBB1002603	0.2788	0.0039
234075_at		CDNA FLJ11204 fis; clone PLACE1007810	0.1201	0.0156
234082_at		CDNA FLJ11831 fis; clone HEMBA1006562	1.8652	0.0105
234084_x_at		CDNA FLJ12075 fis; clone HEMBB1002425	0.4613	0.0061
234096_at		CDNA FLJ13767 fis; clone PLACE4000147	0.1699	0.0173
234098_at	SOBP	Sine oculis binding protein homolog (Drosophila)	0.6822	0.0208
234106_s_at	FLYWCH1	FLYWCH-type zinc finger 1	0.6328	0.0361
234111_at	ZNF81	Zinc finger protein 81	0.557	0.0399
234140_s_at	STIM2	stromal interaction molecule 2	0.5052	0.0024
234182_at			0.2566	0.0024
234196_at		CDNA: FLJ21377 fis; clone COL03255	0.2696	0.0365
234210_x_at	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	0.3514	0.0068

234235_at		MRNA; cDNA DKFZp761I2114 (from clone DKFZp761I2114)	0.1182	0.02
234245_at		MRNA; cDNA DKFZp761M2223 (from clone DKFZp761M2223)	0.7857	0.0266
234260_at		MRNA; cDNA DKFZp434E0572 (from clone DKFZp434E0572)	0.6143	0.0077
234294_x_at	GATAD2A	GATA zinc finger domain containing 2A	0.5883	0.0168
234295_at	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	0.4792	0.031
234299_s_at	NIN	ninein (GSK3B interacting protein)	0.4838	0.0051
234304_s_at	IPO11	importin 11	0.6669	0.0325
234311_s_at	GTPBP10	GTP-binding protein 10 (putative)	1.0436	0.0021
234326_at		CDNA: FLJ21248 fis; clone COL01235	0.2965	0.0132
234341_x_at	LOC91548	hypothetical protein LOC91548	0.6855	0
234344_at	RAP2C	RAP2C; member of RAS oncogene family	0.5055	0.0118
234346_x_at		CDNA FLJ11369 fis; clone HEMBA1000338	0.1523	0.005
234423_x_at		CDNA clone IMAGE:4814259	0.3117	0.0168
234428_at		MRNA; cDNA DKFZp564I1316 (from clone DKFZp564I1316)	0.1072	0.0046
234432_at		Metastasis related protein (MB2)	0.1182	0.0303
234445_at	C6orf12	chromosome 6 open reading frame 12	0.3372	0.0101
234459_at	PPHLN1	periphilin 1	0.2689	0.0365
234488_s_at	GMCL1	germ cell-less homolog 1 (Drosophila)	0.5409	0.0041
234491_s_at	SAV1	salvador homolog 1 (Drosophila)	0.4162	0.0393
234549_at		MRNA; cDNA DKFZp586G1917 (from clone DKFZp586G1917)	0.1089	0.0309
234562_x_at	LOC728678	hypothetical protein LOC728678, hypothetical protein LOC731914	0.8224	0.0022
234578_at		MRNA; cDNA DKFZp434E1812 (from clone DKFZp434E1812)	0.1859	0.0117
234604_at		CDNA: FLJ21228 fis; clone COL00739	0.8269	0.003
234628_at		CDNA: FLJ23374 fis; clone HEP16126	0.2396	0.0026
234643_x_at		CDNA: FLJ21798 fis; clone HEP00573	1.7766	0.0113
234654_at		CDNA: FLJ23314 fis; clone HEP11989	0.2198	0.0083
234672_s_at	TMEM48	transmembrane protein 48	0.4994	0.0469
234675_x_at		CDNA: FLJ23566 fis; clone LNG10880	0.3631	0.014
234697_x_at	C3orf31	chromosome 3 open reading frame 31	0.2691	0.0076
234701_at	ANKRD11	ankyrin repeat domain 11	0.5486	0.0035
234723_x_at		CDNA: FLJ21228 fis; clone COL00739	0.9422	0.0002
234725_s_at	SEMA4B	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4B	0.8094	0.0279
234726_s_at	TMEM168	transmembrane protein 168	0.9163	0.0026

234728_s_at	DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	0.5436	0.019
234731_at		CDNA FLJ12366 fis; clone MAMMA1002411	0.3377	0.0131
234733_s_at	FANCM	Fanconi anemia; complementation group M	0.8829	0.0029
234749_s_at	WDR51A	WD repeat domain 51A	0.4257	0.0047
234762_x_at	NLN	Neurolysin (metallopeptidase M3 family)	0.5918	0.0024
234788_x_at		CDNA: FLJ21166 fis; clone CAS10851	0.8169	0.0003
234801_s_at	ACSS1	acyl-CoA synthetase short-chain family member 1	0.6111	0.0105
234805_at		TNF receptor homolog	0.1393	0.0102
234825_at		MRNA; cDNA DKFZp434P1019 (from clone DKFZp434P1019)	0.1348	0.0113
234863_x_at	FBXO5	F-box protein 5	1.0697	0.014
234907_x_at		Mutant DNA polymerase beta	0.1667	0.0132
234915_s_at	DENR	density-regulated protein	1.0236	0.0059
234921_at	ZNF470	zinc finger protein 470	0.3026	0.0173
234941_s_at	GPHN	gephyrin	0.3648	0.0331
234944_s_at	FAM54A	family with sequence similarity 54; member A	0.7471	0.001
234945_at	FAM54A	family with sequence similarity 54; member A	0.2693	0.0001
234949_at	C20orf80	Chromosome 20 open reading frame 80	1.2721	0
234953_x_at	ZNF19	zinc finger protein 19	0.5707	0
234954_at	LOC442262	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	0.9354	0.0005
234976_x_at	SLC4A5	Solute carrier family 4; sodium bicarbonate cotransporter; member 5	0.3229	0.0001
234977_at	ZADH2	zinc binding alcohol dehydrogenase; domain containing 2	0.3915	0.0075
234979_at	BCDIN3D	BCDIN3 domain containing	0.5873	0.0164
234981_x_at	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	0.3492	0.0017
234983_at		Transcribed locus	1.1792	0
234984_at	NEDD1	neural precursor cell expressed; developmentally down-regulated 1	0.9888	0
234988_at	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	0.3252	0.0383
234990_at		CDNA clone IMAGE:4842353	0.4301	0.0413
234991_at		Transcribed locus; strongly similar to XP_001111447.1 transforming growth factor; beta-induced; 68kDa isoform 6 [Macaca mulatta]	0.572	0.0274
234992_x_at	ECT2	epithelial cell transforming sequence 2 oncogene	0.7837	0.0064
234995_at	CCDC52	coiled-coil domain containing 52	0.908	0.0069
235003_at	UHMK1	U2AF homology motif (UHM) kinase 1	0.8124	0.0251
235008_at		CDNA FLJ25241 fis; clone STM02689	0.9351	0.0223

235009_at	FAM44A	family with sequence similarity 44; member A	0.9547	0.003
235023_at	VPS13C	Vacuolar protein sorting 13 homolog C (S. cerevisiae)	1.1031	0.0003
235025_at	WDR89	WD repeat domain 89	0.7812	0.0105
235026_at	FLJ32549	hypothetical protein FLJ32549	1.113	0.0033
235028_at		CDNA FLJ42313 fis; clone TRACH2019425	1.1965	0.002
235029_at	GINS4	GINS complex subunit 4 (Sld5 homolog)	0.2514	0.0007
235030_at	FAM55C	family with sequence similarity 55; member C	0.8834	0.0045
235032_at	DNAJA5	DnaJ homology subfamily A member 5	0.3977	0.0441
235035_at	SLC35E1	solute carrier family 35; member E1	0.9278	0.0004
235039_x_at	LIN9	lin-9 homolog (C. elegans)	0.718	0.0099
235060_at	DKFZp547E087	hypothetical gene LOC283846	2.2756	0
235061_at	PPM1K	protein phosphatase 1K (PP2C domain containing)	0.7408	0.0215
235079_at		Transcribed locus	1.1659	0.0054
235088_at	LOC201725	hypothetical protein LOC201725	2.5061	0
235113_at	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	1.2726	0.0004
235115_at	PDE8B	phosphodiesterase 8B	0.3796	0.0099
235120_at	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	0.1627	0.023
235123_at		Transcribed locus	1.7835	0
235130_at	PANK2	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	0.3056	0.0379
235146_at		Transcribed locus	1.291	0.003
235147_at		CDNA FLJ39330 fis; clone OCBBF2016405	0.8034	0.0417
235152_at		Homo sapiens; clone IMAGE:5218412; mRNA	1.3381	0.0004
235161_at		Homo sapiens; clone IMAGE:3632683; mRNA	0.2217	0.0313
235167_at	DKFZp547E087	hypothetical gene LOC283846	1.4722	0.0001
235170_at	ZNF92	zinc finger protein 92	1.2016	0.0032
235172_at		Transcribed locus	0.4052	0.0374
235174_s_at		CDNA clone IMAGE:5286843	0.9824	0.015
235176_at	ZNF545	zinc finger protein 545	0.7132	0.0148
235178_x_at	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.3021	0.0025
235179_at	ZNF641	zinc finger protein 641	0.779	0.0473
235180_at	LOC730432	serine/threonine/tyrosine interacting protein, similar to serine/threonine/tyrosine interacting protein	0.1946	0.0456
235182_at	C20orf82	chromosome 20 open reading frame 82	1.9259	0.044
235189_at	NARG2	NMDA receptor regulated 2	0.7535	0.0067
235191_at	LOC148189	Hypothetical protein LOC148189	0.4297	0.0443
235200_at	ZNF561	zinc finger protein 561	0.578	0.0215

235202_x_at	IKIP	IKK interacting protein	1.4565	0.0001
235205_at	LOC346887	similar to solute carrier family 16 (monocarboxylic acid transporters); member 14	1.1274	0.0452
235216_at	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.4063	0.0127
235217_at		CDNA clone IMAGE:5302680	0.5587	0.005
235219_at	LOC116349	hypothetical protein BC014011	0.397	0.0364
235222_x_at	BIRC4	baculoviral IAP repeat-containing 4	0.6709	0.0116
235226_at	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	1.0251	0.0005
235234_at	FLJ36874	FLJ36874 protein	0.6106	0.0146
235239_at	QSOX2	quiescin Q6 sulfhydryl oxidase 2	0.3664	0.0058
235241_at	FLJ90709	hypothetical protein FLJ90709	1.61	0
235253_at	RAD1	RAD1 homolog (S. pombe)	0.741	0.0272
235255_at	ATP6V0A2	ATPase; H+ transporting; lysosomal V0 subunit a2	0.4396	0.0058
235258_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	0.9524	0.0045
235263_at	DKFZP434A0131	DKFZp434A0131 protein	0.724	0.001
235266_at	ATAD2	ATPase family; AAA domain containing 2	0.7147	0.0105
235273_at	DYX1C1	dyslexia susceptibility 1 candidate 1	0.3642	0.0301
235286_at		Transcribed locus	1.0688	0.0014
235287_at	CDK6	cyclin-dependent kinase 6	0.6288	0.0246
235288_at		Transcribed locus	0.43	0.0028
235290_at	ZNF782	Zinc finger protein 782	0.6156	0.0017
235294_at	SIKE	suppressor of IKK epsilon	0.7657	0.0043
235302_at		Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	0.6084	0.0237
235304_at		Transcribed locus	0.4639	0.042
235311_at	FKBP14	FK506 binding protein 14; 22 kDa	0.8945	0.0006
235320_at	ARL6	ADP-ribosylation factor-like 6	0.654	0.0173
235321_at		Transcribed locus	0.4149	0.0144
235322_at			0.6744	0.0074
235327_x_at	UBXD4	UBX domain containing 4	0.4627	0.0018
235328_at	PLXNC1	Plexin C1	0.4158	0.0154
235343_at			0.539	0.0267
235345_at	RUFY2	RUN and FYVE domain containing 2	0.1964	0.0177
235354_s_at	RSRC1	Arginine/serine-rich coiled-coil 1	0.2877	0.0113
235363_at		Transcribed locus	1.2231	0.0175
235369_at	C14orf28	chromosome 14 open reading frame 28	0.5055	0.0178
235374_at	MDH1	Malate dehydrogenase 1; NAD (soluble)	1.9312	0
235387_at	GSTCD	glutathione S-transferase; C-terminal domain containing	0.8841	0.0001

235388_at	CHD9	chromodomain helicase DNA binding protein 9	1.2382	0.0027
235390_at	P18SRP	P18SRP protein	1.2354	0.0035
235406_x_at		CDNA clone IMAGE:4814828	0.7997	0.0069
235409_at	MGA	MAX gene associated	0.9646	0.0025
235411_at	PGBD1	piggyBac transposable element derived 1	0.4717	0.0016
235412_at	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	0.5736	0.0113
235414_at	ZNF383	zinc finger protein 383	0.3272	0.0399
235422_at		Full-length cDNA clone CS0DB008YK14 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	0.4621	0.0083
235425_at	SGOL2	shugoshin-like 2 (S. pombe)	2.0245	0.0003
235435_at	AASDH	2-aminoadipic 6-semialdehyde dehydrogenase	0.8096	0.048
235441_at		CDNA FLJ46476 fis; clone THYMU3024879	0.247	0.046
235444_at	FOXP1	forkhead box P1	0.6906	0.0082
235447_at	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	0.7102	0.0328
235452_at		Transcribed locus	0.8192	0.0071
235453_at	TOR1AIP2	torsin A interacting protein 2	0.4333	0.0287
235455_at	FAM131C	family with sequence similarity 131; member C	0.5056	0.0028
235456_at		CDNA clone IMAGE:4819084	1.2275	0.011
235469_at	FAM133B	family with sequence similarity 133; member B, hypothetical protein LOC728153, hypothetical protein LOC728408, hypothetical protein MGC40405 pseudogene	1.0035	0.0005
235470_at		Transcribed locus	1.4399	0
235473_at	MED6	Mediator of RNA polymerase II transcription; subunit 6 homolog (S. cerevisiae)	0.8201	0.0407
235476_at	TRIM59	tripartite motif-containing 59	0.5271	0.0109
235478_at	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog; S. cerevisiae)	0.4801	0.0449
235484_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	1.3694	0.0001
235486_at	C11orf41	chromosome 11 open reading frame 41	0.8757	0.0204
235487_at		Transcribed locus; strongly similar to XP_001154344.1 hypothetical protein [Pan troglodytes]	0.1796	0.0121
235506_at		Periodontal ligament cell specific protein 2 mRNA; partial sequence	0.2308	0.03
235508_at	PML	promyelocytic leukemia	0.3693	0.0031
235511_at		CDNA FLJ36727 fis; clone UTERU2012286	0.3602	0.0411
235516_at	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.3187	0.0011
235532_at		CDNA clone IMAGE:5302913	0.5062	0.0485
235533_at	COX19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.5598	0.0055

235537_at	OCIAD1	OCIA domain containing 1	0.2708	0.0495
235540_at	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	0.266	0.006
235545_at	DEPDC1	DEP domain containing 1	1.7105	0.0007
235551_at	WDR4	WD repeat domain 4	0.3305	0.0017
235555_at		Transcribed locus; weakly similar to XP_001077486.1 hypothetical protein [Rattus norvegicus]	0.6972	0.0054
235572_at	SPC24	SPC24; NDC80 kinetochore complex component; homolog (S. cerevisiae)	0.4696	0.003
235587_at	LOC202781	hypothetical protein LOC202781	0.709	0.0167
235588_at	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.2906	0.0345
235594_at	SCYE1	Small inducible cytokine subfamily E; member 1 (endothelial monocyte-activating)	0.3256	0.0029
235601_at		Transcribed locus	0.7957	0.0103
235604_x_at	ZNF493	zinc finger protein 493	0.5551	0.0216
235606_at	LOC344595	hypothetical LOC344595	0.7325	0.0205
235607_at		Transcribed locus; strongly similar to XP_517193.1 similar to Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) [Pan troglodytes]	0.5115	0.0004
235609_at		Transcribed locus	1.7493	0
235613_at		Transcribed locus	0.7905	0.0285
235618_at	ZNF507	zinc finger protein 507	0.5324	0.0099
235621_at	LOC285014	hypothetical protein LOC285014	0.4898	0.0109
235640_at		Transcribed locus	0.281	0.0159
235645_at	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.7771	0.0047
235650_at	FLJ23834	hypothetical protein FLJ23834	0.1437	0.0104
235652_at		CDNA FLJ37623 fis; clone BRCOC2014013	1.1325	0.0088
235653_s_at	THAP6	THAP domain containing 6	1.0602	0.0009
235678_at	GM2A	GM2 ganglioside activator	0.9638	0.0065
235679_at		CDNA FLJ42928 fis; clone BRSSN2007076	0.4399	0.025
235681_at		CDNA clone IMAGE:4819084	0.9716	0.0079
235690_at	ZNF594	zinc finger protein 594	0.332	0.0282
235693_at		Transcribed locus	2.5635	0
235697_at		Transcribed locus	0.2607	0.0226
235698_at	ZFP90	zinc finger protein 90 homolog (mouse)	1.6473	0.0002
235709_at	GAS2L3	growth arrest-specific 2 like 3	2.6885	0
235717_at	ZNF229	zinc finger protein 229	0.4339	0.0132
235727_at	KLHL28	kelch-like 28 (Drosophila)	1.0164	0.0017
235729_at	ZNF514	zinc finger protein 514	1.0904	0.001
235738_at		Transcribed locus	0.1377	0.0411

235749_at	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	1.3382	0.0064
235752_at		Transcribed locus	0.428	0.0009
235757_at		Transcribed locus	0.6241	0.0466
235758_at	PNMA6A	paraneoplastic antigen like 6A	1.2925	0.0014
235763_at	SLC44A5	solute carrier family 44; member 5	2.5248	0.0014
235784_at		Transcribed locus	0.2738	0.0022
235785_at		CDNA FLJ43152 fis; clone D3OST2003024	0.3218	0.0199
235788_at		Transcribed locus	0.3521	0.0152
235793_at		Transcribed locus	0.2675	0.0313
235796_at		Transcribed locus	0.3892	0.0451
235803_at		Transcribed locus	0.9329	0.015
235804_at		Transcribed locus	0.751	0.0012
235810_at	ZNF182	zinc finger protein 182	0.9051	0.0004
235812_at	TMEM188	transmembrane protein 188	0.4901	0.0253
235822_at	COQ9	coenzyme Q9 homolog (S. cerevisiae)	0.7194	0.0009
235826_at		CDNA FLJ44257 fis; clone TKIDN2015263, MRNA; cDNA DKFZp564E202 (from clone DKFZp564E202)	0.2682	0.0066
235835_at		CDNA FLJ38721 fis; clone KIDNE2010052	0.3097	0.0084
235836_at	FLJ30594	hypothetical locus FLJ30594	1.0425	0.0413
235840_at	C15orf40	chromosome 15 open reading frame 40	0.5163	0.0097
235846_at		CDNA FLJ23692 fis; clone HEP10227	0.7401	0.0474
235851_s_at	GNAS	GNAS complex locus	0.2374	0.021
235868_at	MGEA5	Meningioma expressed antigen 5 (hyaluronidase)	0.3286	0.0029
235880_at	FLJ37078	hypothetical protein FLJ37078	1.8854	0.0001
235884_at		Transcribed locus	0.3704	0.0006
235901_at		Transcribed locus	0.658	0.0146
235902_at		CDNA FLJ42963 fis; clone BRSTN2012380	0.7751	0.0068
235905_at		Transcribed locus	0.6233	0.002
235918_x_at	LRRIQ2	leucine-rich repeats and IQ motif containing 2	0.7257	0.0036
235925_at	TCF12	Transcription factor 12 (HTF4; helix-loop-helix transcription factors 4)	0.7683	0.0359
235926_at		Transcribed locus	1.7001	0
235927_at			3.2541	0
235937_at	LOC647859	occludin pseudogene	0.1437	0.0121
235948_at	FAM80A	family with sequence similarity 80; member A	0.7933	0.0165
235949_at		Transcribed locus	0.8721	0.0008
235952_at		Transcribed locus	0.3063	0.0162

235954_at		Transcribed locus; strongly similar to XP_529692.1 hypothetical protein XP_529692 [Pan troglodytes]	0.483	0.0007
235959_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.7906	0.041
235968_at	CENTG2	centaurin; gamma 2	0.15	0.0407
235969_at	FLJ33996	hypothetical protein FLJ33996	0.414	0.0177
235970_at	LCORL	ligand dependent nuclear receptor corepressor-like	1.9738	0
235971_at		Transcribed locus	0.1918	0.0359
235984_at			0.7735	0.0102
235996_at	RASSF8	Ras association (RalGDS/AF-6) domain family 8	0.2873	0.0202
236000_s_at		Transcribed locus	0.8021	0.0145
236002_at		CDNA FLJ27180 fis; clone SYN02180	0.1633	0.0429
236006_s_at	AKAP10	A kinase (PRKA) anchor protein 10	0.5268	0.0223
236017_at	CDKL3	cyclin-dependent kinase-like 3	0.3013	0.0004
236018_at			0.26	0.0233
236026_at	GPATCH2	G patch domain containing 2	0.8243	0.0006
236034_at			2.7115	0
236046_at	FLJ44896	FLJ44896 protein	0.7478	0.0448
236047_at	C8orf5	chromosome 8 open reading frame 5	0.8019	0.0056
236060_at		Transcribed locus	0.2802	0.0192
236092_at		CDNA clone IMAGE:4791941	0.3722	0.0299
236097_at		CDNA FLJ25731 fis; clone TST05584	0.7666	0.0243
236103_at		Transcribed locus	0.2764	0.0432
236104_at		CDNA FLJ35303 fis; clone PROST2009571	0.7214	0.0076
236106_at		Transcribed locus	0.3416	0.0171
236122_at		Transcribed locus	0.6186	0.0202
236126_at	ACVR2B	activin A receptor; type IIB	0.763	0.0086
236134_at	WDR68	WD repeat domain 68	0.5844	0.0086
236138_at		CDNA FLJ37302 fis; clone BRAMY2016009	0.2583	0.0211
236149_at		Transcribed locus	1.4632	0.0003
236156_at	LIPA	lipase A; lysosomal acid; cholesterol esterase (Wolman disease)	0.5113	0.0387
236165_at	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	0.2319	0.0441
236179_at		Transcribed locus	2.0989	0.0183
236180_at		Transcribed locus	0.8736	0.0442
236194_at		Transcribed locus; moderately similar to NP_001018860.1 protein LOC401398 [Homo sapiens]	0.6097	0.0101
236207_at	SSFA2	sperm specific antigen 2	0.388	0.02
236210_at		Transcribed locus	0.4226	0.0128
236215_at			0.7067	0

236217_at	SLC31A1	solute carrier family 31 (copper transporters); member 1	0.8166	0.0269
236219_at	TMEM20	transmembrane protein 20	0.4278	0.0255
236227_at	TMEM161B	transmembrane protein 161B	1.2577	0.0002
236229_at		Transcribed locus	1.6141	0.0002
236237_at		Transcribed locus	0.3417	0.0066
236241_at	MED31	mediator complex subunit 31	0.9866	0.0013
236246_x_at	LOC653160	Hypothetical protein LOC653160	0.1459	0.0086
236249_at	IKIP	IKK interacting protein	1.8342	0
236259_at	STK4	serine/threonine kinase 4	0.9301	0.0001
236261_at		CDNA FLJ41254 fis; clone BRAMY2033594	1.2788	0.0004
236267_at	ZNF346	zinc finger protein 346	0.9071	0.0001
236274_at	EIF3B	eukaryotic translation initiation factor 3; subunit B	0.4173	0.016
236282_at		CDNA clone IMAGE:4826240	0.844	0.003
236288_at	RNF34	ring finger protein 34	0.591	0
236291_at	RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	0.327	0.0264
236300_at		CDNA FLJ37884 fis; clone BRSTN2012451	0.5687	0.0247
236305_at	RFESD	Rieske (Fe-S) domain containing	0.4024	0.0051
236310_at		Transcribed locus	0.3158	0.0028
236312_at		Transcribed locus	1.0455	0
236314_at		Transcribed locus	0.6488	0.0052
236322_at		Transcribed locus	1.1826	0.028
236346_at		Transcribed locus	1.5479	0.0002
236353_at		CDNA FLJ43467 fis; clone OCBBF2036752	0.4228	0.0063
236354_at		Transcribed locus	0.1262	0.0315
236368_at	KIAA0368	KIAA0368	0.9475	0.0037
236379_at			0.7585	0.0165
236390_at	C20orf94	chromosome 20 open reading frame 94	0.4171	0.0471
236408_at		Transcribed locus	0.2964	0.002
236409_at		Transcribed locus	0.5259	0.0376
236411_at		Transcribed locus	0.4974	0.0466
236428_at		Transcribed locus	0.3932	0.0341
236429_at		Homo sapiens; clone IMAGE:4423835; mRNA	1.5528	0.0002
236431_at	SR140	U2-associated SR140 protein	0.2465	0.0496
236435_at			0.9067	0.0086
236458_at		Transcribed locus	0.456	0.0039
236462_at		Transcribed locus	1.0711	0.0082
236469_at		MRNA full length insert cDNA clone EUROIMAGE 110216	0.292	0.0103
236472_at		Transcribed locus	0.5035	0.0431

236474_at		Transcribed locus	1.4663	0.0007
236480_at		CDNA FLJ41489 fis; clone BRTHA2004582	0.8937	0.0477
236487_at	SCLT1	sodium channel and clathrin linker 1	0.5605	0.0074
236488_s_at		CDNA FLJ36309 fis; clone THYMU2004986	0.9229	0.0009
236494_x_at		CDNA clone IMAGE:5175565	0.6783	0.0005
236500_at		Transcribed locus	0.3035	0.044
236502_at			0.2229	0.0141
236503_at		Transcribed locus	0.4224	0.0231
236517_at	MEGF10	multiple EGF-like-domains 10	2.5874	0.0005
236533_at	DDEF1	development and differentiation enhancing factor 1	0.3729	0.0379
236535_at	SMC6	structural maintenance of chromosomes 6	0.3491	0.0045
236589_at			0.1503	0.0375
236605_at	EIF3K	eukaryotic translation initiation factor 3; subunit K	0.3262	0.0017
236607_at		Transcribed locus	0.2588	0.0221
236610_at		Transcribed locus	1.0286	0.0261
236612_at		Transcribed locus	0.1213	0.0391
236613_at	RBM25	RNA binding motif protein 25	0.2571	0.0488
236619_at		Transcribed locus	0.6394	0.0001
236620_at	RIF1	RAP1 interacting factor homolog (yeast)	0.9098	0.0161
236634_at	C8orf48	chromosome 8 open reading frame 48	0.5693	0.0085
236635_at	ZNF667	zinc finger protein 667	1.1247	0.0336
236637_at		Transcribed locus	0.3823	0.0027
236641_at	KIF14	kinesin family member 14	2.2607	0.0003
236659_x_at		Transcribed locus	0.4852	0.0015
236664_at	AKT2	v-akt murine thymoma viral oncogene homolog 2	0.3874	0.0288
236671_at			0.2313	0.0468
236676_at		Transcribed locus	0.3102	0.0008
236692_at	LOC729839	similar to DTW domain containing 2	0.4943	0.0306
236696_at	SR140	U2-associated SR140 protein	0.8714	0.0165
236719_at		Transcribed locus; moderately similar to XP_001086437.1 hypothetical protein [Macaca mulatta]	0.2368	0.0274
236751_at		Transcribed locus	0.2075	0.0424
236752_at		Transcribed locus	0.868	0.0073
236766_at		Transcribed locus	0.5345	0.0206
236777_at		Full-length cDNA clone CS0DF025YH20 of Fetal brain of Homo sapiens (human)	0.6142	0.0104
236778_at		Transcribed locus	0.6689	0.0377
236780_at		Transcribed locus	0.2599	0.0453

236808_at	FGFR1OP2	FGFR1 oncogene partner 2	0.9436	0.0056
236811_at	DMRTC2	DMRT-like family C2	0.1164	0.0005
236816_at	C12orf30	chromosome 12 open reading frame 30	0.8638	0.0115
236837_x_at	LOC650794	Similar to FRAS1-related extracellular matrix protein 2 precursor (ECM3 homolog)	0.5993	0.0174
236841_at	FAM39DP	Family with sequence similarity 39; member D pseudogene	0.907	0.002
236852_at	FBXO43	F-box protein 43	0.3446	0.0081
236862_at	GOPC	Golgi associated PDZ and coiled-coil motif containing	0.4916	0.0013
236875_at		Transcribed locus	0.5985	0.0024
236879_at		Transcribed locus	0.5687	0.0123
236880_at	RAD52	RAD52 homolog (S. cerevisiae)	0.1035	0.046
236883_at		Transcribed locus	0.7011	0.0033
236910_at	MRPL39	Mitochondrial ribosomal protein L39	0.8078	0.0211
236911_at	FAM80B	Family with sequence similarity 80; member B	0.2507	0.0453
236915_at			1.5122	0.0161
236923_x_at			0.8403	0.0175
236924_at	GLMN	glomulin; FKBP associated protein	0.9561	0.0136
236930_at	NUMB	Numb homolog (Drosophila)	0.2652	0.0125
236935_at		CDNA clone IMAGE:4813920	0.2296	0.0357
236953_s_at	RP11-50D16.3	similar to RIKEN cDNA 8030451K01	0.7385	0.0058
236955_at		Transcribed locus	0.4031	0.0076
236957_at	CDCA2	cell division cycle associated 2	0.632	0.0164
236961_at		Transcribed locus	0.646	0.0185
236969_at		Transcribed locus	0.3469	0.0221
236985_at		CDNA FLJ37855 fis; clone BRSSN2014636	0.2722	0.0204
236999_at		CDNA FLJ33156 fis; clone UTERU2000377; weakly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C57A10.03 (EC 5.2.1.8)	0.2776	0.0426
237005_at	LOC442075	weakly similar to serine/threonine protein kinase Kp78	0.4428	0.0098
237034_at		Full-length cDNA clone CS0DC025YP03 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	0.6491	0.0251
237051_at		Transcribed locus	0.5175	0.048
237061_at	ZNF347	zinc finger protein 347	0.2865	0.0068
237067_at			0.2173	0.0272
237071_at		Transcribed locus	0.1349	0.0222
237106_at	SLC11A2	Solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	0.4489	0.0119
237110_at		Transcribed locus	0.2389	0.0125

237114_at		Transcribed locus	0.1148	0.0435
237116_at	LOC646903	hypothetical LOC646903	0.5585	0.002
237130_at		Transcribed locus	0.1234	0.0375
237145_at	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	0.2711	0.0138
237158_s_at	MPHOSPH9	M-phase phosphoprotein 9	0.8127	0.0146
237173_at	LOC647500	similar to phosphodiesterase 4D interacting protein isoform 1	0.1168	0.0375
237182_at	LOC653479	Similar to mitochondrial ribosomal protein L45	0.1229	0.0232
237184_at			0.2263	0.0077
237195_at		Transcribed locus	0.133	0.0265
237198_at		Transcribed locus	0.3477	0.0039
237208_at	WDR61	WD repeat domain 61	0.484	0.0032
237215_s_at	TFRC	transferrin receptor (p90; CD71)	0.869	0.0475
237232_at		Transcribed locus	0.2117	0.0375
237246_at		Transcribed locus	1.3485	0.0001
237261_at			1.3581	0
237301_at		Transcribed locus	0.8434	0.0424
237304_at	SYCE2	synaptonemal complex central element protein 2	0.4688	0.0264
237309_at		Transcribed locus	0.2893	0.0231
237330_at		Transcribed locus	0.9043	0.0045
237369_at		Transcribed locus	0.2164	0.0049
237376_at			0.2738	0.0037
237388_at	GLMN	glomulin; FKBP associated protein	0.7762	0.0004
237411_at	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif; 6	0.9786	0.0018
237418_at	CDK5RAP2	CDK5 regulatory subunit associated protein 2	0.5862	0.0008
237441_at			0.7481	0.0425
237456_at		Transcribed locus	0.7986	0.0148
237459_at			0.4336	0.0346
237475_x_at	SEPP1	Selenoprotein P; plasma; 1	0.5205	0.0034
237483_at		Transcribed locus	1.4484	0.008
237502_at	CRLS1	Cardiolipin synthase 1	0.4504	0.011
237504_at	INTS10	integrator complex subunit 10	0.2413	0.0425
237530_at		Transcribed locus	3.1189	0.0008
237560_at	MRPS5	mitochondrial ribosomal protein S5	0.361	0.0216
237577_at	LOC729298	PEST proteolytic signal containing nuclear protein, hypothetical protein LOC729298	0.5361	0.0234
237585_at			0.5694	0.0298
237591_at	FLJ42957	FLJ42957 protein	0.9328	0.0171
237600_at		Transcribed locus	1.0942	0.0024
237626_at		Transcribed locus	1.5069	0.0007

237632_at			0.347	0.0129
237671_at		Transcribed locus	0.1744	0.0176
237681_at		Transcribed locus; weakly similar to NP_001039706.1 protein LOC518880 [Bos taurus]	0.4335	0.0004
237689_at	SARS	Seryl-tRNA synthetase	0.4294	0.01
237725_x_at	SMC5	structural maintenance of chromosomes 5	0.3207	0.0004
237737_at	LOC375010	hypothetical LOC375010, hypothetical LOC401131, hypothetical LOC643166, hypothetical LOC643579, hypothetical protein LOC728295, hypothetical protein LOC728364, hypothetical protein LOC728384, hypothetical protein LOC728759, hypothetical protein LOC728783, similar to Ankyrin repeat domain-containing protein 18A	3.4826	0.0004
237741_at	SLC25A36	Solute carrier family 25; member 36	0.8546	0.0059
237746_at	SFRS11	Splicing factor; arginine/serine-rich 11	0.3763	0.0256
237750_at	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3; putative	0.2884	0.0135
237783_at	PLAC8L1	PLAC8-like 1	0.1859	0.0255
237802_at	XKR4	XK; Kell blood group complex subunit-related family; member 4	1.6075	0.034
237803_x_at		Transcribed locus	0.5807	0.0427
237863_at	TMPO	thymopoietin	0.228	0.0053
237868_x_at		Transcribed locus	0.5691	0.0093
237878_at			0.282	0.014
237884_x_at	TRPM7	transient receptor potential cation channel; subfamily M; member 7	0.5465	0
237942_at		Transcribed locus; strongly similar to XP_001115106.1 similar to SNF related kinase isoform 1 [Macaca mulatta]	0.2004	0.0068
237943_at			0.2686	0.0254
237951_at			0.1892	0.0158
237972_at			0.1378	0.0047
237984_x_at		Transcribed locus	0.1251	0.0372
237999_at			0.3458	0.0116
238000_at		Transcribed locus	1.0091	0.0004
238012_at	DPP7	Dipeptidyl-peptidase 7	0.7713	0.022
238015_at	LOC201725	hypothetical protein LOC201725	1.575	0.0003
238021_s_at	hCG_1815491	hCG1815491	2.9658	0
238022_at	hCG_1815491	hCG1815491	2.0594	0
238037_at	LMLN	leishmanolysin-like (metallopeptidase M8 family)	0.2469	0.0125
238042_at		Transcribed locus	0.9707	0.0028
238070_at	CHD1L	Chromodomain helicase DNA binding protein 1-like	0.6024	0.0438

238075_at		Transcribed locus	1.4454	0.0001
238098_at		Transcribed locus	0.5365	0.0212
238108_at		Transcribed locus	0.7685	0.0163
238109_at		Homo sapiens; clone IMAGE:4346533; mRNA	0.6128	0.0049
238114_at	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.4901	0.0132
238119_at		Transcribed locus	0.6889	0.0022
238122_at	RBM12B	RNA binding motif protein 12B	0.8778	0.0001
238130_at	NFATC2IP	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 2 interacting protein	0.2286	0.0406
238137_at		Transcribed locus	0.154	0.0026
238142_at		CDNA FLJ37584 fis; clone BRCOC2004950	1.0958	0.0003
238146_at		Transcribed locus	0.4348	0.0179
238149_at	ZNF818	zinc finger protein 818	0.5171	0.0375
238154_at	CEP70	Centrosomal protein 70kDa	0.4102	0.0353
238174_at		Transcribed locus	0.6405	0.0035
238176_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.5466	0.0169
238193_at		Transcribed locus	0.4332	0.0381
238220_at	UTX	ubiquitously transcribed tetratricopeptide repeat; X chromosome	0.2715	0.0031
238229_at	TMEM67	Transmembrane protein 67	0.3462	0.0448
238231_at	NFYC	Nuclear transcription factor Y; gamma	0.2339	0.0194
238279_x_at			0.6814	0.001
238295_at	C17orf42	Chromosome 17 open reading frame 42	0.5835	0.0064
238297_at			0.6048	0.0423
238299_at			0.7755	0.0027
238311_at		Transcribed locus	0.9712	0.007
238315_s_at	ZNF567	zinc finger protein 567	0.7139	0.013
238320_at	TncRNA	trophoblast-derived noncoding RNA	1.3891	0.0043
238337_s_at	DNAJA5	DnaJ homology subfamily A member 5	1.3312	0
238341_at			0.9221	0.0001
238342_at			0.5033	0.0109
238346_s_at	TGS1	trimethylguanosine synthase homolog (S. cerevisiae)	0.8203	0.0078
238350_at	FLJ25778	hypothetical protein FLJ25778	0.6272	0.0095
238412_at	CDR2	Cerebellar degeneration-related protein 2; 62kDa	0.8225	0.0045
238416_x_at	NHN1	conserved nuclear protein NHN1	0.1886	0.0297
238418_at	SLC35B4	solute carrier family 35; member B4	0.9675	0.0031
238421_at	RC3H2	Ring finger and CCCH-type zinc finger domains 2	0.6796	0.0097
238427_at	GRPEL2	GrpE-like 2; mitochondrial (E. coli)	0.424	0.0066

238435_at			0.738	0.0001
238437_at	ZNF805	zinc finger protein 805	0.5078	0.0292
238444_at	ZNF618	zinc finger protein 618	1.1697	0.0007
238449_at	LOC595101	PI-3-kinase-related kinase SMG-1 pseudogene	1.334	0.0003
238457_at		CDNA FLJ33029 fis; clone THYMU2000162	0.1737	0.0406
238464_at	ANKRD36	KIAA1641, ankyrin repeat domain 36, similar to ankyrin repeat domain 36, similar to protein immuno-reactive with anti-PTH polyclonal antibodies	0.3541	0.0002
238466_at		CDNA FLJ33443 fis; clone BRALZ1000103	0.9879	0.0336
238475_at	ALG10B	asparagine-linked glycosylation 10 homolog B (yeast; alpha-1;2-glucosyltransferase)	0.5724	0.0029
238484_s_at		MRNA; clone CD 43T7	0.8519	0.009
238490_at	KIAA2026	KIAA2026	0.4185	0.0317
238495_at		CDNA FLJ41444 fis; clone BRSTN2001801	0.3532	0.022
238496_at		Transcribed locus	1.1627	0.0001
238508_at	DBF4B	DBF4 homolog B (S. cerevisiae)	0.4046	0.0295
238511_at	LOC440288	Similar to FLJ16518 protein	0.2248	0.0393
238525_at	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	0.3204	0.0082
238529_at		CDNA clone IMAGE:6342029	0.6371	0.0341
238530_at			0.5851	0.0117
238535_at	CEP152	centrosomal protein 152kDa	0.2706	0.0388
238536_at		CDNA FLJ13474 fis; clone PLACE1003593	1.2129	0.0044
238538_at	ANKRD11	ankyrin repeat domain 11	0.3657	0.0142
238542_at	ULBP2	UL16 binding protein 2	2.4076	0.0004
238548_at		Transcribed locus	0.2158	0.0271
238549_at	CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	2.2724	0
238551_at	FUT11	fucosyltransferase 11 (alpha (1;3) fucosyltransferase)	0.8485	0.0055
238553_at	BMS1P5	BMS1 pseudogene 5, centaurin; gamma-like family; member 2, centaurin; gamma-like family; member 9 pseudogene, hypothetical protein LOC643564	0.2565	0.0368
238562_at		Full-length cDNA clone CS0DI039YF12 of Placenta Cot 25-normalized of Homo sapiens (human)	0.4135	0.0363
238563_at		Transcribed locus	0.9384	0.0027
238571_at		Transcribed locus	1.2461	0
238575_at	OSBPL6	oxysterol binding protein-like 6	1.5255	0.0028
238578_at	TMEM182	transmembrane protein 182	0.2283	0.011
238589_s_at		Transcribed locus	1.0222	0.0001

238593_at	C11orf80	chromosome 11 open reading frame 80	1.2052	0.0029
238596_at	C10orf4	chromosome 10 open reading frame 4	0.2401	0.0316
238610_s_at		Transcribed locus	0.7	0.0129
238611_at		Transcribed locus	0.6215	0.0339
238612_at		Transcribed locus	0.564	0.0142
238614_x_at	ZNF430	zinc finger protein 430	0.9685	0.0076
238620_at		Transcribed locus	0.3632	0.0031
238630_at	OPA3	optic atrophy 3 (autosomal recessive; with chorea and spastic paraplegia)	0.497	0.0117
238635_at	C5orf28	chromosome 5 open reading frame 28	2.0817	0
238637_at		Transcribed locus	0.46	0.0016
238653_at		CDNA FLJ43454 fis; clone OCBBF2034906	0.6178	0.0203
238654_at	LOC147645	hypothetical protein LOC147645	0.8818	0.0093
238656_at		Transcribed locus	1.1026	0.0003
238666_at		Transcribed locus	1.6475	0.0102
238670_at		CDNA FLJ41972 fis; clone SKNMC2003987	0.3182	0.0397
238672_at		Transcribed locus	0.6106	0.0127
238677_at	WDR36	WD repeat domain 36	0.5548	0.0147
238678_at	tcag7.907	hypothetical LOC402483	0.6399	0.0016
238690_at			0.2788	0.0095
238695_s_at	RAB39B	RAB39B; member RAS oncogene family	0.6955	0.0404
238699_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.7192	0.0114
238706_at	PAPD4	PAP associated domain containing 4	1.0836	0
238722_x_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	0.8305	0.0011
238723_at	ATXN3	Ataxin 3	0.3358	0.0456
238733_at		Transcribed locus	0.6472	0.0116
238735_at			0.793	0.0061
238738_at	PSMD7	Proteasome (prosome; macropain) 26S subunit; non-ATPase; 7	0.5973	0.0031
238740_at	AARSD1	alanyl-tRNA synthetase domain containing 1	0.1103	0.0226
238745_at		Transcribed locus; strongly similar to XP_001100143.1 similar to integrator complex subunit 10 isoform 1 [Macaca mulatta]	0.2308	0.0039
238750_at	CCL28	chemokine (C-C motif) ligand 28	0.9908	0.0128
238756_at	GAS2L3	Growth arrest-specific 2 like 3	4.8515	0
238759_at	CCDC88A	coiled-coil domain containing 88A	0.3839	0.0235
238768_at	LOC388969	hypothetical LOC388969	0.861	0.0148
238775_at		Transcribed locus	0.9308	0.0032

238779_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	0.2451	0.0095
238781_at	SFRS12	splicing factor; arginine/serine-rich 12	0.8162	0.0042
238783_at	TMEM161B	transmembrane protein 161B	1.4496	0
238785_at		Transcribed locus	0.995	0.0098
238788_at	LOC494150	prohibitin pseudogene	0.5041	0.0013
238791_at	ZNF100	zinc finger protein 100	0.4474	0.0091
238793_at	TIGD7	tigger transposable element derived 7	1.566	0
238794_at	C10orf78	chromosome 10 open reading frame 78	0.6312	0.0115
238795_at	C10orf18	chromosome 10 open reading frame 18	0.414	0.0096
238796_at		Transcribed locus; weakly similar to XP_001098270.1 similar to YTH domain-containing protein 1 (Putative splicing factor YT521) [Macaca mulatta]	0.1966	0.049
238797_at	TRIM11	tripartite motif-containing 11	0.3759	0.046
238803_at	HECTD2	HECT domain containing 2	0.7361	0.0098
238806_at		Transcribed locus	0.4804	0.0078
238808_at		Transcribed locus	1.8645	0.0001
238811_at	ATP11B	ATPase; Class VI; type 11B	0.2779	0.0119
238818_at	KIAA1429	KIAA1429	0.5175	0.0002
238819_at	ZNF347	zinc finger protein 347	0.6935	0.0035
238831_at		Transcribed locus	0.6155	0.0102
238838_at	TCERG1	Transcription elongation regulator 1	0.4928	0.0009
238842_at			0.4853	0.0073
238848_at	OTUD4	OTU domain containing 4	0.3467	0.0138
238850_at	LOC645323	hypothetical LOC645323	1.5687	0.0107
238851_at	ANKRD13A	ankyrin repeat domain 13A	0.7935	0.0217
238854_at		CDNA: FLJ23130 fis; clone LNG08419	0.3787	0.0167
238859_at	KIAA0974	KIAA0974	0.2134	0.0005
238860_at	C6orf130	chromosome 6 open reading frame 130	0.71	0.0462
238861_at		MRNA; clone CD 43T7	0.7724	0.0374
238862_at	MFSD4	major facilitator superfamily domain containing 4	0.1397	0.0095
238863_x_at		Transcribed locus	0.3129	0.0161
238867_at	TMEM182	transmembrane protein 182	0.4629	0.0171
238874_at	FLJ43663	Hypothetical protein FLJ43663	0.1519	0.0265
238875_at		Clone HLS_IMAGE_731119 mRNA sequence	1.4315	0.0006
238880_at	GTF3A	general transcription factor IIIA	0.8561	0.029
238883_at		Transcribed locus	0.953	0.0241
238884_at		Transcribed locus	0.3598	0.0237
238894_at		Transcribed locus	0.3459	0.0036

238896_at		Transcribed locus	0.2629	0.0122
238902_at		Transcribed locus	1.3235	0.0003
238906_s_at	RHOJ	ras homolog gene family; member J	0.2637	0.0395
238907_at		Transcribed locus	1.0092	0.0046
238908_at	CALU	Calumenin	0.81	0.0045
238917_s_at	MGC24039	hypothetical protein MGC24039	0.3223	0.0148
238918_at		CDNA FLJ42015 fis; clone SPLEN2032813	1.0783	0.0031
238920_at			0.4149	0.0039
238921_at	LOC641767	hypothetical LOC644794, hypothetical protein LOC641767	0.1505	0.0436
238924_at	BMS1P5	BMS1 pseudogene 5, hypothetical protein LOC643564	0.4107	0.0031
238925_at	SNTB2	syntrophin; beta 2 (dystrophin-associated protein A1; 59kDa; basic component 2)	0.1844	0.0082
238932_at		CDNA FLJ41867 fis; clone OCBBF2005546	1.1671	0.0016
238934_at		Transcribed locus	0.4979	0.0385
238937_at	ZNF420	zinc finger protein 420	1.0757	0.0078
238944_at			2.5559	0
238956_at		Transcribed locus; strongly similar to XP_524032.1 similar to ribosomal protein S15; rat insulinoma gene [Pan troglodytes]	0.7999	0.0387
238959_at	LARP4	La ribonucleoprotein domain family; member 4	0.5766	0.0161
238960_s_at	LARP4	La ribonucleoprotein domain family; member 4	0.3533	0.0276
238963_at		MRNA full length insert cDNA clone EUROIMAGE 1652049	0.7697	0.0188
238965_at	C21orf2	Chromosome 21 open reading frame 2	0.7812	0.0144
238970_at		Transcribed locus	0.7723	0.0131
238977_at	MCM6	minichromosome maintenance complex component 6	0.4953	0.0007
238982_at	DENR	density-regulated protein, similar to Density-regulated protein (DRP) (DRP1 protein) (Smooth muscle cell-associated protein 3) (SMAP-3)	0.6519	0.006
238996_x_at	ALDOA	aldolase A; fructose-bisphosphate	0.5377	0.0043
238999_at		Transcribed locus	0.5422	0.0394
239002_at	ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	0.4902	0.0288
239005_at		Transcribed locus	0.6944	0.0143
239008_at		CDNA clone IMAGE:4328048	0.1865	0.0359
239010_at	DUXAP10	Double homeobox A pseudogene 10	2.1542	0.0003
239014_at	CCAR1	Cell division cycle and apoptosis regulator 1	0.8926	0.0129
239018_at	WBSCR18	Williams Beuren syndrome chromosome region 18	0.6797	0.0002
239034_at	CXorf24	chromosome X open reading frame 24	0.7839	0.0005

239043_at	ZNF404	zinc finger protein 404	2.5577	0
239044_at	ITFG1	Integrin alpha FG-GAP repeat containing 1	0.3233	0.0352
239070_at		Full-length cDNA clone CS0CAP004YK07 of Thymus of Homo sapiens (human)	0.2649	0.0034
239071_at	RBBP4	Retinoblastoma binding protein 4	0.5239	0.0195
239083_at	ZNF786	zinc finger protein 786	0.5335	0.0101
239090_at	FLJ13305	hypothetical protein FLJ13305	0.2153	0.0034
239091_at		Transcribed locus	0.9938	0.0098
239106_at		Homo sapiens; clone IMAGE:5244869; mRNA	1.8466	0.0001
239121_at		Transcribed locus	0.3459	0.027
239131_at		Transcribed locus	0.9187	0.0049
239140_at		Transcribed locus	0.3077	0.0121
239147_at	ARSK	arylsulfatase family; member K	1.5506	0.0004
239149_at		Transcribed locus	0.2134	0.0225
239151_at	BMS1P5	BMS1 pseudogene 5, hypothetical protein LOC643564	0.8796	0.0074
239154_at		Transcribed locus; moderately similar to XP_523598.2 tousled-like kinase 2 [Pan troglodytes]	1.2239	0.0001
239163_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.8904	0.0117
239164_at		Transcribed locus	0.4976	0.0027
239171_at			0.3326	0.0036
239177_at		CDNA FLJ38849 fis; clone MESAN2008936	0.1767	0.0277
239179_at			0.2374	0.0398
239188_at	PPP2R3C	Protein phosphatase 2 (formerly 2A); regulatory subunit B''; gamma	0.4047	0.003
239193_at	LOC158301	hypothetical protein LOC158301	1.0987	0.0054
239202_at	RAB3B	RAB3B; member RAS oncogene family	0.8206	0.0333
239203_at	C7orf53	chromosome 7 open reading frame 53	0.7499	0.0023
239208_s_at	C21orf57	Chromosome 21 open reading frame 57	0.3889	0.0272
239223_s_at	FBXL20	F-box and leucine-rich repeat protein 20	0.3539	0.0318
239228_at		Transcribed locus	0.8688	0.0133
239231_at		CDNA FLJ41910 fis; clone PEBLM2007834	0.9208	0.0004
239233_at	CCDC88A	coiled-coil domain containing 88A	0.7287	0.0203
239235_at		Transcribed locus	0.1147	0.0485
239238_at		Transcribed locus	1.0018	0.0025
239240_at		Transcribed locus	0.9645	0
239243_at	ZNF638	Zinc finger protein 638	1.2661	0.0129
239245_at		Transcribed locus	0.5497	0.0471
239251_at		Transcribed locus	1.7939	0
239253_at		Transcribed locus	0.5207	0.0121

239265_at	TMEM20	transmembrane protein 20	0.5253	0.045
239266_at		Transcribed locus	0.5591	0.0016
239289_x_at	MTMR15	myotubularin related protein 15	0.8829	0.0025
239309_at	DLX6	distal-less homeobox 6	0.7249	0.0191
239333_x_at		CDNA FLJ30541 fis; clone BRAWH2001355	0.252	0.0197
239339_at		Transcribed locus	0.2246	0.0234
239343_at	LOC728705	hypothetical protein LOC728705	1.1308	0.0003
239347_at		Transcribed locus	0.4288	0.0022
239348_at			0.7942	0.0062
239355_at		Transcribed locus	0.426	0.0275
239358_at		Transcribed locus	1.3094	0.023
239363_at		Transcribed locus	0.8528	0.0111
239367_at	BDNF	brain-derived neurotrophic factor	0.6376	0.0443
239376_at		CDNA clone IMAGE:4333081	0.9237	0.0009
239377_at	MGC11102	hypothetical protein MGC11102	0.5055	0.0141
239393_at		Transcribed locus	0.7543	0.0073
239413_at	CEP152	centrosomal protein 152kDa	1.1961	0.0047
239418_x_at		Transcribed locus	0.2618	0.0184
239423_at			0.2563	0.0204
239429_at		Transcribed locus	0.1612	0.0095
239432_at	FLJ31306	hypothetical protein FLJ31306	0.7238	0.0177
239435_x_at	SHROOM1	Shroom family member 1	1.3029	0.0017
239442_at	CEP68	centrosomal protein 68kDa	0.7694	0.0053
239448_at		Transcribed locus	0.6153	0.0243
239462_at	ZNF284	zinc finger protein 284	0.4502	0.01
239465_at		Transcribed locus; strongly similar to XP_523485.1 similar to Ubiquinol-cytochrome-c reductase complex core protein 2; mitochondrial precursor (Complex III subunit II) [Pan troglodytes]	0.4035	0.0008
239478_x_at		Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	0.2135	0.0271
239481_at	FAM133A	family with sequence similarity 133; member A	1.6394	0.0174
239482_x_at	ZNF708	zinc finger protein 708	0.7155	0.0071
239489_at		Transcribed locus	0.4426	0.0102
239504_at			0.2011	0.0232
239511_s_at	SFRS4	splicing factor; arginine/serine-rich 4	0.501	0.0053
239512_at	SFRS4	splicing factor; arginine/serine-rich 4	0.7655	0.0245
239516_at		Transcribed locus	1.7457	0.0001
239539_at		Transcribed locus	0.2936	0.017
239540_at			0.2976	0.0043
239545_at		Transcribed locus	1.0218	0.0273

239551_at		Transcribed locus	0.207	0.0371
239557_at		Transcribed locus	0.5585	0.0488
239559_at		Partial unknown mRNA from drug-resistant melanoma cells; 3'UTR; clone DMS-9	0.9297	0.0105
239561_at		Transcribed locus	0.6237	0.0478
239576_at	MTUS1	Mitochondrial tumor suppressor 1	0.9938	0.007
239596_at	SLC30A7	solute carrier family 30 (zinc transporter); member 7	0.2332	0.0174
239601_at		Transcribed locus	0.2476	0.0012
239609_s_at	AGPAT7	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase; eta)	0.3102	0.0023
239610_at		Transcribed locus	0.1299	0.0167
239619_at			1.9047	0.0009
239621_at		Transcribed locus	0.2716	0.0126
239625_at			0.1908	0.0111
239635_at	TMEM137	transmembrane protein 137	0.4451	0.0116
239644_at		CDNA clone IMAGE:5275753	0.9207	0.0022
239646_at		Transcribed locus	1.1005	0.01
239649_at			0.3403	0.0022
239650_at	NAP5	Nck-associated protein 5	0.264	0.0154
239651_at	ANAPC5	anaphase promoting complex subunit 5	0.8007	0.0001
239654_at	CHD9	Chromodomain helicase DNA binding protein 9	1.4768	0.0004
239657_x_at			1.1492	0.0213
239679_at			1.1425	0.0002
239680_at			0.6688	0.0159
239682_at		Full-length cDNA clone CS0DC024YB19 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	0.5983	0.0363
239697_x_at	FLJ42117	FLJ42117 protein	0.7994	0.0017
239699_s_at	PMS2L1	postmeiotic segregation increased 2-like 1	0.2298	0.0364
239716_at		Transcribed locus	0.4434	0.0332
239721_at			1.2081	0.0001
239729_at		Transcribed locus	0.224	0.019
239735_at		MRNA (fetal brain cDNA g6_1g)	1.1452	0
239748_x_at	OCIAD1	OCIA domain containing 1	0.4286	0.0028
239760_at		CDNA FLJ30257 fis; clone BRACE2002467	0.3074	0.0055
239764_at		MRNA; cDNA DKFZp686D1113 (from clone DKFZp686D1113)	0.8185	0.019
239771_at	CAND1	cullin-associated and neddylation-dissociated 1	1.206	0.007
239773_at	GTPBP10	GTP-binding protein 10 (putative)	0.2468	0.0104
239790_s_at		Transcribed locus	0.2939	0.0006
239801_at			0.3187	0.0234

239811_at			1.1552	0
239830_at			0.3725	0.0217
239831_at	TMEM106C	Transmembrane protein 106C	0.5134	0.0177
239832_at		Transcribed locus	1.0187	0.0083
239839_at	ZNF555	zinc finger protein 555	0.3006	0.0058
239841_at		Transcribed locus	0.9068	0.0001
239842_x_at		Transcribed locus	0.7862	0.0014
239843_at	RIT1	Ras-like without CAAX 1	0.7406	0.0356
239851_at			0.1952	0.0336
239853_at	KLC3	kinesin light chain 3	0.3395	0.0168
239857_at		CDNA FLJ37227 fis; clone BRAMY2000277	0.191	0.0133
239863_at		CDNA FLJ43322 fis; clone NT2RI2027975	0.5312	0.0138
239886_at		Transcribed locus	0.3978	0.021
239892_at		Transcribed locus	0.7595	0.0032
239895_at	AQR	Aquarius homolog (mouse)	0.1911	0.0349
239900_x_at			0.2741	0.0032
239902_at		Transcribed locus	0.1062	0.0254
239906_at		Transcribed locus	0.526	0.0157
239917_at	VPS8	Vacuolar protein sorting 8 homolog (S. cerevisiae)	0.5104	0.0476
239924_at	LOC91316	Similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1; pre-B-cell specific)	0.1926	0.0212
239946_at		Transcribed locus	0.4996	0.0104
239950_at	HOXA11S	homeo box A11; antisense	0.4756	0.0309
239954_at	ZNF160	zinc finger protein 160	1.5616	0.0008
239960_x_at	LYRM7	Lyrm7 homolog (mouse)	0.4996	0.014
239963_at		Transcribed locus	0.4073	0.0334
239965_at	LOC151878	hypothetical protein LOC151878	0.6855	0.0281
239969_at		Transcribed locus	0.5105	0.0075
239991_at		Transcribed locus	0.8031	0.0018
240000_at		Transcribed locus	0.3003	0.0023
240011_at	TTBK2	Tau tubulin kinase 2	0.1875	0.0272
240026_x_at		Transcribed locus	0.661	0.0003
240046_at			0.696	0.0004
240052_at	ITPR1	inositol 1;4;5-triphosphate receptor; type 1	0.8766	0.0246
240063_at	LOC441046	glucuronidase; beta pseudogene	0.293	0.0456
240075_at		CDNA FLJ31291 fis; clone KIDNE2007356	0.9888	0.0332
240080_at			0.2069	0.0483
240094_at			0.4097	0.0153
240105_at		Transcribed locus	1.3922	0.0014

240111_at	RHOBTB3	Rho-related BTB domain containing 3	1.3602	0.0005
240121_x_at		Homo sapiens; Similar to LOC148188; clone IMAGE:3867353; mRNA	0.6702	0.0205
240128_at		Transcribed locus	0.4857	0.0131
240139_at		Transcribed locus	0.3302	0.0023
240141_at			0.8071	0.0074
240143_at			0.6022	0.0439
240145_at		Transcribed locus; weakly similar to NP_149931.1 dehydrogenase subunit 1 [Trichosurus vulpecula]	0.1883	0.0454
240146_at			1.1614	0.0039
240155_x_at	ZNF493	zinc finger protein 493, zinc finger protein 738	1.2087	0.0041
240157_at		Transcribed locus	1.8284	0.008
240166_x_at	RG9MTD3	RNA (guanine-9-) methyltransferase domain containing 3	0.4068	0.0119
240168_at	XPO7	exportin 7	0.5042	0.0155
240172_at	ERGIC2	ERGIC and golgi 2	0.8551	0.0007
240174_at		Transcribed locus	0.2772	0.0105
240176_at		Clone HLS_IMAGE_506551 mRNA sequence	0.343	0.0165
240205_x_at			0.4719	0.0054
240206_at	TARS	Threonyl-tRNA synthetase	0.4877	0.0116
240222_at		Transcribed locus; weakly similar to XP_001480255.1 similar to pORF2 [Mus musculus]	0.1839	0.0021
240234_at		Transcribed locus	0.3577	0.033
240239_at	ZNF566	zinc finger protein 566	1.2805	0
240247_at			0.8444	0.0016
240248_at		Transcribed locus	0.3632	0.0093
240254_at			0.4329	0.0415
240258_at	ENO1	enolase 1; (alpha)	0.4924	0.0058
240263_at		Transcribed locus	1.4129	0.0088
240269_at		Transcribed locus	0.2791	0.0093
240270_x_at		CDNA FLJ26264 fis; clone DMC05506	0.121	0.0438
240297_at		Transcribed locus	1.1931	0.0038
240309_at		Transcribed locus	0.2497	0.0046
240314_at		Full length insert cDNA clone ZE12G01	0.6776	0.0356
240324_at			0.407	0.0037
240335_at	SLC35F5	Solute carrier family 35; member F5	0.1864	0.008
240339_at		Transcribed locus	0.4754	0.0007
240344_x_at	LYRM7	Lyrm7 homolog (mouse)	1.4642	0
240351_at			0.1287	0.0445
240365_at	LOC647946	hypothetical protein LOC647946	0.3744	0.0002

240370_at		Transcribed locus	0.357	0.0169
240392_at		MRNA; cDNA DKFZp667J0523 (from clone DKFZp667J0523)	0.5495	0.0314
240417_at		Transcribed locus	0.2245	0.0018
240442_at			0.1941	0.0151
240449_at	ZNF341	zinc finger protein 341	0.2753	0.012
240472_at		MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217)	0.1383	0.0171
240482_at			0.3944	0.0096
240485_at			0.3807	0
240494_at		Transcribed locus	0.1469	0.0327
240513_at	PCID1	PCI domain containing 1 (herpesvirus entry mediator)	0.1618	0.0315
240518_at	LOC729291	hypothetical protein LOC729291	0.4398	0.0014
240521_at			0.2578	0.0076
240528_s_at	EXOC4	exocyst complex component 4	0.9232	0.0008
240529_at			0.4679	0.0041
240538_at		Transcribed locus	0.6339	0.0003
240549_at			0.5198	0.0256
240551_at	ZBTB45	zinc finger and BTB domain containing 45	0.3545	0.001
240554_at	AKAP8L	A kinase (PRKA) anchor protein 8-like	0.3191	0.0026
240557_at		CDNA FLJ41867 fis; clone OCBBF2005546	1.1036	0.0011
240565_at	ZFP28	zinc finger protein 28 homolog (mouse)	0.1481	0.0403
240573_at	LOC374443	CLR pseudogene	0.1728	0.0095
240574_at		CDNA clone IMAGE:5262677	0.8516	0.0433
240579_at	NAG	neuroblastoma-amplified protein	0.2022	0.038
240592_at	LCORL	ligand dependent nuclear receptor corepressor-like	1.4077	0
240593_x_at		Transcribed locus	0.4577	0.0166
240594_at		Transcribed locus	0.6283	0.044
240601_at		Transcribed locus	0.7279	0.0026
240622_at			0.1168	0.0311
240627_x_at		Transcribed locus; strongly similar to XP_001101574.1 similar to KIAA1826 protein isoform 2 [Macaca mulatta]	0.2758	0.0029
240637_at	WDR41	WD repeat domain 41	0.3079	0.0023
240656_at		Transcribed locus	0.4017	0.0224
240659_x_at			0.5353	0.0001
240703_s_at	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	0.4312	0.0013
240733_at		Transcribed locus	0.3628	0.0176
240738_at		Transcribed locus	0.202	0.0329
240751_at		Transcribed locus	0.1857	0.0028

240757_at	CLASP1	Cytoplasmic linker associated protein 1	0.1664	0.0186
240759_at			0.3952	0.0489
240776_at			0.111	0.0416
240787_at			0.1592	0.0056
240788_at		Transcribed locus	0.8902	0.0395
240789_at			0.2459	0.0248
240798_at			0.7204	0.0116
240800_x_at		Transcribed locus	0.2641	0.0062
240824_at		Transcribed locus	1.1176	0.0006
240829_at			0.6565	0.0186
240839_at		Transcribed locus	0.1207	0.0279
240846_at	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	0.2222	0.0009
240859_at	ZFYVE16	zinc finger; FYVE domain containing 16	0.4929	0.0307
240865_at			0.8187	0.0068
240906_at			0.2411	0.0012
240908_at		CDNA FLJ37304 fis; clone BRAMY2016070	0.7375	0.0034
240910_at		Transcribed locus	1.2601	0.0171
240912_x_at	TMEM84	transmembrane protein 84	0.2624	0.0211
240928_at		CDNA FLJ32498 fis; clone SKNSH2000319	0.4377	0.0149
240934_at			0.3526	0.0181
240939_x_at		Transcribed locus	0.4471	0.0049
240965_at			0.1318	0.0182
241018_at	TMEM59	transmembrane protein 59	0.202	0.0349
241065_x_at	CMAS	Cytidine monophosphate N-acetylneuraminic acid synthetase	0.6331	0.0001
241066_at	ZNF449	zinc finger protein 449	0.1719	0.0052
241106_at			0.1357	0.0426
241164_at		Transcribed locus	0.4116	0
241223_x_at		Transcribed locus; weakly similar to NP_001013658.1 protein LOC387873 [Homo sapiens]	0.3967	0.0095
241226_at		Transcribed locus	0.1957	0.0144
241235_at			0.1468	0.0029
241241_at	RPS14	Ribosomal protein S14	0.3899	0.0044
241252_at	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.1204	0.0416
241268_x_at			0.2484	0.0121
241303_x_at			0.3019	0.0338
241328_at	ZMAT1	zinc finger; matrin type 1	0.144	0.0128
241330_x_at			0.1019	0.0071
241342_at	TMEM65	transmembrane protein 65	1.4335	0.0041

241345_at	ZRANB2	zinc finger; RAN-binding domain containing 2	0.4671	0.0273
241366_at	RBAK	RB-associated KRAB zinc finger	0.7379	0.0083
241371_at			0.5351	0.0244
241385_at	LARP7	La ribonucleoprotein domain family; member 7	0.8862	0.0143
241386_at		Transcribed locus	0.796	0.0011
241387_at		Transcribed locus	0.582	0.0386
241388_at		CDNA FLJ40566 fis; clone THYMU2004733	0.7693	0.0034
241393_at	IPP	Intracisternal A particle-promoted polypeptide	0.3812	0.0367
241413_at		Transcribed locus	0.6536	0.0182
241466_at		Transcribed locus	0.2092	0.0206
241468_at		Full length insert cDNA YU76E12	0.1827	0.0143
241472_at	DMXL1	Dmx-like 1	0.6753	0.0055
241487_at		CDNA clone IMAGE:4792502	0.2032	0.0065
241489_at		Transcribed locus	1.0536	0.0002
241492_at		Transcribed locus	0.2193	0.0276
241508_at			0.3042	0.0273
241509_at			1.3912	0.0121
241569_at		Transcribed locus	0.1257	0.0334
241599_at	LSM11	LSM11; U7 small nuclear RNA associated	0.4595	0.0071
241611_s_at	FNDC3A	fibronectin type III domain containing 3A	0.126	0.0273
241613_at		Transcribed locus; weakly similar to XP_001083900.1 similar to zinc finger CCHC-type and RNA binding motif 1 [Macaca mulatta]	0.5342	0.0095
241624_at	LOC389834	hypothetical gene supported by AK123403	0.2255	0.0302
241642_x_at	TLK1	tousled-like kinase 1	0.2464	0.008
241658_at		CDNA FLJ37332 fis; clone BRAMY2019710	0.4588	0.0389
241680_at			0.5471	0.0001
241688_at		Transcribed locus	0.2274	0.0272
241692_at		Transcribed locus	0.911	0.033
241704_x_at	ZNF320	zinc finger protein 320	0.4848	0.0012
241713_s_at	DYX1C1	dyslexia susceptibility 1 candidate 1	0.2698	0.0426
241718_x_at		Transcribed locus	0.2548	0.0205
241720_at	ZNF326	zinc finger protein 326	0.3527	0.0017
241723_at	IQGAP2	IQ motif containing GTPase activating protein 2	0.7957	0.0052
241724_x_at		Transcribed locus	0.2394	0.01
241727_x_at	DHFRL1	dihydrofolate reductase-like 1	0.5214	0.0003
241728_at		Transcribed locus	0.2615	0.0184
241734_at	SRFBP1	serum response factor binding protein 1	0.9871	0.0021

241737_x_at		Transcribed locus	0.613	0.0024
241738_at		Transcribed locus	0.2591	0.0014
241744_x_at		Transcribed locus	0.1245	0.0219
241751_at	OFD1	oral-facial-digital syndrome 1	0.7566	0.0029
241755_at	UQCRC2	ubiquinol-cytochrome c reductase core protein II	1.1734	0.0013
241757_x_at	DYNC2LI1	dynein; cytoplasmic 2; light intermediate chain 1	0.4674	0.0023
241774_at		Transcribed locus	0.8827	0.0017
241775_at		CDNA FLJ26437 fis; clone KDN02067	0.7008	0.011
241777_x_at		Transcribed locus	0.3879	0.0106
241779_at	MTX3	metaxin 3	0.2763	0.0022
241790_at		Transcribed locus	0.5985	0.0081
241794_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	0.1136	0.0323
241798_at			1.0573	0.0018
241804_at		Transcribed locus	0.3144	0.015
241807_x_at		Transcribed locus	0.3522	0.0442
241808_at		CDNA FLJ36977 fis; clone BRACE2006344	1.4259	0
241809_at	C1orf183	chromosome 1 open reading frame 183	0.1981	0.0354
241814_at			0.1774	0.0086
241816_at	C14orf106	Chromosome 14 open reading frame 106	1.3116	0
241818_at		Transcribed locus	0.2621	0.0338
241820_at	RIF1	RAP1 interacting factor homolog (yeast)	0.8078	0.0025
241826_x_at		Transcribed locus	0.3954	0.0406
241832_at	FAM98A	family with sequence similarity 98; member A	0.2092	0.0185
241836_x_at	LRRIQ2	leucine-rich repeats and IQ motif containing 2	0.1689	0.0194
241837_at			0.9286	0.044
241838_at		Transcribed locus	1.285	0.0049
241845_at			0.3109	0.0161
241867_at		Transcribed locus	0.6566	0.0181
241885_at		Transcribed locus	0.6302	0.0143
241903_at		Transcribed locus	1.193	0.0203
241906_at			1.3212	0.0003
241913_at		Transcribed locus	0.2729	0.0034
241928_at		Transcribed locus	0.2758	0.0136
241929_at		Transcribed locus	1.6666	0.0069
241936_x_at		Transcribed locus	1.1734	0.0001
241941_at		Transcribed locus	0.7164	0.0009
241948_at		Transcribed locus	0.7755	0.0033
241954_at	FDFT1	Farnesyl-diphosphate farnesyltransferase 1	1.9324	0.0032

241957_x_at	LIN7B	lin-7 homolog B (C. elegans)	0.8898	0.0004
241970_at		Transcribed locus	0.8915	0.0126
241973_x_at	DPP7	Dipeptidyl-peptidase 7	0.238	0.0263
241988_x_at		Transcribed locus; weakly similar to XP_001091208.1 hypothetical protein [Macaca mulatta]	0.2416	0.0203
241993_x_at		Transcribed locus	0.5232	0.0043
242006_at	LCA5	Leber congenital amaurosis 5	0.3975	0.0073
242016_at		Transcribed locus; weakly similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]	0.5118	0.0172
242017_at	ZNF654	zinc finger protein 654	0.2817	0.0068
242018_at		Transcribed locus	0.1326	0.035
242019_at	LASS6	LAG1 homolog; ceramide synthase 6	0.5844	0.0202
242023_at	ABHD4	Abhydrolase domain containing 4	0.3482	0.0339
242024_at		Transcribed locus	0.97	0.0003
242028_at	ZNF709	zinc finger protein 709	0.7028	0.0149
242041_at	CSPP1	centrosome and spindle pole associated protein 1	0.3472	0.0151
242052_at		CDNA FLJ31445 fis; clone NT2NE2000864	1.9652	0.0005
242059_at		Transcribed locus	0.6979	0.0478
242077_x_at	C6orf150	chromosome 6 open reading frame 150	0.1938	0.0277
242080_at			0.6699	0.0023
242091_at	ZNF720	zinc finger protein 720	0.2248	0.0279
242108_at		MRNA; cDNA DKFZp686F1782 (from clone DKFZp686F1782)	1.7568	0
242110_at		Transcribed locus	1.2942	0.0003
242111_at	METTL3	methyltransferase like 3	1.2534	0.0002
242112_at	LSM11	LSM11; U7 small nuclear RNA associated	0.2858	0.015
242113_at		Transcribed locus	0.3087	0.0049
242115_at			0.137	0.0016
242133_s_at	LOC654342	Similar to lymphocyte-specific protein 1	0.9413	0.0018
242139_s_at			0.8714	0.0385
242144_at			1.1833	0.0037
242146_at	SNRPA1	Small nuclear ribonucleoprotein polypeptide A'	1.2346	0.0078
242154_x_at	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	0.2274	0.004
242167_at			0.2857	0.014
242171_at			0.4306	0.0378
242182_x_at		Transcribed locus	0.2773	0.0063
242189_at			0.3023	0.0206
242191_at	NBPF10	neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11	2.0015	0.0001

242201_at	PMS2L5	Postmeiotic segregation increased 2-like 5	1.1104	0.0002
242202_at		CDNA clone IMAGE:5302136	0.2399	0.0007
242208_at		CDNA FLJ41303 fis; clone BRAMY2042131	0.5947	0.0038
242216_at		Transcribed locus	0.5217	0.0091
242224_at	GPATCH2	G patch domain containing 2	0.8616	0.0064
242225_at		Transcribed locus	1.9403	0
242228_at			0.783	0.0107
242229_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	0.5936	0.008
242233_at		Transcribed locus	1.073	0.0006
242235_x_at	NRD1	Nardilysin (N-arginine dibasic convertase)	0.5607	0.0007
242241_x_at		Transcribed locus	0.3802	0.0001
242248_at	PHKB	phosphorylase kinase; beta	0.5913	0.003
242251_at		Transcribed locus	0.5637	0.0074
242260_at	MATR3	Matrin 3	0.6605	0.0081
242261_at			0.7963	0.0044
242265_at	BRD8	Bromodomain containing 8	0.4705	0.0002
242272_at	ZNF785	zinc finger protein 785	0.7832	0.0073
242282_at	ZFPM1	zinc finger protein; multitype 1	1.1568	0.0038
242287_at			0.6719	0.0086
242293_at	ING3	inhibitor of growth family; member 3	0.7462	0.0047
242307_at	ZNF789	zinc finger protein 789	0.1792	0.038
242309_at		Transcribed locus	0.3028	0.0008
242310_at		Transcribed locus	1.6317	0.0001
242323_at		Full-length cDNA clone CS0DF027YF17 of Fetal brain of Homo sapiens (human)	0.6221	0.0421
242325_at	YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide	0.1215	0.027
242328_at			0.3009	0.0306
242336_at		MRNA; cDNA DKFZp686L15210 (from clone DKFZp686L15210)	0.3987	0.0261
242337_at		Transcribed locus	0.355	0.0143
242343_x_at			1.985	0
242347_at		CDNA clone IMAGE:4715948	0.1824	0.0371
242349_at	HECTD1	HECT domain containing 1	0.6708	0.0199
242352_at	NIPBL	Nipped-B homolog (Drosophila)	1.1782	0.0011
242357_x_at			0.3841	0.0033
242369_x_at		MRNA; cDNA DKFZp313O038 (from clone DKFZp313O038)	0.6344	0.0016
242389_at		CDNA FLJ33355 fis; clone BRACE2005151	0.6685	0.0198

242393_x_at	BMS1P5	BMS1 pseudogene 5, centaurin; gamma-like family; member 2, centaurin; gamma-like family; member 9 pseudogene, hypothetical protein LOC643564	0.4505	0.0212
242398_x_at		Transcribed locus	0.2456	0.0035
242417_at	LOC283278	hypothetical protein LOC283278	0.219	0.0354
242418_at	LOC730719	similar to Protein neurobeachin (Lysosomal trafficking regulator 2) (Protein BCL8B)	0.573	0.0051
242422_at		Full-length cDNA clone CS0DL005YA15 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human)	0.3138	0.0332
242423_x_at		Homo sapiens; clone IMAGE:4346533; mRNA	0.8002	0.0035
242424_at		Transcribed locus	1.2915	0
242426_at	NRG4	neuregulin 4	0.2426	0.0244
242429_at	ZNF567	zinc finger protein 567	1.2025	0.0021
242436_at		Transcribed locus	0.2659	0.0476
242438_at			0.9158	0.0299
242439_s_at			0.5308	0.039
242448_at		CDNA FLJ33367 fis; clone BRACE2005661	1.0959	0.0001
242449_at		Transcribed locus	0.4034	0.0023
242453_at		Transcribed locus	0.2349	0.0165
242456_at	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.3098	0.0055
242458_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	0.3458	0.0342
242463_x_at	ZNF600	zinc finger protein 600	0.836	0.0051
242470_at	EID2B	EP300 interacting inhibitor of differentiation 2B	1.0867	0.0018
242474_s_at	LOC203547	hypothetical protein LOC203547	0.2125	0.0463
242476_at		Transcribed locus	1.6245	0.0047
242477_at	C9orf52	chromosome 9 open reading frame 52	0.194	0.0359
242486_at		Transcribed locus	0.4308	0.0002
242490_at			0.8683	0
242492_at			0.4236	0.0257
242512_at	MYO9A	myosin IXA	1.0343	0.0011
242513_x_at	KIAA2018	KIAA2018	0.1643	0.0032
242514_at		Transcribed locus	0.3736	0.0182
242517_at	KISS1R	KISS1 receptor	1.54	0.0447
242518_at		CDNA FLJ43403 fis; clone OCBBF2016612	0.6214	0.0005
242522_at		Transcribed locus	0.1188	0.0241
242523_at		Transcribed locus	0.7326	0.0268
242526_at		Transcribed locus	0.1118	0.0099
242537_at			0.1929	0.0111

242539_at	LOC730069	nuclear receptor binding factor 2 pseudogene, similar to nuclear receptor binding factor 2	1.0489	0.0117
242546_at	FLJ39632	hypothetical LOC642477	2.412	0.0002
242555_at	LOC388272	similar to RIKEN cDNA 4921524J17	0.1994	0.0449
242560_at	FANCD2	Fanconi anemia; complementation group D2	1.5734	0.0001
242564_at		Full length insert cDNA clone ZD66G01	0.5993	0.0055
242565_x_at	C21orf57	Chromosome 21 open reading frame 57	0.5103	0.0163
242584_at	FLJ13305	hypothetical protein FLJ13305	1.411	0.0032
242586_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	1.413	0.0006
242592_at	GPR137C	G protein-coupled receptor 137C	0.6393	0.0007
242602_x_at	ZNF254	zinc finger protein 254	0.5219	0.0088
242609_x_at		Transcribed locus	0.5383	0
242612_at	NPEPPS	aminopeptidase puromycin sensitive	0.7255	0.0134
242621_at	ZNF498	zinc finger protein 498	0.3149	0.0179
242628_at		Transcribed locus	0.66	0.0035
242633_x_at			0.5898	0
242635_s_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	0.6801	0.0064
242637_at		Transcribed locus	0.6818	0.0024
242640_at	C19orf55	chromosome 19 open reading frame 55	0.4244	0
242645_at		Full length insert cDNA clone YR92A01	0.4151	0.0199
242655_at		Transcribed locus	0.5814	0.0014
242662_at	PCSK6	Proprotein convertase subtilisin/kexin type 6	1.6828	0.0107
242663_at	LOC148189	Hypothetical protein LOC148189	0.4278	0.0001
242673_at		Transcribed locus	1.5163	0.0004
242679_at		CDNA clone IMAGE:5272988	0.3205	0.0175
242691_at		CDNA FLJ41369 fis; clone BRCAN2006117	1.2632	0.0375
242693_at		Transcribed locus	0.8009	0.0008
242696_at		Transcribed locus	0.5463	0.0112
242706_s_at	MED23	mediator complex subunit 23	0.8901	0.0484
242707_at	MED23	mediator complex subunit 23	0.3393	0.0261
242711_x_at	FANCM	Fanconi anemia; complementation group M	0.814	0.0023
242722_at	LMO7	LIM domain 7	0.6273	0.04
242723_at		Transcribed locus	0.3406	0.0039
242724_x_at			0.24	0.0386
242725_at		CDNA FLJ42225 fis; clone THYMU2040427	0.9061	0.0094
242737_at		Transcribed locus	0.7249	0.0016
242739_at	C6orf201	Chromosome 6 open reading frame 201	1.3866	0.0089

242741_x_at		Transcribed locus	0.1466	0.0135
242753_x_at	C4orf16	chromosome 4 open reading frame 16	0.2106	0.0486
242755_at			0.1396	0.0214
242756_at			0.5278	0.0091
242759_at		Transcribed locus	0.7552	0
242772_x_at		Transcribed locus	0.3888	0.0208
242785_at	FLJ42562	similar to echinoderm microtubule associated protein like 5	0.8867	0.0168
242786_at		Full-length cDNA clone CS0DK010YC18 of HeLa cells Cot 25-normalized of Homo sapiens (human)	0.3136	0.0421
242787_at		Transcribed locus	0.5063	0.0109
242796_x_at		Transcribed locus	0.1203	0.0235
242797_x_at			0.5966	0.0321
242804_at	POLN	polymerase (DNA directed) nu	0.2216	0.0484
242807_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	0.874	0.0185
242829_x_at	FBXL3	F-box and leucine-rich repeat protein 3	0.3138	0.023
242851_at	KIAA1919	KIAA1919	1.1397	0.0011
242854_x_at	DLEU2	deleted in lymphocytic leukemia; 2	0.2621	0.0072
242857_at		CDNA FLJ37981 fis; clone CTONG2010566	0.4555	0.0428
242859_at		Transcribed locus	1.3637	0
242872_at	CIT	citron (rho-interacting; serine/threonine kinase 21)	0.2516	0.0261
242873_at		Transcribed locus	1.815	0.0129
242877_at		Transcribed locus	0.9255	0.008
242881_x_at		Clone HLS_IMAGE_626842 mRNA sequence	3.475	0
242886_at		Transcribed locus	0.4448	0.025
242889_x_at	LOC645431	hypothetical protein LOC645431	0.1953	0.039
242890_at		CDNA FLJ34225 fis; clone FCBBF3023372	1.6465	0.0003
242894_at		Transcribed locus	0.482	0.0025
242900_at	ALG10B	asparagine-linked glycosylation 10 homolog B (yeast; alpha-1;2-glucosyltransferase)	0.9203	0.0015
242915_at	ZNF682	zinc finger protein 682	0.8867	0.0112
242918_at	NASP	Nuclear autoantigenic sperm protein (histone-binding)	0.6008	0.0129
242919_at	ZNF253	zinc finger protein 253	0.6062	0.041
242922_at	NOMO1	NODAL modulator 1, NODAL modulator 2, NODAL modulator 3	0.5908	0.0007
242923_at	ZNF678	Zinc finger protein 678	0.5746	0.0375
242926_at		Transcribed locus	0.1958	0.0308
242928_at		Transcribed locus	0.1873	0.0163
242940_x_at	DLX6	distal-less homeobox 6	1.1863	0.0036
242953_at		Transcribed locus	0.36	0.02

242966_x_at		CDNA FLJ31511 fis; clone NT2RI1000035	0.2967	0.0062
242968_at		Transcribed locus	1.1598	0.0005
242969_at		Transcribed locus	0.9612	0.0005
242974_at	CD47	CD47 molecule	1.1605	0.002
242984_at	MKLN1	muskelin 1; intracellular mediator containing kelch motifs	0.3903	0.0167
243003_at		CDNA FLJ45369 fis; clone BRHIP3017325	1.1552	0.0186
243005_at		Transcribed locus	0.3646	0.0004
243009_at	LOC441242	CDNA clone IMAGE:5302136, Hypothetical LOC441242	1.4058	0
243017_at		Transcribed locus	0.5218	0.0312
243026_x_at	BIRC4	baculoviral IAP repeat-containing 4	1.5012	0.0002
243030_at		Transcribed locus	0.4638	0.021
243031_at		Transcribed locus	1.6159	0.0002
243042_at	FAM73A	family with sequence similarity 73; member A	0.8592	0.0095
243051_at	CNIH4	Cornichon homolog 4 (Drosophila)	0.1712	0.0129
243055_at		Transcribed locus	0.3662	0.0007
243069_at			0.236	0.0137
243071_at		Transcribed locus	0.5968	0.0003
243090_at		Transcribed locus	0.7503	0.008
243091_at		Transcribed locus	0.5288	0.0296
243108_at			0.2467	0.022
243113_at		Transcribed locus	0.2539	0.0225
243115_at		Transcribed locus	0.11	0.02
243121_x_at			0.1894	0.0288
243127_x_at	DNASE1	deoxyribonuclease I	0.1726	0.0095
243147_x_at		Transcribed locus	0.2899	0.0123
243150_at		Transcribed locus	0.6344	0.0024
243159_x_at		Transcribed locus	0.5329	0.0072
243162_at		Transcribed locus	0.1918	0.0349
243166_at	SLC30A5	solute carrier family 30 (zinc transporter); member 5	0.4404	0.0462
243181_at	ANKIB1	ankyrin repeat and IBR domain containing 1	0.4398	0.0002
243189_at			0.6128	0.0007
243196_s_at	TRAFD1	TRAF-type zinc finger domain containing 1	0.4128	0.0005
243210_at		CDNA FLJ46024 fis; clone SPLEN2022785	0.46	0.0231
243216_x_at		Transcribed locus	0.3948	0.0034
243224_at		CDNA FLJ34623 fis; clone KIDNE2015073	0.3167	0.0041
243226_at		Transcribed locus	0.1669	0.0021
243229_at		Transcribed locus	0.2283	0.0313

243264_s_at	C8orf44	chromosome 8 open reading frame 44, serum/glucocorticoid regulated kinase family; member 3	0.3489	0.0427
243271_at		Transcribed locus	0.8529	0.0083
243275_at			0.4778	0.0004
243277_x_at	EVI1	Ecotropic viral integration site 1	0.177	0.0009
243282_at	CCDC93	Coiled-coil domain containing 93	0.4746	0.0087
243284_at	FLJ11506	hypothetical protein FLJ11506	0.2577	0.0003
243286_at		Transcribed locus	0.7086	0.033
243287_s_at	OSTM1	osteopetrosis associated transmembrane protein 1	0.1789	0.0134
243294_at	ZNF780B	zinc finger protein 780B	0.43	0.0036
243303_at		CDNA FLJ40827 fis; clone TRACH2011500	0.8285	0.0156
243305_at		Transcribed locus	0.8123	0.0002
243310_at		Transcribed locus	0.5755	0.002
243315_at		Transcribed locus	0.4688	0.0267
243316_x_at	VPS26A	Vacuolar protein sorting 26 homolog A (S. pombe)	0.2301	0.0416
243319_at		Transcribed locus	0.1627	0.0243
243331_at		Transcribed locus	0.1971	0.0329
243332_at		Transcribed locus	0.8744	0.0026
243348_at			0.1886	0.001
243352_at	ALPK1	alpha-kinase 1	0.5335	0.022
243353_at			0.196	0.0152
243361_at	SFRS12	splicing factor; arginine/serine-rich 12	0.5013	0.0038
243367_at		Transcribed locus	0.7343	0.0017
243368_at		Transcribed locus	0.1877	0.009
243375_at		Transcribed locus	0.1397	0.049
243381_at			0.175	0.005
243388_at		Transcribed locus; strongly similar to XP_519898.1 similar to DKFZP564O0463 protein; HSPC064 protein [Pan troglodytes]	0.5644	0.0316
243407_at	MFSD8	Major facilitator superfamily domain containing 8	0.3944	0.0008
243413_at	TTC30B	tetratricopeptide repeat domain 30B	0.5358	0.0001
243428_at	KCNQ1OT1	KCNQ1 overlapping transcript 1	0.9698	0.0119
243435_at	KCNQ1OT1	KCNQ1 overlapping transcript 1	0.9253	0.0092
243461_at		Transcribed locus	0.5976	0.0075
243462_s_at		Transcribed locus	1.2101	0.0045
243465_at		CDNA FLJ32348 fis; clone PROST2007200	0.7871	0.0012
243476_at		Transcribed locus; moderately similar to XP_001109186.1 hypothetical protein [Macaca mulatta]	0.2199	0.0251
243490_at			0.4508	0.0002

243496_at	RAB18	RAB18; member RAS oncogene family	0.846	0.0433
243498_at		Transcribed locus	0.3451	0.0049
243502_at	GJA7	gap junction protein; alpha 7; 45kDa	0.7246	0.0017
243539_at	KIAA1841	KIAA1841	0.7205	0.0074
243542_at	PREPL	prolyl endopeptidase-like	0.1401	0.0229
243546_at		Transcribed locus	0.3726	0.0186
243551_at		Transcribed locus	0.1205	0.0159
243557_at			0.3051	0.0122
243558_at		Transcribed locus	0.2802	0.013
243565_at	FLJ39660	hypothetical protein FLJ39660	0.2014	0.0325
243578_at		Transcribed locus	0.3256	0.0091
243590_at		CDNA FLJ25435 fis; clone TST08040	0.1602	0.036
243592_at	REV1	REV1 homolog (S. cerevisiae)	0.3419	0.0271
243594_x_at	SPIRE2	spire homolog 2 (Drosophila)	0.3999	0.0154
243606_at		Transcribed locus	0.5902	0.04
243608_at	COG2	component of oligomeric golgi complex 2	0.2918	0.0256
243612_at	NSD1	Nuclear receptor binding SET domain protein 1	0.3181	0.0312
243613_at	MGC24039	hypothetical protein MGC24039	0.3621	0
243617_at	LOC152485	Hypothetical protein LOC152485	0.3983	0.0282
243630_at	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 1; 7kDa	0.2599	0.0411
243641_at		Transcribed locus; moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]	0.2556	0.0105
243646_at			1.0171	0.0008
243655_x_at		Transcribed locus	0.1013	0.0339
243660_at	CHD9	Chromodomain helicase DNA binding protein 9	0.3367	0.0116
243661_at	ZNF273	zinc finger protein 273	0.8463	0.001
243664_at	TXNL1	Thioredoxin-like 1	0.7614	0.0221
243667_at		Full length insert cDNA YI30F01	0.2375	0.0374
243673_at		Transcribed locus	0.6123	0.0109
243683_at	MORF4L2	Mortality factor 4 like 2	1.0818	0.035
243689_s_at	C20orf80	Chromosome 20 open reading frame 80	0.1477	0.0284
243691_at			0.7676	0.025
243705_at	DDHD1	DDHD domain containing 1	0.2456	0.0002
243709_at	FLJ90709	hypothetical protein FLJ90709	1.4481	0.0002
243713_at		Transcribed locus	0.192	0.0246
243736_at		Transcribed locus	0.8216	0.0205
243750_x_at	C21orf70	chromosome 21 open reading frame 70	0.4636	0.024
243751_at	CHD2	Chromodomain helicase DNA binding protein 2	0.4955	0.0087

243756_at			1.2183	0.0124
243761_at	PFTK1	PFTAIRE protein kinase 1	0.2984	0.0137
243763_x_at		Transcribed locus	0.2072	0.014
243765_at		Transcribed locus	0.2773	0.0063
243772_at	SDCCAG8	serologically defined colon cancer antigen 8	0.3396	0.0037
243785_at		CDNA FLJ31475 fis; clone NT2NE2001598	0.9972	0.0081
243786_at	ZDHHC20	zinc finger; DHHC-type containing 20	0.4053	0.0144
243790_at	ZNF585A	zinc finger protein 585A	1.3787	0.0001
243792_x_at	PTPN13	Protein tyrosine phosphatase; non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	0.5869	0.0258
243801_x_at		Transcribed locus	0.351	0.022
243808_at		Transcribed locus	0.8147	0.0495
243834_at	TNRC6A	trinucleotide repeat containing 6A	0.6906	0.0213
243835_at	ZDHHC21	Zinc finger; DHHC-type containing 21	0.5512	0.0385
243840_at		Arsenic transactivated protein 1	0.2701	0.0073
243851_at	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	0.6358	0.0426
243852_at	LUC7L2	LUC7-like 2 (S. cerevisiae)	0.617	0.008
243857_at	MORF4L2	Mortality factor 4 like 2	1.7628	0.0004
243858_at			0.1793	0.0129
243861_at		Transcribed locus	0.5953	0.007
243866_x_at			0.2148	0.0033
243871_at		CDNA FLJ42179 fis; clone THYMU2030796	0.1991	0.0049
243894_at	SLC41A2	solute carrier family 41; member 2	0.8515	0.0448
243907_at		Transcribed locus	1.5813	0.009
243908_at			0.6552	0.0396
243910_x_at		CDNA FLJ30383 fis; clone BRACE2008102	0.6808	0.0325
243945_at	TRIM2	tripartite motif-containing 2	0.4489	0.0056
243963_at	SDCCAG8	Serologically defined colon cancer antigen 8	0.6072	0.0214
243973_at		Transcribed locus	0.38	0.0008
243982_at	KLHL28	Kelch-like 28 (Drosophila)	0.4861	0.0403
243985_at	GTF2A2	General transcription factor IIA; 2; 12kDa	0.3451	0.0276
243995_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	0.4103	0.0013
244000_at		CDNA FLJ14364 fis; clone HEMBA1000918	0.6376	0.0191
244010_at		MRNA; cDNA DKFZp686J08131 (from clone DKFZp686J08131)	1.4217	0.0001
244011_at	PPM1K	protein phosphatase 1K (PP2C domain containing)	0.2568	0.0205
244014_x_at		Transcribed locus	0.4854	0
244031_at			0.5049	0.0014

244033_at	C14orf145	chromosome 14 open reading frame 145	0.7664	0.0054
244038_at	WDR89	WD repeat domain 89	0.6473	0.0095
244042_x_at	LOC651466	Similar to retinoic acid receptor responder (tazarotene induced) 2	1.3955	0.0002
244043_at		MRNA; cDNA DKFZp313O196 (from clone DKFZp313O196)	1.0315	0.008
244046_at	URG4	up-regulated gene 4	0.9105	0.0018
244062_at	DAAM1	dishevelled associated activator of morphogenesis 1	0.6654	0.0018
244075_at		Transcribed locus	1.7228	0.0126
244080_at		Full-length cDNA clone CS0DI011YD16 of Placenta Cot 25-normalized of Homo sapiens (human)	0.5247	0.0459
244094_at		Transcribed locus	0.1206	0.0076
244112_x_at			1.0704	0.0196
244115_at	FAM126A	family with sequence similarity 126; member A	0.2633	0.0132
244125_at		Transcribed locus	0.321	0.026
244132_x_at	ZNF518	Zinc finger protein 518	1.1768	0.0009
244133_at		Transcribed locus	0.2046	0.016
244139_s_at			0.3303	0.036
244153_at			0.473	0.0001
244170_at		CDNA FLJ37366 fis; clone BRAMY2024416	1.0183	0.0102
244171_at	MKLN1	muskelin 1; intracellular mediator containing kelch motifs	0.4446	0.0029
244185_at		Transcribed locus	0.8011	0.0228
244187_at	APOOL	Apolipoprotein O-like	0.9535	0.0267
244189_at	KIAA1648	KIAA1648 protein	0.6317	0.0473
244195_at		Transcribed locus	0.1802	0.0185
244197_x_at			0.805	0.0259
244220_at			0.5441	0.0108
244228_at			0.1029	0.0485
244236_at			0.2007	0.0084
244241_x_at		Transcribed locus	0.4171	0.0236
244265_at			0.2547	0.007
244267_at		Transcribed locus	0.3221	0.0317
244271_at		Transcribed locus	0.5748	0.0006
244275_at		Transcribed locus	0.2622	0.0234
244286_at		Transcribed locus	0.4379	0.008
244287_at	SFRS12	splicing factor; arginine/serine-rich 12	1.7757	0.0005
244304_at	LOC730069	nuclear receptor binding factor 2 pseudogene, similar to nuclear receptor binding factor 2	0.4704	0.0217
244315_at	PLSCR1	phospholipid scramblase 1	0.107	0.0313
244324_at	C18orf54	chromosome 18 open reading frame 54	0.5006	0.002

244346_at		Transcribed locus	0.601	0.0247
244347_at		Transcribed locus	0.332	0.0431
244359_s_at		Clone HLS_IMAGE_1699118 mRNA sequence	1.6581	0.0399
244382_at		Transcribed locus	0.3151	0.0202
244401_at	LCA5	Leber congenital amaurosis 5	0.305	0.0021
244407_at	CYP39A1	cytochrome P450; family 39; subfamily A; polypeptide 1	0.8713	0.0218
244427_at	KIF23	Kinesin family member 23	0.9739	0.001
244450_at			0.7488	0.016
244462_at	ZNF224	Zinc finger protein 224	0.9771	0.0008
244472_at	LOC388630	similar to C05G5.5	0.4225	0.016
244473_at		Transcribed locus	0.2086	0.0136
244478_at	LRRC37A3	Leucine rich repeat containing 37; member A3	0.1491	0.0477
244503_at		Transcribed locus	0.7052	0.0367
244505_at		Transcribed locus; strongly similar to XP_001085606.1 similar to phosphoribosyl pyrophosphate amidotransferase proprotein [Macaca mulatta]	0.1677	0.0243
244511_at		Transcribed locus	0.2674	0.0268
244513_at	TMEM161B	transmembrane protein 161B	0.2379	0.0009
244515_at	PSMD7	Proteasome (prosome; macropain) 26S subunit; non-ATPase; 7	0.5716	0.0005
244565_at	HMX2	H6 family homeobox 2	1.0427	0.0192
244567_at		Transcribed locus	0.1616	0.0024
244587_at			0.5755	0.0006
244607_at		Transcribed locus	0.1608	0.0249
244622_at	BRWD1	Bromodomain and WD repeat domain containing 1	0.179	0.0092
244633_at		Transcribed locus	1.0737	0.0397
244638_at			0.2325	0.0076
244640_at	LOC342892	Hypothetical protein LOC342892	1.0805	0.0001
244648_at		Transcribed locus	0.591	0.018
244659_at	TRIP12	Thyroid hormone receptor interactor 12	0.595	0.0413
244660_at	ELAVL1	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 1 (Hu antigen R)	0.5108	0.0199
244664_at		Transcribed locus	0.5523	0.0004
244673_at		Transcribed locus	0.1263	0.0148
244679_at		Transcribed locus	0.1974	0.0093
244703_x_at	IPO9	importin 9	0.4001	0.0169
244731_at			0.2576	0.0035
244749_at		Homo sapiens; clone IMAGE:5218412; mRNA	0.2732	0.0111
244758_at	ZNF452	zinc finger protein 452	1.386	0.0001

244766_at	LOC440345	PI-3-kinase-related kinase SMG-1, PI-3-kinase-related kinase SMG-1 - like locus, PI-3-kinase-related kinase SMG-1 pseudogene, hypothetical protein LOC440345, similar to PI-3-kinase-related kinase SMG-1	1.1566	0.0001
244767_at	C10orf4	chromosome 10 open reading frame 4	0.1997	0.0034
244777_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	0.9405	0.0028
244783_at	YAF2	YY1 associated factor 2	0.4014	0.0274
244786_at	SNHG10	small nucleolar RNA host gene (non-protein coding) 10	0.5841	0.0016
244790_at	MTCP1	mature T-cell proliferation 1	0.6782	0.0025
244795_at	C20orf44	Chromosome 20 open reading frame 44	0.4253	0.0037
244801_at	PSMB7	Proteasome (prosome; macropain) subunit; beta type; 7	0.7626	0.0276
244803_at		Transcribed locus	1.2553	0.0222
244811_at		Full-length cDNA clone CS0DF025YM09 of Fetal brain of Homo sapiens (human)	1.6994	0.0005
244813_at		Transcribed locus	0.6666	0.0001
244842_x_at		Transcribed locus	0.4282	0.0127
244861_at	ZNF527	zinc finger protein 527	0.345	0.0034
244878_at		Transcribed locus	0.898	0.0079
244881_at	LMLN	leishmanolysin-like (metallopeptidase M8 family)	0.9357	0.0018
31637_s_at	NR1D1	nuclear receptor subfamily 1; group D; member 1, thyroid hormone receptor; alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog; avian)	1.7787	0.0004
31807_at	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	0.6478	0.0006
31845_at	ELF4	E74-like factor 4 (ets domain transcription factor)	2.2744	0
32062_at	LRRC14	leucine rich repeat containing 14	0.4378	0.0014
32069_at	N4BP1	Nedd4 binding protein 1	0.6254	0.0008
32137_at	JAG2	jagged 2	0.6661	0.0249
32402_s_at	SYMPK	symplekin	0.6279	0.0006
33132_at	CPSF1	cleavage and polyadenylation specific factor 1; 160kDa	0.6617	0.0079
33148_at	ZFR	zinc finger RNA binding protein	0.5803	0.0053
33646_g_at	GM2A	GM2 ganglioside activator	0.9839	0.0295
33768_at	DMWD	dystrophia myotonica; WD repeat containing	0.5592	0.0043
33814_at	PAK4	p21(CDKN1A)-activated kinase 4	1.0276	0
34031_i_at	KRIT1	KRIT1; ankyrin repeat containing	0.7542	0.0006
34187_at	RBMS2	RNA binding motif; single stranded interacting protein 2	0.2632	0.0099
34221_at	KIAA0194	KIAA0194 protein	0.8603	0.0002
34225_at	WHSC2	Wolf-Hirschhorn syndrome candidate 2	0.6729	0.0016

34449_at	CASP2	caspase 2; apoptosis-related cysteine peptidase (neural precursor cell expressed; developmentally down-regulated 2)	0.2612	0.0026
34697_at	LRP6	low density lipoprotein receptor-related protein 6	0.7894	0.0011
34726_at	CACNB3	calcium channel; voltage-dependent; beta 3 subunit	0.6333	0.0414
35150_at	CD40	CD40 molecule; TNF receptor superfamily member 5	0.5851	0.0479
35160_at	LDB1	LIM domain binding 1	0.7782	0.036
35254_at	TRAFD1	TRAF-type zinc finger domain containing 1	0.8908	0
35436_at	GOLGA2	golgi autoantigen; golgin subfamily a; 2	0.801	0.0028
35666_at	SEMA3F	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3F	1.3744	0.0002
35671_at	GTF3C1	general transcription factor IIIC; polypeptide 1; alpha 220kDa	0.574	0.0007
36030_at	HOM-TES-103	hypothetical protein LOC25900	0.9882	0.0002
36888_at	KIAA0841	KIAA0841	0.7585	0.0002
36994_at	ATP6V0C	ATPase; H+ transporting; lysosomal 16kDa; V0 subunit c	0.3557	0.0232
37254_at	ZNF133	zinc finger protein 133	1.0278	0
37278_at	TAZ	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.3369	0.0337
37462_i_at	SF3A2	splicing factor 3a; subunit 2; 66kDa	0.6814	0.0056
37547_at	BBS9	Bardet-Biedl syndrome 9	0.5996	0.0306
37793_r_at	RAD51L3	RAD51-like 3 (S. cerevisiae)	0.3322	0.0003
37860_at	ZNF337	zinc finger protein 337	0.9239	0.0001
37872_at	JRK	jerky homolog (mouse)	0.219	0.0228
37892_at	COL11A1	collagen; type XI; alpha 1	3.5002	0.0048
38158_at	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	1.8332	0.0004
38269_at	PRKD2	protein kinase D2	1.2996	0
38521_at	CD22	CD22 molecule, myelin associated glycoprotein	0.752	0.0494
38766_at	SRCAP	Snf2-related CBP activator protein	0.2977	0.0111
39313_at	WNK1	WNK lysine deficient protein kinase 1	0.5186	0.0018
40149_at	SH2B1	SH2B adaptor protein 1	0.4233	0.0032
40255_at	DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0.5786	0.0447
40465_at	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	0.7038	0.0008
40472_at	AGPAT7	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase; eta)	1.0115	0.0007
40569_at	MZF1	myeloid zinc finger 1	0.8535	0.0068
41113_at	ZNF500	zinc finger protein 500	0.5968	0.0001
41397_at	LOC55565	hypothetical protein LOC55565	0.2316	0.0141
41512_at		Transcribed locus	0.4102	0.0445

43544_at	MED16	mediator complex subunit 16	0.8256	0.0019
43977_at	TMEM161A	transmembrane protein 161A	0.7811	0.0002
44111_at	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	0.4232	0.0263
44120_at	ADCK2	aarF domain containing kinase 2	0.9554	0.0006
44617_at	OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.6478	0.0005
44669_at	LOC644096	hypothetical protein LOC644096	0.6898	0.0023
44783_s_at	HEY1	hairy/enhancer-of-split related with YRPW motif 1	1.6563	0.0039
44822_s_at	MIER2	mesoderm induction early response 1; family member 2	0.3782	0.0259
45633_at	GINS3	GINS complex subunit 3 (Psf3 homolog)	1.3263	0.0002
45653_at	KCTD13	potassium channel tetramerisation domain containing 13	0.8118	0.0036
45687_at	PRR14	proline rich 14	0.5417	0.0104
46947_at	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	0.3767	0.0201
47560_at	LPHN1	latrophilin 1	0.8943	0.0203
48808_at	DHFR	dihydrofolate reductase	2.3657	0
48825_at	ING4	inhibitor of growth family; member 4	0.5368	0.0105
49485_at	PRDM4	PR domain containing 4	1.1657	0.0002
50314_i_at	C20orf27	chromosome 20 open reading frame 27	0.6488	0.024
50376_at	ZNF444	zinc finger protein 444	0.4258	0.0151
51176_at	MED27	mediator complex subunit 27	0.8115	0.0153
51200_at	C19orf60	chromosome 19 open reading frame 60	0.4392	0.0286
51228_at	RBM12B	RNA binding motif protein 12B	1.495	0
52005_at	WIZ	widely interspaced zinc finger motifs	0.8784	0
52164_at	C11orf24	chromosome 11 open reading frame 24	0.629	0.0455
53202_at	C7orf25	chromosome 7 open reading frame 25	0.3381	0.0372
55065_at	MARK4	MAP/microtubule affinity-regulating kinase 4	0.904	0
55093_at	CSGlcA-T	chondroitin sulfate glucuronyltransferase	0.78	0.0011
55705_at	C19orf22	chromosome 19 open reading frame 22	0.2916	0.0366
55872_at	ZNF512B	zinc finger protein 512B	0.9588	0.001
56821_at	FLJ10815	amino acid transporter	1.0855	0.0008
57516_at	ZNF764	zinc finger protein 764	0.7536	0.0033
57532_at	DVL2	dishevelled; dsh homolog 2 (Drosophila)	0.596	0.0261
58367_s_at	ZNF419	zinc finger protein 419	0.4592	0.0105
58994_at	CC2D1A	coiled-coil and C2 domain containing 1A	0.6267	0.0006
60528_at	PLA2G4B	phospholipase A2; group IVB (cytosolic)	0.3032	0.033
60794_f_at	LOC730051	similar to Zinc finger protein 418, zinc finger protein 814	0.5442	0.0086

60815_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J; 13.3kDa pseudogene	0.995	0.0005
61874_at	C9orf7	chromosome 9 open reading frame 7	0.4859	0.013
63825_at	ABHD2	abhydrolase domain containing 2	0.7776	0.0269
64371_at	SFRS14	splicing factor; arginine/serine-rich 14	0.9234	0
64432_at	C12orf47	chromosome 12 open reading frame 47	0.6311	0.0087
64883_at	MOSPD2	motile sperm domain containing 2	0.7272	0.0001
64900_at	FLJ22167	hypothetical protein FLJ22167	1.1386	0.0022
65086_at	YIPF2	Yip1 domain family; member 2	0.3721	0.0375
65438_at	KIAA1609	KIAA1609	0.8447	0.0001
65770_at	RHOT2	ras homolog gene family; member T2	0.3196	0.0416
65884_at	MAN1B1	mannosidase; alpha; class 1B; member 1	0.7896	0.0265
74694_s_at	RABEP2	rabaptin; RAB GTPase binding effector protein 2	0.7748	0.0162
76897_s_at	FKBP15	FK506 binding protein 15; 133kDa	1.0529	0.0159
78495_at	ZNF783	zinc finger protein 783	0.3375	0.0348
79005_at	SLC35E1	solute carrier family 35; member E1	0.8264	0.0001
81737_at		Homo sapiens; clone IMAGE:4271781	0.297	0.0406
81811_at		CDNA FLJ37304 fis; clone BRAMY2016070	0.6823	0.0112
90610_at	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	0.4864	0.0435
91816_f_at	MEX3D	mex-3 homolog D (C. elegans)	1.1198	0.0118
91952_at	LOC90379	hypothetical protein BC002926	1.0566	0
AFFX-HSAC07/X00351_3_at	ACTB	actin; beta	0.1015	0.0374
AFFX-HSAC07/X00351_5_at	ACTB	actin; beta	0.6314	0.0081
AFFX-HSAC07/X00351_M_at	ACTB	actin; beta	0.3463	0.004
AFFX-HUMGAPDH/M33197_3_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.442	0
AFFX-HUMGAPDH/M33197_5_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.7362	0
AFFX-HUMGAPDH/M33197_M_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.7163	0
AFFX-hum_alu_at			0.1091	0.006
121_at	PAX8	paired box 8	-0.7092	0.0002
1552261_at	WFDC2	WAP four-disulfide core domain 2	-0.1301	0.015
1552278_a_at	SLC46A1	solute carrier family 46; member 1	-1.3729	0.0001
1552279_a_at	SLC46A1	solute carrier family 46; member 1	-0.8726	0.0001
1552281_at	SLC39A5	solute carrier family 39 (metal ion transporter); member 5	-0.2041	0.0325
1552303_a_at	LOC728772	similar to transmembrane protein 106A, transmembrane protein 106A	-0.3029	0.0258

1552307_a_at	C18orf17	chromosome 18 open reading frame 17	-2.3787	0.0003
1552309_a_at	NEXN	nexilin (F actin binding protein)	-2.5976	0
1552316_a_at	GIMAP1	GTPase; IMAP family member 1	-1.0167	0.0119
1552318_at	GIMAP1	GTPase; IMAP family member 1	-0.4435	0.0212
1552320_a_at	CCDC65	coiled-coil domain containing 65	-0.2206	0.0119
1552329_at	RBBP6	retinoblastoma binding protein 6	-1.1524	0.0091
1552349_a_at	PRSS33	protease; serine; 33	-0.1342	0.049
1552354_at	C19orf26	chromosome 19 open reading frame 26	-0.1703	0.0232
1552355_s_at	C19orf26	chromosome 19 open reading frame 26	-0.1558	0.0317
1552364_s_at	MSI2	musashi homolog 2 (Drosophila)	-1.7858	0
1552377_s_at	FAM18B2	family with sequence similarity 18; member B2	-0.2435	0.0151
1552395_at	TSSK3	testis-specific serine kinase 3	-0.2081	0.0003
1552402_at	CALML6	calmodulin-like 6	-0.1683	0.0006
1552409_a_at	ODF4	outer dense fiber of sperm tails 4	-0.1156	0.0285
1552418_at	TTLL10	tubulin tyrosine ligase-like family; member 10	-0.1344	0.006
1552423_at	ETV3	ets variant gene 3	-0.2456	0.0015
1552438_a_at	ANKAR	ankyrin and armadillo repeat containing	-0.1179	0.0482
1552440_at	ADMR	adrenomedullin receptor	-0.9897	0
1552459_a_at	MBD3L1	methyl-CpG binding domain protein 3-like 1	-0.1657	0.0049
1552467_at	DSCR10	Down syndrome critical region gene 10	-0.2076	0.0058
1552482_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-0.2143	0.0099
1552489_s_at	MPP4	membrane protein; palmitoylated 4 (MAGUK p55 subfamily member 4)	-0.1934	0.005
1552491_at	IDI2	isopentenyl-diphosphate delta isomerase 2	-0.3059	0
1552493_s_at	CYP11B1	cytochrome P450; family 11; subfamily B; polypeptide 1	-3.9161	0.0021
1552498_at	ZSCAN20	zinc finger and SCAN domain containing 20	-0.1907	0.0225
1552501_a_at	GPBAR1	G protein-coupled bile acid receptor 1	-0.3946	0
1552509_a_at	CD300LG	CD300 molecule-like family member g	-0.6338	0.005
1552519_at	ACVR1C	activin A receptor; type IC	-0.5458	0.0123
1552541_at	TAGAP	T-cell activation GTPase activating protein	-0.1693	0.0278
1552543_a_at	STON2	stonin 2	-0.1151	0.025
1552548_at	BSND	Bartter syndrome; infantile; with sensorineural deafness (Barttin)	-0.1727	0.0056
1552549_a_at	BSND	Bartter syndrome; infantile; with sensorineural deafness (Barttin)	-0.1413	0.0453
1552553_a_at	NLRC4	NLR family; CARD domain containing 4	-0.488	0.0011
1552568_at	RTP3	receptor (chemosensory) transporter protein 3	-0.1645	0.0124
1552585_s_at	GTF2A1L	general transcription factor IIA; 1-like	-0.1092	0.0313

1552586_at	TRPV3	transient receptor potential cation channel; subfamily V; member 3	-0.1404	0.0315
1552596_at	GAS2L2	growth arrest-specific 2 like 2	-0.1424	0.0217
1552598_at	KCNG4	potassium voltage-gated channel; subfamily G; member 4	-0.1935	0.009
1552602_at	CACNG5	calcium channel; voltage-dependent; gamma subunit 5	-0.2009	0.0094
1552605_s_at	C21orf74	chromosome 21 open reading frame 74	-0.1363	0.0061
1552626_a_at	TMEM163	transmembrane protein 163	-0.8446	0.0283
1552632_a_at	ARSG	arylsulfatase G	-0.5666	0.0035
1552637_at	PTPN11	protein tyrosine phosphatase; non-receptor type 11 (Noonan syndrome 1)	-0.1274	0.0198
1552658_a_at	NAV3	neuron navigator 3	-1.1411	0.0003
1552676_at	UCN3	urocortin 3 (stresscopin)	-0.2546	0.0004
1552690_a_at	CACNA2D4	calcium channel; voltage-dependent; alpha 2/delta subunit 4	-0.1149	0.0124
1552701_a_at	COP1	caspase-1 dominant-negative inhibitor pseudo-ICE	-1.2042	0.0441
1552711_a_at	CYB5D1	cytochrome b5 domain containing 1	-0.5403	0.0338
1552715_a_at	RXFP1	relaxin/insulin-like family peptide receptor 1	-1.3949	0
1552725_s_at	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif; 17	-0.1818	0.0065
1552731_at	ABRA	actin-binding Rho activating protein	-0.1448	0.0042
1552739_s_at	ST7L	suppression of tumorigenicity 7 like	-0.6041	0.0336
1552747_a_at	C3orf48	chromosome 3 open reading frame 48	-0.1323	0.0154
1552750_at	CIB3	calcium and integrin binding family member 3	-0.1767	0.0037
1552755_at	C9orf66	chromosome 9 open reading frame 66	-0.4247	0.0032
1552757_s_at			-0.2269	0.0001
1552761_at	SLC16A11	solute carrier family 16; member 11 (monocarboxylic acid transporter 11)	-0.2171	0.0052
1552767_a_at	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	-0.7095	0.0003
1552789_at	TLOC1	translocation protein 1	-1.1221	0
1552790_a_at	TLOC1	translocation protein 1	-1.9541	0
1552798_a_at	TLR4	toll-like receptor 4	-0.4149	0.0002
1552799_at	TSNARE1	t-SNARE domain containing 1	-0.1347	0.042
1552800_at	ABHD11	abhydrolase domain containing 11	-0.2626	0.0053
1552804_a_at	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	-0.1514	0.0208
1552807_a_at	SIGLEC10	sialic acid binding Ig-like lectin 10	-0.6772	0.0073
1552818_a_at	BRS3	bombesin-like receptor 3	-0.1286	0.0356
1552819_at	C21orf86	chromosome 21 open reading frame 86	-0.1179	0.0462
1552827_s_at	SLC26A7	solute carrier family 26; member 7	-0.1279	0.0104
1552829_at			-0.2603	0.0192
1552856_at	TMEM148	transmembrane protein 148	-0.1393	0.0013

1552857_a_at	HTR6	5-hydroxytryptamine (serotonin) receptor 6	-0.2154	0.0003
1552860_at	TCEB3C	transcription elongation factor B polypeptide 3C (elongin A3)	-0.2006	0.0032
1552863_a_at	CACNG6	calcium channel; voltage-dependent; gamma subunit 6	-0.2427	0.0195
1552865_a_at	IFLTD1	intermediate filament tail domain containing 1	-0.1514	0.0075
1552887_at	C10orf27	chromosome 10 open reading frame 27	-0.1891	0.0356
1552890_a_at	CABP4	calcium binding protein 4	-0.2035	0.0041
1552892_at	TNFRSF13C	tumor necrosis factor receptor superfamily; member 13C	-0.151	0.0026
1552893_at	CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	-0.3702	0
1552897_a_at	KCNG3	potassium voltage-gated channel; subfamily G; member 3	-1.371	0.0008
1552898_a_at	KCNG3	potassium voltage-gated channel; subfamily G; member 3	-0.1229	0.045
1552899_at	RP4-662A9.2	hypothetical protein MGC34034	-0.3644	0.0023
1552903_at	B4GALNT2	beta-1;4-N-acetyl-galactosaminyl transferase 2	-0.18	0.0211
1552917_at	IL29	interleukin 29 (interferon; lambda 1)	-0.1454	0.025
1552930_at	MMEL1	membrane metallo-endopeptidase-like 1	-0.2763	0.0326
1552971_at	SGCZ	sarcoglycan zeta	-0.1561	0.0049
1552988_at	C11orf65	chromosome 11 open reading frame 65	-0.2009	0.0037
1552998_at	DEFB125	defensin; beta 125	-0.1345	0.0291
1553002_at	DEFB105A	defensin; beta 105A, defensin; beta 105B	-0.1458	0.0032
1553009_s_at	REXO1L1	REX1; RNA exonuclease 1 homolog (S. cerevisiae)-like 1	-0.103	0.0417
1553019_at	TMC2	transmembrane channel-like 2	-0.1278	0.0249
1553027_a_at	KLHL4	kelch-like 4 (Drosophila)	-2.2886	0.0008
1553030_a_at	SUOX	sulfite oxidase	-0.6087	0.0001
1553033_at	SYTL5	synaptotagmin-like 5	-0.2721	0.0042
1553041_at	HTR3C	5-hydroxytryptamine (serotonin) receptor 3; family member C	-0.1565	0.0237
1553047_at	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase; type II; beta	-0.3005	0.0018
1553058_at	GIPC3	GIPC PDZ domain containing family; member 3	-0.1364	0.0238
1553059_at	PGLYRP3	peptidoglycan recognition protein 3	-0.1253	0.0023
1553063_at	GPR78	G protein-coupled receptor 78	-0.1751	0.0005
1553064_at	H1FOO	H1 histone family; member O; oocyte-specific	-0.1522	0.0461
1553071_a_at	MYOZ3	myozenin 3	-0.158	0.0184
1553074_at	ASB11	ankyrin repeat and SOCS box-containing 11	-0.157	0.0046
1553077_at	SDR-O	orphan short-chain dehydrogenase / reductase	-0.1779	0.0007
1553078_at	OR5P3	olfactory receptor; family 5; subfamily P; member 3	-0.1134	0.0127
1553082_at	CRYGN	crystallin; gamma N	-0.2397	0.0015

1553086_at	C11orf40	chromosome 11 open reading frame 40	-0.1259	0.0016
1553088_a_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	-0.1869	0.0447
1553089_a_at	WFDC2	WAP four-disulfide core domain 2	-0.1143	0.0148
1553096_s_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	-0.2471	0.0158
1553103_at	NFX1	nuclear transcription factor; X-box binding 1	-0.7263	0.0011
1553111_a_at	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	-0.7989	0.0031
1553114_a_at	PTK6	PTK6 protein tyrosine kinase 6	-0.1449	0.0332
1553118_at	THEM4	thioesterase superfamily member 4	-0.8313	0.002
1553129_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	-0.2318	0.0033
1553133_at	C9orf72	chromosome 9 open reading frame 72	-2.4106	0
1553134_s_at	C9orf72	chromosome 9 open reading frame 72	-0.2828	0.0204
1553156_at	LHX4	LIM homeobox 4	-0.2167	0
1553168_at	GRIK5	glutamate receptor; ionotropic; kainate 5	-0.1209	0.0347
1553174_at	JPH2	junctophilin 2	-0.1951	0.0004
1553176_at	SH2D1B	SH2 domain containing 1B	-0.144	0.0088
1553194_at	NEGR1	neuronal growth regulator 1	-0.2649	0
1553196_a_at	FCRL3	Fc receptor-like 3	-0.144	0.0306
1553202_at	STOX1	storkhead box 1	-0.2606	0.0009
1553204_at	C20orf200	chromosome 20 open reading frame 200	-0.1361	0.0155
1553205_at	C20orf200	Chromosome 20 open reading frame 200	-0.3077	0.0001
1553207_at	ARL10	ADP-ribosylation factor-like 10	-0.1217	0.0351
1553215_s_at	CCDC7	coiled-coil domain containing 7	-0.3134	0.0008
1553220_at	ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 13	-0.5455	0.0004
1553232_at	FAM82A	family with sequence similarity 82; member A	-0.181	0.0006
1553239_at	FAM124A	family with sequence similarity 124A	-0.1254	0.0393
1553255_at	FLJ32214	FLJ32214 protein	-0.1526	0.0236
1553257_at	GAL3ST3	galactose-3-O-sulfotransferase 3	-0.1624	0.0049
1553262_a_at	UTS2R	urotensin 2 receptor	-0.2454	0
1553275_s_at			-0.5562	0.0109
1553279_at	BTNL9	butyrophilin-like 9	-0.2119	0.0194
1553310_at			-0.2045	0.0004
1553314_a_at	KIF19	kinesin family member 19	-0.1456	0.0024
1553316_at	GPR82	G protein-coupled receptor 82	-0.2249	0.0025
1553317_s_at	GPR82	G protein-coupled receptor 82	-0.1789	0.0082
1553327_a_at	C10orf30	chromosome 10 open reading frame 30	-0.1183	0.014
1553328_a_at	SLC18A2	solute carrier family 18 (vesicular monoamine); member 2	-0.1931	0.0002

1553330_at	C7orf45	chromosome 7 open reading frame 45	-0.1345	0.0228
1553350_at	FAM123C	family with sequence similarity 123C	-0.1409	0.0206
1553359_at	FBXL18	F-box and leucine-rich repeat protein 18	-0.1987	0.0211
1553367_a_at	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	-0.1735	0.0227
1553372_at	FLJ23865	hypothetical protein FLJ23865	-0.2212	0.0346
1553395_a_at	CD200R1	CD200 receptor 1	-0.1809	0.0074
1553396_a_at	CCDC13	coiled-coil domain containing 13	-0.319	0.0347
1553412_at	AGBL4	ATP/GTP binding protein-like 4	-0.1294	0.0137
1553417_at	C11orf44	chromosome 11 open reading frame 44	-0.1671	0.0002
1553435_at	C18orf15	chromosome 18 open reading frame 15	-0.141	0.013
1553438_at	C11orf72	chromosome 11 open reading frame 72	-0.1556	0.0233
1553454_at	RPTN	repetin	-0.1023	0.0336
1553482_at	C15orf32	chromosome 15 open reading frame 32	-0.1092	0.0352
1553483_at	TSGA10IP	testis specific; 10 interacting protein	-0.1732	0.0198
1553486_a_at	C17orf78	chromosome 17 open reading frame 78	-0.1092	0.043
1553502_a_at	PALM2	PALM2-AKAP2 protein, paralemmin 2	-0.1168	0.0464
1553512_at	HOXC12	homeobox C12	-0.1738	0.0062
1553514_a_at	VNN3	vanin 3	-0.1615	0.0379
1553523_at	NLRP14	NLR family; pyrin domain containing 14	-0.1149	0.0275
1553537_at	KRT73	keratin 73	-0.1733	0.0031
1553544_at	GPR101	G protein-coupled receptor 101	-0.1207	0.0349
1553545_at	ILDR1	immunoglobulin-like domain containing receptor 1	-0.218	0.0005
1553552_at	TAAR8	trace amine associated receptor 8	-0.1117	0.0243
1553566_at	C12orf53	chromosome 12 open reading frame 53	-0.1385	0.0431
1553573_s_at	EFNA2	ephrin-A2	-0.1357	0.0047
1553583_a_at	THRSP	thyroid hormone responsive (SPOT14 homolog; rat)	-0.3804	0.0003
1553586_at	LOC283932	hypothetical protein LOC283932	-0.1241	0.0259
1553587_a_at	POLE4	polymerase (DNA-directed); epsilon 4 (p12 subunit)	-1.0933	0.0042
1553599_a_at	SYCP3	synaptonemal complex protein 3	-0.2746	0.0012
1553629_a_at	FAM71B	family with sequence similarity 71; member B	-0.1356	0.0368
1553633_s_at	NHEDC1	Na+/H+ exchanger domain containing 1	-0.2159	0.0043
1553637_s_at	TMCO5	transmembrane and coiled-coil domains 5	-0.1291	0.0219
1553644_at	C14orf49	chromosome 14 open reading frame 49	-0.1681	0.0318
1553663_a_at	LOC653419	similar to prepроneuropeptide B	-0.2464	0.0164
1553695_a_at	NLRX1	NLR family member X1	-0.4226	0.0091

1553727_at	B4GALNT3	beta-1;4-N-acetyl-galactosaminyl transferase 3	-0.2572	0.0011
1553730_x_at	LRRC43	leucine rich repeat containing 43	-0.1353	0.0495
1553736_at	CCDC131	coiled-coil domain containing 131	-0.5124	0
1553756_at	C9orf70	chromosome 9 open reading frame 70	-0.124	0.0218
1553757_at	IQCG	IQ motif containing G	-0.1394	0.0472
1553761_at	C22orf30	chromosome 22 open reading frame 30	-0.1242	0.0112
1553785_at	RASGEF1B	RasGEF domain family; member 1B	-0.1548	0.0103
1553787_at	C11orf45	chromosome 11 open reading frame 45	-0.4066	0
1553796_at	FLJ30594	hypothetical locus FLJ30594	-0.1698	0.0066
1553803_at	C17orf46	chromosome 17 open reading frame 46	-0.2194	0.0456
1553804_a_at	C17orf46	chromosome 17 open reading frame 46	-0.2005	0.0287
1553811_at	MGC14436	hypothetical protein MGC14436	-0.1499	0.0063
1553826_a_at	LOC146325	similar to hypothetical protein FLJ13841	-0.2172	0.0004
1553844_a_at	C10orf67	chromosome 10 open reading frame 67	-0.1305	0.0111
1553845_x_at	C10orf67	chromosome 10 open reading frame 67	-0.101	0.0412
1553847_a_at	SPERT	spermatid associated	-0.1305	0.0235
1553860_at	DCST1	DC-STAMP domain containing 1	-0.1374	0.0046
1553872_at	MGC33894	transcript expressed during hematopoiesis 2	-0.1542	0.0335
1553880_at	C10orf91	chromosome 10 open reading frame 91	-0.1397	0.0262
1553882_at			-0.1414	0.018
1553893_at	CCDC105	coiled-coil domain containing 105	-0.1897	0.0116
1553895_at	C11orf42	chromosome 11 open reading frame 42	-0.1778	0.0013
1553906_s_at	FGD2	FYVE; RhoGEF and PH domain containing 2	-2.1264	0
1553918_at	C21orf129	chromosome 21 open reading frame 129	-0.1759	0.0015
1553927_at	C7orf33	chromosome 7 open reading frame 33	-0.1391	0.028
1553945_at	GPHB5	glycoprotein hormone beta 5	-0.1517	0.0187
1553946_at	DCD	dermcidin	-0.1197	0.0261
1553954_at	ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	-1.2447	0.0001
1553955_at	CCDC128	coiled-coil domain containing 128	-0.8822	0.0046
1553960_at	SNX21	sorting nexin family member 21	-1.6185	0
1553961_s_at	SNX21	sorting nexin family member 21	-1.8627	0
1553971_a_at	GATS	opposite strand transcription unit to STAG3	-0.7744	0.0003
1553974_at	LOC128977	hypothetical protein LOC128977	-1.8195	0
1553978_at	MEF2B	myocyte enhancer factor 2B	-0.8836	0.0035
1554003_at	RGNEF	Rho-guanine nucleotide exchange factor	-1.502	0.0004

1554004_a_at	RGNEF	Rho-guanine nucleotide exchange factor	-1.2802	0.0016
1554014_at	CHD2	chromodomain helicase DNA binding protein 2	-1.057	0.0014
1554022_at	CCDC13	coiled-coil domain containing 13	-0.116	0.0209
1554041_at	C20orf141	chromosome 20 open reading frame 141	-0.114	0.0357
1554044_a_at	MRAP	melanocortin 2 receptor accessory protein	-3.903	0
1554049_s_at	WDR42A	WD repeat domain 42A	-0.4057	0.0005
1554065_at	FAM125B	family with sequence similarity 125; member B	-0.1229	0.0325
1554069_at	EPHA8	EPH receptor A8	-0.1374	0.04
1554080_at	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-1.136	0.0064
1554117_at	CCDC60	coiled-coil domain containing 60	-0.2529	0.0003
1554148_a_at	SLC33A1	solute carrier family 33 (acetyl-CoA transporter); member 1	-1.1572	0.0004
1554149_at	CLDND1	claudin domain containing 1	-0.4606	0.0325
1554157_a_at	WFDC8	WAP four-disulfide core domain 8	-0.1006	0.0278
1554173_at	CD300LB	CD300 molecule-like family member b	-0.2614	0.0109
1554176_a_at	C3orf33	chromosome 3 open reading frame 33	-0.3138	0.0064
1554188_at	C11orf53	chromosome 11 open reading frame 53	-0.1226	0.0155
1554192_s_at	C4orf23	chromosome 4 open reading frame 23	-0.1125	0.0399
1554201_at	CABP4	calcium binding protein 4	-0.3032	0.0275
1554205_s_at	ICA1L	islet cell autoantigen 1;69kDa-like	-0.2154	0.0017
1554206_at	TMLHE	trimethyllysine hydroxylase; epsilon	-0.4456	0.01
1554210_at	ZCCHC13	zinc finger; CCHC domain containing 13	-0.1849	0.002
1554222_at	MGC45922	hypothetical gene MGC45922	-0.2569	0.0365
1554237_at	SDCCAG8	serologically defined colon cancer antigen 8	-0.2256	0.0208
1554242_a_at	COCH	coagulation factor C homolog; cochlin (Limulus polyphemus)	-0.7185	0.0012
1554246_at	C1orf210	chromosome 1 open reading frame 210	-0.1685	0.0376
1554259_at	GPSM1	G-protein signaling modulator 1 (AGS3-like; C. elegans)	-0.177	0.0088
1554261_at	KLHL29	kelch-like 29 (Drosophila)	-0.1035	0.009
1554262_s_at	KLHL29	kelch-like 29 (Drosophila)	-0.2252	0.0014
1554281_at			-0.3168	0.0004
1554286_at	FLJ25758	hypothetical locus FLJ25758	-0.1137	0.0284
1554296_at	CYP19A1	cytochrome P450; family 19; subfamily A; polypeptide 1	-0.9638	0.0001
1554312_at	RNF170	ring finger protein 170	-0.1601	0.0173
1554318_at	LOC541473	FK506 binding protein 6; 36kDa pseudogene	-0.1456	0.0444
1554341_a_at	HEL308	DNA helicase HEL308	-0.9075	0.0022
1554342_s_at	HEL308	DNA helicase HEL308	-1.2559	0.0002

1554344_s_at	AQP12A	aquaporin 12A, similar to aquaporin 12A	-0.1648	0.0243
1554372_at			-0.1716	0.0369
1554377_a_at	CNTNAP4	contactin associated protein-like 4	-0.1123	0.0339
1554380_at	NEK11	NIMA (never in mitosis gene a)- related kinase 11	-0.1189	0.0012
1554386_at	CST9	cystatin 9 (testatin)	-0.1382	0.0079
1554405_a_at	C21orf100	chromosome 21 open reading frame 100	-0.1906	0.0029
1554418_s_at	SPOCK3	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 3	-0.1336	0.018
1554428_s_at	NLGN2	neuroligin 2	-0.1531	0.0399
1554438_at	KIAA1217	KIAA1217	-0.5089	0.0002
1554442_at	BEST1	bestrophin 1	-0.3032	0.0041
1554443_s_at	BEST1	bestrophin 1	-0.2056	0.0017
1554459_s_at	CFHR3	complement factor H-related 3	-0.2032	0
1554462_a_at	DNAJB9	DnaJ (Hsp40) homolog; subfamily B; member 9	-0.8733	0.0271
1554474_a_at	MOXD1	monooxygenase; DBH-like 1	-2.7785	0
1554483_at	TMEM37	transmembrane protein 37	-0.2996	0.0142
1554485_s_at	TMEM37	transmembrane protein 37	-1.0848	0.006
1554509_a_at	C10orf97	chromosome 10 open reading frame 97	-0.6082	0.0081
1554517_x_at	LOC203274	CDNA clone IMAGE:3941306, Full-length cDNA clone CS0DD001YM12 of Neuroblastoma Cot 50-normalized of Homo sapiens (human), Hypothetical protein LOC203274	-0.1316	0.0396
1554531_at	TTC12	tetratricopeptide repeat domain 12	-0.2071	0.0011
1554549_a_at	WDR20	WD repeat domain 20	-0.4716	0.0023
1554559_at	GPR62	G protein-coupled receptor 62	-0.2523	0.0017
1554571_at	APBB1IP	amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	-0.1355	0.0038
1554594_at	LOC201175	hypothetical protein LOC201175	-0.1668	0.0012
1554616_at	SERPINB8	serpin peptidase inhibitor; clade B (ovalbumin); member 8	-0.1848	0.0094
1554627_a_at	ASCC1	activating signal cointegrator 1 complex subunit 1	-1.2974	0
1554648_a_at	DUOXA1	dual oxidase maturation factor 1	-0.2019	0.0089
1554650_a_at		CDNA clone IMAGE:4476475	-0.2014	0.0184
1554652_s_at	MAST4	microtubule associated serine/threonine kinase family member 4	-0.1895	0.0282
1554668_a_at	C1orf179	chromosome 1 open reading frame 179	-0.1753	0
1554680_s_at	KCNS2	potassium voltage-gated channel; delayed-rectifier; subfamily S; member 2	-0.1727	0.0134
1554683_a_at	MGC50722	hypothetical MGC50722	-0.2538	0.0028
1554694_at	CCNY	cyclin Y	-0.1514	0.0039

1554707_at	C9orf68	chromosome 9 open reading frame 68	-0.152	0.0103
1554710_at	KCNMB1	potassium large conductance calcium-activated channel; subfamily M; beta member 1	-0.1555	0.0061
1554732_at	MGC24125	hypothetical protein MGC24125	-0.6454	0.0007
1554733_at	MGC24125	hypothetical protein MGC24125	-1.6163	0.026
1554745_at	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	-0.1401	0.0188
1554751_at		CDNA clone IMAGE:3528357	-0.156	0.0251
1554752_a_at		CDNA clone IMAGE:3528357	-0.1773	0.0175
1554759_at	SNIP	SNAP25-interacting protein	-0.209	0.024
1554763_at	UBE2DNL	ubiquitin-conjugating enzyme E2D N-terminal like	-0.1508	0.039
1554765_a_at	C11orf64	chromosome 11 open reading frame 64	-0.2003	0.0412
1554776_at	ZFP42	zinc finger protein 42 homolog (mouse)	-0.1212	0.0098
1554779_s_at	PHLDB2	pleckstrin homology-like domain; family B; member 2	-0.4443	0.0001
1554795_a_at	FBLIM1	filamin binding LIM protein 1	-0.2349	0.0268
1554801_at	C5orf40	chromosome 5 open reading frame 40	-0.1849	0.0164
1554809_at	LOC389199	hypothetical gene supported by BC031673	-0.2333	0.0038
1554821_a_at	ZBED1	zinc finger; BED-type containing 1	-2.8822	0
1554827_a_at	ADCY7	adenylate cyclase 7	-0.1516	0.0047
1554833_at	MCTP2	multiple C2 domains; transmembrane 2	-0.162	0.0005
1554847_at	ATP6V1B1	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B1 (Renal tubular acidosis with deafness)	-0.1546	0.039
1554872_a_at	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	-0.1811	0.0175
1554880_at	DKFZP434K028	DKFZP434K028 protein	-0.1453	0.0047
1554895_a_at	RHBDL2	rhomboid; veinlet-like 2 (Drosophila)	-0.1615	0.019
1554899_s_at	FCER1G	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	-2.5655	0.0004
1554906_a_at	MPHOSPH6	M-phase phosphoprotein 6	-0.4298	0.042
1554941_at	KLHL14	kelch-like 14 (Drosophila)	-0.1614	0.0155
1554942_a_at	KLHL14	kelch-like 14 (Drosophila)	-0.1799	0.0114
1554949_at	LOC554174	hypothetical LOC554174	-0.2117	0.0032
1554966_a_at	FILIP1L	filamin A interacting protein 1-like	-2.0874	0.0029
1554970_at	PDILT	protein disulfide isomerase-like protein of the testis	-0.1086	0.0171
1554974_at	ACY3	aspartoacylase (aminocyclase) 3	-0.1087	0.0238
1554989_at	KIAA0317	KIAA0317	-0.1252	0.0125
1554992_at	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	-0.2411	0.023
1555000_at		OK/SW-CL.36	-0.159	0.0019
1555028_at	BRD3	bromodomain containing 3	-0.1525	0.0006
1555031_at		Angrgm-52	-0.1132	0.0103

1555037_a_at	IDH1	isocitrate dehydrogenase 1 (NADP+); soluble	-0.7302	0.001
1555040_at	C12orf33	chromosome 12 open reading frame 33	-0.1078	0.0396
1555044_a_at	KBTBD5	kelch repeat and BTB (POZ) domain containing 5	-0.2338	0.0001
1555052_a_at	SYT9	synaptotagmin IX	-0.273	0.0036
1555053_at	SYT9	synaptotagmin IX	-0.1089	0.0068
1555060_a_at	IKZF2	IKAROS family zinc finger 2 (Helios)	-0.1512	0.0317
1555076_at	ARHGAP25	Rho GTPase activating protein 25	-0.1383	0.0004
1555083_at	MGC34774	ribosomal protein L13A pseudogene	-0.1953	0.0008
1555084_at			-0.21	0.0234
1555099_at	MPP4	membrane protein; palmitoylated 4 (MAGUK p55 subfamily member 4)	-0.1296	0.0223
1555100_at	C2orf13	chromosome 2 open reading frame 13	-0.1509	0.0086
1555116_s_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1	-0.1433	0.0449
1555129_at			-0.1136	0.0242
1555141_a_at	NHEDC1	Na+/H+ exchanger domain containing 1	-0.4663	0
1555142_at	NHEDC1	Na+/H+ exchanger domain containing 1	-0.1125	0.0415
1555159_at	TMEM74	Transmembrane protein 74	-0.1084	0.0284
1555165_a_at	PGPEP1	pyroglutamyl-peptidase I	-0.2191	0.0071
1555191_a_at	FHL5	four and a half LIM domains 5	-0.7196	0
1555204_at			-0.1439	0.006
1555205_at			-0.1146	0.0237
1555209_at	LOC439951	hypothetical LOC439951	-0.1513	0.0036
1555212_at	OR8B8	olfactory receptor; family 8; subfamily B; member 8	-0.1525	0.0049
1555217_at	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	-0.1384	0.0137
1555231_a_at	C21orf88	chromosome 21 open reading frame 88	-0.1432	0.0263
1555236_a_at	PGC	progastricsin (pepsinogen C)	-0.1481	0.0462
1555237_at		CDNA clone IMAGE:4336144	-0.1331	0.0173
1555238_at	TIP39	tuberoinfundibular 39 residue protein precursor	-0.2575	0.0031
1555245_s_at	RP1L1	retinitis pigmentosa 1-like 1	-0.1467	0.0008
1555265_at	ABCC13	ATP-binding cassette; sub-family C (CFTR/MRP); member 13	-0.1058	0.0347
1555286_at	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-0.108	0.0481
1555289_at	SEC16B	SEC16 homolog B (S. cerevisiae)	-0.1089	0.0308
1555298_a_at	VWA3B	von Willebrand factor A domain containing 3B	-0.1121	0.0053
1555304_a_at	KCNH5	potassium voltage-gated channel; subfamily H (eag-related); member 5	-0.239	0.0002
1555306_a_at	ECE2	endothelin converting enzyme 2	-0.1524	0.0228

1555313_a_at	MCF2	MCF.2 cell line derived transforming sequence	-1.5122	0.0355
1555320_a_at	STAB1	stabilin 1	-0.1609	0.0026
1555321_at	ACOT11	acyl-CoA thioesterase 11	-0.1412	0.0103
1555339_at	RAP1A	RAP1A; member of RAS oncogene family	-0.1478	0.012
1555377_at	OR4D2	olfactory receptor; family 4; subfamily D; member 2	-0.1594	0.0417
1555379_at	MGC52498	hypothetical protein MGC52498	-0.1609	0.0088
1555395_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-0.1429	0.0119
1555396_s_at	LOC340602	similar to CG32656-PA	-0.1388	0.0182
1555401_at	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	-0.1111	0.0303
1555403_a_at	CDH19	cadherin 19; type 2	-0.2455	0
1555404_a_at	DUOXA1	dual oxidase maturation factor 1	-0.1936	0.0032
1555407_s_at	FGD3	FYVE; RhoGEF and PH domain containing 3	-0.1112	0.0161
1555456_at		PRbBP-39	-0.1369	0.0062
1555465_at	MCOLN2	mucolipin 2	-0.8678	0.0065
1555483_x_at	FBLIM1	filamin binding LIM protein 1	-0.1369	0.0135
1555490_s_at	PDZD3	PDZ domain containing 3	-0.1279	0.0067
1555497_a_at	CYP4B1	cytochrome P450; family 4; subfamily B; polypeptide 1	-0.8782	0
1555499_a_at	IL28RA	interleukin 28 receptor; alpha (interferon; lambda receptor)	-0.1167	0.024
1555503_a_at	TMCC2	transmembrane and coiled-coil domain family 2	-0.1641	0.0164
1555516_at	FOXP2	forkhead box P2	-0.1908	0.0225
1555523_a_at	FYCO1	FYVE and coiled-coil domain containing 1	-0.1676	0.0283
1555540_at	TGFB3	transforming growth factor; beta 3	-0.1198	0.0361
1555545_at	KLK2	kallikrein-related peptidase 2	-0.1899	0.0054
1555551_at	SERPINB5	serpin peptidase inhibitor; clade B (ovalbumin); member 5	-0.1122	0.0434
1555553_a_at	SLC22A7	solute carrier family 22 (organic anion transporter); member 7	-0.2412	0.0004
1555554_at	RP11-49G10.8	breast cancer and salivary gland expression gene	-0.1617	0.0307
1555579_s_at	PTPRM	protein tyrosine phosphatase; receptor type; M	-1.0167	0.0272
1555580_at			-0.1647	0.0472
1555585_a_at	FAM71B	family with sequence similarity 71; member B	-0.2069	0.0061
1555587_at	PDZRN3	PDZ domain containing RING finger 3	-0.1211	0.0262
1555600_s_at	APOL4	apolipoprotein L; 4	-0.2458	0.0008
1555616_at			-0.2466	0.0487
1555617_x_at			-0.2184	0.0173
1555620_a_at	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	-0.1815	0.0042
1555626_a_at	SLAMF1	signaling lymphocytic activation molecule family member 1	-0.2104	0.0026

1555630_a_at	RAB34	RAB34; member RAS oncogene family	-4.0485	0
1555634_a_at	LILRA5	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 5	-0.146	0.0475
1555645_at		FGF-2 activity-associated protein 2 (GAFA2)	-0.1148	0.0131
1555646_at			-0.119	0.0173
1555656_at	CD300LG	CD300 molecule-like family member g	-0.1659	0.014
1555666_at	PTPRS	protein tyrosine phosphatase; receptor type; S	-0.1504	0.0054
1555673_at	LOC728285	similar to keratin associated protein 2-4	-0.1583	0.0064
1555678_at	ST3GAL3	ST3 beta-galactoside alpha-2;3-sialyltransferase 3	-0.199	0.0117
1555681_at		MUSP1 (MUSP1)	-0.1009	0.035
1555703_at	ST3GAL3	ST3 beta-galactoside alpha-2;3-sialyltransferase 3	-0.3986	0.0006
1555724_s_at	TAGLN	transgelin	-3.1854	0
1555728_a_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	-2.1177	0.0007
1555740_a_at	MRAP	melanocortin 2 receptor accessory protein	-4.0406	0
1555741_at	MRAP	melanocortin 2 receptor accessory protein	-2.2963	0
1555742_at			-0.428	0.0059
1555746_at	CD79B	CD79b molecule; immunoglobulin-associated beta	-0.2	0.0088
1555752_at	STH	saitohin	-0.1174	0.0355
1555763_x_at	MKL1	Megakaryoblastic leukemia (translocation) 1	-0.2704	0.0168
1555764_s_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	-0.4582	0.0123
1555765_a_at	GNG4	guanine nucleotide binding protein (G protein); gamma 4	-0.3078	0.0039
1555775_a_at	LOC651951	similar to zygote arrest 1, zygote arrest 1	-0.1163	0.0216
1555792_a_at	CCDC116	coiled-coil domain containing 116	-0.1569	0.0363
1555809_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	-0.1825	0.0234
1555811_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-0.2092	0.0124
1555812_a_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-1.1357	0.0126
1555819_s_at	SAMD14	sterile alpha motif domain containing 14	-0.1022	0.0251
1555822_at	FAM138B	family with sequence similarity 138; member B	-0.1659	0.0059
1555867_at	GNG4	guanine nucleotide binding protein (G protein); gamma 4	-0.4172	0.012
1555872_a_at	MGC21881	hypothetical locus MGC21881	-0.8127	0.0213
1555874_x_at	MGC21881	hypothetical locus MGC21881	-1.2074	0.0004
1555878_at	RPS24	Ribosomal protein S24	-1.6418	0.0009
1555886_at	PDSS2	prenyl (decaprenyl) diphosphate synthase; subunit 2	-2.1594	0
1555889_a_at	CRTAP	cartilage associated protein	-0.3758	0.027

1555897_at	AOF2	amine oxidase (flavin containing) domain 2	-0.5693	0.0163
1555914_a_at	FLJ20433	hypothetical protein FLJ20433	-0.1408	0.0449
1555950_a_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-2.3093	0
1555962_at	B3GNT7	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 7	-1.5887	0
1555963_x_at	B3GNT7	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 7	-1.7404	0
1555979_at	FLJ39609	Hypothetical protein FLJ39609	-0.1671	0.0003
1555980_a_at	FLJ39609	Hypothetical protein FLJ39609	-0.2623	0.0004
1555990_at	RP1-127L4.6	hypothetical protein LOC150297	-0.1337	0.0091
1555995_a_at			-0.1307	0.0098
1555997_s_at	IGFBP5	insulin-like growth factor binding protein 5	-1.8269	0
1556001_at	LOC284939	hypothetical protein LOC284939	-0.2365	0.0009
1556014_at	MESP2	mesoderm posterior 2 homolog (mouse)	-0.1498	0.0468
1556017_at	NBEAL2	neurobeachin-like 2	-0.1888	0.0003
1556026_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	-0.3099	0.0477
1556030_at	SMTN	Smoothelin	-0.2866	0
1556037_s_at	HHIP	hedgehog interacting protein	-0.4186	0
1556056_at	SNF1LK2	SNF1-like kinase 2	-0.5153	0
1556075_at			-0.1287	0.0411
1556107_at		MRNA; cDNA DKFZp667C1617 (from clone DKFZp667C1617)	-0.3024	0.0149
1556149_at	ARVCF	armadillo repeat gene deletes in velocardiofacial syndrome	-0.118	0.0244
1556163_a_at	IGSF3	immunoglobulin superfamily; member 3	-0.1542	0.0028
1556185_a_at		CDNA clone IMAGE:5260162	-2.9956	0
1556232_at	KIF6	kinesin family member 6	-0.1413	0.0066
1556247_a_at		CDNA FLJ40468 fis; clone TESTI2042400	-0.2314	0.002
1556253_s_at		CDNA FLJ37989 fis; clone CTONG2011676	-0.4943	0.0237
1556271_at		CDNA clone IMAGE:4830283	-0.129	0.0035
1556274_at		CDNA clone IMAGE:5271140	-0.3309	0.0012
1556281_at		Full length insert cDNA clone YI54A07	-0.1098	0.0457
1556283_s_at	FGFR1OP2	FGFR1 oncogene partner 2	-1.3272	0.0016
1556292_s_at	DKFZp564N2472	hypothetical protein DKFZp564N2472	-0.1353	0.0292
1556294_at		MRNA; cDNA DKFZp547P0115 (from clone DKFZp547P0115)	-0.1252	0.037
1556296_at		CDNA clone IMAGE:5295605	-0.1659	0.0067
1556304_s_at		CDNA clone IMAGE:4829494	-0.1646	0.0174
1556312_at	FLJ34931	similar to cDNA sequence BC027072	-0.1039	0.0183
1556321_a_at		MRNA full length insert cDNA clone EUROIMAGE 283668	-0.9681	0

1556328_at		CDNA clone IMAGE:5301690	-0.4288	0
1556329_a_at		CDNA clone IMAGE:5301690	-1.1963	0
1556332_at		CDNA FLJ38412 fis; clone FEBRA2009385	-0.4993	0
1556340_at	MAPK12	mitogen-activated protein kinase 12	-0.3563	0.0069
1556356_at	ERICH1	glutamate-rich 1	-0.1868	0.008
1556361_s_at	ANKRD13C	ankyrin repeat domain 13C	-1.1885	0
1556365_at	RP3-398D13.1	hypothetical protein FLJ33708	-0.1918	0.0016
1556374_s_at		CDNA clone IMAGE:5270126	-0.13	0.0304
1556385_at		CDNA FLJ39926 fis; clone SPLEN2021157	-0.5426	0
1556411_s_at	KY	kyphoscoliosis peptidase	-0.2265	0.0002
1556413_a_at		Full length insert cDNA clone ZE08G04	-0.1055	0.0287
1556426_at	HEXA	hexosaminidase A (alpha polypeptide)	-0.2105	0.001
1556427_s_at	LOC221091	similar to hypothetical protein	-1.9585	0
1556435_at	LOC400622	hypothetical LOC400622	-0.1791	0.0016
1556447_at	LOC285370	hypothetical protein LOC285370	-0.1049	0.0459
1556451_at		MRNA; cDNA DKFZp667B1520 (from clone DKFZp667B1520)	-0.3653	0.0014
1556456_at	FLJ39739	hypothetical FLJ39739	-0.2345	0.0057
1556467_at	ZNF80	Zinc finger protein 80	-0.1733	0.007
1556477_a_at	LOC283485	hypothetical protein LOC283485	-0.1297	0.0337
1556496_a_at		Full length insert cDNA clone ZD79H01	-0.1216	0.0456
1556507_at		CDNA clone IMAGE:5267328	-0.2328	0.0165
1556508_s_at		CDNA clone IMAGE:5267328	-0.1332	0.0179
1556513_at	ZNF573	zinc finger protein 573	-0.1483	0.0027
1556514_at	LOC338809	hypothetical protein LOC338809	-0.1361	0.0162
1556529_a_at	LOC285326	hypothetical protein LOC285326	-0.1496	0.0421
1556533_at	C17orf52	chromosome 17 open reading frame 52	-0.1608	0.0267
1556558_s_at	FLJ36665	hypothetical protein FLJ36665	-0.1961	0.007
1556573_s_at	LOC286178	hypothetical protein LOC286178	-0.1045	0.0386
1556579_s_at	IGSF10	immunoglobulin superfamily; member 10	-1.6924	0.0001
1556606_at	NAV2	neuron navigator 2	-0.6509	0.0005
1556607_at	EHD4	EH-domain containing 4	-0.2584	0.0094
1556645_s_at		Homo sapiens; clone IMAGE:6016214; mRNA	-0.3754	0.0009
1556669_a_at		Full length insert cDNA clone YR71G12	-0.1146	0.036
1556670_at		CDNA FLJ25849 fis; clone TST08968	-0.1477	0.0082
1556671_s_at		CDNA FLJ25849 fis; clone TST08968	-0.2499	0.0009
1556695_a_at	FLJ42709	Hypothetical gene supported by AK124699	-0.6377	0
1556696_s_at	FLJ42709	Hypothetical gene supported by AK124699	-0.4996	0.0002

1556706_at		CDNA FLJ31687 fis; clone NT2RI2005473	-0.162	0.0424
1556718_s_at		CDNA FLJ35483 fis; clone SMINT2008277	-0.1803	0.0121
1556727_at	PRCD	progressive rod-cone degeneration	-0.1882	0.0165
1556739_at	FLJ35785	hypothetical protein FLJ35785, similar to golgi autoantigen; golgin subfamily a; 8A	-0.1339	0.0209
1556740_at		CDNA FLJ35959 fis; clone TESTI2012444	-0.1111	0.0386
1556747_a_at		CDNA FLJ39784 fis; clone SPLEN2002314	-0.2534	0.0256
1556758_at	C10orf18	chromosome 10 open reading frame 18	-0.2862	0
1556775_at		CDNA clone IMAGE:5271366	-0.536	0
1556797_at	LOC386597	hypothetical protein LOC386597	-0.3226	0.0269
1556805_at		CDNA clone IMAGE:5314388	-0.4497	0
1556822_s_at	LOC116412	Hypothetical protein BC012365	-0.1823	0.0057
1556827_at	LOC339929	hypothetical protein LOC339929	-0.2699	0.0012
1556829_at	LOC732159	TCDD-inducible poly(ADP-ribose) polymerase, hypothetical protein LOC732159	-0.1859	0.01
1556844_at		CDNA clone IMAGE:4827624	-0.1433	0.0071
1556852_a_at		CDNA FLJ33171 fis; clone ADRGL2000644	-0.2783	0.0008
1556854_at	LOC283501	hypothetical protein LOC283501	-0.1923	0.0004
1556856_at		CDNA FLJ25233 fis; clone STM01789	-0.1242	0.0123
1556883_a_at	LOC440896	hypothetical gene supported by AK127288; AY343901	-0.1446	0.0263
1556900_at	LOC149773	hypothetical protein LOC149773	-0.1551	0.0332
1556909_at		CDNA clone IMAGE:4830327	-0.1659	0.0384
1556914_at		CDNA clone IMAGE:4838482	-0.2343	0.0071
1556916_a_at		CDNA clone IMAGE:5295621	-0.1389	0.0362
1556928_at		Full length insert cDNA clone ZE01F11	-0.322	0
1556971_a_at		CDNA clone IMAGE:5272053	-0.1349	0.0337
1556989_at		Full length insert cDNA clone YZ35C05	-1.0579	0.0211
1556990_at	PERP	PERP; TP53 apoptosis effector	-0.1009	0.0385
1557004_at	LOC285389	hypothetical protein LOC285389	-0.1338	0.008
1557007_a_at		CDNA clone IMAGE:4826791	-0.1638	0.016
1557017_at		CDNA clone IMAGE:5312582	-0.13	0.0076
1557018_a_at		CDNA clone IMAGE:5312582	-0.1923	0.0011
1557030_at	GAB1	GRB2-associated binding protein 1	-0.1235	0.0198
1557050_at	HOXA2	Homeobox A2	-1.5376	0
1557051_s_at	HOXA2	Homeobox A2	-2.5652	0
1557105_a_at		MRNA; cDNA DKFZp686P1116 (from clone DKFZp686P1116)	-0.1986	0.0147
1557116_at	APOL6	apolipoprotein L; 6	-0.7767	0.0039
1557121_s_at		Homo sapiens; clone IMAGE:6045023; mRNA	-0.6296	0.005

1557122_s_at	GABRB2	gamma-aminobutyric acid (GABA) A receptor; beta 2	-1.6628	0
1557123_a_at	RP4-756G23.1	hypothetical protein BC012882	-0.4557	0
1557146_a_at	FLJ32252	hypothetical protein FLJ32252	-3.2077	0
1557226_a_at	LOC374569	Similar to Lysophospholipase	-0.2242	0.0031
1557232_at		CDNA clone IMAGE:4797260	-0.2399	0.0027
1557241_a_at		Full length insert cDNA clone ZD89B07	-0.212	0.0012
1557276_at		CDNA clone IMAGE:4828503	-0.1444	0.0176
1557285_at	LOC727738	Similar to Amphiregulin precursor (AR) (Colorectum cell-derived growth factor) (CRDGF)	-0.2982	0.0059
1557286_at		CDNA FLJ10145 fis; clone HEMBA1003322	-1.0844	0
1557287_at		CDNA clone IMAGE:4837072	-0.1437	0.005
1557295_a_at		CDNA FLJ25198 fis; clone REC04733	-0.1099	0.0076
1557334_a_at	C20orf42	chromosome 20 open reading frame 42	-0.1243	0.0117
1557338_x_at		Homo sapiens; clone IMAGE:5396883; mRNA	-0.1553	0.0434
1557341_x_at		Homo sapiens; clone IMAGE:5190399; mRNA	-0.1428	0.0109
1557349_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	-0.1773	0.0195
1557353_at		CDNA FLJ38904 fis; clone NT2NE2001524	-0.7077	0.0191
1557400_at		CDNA FLJ38935 fis; clone NT2NE2014681	-0.4532	0.0007
1557404_at		CDNA clone IMAGE:5266464	-0.1235	0.0192
1557448_a_at		CDNA clone IMAGE:5298376	-0.1131	0.0226
1557457_at		FLJ00054 protein	-0.5459	0.0002
1557459_at		MRNA; cDNA DKFZp547O0210 (from clone DKFZp547O0210)	-1.0714	0.016
1557475_at		CDNA clone IMAGE:5274197	-0.1036	0.0062
1557515_at		Full length insert cDNA clone YA81F02	-0.1073	0.0184
1557532_at	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 7; 14.5kDa	-0.2226	0.0161
1557535_at	PALLD	Palladin; cytoskeletal associated protein	-0.1304	0.0397
1557553_at	PPP1R12B	Protein phosphatase 1; regulatory (inhibitor) subunit 12B	-0.223	0.0292
1557578_at	PHLDB2	Pleckstrin homology-like domain; family B; member 2	-1.4121	0.0004
1557601_s_at	KIAA1257	KIAA1257	-0.1181	0.0139
1557613_at	FLJ39534	hypothetical protein FLJ39534	-0.2256	0.0004
1557624_at		CDNA FLJ34224 fis; clone FCBBF3023078	-0.4678	0.0016
1557628_s_at	LOC283745	hypothetical protein LOC283745	-0.1009	0.0327
1557658_at		CDNA FLJ33670 fis; clone BRAMY2028783	-0.1783	0.035
1557665_at		CDNA FLJ11096 fis; clone PLACE1005480	-0.239	0.0004
1557669_at		CDNA FLJ35343 fis; clone PROST2015932	-0.2248	0.0046

1557672_s_at		CDNA clone IMAGE:5297153	-0.2022	0.0123
1557679_at	C8orf68	chromosome 8 open reading frame 68	-0.1826	0.0022
1557693_at		CDNA clone IMAGE:5303580	-0.1374	0.0478
1557702_at		CDNA clone IMAGE:5265308	-0.1683	0.0154
1557706_at	ZHX2	zinc fingers and homeoboxes 2	-0.8972	0.0001
1557713_at		MRNA; cDNA DKFZp686H1927 (from clone DKFZp686H1927)	-0.1404	0.0082
1557723_at	LOC285847	hypothetical protein LOC285847	-0.124	0.0329
1557731_at	LOC400620	hypothetical gene supported by BC035399	-0.1416	0.0452
1557753_at		CDNA clone IMAGE:5265890	-0.1319	0.0041
1557761_s_at	LOC400794	hypothetical gene supported by BC030596	-0.1823	0.0345
1557774_at		Homo sapiens; clone IMAGE:4498937; mRNA	-0.1406	0.007
1557790_at		CDNA clone IMAGE:5273123	-0.1912	0.004
1557791_at		CDNA clone IMAGE:5303925	-0.1155	0.0131
1557795_s_at	NTRK3	neurotrophic tyrosine kinase; receptor; type 3	-0.1322	0.0076
1557797_a_at		MRNA; cDNA DKFZp566D053 (from clone DKFZp566D053)	-0.529	0.0027
1557807_a_at		Full length insert cDNA clone ZB77E08	-0.1982	0.0167
1557832_at		CDNA FLJ20833 fis; clone ADKA02957	-0.3673	0.0035
1557848_at		CDNA clone IMAGE:5272084	-0.1546	0.0137
1557852_at		CDNA FLJ31245 fis; clone KIDNE2005062	-0.7207	0.0166
1557865_at		CDNA clone IMAGE:5299063	-0.1115	0.0232
1557867_s_at	C9orf117	chromosome 9 open reading frame 117	-0.2018	0.0342
1557892_at		CDNA clone IMAGE:5266893	-0.1218	0.0267
1557897_at	CCDC85A	Coiled-coil domain containing 85A	-0.1836	0.0084
1557898_at		CDNA clone IMAGE:5297808	-0.1512	0.0106
1557907_x_at	MUC12	mucin 12; cell surface associated	-0.1146	0.0076
1557919_a_at	LOC648232	Hypothetical protein LOC648232	-0.1284	0.0015
1557921_s_at		Homo sapiens; clone IMAGE:4447022; mRNA	-1.8013	0
1557943_at	CNP	2';3'-cyclic nucleotide 3' phosphodiesterase	-0.4876	0
1557948_at	LOC653583	pleckstrin homology-like domain; family B; member 3, similar to pleckstrin homology-like domain; family B; member 1	-1.6005	0
1557964_at	EIF4G2	eukaryotic translation initiation factor 4 gamma; 2	-0.1554	0.0032
1557994_at	TTN	titin	-0.2444	0.0157
1558009_at	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter); member 2	-0.1688	0.0047
1558010_s_at	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter); member 2	-0.248	0.0152

1558066_s_at	TBC1D16	TBC1 domain family; member 16	-0.1163	0.026
1558101_at			-0.4534	0.0097
1558102_at		CDNA FLJ30876 fis; clone FEBRA2004412	-0.695	0.0075
1558121_at		CDNA FLJ39178 fis; clone OCBBF2004104	-0.153	0.0335
1558142_at	TNRC6B	trinucleotide repeat containing 6B	-0.7672	0.0213
1558166_at	MGC16275	hypothetical protein MGC16275	-0.4868	0
1558167_a_at	MGC16275	hypothetical protein MGC16275	-0.4654	0
1558168_at	C3orf47	chromosome 3 open reading frame 47	-0.1516	0.0269
1558211_s_at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	-0.2616	0.0001
1558212_at	FLJ35024	hypothetical LOC401491	-0.3565	0.0003
1558225_at		CDNA clone IMAGE:5303125	-0.1372	0.0042
1558238_at	TNRC18	trinucleotide repeat containing 18	-0.1348	0.0133
1558289_at	LOC285398	RFT1 homolog (S. cerevisiae), hypothetical locus LOC285398	-0.1578	0.0054
1558295_a_at	PPFIA2	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 2	-0.1718	0.0082
1558300_at	EFCAB5	EF-hand calcium binding domain 5	-0.1933	0.0051
1558333_at	C22orf15	chromosome 22 open reading frame 15	-0.1617	0.0012
1558343_at		Full length insert cDNA clone YI54B09	-0.1306	0.0252
1558345_a_at	LOC439911	hypothetical gene supported by NM_194304	-1.7593	0
1558387_at		CDNA clone IMAGE:4817707	-0.5422	0.0349
1558388_a_at		CDNA clone IMAGE:4817707	-1.3504	0.025
1558400_x_at	ANKRD24	ankyrin repeat domain 24	-0.1172	0.0122
1558420_at	LOC400258	similar to RIKEN cDNA A530016L24 gene	-0.2865	0
1558421_a_at	LOC400258	similar to RIKEN cDNA A530016L24 gene	-0.4479	0
1558437_at		Epsilon ; IgE=membrane-bound IgE; epsilon m/s isoform {alternative splicing} [human; mRNA Partial; 216 nt], Immunoglobulin epsilon chain	-0.1599	0.0059
1558487_a_at	TMED4	transmembrane emp24 protein transport domain containing 4	-1.6983	0.0002
1558507_at	C1orf53	chromosome 1 open reading frame 53	-0.4263	0.0377
1558508_a_at	C1orf53	chromosome 1 open reading frame 53	-1.5339	0.0038
1558546_at	DNASE1	deoxyribonuclease I	-0.1181	0.0336
1558574_at		CDNA clone IMAGE:6049242	-0.1136	0.0349
1558584_at	UBL4B	ubiquitin-like 4B	-0.2	0.0027
1558586_at	ZNF33B	zinc finger protein 33B	-0.3866	0.0087
1558590_at	LOC731602	methyltransferase 11 domain containing 1, similar to methyltransferase 11 domain containing 1 isoform 2	-0.173	0.0064

1558594_at	C14orf176	Chromosome 14 open reading frame 176	-0.1679	0.0314
1558643_s_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	-0.2638	0.0074
1558647_at	SH3D19	SH3 domain protein D19	-0.1658	0.0338
1558661_at		Homo sapiens; clone IMAGE:5539086; mRNA	-0.1188	0.0077
1558682_at	HMGA2	high mobility group AT-hook 2	-0.2107	0.0011
1558687_a_at		Full length insert cDNA clone ZD83D05	-0.1399	0.0198
1558689_a_at	LOC441461	hypothetical gene supported by BC030123	-0.2642	0.0285
1558703_at	SLC46A1	solute carrier family 46; member 1	-1.6878	0
1558743_at	ZNF620	zinc finger protein 620	-0.1127	0.0267
1558760_at		Homo sapiens; clone IMAGE:5243718; mRNA	-0.1706	0.0156
1558769_s_at	DNAH1	dynein; axonemal; heavy chain 1	-0.1121	0.0201
1558795_at	LOC728052	Hypothetical protein LOC728052	-0.2529	0.0209
1558796_a_at	LOC728052	hypothetical protein LOC728052	-0.3177	0.0154
1558804_at		CDNA clone IMAGE:5263963	-0.2499	0.0159
1558815_at	SORBS2	sorbin and SH3 domain containing 2	-1.9669	0.0006
1558827_a_at	C20orf174	chromosome 20 open reading frame 174	-0.1369	0.0247
1558834_s_at	C1orf62	chromosome 1 open reading frame 62	-0.1305	0.0474
1558847_at		CDNA FLJ34734 fis; clone MESAN2006971	-0.1597	0.0118
1558852_at		CDNA FLJ31186 fis; clone KIDNE2000335	-0.1071	0.0298
1558868_a_at	DSE	Dermatan sulfate epimerase	-0.1104	0.023
1558875_at	SREBF1	sterol regulatory element binding transcription factor 1	-0.4111	0
1558881_at	LOC145820	hypothetical protein LOC145820	-2.3211	0
1558894_a_at	CCDC67	coiled-coil domain containing 67	-0.139	0.0163
1558915_a_at	PEX14	peroxisomal biogenesis factor 14	-0.2146	0.0079
1558944_at	CACNA1A	Calcium channel; voltage-dependent; P/Q type; alpha 1A subunit	-0.2132	0.0041
1558947_at		Full length insert cDNA clone ZD90B10	-0.1258	0.0142
1558950_at		Homo sapiens; clone IMAGE:4647355; mRNA	-0.1154	0.0121
1558954_at	SNORA78	small nucleolar RNA; H/ACA box 78	-0.1392	0.0048
1558960_a_at		CDNA FLJ34838 fis; clone NT2NE2010654	-0.1383	0.0048
1558984_at	MAP3K11	mitogen-activated protein kinase kinase kinase 11	-0.1257	0.0241
1559017_at		CDNA FLJ38915 fis; clone NT2NE2008867	-0.1572	0.0029
1559029_at	LOC286154	Hypothetical protein LOC286154	-0.1062	0.0419
1559034_at	SIRPB2	signal-regulatory protein beta 2	-0.4144	0.0007
1559057_at	CXorf45	chromosome X open reading frame 45	-0.2389	0.0154
1559061_at	LOC253962	hypothetical protein LOC253962	-0.1992	0.0149

1559066_at		Transcribed locus	-0.1078	0.038
1559067_a_at		Transcribed locus	-0.6582	0.0132
1559091_s_at	FGD2	FYVE; RhoGEF and PH domain containing 2	-0.2258	0
1559131_a_at		Homo sapiens; clone IMAGE:5189615; mRNA	-0.1801	0.0334
1559138_a_at	SPATA19	spermatogenesis associated 19	-0.1008	0.0214
1559140_at	FAM87A	family with sequence similarity 87; member A	-0.2828	0.039
1559166_at		CDNA FLJ38526 fis; clone HCHON2000898	-0.1626	0.0059
1559195_at		CDNA clone IMAGE:5302711	-0.1065	0.0319
1559218_s_at	NFYC	nuclear transcription factor Y; gamma	-0.3003	0.0039
1559232_a_at		Homo sapiens; clone IMAGE:4732808; mRNA	-1.2348	0.0005
1559239_s_at	ACAT1	Acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	-0.3113	0.006
1559245_at		Clone IMAGE:121018 mRNA sequence	-0.1524	0.0322
1559254_at	C21orf113	chromosome 21 open reading frame 113	-0.1189	0.034
1559272_at	EXOC3L	exocyst complex component 3-like	-0.1626	0.0132
1559277_at	FLJ35700	hypothetical protein FLJ35700	-0.2919	0.0006
1559321_at		Homo sapiens; clone IMAGE:5528576; mRNA	-0.1785	0.0047
1559351_at		CDNA clone IMAGE:5314400	-1.9522	0
1559362_at		CDNA clone IMAGE:5302421	-0.265	0.0155
1559376_at	C1orf203	chromosome 1 open reading frame 203	-0.1534	0.0061
1559392_s_at	SYT7	synaptotagmin VII	-0.116	0.0489
1559393_at	ALDH1L2	aldehyde dehydrogenase 1 family; member L2	-0.1586	0.0037
1559402_a_at	C1orf61	chromosome 1 open reading frame 61	-0.2221	0.0001
1559409_a_at	KIAA1345	KIAA1345 protein	-0.1238	0.0361
1559412_at	C21orf34	chromosome 21 open reading frame 34	-0.2464	0.0038
1559432_at	CCBP2	chemokine binding protein 2	-0.1604	0.0003
1559478_at		CDNA clone IMAGE:5270289	-0.1223	0.02
1559526_at		CDNA clone IMAGE:5285563	-0.2286	0
1559537_at		Homo sapiens; clone IMAGE:4184655; mRNA	-0.1793	0.0188
1559559_at	C9orf79	chromosome 9 open reading frame 79	-0.132	0.0073
1559571_a_at	ATP13A4	ATPase type 13A4	-0.1565	0.0053
1559582_at	RHOQ	ras homolog gene family; member Q	-0.7721	0.0341
1559590_at	CHDH	choline dehydrogenase	-0.1269	0.0034
1559591_s_at	CHDH	choline dehydrogenase	-0.1662	0.014
1559624_at	STK32A	serine/threonine kinase 32A	-0.1366	0.0114
1559635_at	CASC4	cancer susceptibility candidate 4	-0.1223	0.0399

1559645_at		Non-coding RNA HANC	-0.2254	0.0168
1559655_at		CDNA FLJ42132 fis; clone TESTI2034997	-0.153	0.0281
1559661_at	ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	-0.1042	0.0234
1559664_at		CDNA clone IMAGE:4824541	-0.1431	0.047
1559676_a_at			-0.1321	0.0029
1559683_at		Full length insert cDNA clone YU75B05	-0.202	0.0037
1559692_at			-0.1121	0.0338
1559695_a_at		Full length insert cDNA clone ZC64D07	-0.193	0.0101
1559701_s_at	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	-0.4511	0.0001
1559715_at		CDNA clone IMAGE:4822667	-0.1193	0.0251
1559739_at	CHPT1	Choline phosphotransferase 1	-0.976	0.032
1559745_at		CDNA FLJ34261 fis; clone FEBRA2001772	-0.1324	0.0093
1559748_at	ADAMTSL3	ADAMTS-like 3	-0.2358	0.0003
1559753_at		CDNA FLJ36163 fis; clone TESTI2026014	-0.149	0.0069
1559777_at		CDNA FLJ32866 fis; clone TESTI2003718	-0.1	0.0493
1559785_at	TPPP2	tubulin polymerization-promoting protein family member 2	-0.1578	0.0059
1559901_s_at	C21orf34	chromosome 21 open reading frame 34	-0.9096	0
1559909_a_at	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	-0.1282	0.0085
1559910_at		MRNA full length insert cDNA clone EUROIMAGE 85905	-1.347	0.0025
1559915_at		Homo sapiens; clone IMAGE:4723617; mRNA	-0.197	0.0064
1559917_a_at		CDNA clone IMAGE:5262521	-0.1657	0.0035
1559924_at		CDNA clone IMAGE:5303182	-0.1853	0.0355
1559942_at	MDFIC	MyoD family inhibitor domain containing	-0.7596	0.0001
1559948_at		CDNA FLJ20447 fis; clone KAT05276	-0.1901	0.0479
1559960_x_at		Homo sapiens; clone IMAGE:5728979; mRNA	-0.331	0.0078
1559977_a_at	SLC25A34	solute carrier family 25; member 34	-1.1521	0
1559991_s_at			-0.1644	0.0417
1560024_at		CDNA clone IMAGE:4825318	-0.1139	0.039
1560059_at	VPS37C	vacuolar protein sorting 37 homolog C (S. cerevisiae)	-0.2686	0.0004
1560074_at	PRKCA	protein kinase C; alpha	-0.1506	0.0216
1560115_a_at	KIAA1217	KIAA1217	-0.1796	0.0232
1560132_a_at		Homo sapiens; clone IMAGE:5750475; mRNA	-0.3	0.0001
1560149_at	SLC29A2	solute carrier family 29 (nucleoside transporters); member 2	-0.1957	0.0242
1560151_x_at	SLC29A2	solute carrier family 29 (nucleoside transporters); member 2	-0.1322	0.0321
1560187_at		Homo sapiens; clone IMAGE:5767628; mRNA	-0.1398	0.0476

1560199_x_at	FLJ11903	similar to hypothetical protein MGC40405	-0.9952	0.0017
1560208_at			-0.1057	0.0284
1560219_at	ASB3	Ankyrin repeat and SOCS box-containing 3	-0.1403	0.0149
1560220_a_at	CBY1	chibby homolog 1 (Drosophila)	-0.1095	0.0238
1560240_at		CDNA clone IMAGE:5418341	-0.1193	0.0191
1560253_at	LHX9	LIM homeobox 9	-0.1349	0.0306
1560277_a_at	LOC283403	hypothetical protein LOC283403	-0.1422	0.0192
1560278_at	LOC221122	hypothetical protein LOC221122	-0.1656	0.0147
1560285_at		Homo sapiens; clone IMAGE:3446976; mRNA	-0.1164	0.0156
1560322_at	RBMS3	RNA binding motif; single stranded interacting protein	-0.1609	0.0173
1560378_at	C21orf41	Chromosome 21 open reading frame 41	-0.1526	0.0193
1560402_at	GAS5	growth arrest-specific 5	-0.4417	0.0002
1560409_at		Homo sapiens; clone IMAGE:5211852; mRNA	-0.1096	0.0284
1560424_at		CDNA FLJ40944 fis; clone UTERU2008705	-0.2259	0.0213
1560435_at		CDNA FLJ36444 fis; clone THYMU2012902	-0.1219	0.031
1560472_at	LOC338588	hypothetical protein LOC338588	-0.1397	0.0093
1560477_a_at	SAMD11	sterile alpha motif domain containing 11	-0.2346	0.0014
1560488_at	FLJ45224	FLJ45224 protein	-0.191	0.0027
1560513_at	LOC400568	hypothetical LOC400568	-0.1485	0.0187
1560548_at		CDNA clone IMAGE:4825993	-0.1167	0.0139
1560550_at		Homo sapiens; clone IMAGE:5180210; mRNA	-0.1017	0.0405
1560560_at		Homo sapiens; clone IMAGE:3608699; mRNA	-0.3822	0
1560573_at	LOC387895	hypothetical gene supported by BC040060	-0.2659	0.0006
1560577_at		CDNA clone IMAGE:4827370	-0.2226	0.0233
1560582_a_at		Homo sapiens; clone IMAGE:5741868; mRNA	-0.1992	0.0059
1560619_at	LOC255411	hypothetical LOC255411	-0.1556	0.0012
1560634_a_at		CDNA clone IMAGE:4837645	-0.1195	0.0096
1560639_at		Homo sapiens; clone IMAGE:3935553	-0.126	0.0183
1560647_at	TSPYL1	TSPY-like 1	-0.2182	0.0021
1560648_s_at	TSPYL1	TSPY-like 1	-1.2085	0
1560652_at		MRNA; cDNA DKFZp686L0310 (from clone DKFZp686L0310)	-0.1075	0.0351
1560671_at	KIAA1652	KIAA1652 protein	-0.2372	0.0003
1560705_at	SLC25A28	Solute carrier family 25; member 28	-0.1278	0.0166
1560724_at		CDNA FLJ33564 fis; clone BRAMY2010135	-0.1927	0.0089
1560733_at	ALG5	Asparagine-linked glycosylation 5 homolog (S. cerevisiae; dolichyl-phosphate beta-glucosyltransferase)	-0.1722	0.003

1560762_at	LOC285972	hypothetical protein LOC285972	-0.1446	0.0171
1560765_a_at	ARHGAP22	Rho GTPase activating protein 22	-0.1468	0.0106
1560818_at	LOC387895	Hypothetical gene supported by BC040060	-0.1532	0.0435
1560830_a_at	LOC147646	hypothetical protein LOC147646	-0.2481	0.031
1560832_at		Homo sapiens; clone IMAGE:4063532; mRNA	-0.1003	0.011
1560836_at		Homo sapiens; clone IMAGE:5171361; mRNA	-0.1374	0.0013
1560844_at		Homo sapiens; clone IMAGE:5742838; mRNA	-0.1444	0.0051
1560856_at		Homo sapiens; clone IMAGE:5742065; mRNA	-0.1722	0.004
1560862_at		MRNA; cDNA DKFZp434I235 (from clone DKFZp434I235)	-0.1096	0.0378
1560863_a_at		Full length insert cDNA clone ZA92B11	-0.1085	0.0239
1560878_at	SYT15	synaptotagmin XV	-0.2035	0.0323
1560891_a_at		Full length insert cDNA clone YY75G10	-0.1132	0.0342
1560897_a_at	KRTAP10-11	keratin associated protein 10-11	-0.1731	0.0191
1560901_at	LOC728789	hypothetical protein LOC728789, hypothetical protein LOC728905	-0.1305	0.008
1560940_at		CDNA FLJ32834 fis; clone TESTI2003236	-0.1747	0.0251
1560957_at		CDNA clone IMAGE:5268125	-0.1428	0.0051
1560960_at		Full length insert cDNA clone YX25D06	-0.1812	0.0003
1560962_at		Full length insert cDNA clone YI41H11	-0.1795	0.0038
1560964_at		Full length insert cDNA clone ZE16D09	-0.131	0.0075
1560971_a_at		Full length insert cDNA YQ76C04	-0.1534	0.0175
1560978_at		Full length insert cDNA clone ZD58F01	-0.1449	0.0489
1560989_at		Full length insert cDNA clone YY93H10	-0.1299	0.0167
1561000_at		MRNA; cDNA DKFZp667A015 (from clone DKFZp667A015)	-0.183	0.0028
1561003_at		Full length insert cDNA clone YY79F12	-0.15	0.0032
1561019_at		Full length insert cDNA clone ZD95A07	-0.1158	0.0336
1561034_at		CDNA clone IMAGE:5285971	-0.1408	0.0019
1561041_at		Homo sapiens; clone IMAGE:5534210; mRNA	-0.2292	0.0014
1561044_at		Homo sapiens; clone IMAGE:5548255; mRNA	-0.4058	0.005
1561045_a_at		Homo sapiens; clone IMAGE:5548255; mRNA	-0.147	0.007
1561060_at		CDNA clone IMAGE:5298862	-0.133	0.0119
1561064_a_at		CDNA clone IMAGE:3885734	-0.1118	0.0282
1561076_at		CDNA clone IMAGE:5267701	-0.1096	0.0238
1561078_at		CDNA clone IMAGE:4828251	-0.1817	0.0044
1561083_at		CDNA clone IMAGE:4827605	-0.102	0.0284
1561100_at		CDNA clone IMAGE:5269545	-0.1152	0.0273

1561102_at		CDNA clone IMAGE:5267652	-0.1924	0.0032
1561103_at		CDNA clone IMAGE:5264111	-0.1914	0.0043
1561106_at	C6orf217	chromosome 6 open reading frame 217	-0.391	0
1561133_at		Full length insert cDNA clone ZD60A10	-0.1773	0.0176
1561153_at		Full length insert cDNA YP99H09	-0.4638	0.0094
1561169_at	LOC727818	similar to PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-0.2333	0.0001
1561171_a_at	FLJ36131	FLJ40198 protein, hypothetical protein FLJ36131, similar to Golgin subfamily A member 2 (Cis-Golgi matrix protein GM130), similar to cis-Golgi matrix protein GM130	-0.2094	0.0238
1561185_at	CLONE795723	hypothetical transcript 795723	-0.2768	0.0081
1561202_at		CDNA clone IMAGE:4830882	-0.1183	0.0257
1561211_at		CDNA clone IMAGE:5265906	-0.1315	0.0127
1561214_at		CDNA clone IMAGE:5271518	-0.2095	0.0038
1561228_at		CDNA clone IMAGE:5267471	-0.177	0.039
1561243_at	TMEM105	transmembrane protein 105	-0.1461	0.0167
1561256_at		CDNA clone IMAGE:5272683	-0.1338	0.0226
1561277_at	LOC339298	hypothetical protein LOC339298	-0.1239	0.0072
1561279_at		CDNA clone IMAGE:4821609	-0.1365	0.0246
1561288_at		CDNA clone IMAGE:4838258	-0.1408	0.012
1561304_a_at	C6orf86	chromosome 6 open reading frame 86	-0.1927	0.0028
1561327_at	C6orf122	chromosome 6 open reading frame 122	-0.1535	0.0001
1561336_at	DNASE1L3	deoxyribonuclease I-like 3	-0.504	0
1561352_at		Homo sapiens; clone IMAGE:5528391; mRNA	-0.1094	0.0302
1561355_at	LOC692247	hypothetical locus LOC692247	-0.3598	0.0024
1561383_at	LOC284661	hypothetical protein LOC284661	-0.1521	0.0083
1561384_a_at	LOC284661	hypothetical protein LOC284661	-0.1603	0.0172
1561387_a_at	FAM55A	family with sequence similarity 55; member A	-0.1012	0.0332
1561390_at	FAM41AY	family with sequence similarity 41; member A; Y-linked	-0.1862	0.0082
1561394_s_at	RP5-1054A22.3	KIAA1755 protein	-0.2094	0.0001
1561409_at		CDNA FLJ40393 fis; clone TESTI2036922	-0.1151	0.0356
1561418_at		Homo sapiens; clone IMAGE:5403381; mRNA	-0.1587	0.0004
1561431_at		CDNA clone IMAGE:5259382	-0.1046	0.0348
1561446_at		CDNA clone IMAGE:4829179	-0.2683	0.003
1561449_at	TSPAN18	tetraspanin 18	-0.1219	0.0429
1561452_at		CDNA FLJ35945 fis; clone TESTI2011915	-0.1392	0.0029
1561462_at		CDNA FLJ36107 fis; clone TESTI2021819	-0.1237	0.0233
1561463_at			-0.1761	0.0222

1561471_at	LOC441009	Hypothetical LOC441009	-0.1171	0.0056
1561481_at		CDNA clone IMAGE:4827393	-0.1238	0.0154
1561502_x_at	LOC348180	Hypothetical protein LOC348180	-0.2663	0.0087
1561537_at	LOC388906	hypothetical gene supported by BC039496	-0.1226	0.0333
1561538_at		CDNA clone IMAGE:5271875	-0.179	0.0061
1561539_at		CDNA clone IMAGE:5303543	-0.2032	0.0052
1561543_at		CDNA clone IMAGE:5299981	-0.1567	0.0288
1561546_at		CDNA clone IMAGE:4827685	-0.1511	0.0087
1561554_at		CDNA clone IMAGE:4813826	-0.1449	0.0177
1561571_at	LOC730139	hypothetical protein LOC730139	-0.2383	0.0368
1561579_at	LOC728445	hypothetical protein LOC728445	-0.1636	0.0071
1561590_a_at	BC038740	BC038740	-0.1535	0.013
1561602_at		CDNA FLJ25733 fis; clone TST05652	-0.154	0.0278
1561612_at		CDNA clone IMAGE:5275628	-0.1078	0.0442
1561619_at		CDNA clone IMAGE:5269924	-0.1234	0.049
1561624_at		CDNA clone IMAGE:5270007	-0.1649	0.0447
1561638_at		Full length insert cDNA clone YI46C04	-0.1278	0.0072
1561650_s_at	LOC285692	hypothetical protein LOC285692	-0.128	0.0033
1561666_a_at	KIAA1908	KIAA1908 protein	-0.182	0.0365
1561668_at		CDNA clone IMAGE:5269842	-0.1241	0.006
1561679_at		MRNA; cDNA DKFZp434I039 (from clone DKFZp434I039)	-0.1142	0.0249
1561688_at		CDNA clone IMAGE:5267671	-0.1372	0.0406
1561693_at	LOC400794	hypothetical gene supported by BC030596	-0.101	0.0179
1561707_at		Hypothetical gene supported by AK057431; mRNA (cDNA clone MGC:126199 IMAGE:40033953)	-0.1546	0.0231
1561708_at	C6orf150	chromosome 6 open reading frame 150	-0.11	0.0226
1561723_at	LOC339894	hypothetical protein LOC339894	-0.1197	0.0177
1561728_a_at	LOC400238	hypothetical gene supported by AK093266	-0.1182	0.0395
1561872_at			-0.145	0.0035
1561880_a_at	SIGLECP16	sialic acid binding Ig-like lectin; pseudogene 16	-0.1722	0.0425
1561908_a_at	HS3ST3B1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	-0.1873	0.0011
1561910_at		CDNA clone IMAGE:5300947	-0.1571	0.011
1561927_at	C3orf16	chromosome 3 open reading frame 16	-0.1118	0.0345
1561940_at	POLE	polymerase (DNA directed); epsilon	-0.1624	0.0056
1561942_x_at		CDNA FLJ34475 fis; clone HLUNG2003716; moderately similar to RETROVIRUS-RELATED ENV POLYPROTEIN	-0.3626	0.0169
1561984_at		CDNA clone IMAGE:4822215	-0.1161	0.0187
1561997_at	LOC440061	Hypothetical LOC440061	-0.1562	0.0109

1562002_at	MYOZ3	myozenin 3	-0.2057	0.0013
1562004_x_at	MYOZ3	myozenin 3	-0.1545	0.0052
1562006_at		CDNA clone IMAGE:5286322	-0.1103	0.0107
1562044_at		CDNA clone IMAGE:5270804	-0.1446	0.006
1562059_at		CDNA FLJ90139 fis; clone HEMBB1001026; highly similar to Transmembrane 9 superfamily protein member 3 precursor	-0.2387	0.0071
1562065_at		CDNA clone IMAGE:5270453	-0.1434	0.0419
1562073_at		CDNA clone IMAGE:4830065	-0.1314	0.0436
1562078_at		CDNA FLJ32953 fis; clone TESTI2008099	-0.1235	0.0246
1562144_at		Full length insert cDNA YR39D03	-1.5362	0
1562194_at		Full length insert cDNA clone YW28D08	-1.5737	0.0001
1562234_a_at	LOC652725	neuron navigator 3, similar to neuron navigator 3	-0.2127	0.0048
1562247_at	LOC286058	hypothetical protein LOC286058	-0.2463	0.0001
1562260_at		MRNA; cDNA DKFZp667M0710 (from clone DKFZp667M0710)	-0.7272	0.0018
1562261_at	AMZ1	archaemetzincin-1	-0.1246	0.0453
1562264_at	LOC339685	hypothetical protein LOC339685	-0.1404	0.0315
1562265_at		MRNA; cDNA DKFZp313I1020 (from clone DKFZp313I1020)	-0.4562	0.0028
1562275_at		MRNA; cDNA DKFZp667P1024 (from clone DKFZp667P1024)	-0.8684	0.0177
1562286_at		CDNA clone IMAGE:4274877	-0.1287	0.0137
1562288_at		CDNA clone IMAGE:5262193	-0.1522	0.0297
1562296_at		CDNA clone IMAGE:4828037	-0.1103	0.0161
1562308_at	LOC283682	hypothetical protein LOC283682	-0.142	0.0011
1562310_at		CDNA clone IMAGE:4838759	-0.1013	0.0368
1562317_at	LOC121006	hypothetical protein LOC121006	-0.1443	0.0062
1562319_at	FLJ39743	hypothetical protein FLJ39743	-0.1801	0.0025
1562321_at	PDK4	pyruvate dehydrogenase kinase; isozyme 4	-1.7098	0.042
1562323_at		MRNA; cDNA DKFZp313M0331 (from clone DKFZp313M0331)	-0.1631	0.0237
1562324_a_at		MRNA; cDNA DKFZp313M0331 (from clone DKFZp313M0331)	-0.1788	0.0045
1562348_at	LOC400680	hypothetical gene supported by AK097381; BC040866	-0.3096	0.0004
1562358_at		Homo sapiens; clone IMAGE:4430231; mRNA	-0.1515	0.0143
1562389_at		CDNA clone IMAGE:4818734	-0.1331	0.0122
1562414_at		CDNA clone IMAGE:4797124	-0.1127	0.0226
1562416_at		CDNA clone IMAGE:5272221	-0.2673	0.0099
1562425_at	FARP1	FERM; RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-0.1089	0.0167
1562449_s_at		Homo sapiens; clone IMAGE:5170410; mRNA	-0.1945	0.0001
1562453_at		MRNA; cDNA DKFZp686F1318 (from clone DKFZp686F1318)	-0.1403	0.0313

1562456_at		MRNA; cDNA DKFZp566C0924 (from clone DKFZp566C0924)	-0.1766	0.0105
1562462_at	DNAH10	dynein; axonemal; heavy chain 10	-0.2282	0.0026
1562480_at		CDNA clone IMAGE:5269961	-0.1022	0.0404
1562495_at	ANKFY1	Ankyrin repeat and FYVE domain containing 1	-0.1177	0.0187
1562509_at		CDNA clone IMAGE:5284659	-0.1139	0.033
1562510_at	LOC339442	hypothetical protein LOC339442	-0.1042	0.0402
1562511_at	LYST	lysosomal trafficking regulator	-0.1685	0.0043
1562563_at	HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	-0.1228	0.0297
1562573_at	CYP17A1	cytochrome P450; family 17; subfamily A; polypeptide 1	-1.5344	0.0017
1562577_at		Homo sapiens; clone IMAGE:4546564; mRNA	-0.1487	0.0205
1562586_at		CDNA clone IMAGE:4903593	-0.1685	0.0322
1562601_at	UNQ6975	NGNL6975	-0.1896	0.0033
1562604_at		CDNA FLJ37024 fis; clone BRACE2010837	-0.1996	0.0178
1562610_at		CDNA clone IMAGE:4830466	-0.1415	0.0244
1562617_at	LOC340074	hypothetical protein LOC340074	-0.1457	0.0159
1562637_at	SAMD12	sterile alpha motif domain containing 12	-0.1879	0.0077
1562643_at		CDNA clone IMAGE:5297062	-0.1853	0.0084
1562671_s_at		CDNA FLJ35982 fis; clone TESTI2013604	-0.1259	0.0389
1562674_at		Homo sapiens; clone IMAGE:5165176; mRNA	-0.1304	0.0402
1562689_at	LOC151484	hypothetical protein LOC151484	-0.1922	0.0006
1562693_at		CDNA FLJ40517 fis; clone TESTI2046686	-0.1079	0.0375
1562713_a_at	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	-0.1149	0.0297
1562724_at	LOC286114	hypothetical protein LOC286114	-0.1291	0.0022
1562728_at		CDNA FLJ40174 fis; clone TESTI2016996	-0.1524	0.0026
1562729_at		CDNA clone IMAGE:4110098	-0.1794	0.0177
1562740_at	LOC285224	hypothetical protein LOC285224	-0.1543	0.0039
1562748_at	LOC253044	hypothetical protein LOC253044	-0.1517	0.0092
1562749_at	LOC641912	hypothetical LOC644090, hypothetical protein LOC641912	-0.1332	0.0231
1562751_at		CDNA clone IMAGE:4826129	-0.1792	0.0151
1562771_at		Homo sapiens; clone IMAGE:5759435; mRNA	-0.1265	0.0419
1562785_at	HERC6	Hect domain and RLD 6	-0.1295	0.0165
1562790_at	NCALD	neurocalcin delta	-0.1008	0.0101
1562834_at		CDNA clone IMAGE:5284619	-0.1954	0.0082
1562841_at	LOC339666	hypothetical protein LOC339666	-0.1744	0.0128
1562847_at		Homo sapiens; clone IMAGE:5590223; mRNA	-0.1062	0.013
1562852_at		Homo sapiens; clone IMAGE:5440917; mRNA	-0.352	0.0001

1562853_x_at		Homo sapiens; clone IMAGE:5440917; mRNA	-0.1546	0.0028
1562864_at		Homo sapiens; clone IMAGE:5168221; mRNA	-0.2215	0.0089
1562866_at		Homo sapiens; clone IMAGE:4730399; mRNA	-0.1297	0.0167
1562885_at		Homo sapiens; clone IMAGE:5750288; mRNA	-0.1022	0.0112
1562890_at		CDNA clone IMAGE:4301684	-0.1505	0.0027
1562898_at		MRNA; cDNA DKFZp667K1916 (from clone DKFZp667K1916)	-0.2116	0.0442
1562906_at	LOC340069	hypothetical protein LOC340069	-0.137	0.0027
1562910_at	SH3PXD2B	SH3 and PX domains 2B	-0.2375	0.0008
1562915_at		CDNA clone IMAGE:4823328	-0.182	0.0137
1562916_at	LOC729062	Hypothetical protein LOC729062	-0.2008	0.0013
1562945_at		CDNA clone IMAGE:3920381	-0.1344	0.0167
1562965_at		Homo sapiens; clone IMAGE:5744268; mRNA	-0.1207	0.0096
1562966_at	KIAA1217	KIAA1217	-0.1956	0.0083
1562972_at	LOC503519	hypothetical LOC503519	-0.1474	0.009
1562974_at		CDNA clone IMAGE:5302821	-0.1666	0.0059
1563035_x_at	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.1258	0.005
1563036_at		CDNA clone IMAGE:4795841	-0.1108	0.0449
1563038_at		Homo sapiens; clone IMAGE:3917623; mRNA	-0.1269	0.0264
1563042_at	LOC338694	hypothetical protein LOC338694	-0.2118	0
1563064_at		Homo sapiens; clone IMAGE:5760168; mRNA	-0.1304	0.0478
1563071_at		CDNA clone IMAGE:5223358	-0.2864	0
1563078_at		Homo sapiens; clone IMAGE:5749668; mRNA	-0.124	0.006
1563081_at		Homo sapiens; clone IMAGE:5744960; mRNA	-0.1452	0.0087
1563086_at		CDNA clone IMAGE:5526877	-0.1252	0.0252
1563090_at	CCDC33	coiled-coil domain containing 33	-0.1961	0.0148
1563108_at	LRRC62	leucine rich repeat containing 62	-0.101	0.0487
1563113_at	UBR4	ubiquitin protein ligase E3 component n-recognin 4	-0.3457	0
1563118_at		CDNA: FLJ20923 fis; clone ADSE00893	-0.111	0.0382
1563142_at		Homo sapiens; clone IMAGE:5721993; mRNA	-0.2446	0.0041
1563157_at		Homo sapiens; clone IMAGE:5744232; mRNA	-0.1465	0.0109
1563165_at		CDNA clone IMAGE:3638910	-0.1411	0.0398
1563171_at		CDNA clone IMAGE:5165280	-0.2139	0.0034
1563178_at		Homo sapiens; clone IMAGE:5538207; mRNA	-0.13	0.0181
1563182_at		CDNA clone IMAGE:4796641	-0.2961	0.0045
1563243_at		MRNA; cDNA DKFZp434M242 (from clone DKFZp434M242)	-0.1786	0.0443
1563263_at	PLCG2	Phospholipase C; gamma 2 (phosphatidylinositol-specific)	-0.1619	0.0084

1563300_at	LOC387826	Hypothetical LOC387826	-0.1256	0.0337
1563324_at	LOC389457	hypothetical protein LOC389457	-0.1312	0.0453
1563327_a_at	CXorf31	chromosome X open reading frame 31	-0.1376	0.0133
1563357_at		MRNA; cDNA DKFZp564C203 (from clone DKFZp564C203)	-1.3247	0.0012
1563373_at		CDNA clone IMAGE:5417528	-0.1123	0.0058
1563405_at	ATP4B	ATPase; H+/K+ exchanging; beta polypeptide	-0.2588	0.0062
1563407_x_at	ATP4B	ATPase; H+/K+ exchanging; beta polypeptide	-0.2559	0.0041
1563414_at		Full length insert cDNA clone YW28F05	-1.3927	0.0001
1563425_at		Clone IMAGE:429302; mRNA sequence	-0.1326	0.0201
1563466_at	MYLK	myosin; light chain kinase	-0.1329	0.0087
1563489_at	LOC285638	hypothetical protein LOC285638	-0.1257	0.0235
1563536_at		MRNA; cDNA DKFZp564N093 (from clone DKFZp564N093)	-0.1063	0.0472
1563541_at		MRNA; cDNA DKFZp686N1648 (from clone DKFZp686N1648)	-0.1689	0.0132
1563571_at	LOC285463	hypothetical protein LOC285463	-0.1738	0.0027
1563587_at	CDH4	cadherin 4; type 1; R-cadherin (retinal)	-0.1355	0.0361
1563597_at		MRNA; cDNA DKFZp666P238 (from clone DKFZp666P238)	-0.2374	0.0079
1563610_at	LOC157273	hypothetical protein LOC157273	-0.1241	0.0412
1563632_at	LOC220980	hypothetical protein LOC220980	-0.129	0.0358
1563639_a_at	FHAD1	forkhead-associated (FHA) phosphopeptide binding domain 1	-0.2	0.0279
1563658_a_at	SYT9	synaptotagmin IX	-0.5278	0.001
1563792_at	AMN	Amnionless homolog (mouse)	-0.1045	0.0329
1563793_at		CDNA FLJ36795 fis; clone ADRGL2006767	-0.5387	0
1563800_at	LOC283140	hypothetical protein LOC283140	-0.3164	0.0008
1563808_at	MCF2L	MCF.2 cell line derived transforming sequence-like	-0.3036	0.0082
1563834_a_at	C1orf62	chromosome 1 open reading frame 62	-0.1373	0.0422
1563840_at			-0.1404	0.0341
1563842_at	PIGG	phosphatidylinositol glycan anchor biosynthesis; class G	-0.2763	0.0221
1563860_at	LOC400965	hypothetical gene supported by AK098018	-0.1419	0.0021
1563868_a_at	C9orf79	chromosome 9 open reading frame 79	-0.1677	0.0091
1563878_a_at	LOC338963	hypothetical protein LOC338963	-0.1316	0.03
1563898_at		CDNA FLJ34764 fis; clone NT2NE2002311	-0.1546	0.042
1563900_at	FAM83B	family with sequence similarity 83; member B	-0.1371	0.0059
1563902_at		CDNA FLJ23888 fis; clone LNG14336	-0.2312	0.0001
1563903_x_at		CDNA FLJ23888 fis; clone LNG14336	-0.1785	0.0001

1563943_at	PPARGC1B	peroxisome proliferator-activated receptor gamma; coactivator 1 beta	-0.1883	0.0011
1563946_at			-0.1766	0.0202
1564000_at	ANKRD31	ankyrin repeat domain 31	-0.125	0.0493
1564021_at		CDNA FLJ37693 fis; clone BRHIP2014954	-0.1551	0.0263
1564022_at	ZNF804B	zinc finger protein 804B	-0.1093	0.027
1564044_at	KNCN	kinocilin	-0.1142	0.0408
1564056_at		MRNA; cDNA DKFZp667N093 (from clone DKFZp667N093)	-0.163	0.0094
1564060_at	LOC144742	hypothetical protein LOC144742	-0.1867	0.0023
1564117_at	HMCN2	hemicentin 2	-0.1995	0.001
1564122_at	LOC283875	hypothetical protein LOC283875	-0.1864	0.0062
1564125_at	LOC285857	hypothetical protein LOC285857	-0.1261	0.0428
1564144_at		CDNA FLJ35206 fis; clone PLACE6018843	-0.106	0.038
1564149_at		CDNA FLJ40615 fis; clone THYMU2012882	-0.1307	0.0235
1564193_at	FLJ39061	hypothetical protein FLJ39061	-0.2415	0.0059
1564198_a_at	C10orf90	chromosome 10 open reading frame 90	-0.2591	0.0001
1564203_at	LOC147004	hypothetical protein LOC147004	-0.1203	0.029
1564224_x_at	UNQ2963	hypothetical protein LOC283314	-0.1871	0.0199
1564242_at		CDNA FLJ32713 fis; clone TESTI2000756	-0.215	0.0149
1564251_at	EMID1	EMI domain containing 1	-0.1066	0.009
1564254_at	KY	kyphoscoliosis peptidase	-0.1341	0.0196
1564263_at	LOC144817	hypothetical protein LOC144817	-0.1711	0.0031
1564264_at		Homo sapiens; clone IMAGE:5590162; mRNA	-0.2357	0.0017
1564281_at	LOC285708	hypothetical protein LOC285708	-0.2896	0.0191
1564319_at	C19orf16	chromosome 19 open reading frame 16	-0.1521	0.0321
1564358_at		CDNA: FLJ22631 fis; clone HSI06451	-0.3045	0.0119
1564379_at			-0.1687	0.0024
1564386_at	TXNDC8	thioredoxin domain containing 8 (spermatozoa)	-0.1551	0.002
1564391_at		CDNA: FLJ20911 fis; clone ADSE00547	-0.1361	0.0215
1564403_at	TOPORS	topoisomerase I binding; arginine/serine-rich	-0.2253	0.0015
1564413_at			-0.1199	0.0453
1564421_at		CDNA FLJ36093 fis; clone TESTI2020579	-0.1368	0.0014
1564429_at		MRNA; cDNA DKFZp434C2216 (from clone DKFZp434C2216)	-0.1467	0.0142
1564431_a_at	FLJ45224	FLJ45224 protein	-0.1599	0.0122
1564460_at	LOC286442	hypothetical protein LOC286442	-0.1723	0.0031
1564520_s_at	PRMT5	protein arginine methyltransferase 5	-0.4558	0.0377
1564537_a_at	ASB10	ankyrin repeat and SOCS box-containing 10	-0.1299	0.0307

1564573_at	LOC402778	similar to RIKEN cDNA 6330512M04 gene (mouse)	-1.5356	0.0003
1564584_at		CDNA FLJ25771 fis; clone TST06415	-0.1194	0.0447
1564595_at		Homo sapiens; clone IMAGE:5745181; mRNA	-0.1188	0.0228
1564603_at	NUT	nuclear protein in testis	-0.1725	0.0199
1564620_at			-0.1069	0.0251
1564660_at		CDNA FLJ36900 fis; clone BRACE2001954	-0.1143	0.0316
1564685_a_at		Homo sapiens; clone IMAGE:5168221; mRNA	-0.1421	0.0295
1564713_a_at	FOXN4	forkhead box N4	-0.1727	0.0366
1564729_at		Homo sapiens; clone IMAGE:3891207; mRNA	-0.2136	0.0012
1564760_at		CDNA clone IMAGE:4694535	-0.1126	0.0199
1564778_at		MRNA; cDNA DKFZp434D2122 (from clone DKFZp434D2122)	-0.1934	0.0048
1564783_x_at	OFCC1	orofacial cleft 1 candidate 1	-0.1353	0.0254
1564796_at	EMP1	epithelial membrane protein 1	-1.329	0.0003
1564816_at	C14orf178	chromosome 14 open reading frame 178	-0.2091	0.0127
1564828_at	KIAA1211	KIAA1211 protein	-0.1275	0.0107
1564840_at		MRNA; cDNA DKFZp564B236 (from clone DKFZp564B236)	-0.3298	0
1564876_s_at	FOXP2	forkhead box P2	-0.1158	0.0355
1564905_at		EST from clone DKFZp434P1912; 3' end	-0.1891	0.0039
1564921_at	KRTAP13-1	keratin associated protein 13-1	-0.155	0.0059
1564985_a_at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger); member 1	-0.1882	0.0032
1565002_at		CDNA FLJ20229 fis; clone COLF5247	-0.1298	0.0021
1565082_x_at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	-0.1037	0.0077
1565105_at			-0.1305	0.0449
1565107_x_at			-0.1185	0.0492
1565132_at	RBMY3AP	RNA binding motif protein; Y-linked; family 3; member A pseudogene	-0.1189	0.0474
1565162_s_at	MGST1	microsomal glutathione S-transferase 1	-2.2369	0.0201
1565282_at			-0.1982	0.004
1565320_at	RBMY3AP	RNA binding motif protein; Y-linked; family 3; member A pseudogene	-0.4517	0.0084
1565337_at	DNAH6	dynein; axonemal; heavy chain 6	-0.1956	0.0068
1565358_at	RARA	retinoic acid receptor; alpha	-0.2269	0.0008
1565537_at	NKX1-1	NK1 homeobox 1	-0.1176	0.0463
1565556_at	LOC127841	hypothetical protein LOC127841	-0.1181	0.0249
1565562_at	MAGIX	MAGI family member; X-linked	-0.1864	0.0371
1565581_at		CDNA clone IMAGE:4828937	-0.2303	0.0002
1565587_at		CDNA clone IMAGE:4828283	-0.1163	0.0266

1565598_at		Homo sapiens; clone IMAGE:4275461; mRNA	-1.1599	0.0012
1565603_at	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	-0.1714	0.0268
1565612_at	DYNLRB1	Dynein; light chain; roadblock-type 1	-0.1417	0.0148
1565613_at		CDNA clone IMAGE:6573900	-0.1386	0.0164
1565628_at		Full length insert cDNA clone ZD55G10	-0.2596	0.0008
1565638_at		MRNA; cDNA DKFZp686P21116 (from clone DKFZp686P21116)	-0.2271	0.0146
1565639_a_at		MRNA; cDNA DKFZp686P21116 (from clone DKFZp686P21116)	-0.5686	0.0104
1565650_at			-0.1159	0.0462
1565651_at	ARF1	ADP-ribosylation factor 1	-0.4804	0.0099
1565656_x_at		CDNA FLJ36440 fis; clone THYMU2012565	-0.1248	0.0143
1565660_at	FUT6	Fucosyltransferase 6 (alpha (1;3) fucosyltransferase)	-0.2564	0
1565661_x_at	FUT6	Fucosyltransferase 6 (alpha (1;3) fucosyltransferase)	-0.1661	0.007
1565674_at	FCGR2A	Fc fragment of IgG; low affinity IIa; receptor (CD32)	-0.2954	0.0097
1565714_at		Full length insert cDNA clone YS05E02	-0.2178	0.0018
1565730_at		MRNA; cDNA DKFZp434E145 (from clone DKFZp434E145)	-0.1132	0.0275
1565751_at		Transcribed locus	-0.1268	0.0193
1565752_at	FGD2	FYVE; RhoGEF and PH domain containing 2	-0.2377	0.05
1565768_at		Homo sapiens; clone IMAGE:4272620; mRNA	-0.1431	0.0188
1565784_at		CDNA FLJ36796 fis; clone ADRGL2006817	-0.1286	0.0087
1565795_at	DUOX1	dual oxidase 1	-0.1478	0.001
1565801_at		CDNA clone IMAGE:4796818	-0.1087	0.0412
1565805_at	LOC728011	hypothetical protein LOC728011	-0.1004	0.0284
1565814_at	TRIM36	tripartite motif-containing 36	-0.132	0.0278
1565832_at	ANKRD15	Ankyrin repeat domain 15	-0.1426	0.0482
1565843_s_at	BRPF3	bromodomain and PHD finger containing; 3	-0.1303	0.0265
1565879_at		Full length insert cDNA clone YQ73D03	-0.2019	0.0043
1565882_at		CDNA FLJ12064 fis; clone HEMBB1002232	-0.1948	0.0102
1565911_at		MRNA full length insert cDNA clone EUROIMAGE 209544	-0.2296	0.0115
1565918_a_at		MRNA from chromosome 5q21-22; clone:LI26	-0.1321	0.0046
1565974_at		CDNA FLJ23646 fis; clone COL03258	-0.1372	0.0013
1565998_at	LOC286299	hypothetical protein LOC286299	-0.1931	0.001
1566002_at		CDNA FLJ38745 fis; clone KIDNE2012291	-0.2224	0.0084
1566003_x_at		CDNA FLJ38745 fis; clone KIDNE2012291	-0.1817	0.0286
1566038_at	DGCR7	DiGeorge syndrome critical region gene 7	-0.187	0.0127

1566079_at	LOC647190	similar to 40S ribosomal protein S16	-1.5446	0.0016
1566086_at		MRNA; cDNA DKFZp667A1714 (from clone DKFZp667A1714)	-0.1347	0.0162
1566097_at		MRNA; cDNA DKFZp761K02121 (from clone DKFZp761K02121)	-0.1075	0.0197
1566115_at		MRNA; cDNA DKFZp666E186 (from clone DKFZp666E186)	-0.4054	0.0037
1566123_at	FABP6	fatty acid binding protein 6; ileal (gastrotropin)	-0.1414	0.012
1566136_at			-0.1519	0.0385
1566140_at	HOP	homeodomain-only protein	-0.4978	0.0003
1566141_at		CDNA FLJ37949 fis; clone CTONG2009156	-0.1239	0.0245
1566149_at	CALML4	Calmodulin-like 4	-0.1533	0.0207
1566156_at		Homo sapiens; clone IMAGE:5198544; mRNA	-0.1181	0.0429
1566171_at	RFFL	ring finger and FYVE-like domain containing 1	-0.2019	0.0135
1566195_at		MRNA; cDNA DKFZp313O2015 (from clone DKFZp313O2015)	-0.1474	0.0035
1566208_at	TCEA1	transcription elongation factor A (SII); 1	-0.1361	0.0289
1566209_at		CDNA clone IMAGE:4795866	-0.1211	0.0025
1566231_at		MRNA; cDNA DKFZp667I0318 (from clone DKFZp667I0318)	-0.1456	0.003
1566232_at		MRNA; cDNA DKFZp667I0318 (from clone DKFZp667I0318)	-0.3564	0
1566236_at	DGCR12	DiGeorge syndrome critical region gene 12	-0.1409	0.0431
1566242_at		MRNA; cDNA DKFZp547L144 (from clone DKFZp547L144)	-0.1449	0.0178
1566268_at		Full length insert cDNA YR25G06	-0.2978	0.003
1566301_at	PPP1R11	Protein phosphatase 1; regulatory (inhibitor) subunit 11	-0.1314	0.0074
1566324_a_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	-0.2676	0.0004
1566362_at	DNTT	Deoxynucleotidyltransferase; terminal	-0.1347	0.0301
1566427_at		MRNA; cDNA DKFZp667B046 (from clone DKFZp667B046)	-0.1211	0.041
1566432_at			-0.2002	0.0021
1566438_at	LOC283475	Hypothetical protein LOC283475	-0.1749	0.0004
1566454_at		FLJ00403 protein	-0.1948	0.0074
1566459_at		CDNA clone IMAGE:4801197	-0.147	0.0057
1566463_at		MRNA; cDNA DKFZp667M159 (from clone DKFZp667M159)	-0.1248	0.0084
1566471_at	LOC647305	similar to all-trans-13;14-dihydroretinol saturase	-0.1966	0.0199
1566472_s_at	RETSAT	retinol saturase (all-trans-retinol 13;14-reductase)	-1.5704	0
1566474_at		MRNA; cDNA DKFZp451O1018 (from clone DKFZp451O1018)	-0.2095	0.0062
1566476_at			-0.1223	0.0144
1566477_at		MRNA; cDNA DKFZp547F1316 (from clone DKFZp547F1316)	-0.2992	0.0001

1566484_at		MRNA; cDNA DKFZp666K2010 (from clone DKFZp666K2010)	-0.2197	0.0008
1566490_at		MRNA; cDNA DKFZp547C018 (from clone DKFZp547C018)	-0.1407	0.0148
1566500_at			-0.1254	0.0152
1566501_at		CDNA FLJ20787 fis; clone COL02178	-0.196	0.0011
1566503_at		CDNA clone IMAGE:5265199	-0.1215	0.0382
1566509_s_at	FBXO9	F-box protein 9	-1.2004	0.0013
1566512_at			-0.1352	0.0124
1566517_at			-0.1057	0.0213
1566537_at		CDNA FLJ33736 fis; clone BRAWH2018514	-0.1141	0.0438
1566538_at		MRNA; cDNA DKFZp586G081 (from clone DKFZp586G081)	-0.1313	0.0404
1566543_at		CDNA FLJ40975 fis; clone UTERU2013502	-0.1112	0.0417
1566548_at		MRNA; cDNA DKFZp564C1382 (from clone DKFZp564C1382)	-0.185	0.0004
1566577_at		MRNA; cDNA DKFZp547I1410 (from clone DKFZp547I1410)	-0.1334	0.0253
1566580_at		MRNA; cDNA DKFZp667C1424 (from clone DKFZp667C1424)	-0.1673	0.0008
1566630_at	LOC652806	hypothetical protein LOC652806, protein phosphatase 2 (formerly 2A); regulatory subunit B''; beta	-0.3394	0.006
1566677_at	MMP2	Matrix metallopeptidase 2 (gelatinase A; 72kDa gelatinase; 72kDa type IV collagenase)	-0.1327	0.0289
1566689_at		CDNA clone IMAGE:5273707	-0.1261	0.0179
1566693_at		CDNA: FLJ20947 fis; clone ADSE01841	-0.1083	0.0098
1566696_at		CDNA clone IMAGE:5289071	-0.1438	0.0137
1566700_at	VRK3	vaccinia related kinase 3	-0.1198	0.0031
1566701_at	VRK3	vaccinia related kinase 3	-0.1506	0.0128
1566737_at	hCG_2036596	HCG2036596	-0.1092	0.0173
1566760_at	FLJ34208	hypothetical gene supported by AK091527	-0.1443	0.0364
1566763_at		CDNA clone IMAGE:5277680	-0.1	0.0399
1566775_at	DNAH1	dynein; axonemal; heavy chain 1	-0.1935	0.0358
1566779_at		MRNA; cDNA DKFZp547C083 (from clone DKFZp547C083)	-0.1747	0.0117
1566803_at		CDNA: FLJ20901 fis; clone ADSE00109	-0.1331	0.0387
1566807_a_at		CDNA clone IMAGE:5272727	-0.1024	0.0221
1566814_at	FGF22	Fibroblast growth factor 22	-0.1507	0.0328
1566816_at	FGF22	Fibroblast growth factor 22	-0.12	0.0198
1566821_at		CDNA FLJ32664 fis; clone TESTI1000088	-0.1319	0.0313
1566835_at		MRNA; cDNA DKFZp666I029 (from clone DKFZp666I029)	-0.223	0.0005
1566884_at	C17orf84	Chromosome 17 open reading frame 84	-0.1644	0.002
1566903_at		MRNA; cDNA DKFZp547G039 (from clone DKFZp547G039)	-0.1255	0.0318

1566926_at	C21orf104	chromosome 21 open reading frame 104	-0.1413	0.0461
1566935_at	TYRO3P	TYRO3P protein tyrosine kinase pseudogene	-0.1083	0.034
1566937_at		CDNA FLJ20009 fis; clone ADKA03183	-0.1071	0.0318
1566948_at		MRNA; cDNA DKFZp547K228 (from clone DKFZp547K228)	-0.8199	0.0021
1566957_at	OR7E104P	olfactory receptor; family 7; subfamily E; member 104 pseudogene	-0.4753	0.0139
1566963_at			-0.1589	0.0013
1566967_at		CDNA: FLJ20903 fis; clone ADSE00222	-0.1731	0.0178
1566974_at		MRNA; cDNA DKFZp434M1135 (from clone DKFZp434M1135)	-0.1487	0.0061
1566989_at	ARID1B	AT rich interactive domain 1B (SWI1-like)	-0.2415	0.0141
1566990_x_at	ARID1B	AT rich interactive domain 1B (SWI1-like)	-0.2723	0.0028
1567022_at	OR5AK4P	olfactory receptor; family 5; subfamily AK; member 4 pseudogene	-0.237	0.0133
1567023_at	OR5AK4P	olfactory receptor; family 5; subfamily AK; member 4 pseudogene	-0.1487	0.0051
1567027_at	SH3GLP2	SH3-domain GRB2-like pseudogene 2	-0.1233	0.0058
1567036_at	C20orf181	chromosome 20 open reading frame 181	-0.1314	0.0341
1567068_at	OR4D1	olfactory receptor; family 4; subfamily D; member 1	-0.1386	0.0452
1567140_at		TTY2 gene; clone TTY2L12A	-0.1277	0.0198
1567166_at			-0.1849	0.0014
1567219_at			-0.6592	0
1567223_at	HMGA2	high mobility group AT-hook 2	-0.1772	0.0041
1567252_at	OR10D3P	olfactory receptor; family 10; subfamily D; member 3 pseudogene	-0.1182	0.0258
1567256_at	OR1J2	olfactory receptor; family 1; subfamily J; member 2	-0.1394	0.0172
1567274_at			-0.1325	0.0295
1567282_at	OR1J4	olfactory receptor; family 1; subfamily J; member 4	-0.1421	0.0077
1567284_at	OR1J4	olfactory receptor; family 1; subfamily J; member 4	-0.1283	0.0059
1567297_at	OR13C4	olfactory receptor; family 13; subfamily C; member 4	-0.1554	0.0122
1567298_at	OR13C4	olfactory receptor; family 13; subfamily C; member 4	-0.1731	0.0038
1567319_at	LOC57802	putative ATP-binding cassette protein	-0.1808	0.0045
1567320_at	LOC57802	putative ATP-binding cassette protein	-0.1344	0.0187
1567333_at		MRNA adjacent to 3' end of integrated HPV16 (INT421)	-0.1298	0.0238
1567341_at	FOXD4	forkhead box D4	-0.1889	0.0007
1567375_at		Trapped 3' terminal exon; clone B2E8	-0.1883	0.0268
1567376_at	DNAH1	dynein; axonemal; heavy chain 1	-0.109	0.0479

1567389_at		Trapped 3' terminal exon; clone C2B5	-0.1516	0.0033
1567410_at	ZNF135	zinc finger protein 135	-0.141	0.0291
1567519_at	PLXNA3	plexin A3	-0.155	0.0247
1567539_at	SPAG10	sperm associated antigen 10	-0.1197	0.0406
1567540_at	SPAG10	sperm associated antigen 10	-0.1494	0.0208
1567624_at	TREML2P	triggering receptor expressed on myeloid cells-like 2 pseudogene	-0.1311	0.01
1567628_at	CD74	CD74 molecule; major histocompatibility complex; class II invariant chain	-2.1967	0.0051
1568190_at			-0.2747	0
1568191_at			-0.2333	0.0021
1568406_at			-0.1919	0.0364
1568554_x_at	C6orf142	Chromosome 6 open reading frame 142	-0.1301	0.028
1568589_at		Clone FLB3512 mRNA sequence	-0.1561	0.0434
1568592_at	TRIM69	tripartite motif-containing 69	-0.9387	0.0298
1568612_at	GABRG2	gamma-aminobutyric acid (GABA) A receptor; gamma 2	-0.4118	0.0344
1568613_at	RSPH3	radial spoke head 3 homolog (Chlamydomonas)	-0.271	0.02
1568616_a_at			-0.2773	0.0001
1568633_a_at		CDNA clone IMAGE:3878708	-0.6269	0.0034
1568663_a_at		CDNA clone IMAGE:5266772	-0.2979	0.0067
1568666_at	LSDP5	lipid storage droplet protein 5	-0.1481	0.0016
1568675_at	CHRNA10	Cholinergic receptor; nicotinic; alpha 10	-0.2328	0.0003
1568685_at		Homo sapiens; clone IMAGE:4992489; mRNA	-0.1986	0
1568718_at	C6orf85	chromosome 6 open reading frame 85	-0.1016	0.0312
1568719_s_at	C6orf85	chromosome 6 open reading frame 85	-0.1784	0.0457
1568728_s_at	RNF207	ring finger protein 207	-0.1915	0.0051
1568735_at		CDNA clone IMAGE:4795078	-0.3412	0.0008
1568736_s_at		CDNA clone IMAGE:4795078	-0.9132	0.0002
1568739_at	LOC285692	hypothetical protein LOC285692	-0.1741	0.0081
1568748_at		Homo sapiens; clone IMAGE:5193340; mRNA	-0.2585	0.0002
1568754_at		CDNA clone IMAGE:5267015	-0.1482	0.0488
1568760_at	MYH11	myosin; heavy chain 11; smooth muscle	-0.1414	0.007
1568768_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-4.7912	0
1568789_at	C6orf107	chromosome 6 open reading frame 107	-0.1677	0.0001
1568796_at	LOC550631	hypothetical LOC550631	-0.1534	0.0208
1568821_at	TTC23	tetratricopeptide repeat domain 23	-0.2264	0.001
1568830_at	IRAK3	Interleukin-1 receptor-associated kinase 3	-0.1514	0.0104
1568845_at			-0.1223	0.0455

1568850_at	CCBP2	Chemokine binding protein 2	-0.1306	0.0142
1568859_a_at	SLC8A3	solute carrier family 8 (sodium-calcium exchanger); member 3	-0.1681	0.0201
1568902_at		CDNA clone IMAGE:4914456; with apparent retained intron	-0.139	0.0103
1568921_at		CDNA clone IMAGE:5266271	-0.1023	0.0186
1568943_at	INPP5D	inositol polyphosphate-5-phosphatase; 145kDa	-0.1891	0.0292
1568978_s_at	C11orf21	chromosome 11 open reading frame 21	-0.1632	0.0404
1569020_at	NEDD9	neural precursor cell expressed; developmentally down-regulated 9	-0.3183	0.0008
1569034_a_at	LOC440864	hypothetical gene supported by BC040724	-0.1903	0.0017
1569063_at		CDNA clone IMAGE:4106796	-0.271	0.0063
1569076_a_at	FLJ16287	FLJ16287 protein	-1.2233	0.0155
1569077_x_at	FLJ16287	FLJ16287 protein	-1.3394	0.0122
1569095_at	LOC731424	hypothetical protein LOC731424	-0.1761	0.0187
1569099_at		Homo sapiens; clone IMAGE:4861097; mRNA	-0.1408	0.0217
1569153_at		Homo sapiens; clone IMAGE:4551281; mRNA	-1.654	0
1569154_a_at		Homo sapiens; clone IMAGE:4551281; mRNA	-1.5558	0
1569159_at	LZTS1	Leucine zipper; putative tumor suppressor 1	-0.1077	0.013
1569171_a_at	FXR1	Fragile X mental retardation; autosomal homolog 1	-0.1037	0.0047
1569193_at		CDNA clone IMAGE:4821290	-0.1282	0.0041
1569205_at			-0.1327	0.0057
1569208_a_at		Homo sapiens; clone IMAGE:4704474; mRNA	-0.8225	0
1569235_a_at	LOC729303	hypothetical protein LOC729303	-0.1808	0.0263
1569257_at	FMNL1	formin-like 1	-0.2513	0.005
1569263_at		Pp10472	-0.1158	0.0265
1569283_at	hCG_1646157	hCG1646157	-0.4601	0.0059
1569290_s_at	GRIA3	glutamate receptor; ionotrophic; AMPA 3	-1.5397	0.0303
1569300_at	C1orf148	chromosome 1 open reading frame 148	-0.1784	0.0099
1569303_s_at	RGS20	regulator of G-protein signaling 20	-0.1711	0.0014
1569305_a_at		Homo sapiens; clone IMAGE:5184855; mRNA	-0.1651	0.0026
1569325_at	ARPC5	Actin related protein 2/3 complex; subunit 5; 16kDa	-0.1812	0.0255
1569337_at	SLC5A9	solute carrier family 5 (sodium/glucose cotransporter); member 9	-0.1498	0.0013
1569378_at	FLJ33297	Hypothetical gene supported by AK090616	-0.1148	0.0059
1569393_at	MGC15885	hypothetical protein MGC15885	-0.1032	0.0231
1569401_at	CLEC12A	C-type lectin domain family 12; member A	-0.1227	0.0334
1569421_at	CLDN4	claudin 4	-0.1167	0.0109

1569434_at	C14orf105	chromosome 14 open reading frame 105	-0.1558	0.0288
1569459_a_at		Homo sapiens; clone IMAGE:5191120; mRNA	-0.1342	0.0211
1569465_at	LOC729830	similar to CG3558-PA; isoform A	-0.2083	0.0091
1569473_s_at	LOC791120	hypothetical LOC791120, zinc finger protein 783	-0.1192	0.021
1569487_at	TACC3	Transforming; acidic coiled-coil containing protein 3	-0.1094	0.0068
1569496_s_at	SPON2	Spondin 2; extracellular matrix protein	-0.2615	0.0023
1569516_at		Homo sapiens; clone IMAGE:5585187; mRNA	-0.2163	0.0002
1569518_at		Homo sapiens; clone IMAGE:4153775; mRNA	-0.1959	0.0022
1569523_a_at		Homo sapiens; clone IMAGE:4424208; mRNA	-0.1241	0.0154
1569536_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family; member 2	-0.4458	0
1569615_at		Homo sapiens; clone IMAGE:5163959; mRNA	-0.1144	0.036
1569631_at	NMNAT1	nicotinamide nucleotide adenylyltransferase 1	-0.4189	0.0066
1569644_at		Homo sapiens; clone IMAGE:4708652; mRNA	-0.1347	0.0277
1569647_at	LOC643623	hypothetical LOC643623	-0.192	0.0001
1569670_at		Pp12613	-0.181	0.0006
1569683_at	XYLB	xylulokinase homolog (H. influenzae)	-0.2186	0.0024
1569722_s_at	LOC219731	hypothetical protein LOC219731	-0.1461	0.0301
1569730_at	FLJ40243	hypothetical protein FLJ40243	-0.1936	0.0056
1569741_at		CDNA clone IMAGE:4831311	-0.1865	0.0057
1569763_at		CDNA clone IMAGE:4823272	-0.2134	0
1569785_at		CDNA clone IMAGE:5287047	-0.3577	0
1569793_at	SLC25A18	solute carrier family 25 (mitochondrial carrier); member 18	-0.3392	0.0015
1569817_at		CDNA clone IMAGE:4827374	-0.1429	0.019
1569840_at		Homo sapiens; Similar to HSPC182 protein; clone IMAGE:4431648; mRNA	-0.1172	0.0385
1569847_at	CGNL1	Cingulin-like 1	-0.1703	0.0092
1569887_a_at	LOC286135	hypothetical protein LOC286135	-0.1282	0.0149
1569905_at	HSD11B1L	hydroxysteroid (11-beta) dehydrogenase 1-like	-0.212	0.0078
1569909_at	KRT79	keratin 79	-0.1524	0.0148
1569910_at		CDNA clone IMAGE:5095848	-0.1313	0.0229
1569926_s_at	SLC34A3	solute carrier family 34 (sodium phosphate); member 3	-0.1068	0.0226
1569932_at	RP11-262D11.5	similar to Nance-Horan syndrome protein	-0.1887	0.002
1569933_at		CDNA clone IMAGE:4547814	-0.1509	0.0226
1569937_at		CDNA clone IMAGE:4799216	-0.1514	0.0042
1569953_at		CDNA clone IMAGE:4310445	-0.1105	0.0019
1569956_at		Homo sapiens; clone IMAGE:4413783; mRNA	-0.1648	0.0005

1569963_at		Homo sapiens; clone IMAGE:4662750; mRNA	-0.2048	0.0033
1569979_at	HKR1	GLI-Kruppel family member HKR1	-0.3089	0
1569980_x_at	HKR1	GLI-Kruppel family member HKR1	-0.1409	0.0024
1569991_at	KY	kyphoscoliosis peptidase	-0.1654	0.0156
1569998_at	MMD2	monocyte to macrophage differentiation-associated 2	-0.1231	0.0344
1570038_at	ZNF718	Zinc finger protein 718	-0.1011	0.0493
1570040_at		CDNA clone IMAGE:5267944	-0.179	0.0018
1570065_at		Homo sapiens; clone IMAGE:4340753; mRNA	-0.1327	0.0378
1570082_x_at		CDNA clone IMAGE:4825288	-0.2008	0.0147
1570105_at		Homo sapiens; clone IMAGE:4638342; mRNA	-0.1986	0
1570116_at		CDNA clone IMAGE:3343139	-0.1538	0.0024
1570121_at	ZNF365	zinc finger protein 365	-0.1652	0.0005
1570123_at		CDNA clone IMAGE:4123798	-0.1838	0.0019
1570140_at	LOC653110	hypothetical LOC653110	-0.1424	0.0113
1570167_at		Homo sapiens; clone IMAGE:4214536; mRNA	-0.1119	0.0258
1570171_at		CDNA clone IMAGE:5200896	-0.1333	0.0176
1570186_at	GRASPOS	GRP1-associated scaffold protein opposite strand	-0.1378	0.0053
1570225_at	LOC284417	hCG1651476	-0.1487	0.0012
1570235_at	MGC27382	hypothetical protein MGC27382	-0.13	0.0307
1570238_at	ZNF527	zinc finger protein 527	-0.1196	0.0401
1570239_a_at	MIST	mast cell immunoreceptor signal transducer	-0.1841	0.0255
1570259_at	LIMS1	LIM and senescent cell antigen-like domains 1	-1.2556	0.001
1570266_x_at		Homo sapiens; Similar to otoconin 90; clone IMAGE:4044247; mRNA	-0.3038	0.0214
1570274_at	UNQ9391	tryptophan/serine protease	-0.1311	0.0392
1570279_at	ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	-0.1907	0.0343
1570281_at		CDNA clone IMAGE:5312241	-0.2232	0.003
1570282_at			-0.1303	0.0042
1570302_at		Homo sapiens; clone IMAGE:4178694; mRNA	-0.1072	0.0378
1570315_at	LOC283902	hypothetical gene supported by BC019009	-0.1118	0.0136
1570330_at		Homo sapiens; clone IMAGE:4151631; mRNA	-0.2729	0.0008
1570344_at		CDNA clone IMAGE:4838056	-0.1864	0.0215
1570350_at		Homo sapiens; Similar to hypothetical protein FLJ20234; clone IMAGE:5210552; mRNA	-0.1393	0.0095
1570364_at	ZNF709	zinc finger protein 709	-0.2359	0.03
1570382_at			-0.1726	0.0002
1570385_at		Homo sapiens; clone IMAGE:4040324; mRNA	-0.1553	0.0017
1570405_at		Homo sapiens; clone IMAGE:4543009; mRNA	-0.2121	0.0044

1570470_at	C14orf161	chromosome 14 open reading frame 161	-0.1043	0.0226
1570474_s_at	LOC338579	hypothetical protein LOC338579	-0.1455	0.031
1570506_at		Homo sapiens; clone IMAGE:4093039; mRNA	-0.3911	0.0006
1570511_at	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	-0.4309	0.0001
1570536_at			-0.1111	0.0142
1570546_a_at	TACC2	transforming; acidic coiled-coil containing protein 2	-0.1366	0.0018
1570552_at	C18orf50	chromosome 18 open reading frame 50	-0.9678	0.0001
1570569_at			-0.2474	0.0002
1570601_at		CDNA clone IMAGE:4213015	-0.1439	0.0162
1570627_at	TCEB3	transcription elongation factor B (SIII); polypeptide 3 (110kDa; elongin A)	-0.1094	0.0439
1570630_at		CDNA clone IMAGE:4826992	-0.1893	0.0091
1598_g_at	GAS6	growth arrest-specific 6	-1.4818	0.0001
177_at	PLD1	phospholipase D1; phosphatidylcholine-specific	-1.0824	0
179_at	PMS2L11	postmeiotic segregation increased 2-like 11	-0.1827	0.0388
200000_s_at	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	-0.7586	0
200006_at	PARK7	Parkinson disease (autosomal recessive; early onset) 7	-0.3237	0.0002
200010_at	RPL11	ribosomal protein L11	-0.2398	0.027
200012_x_at	LOC653737	60S ribosomal protein L21 pseudogene, ribosomal protein L21, similar to 60S ribosomal protein L21, similar to ribosomal protein L21	-0.3996	0.0006
200013_at	RPL24	ribosomal protein L24	-0.1918	0.0195
200017_at	RPS27A	ribosomal protein S27a	-0.2095	0.0015
200018_at	RPS13	ribosomal protein S13	-0.1822	0.0041
200019_s_at	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	-0.4717	0.0002
200023_s_at	EIF3F	eukaryotic translation initiation factor 3; subunit F	-0.482	0.008
200025_s_at	RPL27	ribosomal protein L27	-0.1797	0.0024
200026_at	LOC342994	hypothetical protein LOC729536, ribosomal protein L34, similar to ribosomal protein L34	-0.154	0.0016
200029_at	LOC392557	ribosomal protein L19, similar to ribosomal protein L19	-0.2384	0.0025
200033_at	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-0.299	0.0036
200035_at	DULLARD	dullard homolog (Xenopus laevis)	-0.2949	0.0291
200036_s_at	RPL10A	ribosomal protein L10a	-0.3689	0.0051
200038_s_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2273	0.0131
200042_at	C22orf28	chromosome 22 open reading frame 28	-0.4287	0.033

200048_s_at	JTB	jumping translocation breakpoint	-0.2391	0.0268
200055_at	TAF10	TAF10 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 30kDa	-0.7108	0.0006
200056_s_at	C1D	nuclear DNA-binding protein, similar to nuclear DNA-binding protein	-0.3317	0.0276
200061_s_at	RPS24	ribosomal protein S24	-0.1423	0.0252
200070_at	C2orf24	chromosome 2 open reading frame 24	-0.8424	0.0004
200074_s_at	LOC649821	ribosomal protein L14, ribosomal protein L14-like, similar to 60S ribosomal protein L14 (CAG-ISL 7)	-0.2602	0.0176
200075_s_at	GUK1	guanylate kinase 1	-0.5282	0.0039
200081_s_at	RPS6	ribosomal protein S6	-0.2484	0.0484
200084_at	C11orf58	chromosome 11 open reading frame 58	-0.2779	0.0149
200088_x_at	RPL12	ribosomal protein L12	-0.2055	0.0261
200091_s_at	RPS25	ribosomal protein S25	-0.2746	0.0003
200095_x_at	RPS10	ribosomal protein S10	-0.1469	0.0191
200614_at	CLTC	clathrin; heavy chain (Hc)	-0.1977	0.0241
200620_at	TMEM59	transmembrane protein 59	-0.342	0.0163
200621_at	CSRP1	cysteine and glycine-rich protein 1	-2.6839	0
200642_at	SOD1	superoxide dismutase 1; soluble (amyotrophic lateral sclerosis 1 (adult))	-0.2015	0.0336
200645_at	GABARAP	GABA(A) receptor-associated protein	-0.3061	0.0003
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	-0.9416	0.0446
200652_at	SSR2	signal sequence receptor; beta (translocon-associated protein beta)	-0.5263	0.0031
200654_at	P4HB	procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); beta polypeptide	-0.203	0.0362
200659_s_at	PHB	prohibitin	-0.3642	0.0498
200668_s_at	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog; yeast), ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog; yeast)	-0.2189	0.0301
200670_at	XBP1	X-box binding protein 1	-1.6696	0.0002
200672_x_at	SPTBN1	spectrin; beta; non-erythrocytic 1	-1.4178	0.0127
200674_s_at	RPL32	ribosomal protein L32	-0.1636	0.0204
200676_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	-0.692	0.0092
200685_at	SFRS11	splicing factor; arginine/serine-rich 11	-0.73	0.0349
200696_s_at	GSN	gelsolin (amyloidosis; Finnish type)	-0.5516	0.0464
200705_s_at	EEF1B2	eukaryotic translation elongation factor 1 beta 2, eukaryotic translation elongation factor 1 beta 2-like, hCG1983058	-0.3311	0.0147
200710_at	ACADVL	acyl-Coenzyme A dehydrogenase; very long chain	-1.0009	0
200715_x_at	RPL13A	ribosomal protein L13a	-0.3048	0.011
200724_at	RPL10	ribosomal protein L10	-0.1531	0.0298

200725_x_at	RPL10	ribosomal protein L10	-0.1645	0.0254
200730_s_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.9957	0.021
200731_s_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.8061	0.0088
200732_s_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.8671	0.0007
200733_s_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.5526	0.0248
200736_s_at	GPX1	glutathione peroxidase 1	-0.5777	0.0076
200741_s_at	RPS27	ribosomal protein S27 (metallopanstimulin 1)	-0.2078	0.0006
200742_s_at	TPP1	tripeptidyl peptidase I	-0.7973	0.0282
200743_s_at	TPP1	tripeptidyl peptidase I	-0.5117	0.0253
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	-0.5568	0.0421
200748_s_at	FTH1	ferritin; heavy polypeptide 1, ferritin; heavy polypeptide-like 11, ferritin; heavy polypeptide-like 16	-0.452	0.0079
200752_s_at	CAPN1	calpain 1; (mu/I) large subunit	-0.5279	0.0374
200753_x_at	SFRS2	splicing factor; arginine/serine-rich 2	-0.4751	0.031
200761_s_at	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	-0.3941	0.0255
200762_at	DPYSL2	dihydropyrimidinase-like 2	-0.8062	0.0041
200766_at	CTSD	cathepsin D	-0.6744	0.0317
200768_s_at	MAT2A	methionine adenosyltransferase II; alpha	-0.8065	0
200776_s_at	BZW1	basic leucine zipper and W2 domains 1, similar to basic leucine zipper and W2 domains 1	-0.8211	0.0027
200777_s_at	BZW1	basic leucine zipper and W2 domains 1, similar to basic leucine zipper and W2 domains 1	-0.5157	0
200784_s_at	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	-0.4443	0.007
200785_s_at	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	-1.1563	0.0003
200792_at	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen; 70kDa)	-0.6096	0.0035
200797_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-0.4634	0.0102
200798_x_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	-0.9196	0.0051
200807_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.1493	0.0377
200809_x_at	RPL12	ribosomal protein L12	-0.2022	0.0211
200817_x_at	RPS10	ribosomal protein S10	-0.193	0.0069
200823_x_at	RPL29	ribosomal protein L29	-0.2542	0.0105
200824_at	GSTP1	glutathione S-transferase pi	-2.1568	0.0004
200830_at	PSMD2	proteasome (prosome; macropain) 26S subunit; non-ATPase; 2	-0.269	0.0089
200845_s_at	PRDX6	peroxiredoxin 6	-0.3902	0.0112
200848_at	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-0.8998	0

200849_s_at	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-0.8901	0
200850_s_at	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-0.5938	0
200854_at	NCOR1	nuclear receptor co-repressor 1	-0.5714	0.0012
200856_x_at	C20orf191	chromosome 20 open reading frame 191, nuclear receptor co-repressor 1	-0.6038	0.0023
200858_s_at	RPS8	ribosomal protein S8	-0.2392	0.0075
200862_at	DHCR24	24-dehydrocholesterol reductase	-0.728	0.0031
200872_at	S100A10	S100 calcium binding protein A10	-1.0711	0.0302
200878_at	EPAS1	endothelial PAS domain protein 1	-1.4351	0.0002
200881_s_at	DNAJA1	DnaJ (Hsp40) homolog; subfamily A; member 1	-0.4696	0.019
200884_at	CKB	creatine kinase; brain	-2.0099	0
200888_s_at	RPL23	ribosomal protein L23	-0.2231	0.0103
200893_at	SFRS10	splicing factor; arginine/serine-rich 10 (transformer 2 homolog; Drosophila)	-0.252	0.0011
200897_s_at	PALLD	palladin; cytoskeletal associated protein	-1.8377	0.0027
200902_at	15-Sep	15 kDa selenoprotein	-0.338	0.0242
200904_at	HLA-E	major histocompatibility complex; class I; E	-0.8829	0.0223
200906_s_at	PALLD	palladin; cytoskeletal associated protein	-1.1275	0.0174
200907_s_at	PALLD	palladin; cytoskeletal associated protein	-2.1618	0.0039
200908_s_at	RPLP2	ribosomal protein; large; P2	-0.2254	0.0004
200909_s_at	RPLP2	ribosomal protein; large; P2	-0.2572	0.0134
200918_s_at	SRPR	signal recognition particle receptor ('docking protein')	-0.4713	0.0186
200919_at	PHC2	polyhomeotic homolog 2 (Drosophila)	-1.162	0
200937_s_at	RPL5	ribosomal protein L5	-0.3836	0.0013
200938_s_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	-0.1991	0.0113
200940_s_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	-0.9757	0.0013
200946_x_at	GLUD1	glutamate dehydrogenase 1	-1.082	0.0002
200947_s_at	GLUD1	glutamate dehydrogenase 1	-0.9863	0
200963_x_at	RPL31	ribosomal protein L31	-0.1589	0.0268
200965_s_at	ABLIM1	actin binding LIM protein 1	-3.6306	0
200969_at	SERP1	stress-associated endoplasmic reticulum protein 1	-0.4031	0.0389
200970_s_at	SERP1	stress-associated endoplasmic reticulum protein 1	-0.5106	0.0021
200971_s_at	SERP1	stress-associated endoplasmic reticulum protein 1	-0.5698	0.0002
200986_at	SERPING1	serpin peptidase inhibitor; clade G (C1 inhibitor); member 1; (angioedema; hereditary)	-3.4558	0
200991_s_at	SNX17	sorting nexin 17	-0.4729	0.0148
200994_at	IPO7	Importin 7	-0.3289	0.0159

200995_at	IPO7	Importin 7	-0.3398	0.0465
201005_at	CD9	CD9 molecule	-1.0389	0.0274
201007_at	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein); beta subunit	-0.5285	0
201015_s_at	JUP	junction plakoglobin	-0.815	0.0055
201041_s_at	DUSP1	dual specificity phosphatase 1	-0.8361	0
201044_x_at	DUSP1	dual specificity phosphatase 1	-2.0201	0.0001
201056_at	GOLGB1	golgin B1; golgi integral membrane protein	-0.5614	0.0094
201059_at	CTTN	cortactin	-0.6693	0.0001
201069_at	MMP2	matrix metallopeptidase 2 (gelatinase A; 72kDa gelatinase; 72kDa type IV collagenase)	-4.2588	0
201076_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	-1.0461	0
201077_s_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	-0.9382	0
201080_at	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase; type II; beta	-0.6057	0.002
201092_at	RBBP7	retinoblastoma binding protein 7	-0.4932	0.0022
201094_at	RPS29	ribosomal protein S29	-0.2406	0.0066
201106_at	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	-0.3398	0.0119
201107_s_at	THBS1	thrombospondin 1	-0.2649	0
201108_s_at	THBS1	thrombospondin 1	-1.734	0
201109_s_at	THBS1	thrombospondin 1	-3.2646	0
201110_s_at	THBS1	thrombospondin 1	-2.9702	0
201116_s_at	CPE	carboxypeptidase E	-2.0244	0.0003
201117_s_at	CPE	carboxypeptidase E	-2.1288	0
201135_at	ECHS1	enoyl Coenzyme A hydratase; short chain; 1; mitochondrial	-0.3314	0.0433
201137_s_at	HLA-DPB1	major histocompatibility complex; class II; DP beta 1	-2.0011	0.0029
201146_at	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	-0.3088	0.0429
201150_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy; pseudoinflammatory)	-1.4615	0.0064
201153_s_at	MBNL1	muscleblind-like (Drosophila)	-0.3079	0.0216
201160_s_at	CSDA	cold shock domain protein A	-0.4835	0.0029
201173_x_at	NUDC	nuclear distribution gene C homolog (A. nidulans)	-0.5683	0.0016
201175_at	TXNDC14	thioredoxin domain containing 14	-0.4731	0.0159
201178_at	FBXO7	F-box protein 7	-0.538	0.0044
201190_s_at	PITPNA	phosphatidylinositol transfer protein; alpha	-0.5511	0.0002
201191_at	PITPNA	phosphatidylinositol transfer protein; alpha	-0.7681	0.0002
201193_at	IDH1	isocitrate dehydrogenase 1 (NADP+); soluble	-0.6736	0.0007

201200_at	CREG1	cellular repressor of E1A-stimulated genes 1	-1.2008	0
201217_x_at	RPL3	ribosomal protein L3	-0.1963	0.0062
201219_at	CTBP2	C-terminal binding protein 2	-0.6275	0.0369
201225_s_at	SRRM1	serine/arginine repetitive matrix 1	-0.4046	0.0023
201232_s_at	PSMD13	proteasome (prosome; macropain) 26S subunit; non-ATPase; 13	-0.4231	0.0476
201234_at	ILK	integrin-linked kinase	-0.7059	0.0012
201235_s_at	BTG2	BTG family; member 2	-1.1634	0.0001
201236_s_at	BTG2	BTG family; member 2	-2.7235	0
201239_s_at	LOC653566	signal peptidase complex subunit 2 homolog (S. cerevisiae), signal peptidase complex subunit 2 homolog pseudogene	-0.4271	0.0364
201240_s_at	SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	-0.3218	0.0031
201241_at	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	-0.3441	0.023
201254_x_at	RPS6	ribosomal protein S6	-0.2106	0.014
201255_x_at	BAT3	HLA-B associated transcript 3	-0.3132	0.031
201256_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	-0.2481	0.0202
201261_x_at	BGN	biglycan	-1.0101	0.011
201272_at	AKR1B1	aldo-keto reductase family 1; member B1 (aldose reductase)	-0.8727	0.0002
201288_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-1.0147	0.0015
201289_at	CYR61	cysteine-rich; angiogenic inducer; 61	-2.5734	0.0001
201290_at	SEC11A	SEC11 homolog A (S. cerevisiae)	-0.2487	0.0137
201300_s_at	PRNP	prion protein (p27-30) (Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; fatal familial insomnia)	-0.6641	0.0489
201303_at	EIF4A3	eukaryotic translation initiation factor 4A; isoform 3	-1.2708	0
201315_x_at	IFITM2	interferon induced transmembrane protein 2 (1-8D)	-0.9118	0.0006
201318_s_at	MRCL3	myosin regulatory light chain MRCL3, myosin regulatory light chain MRLC2	-0.2171	0.0425
201319_at	LOC645094	myosin regulatory light chain MRCL3, similar to myosin regulatory light chain-like	-0.3121	0.0138
201324_at	EMP1	epithelial membrane protein 1	-1.9902	0.0003
201325_s_at	EMP1	epithelial membrane protein 1	-1.497	0.0002
201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-1.6994	0.0002
201329_s_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-0.8299	0.001
201334_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	-0.5399	0.0002
201336_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	-0.2827	0.0053
201338_x_at	GTF3A	general transcription factor IIIA	-0.5589	0.0179
201339_s_at	SCP2	sterol carrier protein 2	-0.5079	0.0276

201347_x_at	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.663	0.0153
201348_at	GPX3	glutathione peroxidase 3 (plasma)	-2.5368	0.0002
201349_at	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger); member 3 regulator 1	-2.5392	0.0001
201356_at	SF3A1	splicing factor 3a; subunit 1; 120kDa	-0.5864	0.038
201367_s_at	ZFP36L2	zinc finger protein 36; C3H type-like 2	-0.9818	0.0144
201368_at	ZFP36L2	zinc finger protein 36; C3H type-like 2	-1.0946	0
201369_s_at	ZFP36L2	zinc finger protein 36; C3H type-like 2	-1.6946	0.0001
201382_at	CACYBP	calcyclin binding protein	-0.2248	0.0218
201384_s_at	LOC727732	neighbor of BRCA1 gene 1, similar to neighbor of BRCA1 gene 1	-0.4184	0.0009
201400_at	PSMB3	proteasome (prosome; macropain) subunit; beta type; 3	-0.4055	0.0005
201407_s_at	PPP1CB	protein phosphatase 1; catalytic subunit; beta isoform	-0.3851	0.0073
201408_at	PPP1CB	protein phosphatase 1; catalytic subunit; beta isoform	-0.8646	0.0034
201409_s_at	PPP1CB	protein phosphatase 1; catalytic subunit; beta isoform	-0.4323	0.0065
201413_at	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	-0.4815	0.0098
201425_at	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	-0.9988	0.0032
201427_s_at	SEPP1	selenoprotein P; plasma; 1	-0.6942	0.0015
201432_at	CAT	catalase	-1.3665	0
201445_at	CNN3	calponin 3; acidic	-0.8088	0.0458
201455_s_at	NPEPPS	aminopeptidase puromycin sensitive	-0.5084	0.0115
201460_at	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	-1.0257	0
201461_s_at	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	-1.0001	0.0016
201463_s_at	TALDO1	transaldolase 1	-0.5467	0.0023
201473_at	JUNB	jun B proto-oncogene	-2.032	0
201474_s_at	ITGA3	integrin; alpha 3 (antigen CD49C; alpha 3 subunit of VLA-3 receptor)	-0.8179	0.0015
201484_at	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	-0.5271	0.0155
201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)	-0.4325	0.03
201497_x_at	MYH11	myosin; heavy chain 11; smooth muscle	-1.1538	0.018
201502_s_at	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; alpha	-1.0435	0
201506_at	TGFBI	transforming growth factor; beta-induced; 68kDa	-1.6288	0.0122
201508_at	IGFBP4	insulin-like growth factor binding protein 4	-2.3087	0.0001
201516_at	SRM	spermidine synthase	-0.5377	0.0408
201517_at	NCBP2	nuclear cap binding protein subunit 2; 20kDa	-0.4648	0.0002

201525_at	APOD	apolipoprotein D	-3.4519	0
201530_x_at	EIF4A1	eukaryotic translation initiation factor 4A; isoform 1	-0.2387	0.0155
201531_at	ZFP36	zinc finger protein 36; C3H type; homolog (mouse)	-1.8644	0.0001
201540_at	FHL1	four and a half LIM domains 1	-1.8166	0.0002
201547_at	JARID1B	jumonji; AT rich interactive domain 1B	-0.1223	0.0301
201556_s_at	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	-0.832	0.0008
201557_at	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	-0.9649	0
201560_at	CLIC4	chloride intracellular channel 4	-0.5548	0.0102
201562_s_at	LOC653381	similar to Sorbitol dehydrogenase (L-iditol 2-dehydrogenase), sorbitol dehydrogenase	-0.9098	0.0093
201563_at	SORD	sorbitol dehydrogenase	-1.3068	0.0004
201572_x_at	DCTD	dCMP deaminase	-0.3651	0.0306
201573_s_at	ETF1	eukaryotic translation termination factor 1	-0.5571	0.0148
201578_at	PODXL	podocalyxin-like	-0.7909	0.019
201586_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-0.3515	0.0453
201595_s_at	ZC3H15	zinc finger CCCH-type containing 15	-0.3703	0.0122
201599_at	OAT	ornithine aminotransferase (gyrate atrophy)	-0.4359	0.0335
201601_x_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	-1.3026	0.0032
201605_x_at	CNN2	calponin 2	-0.5493	0.0056
201612_at	ALDH9A1	aldehyde dehydrogenase 9 family; member A1	-0.3113	0.0058
201616_s_at	CALD1	caldesmon 1	-1.2892	0.0042
201617_x_at	CALD1	caldesmon 1	-1.3894	0.0024
201628_s_at	RRAGA	Ras-related GTP binding A	-0.5215	0.0029
201631_s_at	IER3	immediate early response 3	-3.69	0
201637_s_at	FXR1	fragile X mental retardation; autosomal homolog 1	-0.4116	0.0113
201650_at	KRT19	keratin 19	-0.2641	0.0109
201651_s_at	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	-0.6089	0.0004
201662_s_at	ACSL3	acyl-CoA synthetase long-chain family member 3	-0.4732	0.0031
201665_x_at	RPS17	ribosomal protein S17	-0.1313	0.0152
201667_at	GJA1	gap junction protein; alpha 1; 43kDa	-0.8707	0.0207
201677_at	C3orf37	Chromosome 3 open reading frame 37	-0.6007	0.0017
201681_s_at	DLG5	discs; large homolog 5 (Drosophila)	-0.6618	0.0004
201687_s_at	API5	apoptosis inhibitor 5	-0.7566	0
201693_s_at	EGR1	early growth response 1	-3.3174	0
201694_s_at	EGR1	early growth response 1	-2.4073	0.0001
201703_s_at	PPP1R10	protein phosphatase 1; regulatory (inhibitor) subunit 10	-0.79	0.0327

201706_s_at	PEX19	peroxisomal biogenesis factor 19	-0.8751	0
201707_at	PEX19	peroxisomal biogenesis factor 19	-0.7718	0
201711_x_at	RANBP2	RAN binding protein 2	-1.4384	0.0009
201712_s_at	RANBP2	RAN binding protein 2	-2.2623	0
201713_s_at	RANBP2	RAN binding protein 2	-1.8732	0
201717_at	MRPL49	mitochondrial ribosomal protein L49	-0.9818	0.0001
201719_s_at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	-0.8166	0.0469
201721_s_at	LAPTM5	lysosomal associated multispanning membrane protein 5	-1.1177	0.0069
201729_s_at	KIAA0100	KIAA0100	-0.9337	0.0004
201734_at	CLCN3	Chloride channel 3	-0.6255	0.0065
201739_at	SGK	serum/glucocorticoid regulated kinase	-1.9961	0
201740_at	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3; 30kDa (NADH-coenzyme Q reductase)	-0.6397	0.0004
201743_at	CD14	CD14 molecule	-4.1525	0
201744_s_at	LUM	lumican	-3.0717	0.0008
201749_at	ECE1	Endothelin converting enzyme 1	-0.8795	0
201751_at	JOSD1	Josephin domain containing 1	-1.1467	0.0004
201758_at	TSG101	tumor susceptibility gene 101	-0.4348	0.004
201767_s_at	ELAC2	elaC homolog 2 (E. coli)	-0.4847	0.0157
201778_s_at	KIAA0494	KIAA0494	-0.5393	0
201783_s_at	RELA	v-rel reticuloendotheliosis viral oncogene homolog A; nuclear factor of kappa light polypeptide gene enhancer in B-cells 3; p65 (avian)	-0.3509	0.023
201784_s_at	C11orf58	chromosome 11 open reading frame 58	-0.3977	0.0345
201785_at	RNASE1	ribonuclease; RNase A family; 1 (pancreatic)	-1.6462	0.0036
201787_at	FBLN1	fibulin 1	-2.0942	0.0001
201792_at	AEBP1	AE binding protein 1	-2.4258	0.0002
201799_s_at	OSBP	oxysterol binding protein	-0.8555	0.0059
201800_s_at	OSBP	oxysterol binding protein	-0.7858	0
201808_s_at	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	-0.1472	0.0421
201809_s_at	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	-1.3266	0.0001
201810_s_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-0.9897	0.0119
201811_x_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-0.6238	0.0187
201812_s_at	LOC201725	hypothetical protein LOC201725, translocase of outer mitochondrial membrane 7 homolog (yeast)	-0.2657	0.0323
201814_at	TBC1D5	TBC1 domain family; member 5	-0.4741	0.0021
201816_s_at	GBAS	glioblastoma amplified sequence	-0.9414	0.0001
201825_s_at	SCCPDH	saccharopine dehydrogenase (putative)	-2.1071	0

201826_s_at	SCCPDH	saccharopine dehydrogenase (putative)	-1.6944	0
201842_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	-2.8959	0.0021
201843_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	-2.7909	0.0008
201859_at	SRGN	serglycin	-0.7271	0.0043
201860_s_at	PLAT	plasminogen activator; tissue	-4.0632	0
201871_s_at	LOC51035	SAPK substrate protein 1	-1.0005	0.0001
201882_x_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 1	-0.1846	0.0148
201883_s_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 1	-0.9818	0
201887_at	IL13RA1	interleukin 13 receptor; alpha 1	-0.7755	0.0035
201893_x_at	DCN	decorin	-3.7936	0.0008
201909_at	RPS4Y1	ribosomal protein S4; Y-linked 1	-3.9755	0.003
201921_at	GNG10	guanine nucleotide binding protein (G protein); gamma 10, hypothetical protein LOC552891	-0.2488	0.0393
201924_at	AFF1	AF4/FMR2 family; member 1	-0.393	0.0152
201925_s_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-2.5472	0
201926_s_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-2.6316	0
201931_at	ETFA	electron-transfer-flavoprotein; alpha polypeptide (glutaric aciduria II)	-0.5895	0.0007
201936_s_at	EIF4G3	eukaryotic translation initiation factor 4 gamma; 3	-0.3752	0.02
201949_x_at	CAPZB	capping protein (actin filament) muscle Z-line; beta	-0.1642	0.0487
201957_at	PPP1R12B	protein phosphatase 1; regulatory (inhibitor) subunit 12B	-0.8603	0.0016
201966_at	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2; 49kDa (NADH-coenzyme Q reductase)	-0.7409	0.0005
201968_s_at	PGM1	phosphoglucomutase 1	-0.688	0.0037
201978_s_at	KIAA0141	KIAA0141	-0.6444	0.0013
201988_s_at	CREBL2	cAMP responsive element binding protein-like 2	-1.6316	0.0001
201989_s_at	CREBL2	cAMP responsive element binding protein-like 2	-1.0604	0
201990_s_at	CREBL2	cAMP responsive element binding protein-like 2	-1.6918	0
202000_at	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 6; 14kDa	-0.857	0.0213
202003_s_at	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	-1.7004	0.0002
202007_at	NID1	nidogen 1	-1.4298	0.0007
202008_s_at	NID1	nidogen 1	-0.5577	0.031
202010_s_at	ZNF410	zinc finger protein 410	-0.8052	0.0003
202016_at	MEST	mesoderm specific transcript homolog (mouse)	-1.6687	0.012
202017_at	EPHX1	epoxide hydrolase 1; microsomal (xenobiotic)	-0.5906	0.0416

202021_x_at	EIF1	eukaryotic translation initiation factor 1	-0.2416	0.003
202023_at	EFNA1	ephrin-A1	-0.7683	0.028
202025_x_at	ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	-0.4509	0.0017
202026_at	SDHD	succinate dehydrogenase complex; subunit D; integral membrane protein	-0.5313	0.0103
202028_s_at	RPL38	ribosomal protein L38	-0.4826	0.037
202029_x_at	RPL38	ribosomal protein L38	-0.1633	0.0486
202038_at	UBE4A	ubiquitination factor E4A (UFD2 homolog; yeast)	-0.331	0.0203
202048_s_at	CBX6	chromobox homolog 6	-0.5449	0.0038
202053_s_at	ALDH3A2	aldehyde dehydrogenase 3 family; member A2	-1.2416	0
202054_s_at	ALDH3A2	aldehyde dehydrogenase 3 family; member A2	-1.5267	0
202055_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	-0.3662	0.0221
202057_at	KPNA1	karyopherin alpha 1 (importin alpha 5)	-0.6988	0.0005
202060_at	CTR9	Ctr9; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	-0.4966	0.0034
202071_at	SDC4	syndecan 4	-1.4405	0.0031
202075_s_at	PLTP	phospholipid transfer protein	-3.088	0
202081_at	IER2	immediate early response 2	-1.2042	0
202082_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-0.8382	0.0043
202083_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-1.8109	0
202084_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-1.1379	0
202096_s_at	TSPO	translocator protein (18kDa)	-1.3419	0.0155
202108_at	PEPD	peptidase D	-0.4634	0.007
202109_at	ARFIP2	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	-0.7011	0.0086
202121_s_at	CHMP2A	chromatin modifying protein 2A	-0.217	0.0466
202125_s_at	TRAK2	trafficking protein; kinesin binding 2	-0.7182	0.0089
202126_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.3248	0.017
202135_s_at	ACTR1B	ARP1 actin-related protein 1 homolog B; centractin beta (yeast)	-0.5761	0.0009
202139_at	AKR7A2	aldo-keto reductase family 7; member A2 (aflatoxin aldehyde reductase)	-1.5239	0
202149_at	NEDD9	neural precursor cell expressed; developmentally down-regulated 9	-2.0846	0
202150_s_at	NEDD9	neural precursor cell expressed; developmentally down-regulated 9	-0.9901	0
202157_s_at	CUGBP2	CUG triplet repeat; RNA binding protein 2	-1.698	0.0153
202172_at	VEZF1	vascular endothelial zinc finger 1	-0.493	0.0127
202177_at	GAS6	growth arrest-specific 6	-1.16	0
202178_at	PRKCZ	protein kinase C; zeta	-1.036	0.0091
202192_s_at	GAS7	growth arrest-specific 7	-0.7206	0.0317

202196_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	-3.0544	0
202197_at	MTMR3	myotubularin related protein 3	-0.6493	0.0398
202211_at	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3	-1.3904	0
202218_s_at	FADS2	fatty acid desaturase 2	-0.6835	0.0397
202222_s_at	DES	desmin	-0.1346	0.0403
202225_at	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	-0.516	0.0059
202231_at	EIF3M	eukaryotic translation initiation factor 3; subunit M	-0.4142	0.0021
202232_s_at	EIF3M	eukaryotic translation initiation factor 3; subunit M	-0.4202	0.0128
202237_at	NNMT	nicotinamide N-methyltransferase	-2.3359	0.0031
202238_s_at	NNMT	nicotinamide N-methyltransferase	-1.695	0.0107
202239_at	PARP4	poly (ADP-ribose) polymerase family; member 4	-0.5173	0.0106
202241_at	TRIB1	tribbles homolog 1 (Drosophila)	-1.6159	0.002
202250_s_at	WDR42A	WD repeat domain 42A	-0.6626	0.0251
202258_s_at	PFAAP5	phosphonoformate immuno-associated protein 5	-0.6532	0.0141
202271_at	FBXO28	F-box protein 28	-0.759	0.007
202280_at			-0.1524	0.0275
202283_at	SERPINF1	serpin peptidase inhibitor; clade F (alpha-2 antiplasmin; pigment epithelium derived factor); member 1	-2.7235	0.0005
202287_s_at	TACSTD2	tumor-associated calcium signal transducer 2	-0.1705	0.0047
202291_s_at	MGP	matrix Gla protein	-1.5657	0.0001
202294_at	STAG1	stromal antigen 1	-0.5627	0.003
202295_s_at	CTSH	cathepsin H	-1.3945	0.0019
202305_s_at	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	-0.5005	0.0475
202308_at	SREBF1	sterol regulatory element binding transcription factor 1	-2.4836	0
202317_s_at	UBE4B	ubiquitination factor E4B (UFD2 homolog; yeast)	-0.9938	0.0013
202318_s_at	SENP6	SUMO1/sentrin specific peptidase 6	-0.3858	0.0452
202321_at	GGPS1	geranylgeranyl diphosphate synthase 1	-0.7808	0.0224
202340_x_at	NR4A1	nuclear receptor subfamily 4; group A; member 1	-2.6239	0
202350_s_at	MATN2	matrilin 2	-3.3857	0
202351_at	ITGAV	integrin; alpha V (vitronectin receptor; alpha polypeptide; antigen CD51)	-0.4461	0.0143
202352_s_at	PSMD12	proteasome (prosome; macropain) 26S subunit; non-ATPase; 12	-0.7514	0.0029
202359_s_at	SNX19	sorting nexin 19	-0.9854	0.0016
202377_at	LEPROT	leptin receptor overlapping transcript	-0.6117	0.0017
202387_at	BAG1	BCL2-associated athanogene	-0.8107	0.0015
202388_at	RGS2	regulator of G-protein signaling 2; 24kDa	-2.1377	0.0003

202390_s_at	HD	huntingtin (Huntington disease)	-0.5828	0.0148
202394_s_at	ABCF3	ATP-binding cassette; sub-family F (GCN20); member 3	-0.7683	0.0061
202426_s_at	RXRA	retinoid X receptor; alpha	-0.3277	0.0165
202427_s_at	BRP44	brain protein 44	-0.6002	0.0458
202429_s_at	PPP3CA	protein phosphatase 3 (formerly 2B); catalytic subunit; alpha isoform	-0.6869	0.0012
202431_s_at	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-2.3576	0
202432_at	PPP3CB	protein phosphatase 3 (formerly 2B); catalytic subunit; beta isoform	-0.498	0.0001
202435_s_at	CYP1B1	cytochrome P450; family 1; subfamily B; polypeptide 1	-1.9162	0.0006
202436_s_at	CYP1B1	cytochrome P450; family 1; subfamily B; polypeptide 1	-2.7869	0.0001
202437_s_at	CYP1B1	cytochrome P450; family 1; subfamily B; polypeptide 1	-3.1938	0
202449_s_at	RXRA	retinoid X receptor; alpha	-1.2703	0.0001
202454_s_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-0.2781	0.0011
202468_s_at	CTNNAL1	catenin (cadherin-associated protein); alpha-like 1	-0.7368	0.0131
202481_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	-0.7723	0.0475
202484_s_at	MBD2	methyl-CpG binding domain protein 2	-0.6562	0
202485_s_at	MBD2	methyl-CpG binding domain protein 2	-0.1017	0.0138
202488_s_at	FXYD3	FXYD domain containing ion transport regulator 3	-0.3961	0.0022
202500_at	DNAJB2	DnaJ (Hsp40) homolog; subfamily B; member 2	-0.6698	0.0021
202502_at	ACADM	acyl-Coenzyme A dehydrogenase; C-4 to C-12 straight chain	-0.5796	0.006
202509_s_at	TNFAIP2	tumor necrosis factor; alpha-induced protein 2	-0.3273	0.0001
202510_s_at	TNFAIP2	tumor necrosis factor; alpha-induced protein 2	-1.7852	0.0009
202523_s_at	SPOCK2	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 2	-1.0676	0
202524_s_at	SPOCK2	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 2	-2.8028	0
202526_at	SMAD4	SMAD family member 4	-0.3355	0.0001
202537_s_at	CHMP2B	chromatin modifying protein 2B	-0.5644	0.01
202541_at	SCYE1	small inducible cytokine subfamily E; member 1 (endothelial monocyte-activating)	-0.651	0.0005
202546_at	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	-2.1593	0.0002
202550_s_at	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	-0.5167	0.0012
202551_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-0.8354	0.0158
202552_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.0252	0.0041
202553_s_at	SYF2	SYF2 homolog; RNA splicing factor (S. cerevisiae)	-0.4083	0.0017

202555_s_at	MYLK	myosin; light chain kinase	-3.0704	0
202565_s_at	SVIL	supervillin	-1.8426	0.0007
202568_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	-0.532	0.0342
202584_at	NFX1	nuclear transcription factor; X-box binding 1	-0.6257	0.0007
202590_s_at	PDK2	pyruvate dehydrogenase kinase; isozyme 2	-1.5921	0.0001
202595_s_at	LEPROTL1	leptin receptor overlapping transcript-like 1	-0.4714	0.0446
202598_at	S100A13	S100 calcium binding protein A13	-1.3498	0.0467
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	-1.1663	0.0023
202615_at	GNAQ	Guanine nucleotide binding protein (G protein); q polypeptide	-0.4011	0.0154
202623_at	EAPP	E2F-associated phosphoprotein	-0.5028	0.003
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	-1.3	0.0058
202626_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	-1.3812	0.0134
202630_at	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-0.5775	0.013
202637_s_at	ICAM1	intercellular adhesion molecule 1 (CD54); human rhinovirus receptor	-1.0454	0.0495
202646_s_at	CSDE1	cold shock domain containing E1; RNA-binding, neuroblastoma RAS viral (v-ras) oncogene homolog	-0.6816	0.0001
202650_s_at	KIAA0195	KIAA0195	-0.8009	0.0101
202664_at	WIPF1	WAS/WASL interacting protein family; member 1	-1.3476	0.0098
202668_at	EFNB2	ephrin-B2	-0.9687	0.0489
202672_s_at	ATF3	activating transcription factor 3	-3.114	0.0001
202673_at	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	-0.3859	0.0188
202675_at	SDHB	succinate dehydrogenase complex; subunit B; iron sulfur (Ip)	-0.4971	0.0358
202679_at	NPC1	Niemann-Pick disease; type C1	-2.1672	0
202681_at	USP4	ubiquitin specific peptidase 4 (proto-oncogene)	-0.3824	0.0248
202684_s_at	RNMT	RNA (guanine-7-) methyltransferase	-0.5269	0.0002
202685_s_at	AXL	AXL receptor tyrosine kinase	-0.6279	0
202686_s_at	AXL	AXL receptor tyrosine kinase	-3.8518	0
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily; member 10	-1.4905	0.0001
202688_at	TNFSF10	tumor necrosis factor (ligand) superfamily; member 10	-1.4601	0.0001
202689_at	RBM15B	RNA binding motif protein 15B	-0.3107	0.0373
202692_s_at	UBTF	upstream binding transcription factor; RNA polymerase I	-0.4468	0.0358
202701_at	BMP1	bone morphogenetic protein 1	-0.8004	0.0136
202704_at	TOB1	transducer of ERBB2; 1	-1.3777	0
202709_at	FMOD	fibromodulin	-1.1379	0.0001
202725_at	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A; 220kDa	-0.8255	0.0073

202740_at	ACY1	aminoacylase 1	-0.7966	0.0199
202746_at	ITM2A	integral membrane protein 2A	-2.0634	0.0001
202747_s_at	ITM2A	integral membrane protein 2A	-1.022	0.0016
202748_at	GBP2	guanylate binding protein 2; interferon-inducible	-2.4656	0.0001
202764_at	STIM1	stromal interaction molecule 1	-0.2159	0.0429
202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-4.3781	0
202772_at	HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	-0.8186	0.0006
202776_at	DNTTIP2	deoxynucleotidyltransferase; terminal; interacting protein 2	-0.6058	0.0012
202781_s_at	SKIP	skeletal muscle and kidney enriched inositol phosphatase	-0.6621	0.0001
202782_s_at	SKIP	skeletal muscle and kidney enriched inositol phosphatase	-0.4782	0.0053
202792_s_at	SAPS2	SAPS domain family; member 2	-0.9155	0.0012
202803_s_at	ITGB2	integrin; beta 2 (complement component 3 receptor 3 and 4 subunit)	-1.2845	0.0318
202807_s_at	TOM1	target of myb1 (chicken)	-0.4893	0.0083
202808_at	C10orf26	chromosome 10 open reading frame 26	-0.8422	0.0009
202810_at	DRG1	developmentally regulated GTP binding protein 1	-0.7556	0.0018
202814_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	-1.746	0
202815_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	-1.7209	0
202817_s_at	SS18	synovial sarcoma translocation; chromosome 18	-0.9032	0.0116
202822_at	LPP	LIM domain containing preferred translocation partner in lipoma	-0.923	0
202832_at	GCC2	GRIP and coiled-coil domain containing 2	-0.586	0.0149
202838_at	FUCA1	fucosidase; alpha-L- 1; tissue	-0.8129	0.0112
202842_s_at	DNAJB9	DnaJ (Hsp40) homolog; subfamily B; member 9	-0.6165	0.0119
202843_at	DNAJB9	DnaJ (Hsp40) homolog; subfamily B; member 9	-0.9332	0.0058
202853_s_at	RYK	RYK receptor-like tyrosine kinase	-0.5435	0.0052
202861_at	PER1	period homolog 1 (Drosophila)	-1.6052	0
202862_at	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	-0.9465	0.0092
202863_at	SP100	SP100 nuclear antigen	-0.8039	0.0221
202867_s_at	DNAJB12	DnaJ (Hsp40) homolog; subfamily B; member 12	-0.5178	0.0286
202883_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A); regulatory subunit A; beta isoform	-1.5916	0.0004
202885_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A); regulatory subunit A; beta isoform	-0.1358	0.0008
202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A); regulatory subunit A; beta isoform	-1.5564	0.0003

202889_x_at	MAP7	microtubule-associated protein 7	-0.5471	0.0003
202890_at	MAP7	microtubule-associated protein 7	-1.9706	0
202891_at	NIT1	nitrilase 1	-0.7781	0.0007
202893_at	UNC13B	unc-13 homolog B (C. elegans)	-0.6635	0.0407
202900_s_at	NUP88	nucleoporin 88kDa	-0.9059	0.0025
202916_s_at	FAM20B	family with sequence similarity 20; member B	-0.4674	0.0139
202917_s_at	S100A8	S100 calcium binding protein A8	-1.9245	0.0197
202918_s_at	MOBKL3	MOB1; Mps One Binder kinase activator-like 3 (yeast)	-1.1957	0.0069
202919_at	MOBKL3	MOB1; Mps One Binder kinase activator-like 3 (yeast)	-0.9789	0.008
202920_at	ANK2	ankyrin 2; neuronal	-2.5882	0.0031
202930_s_at	SUCLA2	succinate-CoA ligase; ADP-forming; beta subunit	-0.8166	0.0013
202931_x_at	BIN1	bridging integrator 1	-1.2242	0.0052
202941_at	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2; 24kDa	-0.5557	0.0002
202947_s_at	GYPC	glycophorin C (Gerbich blood group)	-2.69	0
202948_at	IL1R1	interleukin 1 receptor; type I	-1.532	0.0009
202949_s_at	FHL2	four and a half LIM domains 2	-1.5636	0.0091
202953_at	C1QB	complement component 1; q subcomponent; B chain	-2.2889	0.0005
202957_at	HCLS1	hematopoietic cell-specific Lyn substrate 1	-2.99	0
202962_at	KIF13B	kinesin family member 13B	-0.6237	0.0321
202967_at	GSTA4	glutathione S-transferase A4	-1.5287	0
202974_at	MPP1	membrane protein; palmitoylated 1; 55kDa	-0.7252	0.0253
202982_s_at	ACOT1	acyl-CoA thioesterase 1, acyl-CoA thioesterase 2	-1.509	0.0002
202988_s_at	RGS1	regulator of G-protein signaling 1	-1.5591	0.0276
202990_at	PYGL	phosphorylase; glycogen; liver (Hers disease; glycogen storage disease type VI)	-1.8906	0
202992_at	C7	complement component 7	-2.116	0.0008
202994_s_at	FBLN1	fibulin 1	-4.328	0
202995_s_at	FBLN1	fibulin 1	-4.7971	0
203002_at	AMOTL2	angiomotin like 2	-1.2061	0.0145
203003_at	MEF2D	myocyte enhancer factor 2D	-0.3791	0.0019
203004_s_at	MEF2D	myocyte enhancer factor 2D	-0.2696	0.0337
203010_at	STAT5A	signal transducer and activator of transcription 5A	-1.5908	0
203012_x_at	RPL23A	ribosomal protein L23a	-0.1679	0.0013
203028_s_at	CYBA	cytochrome b-245; alpha polypeptide	-1.167	0.022
203034_s_at	hCG_21078	hCG21078, ribosomal protein L27a	-0.1807	0.0111
203039_s_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1; 75kDa (NADH-coenzyme Q reductase)	-0.6239	0.001
203043_at	ZBED1	zinc finger; BED-type containing 1	-2.5333	0

203045_at	NINJ1	ninjurin 1	-0.8968	0.0243
203052_at	C2	complement component 2	-0.6948	0.0452
203053_at	BCAS2	breast carcinoma amplified sequence 2	-0.719	0.0015
203054_s_at	TCTA	T-cell leukemia translocation altered gene	-1.1446	0.0143
203058_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.51	0.0138
203059_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.1787	0.0206
203060_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.2381	0.0301
203063_at	PPM1F	protein phosphatase 1F (PP2C domain containing)	-0.7191	0.0005
203064_s_at	FOXK2	forkhead box K2	-1.5461	0
203066_at	GALNAC4S-6ST	B cell RAG associated protein	-2.2152	0.0001
203071_at	SEMA3B	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3B	-3.3549	0
203074_at	ANXA8	annexin A8, annexin A8-like 1, annexin A8-like 2	-0.2844	0.0031
203075_at	SMAD2	SMAD family member 2	-0.5516	0.0082
203088_at	FBLN5	fibulin 5	-3.9232	0
203090_at	SDF2	stromal cell-derived factor 2	-1.2469	0
203102_s_at	MGAT2	mannosyl (alpha-1;6-)-glycoprotein beta-1;2-N-acetylglucosaminyltransferase	-0.3977	0.0229
203104_at	CSF1R	colony stimulating factor 1 receptor; formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	-2.6776	0
203111_s_at	PTK2B	PTK2B protein tyrosine kinase 2 beta	-0.1916	0.0069
203113_s_at	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	-0.4109	0.0459
203114_at	SSSCA1	Sjogren's syndrome/scleroderma autoantigen 1	-0.7326	0.0003
203115_at	FECH	ferrochelatase (protoporphyria)	-0.6445	0.0043
203116_s_at	FECH	ferrochelatase (protoporphyria)	-0.5507	0.0134
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	-1.0809	0.0006
203131_at	PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	-5.0204	0
203143_s_at	KIAA0040	KIAA0040	-0.5277	0.0215
203144_s_at	KIAA0040	KIAA0040	-0.3918	0.0005
203152_at	MRPL40	mitochondrial ribosomal protein L40	-1.0138	0.0005
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	-0.7975	0.0412
203156_at	AKAP11	A kinase (PRKA) anchor protein 11	-0.4621	0.0285
203157_s_at	GLS	glutaminase	-1.2174	0.0242
203159_at	GLS	glutaminase	-1.0295	0.0057
203161_s_at	RNF8	ring finger protein 8	-0.2582	0.0001
203164_at	SLC33A1	solute carrier family 33 (acetyl-CoA transporter); member 1	-1.6538	0

203165_s_at	SLC33A1	solute carrier family 33 (acetyl-CoA transporter); member 1	-1.35	0
203170_at	KIAA0409	KIAA0409	-0.1947	0.0028
203178_at	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	-1.5061	0.0237
203179_at	GALT	galactose-1-phosphate uridylyltransferase	-0.5729	0.0236
203180_at	ALDH1A3	aldehyde dehydrogenase 1 family; member A3	-2.3242	0.0014
203185_at	RASSF2	Ras association (RalGDS/AF-6) domain family 2	-2.5797	0
203186_s_at	S100A4	S100 calcium binding protein A4	-2.0781	0.0023
203188_at	B3GNT1	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 1	-0.5558	0.0133
203189_s_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8; 23kDa (NADH-coenzyme Q reductase)	-0.6846	0.0014
203190_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8; 23kDa (NADH-coenzyme Q reductase)	-0.588	0.0003
203197_s_at	C1orf123	chromosome 1 open reading frame 123	-0.6385	0.0038
203200_s_at	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	-0.5156	0.0363
203206_at	FAM53B	family with sequence similarity 53; member B	-0.675	0.0035
203233_at	IL4R	interleukin 4 receptor	-1.1061	0.0001
203237_s_at	NOTCH3	Notch homolog 3 (Drosophila)	-0.1417	0.0164
203240_at	FCGBP	Fc fragment of IgG binding protein	-3.1634	0.0001
203241_at	UVRAG	UV radiation resistance associated gene	-1.0895	0
203243_s_at	PDLIM5	PDZ and LIM domain 5	-0.565	0.0269
203252_at	CDK2AP2	CDK2-associated protein 2	-2.3935	0
203255_at	FBXO11	F-box protein 11	-0.7945	0.0047
203259_s_at	HDDC2	HD domain containing 2	-0.9339	0
203260_at	HDDC2	HD domain containing 2	-0.6201	0.0178
203266_s_at	MAP2K4	mitogen-activated protein kinase kinase 4	-0.4696	0.0148
203267_s_at	DRG2	developmentally regulated GTP binding protein 2	-0.3271	0.0246
203268_s_at	DRG2	developmentally regulated GTP binding protein 2	-0.2554	0.0328
203292_s_at	VPS11	vacuolar protein sorting 11 homolog (S. cerevisiae)	-0.7823	0.0001
203303_at	DYNLT3	dynein; light chain; Tctex-type 3	-0.7665	0.0012
203305_at	F13A1	coagulation factor XIII; A1 polypeptide	-3.7126	0
203310_at	STXBP3	syntaxin binding protein 3	-0.3801	0.0254
203314_at	GTPBP6	GTP binding protein 6 (putative)	-0.5451	0.0215
203320_at	SH2B3	SH2B adaptor protein 3	-1.1425	0.0005
203327_at	IDE	insulin-degrading enzyme	-0.5959	0.0124
203330_s_at	STX5	syntaxin 5	-0.4712	0.0028

203331_s_at	INPP5D	inositol polyphosphate-5-phosphatase; 145kDa	-0.2317	0.0088
203335_at	PHYH	phytanoyl-CoA 2-hydroxylase	-0.5641	0.0015
203341_at	CEBPZ	CCAAT/enhancer binding protein zeta	-0.5123	0.0072
203343_at	UGDH	UDP-glucose dehydrogenase	-0.962	0.0004
203363_s_at	KIAA0652	KIAA0652	-0.4014	0.0115
203364_s_at	KIAA0652	KIAA0652	-0.4804	0.0103
203371_s_at	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 3; 12kDa	-0.2645	0.0259
203372_s_at	SOCS2	suppressor of cytokine signaling 2	-2.1473	0.0001
203373_at	SOCS2	suppressor of cytokine signaling 2	-1.8435	0
203380_x_at	SFRS5	splicing factor; arginine/serine-rich 5	-0.5285	0.0002
203381_s_at	APOE	apolipoprotein E	-1.5197	0.0048
203382_s_at	APOE	apolipoprotein E	-1.642	0.0033
203385_at	DGKA	diacylglycerol kinase; alpha 80kDa	-1.711	0.001
203386_at	TBC1D4	TBC1 domain family; member 4	-1.1377	0.0001
203387_s_at	TBC1D4	TBC1 domain family; member 4	-1.849	0.0001
203388_at	ARRB2	arrestin; beta 2	-1.7151	0
203391_at	FKBP2	FK506 binding protein 2; 13kDa	-0.4887	0.001
203401_at	PRPS2	phosphoribosyl pyrophosphate synthetase 2	-2.981	0.0002
203413_at	NELL2	NEL-like 2 (chicken)	-0.8753	0.0094
203414_at	MMD	monocyte to macrophage differentiation-associated	-1.6495	0.0004
203416_at	CD53	CD53 molecule	-2.0035	0.0024
203420_at	FAM8A1	family with sequence similarity 8; member A1	-0.3238	0.0024
203424_s_at	IGFBP5	insulin-like growth factor binding protein 5	-3.2291	0
203425_s_at	IGFBP5	insulin-like growth factor binding protein 5	-1.7855	0
203426_s_at	IGFBP5	insulin-like growth factor binding protein 5	-0.7388	0
203430_at	HEBP2	heme binding protein 2	-1.24	0.0046
203440_at	CDH2	cadherin 2; type 1; N-cadherin (neuronal)	-3.6018	0.0005
203441_s_at	CDH2	cadherin 2; type 1; N-cadherin (neuronal)	-2.2382	0.0006
203442_x_at	EML3	echinoderm microtubule associated protein like 3	-0.6345	0.0007
203443_at	EML3	echinoderm microtubule associated protein like 3	-0.1712	0.0204
203447_at	PSMD5	proteasome (prosome; macropain) 26S subunit; non-ATPase; 5	-0.5815	0.0184
203450_at	CBY1	chibby homolog 1 (Drosophila)	-0.7012	0.0035
203453_at	SCNN1A	sodium channel; nonvoltage-gated 1 alpha	-5.0139	0
203455_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	-0.6313	0.0003
203465_at	MRPL19	mitochondrial ribosomal protein L19	-0.4333	0.0334
203466_at	MPV17	MpV17 mitochondrial inner membrane protein	-1.2028	0.0004

203467_at	PMM1	phosphomannomutase 1	-0.6336	0.0346
203471_s_at	PLEK	pleckstrin	-1.1296	0.0192
203472_s_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	-0.4836	0.0121
203473_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	-2.9263	0
203475_at	CYP19A1	cytochrome P450; family 19; subfamily A; polypeptide 1	-1.7957	0.0036
203499_at	EPHA2	EPH receptor A2	-1.0971	0
203504_s_at	ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	-2.2855	0.0001
203505_at	ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	-1.3596	0.0001
203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily; member 1B	-0.7977	0.041
203511_s_at	TRAPPC3	trafficking protein particle complex 3	-0.653	0.0448
203512_at	TRAPPC3	trafficking protein particle complex 3	-0.6045	0.0172
203514_at	MAP3K3	mitogen-activated protein kinase kinase kinase 3	-0.4347	0.0469
203515_s_at	PMVK	phosphomevalonate kinase	-1.0075	0.0005
203518_at	LYST	lysosomal trafficking regulator	-0.7322	0.0116
203522_at	CCS	copper chaperone for superoxide dismutase	-0.6757	0.0093
203528_at	SEMA4D	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4D	-1.3249	0.0007
203531_at	CUL5	cullin 5	-0.5031	0.0027
203533_s_at	CUL5	cullin 5	-0.2575	0.0272
203540_at	GFAP	glial fibrillary acidic protein	-0.1787	0.0102
203542_s_at	KLF9	Kruppel-like factor 9	-1.0062	0.0291
203543_s_at	KLF9	Kruppel-like factor 9	-1.1801	0.0011
203545_at	ALG8	asparagine-linked glycosylation 8 homolog (S. cerevisiae; alpha-1;3-glucosyltransferase)	-0.5756	0.003
203547_at	CD4	CD4 molecule	-0.6876	0.0335
203551_s_at	COX11	COX11 homolog; cytochrome c oxidase assembly protein (yeast)	-0.5906	0.0022
203556_at	ZHX2	zinc fingers and homeoboxes 2	-0.7468	0.0172
203557_s_at	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	-0.8188	0.032
203559_s_at	ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	-0.1208	0.0391
203561_at	FCGR2A	Fc fragment of IgG; low affinity IIa; receptor (CD32)	-1.3657	0.0047
203571_s_at	C10orf116	chromosome 10 open reading frame 116	-2.0896	0
203574_at	NFIL3	nuclear factor; interleukin 3 regulated	-2.6989	0
203576_at	BCAT2	branched chain aminotransferase 2; mitochondrial	-0.7668	0.0052
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	-3.3754	0

203592_s_at	FSTL3	follistatin-like 3 (secreted glycoprotein)	-2.1327	0
203599_s_at	WBP4	WW domain binding protein 4 (formin binding protein 21)	-0.8931	0.025
203603_s_at	ZEB2	zinc finger E-box binding homeobox 2	-2.0998	0
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family; member A1 (succinate-semialdehyde dehydrogenase)	-1.5072	0.0008
203615_x_at	SULT1A1	sulfotransferase family; cytosolic; 1A; phenol-preferring; member 1	-1.0278	0.0278
203618_at	FAIM2	Fas apoptotic inhibitory molecule 2	-0.1744	0.014
203620_s_at	FCHSD2	FCH and double SH3 domains 2	-0.5133	0.0374
203621_at	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 5; 16kDa	-0.3174	0.0105
203632_s_at	GPRC5B	G protein-coupled receptor; family C; group 5; member B	-1.3978	0.0109
203633_at	CPT1A	carnitine palmitoyltransferase 1A (liver)	-1.1247	0.0003
203638_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-2.443	0.0036
203639_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-1.736	0.0016
203640_at	MBNL2	muscleblind-like 2 (Drosophila)	-0.8607	0.0173
203641_s_at	COBLL1	COBL-like 1	-2.9911	0
203642_s_at	COBLL1	COBL-like 1	-2.101	0
203645_s_at	CD163	CD163 molecule	-2.9706	0.0001
203646_at	FDX1	ferredoxin 1	-0.6882	0.0251
203647_s_at	FDX1	ferredoxin 1	-0.8616	0.0072
203650_at	PROCR	protein C receptor; endothelial (EPCR)	-0.5836	0.0305
203657_s_at	CTSF	cathepsin F	-1.4884	0.0001
203658_at	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase); member 20	-0.9657	0.0003
203661_s_at	TMOD1	tropomodulin 1	-2.7978	0
203662_s_at	TMOD1	tropomodulin 1	-3.3048	0
203666_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	-2.1494	0
203668_at	MAN2C1	mannosidase; alpha; class 2C; member 1	-1.2785	0
203669_s_at	DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	-1.497	0.0018
203671_at	TPMT	thiopurine S-methyltransferase	-0.5721	0.0005
203672_x_at	TPMT	thiopurine S-methyltransferase	-0.7712	0.0001
203673_at	TG	thyroglobulin	-0.3238	0.0031
203682_s_at	IVD	isovaleryl Coenzyme A dehydrogenase	-0.6639	0.0486

203688_at	PKD2	polycystic kidney disease 2 (autosomal dominant)	-0.8109	0.0031
203699_s_at	DIO2	deiodinase; iodothyronine; type II	-1.223	0
203700_s_at	DIO2	deiodinase; iodothyronine; type II	-1.5091	0
203704_s_at			-0.4822	0.0003
203711_s_at	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	-1.6332	0
203733_at	DEXI	dexamethasone-induced transcript	-0.8049	0.0149
203749_s_at	RARA	retinoic acid receptor; alpha	-1.4124	0
203751_x_at	JUND	jun D proto-oncogene	-0.6963	0.0432
203756_at	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	-0.3837	0.0032
203759_at	ST3GAL4	ST3 beta-galactoside alpha-2;3-sialyltransferase 4	-1.1018	0
203760_s_at	SLA	Src-like-adaptor	-1.2414	0.0003
203761_at	SLA	Src-like-adaptor	-2.7188	0
203766_s_at	LMOD1	leiomodin 1 (smooth muscle)	-4.4445	0
203781_at	MRPL33	mitochondrial ribosomal protein L33	-1.0545	0
203786_s_at	TPD52L1	tumor protein D52-like 1	-1.3716	0.0044
203793_x_at	PCGF2	polycomb group ring finger 2	-0.3683	0.0315
203794_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	-0.5932	0.0418
203797_at	VSNL1	visinin-like 1	-2.5365	0.0016
203798_s_at	VSNL1	visinin-like 1	-2.216	0.0037
203799_at	CD302	CD302 molecule	-2.2984	0
203801_at	MRPS14	mitochondrial ribosomal protein S14	-0.7478	0.0042
203810_at	DNAJB4	DnaJ (Hsp40) homolog; subfamily B; member 4	-0.8921	0.0027
203812_at		CDNA clone IMAGE:5922621	-1.4535	0
203813_s_at	SLIT3	slit homolog 3 (Drosophila)	-1.3778	0.0004
203814_s_at	NQO2	NAD(P)H dehydrogenase; quinone 2	-0.9894	0.0041
203821_at	HBEGF	heparin-binding EGF-like growth factor	-1.2611	0.0034
203826_s_at	PITPNM1	phosphatidylinositol transfer protein; membrane-associated 1	-1.0401	0.0001
203835_at	LRRC32	leucine rich repeat containing 32	-2.3679	0
203836_s_at	MAP3K5	mitogen-activated protein kinase kinase kinase 5	-1.9337	0.0001
203837_at	LOC729144	hypothetical protein LOC729144, mitogen-activated protein kinase kinase kinase 5	-1.6017	0
203838_s_at	TNK2	tyrosine kinase; non-receptor; 2	-0.224	0.0191
203851_at	IGFBP6	insulin-like growth factor binding protein 6	-4.1769	0
203860_at	PCCA	propionyl Coenzyme A carboxylase; alpha polypeptide	-1.1785	0.0005
203866_at	NLE1	notchless homolog 1 (Drosophila)	-0.2255	0
203867_s_at	NLE1	notchless homolog 1 (Drosophila)	-0.3353	0.0312
203869_at	USP46	ubiquitin specific peptidase 46	-0.9408	0.0027

203870_at	USP46	ubiquitin specific peptidase 46	-0.7921	0.0082
203874_s_at	SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	-0.8923	0.0099
203875_at	SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	-0.6604	0.0447
203877_at			-0.1577	0.0052
203881_s_at	DMD	dystrophin (muscular dystrophy; Duchenne and Becker types)	-1.8686	0.0023
203887_s_at	THBD	thrombomodulin	-2.0684	0.0016
203888_at	THBD	thrombomodulin	-1.3654	0.0016
203897_at	LYRM1	LYR motif containing 1	-0.6466	0.0137
203903_s_at	HEPH	hephaestin	-2.8606	0.0008
203911_at	RAP1GAP	RAP1 GTPase activating protein	-1.2869	0.0054
203916_at	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	-0.4662	0.0133
203920_at	NR1H3	nuclear receptor subfamily 1; group H; member 3	-1.5613	0.0004
203922_s_at	CYBB	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	-0.5863	0.0307
203923_s_at	CYBB	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	-2.5812	0
203924_at	GSTA1	glutathione S-transferase A1	-3.5296	0.004
203925_at	GCLM	glutamate-cysteine ligase; modifier subunit	-1.3266	0.0014
203932_at	HLA-DMB	major histocompatibility complex; class II; DM beta	-1.5143	0.0027
203934_at	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	-0.9921	0.0158
203941_at	INTS9	integrator complex subunit 9	-0.9131	0.0084
203946_s_at	ARG2	arginase; type II	-1.7414	0.0219
203949_at	MPO	myeloperoxidase	-0.1419	0.0008
203951_at	CNN1	calponin 1; basic; smooth muscle	-1.1657	0
203960_s_at	C1orf41	chromosome 1 open reading frame 41	-0.8087	0.0011
203970_s_at	PEX3	peroxisomal biogenesis factor 3	-0.7931	0.004
203972_s_at	PEX3	peroxisomal biogenesis factor 3	-0.8221	0.0254
203973_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP); delta	-1.258	0.0001
203980_at	FABP4	fatty acid binding protein 4; adipocyte	-2.5515	0.0092
203982_s_at	ABCD4	ATP-binding cassette; sub-family D (ALD); member 4	-0.1762	0.0059
203984_s_at	CASP9	caspase 9; apoptosis-related cysteine peptidase	-3.8023	0
203996_s_at	C21orf2	chromosome 21 open reading frame 2	-0.2032	0.0324
203999_at	SYT1	synaptotagmin I	-1.1236	0.0091
204002_s_at	ICA1	islet cell autoantigen 1; 69kDa	-0.2565	0.0002
204004_at	PAWR	PRKC; apoptosis; WT1; regulator	-1.7464	0.0047
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-1.4799	0.001

204018_x_at	HBA1	hemoglobin; alpha 1, hemoglobin; alpha 2	-1.3636	0.0245
204025_s_at	PDCD2	programmed cell death 2	-0.7403	0.0034
204034_at	ETHE1	ethylmalonic encephalopathy 1	-1.1793	0.0038
204036_at	EDG2	endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 2	-2.601	0.0006
204037_at	EDG2	endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 2	-1.0254	0.0018
204038_s_at	EDG2	endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 2	-0.6934	0.0111
204040_at	RNF144A	ring finger protein 144A	-0.8284	0.0148
204041_at	MAOB	monoamine oxidase B	-1.7016	0.0311
204043_at	TCN2	transcobalamin II; macrocytic anemia	-0.9281	0.0019
204046_at	PLCB2	phospholipase C; beta 2	-0.2465	0.033
204048_s_at	PHACTR2	phosphatase and actin regulator 2	-0.9457	0.0289
204049_s_at	PHACTR2	phosphatase and actin regulator 2	-1.0113	0.0218
204057_at	IRF8	interferon regulatory factor 8	-1.6558	0.0001
204067_at	SUOX	sulfite oxidase	-1.2707	0.0007
204070_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	-1.5573	0.0032
204071_s_at	TOPORS	topoisomerase I binding; arginine/serine-rich	-0.4789	0.0252
204079_at	TPST2	tyrosylprotein sulfotransferase 2	-0.8932	0.0359
204082_at	PBX3	pre-B-cell leukemia homeobox 3	-1.4359	0.0008
204083_s_at	TPM2	tropomyosin 2 (beta)	-1.4336	0.0095
204085_s_at	CLN5	ceroid-lipofuscinosis; neuronal 5	-0.9373	0.0385
204093_at	CCNH	cyclin H	-0.6469	0.0087
204105_s_at	NRCAM	neuronal cell adhesion molecule	-2.8504	0.0025
204106_at	TESK1	testis-specific kinase 1	-0.9484	0.0079
204111_at	HNMT	histamine N-methyltransferase	-0.2576	0.0016
204112_s_at	HNMT	histamine N-methyltransferase	-2.3823	0.0005
204121_at	GADD45G	growth arrest and DNA-damage-inducible; gamma	-0.9315	0.0119
204122_at	TYROBP	TYRO protein tyrosine kinase binding protein	-1.8785	0.0014
204135_at	FILIP1L	filamin A interacting protein 1-like	-2.2307	0.001
204142_at	ENOSF1	enolase superfamily member 1	-0.8866	0.0001
204143_s_at	ENOSF1	enolase superfamily member 1	-1.0162	0.0003
204150_at	STAB1	stabilin 1	-3.2391	0
204153_s_at	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-0.9246	0
204155_s_at	KIAA0999	KIAA0999 protein	-0.3887	0.0187
204157_s_at	KIAA0999	KIAA0999 protein	-0.9107	0.0069
204158_s_at	TCIRG1	T-cell; immune regulator 1; ATPase; H+ transporting; lysosomal V0 subunit A3	-2.112	0.0075

204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	-1.4276	0.0312
204163_at	EMILIN1	elastin microfibril interfacer 1	-1.1464	0
204167_at	BTD	biotinidase	-0.6495	0.0003
204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	-2.8845	0.0002
204183_s_at	ADRBK2	adrenergic; beta; receptor kinase 2	-0.3007	0.0265
204187_at	GMPR	guanosine monophosphate reductase	-1.2179	0.0012
204193_at	CHKB	carnitine palmitoyltransferase 1B (muscle), choline kinase beta	-1.3201	0.0002
204205_at	APOBEC3G	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 3G	-1.9937	0.0007
204213_at	PIGR	polymeric immunoglobulin receptor	-0.2215	0.011
204218_at	C11orf51	chromosome 11 open reading frame 51	-1.1237	0
204220_at	GMFG	glia maturation factor; gamma	-0.9372	0.0133
204223_at	PRELP	proline/arginine-rich end leucine-rich repeat protein	-2.8009	0
204225_at	HDAC4	histone deacetylase 4	-0.8867	0.0482
204231_s_at	FAAH	fatty acid amide hydrolase	-0.5642	0.0005
204232_at	FCER1G	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	-2.2664	0.0005
204238_s_at	C6orf108	chromosome 6 open reading frame 108	-1.2285	0.0005
204239_s_at	NNAT	neuronatin	-0.2944	0.0006
204258_at	CHD1	chromodomain helicase DNA binding protein 1	-1.2069	0
204264_at	CPT2	carnitine palmitoyltransferase II	-0.6189	0.007
204265_s_at	GPSM3	G-protein signaling modulator 3 (AGS3-like; C. elegans)	-0.8837	0.0192
204271_s_at	EDNRB	endothelin receptor type B	-1.6084	0.0155
204273_at	EDNRB	endothelin receptor type B	-2.229	0.0011
204288_s_at	SORBS2	sorbin and SH3 domain containing 2	-2.2884	0.0014
204290_s_at	ALDH6A1	aldehyde dehydrogenase 6 family; member A1	-0.8611	0.0391
204294_at	AMT	aminomethyltransferase	-3.011	0
204295_at	SURF1	surfeit 1	-0.6345	0.0041
204297_at	PIK3C3	phosphoinositide-3-kinase; class 3	-0.3634	0.0307
204301_at	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	-1.3829	0.0255
204305_at	MIPEP	mitochondrial intermediate peptidase	-0.5344	0.0355
204307_at	KIAA0329	KIAA0329	-0.3953	0.0017
204310_s_at	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	-0.8365	0.0006
204319_s_at	RGS10	regulator of G-protein signaling 10	-1.3383	0.0173
204326_x_at	MT1X	metallothionein 1X	-0.9381	0.0061
204332_s_at	AGA	aspartylglucosaminidase	-0.956	0.0169

204336_s_at	RGS19	regulator of G-protein signaling 19	-0.9884	0.0051
204363_at	F3	coagulation factor III (thromboplastin; tissue factor)	-1.2225	0.0133
204367_at	SP2	Sp2 transcription factor	-0.4027	0.0047
204368_at	SLCO2A1	solute carrier organic anion transporter family; member 2A1	-3.827	0
204385_at	KYNU	kynureninase (L-kynurenine hydrolase)	-0.3502	0.0024
204386_s_at	MRP63	mitochondrial ribosomal protein 63	-0.3015	0.036
204390_at			-0.1666	0.0051
204392_at	CAMK1	calcium/calmodulin-dependent protein kinase I	-2.9403	0
204396_s_at	GRK5	G protein-coupled receptor kinase 5	-1.9831	0.0021
204400_at	EFS	embryonal Fyn-associated substrate	-0.6833	0.0031
204404_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters); member 2	-1.4542	0.012
204409_s_at	EIF1AY	eukaryotic translation initiation factor 1A; Y-linked	-3.3156	0.0007
204410_at	EIF1AY	eukaryotic translation initiation factor 1A; Y-linked	-2.0633	0.0045
204412_s_at	NEFH	neurofilament; heavy polypeptide 200kDa	-1.1193	0.0127
204414_at	LARGE	like-glycosyltransferase	-0.1388	0.0187
204416_x_at	APOC1	apolipoprotein C-I	-2.8878	0.0003
204417_at	GALC	galactosylceramidase	-0.6848	0.037
204418_x_at	GSTM2	glutathione S-transferase M2 (muscle)	-1.4421	0.0338
204420_at	FOSL1	FOS-like antigen 1	-0.9312	0.0005
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter); member 5	-1.8619	0.0003
204431_at	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog; Drosophila)	-0.9856	0
204436_at	PLEKHQ1	pleckstrin homology domain containing; family Q member 1	-1.0175	0.002
204437_s_at	FOLR1	folate receptor 1 (adult)	-0.7376	0
204438_at	MRC1	mannose receptor; C type 1, mannose receptor; C type 1-like 1	-3.5147	0
204446_s_at	ALOX5	arachidonate 5-lipoxygenase	-2.9644	0.0001
204451_at	FZD1	frizzled homolog 1 (Drosophila)	-1.1295	0.0022
204457_s_at	GAS1	growth arrest-specific 1	-1.7931	0.0004
204462_s_at	SLC16A2	solute carrier family 16; member 2 (monocarboxylic acid transporter 8)	-2.3685	0.0002
204470_at	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity; alpha)	-0.3412	0.0177
204472_at	GEM	GTP binding protein overexpressed in skeletal muscle	-2.6998	0
204476_s_at	PC	pyruvate carboxylase	-2.0518	0
204480_s_at	C9orf16	chromosome 9 open reading frame 16	-0.6542	0.041
204485_s_at	TOM1L1	target of myb1 (chicken)-like 1	-0.9733	0.006

204487_s_at	KCNQ1	potassium voltage-gated channel; KQT-like subfamily; member 1	-4.1956	0
204501_at	NOV	nephroblastoma overexpressed gene	-3.3997	0.0014
204503_at	EVPL	envoplakin	-0.1872	0.0346
204509_at	CA12	carbonic anhydrase XII	-0.1682	0.0132
204516_at	ATXN7	ataxin 7	-0.6452	0.0012
204522_at	DOM3Z	dom-3 homolog Z (C. elegans)	-1.3064	0.0001
204534_at	VTN	vitronectin	-1.9859	0.0045
204564_at	PCGF3	polycomb group ring finger 3	-0.4853	0.0005
204567_s_at	ABCG1	ATP-binding cassette; sub-family G (WHITE); member 1	-2.4868	0.0005
204569_at	ICK	intestinal cell (MAK-like) kinase	-0.8081	0.0482
204570_at	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	-1.4595	0.0121
204575_s_at	LOC732415	matrix metallopeptidase 19, similar to Matrix metalloproteinase-19 precursor (MMP-19) (Matrix metalloproteinase RASI) (MMP-18)	-1.3103	0.0085
204584_at	L1CAM	L1 cell adhesion molecule	-0.7627	0.0107
204588_s_at	SLC7A7	solute carrier family 7 (cationic amino acid transporter; y+ system); member 7	-1.1099	0.009
204610_s_at	CCDC85B	coiled-coil domain containing 85B	-1.1059	0.0007
204613_at	PLCG2	phospholipase C; gamma 2 (phosphatidylinositol-specific)	-1.4598	0.0105
204616_at	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	-0.8235	0.0083
204619_s_at	VCAN	versican	-2.5271	0.0034
204620_s_at	VCAN	versican	-2.629	0.0078
204621_s_at	NR4A2	nuclear receptor subfamily 4; group A; member 2	-5.4471	0
204622_x_at	NR4A2	nuclear receptor subfamily 4; group A; member 2	-5.7822	0
204623_at	TFF3	trefoil factor 3 (intestinal)	-0.6157	0.0003
204629_at	PARVB	parvin; beta	-1.2706	0.0007
204636_at	COL17A1	collagen; type XVII; alpha 1	-0.1479	0.0059
204637_at	CGA	glycoprotein hormones; alpha polypeptide	-0.2952	0
204642_at	EDG1	endothelial differentiation; sphingolipid G-protein-coupled receptor; 1	-0.5606	0.009
204646_at	DPYD	dihydropyrimidine dehydrogenase	-2.29	0.0007
204664_at	ALPP	alkaline phosphatase; placental (Regan isozyme)	-0.1338	0.0345
204670_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1	-1.9601	0.0027
204686_at	IRS1	insulin receptor substrate 1	-1.6039	0.0004
204687_at	DKFZP564O0823	DKFZP564O0823 protein	-1.8692	0.0001
204688_at	SGCE	sarcoglycan; epsilon	-1.3708	0.0237
204690_at	STX8	syntaxin 8	-0.7974	0

204693_at	CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	-0.9124	0.0155
204697_s_at	CHGA	chromogranin A (parathyroid secretory protein 1)	-2.3983	0.0004
204708_at	MAPK4	mitogen-activated protein kinase 4	-0.1783	0.0011
204718_at	EPHB6	EPH receptor B6	-0.5494	0
204719_at	ABCA8	ATP-binding cassette; sub-family A (ABC1); member 8	-2.6817	0.0033
204735_at	PDE4A	phosphodiesterase 4A; cAMP-specific (phosphodiesterase E2 dunce homolog; Drosophila)	-1.3054	0.0001
204739_at	CENPC1	centromere protein C 1	-0.3812	0.0213
204743_at	TAGLN3	transgelin 3	-0.5623	0.0046
204745_x_at	MT1G	metallothionein 1G	-1.5087	0
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-2.5823	0.0001
204751_x_at	DSC2	desmocollin 2	-0.2177	0.0126
204753_s_at	HLF	hepatic leukemia factor	-1.9421	0.0343
204754_at	HLF	hepatic leukemia factor	-1.8149	0.0081
204759_at	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	-1.1448	0
204765_at	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	-0.4906	0.0023
204781_s_at	FAS	Fas (TNF receptor superfamily; member 6)	-1.391	0.0068
204787_at	VSIG4	V-set and immunoglobulin domain containing 4	-3.329	0
204788_s_at	PPOX	protoporphyrinogen oxidase	-0.6651	0.0039
204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1	-1.6377	0.0021
204800_s_at	DHRS12	dehydrogenase/reductase (SDR family) member 12	-0.6478	0.0094
204813_at	MAPK10	mitogen-activated protein kinase 10	-1.1693	0.0308
204821_at	BTN3A3	butyrophilin; subfamily 3; member A3	-0.8702	0.0154
204823_at	NAV3	neuron navigator 3	-3.2796	0
204829_s_at	FOLR2	folate receptor 2 (fetal)	-2.2184	0
204834_at	FGL2	fibrinogen-like 2	-1.5482	0.0008
204850_s_at	DCX	doublecortex; lissencephaly; X-linked (doublecortin)	-0.1338	0.0063
204851_s_at	DCX	doublecortex; lissencephaly; X-linked (doublecortin)	-0.1372	0.0097
204862_s_at	NME3	non-metastatic cells 3; protein expressed in	-0.6662	0.0487
204863_s_at	IL6ST	interleukin 6 signal transducer (gp130; oncostatin M receptor)	-0.8791	0.042
204866_at	PHF16	PHD finger protein 16	-1.2151	0.0032
204868_at	ICT1	immature colon carcinoma transcript 1	-0.6583	0.0153
204880_at	MGMT	O-6-methylguanine-DNA methyltransferase	-0.7912	0.0087
204882_at	ARHGAP25	Rho GTPase activating protein 25	-0.535	0.0012

204894_s_at	AOC3	amine oxidase; copper containing 3 (vascular adhesion protein 1)	-1.5973	0.0336
204896_s_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	-0.1494	0.0008
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	-3.8737	0
204904_at	GJA4	gap junction protein; alpha 4; 37kDa	-0.4331	0.0476
204906_at	RPS6KA2	ribosomal protein S6 kinase; 90kDa; polypeptide 2	-1.0104	0.0189
204908_s_at	BCL3	B-cell CLL/lymphoma 3	-0.6628	0.0254
204909_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	-0.4527	0.0002
204911_s_at	TRIM3	tripartite motif-containing 3	-0.1476	0.0364
204912_at	IL10RA	interleukin 10 receptor; alpha	-2.5362	0
204916_at	RAMP1	receptor (G protein-coupled) activity modifying protein 1	-0.4453	0
204923_at	CXorf9	chromosome X open reading frame 9	-1.2598	0.0008
204924_at	TLR2	toll-like receptor 2	-1.1383	0.0063
204925_at	CTNS	cystinosis; nephropathic	-0.8566	0.0056
204926_at	INHBA	inhibin; beta A	-0.1065	0.0267
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	-1.8153	0.0003
204931_at	TCF21	transcription factor 21	-1.9732	0
204932_at	TNFRSF11B	tumor necrosis factor receptor superfamily; member 11b (osteoprotegerin)	-0.6286	0.0086
204933_s_at	TNFRSF11B	tumor necrosis factor receptor superfamily; member 11b (osteoprotegerin)	-0.5884	0.0017
204938_s_at	PLN	phospholamban	-0.8896	0
204939_s_at	PLN	phospholamban	-2.6934	0
204940_at	PLN	phospholamban	-1.2297	0.0002
204944_at	PTPRG	protein tyrosine phosphatase; receptor type; G	-1.3503	0.0117
204952_at	LYPD3	LY6/PLAUR domain containing 3	-1.1756	0
204955_at	SRPX	sushi-repeat-containing protein; X-linked	-1.7784	0.0225
204956_at	MTAP	methylthioadenosine phosphorylase	-0.3808	0.0006
204959_at	MNDA	myeloid cell nuclear differentiation antigen	-2.3569	0.0007
204961_s_at	NCF1	neutrophil cytosolic factor 1; (chronic granulomatous disease; autosomal 1), neutrophil cytosolic factor 1B pseudogene, neutrophil cytosolic factor 1C pseudogene	-0.3678	0.0137
204963_at	SSPN	sarcospan (Kras oncogene-associated gene)	-1.3444	0.0019
204969_s_at	RDX	radixin	-1.1152	0.0382
204971_at	CSTA	cystatin A (stefin A)	-1.381	0.0343
204973_at	GJB1	gap junction protein; beta 1; 32kDa	-0.2077	0.0072
204979_s_at	SH3BGR	SH3 domain binding glutamic acid-rich protein	-1.2104	0.0077
204984_at	GPC4	glypican 4	-1.3579	0.0274

204985_s_at	TRAPPC6A	trafficking protein particle complex 6A	-0.6723	0.035
204990_s_at	ITGB4	integrin; beta 4	-0.2022	0.0181
204991_s_at	NF2	neurofibromin 2 (bilateral acoustic neuroma)	-0.1928	0.013
205000_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3; Y-linked	-3.7682	0.0017
205007_s_at	CIB2	calcium and integrin binding family member 2	-0.4289	0.0443
205008_s_at	CIB2	calcium and integrin binding family member 2	-1.1344	0.0059
205011_at	LOH11CR2A	loss of heterozygosity; 11; chromosomal region 2; gene A	-1.3268	0.0148
205012_s_at	HAGH	hydroxyacylglutathione hydrolase	-1.0367	0.0065
205013_s_at	ADORA2A	adenosine A2a receptor	-0.2682	0.0034
205014_at	FGFBP1	fibroblast growth factor binding protein 1	-0.1559	0.0032
205019_s_at	VIPR1	vasoactive intestinal peptide receptor 1	-0.7316	0
205021_s_at	FOXN3	forkhead box N3	-0.4195	0
205022_s_at	FOXN3	forkhead box N3	-0.6085	0.0237
205027_s_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8	-1.8687	0.0001
205029_s_at	FABP7	fatty acid binding protein 7; brain	-0.1143	0.0019
205032_at	ITGA2	integrin; alpha 2 (CD49B; alpha 2 subunit of VLA-2 receptor)	-0.916	0.0466
205052_at	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	-0.9316	0.0023
205054_at	NEB	nebulin	-1.2901	0
205077_s_at	PIGF	phosphatidylinositol glycan anchor biosynthesis; class F	-0.6435	0.0008
205078_at	PIGF	phosphatidylinositol glycan anchor biosynthesis; class F	-1.1551	0.0008
205080_at	RARB	retinoic acid receptor; beta	-0.7647	0.0288
205082_s_at	AOX1	aldehyde oxidase 1	-3.0199	0
205083_at	AOX1	aldehyde oxidase 1	-2.6958	0
205098_at	CCR1	chemokine (C-C motif) receptor 1	-1.7783	0.0025
205099_s_at	CCR1	chemokine (C-C motif) receptor 1	-0.7717	0.0366
205102_at	TMPRSS2	transmembrane protease; serine 2	-0.1922	0.0054
205116_at	LAMA2	laminin; alpha 2 (merosin; congenital muscular dystrophy)	-1.2127	0.0042
205119_s_at	FPR1	formyl peptide receptor 1	-1.456	0.0152
205133_s_at	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	-0.4872	0.0028
205136_s_at	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	-0.4411	0.0192
205137_x_at	USH1C	Usher syndrome 1C (autosomal recessive; severe)	-0.1336	0.0304
205147_x_at	NCF4	neutrophil cytosolic factor 4; 40kDa	-0.9094	0.0013
205154_at	LRRN2	leucine rich repeat neuronal 2	-0.3031	0.0399
205155_s_at	SPTBN2	spectrin; beta; non-erythrocytic 2	-0.3204	0.0029
205160_at	PEX11A	Peroxisomal biogenesis factor 11A	-0.8465	0.0027
205163_at	MYLPF	fast skeletal myosin light chain 2	-0.1738	0.0386

205168_at	DDR2	discoidin domain receptor family; member 2	-1.3594	0.0435
205177_at	TNNI1	troponin I type 1 (skeletal; slow)	-0.1628	0.0273
205184_at	GNG4	guanine nucleotide binding protein (G protein); gamma 4	-0.3406	0.0007
205193_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	-2.3728	0
205200_at	CLEC3B	C-type lectin domain family 3; member B	-3.1983	0
205203_at	PLD1	phospholipase D1; phosphatidylcholine-specific	-1.0989	0
205204_at	NMB	neuromedin B	-1.9946	0
205208_at	ALDH1L1	aldehyde dehydrogenase 1 family; member L1	-2.4187	0.0001
205225_at	ESR1	estrogen receptor 1	-1.6156	0
205229_s_at	COCH	coagulation factor C homolog; cochlin (Limulus polyphemus)	-2.1296	0
205231_s_at	EPM2A	epilepsy; progressive myoclonus type 2A; Lafora disease (laforin)	-0.579	0.0078
205234_at	SLC16A4	solute carrier family 16; member 4 (monocarboxylic acid transporter 5)	-1.3494	0
205241_at	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	-1.2203	0.0058
205245_at	PARD6A	par-6 partitioning defective 6 homolog alpha (C. elegans)	-0.3637	0.0029
205251_at	PER2	period homolog 2 (Drosophila)	-0.8409	0.0187
205269_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-1.9924	0.0001
205270_s_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-1.2902	0.0039
205275_at	GTPBP1	GTP binding protein 1	-0.1481	0.0125
205276_s_at	GTPBP1	GTP binding protein 1	-0.226	0.049
205281_s_at	PIGA	phosphatidylinositol glycan anchor biosynthesis; class A (paroxysmal nocturnal hemoglobinuria)	-1.0171	0.0019
205297_s_at	CD79B	CD79b molecule; immunoglobulin-associated beta	-0.2251	0.0345
205303_at	KCNJ8	potassium inwardly-rectifying channel; subfamily J; member 8	-2.0764	0
205304_s_at	KCNJ8	potassium inwardly-rectifying channel; subfamily J; member 8	-2.4313	0
205307_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-0.1936	0.003
205311_at	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-1.0696	0.0018
205312_at	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	-0.2188	0.0378
205314_x_at	SNTB2	syntrophin; beta 2 (dystrophin-associated protein A1; 59kDa; basic component 2)	-0.1488	0.0466
205320_at	APC2	adenomatosis polyposis coli 2	-0.174	0.0425
205322_s_at	MTF1	metal-regulatory transcription factor 1	-1.041	0
205323_s_at	MTF1	metal-regulatory transcription factor 1	-0.5811	0.0006

205325_at	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	-3.8157	0
205326_at	RAMP3	receptor (G protein-coupled) activity modifying protein 3	-1.5769	0.0006
205333_s_at	RCE1	RCE1 homolog; prenyl protein peptidase (S. cerevisiae)	-0.3076	0.0198
205334_at	S100A1	S100 calcium binding protein A1	-0.2178	0.0045
205353_s_at	PEBP1	phosphatidylethanolamine binding protein 1	-0.4896	0.0025
205356_at	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	-1.6472	0
205357_s_at	AGTR1	angiotensin II receptor; type 1	-1.7866	0.0416
205360_at			-0.177	0.0179
205364_at	ACOX2	acyl-Coenzyme A oxidase 2; branched chain	-1.269	0.0129
205382_s_at	CFD	complement factor D (adipsin)	-3.0787	0
205384_at	FXYD1	FXYD domain containing ion transport regulator 1 (phospholemman)	-0.8662	0
205388_at	TNNC2	troponin C type 2 (fast)	-0.4639	0.0003
205392_s_at	CCL14	chemokine (C-C motif) ligand 14, chemokine (C-C motif) ligand 15	-2.9977	0
205404_at	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	-1.6272	0
205407_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	-0.934	0.002
205409_at	FOSL2	FOS-like antigen 2	-1.6564	0
205412_at	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	-1.0147	0
205417_s_at	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	-0.4222	0.028
205418_at	FES	feline sarcoma oncogene	-0.6179	0
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	-1.614	0.0043
205420_at	PEX7	peroxisomal biogenesis factor 7	-0.908	0.0007
205421_at	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter); member 3	-1.4005	0.0191
205423_at	AP1B1	adaptor-related protein complex 1; beta 1 subunit	-0.8015	0.0008
205440_s_at	NPY1R	neuropeptide Y receptor Y1	-3.9671	0
205471_s_at	DACH1	dachshund homolog 1 (Drosophila)	-1.6501	0.0399
205475_at	SCRG1	scrapie responsive protein 1	-0.3343	0.0011
205478_at	PPP1R1A	protein phosphatase 1; regulatory (inhibitor) subunit 1A	-0.7264	0.0002
205487_s_at	VGLL1	vestigial like 1 (Drosophila)	-0.1609	0.0105
205490_x_at	GJB3	gap junction protein; beta 3; 31kDa	-0.126	0.0399
205491_s_at	GJB3	gap junction protein; beta 3; 31kDa	-0.1122	0.0375
205499_at	SRPX2	sushi-repeat-containing protein; X-linked 2	-1.7456	0
205506_at	VIL1	villin 1	-0.1518	0.0295
205508_at	SCN1B	sodium channel; voltage-gated; type I; beta	-0.8937	0.0004

205518_s_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	-1.2846	0.0042
205525_at	CALD1	caldesmon 1	-1.5326	0.0009
205530_at	ETFDH	electron-transferring-flavoprotein dehydrogenase	-1.109	0.0001
205543_at	HSPA4L	heat shock 70kDa protein 4-like	-0.6505	0.0454
205547_s_at	TAGLN	transgelin	-2.979	0
205550_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.9464	0
205554_s_at	DNASE1L3	deoxyribonuclease I-like 3	-4.547	0
205557_at	BPI	bactericidal/permeability-increasing protein	-0.15	0.0421
205563_at	KISS1	KiSS-1 metastasis-suppressor	-0.1988	0.0128
205564_at	PAGE4	P antigen family; member 4 (prostate associated)	-0.3751	0.0081
205571_at	LIPT1	lipoyltransferase 1	-0.8933	0.0021
205577_at	PYGM	phosphorylase; glycogen; muscle (McArdle syndrome; glycogen storage disease type V)	-0.4338	0
205582_s_at	GGTLA1	gamma-glutamyltransferase-like activity 1	-1.9103	0
205583_s_at	CXorf45	chromosome X open reading frame 45	-0.7799	0.0215
205589_at	MYL3	myosin; light chain 3; alkali; ventricular; skeletal; slow	-0.1698	0
205609_at	ANGPT1	angiopoietin 1	-1.2212	0.0055
205611_at	TNFSF12	tumor necrosis factor (ligand) superfamily; member 12	-0.7971	0
205633_s_at	ALAS1	aminolevulinate; delta-; synthase 1	-1.7221	0
205639_at	AOAH	acyloxyacyl hydrolase (neutrophil)	-0.5935	0.0337
205640_at	ALDH3B1	aldehyde dehydrogenase 3 family; member B1	-2.0828	0
205651_x_at	RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4	-3.0702	0.0001
205653_at	CTSG	cathepsin G	-0.2225	0.0069
205657_at	HAAO	3-hydroxyanthranilate 3;4-dioxygenase	-0.3193	0
205666_at	FMO1	flavin containing monooxygenase 1	-1.6826	0.0071
205672_at	XPA	xeroderma pigmentosum; complementation group A	-0.4409	0.0296
205682_x_at	APOM	apolipoprotein M	-0.6077	0
205692_s_at	CD38	CD38 molecule	-0.6837	0.0023
205695_at	SDS	serine dehydratase	-1.4327	0.0098
205696_s_at	GFRA1	GDNF family receptor alpha 1	-0.1332	0.0487
205703_at			-0.1018	0.0183
205711_x_at	ATP5C1	ATP synthase; H+ transporting; mitochondrial F1 complex; gamma polypeptide 1	-0.2485	0.0309
205737_at	KCNQ2	potassium voltage-gated channel; KQT-like subfamily; member 2	-0.2598	0.0118
205752_s_at	GSTM5	glutathione S-transferase M5	-0.972	0

205756_s_at	F8	coagulation factor VIII; procoagulant component (hemophilia A)	-0.7943	0.0488
205768_s_at	SLC27A2	solute carrier family 27 (fatty acid transporter); member 2	-1.5319	0.0364
205771_s_at	AKAP7	A kinase (PRKA) anchor protein 7	-1.0356	0.0088
205776_at	FMO5	flavin containing monooxygenase 5	-1.0224	0.0001
205778_at	KLK7	kallikrein-related peptidase 7	-0.1466	0.0251
205786_s_at	ITGAM	integrin; alpha M (complement component 3 receptor 3 subunit)	-2.1624	0
205790_at	SKAP1	src kinase associated phosphoprotein 1	-1.2461	0.0058
205814_at	GRM3	glutamate receptor; metabotropic 3	-0.4927	0.0009
205819_at	MARCO	macrophage receptor with collagenous structure	-1.3578	0
205824_at	HSPB2	heat shock 27kDa protein 2	-0.3599	0.0007
205832_at	CPA4	carboxypeptidase A4	-0.5135	0
205834_s_at	PART1	prostate androgen-regulated transcript 1	-0.1459	0.0388
205838_at	GYPA	glycophorin A (MNS blood group)	-0.1091	0.0371
205839_s_at	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	-0.3879	0.02
205843_x_at	CRAT	carnitine acetyltransferase	-0.314	0.0162
205846_at	PTPRB	protein tyrosine phosphatase; receptor type; B	-1.0232	0
205853_at	ZBTB7B	zinc finger and BTB domain containing 7B	-0.2867	0.0051
205856_at	SLC14A1	solute carrier family 14 (urea transporter); member 1 (Kidd blood group)	-0.4265	0
205857_at	SLC18A2	solute carrier family 18 (vesicular monoamine); member 2	-0.2904	0.0028
205858_at	NGFR	nerve growth factor receptor (TNFR superfamily; member 16)	-1.3077	0
205859_at	LY86	lymphocyte antigen 86	-1.7174	0.0017
205866_at	FCN3	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	-1.7644	0.0021
205877_s_at	ZC3H7B	zinc finger CCCH-type containing 7B	-0.5584	0
205879_x_at	RET	ret proto-oncogene	-0.3477	0.0018
205894_at	ARSE	arylsulfatase E (chondrodysplasia punctata 1)	-0.1304	0.0147
205896_at	SLC22A4	solute carrier family 22 (organic cation transporter); member 4	-0.589	0.0444
205907_s_at	OMD	osteomodulin	-2.2502	0
205908_s_at	OMD	osteomodulin	-1.6962	0
205911_at	PTHR1	parathyroid hormone receptor 1	-4.1114	0
205913_at	PLIN	perilipin	-1.4131	0
205914_s_at	GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1, similar to glutamate receptor; ionotropic; N-methyl D-aspartate 1	-0.2286	0.0322
205915_x_at	GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1	-0.1506	0.0391
205919_at	HBE1	hemoglobin; epsilon 1	-0.1556	0.042
205933_at	SETBP1	SET binding protein 1	-1.3979	0

205934_at	PLCL1	phospholipase C-like 1	-0.9178	0.0099
205936_s_at	HK3	hexokinase 3 (white cell)	-0.4503	0.0131
205944_s_at	CLTCL1	clathrin; heavy chain-like 1	-1.0914	0.0002
205954_at	RXRG	retinoid X receptor; gamma	-0.1797	0.0014
205969_at	AADAC	arylacetamide deacetylase (esterase)	-5.9773	0
205977_s_at	EPHA1	EPH receptor A1	-0.1717	0.0189
205982_x_at	SFTPC	surfactant; pulmonary-associated protein C	-0.1122	0.0166
205983_at	DPEP1	dipeptidase 1 (renal)	-0.2629	0.0003
205984_at	CRHBP	corticotropin releasing hormone binding protein	-1.7507	0
206001_at	NPY	neuropeptide Y	-0.5397	0
206002_at	GPR64	G protein-coupled receptor 64	-0.2327	0.0023
206020_at	SOCS6	suppressor of cytokine signaling 6	-0.4675	0.0064
206030_at	ASPA	aspartoacylase (Canavan disease)	-1.3446	0.0015
206032_at	DSC3	desmocollin 3	-0.1532	0.029
206034_at	SERPINB8	serpin peptidase inhibitor; clade B (ovalbumin); member 8	-0.5725	0.005
206035_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	-0.1609	0.0023
206036_s_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	-0.8967	0.0228
206045_s_at	NOL4	nucleolar protein 4	-0.2011	0.0002
206050_s_at	RNH1	ribonuclease/angiogenin inhibitor 1	-0.4247	0.0039
206051_at	ELAVL4	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 4 (Hu antigen D)	-0.5311	0.0001
206057_x_at	SPN	sialophorin (leukosialin; CD43)	-0.1664	0.0161
206065_s_at	DPYS	dihydropyrimidinase	-1.9451	0
206066_s_at	RAD51C	RAD51 homolog C (S. cerevisiae)	-0.5504	0.0026
206072_at	UCN	urocortin	-0.6313	0.0046
206080_at	PLCH2	phospholipase C; eta 2	-0.2445	0.0295
206085_s_at	CTH	cystathionase (cystathionine gamma-lyase)	-4.7201	0
206097_at	SLC22A18AS	solute carrier family 22 (organic cation transporter); member 18 antisense	-0.1333	0.0171
206101_at	ECM2	extracellular matrix protein 2; female organ and adipocyte specific	-1.9108	0.0123
206107_at	RGS11	regulator of G-protein signaling 11	-0.1681	0.0335
206111_at	RNASE2	ribonuclease; RNase A family; 2 (liver; eosinophil-derived neurotoxin)	-0.6696	0.0263
206115_at	EGR3	early growth response 3	-3.9831	0
206120_at	CD33	CD33 molecule	-0.7365	0.0002
206123_at	LLGL1	lethal giant larvae homolog 1 (Drosophila)	-0.3839	0.003
206124_s_at	LLGL1	lethal giant larvae homolog 1 (Drosophila)	-0.133	0.0432

206126_at	BLR1	Burkitt lymphoma receptor 1; GTP binding protein (chemokine (C-X-C motif) receptor 5)	-0.1814	0.0476
206136_at	FZD5	frizzled homolog 5 (Drosophila)	-0.3463	0.0001
206137_at	RIMS2	regulating synaptic membrane exocytosis 2	-1.3618	0.019
206154_at	RLBP1	retinaldehyde binding protein 1	-0.1208	0.0132
206158_s_at	CNBP	CCHC-type zinc finger; nucleic acid binding protein	-0.282	0.0058
206170_at	ADRB2	adrenergic; beta-2-; receptor; surface	-0.2561	0.0223
206171_at	ADORA3	adenosine A3 receptor	-2.0512	0
206179_s_at	TPPP	tubulin polymerization promoting protein	-0.1776	0.0482
206185_at	CRYBB1	crystallin; beta B1	-0.3027	0.0003
206187_at	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	-0.4281	0
206189_at	UNC5C	unc-5 homolog C (C. elegans)	-0.3234	0.0374
206190_at	GPR17	G protein-coupled receptor 17	-0.1069	0.021
206195_x_at	GH2	growth hormone 2	-0.1687	0.0228
206203_at	RCVRN	recoverin	-0.153	0.0172
206204_at	GRB14	growth factor receptor-bound protein 14	-2.044	0.0121
206210_s_at	CETP	cholesteryl ester transfer protein; plasma	-0.3694	0.0443
206211_at	SELE	selectin E (endothelial adhesion molecule 1)	-0.9899	0.0268
206212_at	CPA2	carboxypeptidase A2 (pancreatic)	-0.216	0.0032
206219_s_at	VAV1	vav 1 guanine nucleotide exchange factor	-0.3452	0.0008
206220_s_at	RASA3	RAS p21 protein activator 3	-0.1502	0.0491
206233_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 6	-2.0088	0
206242_at	TM4SF5	transmembrane 4 L six family member 5	-0.1363	0.0404
206243_at	TIMP4	TIMP metallopeptidase inhibitor 4	-2.6143	0
206244_at	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	-0.134	0.0291
206250_x_at	AVPR1A	arginine vasopressin receptor 1A	-0.1458	0.0104
206251_s_at	AVPR1A	arginine vasopressin receptor 1A	-0.6976	0
206252_s_at	AVPR1A	arginine vasopressin receptor 1A	-0.9471	0
206253_at	DLG2	discs; large homolog 2; chapsyn-110 (Drosophila)	-0.602	0.0462
206255_at	BLK	B lymphoid tyrosine kinase	-0.1209	0.0402
206256_at	CPN1	carboxypeptidase N; polypeptide 1	-0.1682	0.0267
206270_at	PRKCG	protein kinase C; gamma	-0.1446	0.0142
206283_s_at	TAL1	T-cell acute lymphocytic leukemia 1	-0.5807	0.0059
206289_at	HOXA4	homeobox A4	-0.4336	0.0133
206290_s_at	RGS7	regulator of G-protein signaling 7	-1.375	0.0261
206294_at	HSD3B2	hydroxy-delta-5-steroid dehydrogenase; 3 beta- and steroid delta-isomerase 2	-3.7826	0.0009

206295_at	IL18	interleukin 18 (interferon-gamma-inducing factor)	-0.7293	0.0103
206305_s_at	C8A	complement component 8; alpha polypeptide	-0.1904	0.0037
206309_at	LECT1	leukocyte cell derived chemotaxin 1	-0.1804	0.0044
206313_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	-0.3172	0.008
206315_at	CRLF1	cytokine receptor-like factor 1	-0.6529	0.0002
206323_x_at	OPHN1	oligophrenin 1	-0.2895	0.0074
206330_s_at	SHC3	SHC (Src homology 2 domain containing) transforming protein 3	-1.2636	0.0001
206339_at	CARTPT	CART prepropeptide	-0.9346	0.0003
206341_at	IL2RA	interleukin 2 receptor; alpha	-0.1805	0.0285
206344_at	PON1	paraoxonase 1	-0.3683	0.0002
206345_s_at	PON1	paraoxonase 1	-3.6453	0
206354_at	SLCO1B3	solute carrier organic anion transporter family; member 1B3	-0.1345	0.0239
206359_at	SOCS3	suppressor of cytokine signaling 3	-1.1123	0.002
206360_s_at	SOCS3	suppressor of cytokine signaling 3	-0.3534	0.0041
206362_x_at	MAP3K10	mitogen-activated protein kinase kinase kinase 10	-0.2027	0.0366
206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	-1.351	0.0123
206380_s_at	CFP	complement factor properdin	-0.8399	0
206395_at	DGKG	diacylglycerol kinase; gamma 90kDa	-0.5565	0.0118
206399_x_at	CACNA1A	calcium channel; voltage-dependent; P/Q type; alpha 1A subunit	-0.2594	0.0158
206407_s_at	CCL13	chemokine (C-C motif) ligand 13	-0.8617	0
206417_at	CNGA1	cyclic nucleotide gated channel alpha 1	-0.4012	0.0001
206421_s_at	SERPINB7	serpin peptidase inhibitor; clade B (ovalbumin); member 7	-0.1477	0.0037
206423_at	ANGPTL7	angiopoietin-like 7	-0.1953	0
206428_s_at	ZNF143	zinc finger protein 143	-0.1365	0.0034
206430_at	CDX1	caudal type homeobox 1	-0.3622	0.0001
206434_at	SPOCK3	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 3	-0.1408	0.033
206437_at	EDG6	endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 6	-0.2995	0.0199
206450_at	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	-1.1984	0.0004
206453_s_at	NDRG2	NDRG family member 2	-1.6297	0.0001
206458_s_at	WNT2B	wingless-type MMTV integration site family; member 2B	-0.1708	0.0041
206459_s_at	WNT2B	wingless-type MMTV integration site family; member 2B	-0.1205	0.0192
206461_x_at	MT1H	metallothionein 1 pseudogene 2, metallothionein 1H	-0.876	0.0006
206462_s_at	NTRK3	neurotrophic tyrosine kinase; receptor; type 3	-0.2395	0

206465_at	ACSBG1	acyl-CoA synthetase bubblegum family member 1	-1.609	0.0004
206466_at	ACSBG1	acyl-CoA synthetase bubblegum family member 1	-0.2004	0.0068
206469_x_at	AKR7A3	aldo-keto reductase family 7; member A3 (aflatoxin aldehyde reductase)	-1.6039	0
206475_x_at	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	-0.1498	0.0025
206480_at	LTC4S	leukotriene C4 synthase	-0.551	0
206489_s_at	DLGAP1	discs; large (Drosophila) homolog-associated protein 1	-0.6367	0
206490_at	DLGAP1	discs; large (Drosophila) homolog-associated protein 1	-0.8429	0
206492_at	FHIT	fragile histidine triad gene	-1.198	0.0141
206496_at	FMO3	flavin containing monooxygenase 3	-3.6079	0
206502_s_at	INSM1	insulinoma-associated 1	-0.6967	0.0044
206525_at	GABRR1	gamma-aminobutyric acid (GABA) receptor; rho 1	-0.1852	0
206538_at	MRAS	muscle RAS oncogene homolog	-1.0906	0
206540_at	GLB1L	galactosidase; beta 1-like	-0.4533	0.0015
206542_s_at	SMARCA2	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 2	-0.6431	0.0062
206549_at	INSL4	insulin-like 4 (placenta)	-0.1468	0.001
206552_s_at	TAC1	tachykinin; precursor 1 (substance K; substance P; neurokinin 1; neurokinin 2; neuromedin L; neurokinin alpha; neuropeptide K; neuropeptide gamma)	-2.9932	0
206554_x_at	SETMAR	SET domain and mariner transposase fusion gene	-0.674	0.0083
206569_at	IL24	interleukin 24	-0.1169	0.0104
206575_at	CDKL5	cyclin-dependent kinase-like 5	-0.155	0.0087
206577_at	VIP	vasoactive intestinal peptide	-0.1742	0.0056
206580_s_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	-1.9611	0.0002
206590_x_at	DRD2	dopamine receptor D2	-0.1415	0.0092
206595_at	CST6	cystatin E/M	-0.1247	0.0247
206598_at	INS	insulin	-0.1435	0.0153
206608_s_at	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	-0.1069	0.0415
206610_s_at	F11	coagulation factor XI (plasma thromboplastin antecedent)	-0.1722	0.0291
206612_at	CACNG1	calcium channel; voltage-dependent; gamma subunit 1	-0.3298	0.0003
206619_at	DKK4	dickkopf homolog 4 (Xenopus laevis)	-0.1104	0.0095
206624_at	USP9Y	ubiquitin specific peptidase 9; Y-linked (fat facets-like; Drosophila)	-1.3696	0.0311
206625_at	PRPH2	peripherin 2 (retinal degeneration; slow)	-0.2992	0.0056
206629_at	ADAMTSL2	ADAMTS-like 2	-1.1028	0
206634_at	SIX3	SIX homeobox 3	-0.1526	0.0336

206635_at	CHRNB2	cholinergic receptor; nicotinic; beta 2 (neuronal)	-0.2621	0.0091
206637_at	P2RY14	purinergic receptor P2Y; G-protein coupled; 14	-0.5074	0.0469
206638_at	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	-4.2302	0
206642_at	DSG1	desmoglein 1	-0.1199	0.0291
206648_at	ZNF571	zinc finger protein 571	-2.7621	0
206662_at	GLRX	glutaredoxin (thioltransferase)	-0.8022	0.0003
206674_at	FLT3	fms-related tyrosine kinase 3	-0.1535	0.0116
206677_at	KRT31	keratin 31	-0.2052	0.0039
206678_at	GABRA1	gamma-aminobutyric acid (GABA) A receptor; alpha 1	-0.1567	0.0076
206682_at	CLEC10A	C-type lectin domain family 10; member A	-0.5466	0.0269
206689_x_at	HTATIP	HIV-1 Tat interacting protein; 60kDa	-0.4321	0.0019
206690_at	ACCN1	amiloride-sensitive cation channel 1; neuronal (degenerin)	-0.3642	0
206692_at	KCNJ10	potassium inwardly-rectifying channel; subfamily J; member 10	-0.2204	0.0013
206699_x_at	NPAS1	neuronal PAS domain protein 1	-0.172	0.0411
206700_s_at	JARID1D	jumonji; AT rich interactive domain 1D	-3.643	0.001
206702_at	TEK	TEK tyrosine kinase; endothelial (venous malformations; multiple cutaneous and mucosal)	-3.0319	0
206705_at	TULP1	tubby like protein 1	-0.2078	0.0036
206706_at	NTF3	neurotrophin 3	-0.3009	0
206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-1.9514	0.0005
206714_at	ALOX15B	arachidonate 15-lipoxygenase; type B	-0.706	0.0002
206716_at	UMOD	uromodulin (uromucoid; Tamm-Horsfall glycoprotein)	-0.1066	0.0427
206726_at	PGDS	prostaglandin D2 synthase; hematopoietic	-0.8354	0.0058
206728_at	ECE2	endothelin converting enzyme 2	-0.1948	0.0095
206729_at	TNFRSF8	tumor necrosis factor receptor superfamily; member 8	-0.131	0.019
206737_at	WNT11	wingless-type MMTV integration site family; member 11	-1.0932	0.0038
206767_at	RBMS3	RNA binding motif; single stranded interacting protein	-0.8702	0.0085
206769_at	TMSB4Y	thymosin; beta 4; Y-linked	-0.359	0.0001
206771_at	UPK3A	uroplakin 3A	-0.163	0.0203
206782_s_at	DNAJC4	DnaJ (Hsp40) homolog; subfamily C; member 4	-0.7922	0.0014
206790_s_at	NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 1; 7kDa	-0.2237	0.0175
206793_at	PNMT	phenylethanolamine N-methyltransferase	-1.0508	0.0011
206795_at	F2RL2	coagulation factor II (thrombin) receptor-like 2	-0.136	0.0049
206796_at	WISP1	WNT1 inducible signaling pathway protein 1	-1.1122	0.0089
206800_at	MTHFR	5;10-methylenetetrahydrofolate reductase (NADPH)	-0.2953	0.0057

206802_at	PAX5	paired box 5	-0.1601	0.039
206803_at	PDYN	prodynorphin	-0.1101	0.0224
206804_at	CD3G	CD3g molecule; gamma (CD3-TCR complex)	-0.2542	0.0158
206815_at	SPAG8	sperm associated antigen 8	-0.1594	0.0291
206816_s_at	SPAG8	sperm associated antigen 8	-0.2124	0.0279
206818_s_at	CNNM2	cyclin M2	-0.6607	0.0186
206826_at	PMP2	peripheral myelin protein 2	-0.1694	0.0013
206831_s_at	ARSD	arylsulfatase D	-0.1733	0.0327
206833_s_at	ACYP2	acylphosphatase 2; muscle type	-0.8251	0.0066
206839_at	C22orf31	chromosome 22 open reading frame 31	-0.1782	0.0242
206844_at	FBP2	fructose-1;6-bisphosphatase 2	-0.1857	0.0023
206848_at	HOXA7	homeobox A7	-1.0978	0.0398
206851_at	RNASE3	ribonuclease; RNase A family; 3 (eosinophil cationic protein)	-0.1828	0.0092
206853_s_at	MAP3K7	mitogen-activated protein kinase kinase kinase 7	-0.4516	0.0212
206867_at	GCKR	glucokinase (hexokinase 4) regulator	-0.3491	0.0008
206868_at	STARD8	StAR-related lipid transfer (START) domain containing 8	-0.5518	0
206869_at	CHAD	chondroadherin	-2.0245	0
206878_at	DAO	D-amino-acid oxidase	-0.1191	0.0449
206880_at	P2RXL1	purinergic receptor P2X-like 1; orphan receptor	-0.2034	0.0074
206890_at	IL12RB1	interleukin 12 receptor; beta 1	-0.159	0.0056
206894_at	APOA4	apolipoprotein A-IV	-0.1967	0.0446
206897_at	PAGE1	P antigen family; member 1 (prostate associated)	-0.3067	0
206898_at	CDH19	cadherin 19; type 2	-1.6907	0
206908_s_at	CLDN11	claudin 11 (oligodendrocyte transmembrane protein)	-0.1518	0.0026
206910_x_at	CFHR2	complement factor H-related 2	-0.5571	0.0002
206931_at	ZNF141	zinc finger protein 141	-2.4523	0
206932_at	CH25H	cholesterol 25-hydroxylase	-1.438	0
206936_x_at			-0.2621	0.0207
206939_at	DCC	deleted in colorectal carcinoma	-0.1481	0.0069
206955_at	AQP7	aquaporin 7	-0.4166	0.0007
206963_s_at	NAT8	N-acetyltransferase 8, N-acetyltransferase 8B (gene/pseudogene)	-0.1617	0.0176
206973_at	PPFIA2	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 2	-0.1951	0.003
206982_at	CRYBA1	crystallin; beta A1	-0.1231	0.0367
206988_at	CCL25	chemokine (C-C motif) ligand 25	-0.1411	0.0351
206993_at	ATP5S	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit s (factor B)	-0.6062	0.0109

207006_s_at	CCDC106	coiled-coil domain containing 106	-0.6017	0.0069
207009_at	PHOX2B	paired-like homeobox 2b	-0.4378	0.0013
207024_at	CHRND	cholinergic receptor; nicotinic; delta	-0.2294	0.0046
207025_at	GJA12	gap junction protein; alpha 12; 47kDa	-0.2625	0.0045
207027_at	HGFAC	HGF activator	-0.1426	0.0197
207028_at	MYCNOS	v-myc myelocytomatosis viral related oncogene; neuroblastoma derived (avian) opposite strand	-0.1808	0.0084
207037_at	TNFRSF11A	tumor necrosis factor receptor superfamily; member 11a; NFKB activator	-0.1623	0.0306
207040_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	-0.5545	0.0068
207043_s_at	SLC6A9	solute carrier family 6 (neurotransmitter transporter; glycine); member 9	-1.2654	0.0013
207044_at	THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	-0.2574	0.0002
207048_at	SLC6A11	solute carrier family 6 (neurotransmitter transporter; GABA); member 11	-0.1598	0.0102
207055_at	GPR37L1	G protein-coupled receptor 37 like 1	-0.123	0.0165
207058_s_at	PARK2	Parkinson disease (autosomal recessive; juvenile) 2; parkin	-0.2785	0.0145
207059_at	PAX9	paired box 9	-0.1377	0.0297
207061_at	ERN1	endoplasmic reticulum to nucleus signaling 1	-0.2817	0.0008
207063_at	CYorf14	chromosome Y open reading frame 14	-1.3146	0
207070_at	RGR	retinal G protein coupled receptor	-0.2564	0.0082
207071_s_at	ACO1	aconitase 1; soluble	-1.3982	0
207074_s_at	SLC18A1	solute carrier family 18 (vesicular monoamine); member 1	-0.5871	0.0031
207075_at	NLRP3	NLR family; pyrin domain containing 3	-0.2591	0.02
207082_at	CSF1	colony stimulating factor 1 (macrophage)	-0.4771	0.0001
207092_at	LEP	leptin (obesity homolog; mouse)	-0.2396	0.0017
207095_at	SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	-0.1378	0.0421
207113_s_at	TNF	tumor necrosis factor (TNF superfamily; member 2)	-0.1666	0.004
207114_at	LY6G6C	lymphocyte antigen 6 complex; locus G6C	-0.1447	0.0231
207119_at	PRKG1	protein kinase; cGMP-dependent; type I	-0.4986	0.0009
207122_x_at	SULT1A2	sulfotransferase family; cytosolic; 1A; phenol-preferring; member 2	-0.6673	0.0288
207131_x_at	GGT1	gamma-glutamyltransferase 1	-0.2021	0.0378
207138_at	PHF2	PHD finger protein 2	-0.1263	0.0364
207139_at	ATP4A	ATPase; H+/K+ exchanging; alpha polypeptide	-1.9626	0.0093

207152_at	NTRK2	neurotrophic tyrosine kinase; receptor; type 2	-0.1727	0.0079
207175_at	ADIPOQ	adiponectin; C1Q and collagen domain containing	-2.5519	0
207191_s_at	ISLR	immunoglobulin superfamily containing leucine-rich repeat	-1.742	0
207195_at	CNTN6	contactin 6	-1.2302	0.0101
207205_at	CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4	-0.1646	0.0181
207212_at	SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger); member 3	-0.1204	0.0034
207220_at	ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	-0.5548	0.0004
207224_s_at	SIGLEC7	sialic acid binding Ig-like lectin 7	-0.6994	0.0128
207225_at	AANAT	arylalkylamine N-acetyltransferase	-0.1223	0.0002
207226_at	HIST1H2BN	histone cluster 1; H2bn	-0.1862	0.0071
207230_at	CDON	Cdon homolog (mouse)	-0.2301	0.0001
207233_s_at	MITF	microphthalmia-associated transcription factor	-0.94	0.034
207237_at	KCNA3	potassium voltage-gated channel; shaker-related subfamily; member 3	-0.1162	0.0089
207252_at	INE1	inactivation escape 1	-0.1868	0.0096
207259_at	C17orf73	chromosome 17 open reading frame 73	-0.1102	0.0237
207260_at	FEV	FEV (ETS oncogene family)	-0.2131	0.0228
207277_at	CD209	CD209 molecule	-0.6786	0.0399
207302_at	SGCG	sarcoglycan; gamma (35kDa dystrophin-associated glycoprotein)	-0.2813	0.0003
207309_at	NOS1	nitric oxide synthase 1 (neuronal)	-0.2188	0.0213
207313_x_at	KIR3DL2	killer cell immunoglobulin-like receptor; three domains; long cytoplasmic tail; 2	-0.1901	0.0005
207330_at	PZP	pregnancy-zone protein	-0.1326	0.0463
207349_s_at	UCP3	uncoupling protein 3 (mitochondrial; proton carrier)	-0.1906	0.0071
207355_at	SLC1A7	solute carrier family 1 (glutamate transporter); member 7	-0.1834	0.0206
207356_at	DEFB4	defensin; beta 4, defensin; beta 4; pseudogene	-0.1336	0.046
207358_x_at	MACF1	microtubule-actin crosslinking factor 1	-0.5707	0.0101
207363_at	RS1	retinoschisis (X-linked; juvenile) 1	-0.1191	0.0333
207364_at	TEX28	testis expressed 28, testis expressed 28 pseudogene 1, testis expressed 28 pseudogene 2	-0.1732	0.0079
207368_at	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D	-0.1344	0.0071
207376_at	VENTX	VENT homeobox homolog (Xenopus laevis)	-0.1533	0.0233
207377_at	PPP1R2P9	protein phosphatase 1; regulatory (inhibitor) subunit 2 pseudogene 9	-0.1738	0.0071
207390_s_at	SMTN	smoothelin	-1.283	0
207399_at	BFSP2	beaded filament structural protein 2; phakinin	-0.1964	0.0055
207400_at	NPY5R	neuropeptide Y receptor Y5	-0.8692	0

207403_at	IRS4	insulin receptor substrate 4	-0.1172	0.0479
207422_at	ADAM20	ADAM metallopeptidase domain 20	-0.1203	0.0362
207423_s_at	ADAM20	ADAM metallopeptidase domain 20	-0.1657	0.02
207428_x_at	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins), cell division cycle 2-like 2 (PITSLRE proteins)	-0.4187	0.0103
207433_at	IL10	interleukin 10	-0.4669	0.0002
207441_at	SMR3B	submaxillary gland androgen regulated protein 3 homolog B (mouse)	-0.5196	0
207448_at	POFUT2	protein O-fucosyltransferase 2	-0.1836	0.001
207459_x_at	GYPB	glycophorin B (MNS blood group)	-0.1296	0.0022
207462_at	GLRA2	glycine receptor; alpha 2	-0.1409	0.0264
207468_s_at	SFRP5	secreted frizzled-related protein 5	-0.2805	0.0003
207473_at	MLN	motilin	-0.1691	0.0176
207480_s_at	MEIS2	Meis homeobox 2	-1.2268	0.0056
207490_at	TUBA4B	tubulin; alpha 4b (pseudogene)	-0.1499	0.0467
207494_s_at	ZNF76	zinc finger protein 76 (expressed in testis)	-0.3995	0.0041
207501_s_at	FGF12	fibroblast growth factor 12	-2.8042	0
207502_at	GUCA2B	guanylate cyclase activator 2B (uroguanylin)	-0.1225	0.0434
207505_at	PRKG2	protein kinase; cGMP-dependent; type II	-0.1755	0.0088
207511_s_at	C2orf24	chromosome 2 open reading frame 24	-0.7779	0.0012
207517_at	LAMC2	laminin; gamma 2	-0.1738	0.0026
207519_at	SLC6A4	solute carrier family 6 (neurotransmitter transporter; serotonin); member 4	-0.1486	0.0349
207524_at	ST7	suppression of tumorigenicity 7	-0.9006	0.0009
207526_s_at	IL1RL1	interleukin 1 receptor-like 1	-3.4915	0
207527_at	KCNJ9	potassium inwardly-rectifying channel; subfamily J; member 9	-0.1501	0.026
207537_at	PFKFB1	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 1	-0.1519	0.0178
207538_at	IL4	interleukin 4	-0.1472	0.0059
207540_s_at	SYK	spleen tyrosine kinase	-0.6443	0.0065
207550_at	MPL	myeloproliferative leukemia virus oncogene	-0.2235	0.0001
207571_x_at	C1orf38	chromosome 1 open reading frame 38	-1.6351	0.0029
207573_x_at	ATP5L	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit G	-0.5202	0.001
207574_s_at	GADD45B	growth arrest and DNA-damage-inducible; beta	-0.8156	0.0369
207576_x_at	OXT	oxytocin; prepro- (neurophysin I)	-0.3655	0
207578_s_at	HTR4	5-hydroxytryptamine (serotonin) receptor 4	-0.2583	0.027
207585_s_at	RPL36AL	ribosomal protein L36a-like	-0.4331	0.004
207587_at	CRYGA	crystallin; gamma A	-0.133	0.0295

207609_s_at	CYP1A2	cytochrome P450; family 1; subfamily A; polypeptide 2	-0.1879	0.0026
207613_s_at	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	-0.1469	0.0081
207618_s_at	BCS1L	BCS1-like (yeast)	-0.6322	0.0211
207621_s_at	PEMT	phosphatidylethanolamine N-methyltransferase	-0.6372	0.0017
207630_s_at	CREM	cAMP responsive element modulator	-2.8361	0
207632_at	MUSK	muscle; skeletal; receptor tyrosine kinase	-0.1306	0.0013
207635_s_at	KCNH1	potassium voltage-gated channel; subfamily H (eag-related); member 1	-0.1581	0.0232
207640_x_at	NTN2L	netrin 2-like (chicken)	-0.1715	0.0186
207643_s_at	TNFRSF1A	tumor necrosis factor receptor superfamily; member 1A	-0.6191	0.0094
207648_at	DRP2	dystrophin related protein 2	-0.2207	0.0073
207649_at	KRT37	keratin 37	-0.1068	0.0154
207652_s_at	CMKLR1	chemokine-like receptor 1	-0.254	0.0047
207656_s_at	ACOX1	acyl-Coenzyme A oxidase 1; palmitoyl	-0.1372	0.0071
207667_s_at	MAP2K3	mitogen-activated protein kinase kinase 3	-0.462	0.0055
207670_at	KRT85	keratin 85	-0.1484	0.0033
207672_at			-0.1686	0.0055
207677_s_at	NCF4	neutrophil cytosolic factor 4; 40kDa	-1.0559	0.0023
207679_at	PAX3	paired box 3	-0.1074	0.0259
207688_s_at	INHBC	inhibin; beta C	-0.7662	0.0075
207689_at	TBX10	T-box 10	-0.1934	0.0015
207695_s_at	IGSF1	immunoglobulin superfamily; member 1	-0.2535	0.0369
207698_at	C6orf123	chromosome 6 open reading frame 123	-0.1085	0.0358
207703_at	NLGN4Y	neuroligin 4; Y-linked	-0.5368	0.0216
207752_x_at	PRB1	proline-rich protein BstNI subfamily 1, proline-rich protein BstNI subfamily 2	-0.371	0.0059
207762_at	LPAL2	lipoprotein; Lp(a)-like 2	-0.1171	0.0329
207763_at	S100A5	S100 calcium binding protein A5	-0.1393	0.0125
207778_at	REGL	regenerating islet-derived-like; pancreatic stone protein-like; pancreatic thread protein-like (rat)	-0.1468	0.0339
207814_at	DEFA6	defensin; alpha 6; Paneth cell-specific	-0.1464	0.0026
207820_at	ADH1A	alcohol dehydrogenase 1A (class I); alpha polypeptide	-0.2645	0.023
207834_at	FBLN1	fibulin 1	-0.1012	0.0013
207835_at	FBLN1	fibulin 1	-0.1514	0.0282
207837_at	RBPMS	RNA binding protein with multiple splicing	-0.2013	0.0424
207842_s_at	CASC3	cancer susceptibility candidate 3	-0.5214	0.0036
207843_x_at	CYB5A	cytochrome b5 type A (microsomal)	-2.3808	0

207844_at	IL13	interleukin 13	-0.1941	0.0207
207857_at	LILRA2	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 2	-0.8308	0
207859_s_at	CHRNB3	cholinergic receptor; nicotinic; beta 3	-0.1139	0.0307
207864_at	SCN7A	sodium channel; voltage-gated; type VII; alpha	-0.4099	0
207866_at	BMP8A	bone morphogenetic protein 8a	-0.147	0.0051
207868_at	CHRNA2	cholinergic receptor; nicotinic; alpha 2 (neuronal)	-0.1487	0.0275
207878_at	KRT76	keratin 76	-0.1161	0.0313
207888_at			-0.1111	0.0411
207897_at	CRHR2	corticotropin releasing hormone receptor 2	-0.1563	0.0039
207900_at	CCL17	chemokine (C-C motif) ligand 17	-0.1276	0.0428
207914_x_at	EVX1	even-skipped homeobox 1	-0.4566	0.0025
207921_x_at	PAX8	paired box 8	-0.1846	0.0153
207923_x_at	PAX8	paired box 8	-0.1877	0.0231
207924_x_at	PAX8	paired box 8	-0.1444	0.0429
207933_at	ZP2	zona pellucida glycoprotein 2 (sperm receptor)	-0.1169	0.0182
207935_s_at	KRT13	keratin 13	-0.1733	0.0022
207944_at	LOC4951	parvalbumin	-0.1108	0.0304
207946_at			-0.1226	0.0474
207954_at	GATA2	GATA binding protein 2	-0.1039	0.0282
207960_at			-0.1307	0.0318
207961_x_at	MYH11	myosin; heavy chain 11; smooth muscle	-0.9661	0.0184
207962_at	CAPN11	calpain 11	-0.1249	0.0184
207977_s_at	DPT	dermatopontin	-1.0134	0
207978_s_at	NR4A3	nuclear receptor subfamily 4; group A; member 3	-3.1947	0
207992_s_at	AMPD3	adenosine monophosphate deaminase (isoform E)	-1.8517	0.012
207994_s_at	OPRM1	opioid receptor; mu 1	-0.1348	0.029
207996_s_at	C18orf1	chromosome 18 open reading frame 1	-1.6103	0.0055
208007_at			-0.1578	0.0297
208017_s_at	MCF2	MCF.2 cell line derived transforming sequence	-2.9426	0.0007
208018_s_at	HCK	hemopoietic cell kinase	-1.8953	0.0002
208041_at	GRK1	G protein-coupled receptor kinase 1	-0.1588	0.0171
208052_x_at	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	-0.2148	0.0124
208060_at	PAX7	paired box 7	-0.1765	0.0022
208063_s_at	CAPN9	calpain 9	-0.1913	0.0111
208066_s_at	GTF2B	general transcription factor IIB	-0.8497	0.0011

208069_x_at	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen), chorionic somatomammotropin hormone 2, chorionic somatomammotropin hormone-like 1, growth hormone 1, growth hormone 2	-0.1433	0.0021
208078_s_at	SNF1LK	SNF1-like kinase	-2.0479	0.0006
208084_at	ITGB6	integrin; beta 6	-0.155	0.0017
208085_s_at	ARHGAP6	Rho GTPase activating protein 6	-0.1853	0.0021
208090_s_at	AIRE	autoimmune regulator	-0.1569	0.0325
208092_s_at	FAM49A	family with sequence similarity 49; member A	-0.9454	0.01
208093_s_at	NDEL1	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	-1.4724	0
208116_s_at	MAN1A1	mannosidase; alpha; class 1A; member 1	-1.9702	0.003
208123_at	KCNB2	potassium voltage-gated channel; Shab-related subfamily; member 2	-0.126	0.041
208128_x_at	KIF25	kinesin family member 25	-0.1197	0.0027
208130_s_at	TBXAS1	thromboxane A synthase 1 (platelet; cytochrome P450; family 5; subfamily A)	-0.9699	0
208131_s_at	PTGIS	prostaglandin I2 (prostacyclin) synthase	-1.5382	0.0048
208133_at	RFC1	replication factor C (activator 1) 1; 145kDa	-0.1388	0.0092
208136_s_at	MGC3771	hypothetical protein MGC3771	-0.1029	0.0465
208138_at	GAST	gastrin	-0.1743	0.0016
208158_s_at	OSBPL1A	oxysterol binding protein-like 1A	-0.6045	0.0263
208160_at	FLJ10232	hypothetical protein FLJ10232	-0.1298	0.0079
208161_s_at	ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	-2.6836	0.0005
208169_s_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-0.1609	0.0047
208173_at	IFNB1	interferon; beta 1; fibroblast	-0.1716	0.013
208183_at	TACR3	tachykinin receptor 3	-0.1436	0.0244
208188_at	KRT9	keratin 9 (epidermolytic palmoplantar keratoderma)	-0.102	0.0458
208189_s_at	MYO7A	myosin VIIA	-2.3613	0
208201_at	DUX3	double homeobox; 3, double homeobox; 4, similar to double homeobox 4c, similar to double homeobox; 4	-0.2121	0.0001
208204_s_at	CAV3	caveolin 3	-0.1405	0.0164
208206_s_at	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-0.791	0
208210_at	MAS1	MAS1 oncogene	-0.1253	0.0369
208215_x_at	DRD4	dopamine receptor D4	-0.1081	0.0458
208217_at	GABRR2	gamma-aminobutyric acid (GABA) receptor; rho 2	-0.187	0.032

208228_s_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-2.1561	0.0041
208234_x_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-0.2345	0.0102
208242_at	RAX	retina and anterior neural fold homeobox	-0.1737	0.0275
208250_s_at	DMBT1	deleted in malignant brain tumors 1	-0.1894	0.003
208251_at	KCNC4	potassium voltage-gated channel; Shaw-related subfamily; member 4	-0.2065	0.0004
208253_at	SIGLEC8	sialic acid binding Ig-like lectin 8	-0.5409	0
208254_at	C15orf31	chromosome 15 open reading frame 31	-0.1254	0.0033
208259_x_at	IFNA7	interferon; alpha 7	-0.1019	0.033
208265_at	DKFZp547H025	hypothetical protein DKFZp547H025	-0.1822	0.0072
208266_at	C8orf17	chromosome 8 open reading frame 17	-0.1355	0.0075
208284_x_at	GGT1	gamma-glutamyltransferase 1	-0.2048	0.013
208288_at	ABCB11	ATP-binding cassette; sub-family B (MDR/TAP); member 11	-0.117	0.0473
208291_s_at	TH	tyrosine hydroxylase	-1.7825	0
208297_s_at	EVI5	ecotropic viral integration site 5	-0.2873	0.005
208299_at	CACNA1I	calcium channel; voltage-dependent; T type; alpha 1I subunit	-0.136	0.0263
208306_x_at	HLA-DRB1	Major histocompatibility complex; class II; DR beta 1	-1.6792	0.0058
208307_at	RBMY1A1	RNA binding motif protein; Y-linked; family 1; member A1, RNA binding motif protein; Y-linked; family 1; member B, RNA binding motif protein; Y-linked; family 1; member D, RNA binding motif protein; Y-linked; family 1; member E, RNA binding motif protein; Y-linked; family 1; member F, RNA binding motif protein; Y-linked; family 1; member J	-0.1165	0.0254
208313_s_at	SF1	splicing factor 1	-0.6899	0.0006
208329_at	PBOV1	prostate and breast cancer overexpressed 1	-0.2091	0.0112
208338_at	P2RX3	purinergic receptor P2X; ligand-gated ion channel; 3	-0.1143	0.0347
208344_x_at	IFNA1	interferon; alpha 1, interferon; alpha 13	-0.1702	0.0447
208373_s_at	P2RY6	pyrimidinergic receptor P2Y; G-protein coupled; 6	-0.2677	0.0072
208380_at	LBX1	ladybird homeobox 1	-0.1539	0.0011
208387_s_at	MMP24	matrix metallopeptidase 24 (membrane-inserted)	-0.1122	0.0406

208389_s_at	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter); member 2	-1.0422	0
208397_x_at	KCNJ5	potassium inwardly-rectifying channel; subfamily J; member 5	-0.3294	0.0007
208399_s_at	EDN3	endothelin 3	-0.7649	0.0246
208404_x_at	KCNJ5	potassium inwardly-rectifying channel; subfamily J; member 5	-1.2414	0
208407_s_at	CTNND1	catenin (cadherin-associated protein); delta 1	-0.8276	0.0162
208410_x_at	AMELX	amelogenin (amelogenesis imperfecta 1; X-linked)	-0.102	0.016
208417_at	FGF6	fibroblast growth factor 6	-0.2912	0.0131
208420_x_at	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	-0.7399	0.0003
208437_at	CLCN1	chloride channel 1; skeletal muscle (Thomsen disease; autosomal dominant)	-0.1533	0.0473
208438_s_at	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	-1.0445	0.0164
208449_s_at	FGF8	fibroblast growth factor 8 (androgen-induced)	-0.1431	0.0101
208461_at	HIC1	hypermethylated in cancer 1	-0.1242	0.0384
208462_s_at	ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	-0.1466	0.0057
208465_at	GRM2	glutamate receptor; metabotropic 2	-0.1247	0.0247
208468_at	SOX21	SRY (sex determining region Y)-box 21	-0.1881	0.0039
208483_x_at	KRT33A	keratin 33A	-0.1305	0.0175
208487_at	LMX1B	LIM homeobox transcription factor 1; beta	-0.1075	0.0471
208489_at	GJA8	gap junction protein; alpha 8; 50kDa	-0.25	0.0085
208495_at	TLX3	T-cell leukemia homeobox 3	-0.2129	0.0005
208507_at	OR7C2	olfactory receptor; family 7; subfamily C; member 2	-0.1243	0.0101
208513_at	FOXB1	forkhead box B1	-0.1651	0.0175
208514_at	KCNE1	potassium voltage-gated channel; Isk-related family; member 1	-0.1358	0.0202
208526_at	OR2F1	olfactory receptor; family 2; subfamily F; member 1, olfactory receptor; family 2; subfamily F; member 2	-0.1986	0.0033
208533_at	SOX1	SRY (sex determining region Y)-box 1	-0.126	0.0273
208534_s_at	FLJ21767	RAS p21 protein activator 4, hypothetical protein FLJ21767	-0.7024	0.0189
208538_at	ANP32C	acidic (leucine-rich) nuclear phosphoprotein 32 family; member C	-0.144	0.0213
208556_at	GPR31	G protein-coupled receptor 31	-0.1582	0.0112
208557_at	HOXA6	homeobox A6	-0.302	0.0131
208559_at	PDX1	pancreatic and duodenal homeobox 1	-0.1945	0.0133
208560_at	KCNA10	potassium voltage-gated channel; shaker-related subfamily; member 10	-0.1558	0.023
208561_at	ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	-0.3189	0.0196

208564_at	KCNA2	potassium voltage-gated channel; shaker-related subfamily; member 2	-0.1991	0.0078
208566_at	KCNJ12	potassium inwardly-rectifying channel; subfamily J; member 12	-0.1523	0.0038
208568_at	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	-2.1446	0.0115
208571_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family; member A, acidic (leucine-rich) nuclear phosphoprotein 32 family; member C, acidic (leucine-rich) nuclear phosphoprotein 32 family; member D, hepatopoietin PCn127	-0.1525	0.0304
208572_at	HIST3H3	histone cluster 3; H3	-0.1009	0.0115
208578_at	SCN10A	sodium channel; voltage-gated; type X; alpha subunit	-0.1688	0.0302
208581_x_at	MT1X	metallothionein 1X	-0.876	0.0016
208584_at	SNCG	synuclein; gamma (breast cancer-specific protein 1)	-0.1698	0.0098
208585_at	BTN2A3	butyrophilin; subfamily 2; member A3	-0.1452	0.017
208588_at	FKSG2	apoptosis inhibitor	-0.2162	0.0016
208604_s_at	HOXA3	homeobox A3	-0.1411	0.0147
208607_s_at	SAA1	serum amyloid A1, serum amyloid A2	-0.4519	0.0031
208613_s_at	FLNB	filamin B; beta (actin binding protein 278)	-1.2014	0.0014
208614_s_at	FLNB	filamin B; beta (actin binding protein 278)	-1.2978	0.0008
208615_s_at	PTP4A2	protein tyrosine phosphatase type IVA; member 2	-0.5239	0.0152
208617_s_at	PTP4A2	protein tyrosine phosphatase type IVA; member 2	-0.556	0.0008
208619_at	DDB1	damage-specific DNA binding protein 1; 127kDa	-0.4207	0.0021
208620_at	PCBP1	poly(rC) binding protein 1	-0.4375	0.0044
208622_s_at	VIL2	villin 2 (ezrin)	-1.0545	0.0149
208623_s_at	VIL2	villin 2 (ezrin)	-0.8514	0
208626_s_at	VAT1	vesicle amine transport protein 1 homolog (T. californica)	-0.8294	0.0072
208630_at	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein); alpha subunit	-0.5399	0
208631_s_at	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein); alpha subunit	-0.6708	0.0024
208634_s_at	MACF1	microtubule-actin crosslinking factor 1	-0.504	0.0023
208643_s_at	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kDa)	-0.3997	0.008
208666_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	-0.8133	0.0037

208667_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	-0.3938	0.0286
208669_s_at	EID1	EP300 interacting inhibitor of differentiation 1	-0.2976	0.0479
208672_s_at	SFRS3	splicing factor; arginine/serine-rich 3	-0.3811	0.0005
208673_s_at	SFRS3	splicing factor; arginine/serine-rich 3	-0.3947	0.0161
208683_at	CAPN2	calpain 2; (m/II) large subunit	-0.3108	0.0206
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	-0.9613	0.041
208706_s_at	EIF5	eukaryotic translation initiation factor 5	-0.5488	0.0111
208728_s_at	CDC42	cell division cycle 42 (GTP binding protein; 25kDa)	-0.1987	0.0421
208730_x_at	RAB2A	RAB2A; member RAS oncogene family	-0.2903	0.0321
208745_at	ATP5L	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit G	-0.7718	0.0001
208746_x_at	ATP5L	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit G	-0.5141	0.0008
208747_s_at	C1S	complement component 1; s subcomponent	-1.9138	0.002
208749_x_at	FLOT1	flotillin 1	-0.784	0
208768_x_at	RPL22	ribosomal protein L22	-0.2716	0.0057
208771_s_at	LTA4H	leukotriene A4 hydrolase	-0.474	0.0002
208780_x_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A; 33kDa	-0.2656	0.0064
208782_at	FSTL1	follistatin-like 1	-0.6834	0.0436
208788_at	ELOVL5	ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast)	-0.4161	0.0275
208804_s_at	SFRS6	splicing factor; arginine/serine-rich 6	-0.6537	0.0001
208806_at	CHD3	chromodomain helicase DNA binding protein 3	-0.5218	0.0302
208813_at	GOT1	glutamic-oxaloacetic transaminase 1; soluble (aspartate aminotransferase 1)	-1.3924	0.0002
208825_x_at	RPL23A	ribosomal protein L23a	-0.1488	0.0008
208827_at	PSMB6	proteasome (prosome; macropain) subunit; beta type; 6	-0.4594	0.002
208830_s_at	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	-0.614	0.0044
208831_x_at	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	-0.6891	0.0011
208832_at	ATXN10	ataxin 10	-1.2123	0
208833_s_at	ATXN10	ataxin 10	-0.7115	0.0001
208834_x_at	hCG_16001	ribosomal protein L23a, similar to ribosomal protein L23A	-0.1292	0.0014
208836_at	ATP1B3	ATPase; Na+/K+ transporting; beta 3 polypeptide	-1.7356	0
208863_s_at	SFRS1	splicing factor; arginine/serine-rich 1 (splicing factor 2; alternate splicing factor)	-0.3606	0.0206

208870_x_at	ATP5C1	ATP synthase; H+ transporting; mitochondrial F1 complex; gamma polypeptide 1	-0.217	0.0408
208877_at	PAK2	p21 (CDKN1A)-activated kinase 2	-0.5394	0.0146
208894_at	HLA-DRA	major histocompatibility complex; class II; DR alpha	-1.998	0.0051
208896_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-0.3849	0.0257
208898_at	ATP6V1D	ATPase; H+ transporting; lysosomal 34kDa; V1 subunit D	-0.6266	0.0003
208899_x_at	ATP6V1D	ATPase; H+ transporting; lysosomal 34kDa; V1 subunit D	-0.5356	0.022
208903_at	RPS28	ribosomal protein S28	-0.633	0.024
208910_s_at	C1QBP	complement component 1; q subcomponent binding protein	-0.4642	0.0142
208911_s_at	PDHB	pyruvate dehydrogenase (lipoamide) beta	-0.4463	0.0218
208912_s_at	CNP	2';3'-cyclic nucleotide 3' phosphodiesterase	-0.6009	0.0275
208916_at	SLC1A5	solute carrier family 1 (neutral amino acid transporter); member 5	-0.8528	0.0001
208919_s_at	NADK	NAD kinase	-0.5977	0.0074
208920_at	SRI	sorcin	-0.8504	0.0326
208922_s_at	NXF1	nuclear RNA export factor 1	-0.7625	0.0001
208923_at	CYFIP1	cytoplasmic FMR1 interacting protein 1	-0.38	0.0332
208924_at	RNF11	ring finger protein 11	-0.505	0.0027
208937_s_at	ID1	inhibitor of DNA binding 1; dominant negative helix-loop-helix protein	-2.1292	0.0012
208943_s_at	TLOC1	translocation protein 1	-0.2707	0.0069
208944_at	TGFBR2	transforming growth factor; beta receptor II (70/80kDa)	-1.6087	0.0002
208945_s_at	BECN1	beclin 1 (coiled-coil; myosin-like BCL2 interacting protein)	-0.4456	0.0453
208946_s_at	BECN1	beclin 1 (coiled-coil; myosin-like BCL2 interacting protein)	-0.518	0.0021
208950_s_at	ALDH7A1	aldehyde dehydrogenase 7 family; member A1	-0.6516	0.004
208951_at	ALDH7A1	aldehyde dehydrogenase 7 family; member A1	-0.6831	0.0062
208962_s_at	FADS1	fatty acid desaturase 1	-1.3193	0.0142
208963_x_at	FADS1	fatty acid desaturase 1	-1.2876	0.0158
208964_s_at	FADS1	fatty acid desaturase 1	-1.428	0.0057
208970_s_at	UROD	uroporphyrinogen decarboxylase	-0.4723	0.0088
208984_x_at	RBM10	RNA binding motif protein 10	-0.4602	0.0189
208991_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	-0.493	0.0112
208997_s_at	UCP2	uncoupling protein 2 (mitochondrial; proton carrier)	-1.3841	0.0264
208998_at	UCP2	uncoupling protein 2 (mitochondrial; proton carrier)	-1.9593	0.0038
209005_at	FBXL5	F-box and leucine-rich repeat protein 5	-0.7696	0.0121
209008_x_at	KRT8	keratin 8	-1.246	0.0217
209018_s_at	PINK1	PTEN induced putative kinase 1	-0.9136	0.0196

209019_s_at	PINK1	PTEN induced putative kinase 1	-0.7671	0.0013
209021_x_at	KIAA0652	KIAA0652	-0.4466	0.0001
209034_at	PNRC1	proline-rich nuclear receptor coactivator 1	-0.3473	0.0174
209072_at	MBP	myelin basic protein	-0.2403	0.0087
209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	-0.3914	0.0286
209076_s_at	WDR45L	WDR45-like	-0.8924	0
209077_at	TXN2	thioredoxin 2	-0.7542	0.0008
209078_s_at	TXN2	thioredoxin 2	-0.8118	0.0129
209083_at	CORO1A	coronin; actin binding protein; 1A	-1.435	0.001
209086_x_at	MCAM	melanoma cell adhesion molecule	-0.7229	0.0179
209087_x_at	MCAM	melanoma cell adhesion molecule	-1.1353	0.004
209094_at	DDAH1	dimethylarginine dimethylaminohydrolase 1	-1.7911	0.002
209101_at	CTGF	connective tissue growth factor	-3.0808	0.0005
209102_s_at	HBP1	HMG-box transcription factor 1	-0.4781	0.0006
209105_at	NCOA1	nuclear receptor coactivator 1	-0.6239	0.0421
209106_at	NCOA1	nuclear receptor coactivator 1	-0.6537	0.0036
209109_s_at	TSPAN6	tetraspanin 6	-0.7182	0.0318
209111_at	RNF5	ring finger protein 5	-0.366	0.0399
209116_x_at	HBB	hemoglobin; beta	-1.781	0.0208
209120_at	NR2F2	nuclear receptor subfamily 2; group F; member 2	-0.819	0.0002
209121_x_at	NR2F2	nuclear receptor subfamily 2; group F; member 2	-0.6865	0.0455
209122_at	ADFP	adipose differentiation-related protein	-1.5798	0.0028
209129_at	TRIP6	thyroid hormone receptor interactor 6	-1.52	0.0072
209134_s_at	RPS6	ribosomal protein S6	-0.1841	0.0205
209139_s_at	PRKRA	protein kinase; interferon-inducible double stranded RNA dependent activator	-0.3523	0.0335
209143_s_at	CLNS1A	chloride channel; nucleotide-sensitive; 1A	-0.4112	0.0033
209147_s_at	PPAP2A	phosphatidic acid phosphatase type 2A	-0.6507	0.0176
209159_s_at	NDRG4	NDRG family member 4	-3.0758	0.0042
209163_at	CYB561	cytochrome b-561	-1.3001	0.0104
209167_at	GPM6B	glycoprotein M6B	-3.2524	0
209168_at	GPM6B	glycoprotein M6B	-0.6722	0
209169_at	GPM6B	glycoprotein M6B	-0.6948	0
209170_s_at	GPM6B	glycoprotein M6B	-3.061	0
209174_s_at	QRICH1	glutamine-rich 1	-0.4914	0.0026
209177_at	C3orf60	chromosome 3 open reading frame 60	-0.9618	0.0004
209182_s_at	C10orf10	chromosome 10 open reading frame 10	-0.6203	0.0075

209183_s_at	C10orf10	chromosome 10 open reading frame 10	-2.1175	0.0001
209186_at	ATP2A2	ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	-0.4239	0.009
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	-2.7161	0.0003
209192_x_at	HTATIP	HIV-1 Tat interacting protein; 60kDa	-0.3448	0.0084
209199_s_at	MEF2C	myocyte enhancer factor 2C	-0.8005	0.0121
209200_at	MEF2C	myocyte enhancer factor 2C	-1.0754	0.0089
209208_at	MPDU1	mannose-P-dolichol utilization defect 1	-0.7125	0.0031
209210_s_at	PLEKHC1	pleckstrin homology domain containing; family C (with FERM domain) member 1	-0.7928	0.042
209211_at	KLF5	Kruppel-like factor 5 (intestinal)	-0.997	0.0005
209212_s_at	KLF5	Kruppel-like factor 5 (intestinal)	-0.6745	0.0026
209214_s_at	EWSR1	Ewing sarcoma breakpoint region 1	-0.452	0.0071
209216_at	WDR45	WD repeat domain 45	-0.7072	0.0053
209217_s_at	WDR45	WD repeat domain 45	-0.6243	0.0159
209219_at	RDBP	RD RNA binding protein	-0.5702	0.0142
209220_at	GPC3	glypican 3	-2.2201	0
209230_s_at	NUPR1	nuclear protein 1	-1.7185	0.0386
209234_at	KIF1B	kinesin family member 1B	-1.024	0.0057
209236_at	SLC23A2	solute carrier family 23 (nucleobase transporters); member 2	-1.527	0.0006
209239_at	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-0.9345	0.0024
209244_s_at	KIF1C	kinesin family member 1C	-0.3886	0.0013
209253_at	SORBS3	sorbin and SH3 domain containing 3	-0.585	0.0256
209263_x_at	TSPAN4	tetraspanin 4	-1.4634	0.0009
209264_s_at	TSPAN4	tetraspanin 4	-1.0332	0.046
209268_at	VPS45	vacuolar protein sorting 45 homolog (S. cerevisiae)	-0.8698	0.0002
209269_s_at	SYK	spleen tyrosine kinase	-0.2289	0.007
209272_at	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	-0.5451	0.0063
209273_s_at	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-0.5333	0.0062
209274_s_at	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-0.6195	0.0009
209276_s_at	GLRX	glutaredoxin (thioltransferase)	-1.5399	0.0001
209283_at	CRYAB	crystallin; alpha B	-1.8925	0.0049
209286_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	-1.0416	0.0253
209287_s_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	-0.2481	0.0261
209288_s_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	-1.1199	0.0253
209290_s_at	NFIB	nuclear factor I/B	-0.3845	0.0231
209298_s_at	ITSN1	intersectin 1 (SH3 domain protein)	-0.779	0.0117

209304_x_at	GADD45B	growth arrest and DNA-damage-inducible; beta	-0.8857	0.0343
209312_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1	-2.0029	0.0045
209323_at	PRKRIR	protein-kinase; interferon-inducible double stranded RNA dependent inhibitor; repressor of (P58 repressor)	-0.6827	0.002
209335_at	DCN	decorin	-4.2802	0
209339_at	SIAH2	seven in absentia homolog 2 (Drosophila)	-0.7737	0.0098
209340_at	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	-1.207	0
209348_s_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	-1.3557	0.0069
209351_at	KRT14	keratin 14 (epidermolysis bullosa simplex; Dowling-Meara; Koebner)	-0.1977	0.0017
209353_s_at			-0.1719	0.0062
209354_at	TNFRSF14	tumor necrosis factor receptor superfamily; member 14 (herpesvirus entry mediator)	-0.8799	0.0051
209355_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	-1.7774	0.0009
209356_x_at	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	-1.7338	0.0003
209364_at	BAD	BCL2-antagonist of cell death	-0.4638	0.0319
209365_s_at	ECM1	extracellular matrix protein 1	-1.2951	0.0079
209366_x_at	CYB5A	cytochrome b5 type A (microsomal)	-2.4596	0
209368_at	EPHX2	epoxide hydrolase 2; cytoplasmic	-2.6223	0
209370_s_at	SH3BP2	SH3-domain binding protein 2	-0.3297	0.0034
209386_at	TM4SF1	transmembrane 4 L six family member 1	-1.9466	0.0002
209387_s_at	TM4SF1	transmembrane 4 L six family member 1	-2.4501	0.0001
209397_at	ME2	malic enzyme 2; NAD(+)-dependent; mitochondrial	-0.5727	0.0271
209407_s_at	DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila)	-1.0988	0.0042
209414_at	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-0.5129	0.0224
209417_s_at	IFI35	interferon-induced protein 35	-2.2009	0
209427_at	SMTN	smoothelin	-1.3439	0
209429_x_at	EIF2B4	eukaryotic translation initiation factor 2B; subunit 4 delta; 67kDa	-0.8618	0.003
209436_at	SPON1	spondin 1; extracellular matrix protein	-4.1679	0
209437_s_at	SPON1	spondin 1; extracellular matrix protein	-0.6768	0
209451_at	TANK	TRAF family member-associated NFKB activator	-0.6198	0.0052
209454_s_at	TEAD3	TEA domain family member 3	-0.4416	0.0095
209457_at	DUSP5	dual specificity phosphatase 5	-1.1306	0.0278
209458_x_at	HBA1	hemoglobin; alpha 1, hemoglobin; alpha 2	-1.4089	0.0276

209467_s_at	MKNK1	MAP kinase interacting serine/threonine kinase 1	-1.095	0.0019
209468_at	LRP5	low density lipoprotein receptor-related protein 5	-1.529	0.0004
209469_at	GPM6A	glycoprotein M6A	-2.2815	0
209470_s_at	GPM6A	glycoprotein M6A	-2.5626	0
209472_at	CCBL2	cysteine conjugate-beta lyase 2	-1.1198	0.0002
209479_at	CCDC28A	coiled-coil domain containing 28A	-0.8505	0
209481_at	SNRK	SNF related kinase	-0.3799	0.0349
209486_at	SAS10	disrupter of silencing 10	-0.5788	0.0009
209487_at	RBPMS	RNA binding protein with multiple splicing	-1.5274	0.0015
209488_s_at	RBPMS	RNA binding protein with multiple splicing	-1.4633	0.0024
209493_at	PDZD2	PDZ domain containing 2	-0.7724	0.0053
209496_at	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	-2.1468	0.0102
209499_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	-1.8603	0
209500_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	-1.8359	0
209503_s_at	PSMC5	proteasome (prosome; macropain) 26S subunit; ATPase; 5	-0.5038	0.0026
209505_at	NR2F1	Nuclear receptor subfamily 2; group F; member 1	-2.939	0
209506_s_at	NR2F1	nuclear receptor subfamily 2; group F; member 1	-1.988	0
209512_at	HSDL2	hydroxysteroid dehydrogenase like 2	-1.1324	0.0009
209513_s_at	HSDL2	hydroxysteroid dehydrogenase like 2	-0.9009	0.0005
209521_s_at	AMOT	angiomotin	-0.1002	0.0481
209525_at	HDGFRP3	Hepatoma-derived growth factor; related protein 3	-0.2934	0.0163
209531_at	GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	-1.0696	0.0011
209540_at	IGF1	insulin-like growth factor 1 (somatomedin C)	-2.622	0
209541_at	IGF1	insulin-like growth factor 1 (somatomedin C)	-2.4101	0
209542_x_at	IGF1	insulin-like growth factor 1 (somatomedin C)	-0.8266	0.0006
209543_s_at	CD34	CD34 molecule	-0.6076	0.005
209552_at	PAX8	paired box 8	-0.4708	0.0011
209558_s_at	HIP1R	huntingtin interacting protein 1 related, similar to huntingtin interacting protein 1 related	-1.8124	0
209559_at	HIP1R	huntingtin interacting protein 1 related	-0.5279	0.0031
209580_s_at	MBD4	methyl-CpG binding domain protein 4	-0.6201	0.0018
209581_at	HRASLS3	HRAS-like suppressor 3	-1.6591	0.0029

209595_at	GTF2F2	general transcription factor IIF; polypeptide 2; 30kDa	-0.4887	0.0141
209596_at	MXRA5	matrix-remodelling associated 5	-2.7465	0.0088
209600_s_at	ACOX1	acyl-Coenzyme A oxidase 1; palmitoyl	-1.1286	0.0029
209605_at	TST	thiosulfate sulfurtransferase (rhodanese)	-1.2718	0.0064
209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter); member 4	-1.6002	0.0008
209612_s_at	ADH1B	alcohol dehydrogenase 1C (class I); gamma polypeptide, alcohol dehydrogenase IB (class I); beta polypeptide	-6.142	0
209613_s_at	ADH1B	alcohol dehydrogenase 1C (class I); gamma polypeptide, alcohol dehydrogenase IB (class I); beta polypeptide	-6.1984	0
209614_at	ADH1C	alcohol dehydrogenase 1C (class I); gamma polypeptide	-3.6659	0
209616_s_at	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	-1.7303	0.0393
209619_at	CD74	CD74 molecule; major histocompatibility complex; class II invariant chain	-1.7451	0.0024
209633_at	PPP2R3A	protein phosphatase 2 (formerly 2A); regulatory subunit B''; alpha	-0.866	0.0037
209641_s_at	ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	-2.5544	0.0001
209643_s_at	PLD2	phospholipase D2	-0.303	0.0287
209650_s_at	TBC1D22A	TBC1 domain family; member 22A	-0.4471	0.0009
209664_x_at	NFATC1	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 1	-0.1014	0.042
209674_at	CRY1	cryptochrome 1 (photolyase-like)	-0.6295	0.0017
209681_at	SLC19A2	solute carrier family 19 (thiamine transporter); member 2	-1.4032	0.0002
209683_at	FAM49A	family with sequence similarity 49; member A	-1.8282	0.0022
209686_at	S100B	S100 calcium binding protein B	-0.7532	0
209687_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	-5.1303	0
209696_at	FBP1	fructose-1;6-bisphosphatase 1	-2.7121	0
209706_at	NKX3-1	NK3 homeobox 1	-0.9456	0.0156
209708_at	MOXD1	monooxygenase; DBH-like 1	-2.9858	0
209716_at	CSF1	colony stimulating factor 1 (macrophage)	-0.9892	0.0002
209717_at	EVI5	ecotropic viral integration site 5	-0.9019	0.0006
209718_at	NCAPH2	non-SMC condensin II complex; subunit H2	-0.1839	0.0366
209723_at	SERPINB9	serpin peptidase inhibitor; clade B (ovalbumin); member 9	-3.4238	0
209734_at	NCKAP1L	NCK-associated protein 1-like	-0.8901	0.0065
209735_at	ABCG2	ATP-binding cassette; sub-family G (WHITE); member 2	-1.7991	0
209736_at	SOX13	SRY (sex determining region Y)-box 13	-0.3121	0.0352

209747_at	TGFB3	transforming growth factor; beta 3	-0.602	0.0061
209751_s_at	SEDLP	spondyloepiphyseal dysplasia; late; pseudogene, trafficking protein particle complex 2	-0.7869	0.0009
209758_s_at	MFAP5	microfibrillar associated protein 5	-2.0052	0
209763_at	CHRDL1	chordin-like 1	-1.5945	0
209771_x_at	CD24	CD24 molecule	-1.4488	0.0275
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	-2.5442	0.0011
209789_at	CORO2B	coronin; actin binding protein; 2B	-0.877	0
209794_at	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	-0.9791	0
209798_at	NPAT	nuclear protein; ataxia-telangiectasia locus	-0.743	0.0031
209821_at	IL33	interleukin 33	-2.5483	0
209824_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-1.9109	0
209827_s_at	IL16	interleukin 16 (lymphocyte chemoattractant factor)	-0.3749	0.0333
209828_s_at	IL16	interleukin 16 (lymphocyte chemoattractant factor)	-0.2138	0.006
209830_s_at	SLC9A3R2	solute carrier family 9 (sodium/hydrogen exchanger); member 3 regulator 2	-0.1856	0.0075
209840_s_at	LRRN3	leucine rich repeat neuronal 3	-3.2733	0.0006
209841_s_at	LRRN3	leucine rich repeat neuronal 3	-3.227	0.0002
209842_at	SOX10	SRY (sex determining region Y)-box 10	-0.2572	0.008
209843_s_at	SOX10	SRY (sex determining region Y)-box 10	-0.2402	0.0121
209850_s_at	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	-0.3557	0
209851_at	ZC3H13	zinc finger CCCH-type containing 13	-0.2096	0.0031
209879_at	SELPLG	selectin P ligand	-1.0635	0.0099
209888_s_at	MYL1	myosin; light chain 1; alkali; skeletal; fast	-0.1509	0.009
209897_s_at	SLIT2	slit homolog 2 (Drosophila)	-3.254	0.0009
209898_x_at	ITSN2	intersectin 2	-0.4096	0.0258
209901_x_at	AIF1	allograft inflammatory factor 1	-3.0142	0
209904_at	TNNC1	troponin C type 1 (slow)	-0.7637	0
209906_at	C3AR1	complement component 3a receptor 1	-1.7644	0.0011
209907_s_at	ITSN2	intersectin 2	-0.6566	0.0271
209939_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	-0.6717	0.0178
209943_at	FBXL4	F-box and leucine-rich repeat protein 4	-0.6173	0.0105
209944_at	ZNF410	zinc finger protein 410	-0.6638	0.0001
209948_at	KCNMB1	potassium large conductance calcium-activated channel; subfamily M; beta member 1	-0.2664	0.0345
209950_s_at	VILL	villin-like	-0.318	0.0007
209959_at	NR4A3	nuclear receptor subfamily 4; group A; member 3	-3.8063	0

209960_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	-3.757	0
209964_s_at	ATXN7	ataxin 7	-1.0069	0.0012
209967_s_at	CREM	cAMP responsive element modulator	-2.0119	0
209981_at	CSDC2	cold shock domain containing C2; RNA binding	-2.8498	0.0002
209987_s_at	ASCL1	achaete-scute complex homolog 1 (Drosophila)	-0.1643	0.0024
209993_at	ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	-2.5109	0.0014
209994_s_at	ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1, ATP-binding cassette; sub-family B (MDR/TAP); member 4	-2.2004	0.0043
210000_s_at	SOCS1	suppressor of cytokine signaling 1	-0.1093	0.0112
210002_at	GATA6	GATA binding protein 6	-1.5192	0.0025
210006_at	ABHD14A	abhydrolase domain containing 14A	-0.8581	0.0044
210016_at	MYT1L	myelin transcription factor 1-like	-0.1229	0.035
210027_s_at	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-0.4977	0.0018
210042_s_at	CTSZ	cathepsin Z	-1.1245	0.0158
210044_s_at	LYL1	lymphoblastic leukemia derived sequence 1	-0.5378	0.0105
210055_at	TSHR	thyroid stimulating hormone receptor	-0.1433	0.0492
210058_at	MAPK13	mitogen-activated protein kinase 13	-2.167	0.0006
210059_s_at	MAPK13	mitogen-activated protein kinase 13	-1.7428	0.0003
210063_at	SARDH	sarcosine dehydrogenase	-0.2275	0.0006
210066_s_at	AQP4	aquaporin 4	-0.1484	0.0015
210073_at	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 1	-1.4116	0
210078_s_at	KCNAB1	potassium voltage-gated channel; shaker-related subfamily; beta member 1	-1.0038	0
210079_x_at	KCNAB1	potassium voltage-gated channel; shaker-related subfamily; beta member 1	-0.1408	0.0165
210082_at	ABCA4	ATP-binding cassette; sub-family A (ABC1); member 4	-0.1878	0.0043
210090_at	ARC	activity-regulated cytoskeleton-associated protein	-0.1472	0.0316
210096_at	CYP4B1	cytochrome P450; family 4; subfamily B; polypeptide 1	-3.3613	0
210099_at	ABCA2	ATP-binding cassette; sub-family A (ABC1); member 2	-0.1501	0.0177
210102_at	LOH11CR2A	loss of heterozygosity; 11; chromosomal region 2; gene A	-1.3794	0.006
210121_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 2	-0.311	0.0152
210130_s_at	TM7SF2	transmembrane 7 superfamily member 2	-2.0505	0.0046
210139_s_at	PMP22	peripheral myelin protein 22	-1.3755	0.0024
210142_x_at	FLOT1	flotillin 1	-0.8727	0
210144_at	TBC1D22A	TBC1 domain family; member 22A	-0.4811	0.0054

210145_at	PLA2G4A	phospholipase A2; group IVA (cytosolic; calcium-dependent)	-4.7472	0
210155_at	MYOC	myocilin; trabecular meshwork inducible glucocorticoid response	-0.1966	0.0023
210162_s_at	NFATC1	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 1	-0.3215	0.0155
210168_at	C6	complement component 6	-0.5964	0
210171_s_at	CREM	cAMP responsive element modulator	-0.3192	0.0023
210190_at	STX11	syntaxin 11	-0.2385	0.0042
210198_s_at	PLP1	proteolipid protein 1 (Pelizaeus-Merzbacher disease; spastic paraplegia 2; uncomplicated)	-0.7638	0.0059
210199_at	CRYAA	crystallin; alpha A	-0.1693	0.0006
210201_x_at	BIN1	bridging integrator 1	-1.1695	0.0053
210202_s_at	BIN1	bridging integrator 1	-1.7158	0.0046
210205_at	B3GALT4	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 4	-0.5371	0.0114
210208_x_at	BAT3	HLA-B associated transcript 3	-0.2709	0.0415
210214_s_at	BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	-0.6872	0.0029
210221_at	CHRNA3	cholinergic receptor; nicotinic; alpha 3	-0.9501	0.0322
210225_x_at	LILRB3	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 3	-0.2968	0.0334
210227_at	DLGAP2	discs; large (Drosophila) homolog-associated protein 2	-0.1086	0.0307
210229_s_at	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	-0.1395	0.0416
210239_at	IRX5	iroquois homeobox 5	-0.204	0.0003
210243_s_at	B4GALT3	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 3	-0.41	0.0457
210245_at	ABCC8	ATP-binding cassette; sub-family C (CFTR/MRP); member 8	-0.1578	0.0246
210246_s_at	ABCC8	ATP-binding cassette; sub-family C (CFTR/MRP); member 8	-0.2626	0.0031
210248_at	WNT7A	wingless-type MMTV integration site family; member 7A	-0.1508	0.0065
210253_at	HTATIP2	HIV-1 Tat interactive protein 2; 30kDa	-1.031	0.0141
210254_at	MS4A3	membrane-spanning 4-domains; subfamily A; member 3 (hematopoietic cell-specific)	-0.1197	0.0152
210255_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	-0.1739	0.023
210261_at	KCNK2	potassium channel; subfamily K; member 2	-2.9588	0
210262_at	CRISP2	cysteine-rich secretory protein 2	-0.1538	0.0093
210263_at	KCNF1	potassium voltage-gated channel; subfamily F; member 1	-0.1829	0.0275
210270_at	RGS6	regulator of G-protein signaling 6	-0.1701	0.0282
210275_s_at	ZFAND5	zinc finger; AN1-type domain 5	-0.7827	0
210289_at	NAT8	N-acetyltransferase 8, N-acetyltransferase 8B (gene/pseudogene)	-0.1275	0.0185

210292_s_at	PCDH11X	protocadherin 11 X-linked, protocadherin 11 Y-linked	-0.2364	0.0047
210293_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	-0.307	0.0117
210295_at	MAGEA10	melanoma antigen family A; 10	-0.1385	0.0276
210298_x_at	FHL1	four and a half LIM domains 1	-0.5602	0.0437
210299_s_at	FHL1	four and a half LIM domains 1	-1.7985	0
210300_at	REM1	RAS (RAD and GEM)-like GTP-binding 1	-0.5298	0
210304_at	PDE6B	phosphodiesterase 6B; cGMP-specific; rod; beta (congenital stationary night blindness 3; autosomal dominant)	-0.135	0.0277
210314_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	-2.4626	0
210316_at	FLT4	fms-related tyrosine kinase 4	-0.1167	0.0494
210318_at	RBP3	retinol binding protein 3; interstitial	-0.1636	0.0097
210324_at	C8G	complement component 8; gamma polypeptide	-0.2645	0.0007
210340_s_at	CSF2RA	colony stimulating factor 2 receptor; alpha; low-affinity (granulocyte-macrophage)	-0.3224	0.0009
210342_s_at	TPO	thyroid peroxidase	-0.1753	0.0011
210363_s_at	SCN2B	sodium channel; voltage-gated; type II; beta	-0.2221	0.0018
210372_s_at	TPD52L1	tumor protein D52-like 1	-2.216	0.0005
210375_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-0.5387	0.0008
210381_s_at	CCKBR	cholecystokinin B receptor	-0.1479	0.0263
210390_s_at	CCL14	chemokine (C-C motif) ligand 14, chemokine (C-C motif) ligand 15	-0.1511	0.0232
210403_s_at	KCNJ1	potassium inwardly-rectifying channel; subfamily J; member 1	-0.1748	0.0108
210408_s_at	CPNE6	copine VI (neuronal)	-0.1037	0.0133
210422_x_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1	-0.3635	0
210423_s_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1	-0.9505	0.0209
210442_at	IL1RL1	interleukin 1 receptor-like 1	-0.1374	0.0162
210445_at	FABP6	fatty acid binding protein 6; ileal (gastrotropin)	-2.1875	0.0171
210450_at	LOC90925	hypothetical protein LOC90925	-0.1885	0.0222
210451_at	PKLR	pyruvate kinase; liver and RBC	-0.1071	0.0459
210453_x_at	ATP5L	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit G	-0.532	0.0007
210461_s_at	ABLIM1	actin binding LIM protein 1	-1.6952	0
210469_at	DLG5	discs; large homolog 5 (Drosophila)	-1.2845	0.0005
210471_s_at	KCNAB1	potassium voltage-gated channel; shaker-related subfamily; beta member 1	-0.3234	0.0002

210474_s_at	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins), cell division cycle 2-like 2 (PITSLRE proteins)	-0.2812	0.0307
210475_at	POU3F1	POU class 3 homeobox 1	-0.5747	0.0006
210487_at	DNTT	deoxynucleotidyltransferase; terminal	-0.1045	0.038
210506_at	FUT7	fucosyltransferase 7 (alpha (1;3) fucosyltransferase)	-0.1294	0.0126
210515_at	TCF1	transcription factor 1; hepatic; LF-B1; hepatic nuclear factor (HNF1); albumin proximal factor	-0.1521	0.0319
210517_s_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-2.018	0.0018
210524_x_at			-1.1686	0.0086
210532_s_at	C14orf2	chromosome 14 open reading frame 2	-0.2341	0.0225
210536_s_at	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase; zona pellucida binding)	-0.1297	0.0145
210544_s_at	ALDH3A2	aldehyde dehydrogenase 3 family; member A2	-1.9591	0
210545_at	ITSN2	intersectin 2	-0.1543	0.006
210548_at	CCL23	chemokine (C-C motif) ligand 23	-0.2837	0
210549_s_at	CCL23	chemokine (C-C motif) ligand 23	-0.3966	0.0006
210557_x_at	CSF1	colony stimulating factor 1 (macrophage)	-0.2272	0.0064
210560_at	GBX2	gastrulation brain homeobox 2	-0.1373	0.032
210563_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	-0.7464	0.0185
210565_at	GCGR	glucagon receptor	-0.1182	0.0162
210569_s_at	SIGLEC9	sialic acid binding Ig-like lectin 9	-0.3057	0.001
210571_s_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	-0.4206	0.0043
210574_s_at	NUDC	nuclear distribution gene C homolog (A. nidulans)	-0.4949	0.0009
210575_at	NUDC	nuclear distribution gene C homolog (A. nidulans)	-0.1707	0.0002
210579_s_at	TRIM10	tripartite motif-containing 10	-0.1074	0.0229
210583_at	POLDIP3	polymerase (DNA-directed); delta interacting protein 3	-0.1527	0.0283
210592_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	-0.7714	0.0001
210597_x_at	PRB1	proline-rich protein BstNI subfamily 1, proline-rich protein BstNI subfamily 2	-0.3783	0.013
210609_s_at	TP53I3	tumor protein p53 inducible protein 3	-1.2023	0.0479
210613_s_at	SYNGR1	synaptogyrin 1	-1.1168	0.019
210618_at	RAP1GAP	RAP1 GTPase activating protein	-0.1448	0.0095
210626_at	AKAP1	A kinase (PRKA) anchor protein 1	-0.2291	0.0012
210628_x_at	LTBP4	latent transforming growth factor beta binding protein 4	-0.3736	0.0001
210629_x_at	LST1	leukocyte specific transcript 1	-0.6177	0.0231

210632_s_at	SGCA	sarcoglycan; alpha (50kDa dystrophin-associated glycoprotein)	-0.1319	0.04
210638_s_at	FBXO9	F-box protein 9	-0.8816	0
210644_s_at	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	-0.9991	0.0472
210653_s_at	BCKDHB	branched chain keto acid dehydrogenase E1; beta polypeptide (maple syrup urine disease)	-0.8431	0.0006
210657_s_at	4-Sep	septin 4	-3.465	0
210659_at	CMKLR1	chemokine-like receptor 1	-0.3613	0.0001
210660_at	LILRA1	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 1	-0.2572	0.0062
210663_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	-0.4017	0.0191
210677_at	SOAT2	sterol O-acyltransferase 2	-0.1398	0.0045
210687_at	CPT1A	carnitine palmitoyltransferase 1A (liver)	-0.5442	0
210702_s_at	PTGIS	prostaglandin I2 (prostacyclin) synthase	-0.1208	0.0311
210705_s_at	TRIM5	tripartite motif-containing 5	-0.4969	0.0116
210715_s_at	SPINT2	serine peptidase inhibitor; Kunitz type; 2	-1.2756	0.0063
210728_s_at	CALCA	calcitonin/calcitonin-related polypeptide; alpha	-0.1438	0.029
210737_at	TUB	tubby homolog (mouse)	-0.2282	0.0032
210750_s_at	DLGAP1	discs; large (Drosophila) homolog-associated protein 1	-0.2074	0.0027
210751_s_at	RGN	regucalcin (senescence marker protein-30)	-1.6886	0.0002
210752_s_at	MLX	MAX-like protein X	-0.3787	0.0059
210764_s_at	CYR61	cysteine-rich; angiogenic inducer; 61	-3.2213	0.0001
210773_s_at	FPRL1	formyl peptide receptor-like 1	-0.1178	0.0129
210774_s_at	NCOA4	nuclear receptor coactivator 4	-0.2435	0.0268
210775_x_at	CASP9	caspase 9; apoptosis-related cysteine peptidase	-4.3135	0
210781_x_at	GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1	-0.2064	0.0055
210785_s_at	C1orf38	chromosome 1 open reading frame 38	-1.639	0.0058
210789_x_at	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	-0.1698	0.0397
210793_s_at	NUP98	nucleoporin 98kDa	-1.366	0.0001
210798_x_at	MASP2	mannan-binding lectin serine peptidase 2	-0.1794	0.0029
210810_s_at	SLC6A5	solute carrier family 6 (neurotransmitter transporter; glycine); member 5	-0.1053	0.0483
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	-0.8056	0
210819_x_at	DIO2	deiodinase; iodothyronine; type II	-0.1369	0.0253
210825_s_at	PEBP1	phosphatidylethanolamine binding protein 1	-0.3242	0.0099
210838_s_at	ACVRL1	activin A receptor type II-like 1	-0.3669	0

210841_s_at	NRP2	neuropilin 2	-0.217	0.0346
210847_x_at	PLEKHG5	pleckstrin homology domain containing; family G (with RhoGef domain) member 5, tumor necrosis factor receptor superfamily; member 25	-0.2347	0.0335
210864_x_at	HFE	hemochromatosis	-0.1974	0.0174
210869_s_at	MCAM	melanoma cell adhesion molecule	-0.9124	0.0376
210880_s_at	EFS	embryonal Fyn-associated substrate	-0.2078	0.0095
210909_x_at	LPAL2	lipoprotein; Lp(a)-like 2	-0.1538	0.0199
210923_at	SLC1A7	solute carrier family 1 (glutamate transporter); member 7	-0.1435	0.0297
210924_at	OLFM1	olfactomedin 1	-0.1417	0.0391
210942_s_at	ST3GAL6	ST3 beta-galactoside alpha-2;3-sialyltransferase 6	-1.592	0.0016
210946_at	PPAP2A	phosphatidic acid phosphatase type 2A	-0.8751	0.0021
210952_at	AP4S1	adaptor-related protein complex 4; sigma 1 subunit	-0.1883	0.0267
210955_at	CASP10	caspase 10; apoptosis-related cysteine peptidase	-0.2198	0.022
210958_s_at	MAST4	microtubule associated serine/threonine kinase family member 4	-0.6689	0.0398
210960_at	ADRA1D	adrenergic; alpha-1D-; receptor	-0.167	0.0068
210967_x_at	CACNB1	calcium channel; voltage-dependent; beta 1 subunit	-0.1724	0.0151
210971_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-1.1503	0.0032
210982_s_at	HLA-DRA	major histocompatibility complex; class II; DR alpha	-2.2024	0.0075
210986_s_at	TPM1	tropomyosin 1 (alpha)	-0.5418	0.0213
211001_at	TRIM29	tripartite motif-containing 29	-0.1204	0.0265
211002_s_at	TRIM29	tripartite motif-containing 29	-0.1387	0.0474
211004_s_at	ALDH3B1	aldehyde dehydrogenase 3 family; member B1	-0.8552	0
211023_at	PDHB	pyruvate dehydrogenase (lipoamide) beta	-0.5755	0
211032_at	COBLL1	COBL-like 1	-0.9049	0
211033_s_at	PEX7	peroxisomal biogenesis factor 7	-1.004	0.0006
211067_s_at	GAS7	growth arrest-specific 7	-0.2961	0.0062
211069_s_at	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	-0.2555	0.042
211073_x_at	RPL3	ribosomal protein L3	-0.1917	0.0114
211101_x_at	LILRA2	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 2	-0.251	0.0038
211102_s_at	LILRA2	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 2	-0.1263	0.0427
211104_s_at	MYO7A	myosin VIIA	-0.2031	0.0481
211105_s_at	NFATC1	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 1	-0.8792	0.0006

211113_s_at	ABCG1	ATP-binding cassette; sub-family G (WHITE); member 1	-1.4341	0.0013
211125_x_at	GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1	-0.1725	0.0087
211135_x_at	LILRB3	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 3	-0.4031	0.026
211142_x_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	-0.2616	0.0106
211143_x_at	NR4A1	nuclear receptor subfamily 4; group A; member 1	-1.1459	0
211149_at	UTY	ubiquitously transcribed tetratricopeptide repeat gene; Y-linked	-1.2118	0.0198
211175_at	GPR45	G protein-coupled receptor 45	-0.1369	0.0166
211177_s_at	TXNRD2	thioredoxin reductase 2	-0.9615	0.0001
211181_x_at	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	-0.1103	0.0434
211182_x_at	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	-0.1545	0.0025
211184_s_at	USH1C	Usher syndrome 1C (autosomal recessive; severe)	-0.2241	0.0011
211197_s_at	ICOSLG	inducible T-cell co-stimulator ligand	-0.413	0
211198_s_at	ICOSLG	inducible T-cell co-stimulator ligand	-0.1443	0.035
211199_s_at	ICOSLG	inducible T-cell co-stimulator ligand	-0.1279	0.0248
211203_s_at	CNTN1	contactin 1	-0.3464	0.0091
211215_x_at	DIO2	deiodinase; iodothyronine; type II	-0.2536	0.0001
211217_s_at	KCNQ1	potassium voltage-gated channel; KQT-like subfamily; member 1	-3.3918	0
211218_at	PRO1848	PRO1848 protein	-0.1056	0.0226
211223_at	PROP1	PROP paired-like homeobox 1	-0.1642	0.0169
211226_at	GALR2	galanin receptor 2	-0.1053	0.03
211231_x_at	CYP4A11	cytochrome P450; family 4; subfamily A; polypeptide 11	-0.1678	0.0143
211235_s_at	ESR1	estrogen receptor 1	-0.1462	0.0307
211240_x_at	CTNND1	catenin (cadherin-associated protein); delta 1	-0.3237	0.049
211241_at	ANXA2P3	annexin A2 pseudogene 3	-0.2319	0.0389
211242_x_at	KIR2DL4	killer cell immunoglobulin-like receptor; two domains; long cytoplasmic tail; 4	-0.2254	0.0009
211248_s_at	CHRD	chordin	-0.4335	0.0038
211253_x_at	PYY	peptide YY	-0.1451	0.0327
211261_at			-0.1717	0.0189
211269_s_at	IL2RA	interleukin 2 receptor; alpha	-0.3497	0.0015
211275_s_at	GYG1	glycogenin 1	-0.6367	0.006
211276_at	TCEAL2	transcription elongation factor A (SII)-like 2	-1.3259	0.02
211282_x_at	TNFRSF25	tumor necrosis factor receptor superfamily; member 25	-0.3348	0.004

211289_x_at	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins), cell division cycle 2-like 2 (PITSLRE proteins)	-0.3351	0.0268
211304_x_at	KCNJ5	potassium inwardly-rectifying channel; subfamily J; member 5	-0.4122	0.0003
211307_s_at	FCAR	Fc fragment of IgA; receptor for	-0.1747	0.0062
211313_s_at	BAZ1B	bromodomain adjacent to zinc finger domain; 1B	-0.2133	0.0344
211315_s_at	CACNA1G	calcium channel; voltage-dependent; T type; alpha 1G subunit	-0.1807	0.0336
211324_s_at	RGPD5	RANBP2-like and GRIP domain containing 5, RANBP2-like and GRIP domain containing 6, RANBP2-like and GRIP domain containing 7, RANBP2-like and GRIP domain containing 8	-0.4899	0.0121
211340_s_at	MCAM	melanoma cell adhesion molecule	-0.8037	0.0134
211359_s_at	OPRM1	opioid receptor; mu 1	-0.1079	0.0474
211377_x_at	MYCN	v-myc myelocytomatosis viral related oncogene; neuroblastoma derived (avian)	-0.1218	0.0377
211381_x_at	SPAG11B	sperm associated antigen 11B	-0.1765	0.0047
211384_s_at	CASR	calcium-sensing receptor (hypocalciuric hypercalcemia 1; severe neonatal hyperparathyroidism)	-0.1426	0.0419
211385_x_at	SULT1A2	sulfotransferase family; cytosolic; 1A; phenol-preferring; member 2	-0.6562	0.0283
211407_at	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 7; 18kDa	-0.1586	0.0453
211413_s_at	PADI4	peptidyl arginine deiminase; type IV	-0.1997	0.0328
211414_at	GLS	glutaminase	-0.1191	0.0281
211421_s_at	RET	ret proto-oncogene	-0.9713	0.0048
211436_at		Clone FLB4228 PRO1095	-0.1032	0.0427
211438_at	TRHR	thyrotropin-releasing hormone receptor	-0.1013	0.0493
211439_at	SFRS7	splicing factor; arginine/serine-rich 7; 35kDa	-0.244	0.0002
211447_s_at	PDE4A	phosphodiesterase 4A; cAMP-specific (phosphodiesterase E2 dunce homolog; Drosophila)	-0.2641	0.0172
211455_at	LOC651198	similar to IFP38	-0.1507	0.005
211456_x_at	MT1P2	metallothionein 1 pseudogene 2	-0.6553	0.0015
211460_at	TTTY9A	testis-specific transcript; Y-linked 9A, testis-specific transcript; Y-linked 9B	-0.1176	0.0195
211461_at	CSPG4LYP1	chondroitin sulfate proteoglycan 4-like; Y-linked pseudogene 1, chondroitin sulfate proteoglycan 4-like; Y-linked pseudogene 2	-0.1621	0.0033
211472_at	PLXNB2	Plexin B2	-0.1412	0.0266
211473_s_at	COL4A6	collagen; type IV; alpha 6	-0.1352	0.0093
211474_s_at	SERPINB6	serpin peptidase inhibitor; clade B (ovalbumin); member 6	-0.5873	0.002
211475_s_at	BAG1	BCL2-associated athanogene	-0.7841	0.0073

211485_s_at	FGF18	fibroblast growth factor 18	-0.1149	0.0407
211495_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	-1.1103	0
211498_s_at	NKX3-1	NK3 homeobox 1	-0.187	0.0277
211531_x_at	PRB1	proline-rich protein BstNI subfamily 1, proline-rich protein BstNI subfamily 2	-0.4899	0.0074
211542_x_at	RPS10	ribosomal protein S10	-0.1778	0.0085
211557_x_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	-0.8645	0.0002
211562_s_at	LMOD1	leiomodin 1 (smooth muscle)	-0.8205	0
211566_x_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.8506	0
211567_at			-0.1282	0.048
211571_s_at	VCAN	versican	-2.3491	0.0075
211577_s_at	IGF1	insulin-like growth factor 1 (somatomedin C)	-0.5241	0.0023
211581_x_at	LST1	leukocyte specific transcript 1	-0.7826	0.0177
211582_x_at	LST1	leukocyte specific transcript 1	-1.0068	0.0078
211597_s_at	HOP	homeodomain-only protein	-3.5845	0.0001
211608_at		Rearranged TCR Vbeta 12.3 mRNA for T cell receptor	-0.1212	0.0494
211619_s_at	ALPP	alkaline phosphatase; placental (Regan isozyme), alkaline phosphatase; placental-like 2	-0.1837	0.005
211620_x_at	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	-0.1332	0.0005
211628_x_at	FTHP1	ferritin; heavy polypeptide pseudogene 1	-0.3603	0.0073
211641_x_at		Isolate Middle91 immunoglobulin heavy chain variable region (IGVH)	-0.1299	0.0382
211656_x_at	HLA-DQB1	major histocompatibility complex; class II; DQ beta 1	-1.3141	0.0399
211659_at	GPR135	G protein-coupled receptor 135	-0.3226	0.0008
211663_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-3.8751	0
211666_x_at	RPL3	ribosomal protein L3	-0.31	0.0213
211667_x_at		T cell receptor alpha chain (TRCAV2S1-N-AJ41-C) mRNA; anti-melanoma cytotoxic T lymphocyte clone MU-45; -63; -79	-0.1406	0.0254
211694_at	TSSK1B	testis-specific serine kinase 1B	-0.1384	0.0068
211696_x_at	HBB	hemoglobin; beta	-1.5903	0.021
211697_x_at	PNO1	partner of NOB1 homolog (S. cerevisiae)	-0.3953	0.0224
211698_at	EID1	EP300 interacting inhibitor of differentiation 1	-0.424	0.0074
211699_x_at	HBA1	hemoglobin; alpha 1, hemoglobin; alpha 2	-1.3365	0.0398
211703_s_at	TM2D1	TM2 domain containing 1	-0.8764	0.0215
211705_s_at	SORBS1	sorbin and SH3 domain containing 1	-0.1436	0.0068

211717_at	ANKRD40	ankyrin repeat domain 40	-0.3085	0.049
211726_s_at	FMO2	flavin containing monooxygenase 2 (non-functional)	-5.5456	0
211730_s_at	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L; 7.6kDa	-0.4894	0.0014
211733_x_at	SCP2	sterol carrier protein 2	-0.4556	0.0012
211735_x_at	SFTPC	surfactant; pulmonary-associated protein C	-0.132	0.0397
211742_s_at	EVI2B	ecotropic viral integration site 2B	-1.4289	0.0075
211745_x_at	HBA1	hemoglobin; alpha 1	-1.3329	0.0273
211748_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-5.3206	0
211754_s_at	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein; 34kDa); member 17	-0.6113	0.0053
211760_s_at	VAMP4	vesicle-associated membrane protein 4	-0.8002	0.0096
211764_s_at	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog; yeast)	-0.7678	0.005
211772_x_at	CHRNA3	cholinergic receptor; nicotinic; alpha 3	-0.2503	0.0096
211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-1.8695	0.0015
211781_x_at			-0.2228	0.0062
211784_s_at	SFRS1	splicing factor; arginine/serine-rich 1 (splicing factor 2; alternate splicing factor)	-0.2677	0.0163
211787_s_at	EIF4A1	eukaryotic translation initiation factor 4A; isoform 1	-0.2986	0.0033
211813_x_at	DCN	decorin	-3.9598	0.0004
211815_s_at	GGA3	golgi associated; gamma adaptin ear containing; ARF binding protein 3	-0.1561	0.0267
211817_s_at	KCNJ5	potassium inwardly-rectifying channel; subfamily J; member 5	-0.9938	0.0006
211819_s_at	SORBS1	sorbin and SH3 domain containing 1	-0.1731	0.001
211826_s_at	AFF1	AF4/FMR2 family; member 1	-0.1022	0.0177
211835_at	C12orf32	chromosome 12 open reading frame 32, immunoglobulin heavy constant alpha 1, immunoglobulin heavy constant alpha 2 (A2m marker), immunoglobulin heavy constant delta, immunoglobulin heavy constant gamma 1 (G1m marker), immunoglobulin heavy constant gamma 3 (G3m marker), immunoglobulin heavy constant gamma 4 (G4m marker), immunoglobulin heavy constant mu, immunoglobulin heavy locus, immunoglobulin heavy variable 3-48, immunoglobulin heavy variable 4-31, interleukin 8	-0.1011	0.0219
211839_s_at	CSF1	colony stimulating factor 1 (macrophage)	-0.2986	0.0001
211841_s_at	TNFRSF25	tumor necrosis factor receptor superfamily; member 25	-0.268	0.0015

211845_at	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	-0.3156	0.0005
211848_s_at	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	-0.1407	0.0092
211852_s_at	ATRN	attractin	-0.9342	0.0022
211873_s_at	PCDHGA9	protocadherin gamma subfamily A; 9	-0.1149	0.0189
211885_x_at	FUT6	fucosyltransferase 6 (alpha (1;3) fucosyltransferase)	-0.3005	0.0005
211886_s_at	TBX5	T-box 5	-0.1458	0.0345
211896_s_at	DCN	decorin	-4.0977	0.0003
211897_s_at	CRHR1	corticotropin releasing hormone receptor 1	-0.1237	0.0011
211903_s_at	MPL	myeloproliferative leukemia virus oncogene	-0.1899	0.0076
211922_s_at	CAT	catalase	-2.0499	0
211941_s_at	PEBP1	phosphatidylethanolamine binding protein 1	-0.4825	0.0013
211943_x_at	TPT1	tumor protein; translationally-controlled 1	-0.1332	0.0017
211950_at	UBR4	ubiquitin protein ligase E3 component n-recognin 4	-0.5278	0.0214
211958_at	IGFBP5	insulin-like growth factor binding protein 5	-2.8957	0
211959_at	IGFBP5	insulin-like growth factor binding protein 5	-2.9215	0.0001
211975_at	ZNF289	zinc finger protein 289; ID1 regulated	-0.835	0.0063
211976_at		CDNA: FLJ22515 fis; clone HRC12122; highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence	-0.6473	0.0021
211986_at	AHNAK	AHNAK nucleoprotein	-1.1368	0.0058
211990_at	HLA-DPA1	major histocompatibility complex; class II; DP alpha 1	-1.5358	0.0019
211991_s_at	HLA-DPA1	major histocompatibility complex; class II; DP alpha 1	-2.3026	0.003
211998_at	H3F3B	H3 histone; family 3B (H3.3B)	-1.4987	0.0006
212010_s_at	CDV3	CDV3 homolog (mouse)	-0.3399	0.0087
212024_x_at	FLII	flightless I homolog (Drosophila)	-0.315	0.0135
212026_s_at	EXOC7	exocyst complex component 7	-0.632	0.0165
212039_x_at	RPL3	ribosomal protein L3	-0.1678	0.037
212040_at	TGOLN2	trans-golgi network protein 2	-0.4581	0.0204
212043_at	TGOLN2	trans-golgi network protein 2	-0.4051	0.0001
212044_s_at	RPL27A	Ribosomal protein L27a	-0.5818	0.0006
212055_at	C18orf10	chromosome 18 open reading frame 10	-0.5319	0.0433
212063_at	CD44	CD44 molecule (Indian blood group)	-1.8845	0.0048
212067_s_at	C1R	complement component 1; r subcomponent	-1.6886	0.0073
212071_s_at	SPTBN1	spectrin; beta; non-erythrocytic 1	-0.865	0
212077_at	CALD1	caldesmon 1	-1.082	0.0004
212083_at	TEX261	testis expressed 261	-0.8862	0.0005

212092_at	PEG10	paternally expressed 10	-2.3812	0.0198
212094_at	PEG10	paternally expressed 10	-1.5928	0.0109
212099_at	RHOB	ras homolog gene family; member B	-0.6601	0.0036
212103_at	KPNA6	karyopherin alpha 6 (importin alpha 7)	-0.3207	0.0429
212117_at	RHOQ	ras homolog gene family; member Q	-0.5107	0.0366
212119_at	RHOQ	ras homolog gene family; member Q	-0.7477	0.0063
212120_at	RHOQ	ras homolog gene family; member Q	-0.7661	0.0011
212122_at	RHOQ	ras homolog gene family; member Q	-0.9147	0.0007
212130_x_at	EIF1	eukaryotic translation initiation factor 1	-0.2185	0.005
212134_at	PHLDB1	pleckstrin homology-like domain; family B; member 1	-0.374	0.0399
212136_at	ATP2B4	ATPase; Ca++ transporting; plasma membrane 4	-0.5396	0.0237
212146_at	PLEKHM2	pleckstrin homology domain containing; family M (with RUN domain) member 2	-0.6854	0.0013
212148_at	PBX1	pre-B-cell leukemia homeobox 1	-1.0845	0.0033
212151_at	PBX1	pre-B-cell leukemia homeobox 1	-0.8588	0.0307
212168_at	RBM12	RNA binding motif protein 12	-0.7721	0.0069
212169_at	FKBP9	FK506 binding protein 9; 63 kDa	-0.4833	0.0449
212185_x_at	MT2A	metallothionein 2A	-0.7562	0.0003
212186_at	ACACA	acetyl-Coenzyme A carboxylase alpha	-0.5098	0.0359
212187_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-5.0038	0
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	-0.9977	0.0306
212192_at	KCTD12	potassium channel tetramerisation domain containing 12	-1.1888	0.0105
212195_at	IL6ST	Interleukin 6 signal transducer (gp130; oncostatin M receptor)	-0.4684	0.0001
212196_at	IL6ST	Interleukin 6 signal transducer (gp130; oncostatin M receptor)	-0.6666	0.0097
212197_x_at	M-RIP	myosin phosphatase-Rho interacting protein	-0.6415	0.0004
212203_x_at	IFITM3	interferon induced transmembrane protein 3 (1-8U)	-0.6621	0.0032
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family; member A1	-3.7727	0.0002
212226_s_at	PPAP2B	phosphatidic acid phosphatase type 2B	-1.5279	0.0008
212227_x_at	EIF1	eukaryotic translation initiation factor 1	-0.2382	0.0031
212230_at	PPAP2B	phosphatidic acid phosphatase type 2B	-1.6512	0.0001
212242_at	TUBA4A	tubulin; alpha 4a	-1.5448	0.0105
212245_at	MCFD2	multiple coagulation factor deficiency 2	-0.3083	0.0045
212246_at	MCFD2	multiple coagulation factor deficiency 2	-0.5651	0.0442
212260_at	TNRC15	trinucleotide repeat containing 15	-0.5538	0.0342

212261_at	TNRC15	trinucleotide repeat containing 15	-0.54	0.0159
212262_at	QKI	quaking homolog; KH domain RNA binding (mouse)	-0.7453	0.014
212266_s_at	SFRS5	splicing factor; arginine/serine-rich 5	-0.3026	0.0219
212268_at	SERPINB1	serpin peptidase inhibitor; clade B (ovalbumin); member 1	-0.6704	0.0286
212270_x_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2248	0.0072
212293_at	HIPK1	homeodomain interacting protein kinase 1	-0.6937	0
212294_at	GNG12	guanine nucleotide binding protein (G protein); gamma 12	-0.7414	0.025
212313_at	CHMP7	CHMP family; member 7	-0.7529	0.0011
212319_at	SGSM2	small G protein signaling modulator 2	-0.7427	0.0004
212325_at	LIMCH1	LIM and calponin homology domains 1	-1.4934	0.0038
212326_at	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	-0.689	0.0004
212327_at	LIMCH1	LIM and calponin homology domains 1	-2.2815	0.0004
212328_at	LIMCH1	LIM and calponin homology domains 1	-1.9823	0.0005
212329_at	SCAP	SREBF chaperone	-1.0199	0.0228
212338_at	MYO1D	myosin ID	-0.8022	0.0355
212345_s_at	CREB3L2	cAMP responsive element binding protein 3-like 2	-0.5739	0.0182
212361_s_at	ATP2A2	ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	-1.6712	0
212386_at	TCF4	transcription factor 4	-0.6011	0.038
212393_at	SBF1	SET binding factor 1	-0.4539	0.0383
212394_at	KIAA0090	KIAA0090	-0.414	0.0007
212397_at	RDX	radixin	-0.8107	0
212398_at	RDX	radixin	-0.9479	0.0132
212401_s_at	CDC2L2	cell division cycle 2-like 2 (PITSLRE proteins)	-0.7609	0.0019
212405_s_at	KIAA0859	KIAA0859	-0.4826	0.0344
212408_at	TOR1AIP1	torsin A interacting protein 1	-0.5923	0.0017
212410_at	EFHA1	EF-hand domain family; member A1	-0.5587	0.0024
212412_at	PDLIM5	PDZ and LIM domain 5	-0.6617	0.0013
212418_at	ELF1	E74-like factor 1 (ets domain transcription factor)	-0.8262	0.003
212419_at	C10orf56	chromosome 10 open reading frame 56	-1.3639	0.0001
212420_at	ELF1	E74-like factor 1 (ets domain transcription factor)	-0.5809	0.0328
212421_at	C22orf9	chromosome 22 open reading frame 9	-0.841	0.0007
212423_at	C10orf56	chromosome 10 open reading frame 56	-0.9251	0.0005
212434_at	GRPEL1	GrpE-like 1; mitochondrial (E. coli)	-0.4919	0.0187
212435_at	TRIM33	tripartite motif-containing 33	-0.3952	0.0079
212440_at	RY1	putative nucleic acid binding protein RY-1	-0.2533	0.0427

212448_at	NEDD4L	neural precursor cell expressed; developmentally down-regulated 4-like	-1.158	0.0058
212450_at	KIAA0256	KIAA0256 gene product	-0.5016	0.0107
212459_x_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	-1.0134	0
212460_at	C14orf147	chromosome 14 open reading frame 147	-0.7747	0.0156
212472_at	MICAL2	microtubule associated monoxygenase; calponin and LIM domain containing 2	-1.084	0
212473_s_at	MICAL2	microtubule associated monoxygenase; calponin and LIM domain containing 2	-1.9271	0.0003
212480_at	SPECC1L	SPECC1-like	-0.6347	0.0453
212490_at	DNAJC8	DnaJ (Hsp40) homolog; subfamily C; member 8	-0.3777	0.0024
212494_at	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	-1.0849	0.0206
212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP); beta	-0.6527	0
212508_at	MOAP1	modulator of apoptosis 1	-0.8711	0.0003
212510_at	GPD1L	glycerol-3-phosphate dehydrogenase 1-like	-0.8313	0.0012
212513_s_at	USP33	ubiquitin specific peptidase 33	-0.2948	0.0458
212516_at	CENTD2	centaurin; delta 2	-0.7565	0.0002
212526_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	-0.7914	0.0075
212527_at	D15Wsu75e	DNA segment; Chr 15; Wayne State University 75; expressed	-1.2374	0.0017
212528_at		CDNA clone IMAGE:3878236	-0.686	0.0264
212530_at	NEK7	NIMA (never in mitosis gene a)-related kinase 7	-0.6443	0.0002
212535_at	MEF2A	myocyte enhancer factor 2A	-0.3973	0.0158
212537_x_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2474	0.0032
212538_at	DOCK9	dedicator of cytokinesis 9	-0.8493	0.0177
212549_at	STAT5B	signal transducer and activator of transcription 5B	-1.512	0
212550_at	STAT5B	signal transducer and activator of transcription 5B	-0.7895	0
212552_at	HPCAL1	hippocalcin-like 1	-0.7869	0.0337
212558_at	SPRY1	sprouty homolog 1; antagonist of FGF signaling (Drosophila)	-1.5959	0.0016
212578_x_at	RPS17	ribosomal protein S17	-0.1284	0.0217
212588_at	PTPRC	protein tyrosine phosphatase; receptor type; C	-1.2756	0.0485
212589_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	-1.087	0.016
212590_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	-0.9043	0.0153
212597_s_at	HMG2L1	high-mobility group protein 2-like 1	-0.6002	0.0101
212603_at	MRPS31	mitochondrial ribosomal protein S31	-0.6243	0.0469
212604_at	MRPS31	mitochondrial ribosomal protein S31	-0.663	0.0413

212605_s_at		AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig	-0.8804	0.0145
212607_at	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B; gamma)	-1.7609	0.0028
212609_s_at	AKT3	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B; gamma)	-2.0669	0
212627_s_at	EXOSC7	exosome component 7	-0.6299	0.0007
212636_at	QKI	quaking homolog; KH domain RNA binding (mouse)	-1.0672	0.0189
212643_at	C14orf32	chromosome 14 open reading frame 32	-0.2448	0.0491
212645_x_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.6865	0
212646_at	RFTN1	raftlin; lipid raft linker 1	-1.5527	0.001
212647_at	RRAS	related RAS viral (r-ras) oncogene homolog	-1.4073	0.0011
212653_s_at	EHBP1	EH domain binding protein 1	-0.9603	0.008
212665_at	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	-4.0215	0
212671_s_at	HLA-DQA1	major histocompatibility complex; class II; DQ alpha 1, major histocompatibility complex; class II; DQ alpha 2, similar to HLA class II histocompatibility antigen; DQ(1) alpha chain precursor (DC-4 alpha chain)	-2.9832	0.0031
212681_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-1.8964	0.0002
212687_at	LIMS1	LIM and senescent cell antigen-like domains 1	-0.8951	0
212693_at	MDN1	MDN1; midasin homolog (yeast)	-0.9676	0.001
212694_s_at	PCCB	propionyl Coenzyme A carboxylase; beta polypeptide	-0.9965	0.0001
212695_at	CRY2	cryptochrome 2 (photolyase-like)	-1.3486	0.0001
212701_at		Clone 23962 mRNA sequence	-0.3815	0.0491
212703_at	TLN2	talin 2	-0.4655	0.0015
212704_at	ZCCHC11	zinc finger; CCHC domain containing 11	-0.5789	0.0307
212705_x_at	PNPLA2	patatin-like phospholipase domain containing 2	-0.3398	0.0384
212707_s_at	FLJ21767	RAS p21 protein activator 4, hypothetical protein FLJ21767	-0.3988	0.0151
212713_at	MFAP4	microfibrillar-associated protein 4	-1.0327	0.0035
212717_at	PLEKHM1	pleckstrin homology domain containing; family M (with RUN domain) member 1	-0.5814	0.0072
212719_at	PHLPP	PH domain and leucine rich repeat protein phosphatase	-1.4423	0.0006
212724_at	RND3	Rho family GTPase 3	-1.1391	0.0189
212731_at	ANKRD46	ankyrin repeat domain 46	-1.0071	0.0017
212740_at	PIK3R4	phosphoinositide-3-kinase; regulatory subunit 4; p150	-0.4488	0.0078
212747_at	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	-1.7921	0

212753_at	PCGF3	polycomb group ring finger 3	-0.7316	0.001
212760_at	UBR2	ubiquitin protein ligase E3 component n-recognin 2	-0.7075	0.0017
212787_at	YLPM1	YLP motif containing 1	-0.5958	0.0062
212793_at	DAAM2	dishevelled associated activator of morphogenesis 2	-2.8119	0.0009
212810_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter); member 4	-1.7868	0.0004
212811_x_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter); member 4	-1.5236	0.0019
212813_at	JAM3	junctional adhesion molecule 3	-1.3751	0.0044
212817_at	DNAJB5	DnaJ (Hsp40) homolog; subfamily B; member 5	-0.4295	0.0334
212823_s_at	PLEKHG3	pleckstrin homology domain containing; family G (with RhoGef domain) member 3	-0.2606	0.0418
212829_at	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase; type II; alpha	-0.9898	0.0116
212841_s_at	PPFIBP2	PTPRF interacting protein; binding protein 2 (liprin beta 2)	-1.1405	0.0106
212845_at	SAMD4A	sterile alpha motif domain containing 4A	-0.8893	0.0247
212848_s_at	C9orf3	chromosome 9 open reading frame 3	-1.5956	0
212856_at	DIP	death-inducing-protein	-3.3266	0
212859_x_at	MT1E	metallothionein 1E	-1.0716	0.0032
212873_at	HMHA1	histocompatibility (minor) HA-1	-0.7792	0.0137
212874_at	APOE	Apolipoprotein E	-0.1934	0.0023
212880_at	WDR7	WD repeat domain 7	-0.5999	0.0012
212883_at	APOE	Apolipoprotein E	-0.4592	0.0001
212884_x_at	APOE	Apolipoprotein E	-0.8054	0.0073
212890_at	MGC15523	hypothetical protein MGC15523	-0.9055	0.0034
212908_at	DNAJC16	DnaJ (Hsp40) homolog; subfamily C; member 16	-0.7702	0.0297
212911_at	DNAJC16	DnaJ (Hsp40) homolog; subfamily C; member 16	-1.3909	0.0001
212912_at	RPS6KA2	ribosomal protein S6 kinase; 90kDa; polypeptide 2	-1.5365	0.008
212914_at	CBX7	chromobox homolog 7	-1.1053	0.0001
212915_at	PDZRN3	PDZ domain containing RING finger 3	-3.4462	0
212923_s_at	C6orf145	chromosome 6 open reading frame 145	-0.9287	0.0012
212928_at	TSPYL4	TSPY-like 4	-1.022	0
212933_x_at	RPL13	ribosomal protein L13	-0.1159	0.048
212939_at	COL6A1	collagen; type VI; alpha 1	-0.1626	0.0003
212946_at	RP11-125A7.3	KIAA0564 protein	-1.2333	0.0004
212947_at	SLC9A8	solute carrier family 9 (sodium/hydrogen exchanger); member 8	-0.6343	0.0013
212950_at	GPR116	G protein-coupled receptor 116	-1.9415	0
212951_at	GPR116	G protein-coupled receptor 116	-1.7063	0.0001

212952_at		Transcribed locus	-0.6582	0.0011
212961_x_at	CXorf40B	chromosome X open reading frame 40B	-1.8444	0
212963_at	TM2D1	TM2 domain containing 1	-0.2017	0.0209
212969_x_at	EML3	echinoderm microtubule associated protein like 3	-0.516	0.0061
212970_at		Full-length cDNA clone CS0DC015YK09 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	-0.6059	0.043
212973_at	RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	-0.4733	0.0458
212974_at	DENND3	DENN/MADD domain containing 3	-0.2487	0.0096
212975_at	DENND3	DENN/MADD domain containing 3	-0.5713	0.0001
212976_at			-0.8256	0.0018
212978_at	LRRC8B	Leucine rich repeat containing 8 family; member B	-2.2097	0
212987_at	FBXO9	F-box protein 9	-0.8615	0
212989_at	SGMS1	sphingomyelin synthase 1	-1.2209	0
212991_at	FBXO9	F-box protein 9	-1.1616	0.0017
212993_at		MRNA; cDNA DKFZp667B1718 (from clone DKFZp667B1718)	-0.8325	0.0163
212998_x_at	HLA-DQB1	major histocompatibility complex; class II; DQ beta 1	-2.4294	0.0081
213003_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP); delta	-0.3454	0
213005_s_at	ANKRD15	ankyrin repeat domain 15	-1.1675	0.0091
213006_at	CEBPD	CCAAT/enhancer binding protein (C/EBP); delta	-1.8387	0.0001
213010_at	PRKCDBP	protein kinase C; delta binding protein	-0.7675	0.0194
213019_at	RANBP6	RAN binding protein 6	-0.3738	0.0123
213020_at	GOSR1	golgi SNAP receptor complex member 1	-0.546	0.0087
213029_at	NFIB	nuclear factor I/B	-0.6873	0.0158
213034_at	KIAA0999	KIAA0999 protein	-0.7129	0.0127
213038_at	RNF19B	ring finger protein 19B	-1.5823	0
213041_s_at	ATP5D	ATP synthase; H+ transporting; mitochondrial F1 complex; delta subunit	-0.2813	0.0458
213056_at	FRMD4B	FERM domain containing 4B	-1.638	0.0003
213058_at	TTC28	tetratricopeptide repeat domain 28	-0.9675	0.0055
213059_at	CREB3L1	cAMP responsive element binding protein 3-like 1	-0.9316	0.0394
213068_at	DPT	dermatopontin	-2.6413	0
213070_at	PIK3C2A	phosphoinositide-3-kinase; class 2; alpha polypeptide	-0.4228	0.0114
213071_at	DPT	dermatopontin	-1.8037	0
213080_x_at	RPL5	ribosomal protein L5	-0.2978	0
213084_x_at	hCG_16001	ribosomal protein L23a, similar to ribosomal protein L23A	-0.1452	0.0035
213087_s_at		CDNA clone IMAGE:4838699	-0.1448	0.0353
213093_at	PRKCA	protein kinase C; alpha	-2.2868	0.0019

213094_at	GPR126	G protein-coupled receptor 126	-1.2716	0
213095_x_at	AIF1	allograft inflammatory factor 1	-2.3329	0
213102_at	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	-0.4565	0.0021
213103_at	STARD13	StAR-related lipid transfer (START) domain containing 13	-1.046	0.0119
213106_at			-1.7064	0.0003
213111_at	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase; type III	-0.4254	0.0441
213132_s_at	MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	-0.5795	0.0302
213146_at	JMJD3	jumonji domain containing 3	-0.823	0.0115
213158_at		Homo sapiens; clone IMAGE:4214654; mRNA	-0.8726	0.0168
213160_at	DOCK2	dedicator of cytokinesis 2	-0.8914	0.034
213179_at	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-0.6234	0.0351
213181_s_at	MOCS1	molybdenum cofactor synthesis 1	-0.8004	0.0405
213182_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57; Kip2)	-3.385	0
213183_s_at	CDKN1C	Cyclin-dependent kinase inhibitor 1C (p57; Kip2)	-2.9501	0
213195_at	LOC201229	hypothetical protein LOC201229	-1.3554	0
213220_at	LOC92482	hypothetical protein LOC92482	-0.3771	0.028
213221_s_at			-1.6631	0
213236_at	SASH1	SAM and SH3 domain containing 1	-0.5039	0.0441
213247_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	-2.4628	0
213252_at	SH3PXD2A	SH3 and PX domains 2A	-0.229	0.0055
213260_at	FOXC1	forkhead box C1	-0.5108	0.0141
213263_s_at	PCBP2	poly(rC) binding protein 2	-0.7139	0.0073
213264_at	PCBP2	poly(rC) binding protein 2	-0.7221	0.0053
213265_at	PGA3	pepsinogen 3; group I (pepsinogen A), pepsinogen 4; group I (pepsinogen A), pepsinogen 5; group I (pepsinogen A)	-0.3348	0.001
213271_s_at	DOPEY1	dopey family member 1	-0.3826	0.025
213273_at	ODZ4	odz; odd Oz/ten-m homolog 4 (Drosophila)	-0.5995	0.0356
213279_at	DHRS1	dehydrogenase/reductase (SDR family) member 1	-1.6049	0
213290_at	COL6A2	collagen; type VI; alpha 2	-0.7719	0.0005
213293_s_at	TRIM22	tripartite motif-containing 22	-2.0877	0.001
213296_at	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	-1.1403	0
213306_at	MPDZ	multiple PDZ domain protein	-1.2956	0.0026
213315_x_at	CXorf40A	chromosome X open reading frame 40A	-1.8197	0
213316_at	KIAA1462	KIAA1462	-0.8787	0.0396
213317_at	CLIC5	chloride intracellular channel 5	-0.6481	0.0192

213318_s_at	BAT3	HLA-B associated transcript 3	-0.3066	0.041
213321_at	BCKDHB	branched chain keto acid dehydrogenase E1; beta polypeptide (maple syrup urine disease)	-0.375	0.0045
213323_s_at	ZC3H7B	zinc finger CCCH-type containing 7B	-0.3427	0.0008
213324_at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	-0.8216	0.0127
213327_s_at	USP12	ubiquitin specific peptidase 12	-0.5155	0.0079
213331_s_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1	-0.6714	0.0388
213344_s_at	H2AFX	H2A histone family; member X	-0.2455	0.0124
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57; Kip2)	-3.7474	0
213350_at	RPS11	Ribosomal protein S11	-0.5498	0.0008
213355_at	ST3GAL6	ST3 beta-galactoside alpha-2;3-sialyltransferase 6	-1.5434	0.0014
213357_at	GTF2H5	general transcription factor IIH; polypeptide 5	-0.6433	0.0001
213366_x_at	ATP5C1	ATP synthase; H+ transporting; mitochondrial F1 complex; gamma polypeptide 1	-0.2512	0.014
213374_x_at	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	-1.7348	0
213375_s_at	CG018	hypothetical gene CG018	-1.0593	0.0064
213379_at	COQ2	coenzyme Q2 homolog; prenyltransferase (yeast)	-0.9064	0.0005
213381_at	C10orf72	Chromosome 10 open reading frame 72	-1.2673	0.0198
213382_at	MST1	macrophage stimulating 1 (hepatocyte growth factor-like), macrophage stimulating; pseudogene 9	-0.1054	0.047
213383_at		Full-length cDNA clone CS0DF026YC16 of Fetal brain of Homo sapiens (human)	-0.2287	0.0279
213398_s_at	C14orf124	chromosome 14 open reading frame 124	-0.5968	0.0021
213403_at		Clone 23908 mRNA sequence	-0.1614	0.0331
213411_at		MRNA; cDNA DKFZp434E0528 (from clone DKFZp434E0528)	-1.5977	0.0007
213413_at	STON1	stonin 1	-2.7396	0
213418_at	HSPA6	heat shock 70kDa protein 6 (HSP70B')	-1.1733	0.0437
213421_x_at	PRSS3	protease; serine; 3 (mesotrypsin)	-0.1537	0.0317
213422_s_at	LOC727882	matrix-remodelling associated 8, similar to matrix-remodelling associated 8	-1.1693	0.0042
213429_at	BICC1	bicaudal C homolog 1 (Drosophila)	-1.9895	0.0001
213450_s_at	ICOSLG	inducible T-cell co-stimulator ligand	-0.5222	0
213469_at	PGAP1	GPI deacylase	-3.0419	0
213489_at	MAPRE2	Microtubule-associated protein; RP/EB family; member 2	-0.683	0.041
213497_at	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	-3.9806	0
213500_at		Clone 24627 mRNA sequence	-1.4364	0.0001

213508_at	C14orf147	chromosome 14 open reading frame 147	-1.3452	0.0005
213519_s_at	LAMA2	laminin; alpha 2 (merosin; congenital muscular dystrophy)	-2.6441	0.0002
213521_at	PTPN18	protein tyrosine phosphatase; non-receptor type 18 (brain-derived)	-0.5009	0.0387
213524_s_at	G0S2	G0/G1switch 2	-2.4084	0.0056
213537_at	HLA-DPA1	major histocompatibility complex; class II; DP alpha 1	-2.6073	0.0006
213540_at	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	-1.6954	0
213547_at	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	-0.8205	0.0134
213550_s_at	TMCO6	transmembrane and coiled-coil domains 6	-0.3002	0.0193
213551_x_at	PCGF2	polycomb group ring finger 2	-0.3948	0.0468
213553_x_at	APOC1	apolipoprotein C-I	-1.9441	0.0005
213554_s_at	CDV3	CDV3 homolog (mouse)	-0.6463	0.0213
213560_at	GADD45B	Growth arrest and DNA-damage-inducible; beta	-0.2584	0.0023
213563_s_at	TUBGCP2	Tubulin; gamma complex associated protein 2	-0.4328	0
213566_at	RNASE6	ribonuclease; RNase A family; k6	-2.6582	0.0001
213572_s_at	SERPINB1	serpin peptidase inhibitor; clade B (ovalbumin); member 1	-1.0509	0.0004
213581_at	PDCD2	programmed cell death 2	-0.732	0.0103
213582_at	ATP11A	ATPase; Class VI; type 11A	-0.329	0.015
213588_x_at	RPL14	ribosomal protein L14	-0.2109	0.0146
213591_at	ALDH7A1	aldehyde dehydrogenase 7 family; member A1	-0.5565	0.001
213604_at	TCEB3	transcription elongation factor B (SIII); polypeptide 3 (110kDa; elongin A)	-0.3828	0.0166
213624_at	SMPDL3A	sphingomyelin phosphodiesterase; acid-like 3A	-1.0285	0.002
213628_at	CLCC1	chloride channel CLIC-like 1	-0.3606	0.0324
213629_x_at	MT1F	metallothionein 1F	-1.4739	0.0057
213636_at	KIAA1045	KIAA1045	-0.1087	0.0424
213648_at	EXOSC7	exosome component 7	-0.6378	0.0068
213661_at	DKFZP586H2123	regeneration associated muscle protease	-1.2533	0.0001
213673_x_at	NENF	Neuron derived neurotrophic factor	-0.2017	0.0111
213674_x_at	IGHD	immunoglobulin heavy constant delta	-0.1015	0.0454
213675_at		CDNA FLJ25106 fis; clone CBR01467	-1.6679	0
213687_s_at	RPL35A	ribosomal protein L35a	-0.3945	0.0015
213695_at	PON3	paraoxonase 3	-1.4617	0.0002
213705_at		CDNA FLJ30007 fis; clone 3NB692000012	-0.5394	0.0024
213706_at	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.5865	0.0005
213711_at	KRT81	keratin 81	-0.1899	0.0364
213715_s_at	ANKRD47	ankyrin repeat domain 47	-0.3626	0.0043

213724_s_at	PDK2	pyruvate dehydrogenase kinase; isozyme 2	-1.1549	0
213732_at	TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	-0.1131	0.016
213733_at	MYO1F	myosin IF	-1.1703	0.0028
213738_s_at	ATP5A1	ATP synthase; H+ transporting; mitochondrial F1 complex; alpha subunit 1; cardiac muscle	-0.1911	0.01
213744_at	ATRNL1	attractin-like 1	-1.6434	0
213755_s_at	SKI	V-ski sarcoma viral oncogene homolog (avian)	-0.1417	0.0288
213764_s_at	MFAP5	microfibrillar associated protein 5	-2.3357	0
213765_at	MFAP5	microfibrillar associated protein 5	-1.8968	0
213768_s_at	ASCL1	achaete-scute complex homolog 1 (Drosophila)	-0.2177	0.0054
213769_at	KSR1	kinase suppressor of ras 1	-0.2226	0.0092
213774_s_at			-0.1295	0.0078
213777_s_at			-0.1086	0.0412
213789_at	TBC1D25	TBC1 domain family; member 25	-0.9056	0.0338
213791_at	PENK	proenkephalin	-2.7119	0
213800_at	CFH	complement factor H	-2.7997	0
213801_x_at	LOC387867	ribosomal protein SA, ribosomal protein SA pseudogene, similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag), similar to laminin receptor 1 (ribosomal protein SA)	-0.2218	0.0227
213806_at	PURA	Purine-rich element binding protein A	-0.103	0.0486
213813_x_at			-0.3617	0.0054
213817_at		CDNA FLJ13601 fis; clone PLACE1010069	-2.0997	0
213819_s_at	FLOT1	Flotillin 1	-0.1336	0.0011
213824_at	OLIG2	oligodendrocyte lineage transcription factor 2	-0.1713	0.0013
213826_s_at			-0.3674	0.0017
213844_at	HOXA5	homeobox A5	-3.8358	0
213847_at	PRPH	peripherin	-0.2524	0.0047
213848_at		MRNA; cDNA DKFZp586F2224 (from clone DKFZp586F2224)	-0.6775	0.0015
213852_at	RBM8A	RNA binding motif protein 8A	-0.6521	0.0093
213854_at	SYNGR1	synaptogyrin 1	-0.3507	0.0049
213862_at	PNPLA2	Patatin-like phospholipase domain containing 2	-0.1677	0.0195
213871_s_at	C6orf108	Chromosome 6 open reading frame 108	-0.2398	0.0038
213883_s_at	TM2D1	TM2 domain containing 1	-0.4477	0.0027
213884_s_at	TRIM3	tripartite motif-containing 3	-0.2163	0.0026
213891_s_at	TCF4	transcription factor 4	-0.735	0.035

213895_at	EMP1	epithelial membrane protein 1	-0.4065	0.0064
213897_s_at	MRPL23	mitochondrial ribosomal protein L23	-1.1041	0.001
213900_at	C9orf61	chromosome 9 open reading frame 61	-0.9422	0.0092
213904_at		Clone 23555 mRNA sequence	-2.0262	0.0026
213905_x_at	BGN	biglycan	-1.1597	0.0148
213907_at	EEF1E1	Eukaryotic translation elongation factor 1 epsilon 1	-0.2326	0.0014
213914_s_at	SPTBN1	Spectrin; beta; non-erythrocytic 1	-0.2014	0.0007
213921_at	SST	somatostatin	-1.1908	0.0001
213923_at	RAP2B	RAP2B; member of RAS oncogene family	-0.7919	0.0223
213933_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-2.019	0.0001
213935_at	ABHD5	abhydrolase domain containing 5	-0.4932	0.0081
213942_at	MEGF6	multiple EGF-like-domains 6	-0.2322	0.0001
213948_x_at	CADM3	cell adhesion molecule 3	-0.1365	0.0357
213952_s_at	ALOX5	Arachidonate 5-lipoxygenase	-0.1322	0.0056
213960_at		CDNA FLJ37610 fis; clone BRCOC2011398	-0.5474	0
213961_s_at			-0.151	0.0095
213967_at	RALYL	RALY RNA binding protein-like	-3.784	0.0001
213969_x_at	RPL29	ribosomal protein L29	-0.2096	0.0016
213970_at	LOC653256	RAB; member of RAS oncogene family-like 3, similar to RAB; member of RAS oncogene family-like 3	-1.5724	0.0001
213974_at	ADAMTSL3	ADAMTS-like 3	-2.2369	0
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	-1.3595	0.0013
213987_s_at	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	-0.1277	0.0496
213988_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	-0.9678	0.0002
213991_s_at	HS3ST1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-0.1498	0.0179
213993_at	SPON1	spondin 1; extracellular matrix protein	-2.0441	0
213994_s_at	SPON1	spondin 1; extracellular matrix protein	-3.3632	0
213999_at	YIPF4	Yip1 domain family; member 4	-0.142	0.0129
214001_x_at		CDNA: FLJ21700 fis; clone COL09849; highly similar to HSU14972 Human ribosomal protein S10 mRNA	-0.2695	0.0056
214005_at	GGCX	gamma-glutamyl carboxylase	-0.7025	0.0193
214012_at	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	-1.1856	0.0127
214014_at	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	-0.2878	0.0001
214022_s_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	-1.1963	0.0055

214024_s_at	DGCR6L	DiGeorge syndrome critical region gene 6-like	-0.1532	0.0011
214027_x_at	DES	desmin, family with sequence similarity 48; member A	-0.3504	0.049
214029_at	SLC25A42	Solute carrier family 25; member 42	-0.1502	0.0067
214030_at	DKFZp667G2110	hypothetical protein DKFZp667G2110	-1.0672	0.0013
214031_s_at	KRT7	Keratin 7	-0.1116	0.036
214038_at	CCL8	chemokine (C-C motif) ligand 8	-2.5479	0
214042_s_at	RPL22	ribosomal protein L22	-0.5279	0.0002
214047_s_at	MBD4	methyl-CpG binding domain protein 4	-0.6657	0.002
214054_at	DOK2	docking protein 2; 56kDa	-0.5874	0.006
214056_at	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	-1.4231	0
214057_at	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	-0.4243	0.002
214064_at	TF	transferrin	-0.2429	0.0018
214066_x_at	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	-1.0032	0
214072_x_at	NENF	Neuron derived neurotrophic factor	-0.2168	0.0094
214073_at	CTTN	cortactin	-1.9811	0.0001
214074_s_at	CTTN	cortactin	-0.983	0.0029
214077_x_at	MEIS3P1	Meis homeobox 3 pseudogene 1	-1.1604	0.0018
214083_at	PPP2R5C	Protein phosphatase 2; regulatory subunit B'; gamma isoform	-1.0296	0
214084_x_at	LOC648998	neutrophil cytosolic factor 1; (chronic granulomatous disease; autosomal 1), neutrophil cytosolic factor 1B pseudogene, neutrophil cytosolic factor 1C pseudogene, similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2)	-0.4561	0.0138
214091_s_at	GPX3	glutathione peroxidase 3 (plasma)	-2.8054	0.0001
214101_s_at		Transcribed locus	-0.4534	0.0272
214103_s_at	RAP2A	RAP2A; member of RAS oncogene family	-0.2229	0.0003
214106_s_at	GMDS	GDP-mannose 4;6-dehydratase	-0.2964	0.0481
214110_s_at	LOC654342	Similar to lymphocyte-specific protein 1	-0.8435	0.0032
214112_s_at	CXorf40A	chromosome X open reading frame 40A, chromosome X open reading frame 40B	-1.6366	0
214115_at	VAMP5	Vesicle-associated membrane protein 5 (myobrevin)	-0.1466	0.0246
214124_x_at	FGFR1OP	FGFR1 oncogene partner	-0.5114	0.034
214127_s_at	ARS2	ARS2 protein	-0.1394	0.0231
214135_at	CLDN18	claudin 18	-0.136	0.0269

214141_x_at	SFRS7	splicing factor; arginine/serine-rich 7; 35kDa	-0.5681	0.0246
214143_x_at	RPL24	ribosomal protein L24, solute carrier family 36 (proton/amino acid symporter); member 2	-0.2102	0.001
214149_s_at	ATP6V0E1	ATPase; H+ transporting; lysosomal 9kDa; V0 subunit e1	-0.4338	0.0212
214153_at	ELOVL5	ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast)	-0.9678	0.0003
214161_at	OSGIN2	Oxidative stress induced growth inhibitor family member 2	-0.105	0.0216
214181_x_at	LST1	leukocyte specific transcript 1	-1.0002	0.0086
214183_s_at	TKTL1	transketolase-like 1	-0.1385	0.0219
214191_at	ICA1	islet cell autoantigen 1; 69kDa	-0.1467	0.0063
214194_at	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	-0.4785	0.0489
214207_s_at	CARD10	Caspase recruitment domain family; member 10	-0.1681	0.0079
214210_at	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein; 34kDa); member 17	-0.5885	0
214211_at	FTH1	ferritin; heavy polypeptide 1, ferritin; heavy polypeptide-like 16	-0.8761	0.0045
214214_s_at	C1QBP	complement component 1; q subcomponent binding protein	-0.5698	0.0005
214231_s_at	RP11-125A7.3	KIAA0564 protein	-0.6805	0.0001
214233_at	GGA2	Golgi associated; gamma adaptin ear containing; ARF binding protein 2	-0.2185	0.0018
214239_x_at	PCGF2	polycomb group ring finger 2	-0.9203	0.0104
214243_s_at	SERHL	serine hydrolase-like, serine hydrolase-like 2	-0.4226	0.0009
214247_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	-3.5191	0
214255_at	ATP10A	ATPase; Class V; type 10A	-3.2664	0
214256_at	ATP10A	ATPase; Class V; type 10A	-0.1802	0.0124
214258_x_at	HTATIP	HIV-1 Tat interacting protein; 60kDa	-0.4022	0.0296
214259_s_at	AKR7A2	aldo-keto reductase family 7; member A2 (aflatoxin aldehyde reductase)	-1.2244	0
214262_at	TRIP6	thyroid hormone receptor interactor 6	-0.1586	0.0108
214265_at	ITGA8	integrin; alpha 8	-1.5206	0.001
214274_s_at	ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	-0.7853	0
214275_at	MED12	Mediator of RNA polymerase II transcription; subunit 12 homolog (S. cerevisiae)	-0.1267	0.0008
214278_s_at	NDRG2	NDRG family member 2	-0.2279	0.0003
214279_s_at	NDRG2	NDRG family member 2	-2.4094	0.0003
214309_s_at	C21orf2	Chromosome 21 open reading frame 2	-0.1308	0.0271
214317_x_at	RPS9	ribosomal protein S9	-0.165	0.002

214321_at	NOV	nephroblastoma overexpressed gene	-3.0072	0.004
214325_at	GP2	glycoprotein 2 (zymogen granule membrane)	-0.1077	0.0204
214326_x_at	JUND	jun D proto-oncogene	-0.7003	0.008
214327_x_at	TPT1	tumor protein; translationally-controlled 1	-0.147	0.0216
214329_x_at	TNFSF10	tumor necrosis factor (ligand) superfamily; member 10	-1.4974	0.0002
214330_at	ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2	-0.5802	0
214342_at	ATXN7L1	ataxin 7-like 1	-0.1318	0.028
214344_at	LOC92973	hypothetical protein LOC92973	-0.1508	0.0031
214347_s_at	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	-0.1846	0.0046
214350_at	SNTB2	Syntrophin; beta 2 (dystrophin-associated protein A1; 59kDa; basic component 2)	-0.1284	0.0362
214360_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-0.105	0.01
214366_s_at	ALOX5	arachidonate 5-lipoxygenase	-0.3482	0.0005
214368_at	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-0.3584	0.0114
214369_s_at	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-1.0093	0
214379_at		Transcribed locus	-0.2049	0.005
214382_at	UNC93A	unc-93 homolog A (C. elegans)	-0.1262	0.0337
214391_x_at	PTGER1	prostaglandin E receptor 1 (subtype EP1); 42kDa	-0.1143	0.0221
214393_at	RND2	Rho family GTPase 2	-0.1581	0.0081
214394_x_at	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein), eukaryotic translation elongation factor 1 delta pseudogene 1	-0.3126	0.0232
214395_x_at		CDNA clone IMAGE:4838699	-0.2429	0.0333
214396_s_at	MBD2	methyl-CpG binding domain protein 2	-0.1246	0.0228
214399_s_at	KRT4	Keratin 4	-0.1033	0.043
214404_x_at	SPDEF	SAM pointed domain containing ets transcription factor	-0.2733	0.004
214414_x_at	HBA2	hemoglobin; alpha 2	-1.3601	0.0196
214417_s_at	FETUB	Fetuin B	-0.103	0.0239
214424_s_at		CDNA FLJ46657 fis; clone TRACH3006264	-0.1053	0.0378
214429_at	MTMR6	myotubularin related protein 6	-1.0387	0
214433_s_at	SELENBP1	selenium binding protein 1	-2.9006	0
214434_at	HSPA12A	heat shock 70kDa protein 12A	-1.2313	0.0208
214439_x_at	BIN1	bridging integrator 1	-1.6205	0.0037
214446_at	ELL2	elongation factor; RNA polymerase II; 2	-1.3629	0
214449_s_at	RHOQ	ras homolog gene family; member Q	-0.6053	0.0406

214451_at	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	-0.2919	0.0012
214454_at	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif; 2	-0.4785	0
214456_x_at	SAA1	serum amyloid A1	-1.014	0
214457_at	HOXA2	homeobox A2	-0.9483	0
214467_at	GPR65	G protein-coupled receptor 65	-0.6414	0.0233
214480_at	ETV3	ets variant gene 3	-0.1214	0.0067
214490_at	ARSF	arylsulfatase F	-0.2375	0.0073
214503_x_at	GPR135	G protein-coupled receptor 135	-0.138	0.047
214506_at	ADMR	adrenomedullin receptor	-0.5037	0
214508_x_at	CREM	cAMP responsive element modulator	-3.3046	0
214521_at	HES2	hairy and enhancer of split 2 (Drosophila)	-0.1659	0.0071
214524_at	GHRH	growth hormone releasing hormone	-0.2051	0.0024
214528_s_at	PAX8	paired box 8	-0.2128	0.0002
214534_at	HIST1H1B	histone cluster 1; H1b	-0.169	0.0029
214535_s_at	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif; 2	-0.2164	0.0009
214536_at	SLURP1	secreted LY6/PLAUR domain containing 1	-0.1755	0.038
214538_x_at	RGS6	regulator of G-protein signaling 6	-0.1419	0.0124
214565_s_at	SMR3A	submaxillary gland androgen regulated protein 3 homolog A (mouse), submaxillary gland androgen regulated protein 3 homolog B (mouse)	-0.4011	0
214574_x_at	LST1	leukocyte specific transcript 1	-1.1403	0.0019
214583_at	DDI2	DDI1; DNA-damage inducible 1; homolog 2 (S. cerevisiae)	-0.8822	0
214585_s_at	VPS52	vacuolar protein sorting 52 homolog (S. cerevisiae)	-0.6178	0.0008
214589_at	FGF12	fibroblast growth factor 12	-1.7715	0
214591_at	KLHL4	kelch-like 4 (Drosophila)	-4.2891	0
214599_at	IVL	involucrin	-0.1883	0.0181
214602_at	COL4A4	collagen; type IV; alpha 4	-1.8991	0
214607_at	PAK3	p21 (CDKN1A)-activated kinase 3	-0.7626	0.001
214609_at	PHOX2A	paired-like homeobox 2a	-0.3761	0.0009
214610_at	CYP11B1	cytochrome P450; family 11; subfamily B; polypeptide 1	-3.3192	0.0058
214622_at	CYP21A2	cytochrome P450; family 21; subfamily A; polypeptide 2	-1.7906	0.0216
214625_s_at	MINK1	misshapen-like kinase 1 (zebrafish)	-0.2566	0.0284
214630_at	CYP11B2	cytochrome P450; family 11; subfamily B; polypeptide 2	-1.5415	0.0311
214635_at	CLDN9	claudin 9	-0.1824	0.0422
214636_at	CALCB	calcitonin-related polypeptide; beta	-0.1482	0.0036
214637_at	OSM	oncostatin M	-0.1273	0.0487
214641_at	COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	-1.7863	0

214643_x_at	BIN1	bridging integrator 1	-0.4348	0.0256
214648_at	GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	-0.1383	0.0199
214665_s_at	CHP	calcium binding protein P22	-0.2823	0.0223
214674_at	USP19	ubiquitin specific peptidase 19	-0.4813	0
214683_s_at	CLK1	CDC-like kinase 1	-0.9496	0
214684_at	MEF2A	myocyte enhancer factor 2A	-0.3789	0.0184
214688_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	-0.2383	0.0027
214689_at	PAPPA2	pappalysin 2	-0.1976	0.0108
214696_at	MGC14376	hypothetical protein MGC14376	-2.5527	0
214708_at	SNTB1	syntrophin; beta 1 (dystrophin-associated protein A1; 59kDa; basic component 1)	-1.8689	0.0012
214713_at	YLPM1	YLP motif containing 1	-0.2577	0.0173
214721_x_at	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	-1.253	0
214724_at	DIXDC1	DIX domain containing 1	-1.1448	0.0115
214733_s_at	YIPF1	Yip1 domain family; member 1	-0.4274	0.0229
214744_s_at		Transcribed locus; strongly similar to XP_001102967.1 similar to 60S ribosomal protein L23 [Macaca mulatta]	-0.7108	0
214770_at	MSR1	macrophage scavenger receptor 1	-1.9671	0.0004
214771_x_at	M-RIP	myosin phosphatase-Rho interacting protein	-0.6034	0.0006
214774_x_at	TOX3	TOX high mobility group box family member 3	-0.4443	0.0116
214779_s_at	SGSM3	small G protein signaling modulator 3	-0.6143	0.0068
214792_x_at	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	-1.2094	0.0007
214801_at		CDNA FLJ11392 fis; clone HEMBA1000575	-0.8137	0.0007
214805_at	EIF4A1	Eukaryotic translation initiation factor 4A; isoform 1	-1.4415	0.0008
214822_at	FAM5B	family with sequence similarity 5; member B	-1.3663	0
214823_at	ZNF204	zinc finger protein 204	-0.7661	0.0348
214824_at			-0.2362	0.001
214835_s_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	-1.0389	0
214847_s_at	GPSM3	G-protein signaling modulator 3 (AGS3-like; C. elegans)	-0.2441	0.0205
214858_at		Pp14571	-0.163	0.0018
214864_s_at	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.5842	0.0124
214880_x_at	CALD1	caldesmon 1	-0.4563	0.0144
214894_x_at	MACF1	microtubule-actin crosslinking factor 1	-0.6142	0.0007
214910_s_at	APOM	apolipoprotein M	-0.394	0.0001

214919_s_at	EIF4EBP3	MASK-4E-BP3 alternate reading frame gene, eukaryotic translation initiation factor 4E binding protein 3	-1.1281	0.0012
214921_at	KCNMA1	potassium large conductance calcium-activated channel; subfamily M; alpha member 1	-0.1225	0.0497
214940_s_at	SMG6	Smg-6 homolog; nonsense mediated mRNA decay factor (C. elegans)	-0.3813	0.0031
214945_at	LOC202134	NY-REN-7 antigen, hypothetical protein LOC202134, hypothetical protein LOC653316	-2.4362	0.0015
214955_at	TMPRSS6	transmembrane protease; serine 6	-0.1821	0.0271
214956_at	AAK1	AP2 associated kinase 1	-0.2219	0.013
214957_at	ACTL8	actin-like 8	-0.1652	0.0333
214965_at	SPATA2L	spermatogenesis associated 2-like	-1.2032	0.0001
214979_at	ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	-0.1776	0.0033
214990_at			-0.2208	0.0421
214998_at	AAK1	AP2 associated kinase 1	-0.1665	0.0034
215000_s_at	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)	-0.761	0.0025
215001_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	-1.1124	0.0004
215016_x_at	DST	dystonin	-0.5202	0.0306
215019_x_at	ZNF528	zinc finger protein 528	-0.1994	0.0147
215025_at	NTRK3	neurotrophic tyrosine kinase; receptor; type 3	-0.165	0.01
215028_at	SEMA6A	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6A	-4.1665	0
215034_s_at	TM4SF1	transmembrane 4 L six family member 1	-2.7156	0.0001
215036_at		Immunoglobulin anti-HBsAg lambda light chain (LM25)	-0.1317	0.005
215041_s_at	DOCK9	dedicator of cytokinesis 9	-0.1353	0.0134
215042_at	BMP6	bone morphogenetic protein 6	-0.1687	0.0072
215049_x_at	CD163	CD163 molecule	-3.0707	0
215050_x_at	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	-0.7372	0.0002
215051_x_at	AIF1	allograft inflammatory factor 1	-2.7352	0
215055_at	B3GNTL1	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase-like 1	-0.2339	0.0021
215061_at	LOC399818	similar to CG9643-PA	-0.1391	0.0285
215065_at	PHF8	PHD finger protein 8	-0.1194	0.0257
215073_s_at	NR2F2	nuclear receptor subfamily 2; group F; member 2	-1.3188	0.0007
215081_at	KIAA1024	KIAA1024 protein	-2.7825	0
215085_x_at	DLEC1	deleted in lung and esophageal cancer 1	-0.2852	0.001
215088_s_at	SDHC	succinate dehydrogenase complex; subunit C; integral membrane protein; 15kDa	-0.5791	0.0114
215091_s_at	GTF3A	general transcription factor IIIA	-0.5952	0.0071

215106_at	TTC22	tetratricopeptide repeat domain 22	-0.1106	0.0222
215108_x_at	TOX3	TOX high mobility group box family member 3	-0.3324	0.0042
215115_x_at	NTRK3	neurotrophic tyrosine kinase; receptor; type 3	-0.2225	0.0105
215129_at	PIK3C2G	phosphoinositide-3-kinase; class 2; gamma polypeptide	-0.2315	0.0002
215137_at	KIAA0508	KIAA0508 protein	-0.1748	0.0156
215141_at	C4orf10	chromosome 4 open reading frame 10	-0.1374	0.0067
215146_s_at	TTC28	tetratricopeptide repeat domain 28	-0.5101	0.0486
215154_at	ULK2	Unc-51-like kinase 2 (C. elegans)	-0.4075	0
215173_at	LRRC50	leucine rich repeat containing 50	-0.1525	0.0107
215183_at		Clone HQ0072	-0.1326	0.0038
215193_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1, major histocompatibility complex; class II; DR beta 3	-2.05	0.0046
215195_at	PRKCA	protein kinase C; alpha	-1.3015	0.0064
215198_s_at	CALD1	caldesmon 1	-0.4972	0.005
215199_at	CALD1	caldesmon 1	-0.9597	0
215217_at			-0.139	0.0182
215225_s_at	GPR17	G protein-coupled receptor 17	-0.1226	0.0091
215237_at	DOCK9	dedicator of cytokinesis 9	-0.1905	0.0106
215243_s_at	GJB3	gap junction protein; beta 3; 31kDa	-0.2113	0.0091
215261_at		Clone 23578 mRNA sequence	-0.1317	0.0265
215265_at	EMX1	empty spiracles homeobox 1	-0.196	0.0084
215266_at	DNAH3	dynein; axonemal; heavy chain 3	-0.1707	0.0195
215271_at	TNN	tenascin N	-0.2484	0
215273_s_at	TADA3L	transcriptional adaptor 3 (NGG1 homolog; yeast)-like	-0.775	0.0039
215288_at	LOC650465	similar to Short transient receptor potential channel 2 (TrpC2) (mTrp2)	-0.1397	0.0005
215292_s_at	MKL1	megakaryoblastic leukemia (translocation) 1	-0.2404	0.0024
215294_s_at	SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	-0.9429	0.0242
215299_x_at	SULT1A1	sulfotransferase family; cytosolic; 1A; phenol-preferring; member 1	-0.9174	0.0284
215305_at	PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	-0.4312	0
215306_at		MRNA; cDNA DKFZp586N2020 (from clone DKFZp586N2020)	-1.1919	0
215311_at		CDNA FLJ37610 fis; clone BRCOC2011398	-0.3622	0
215325_x_at	C19orf26	chromosome 19 open reading frame 26	-0.2335	0.0007
215332_s_at	CD8B	CD8b molecule	-0.1634	0.0287
215333_x_at	GSTM1	glutathione S-transferase M1	-1.3214	0.0393
215353_at			-0.1288	0.0254

215388_s_at	CFH	complement factor H, complement factor H-related 1	-2.2632	0
215389_s_at	TNNT2	troponin T type 2 (cardiac)	-0.2772	0.0003
215393_s_at	COBLL1	COBL-like 1	-0.3995	0
215403_at		CDNA: FLJ21207 fis; clone COL00362	-0.1649	0.0094
215405_at		CDNA: FLJ21419 fis; clone COL04084	-0.101	0.0442
215410_at	LOC392713	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)-like, postmeiotic segregation increased 2-like 1, postmeiotic segregation increased 2-like 2, postmeiotic segregation increased 2-like 5, similar to PMS1 protein homolog 2 (DNA mismatch repair protein PMS2), similar to postmeiotic segregation increased 2-like 2	-0.1483	0.0457
215414_at	FARS2	Phenylalanyl-tRNA synthetase 2; mitochondrial	-0.1754	0.0056
215418_at	PARVA	parvin; alpha	-0.4028	0.0013
215423_at		Cri-du-chat region mRNA; clone NIBB11	-0.3015	0
215442_s_at	TSHR	thyroid stimulating hormone receptor	-0.1422	0.0462
215444_s_at	TRIM31	tripartite motif-containing 31	-0.1364	0.0141
215449_at	BZRPL1	benzodiazapine receptor (peripheral)-like 1	-0.1405	0.0095
215471_s_at	MAP7	microtubule-associated protein 7	-0.4433	0.0019
215479_at		CDNA FLJ20780 fis; clone COL04256	-1.3928	0
215482_s_at	EIF2B4	eukaryotic translation initiation factor 2B; subunit 4 delta; 67kDa	-0.8275	0.0007
215490_at	C1orf69	chromosome 1 open reading frame 69	-0.2596	0.0006
215496_at	SAMD4A	sterile alpha motif domain containing 4A	-0.1469	0.0049
215534_at		MRNA; cDNA DKFZp586C1923 (from clone DKFZp586C1923)	-0.1242	0.018
215543_s_at	LARGE	like-glycosyltransferase	-0.4954	0.0295
215552_s_at	ESR1	estrogen receptor 1	-0.1228	0.0295
215583_at	TMEM63A	Transmembrane protein 63A	-0.2088	0.0225
215584_at	HECW1	HECT; C2 and WW domain containing E3 ubiquitin protein ligase 1	-0.1439	0.0316
215594_at		PTR2 mRNA for repetitive sequence	-0.1072	0.0399
215598_at	TTC12	Tetratricopeptide repeat domain 12	-0.1816	0.0066
215602_at	FGD2	FYVE; RhoGEF and PH domain containing 2	-0.162	0.0152
215610_at	LOC728263	similar to beta-1;4-mannosyltransferase	-0.1537	0.0135
215617_at		CDNA FLJ11754 fis; clone HEMBA1005588	-0.3866	0.0061
215630_at		CDNA FLJ14102 fis; clone MAMMA1000940	-0.1392	0.0181
215633_x_at	LST1	leukocyte specific transcript 1	-0.8485	0.009

215643_at		CDNA FLJ11740 fis; clone HEMBA1005500	-0.3232	0.0001
215646_s_at	VCAN	versican	-2.4715	0.0107
215651_at			-0.1189	0.026
215662_at		CDNA: FLJ21699 fis; clone COL09829	-0.3191	0.0028
215665_at	HSD3B2	hydroxy-delta-5-steroid dehydrogenase; 3 beta- and steroid delta-isomerase 2, similar to 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I (3Beta-HSD I) (Trophoblast antigen FDO161G)	-4.3715	0
215677_s_at	BRF1	BRF1 homolog; subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	-0.139	0.0151
215678_at	LOC440792	proline dehydrogenase (oxidase) 1 pseudogene	-0.1161	0.044
215684_s_at	ASCC2	activating signal cointegrator 1 complex subunit 2	-0.9485	0.0011
215686_x_at	TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	-0.1537	0.0247
215689_s_at	SHBG	sex hormone-binding globulin	-0.1637	0.0118
215693_x_at	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	-0.5549	0.0054
215709_at	PRIM2	primase; DNA; polypeptide 2 (58kDa)	-0.1433	0.0389
215723_s_at	PLD1	phospholipase D1; phosphatidylcholine-specific	-1.186	0.0001
215724_at	PLD1	phospholipase D1; phosphatidylcholine-specific	-0.2265	0.0015
215725_at	DGCR11	DiGeorge syndrome critical region gene 11	-0.2038	0.0429
215726_s_at	CYB5A	cytochrome b5 type A (microsomal)	-2.4928	0
215748_at	FLJ33790	Hypothetical protein FLJ33790	-0.1371	0.0019
215759_at	ANKRD53	ankyrin repeat domain 53	-0.1959	0.0031
215771_x_at	RET	ret proto-oncogene	-0.2918	0.0148
215772_x_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	-0.971	0
215775_at	THBS1	Thrombospondin 1	-0.3979	0
215792_s_at	DNAJC11	DnaJ (Hsp40) homolog; subfamily C; member 11	-0.494	0.0065
215794_x_at	GLUD2	glutamate dehydrogenase 2	-0.8581	0.0221
215800_at	DUOX1	dual oxidase 1	-0.4181	0.0031
215804_at	EPHA1	EPH receptor A1	-0.1496	0.0147
215809_at	CYP2D6	cytochrome P450; family 2; subfamily D; polypeptide 6	-0.1404	0.0229
215834_x_at	SCARB1	scavenger receptor class B; member 1	-1.0513	0.0329
215835_at	SCARB1	scavenger receptor class B; member 1	-0.183	0.0048
215839_at	LILRA5	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 5	-0.1119	0.037
215849_x_at		CDNA FLJ12173 fis; clone MAMMA1000696	-0.2709	0

215865_at	SYT12	Synaptotagmin XII	-0.1725	0.0012
215869_at		CDNA FLJ12192 fis; clone MAMMA1000851	-0.1744	0.011
215872_at			-0.1702	0.0007
215875_at		CDNA: FLJ23167 fis; clone LNG09902	-0.1473	0.04
215881_x_at	LOC652163	similar to synovial sarcoma; X breakpoint 9, synovial sarcoma; X breakpoint 2, synovial sarcoma; X breakpoint 2B, synovial sarcoma; X breakpoint 3, synovial sarcoma; X breakpoint 5, synovial sarcoma; X breakpoint 7, synovial sarcoma; X breakpoint 9	-0.1574	0.0433
215918_s_at	SPTBN1	spectrin; beta; non-erythrocytic 1	-0.8865	0.0003
215935_at	FAM75A1	family with sequence similarity 75; member A1, family with sequence similarity 75; member A2, family with sequence similarity 75; member A3, family with sequence similarity 75; member A4, family with sequence similarity 75; member A5, family with sequence similarity 75; member A7	-0.1791	0.006
215937_at	PTGDR	prostaglandin D2 receptor (DP)	-0.1831	0.0005
215951_at	TBC1D2B	TBC1 domain family; member 2B	-0.142	0.0065
215963_x_at	LOC642741	similar to ribosomal protein L3 isoform a	-0.2816	0.0023
215975_x_at	GK	glycerol kinase	-0.1551	0.0083
215982_s_at	DOM3Z	dom-3 homolog Z (C. elegans)	-1.4918	0.0011
215983_s_at	UBXD6	UBX domain containing 6	-0.7824	0.0028
216001_at	PRAMEF12	PRAME family member 12	-0.1188	0.0461
216042_at	TNFRSF25	tumor necrosis factor receptor superfamily; member 25	-0.2338	0.0033
216061_x_at	PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	-0.3171	0.0431
216064_s_at	AGA	aspartylglucosaminidase	-1.0914	0.0186
216065_at		Transcribed locus; strongly similar to XP_530916.1 hypothetical protein XP_530916 [Pan troglodytes]	-0.1717	0.0049
216079_at	EPM2A	epilepsy; progressive myoclonus type 2A; Lafora disease (laforin)	-0.135	0.0086
216082_at	NEU3	sialidase 3 (membrane sialidase)	-0.2338	0.0246
216102_at	PHLDB1	pleckstrin homology-like domain; family B; member 1	-0.1852	0.0014
216122_at		CDNA: FLJ20890 fis; clone ADKA03323	-0.1599	0.0317
216133_at		T cell receptor V alpha gene segment V-alpha-w23; clone IGRa01	-0.1266	0.0204
216137_s_at	MAPK8IP3	Mitogen-activated protein kinase 8 interacting protein 3	-0.14	0.0188
216141_at			-0.186	0.0086
216143_at		MRNA; cDNA DKFZp434L092 (from clone DKFZp434L092)	-0.1784	0.0129

216145_at		Velo-cardio-facial syndrome 22q11 region mRNA sequence	-0.1711	0.0124
216152_at		CDNA FLJ11571 fis; clone HEMBA1003328	-0.1282	0.0329
216164_at	LRRN2	leucine rich repeat neuronal 2	-0.1791	0.0061
216177_at	LOC391132	similar to 60S ribosomal protein L29 (P23)	-0.4285	0.0034
216179_x_at		CDNA: FLJ23520 fis; clone LNG04926	-0.1994	0.0085
216182_at	SYNJ2	Synaptojanin 2	-0.156	0.0277
216184_s_at	RIMS1	regulating synaptic membrane exocytosis 1	-0.1597	0.0364
216217_at	PLCL2	phospholipase C-like 2	-0.2376	0.0069
216225_at		Clone IMAGE 25997	-1.1469	0
216233_at	CD163	CD163 molecule	-2.1217	0
216240_at			-0.1412	0.0151
216246_at			-0.3465	0.0037
216248_s_at	NR4A2	nuclear receptor subfamily 4; group A; member 2	-5.8788	0
216253_s_at	PARVB	parvin; beta	-0.3232	0.029
216257_at	HSHUR7SEQ	UV-B repressed sequence; HUR 7	-0.1203	0.0429
216260_at	DICER1	Dicer1; Dcr-1 homolog (Drosophila)	-0.1851	0.0065
216270_at	ILVBL	ilvB (bacterial acetolactate synthase)-like	-0.157	0.0041
216271_x_at	SYDE1	synapse defective 1; Rho GTPase; homolog 1 (C. elegans)	-0.1359	0.0273
216293_at	CLTA	Clathrin; light chain (Lca)	-0.2423	0.0114
216300_x_at	RARA	retinoic acid receptor; alpha	-0.4321	0.0005
216301_at		Ig lambda light chain variable region	-0.1727	0.0151
216308_x_at	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.6263	0.0081
216311_at	LOC644099	similar to ovo-like 2 isoform A	-0.103	0.0428
216324_at			-0.1234	0.0136
216328_at	SIGLEC8	sialic acid binding Ig-like lectin 8	-0.1692	0.0328
216336_x_at	MT1A	metallothionein 1 pseudogene 2, metallothionein 1A, metallothionein 1M	-1.1144	0.0004
216340_s_at	CYP2A7P1	cytochrome P450; family 2; subfamily A; polypeptide 7 pseudogene 1	-0.226	0.0014
216343_at	PCDHGA3	protocadherin gamma subfamily A; 3	-0.1821	0.0009
216348_at	LOC402057	ribosomal protein S17, similar to 40S ribosomal protein S17	-0.4075	0.0018
216349_at	LOC341651	similar to Fumarate hydratase; mitochondrial precursor (Fumarase)	-0.192	0.0235
216350_s_at	ZNF10	zinc finger protein 10	-1.2415	0
216354_at			-0.2141	0.0009
216363_at			-0.2064	0.0022
216365_x_at	CPVL	carboxypeptidase; vitellogenic-like, immunoglobulin lambda locus	-0.133	0.0117

216367_at	COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	-0.1117	0.0117
216369_at			-0.1181	0.0302
216371_at			-0.3419	0.0017
216376_x_at			-0.162	0.0028
216379_x_at	CD24	CD24 molecule	-1.4134	0.0323
216381_x_at	AKR7A3	aldo-keto reductase family 7; member A3 (aflatoxin aldehyde reductase)	-1.6502	0
216382_s_at	TNRC21	trinucleotide repeat containing 21	-0.1492	0.0049
216383_at	hCG_2040224	hCG2040224, ribosomal protein L18a, similar to ribosomal protein L18a, similar to ribosomal protein L18a; 60S ribosomal protein L18a	-0.2044	0.0424
216409_at	ACSL6	Acyl-CoA synthetase long-chain family member 6	-0.1312	0.0365
216410_at	LOC643875	similar to calponin 3; acidic	-0.1259	0.0285
216412_x_at	IVD	Isovaleryl Coenzyme A dehydrogenase	-0.1648	0.0354
216414_at			-0.1373	0.0261
216416_at		CDNA: FLJ23601 fis; clone LNG15501	-0.1301	0.0247
216421_at			-0.338	0.017
216431_at			-0.1202	0.0443
216434_at	FLJ20699	Hypothetical protein FLJ20699	-0.2255	0.0215
216438_s_at	TMSB4X	thymosin-like 3, thymosin; beta 4; X-linked	-0.1737	0.0399
216443_at		CDNA: FLJ20962 fis; clone ADSH00804	-0.1295	0.0232
216451_at	STK38	Serine/threonine kinase 38	-0.1726	0.0379
216456_at		MRNA; cDNA DKFZp761L0812 (from clone DKFZp761L0812); partial cds	-0.2061	0.0103
216457_s_at	SF3A1	splicing factor 3a; subunit 1; 120kDa	-0.7989	0.0114
216477_at			-0.1374	0.0133
216479_at	LOC387753	60S ribosomal protein L21 pseudogene, ribosomal protein L21, ribosomal protein L21 pseudogene, similar to 60S ribosomal protein L21, similar to ribosomal protein L21, similar to ribosomal protein L21 isoform 1	-0.3859	0.0005
216490_x_at	LOC442175	similar to 60S acidic ribosomal protein P2 (NY-REN-44 antigen)	-0.2482	0.0004
216492_at	KIR3DX1	killer cell immunoglobulin-like receptor; three domains; X1	-0.2368	0.0009
216495_x_at	IVD	Isovaleryl Coenzyme A dehydrogenase	-0.1945	0.002
216502_at	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	-0.1541	0.023
216505_x_at	LOC133569	ribosomal protein S10, ribosomal protein S10 pseudogene 3, similar to 40S ribosomal protein S10, similar to ribosomal protein S10	-0.3723	0.0021
216507_at	TAPT1	transmembrane anterior posterior transformation 1	-0.1511	0.038

216513_at	DCT	dopachrome tautomerase (dopachrome delta-isomerase; tyrosine-related protein 2)	-0.1141	0.0409
216516_at			-0.1483	0.0186
216520_s_at	TPT1	tumor protein; translationally-controlled 1	-0.1611	0.0013
216547_at	LOC127406	similar to laminin receptor 1 (ribosomal protein SA)	-0.3	0.0022
216562_at			-0.1618	0.0005
216564_at			-0.1076	0.0345
216565_x_at	LOC391020	interferon induced transmembrane protein pseudogene	-0.4987	0.0035
216566_at		Immunoglobulin (mAb56) light chain V region mRNA; partial sequence	-0.1122	0.0174
216567_at			-0.1248	0.0253
216570_x_at	LOC646417	similar to 60S ribosomal protein L29 (P23)	-0.3828	0.0007
216577_at			-0.1693	0.0236
216580_at	hCG_2015956	hCG2015956, hCG31916, hypothetical LOC120872, hypothetical LOC439954, ribosomal protein L7, similar to 60S ribosomal protein L7	-0.1047	0.0478
216581_at	KRT18P38	keratin 18 pseudogene 38	-0.1147	0.0449
216598_s_at	CCL2	chemokine (C-C motif) ligand 2	-4.9062	0
216613_at		MRNA; cDNA DKFZp566L0824 (from clone DKFZp566L0824)	-0.1109	0.0245
216615_s_at	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	-0.13	0.0218
216623_x_at	TOX3	TOX high mobility group box family member 3	-0.4383	0.0375
216631_s_at	LOC642043	similar to HLA class II histocompatibility antigen; DP alpha chain precursor (HLA-SB alpha chain) (MHC class II DP3-alpha) (DP(W3)) (DP(W4))	-0.1985	0.0164
216635_at		MRNA; cDNA DKFZp566M0524 (from clone DKFZp566M0524)	-0.1268	0.0408
216636_at		MRNA; cDNA DKFZp566M0524 (from clone DKFZp566M0524)	-0.1369	0.0178
216637_at		MRNA; cDNA DKFZp586A0617 (from clone DKFZp586A0617)	-0.1513	0.0145
216650_at	LOC650303	similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP), similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP)	-0.3611	0.0003
216654_at	TNXB	tenascin XB	-0.1502	0.015
216679_at	TIGD1L	tigger transposable element derived 1-like	-0.234	0.0194
216696_s_at	PRODH2	proline dehydrogenase (oxidase) 2	-0.1838	0.0428

216698_x_at	LOC441453	olfactory receptor; family 7; subfamily E; member 18 pseudogene, olfactory receptor; family 7; subfamily E; member 35 pseudogene, olfactory receptor; family 7; subfamily E; member 37 pseudogene, olfactory receptor; family 7; subfamily E; member 47 pseudogene, similar to olfactory receptor; family 7; subfamily A; member 17	-0.2169	0.0409
216700_at	TRIO	Triple functional domain (PTPRF interacting)	-0.1203	0.0135
216703_at			-0.1189	0.0239
216704_at		MRNA; cDNA DKFZp761P1114 (from clone DKFZp761P1114)	-0.1575	0.0081
216707_at		MRNA; cDNA DKFZp761L0812 (from clone DKFZp761L0812); partial cds	-0.192	0.0168
216708_x_at	IGL@	Immunoglobulin lambda locus	-0.2069	0.0073
216710_x_at	ZNF287	zinc finger protein 287	-0.1338	0.013
216715_at			-0.1494	0.0361
216739_at		CDNA: FLJ20874 fis; clone ADKA02818	-0.1261	0.0389
216756_at		CDNA: FLJ21342 fis; clone COL02673	-0.3241	0.0169
216784_at		CDNA: FLJ21769 fis; clone COLF7354	-0.252	0.0218
216790_at		CDNA: FLJ22812 fis; clone KAIA2955	-0.1329	0.0168
216795_at		CDNA: FLJ23194 fis; clone REC00490	-0.1725	0.0106
216800_at		CDNA: FLJ23416 fis; clone HEP20790	-0.1269	0.0353
216806_at	LOC652411	similar to laminin receptor 1 (ribosomal protein SA)	-0.1688	0.0245
216811_at			-0.1336	0.0467
216815_at			-0.1187	0.0124
216817_s_at	OR2H1	olfactory receptor; family 2; subfamily H; member 1	-0.1346	0.0082
216819_at	LOC391076	similar to 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type II (3Beta-HSD II)	-0.4218	0
216823_at	LOC146053	40S ribosomal protein S3a pseudogene, ribosomal protein S3A, similar to 40S ribosomal protein S3a, similar to 40S ribosomal protein S3a (V-fos transformation effector protein), similar to ribosomal protein S3a	-0.3017	0.0001
216824_at			-0.1105	0.0395
216826_at			-0.1723	0.0005
216834_at	RGS1	regulator of G-protein signaling 1	-1.2862	0.0167
216840_s_at	LAMA2	laminin; alpha 2 (merosin; congenital muscular dystrophy)	-2.2635	0.0001
216848_at	KIAA1660	KIAA1660 protein	-0.1437	0.0281
216854_at	GDF11	growth differentiation factor 11	-0.1106	0.0456

216872_at	HR44	Hr44 antigen	-0.1369	0.0013
216875_x_at	HAB1	B1 for mucin	-0.1275	0.0219
216881_x_at	PRB4	proline-rich protein BstNI subfamily 4	-0.4021	0.0035
216886_at	CHRNA4	cholinergic receptor; nicotinic; alpha 4	-0.1128	0.0382
216893_s_at	COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	-0.6882	0
216894_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57; Kip2)	-2.3755	0
216898_s_at	COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	-1.0985	0
216909_at	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	-0.1422	0.007
216914_at	CDC25C	cell division cycle 25 homolog C (S. pombe)	-0.1143	0.0302
216932_at			-0.1094	0.0295
216936_at			-0.2886	0.0014
216938_x_at	DRD2	dopamine receptor D2	-0.1924	0.0058
216946_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	-0.202	0.0015
216953_s_at	WT1	Wilms tumor 1	-0.1316	0.0472
216958_s_at	IVD	isovaleryl Coenzyme A dehydrogenase	-0.9379	0.0101
216962_at	OR5T2	RPA interacting protein, olfactory receptor; family 5; subfamily T; member 2	-0.1989	0.0002
216965_x_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	-0.3088	0.0001
216979_at	NR4A3	nuclear receptor subfamily 4; group A; member 3	-1.8729	0
216981_x_at	SPN	sialophorin (leukosialin; CD43)	-0.2171	0.0033
216991_at	ZNF224	zinc finger protein 224	-0.115	0.0292
217000_at	KRT18P50	keratin 18 pseudogene 50	-0.1801	0.0188
217001_x_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	-0.1837	0.0081
217004_s_at	MCF2	MCF.2 cell line derived transforming sequence	-1.7667	0.0098
217005_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	-0.1471	0.0067
217014_s_at	AZGP1	alpha-2-glycoprotein 1; zinc-binding, similar to alpha-2-glycoprotein 1; zinc	-0.2317	0.0175
217015_at	LOC727842	similar to retinoblastoma binding protein 4	-0.115	0.0149
217017_at	OSBPL10	oxysterol binding protein-like 10	-0.183	0.0013
217021_at	CYB5A	cytochrome b5 type A (microsomal)	-0.186	0.0016
217035_at		Immunoglobulin heavy chain variable region (clone Agamma5-3)	-0.2666	0.0041
217036_at		Immunoglobulin kappa chain; V-region (SPK.3)	-0.1776	0.0039
217041_at	NPTXR	neuronal pentraxin receptor	-0.2037	0.008
217047_s_at	FAM13A1	family with sequence similarity 13; member A1	-0.5997	0.05
217058_at	GNAS	GNAS complex locus	-0.2552	0.0312
217072_at	CD300A	CD300a molecule	-0.1092	0.0191

217083_at	MAPKAPK5	Mitogen-activated protein kinase-activated protein kinase 5	-0.1183	0.0152
217087_at	C1orf68	chromosome 1 open reading frame 68	-0.1667	0.0016
217088_s_at	NCR1	natural cytotoxicity triggering receptor 1	-0.1729	0.0016
217095_x_at	NCR1	natural cytotoxicity triggering receptor 1	-0.2392	0.0009
217103_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	-0.1544	0.0097
217113_at	AMACR	alpha-methylacyl-CoA racemase	-0.1188	0.0175
217118_s_at	C22orf9	chromosome 22 open reading frame 9	-1.2137	0.004
217120_s_at	MED14	mediator complex subunit 14	-0.1511	0.0058
217122_s_at	LOC728661	similar to solute carrier family 35; member E2, solute carrier family 35; member E2	-0.5476	0.0142
217127_at	CTH	cystathionase (cystathionine gamma-lyase)	-5.9921	0
217131_at			-0.1903	0.0052
217144_at	LOC648390	similar to ubiquitin B precursor, ubiquitin B	-0.5153	0.0386
217149_x_at	TNK1	tyrosine kinase; non-receptor; 1	-0.1831	0.0172
217153_at	ARHGAP1	Rho GTPase activating protein 1	-0.1373	0.0073
217156_at			-0.2192	0.0268
217159_x_at	SIGLEC7	sialic acid binding Ig-like lectin 7	-0.1774	0.0269
217162_at	TSPY1	testis specific protein; Y-linked 1	-0.1764	0.0165
217165_x_at	MT1F	metallothionein 1F	-1.5125	0.003
217174_s_at	APC2	adenomatosis polyposis coli 2	-0.1118	0.0388
217177_s_at		CDNA FLJ13658 fis; clone PLACE1011567	-0.5186	0
217182_at	MUC5AC	mucin 5AC; oligomeric mucus/gel-forming	-0.2342	0.0205
217187_at	MUC5AC	mucin 5AC; oligomeric mucus/gel-forming	-0.243	0.0492
217190_x_at	ESR1	estrogen receptor 1	-0.1569	0.0025
217193_x_at	IL8	Interleukin 8	-0.181	0.0094
217198_x_at	IGH@	immunoglobulin heavy constant delta, immunoglobulin heavy constant gamma 1 (G1m marker), immunoglobulin heavy locus, immunoglobulin heavy variable 4-31	-0.1848	0.0058
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	-1.0653	0.0264
217205_at			-0.1881	0.0012
217207_s_at	BTNL3	butyrophilin-like 3	-0.2282	0.027
217217_at	SKAP2	Immunoglobulin epsilon chain, Src kinase associated phosphoprotein 2	-0.1331	0.0041
217219_at	DKFZP434A062	DKFZP434A062 protein	-0.2758	0.0068
217230_at	VIL2	villin 2 (ezrin)	-0.2097	0.0006
217232_x_at	HBB	hemoglobin; beta	-1.7628	0.0245
217233_at			-0.1524	0.023
217252_at	SQSTM1	sequestosome 1	-0.1001	0.0362

217263_x_at	RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	-0.1533	0.004
217266_at	LOC646672	ribosomal protein L15, similar to ribosomal protein L15	-0.3347	0.0322
217273_at	LOC645399	PRAME family member 10, similar to PRAME family member 10	-0.113	0.0347
217283_at		Homeobox protein Og12 (OGL12)	-0.168	0.0149
217286_s_at	NDRG3	NDRG family member 3	-0.4187	0.0479
217291_at	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	-0.1452	0.0032
217303_s_at	ADRB3	adrenergic; beta-3-; receptor	-0.1202	0.0376
217307_at			-0.1829	0.018
217332_at	LOC647288	similar to CTAGE family; member 5	-0.1206	0.0403
217333_at	KRT18P44	keratin 18 pseudogene 44	-0.159	0.0189
217336_at	LOC133569	hypothetical LOC376693, ribosomal protein S10, ribosomal protein S10 pseudogene 3, similar to 40S ribosomal protein S10, similar to ribosomal protein S10	-0.4466	0.0413
217340_at	LOC645452	similar to 60S ribosomal protein L21	-0.2523	0.0004
217341_at			-0.2174	0.0454
217347_at	LOC643653	similar to 60S ribosomal protein L35	-0.3369	0.0083
217350_at	KRT19P2	keratin 19 pseudogene 2	-0.1134	0.022
217358_at	DNAJC16	DnaJ (Hsp40) homolog; subfamily C; member 16	-0.1674	0.0158
217361_at			-0.1237	0.0394
217362_x_at	HLA-DRB6	major histocompatibility complex; class II; DR beta 6 (pseudogene)	-0.8866	0.0032
217363_x_at			-0.3178	0
217367_s_at	ZHX3	zinc fingers and homeoboxes 3	-0.5506	0.0382
217377_x_at	NTRK3	neurotrophic tyrosine kinase; receptor; type 3	-0.3524	0.0013
217379_at	LOC442171	similar to ribosomal protein L10	-0.4023	0.0027
217388_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	-1.9463	0.0003
217395_at	MT4	metallothionein 4	-0.1279	0.0196
217397_at	TRA@	T cell receptor V alpha gene segment V-alpha-w24; clone IGRa02, T cell receptor alpha locus	-0.1237	0.0304
217408_at	MRPS18B	mitochondrial ribosomal protein S18B	-0.2351	0.0404
217412_at		Rearranged T-cell receptor alpha chain mRNA; variable region	-0.1053	0.0075
217413_s_at	TNXB	tenascin XB	-0.1393	0.0387
217414_x_at	HBA1	hemoglobin; alpha 1, hemoglobin; alpha 2	-1.371	0.0325
217421_at	PIWIL2	piwi-like 2 (Drosophila)	-0.159	0.0014
217425_at	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	-1.1314	0
217433_at	TACC1	transforming; acidic coiled-coil containing protein 1	-0.127	0.0433
217434_at	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	-2.6817	0.0019

217449_at		MRNA; cDNA DKFZp434D1516 (from clone DKFZp434D1516)	-0.1138	0.0394
217452_s_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 2	-0.3813	0.0036
217454_at			-0.1634	0.0295
217459_at		MRNA; cDNA DKFZp434L1016 (from clone DKFZp434L1016)	-0.1701	0.0075
217464_at			-0.2217	0.0027
217473_x_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1	-0.2247	0.0255
217478_s_at	HLA-DMA	major histocompatibility complex; class II; DM alpha	-2.5251	0.0009
217493_x_at	NCR2	natural cytotoxicity triggering receptor 2	-0.1495	0.0464
217499_x_at	OR7E37P	olfactory receptor; family 7; subfamily E; member 37 pseudogene	-0.9575	0.0385
217504_at	ABCA6	ATP-binding cassette; sub-family A (ABC1); member 6	-1.3988	0
217507_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1	-0.3759	0.0059
217513_at	C17orf60	chromosome 17 open reading frame 60	-0.198	0.0352
217515_s_at	CACNA1S	calcium channel; voltage-dependent; L type; alpha 1S subunit	-0.2368	0.0031
217525_at	OLFML1	olfactomedin-like 1	-1.1436	0
217532_x_at		Transcribed locus	-0.31	0.0002
217546_at	MT1M	metallothionein 1M	-3.5843	0
217559_at	RPL10L	ribosomal protein L10-like	-0.3058	0.0006
217570_x_at			-0.1575	0.0045
217582_at			-0.2059	0.0065
217584_at	NPC1	Niemann-Pick disease; type C1	-2.6289	0
217590_s_at	TRPA1	transient receptor potential cation channel; subfamily A; member 1	-0.1248	0.0082
217597_x_at	RAB40B	RAB40B; member RAS oncogene family	-0.2445	0.0119
217600_at	SCUBE3	Signal peptide; CUB domain; EGF-like 3	-0.2324	0.0007
217604_at		Transcribed locus	-0.6926	0.0361
217614_at		Transcribed locus	-0.1429	0.0135
217616_at		Transcribed locus	-0.1353	0.0205
217622_at	RHBDD3	rhomboid domain containing 3	-0.293	0.025
217625_x_at		Homo sapiens; clone IMAGE:3851018; mRNA	-0.4894	0.046
217629_at		Transcribed locus	-0.137	0.0122
217631_at	GTPBP4	GTP binding protein 4	-1.1499	0
217633_at	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	-0.2245	0.0006
217634_at	LOC645954	similar to supervillin isoform 2	-0.1443	0.0159
217641_at	GPR135	G protein-coupled receptor 135	-0.4884	0.0012
217645_at	C14orf112	chromosome 14 open reading frame 112	-1.8957	0

217647_at		CDNA FLJ40920 fis; clone UTERU2005905	-0.1211	0.0495
217649_at	LOC732229	Similar to Zinc finger A20 domain-containing protein 2 (Zinc finger protein 216)	-1.6808	0.0002
217652_at	KIAA0892	KIAA0892	-0.105	0.0019
217670_at	RPLP2	Ribosomal protein; large; P2	-0.2495	0.0001
217672_x_at			-0.2009	0.0115
217674_at		Transcribed locus	-0.1464	0.0115
217676_at		Transcribed locus; moderately similar to XP_001090216.1 ATP synthase; H+ transporting; mitochondrial F1 complex; O subunit (oligomycin sensitivity conferring protein) [Macaca mulatta]	-0.1886	0.0034
217681_at	LOC647836	similar to wingless-type MMTV integration site family; member 7B precursor, wingless-type MMTV integration site family; member 7B	-0.1894	0.0204
217683_at	HBE1	Hemoglobin; epsilon 1	-0.1167	0.0001
217685_at	SLC16A3	Solute carrier family 16; member 3 (monocarboxylic acid transporter 4)	-0.1752	0.0069
217687_at	ADCY2	adenylate cyclase 2 (brain)	-0.1754	0.003
217689_at	PTPN1	Protein tyrosine phosphatase; non-receptor type 1	-0.1478	0.0372
217702_at	IL27RA	interleukin 27 receptor; alpha	-0.1818	0.0104
217707_x_at	SMARCA2	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 2	-0.8026	0.0044
217708_x_at		Transcribed locus	-0.1708	0.044
217710_x_at	ITPK1	inositol 1;3;4-triphosphate 5/6 kinase	-0.1766	0.0286
217719_at	EIF3EIP	eukaryotic translation initiation factor 3; subunit E interacting protein	-0.5557	0.0009
217721_at		Full-length cDNA clone CS0DB003YD12 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	-0.2236	0.0271
217723_x_at			-0.1635	0.0409
217728_at	S100A6	S100 calcium binding protein A6	-1.8237	0.0017
217730_at	TMBIM1	transmembrane BAX inhibitor motif containing 1	-1.4268	0.0003
217731_s_at	ITM2B	integral membrane protein 2B	-0.2538	0.0243
217732_s_at	ITM2B	integral membrane protein 2B	-0.3462	0.0032
217734_s_at	WDR6	WD repeat domain 6	-0.726	0.0143
217738_at	PBEF1	pre-B-cell colony enhancing factor 1	-0.53	0.033
217739_s_at	PBEF1	pre-B-cell colony enhancing factor 1	-0.8235	0.0015
217741_s_at	ZFAND5	zinc finger; AN1-type domain 5	-1.291	0
217747_s_at	RPS9	ribosomal protein S9	-0.323	0.0075
217757_at	A2M	alpha-2-macroglobulin	-0.6772	0.0079
217762_s_at	RAB31	RAB31; member RAS oncogene family	-0.8607	0.0113

217763_s_at	RAB31	RAB31; member RAS oncogene family	-0.9226	0.0229
217764_s_at	RAB31	RAB31; member RAS oncogene family	-1.0361	0.003
217766_s_at	TMEM50A	transmembrane protein 50A	-0.9233	0.0021
217767_at	LOC653879	similar to Complement C3 precursor	-3.3996	0.0017
217771_at	GOLM1	golgi membrane protein 1	-1.0855	0.0044
217774_s_at	HSPC152	hypothetical protein HSPC152	-0.1753	0.0452
217779_s_at	PNRC2	proline-rich nuclear receptor coactivator 2	-0.4363	0.019
217783_s_at	YPEL5	yippee-like 5 (Drosophila)	-0.5184	0.0015
217797_at	UFC1	ubiquitin-fold modifier conjugating enzyme 1	-0.5455	0.0001
217806_s_at	POLDIP2	polymerase (DNA-directed); delta interacting protein 2	-0.7885	0.0001
217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.3087	0.0115
217817_at	ARPC4	actin related protein 2/3 complex; subunit 4; 20kDa	-0.3681	0.0427
217824_at	UBE2J1	ubiquitin-conjugating enzyme E2; J1 (UBC6 homolog; yeast)	-1.2814	0
217825_s_at	UBE2J1	ubiquitin-conjugating enzyme E2; J1 (UBC6 homolog; yeast)	-1.1572	0
217830_s_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-0.8828	0.001
217831_s_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-0.4851	0.0093
217837_s_at	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	-0.4367	0.006
217838_s_at	EVL	Enah/Vasp-like	-0.7364	0.0173
217843_s_at	MED4	mediator complex subunit 4	-0.5145	0.0279
217844_at	CTDSP1	CTD (carboxy-terminal domain; RNA polymerase II; polypeptide A) small phosphatase 1	-0.3567	0.0258
217845_x_at	HIGD1A	HIG1 domain family; member 1A	-0.3814	0.0134
217848_s_at	PPA1	pyrophosphatase (inorganic) 1	-0.5851	0.0046
217850_at	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	-0.4103	0.0337
217853_at	TNS3	tensin 3	-0.8585	0.0467
217868_s_at	METTL9	methyltransferase like 9	-0.4637	0.0088
217874_at	SUCLG1	succinate-CoA ligase; GDP-forming; alpha subunit	-0.4095	0.0038
217875_s_at	TMEPAI	transmembrane; prostate androgen induced RNA	-2.021	0
217886_at	EPS15	epidermal growth factor receptor pathway substrate 15	-1.1077	0.0001
217887_s_at	EPS15	epidermal growth factor receptor pathway substrate 15	-0.8297	0.0006
217889_s_at	CYBRD1	cytochrome b reductase 1	-2.5295	0
217890_s_at	PARVA	parvin; alpha	-1.9599	0
217892_s_at	LIMA1	LIM domain and actin binding 1	-1.2615	0.0086
217894_at	KCTD3	potassium channel tetramerisation domain containing 3	-0.7393	0.0112
217908_s_at	IQWD1	IQ motif and WD repeats 1	-0.9578	0.0006
217922_at	MAN1A2	mannosidase; alpha; class 1A; member 2	-0.9257	0.0001

217923_at	PEF1	penta-EF-hand domain containing 1	-0.4006	0.0237
217932_at	MRPS7	mitochondrial ribosomal protein S7	-0.7242	0.0048
217955_at	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-0.8168	0.0013
217958_at	TRAPPC4	trafficking protein particle complex 4	-0.3355	0.0319
217964_at	TTC19	tetratricopeptide repeat domain 19	-0.7237	0
217969_at	C11orf2	chromosome 11 open reading frame2	-1.2013	0.0001
217980_s_at	MRPL16	mitochondrial ribosomal protein L16	-0.8333	0
217987_at	ASNSD1	asparagine synthetase domain containing 1	-0.4553	0.0005
217995_at	SQRDL	sulfide quinone reductase-like (yeast)	-2.0792	0.0002
217996_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-2.0997	0.01
218004_at	BSDC1	BSD domain containing 1	-0.5145	0.0053
218016_s_at	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	-0.6888	0.006
218026_at	CCDC56	coiled-coil domain containing 56	-0.4256	0.0039
218031_s_at	FOXN3	forkhead box N3	-0.9807	0.0016
218032_at	SNN	stannin	-0.7888	0.0034
218035_s_at	FLJ20273	RNA-binding protein	-0.6209	0.0319
218041_x_at	SLC38A2	solute carrier family 38; member 2	-0.3623	0.0382
218043_s_at	AZI2	5-azacytidine induced 2	-0.56	0.0003
218044_x_at	PTMS	parathymosin	-0.1951	0.0112
218047_at	OSBPL9	oxysterol binding protein-like 9	-0.5632	0.0055
218050_at	UFM1	ubiquitin-fold modifier 1	-0.4537	0.0128
218062_x_at	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4	-1.601	0
218065_s_at	TMEM9B	TMEM9 domain family; member B	-0.5395	0.0021
218072_at	COMMD9	COMM domain containing 9	-0.6504	0.0005
218077_s_at	ZDHHC3	zinc finger; DHHC-type containing 3	-0.5632	0.0015
218078_s_at	ZDHHC3	zinc finger; DHHC-type containing 3	-1.2043	0
218087_s_at	SORBS1	sorbin and SH3 domain containing 1	-2.618	0
218091_at	HRB	HIV-1 Rev binding protein	-0.759	0.002
218098_at	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	-0.4949	0.0019
218101_s_at	NDUFC2	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 2; 14.5kDa	-0.4664	0
218103_at	FTSJ3	FtsJ homolog 3 (E. coli)	-0.5038	0.0132
218109_s_at	MFSD1	major facilitator superfamily domain containing 1	-0.3491	0.0405
218124_at	RETSAT	retinol saturase (all-trans-retinol 13;14-reductase)	-1.4313	0
218150_at	ARL5A	ADP-ribosylation factor-like 5A	-0.4995	0.0002
218153_at	CARS2	cysteinyl-tRNA synthetase 2; mitochondrial (putative)	-0.7567	0.0078
218157_x_at	CDC42SE1	CDC42 small effector 1	-0.4689	0.0006

218162_at	OLFML3	olfactomedin-like 3	-4.7311	0
218164_at	SPATA20	spermatogenesis associated 20	-1.5534	0.0011
218166_s_at	RSF1	remodeling and spacing factor 1	-0.6483	0.0249
218168_s_at	CABC1	chaperone; ABC1 activity of bc1 complex homolog (S. pombe)	-1.2014	0.0021
218177_at	CHMP1B	chromatin modifying protein 1B	-1.1149	0.0004
218178_s_at	CHMP1B	chromatin modifying protein 1B	-0.9247	0.0005
218182_s_at	CLDN1	claudin 1	-1.0215	0.0354
218187_s_at	C8orf33	chromosome 8 open reading frame 33	-0.6034	0.0207
218190_s_at	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD)	-0.2442	0.0486
218191_s_at	LMBRD1	LMBR1 domain containing 1	-0.8974	0
218202_x_at	MRPL44	mitochondrial ribosomal protein L44	-0.361	0.0023
218203_at	ALG5	asparagine-linked glycosylation 5 homolog (S. cerevisiae; dolichyl-phosphate beta-glucosyltransferase)	-0.6377	0.0089
218204_s_at	FYCO1	FYVE and coiled-coil domain containing 1	-1.3008	0
218208_at	PQLC1	PQ loop repeat containing 1	-0.5943	0.0009
218213_s_at	C11orf10	chromosome 11 open reading frame 10	-0.2249	0.0061
218217_at	SCPEP1	serine carboxypeptidase 1	-1.057	0
218221_at	ARNT	aryl hydrocarbon receptor nuclear translocator	-0.9663	0.0003
218223_s_at	PLEKHO1	pleckstrin homology domain containing; family O member 1	-2.0304	0
218224_at	PNMA1	paraneoplastic antigen MA1	-0.4769	0.0337
218226_s_at	LOC727762	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 4; 15kDa, similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 4; 15kDa	-0.4194	0
218232_at	C1QA	complement component 1; q subcomponent; A chain	-2.57	0
218233_s_at	C6orf49	chromosome 6 open reading frame 49	-0.3247	0.0027
218235_s_at	UTP11L	UTP11-like; U3 small nucleolar ribonucleoprotein; (yeast)	-1.2203	0.0001
218238_at	GTPBP4	GTP binding protein 4	-0.9187	0.0155
218239_s_at	GTPBP4	GTP binding protein 4	-0.7549	0.0012
218247_s_at	MEX3C	mex-3 homolog C (C. elegans)	-0.4719	0.0264
218253_s_at	LGTN	ligatin	-1.5166	0
218265_at	SECISBP2	SECIS binding protein 2	-0.3686	0.0246
218267_at	CINP	cyclin-dependent kinase 2-interacting protein	-0.2779	0.0195
218270_at	MRPL24	mitochondrial ribosomal protein L24	-0.5913	0
218272_at	FLJ20699	hypothetical protein FLJ20699	-0.8594	0.0023
218273_s_at	PPM2C	protein phosphatase 2C; magnesium-dependent; catalytic subunit	-1.452	0.009
218281_at	MRPL48	mitochondrial ribosomal protein L48	-0.8925	0.0003

218285_s_at	BDH2	3-hydroxybutyrate dehydrogenase; type 2	-0.9012	0.0076
218288_s_at	CCDC90B	coiled-coil domain containing 90B	-0.8374	0
218289_s_at	UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1	-0.6477	0.016
218297_at	C10orf97	chromosome 10 open reading frame 97	-0.6938	0.0001
218301_at	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	-0.4018	0.0115
218307_at	RSAD1	radical S-adenosyl methionine domain containing 1	-0.7534	0.0054
218310_at	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	-0.4704	0.0011
218319_at	PELI1	pellino homolog 1 (Drosophila)	-0.9524	0.0058
218322_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5	-0.8417	0.0006
218326_s_at	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	-1.4037	0.001
218333_at	DERL2	Der1-like domain family; member 2	-0.5421	0
218334_at	THOC7	THO complex 7 homolog (Drosophila)	-0.5489	0.0001
218342_s_at	ERMP1	endoplasmic reticulum metallopeptidase 1	-2.1789	0.0001
218347_at	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	-0.7109	0.0064
218352_at	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	-0.7959	0.0138
218354_at	TRAPPC2L	trafficking protein particle complex 2-like	-0.5498	0.0374
218358_at	CRELD2	cysteine-rich with EGF-like domains 2	-0.5665	0.0419
218360_at	RAB22A	RAB22A; member RAS oncogene family	-0.5256	0.0397
218379_at	RBM7	RNA binding motif protein 7	-0.8639	0.0183
218383_at	C14orf94	chromosome 14 open reading frame 94	-0.6883	0.0498
218391_at	SNF8	SNF8; ESCRT-II complex subunit; homolog (S. cerevisiae)	-0.3991	0.0499
218406_x_at	NENF	neuron derived neurotrophic factor	-0.1817	0.0314
218408_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	-0.4869	0.022
218418_s_at	ANKRD25	ankyrin repeat domain 25	-0.6317	0.0154
218419_s_at	TMUB2	transmembrane and ubiquitin-like domain containing 2	-0.5116	0.0004
218421_at	CERK	ceramide kinase	-2.6166	0
218440_at	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-0.8029	0.0003
218443_s_at	DAZAP1	DAZ associated protein 1	-1.048	0
218444_at	ALG12	asparagine-linked glycosylation 12 homolog (S. cerevisiae; alpha-1;6-mannosyltransferase)	-0.3412	0.018
218446_s_at	FAM18B	family with sequence similarity 18; member B	-0.5588	0.0015
218449_at	C4orf20	chromosome 4 open reading frame 20	-0.3886	0.0293
218467_at	TNFSF5IP1	tumor necrosis factor superfamily; member 5-induced protein 1	-0.2502	0.0252

218471_s_at	BBS1	Bardet-Biedl syndrome 1	-0.5995	0.0111
218475_at	HTF9C	HpaII tiny fragments locus 9C	-0.2902	0.034
218480_at	AGBL5	ATP/GTP binding protein-like 5	-0.758	0.0094
218486_at	KLF11	Kruppel-like factor 11	-0.8003	0.0226
218487_at	ALAD	aminolevulinate; delta-; dehydratase	-1.4584	0
218488_at	EIF2B3	eukaryotic translation initiation factor 2B; subunit 3 gamma; 58kDa	-0.9864	0.0006
218489_s_at	ALAD	aminolevulinate; delta-; dehydratase	-1.2016	0.002
218501_at	ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	-1.0618	0.0059
218503_at	KIAA1797	KIAA1797	-0.8088	0.0021
218511_s_at	PNPO	pyridoxamine 5'-phosphate oxidase	-0.514	0.0082
218523_at	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-1.2707	0.0004
218526_s_at	RANGRF	RAN guanine nucleotide release factor	-0.6003	0.0053
218527_at	APTX	aprataxin	-0.5331	0.0459
218540_at	THTPA	thiamine triphosphatase	-1.2264	0
218541_s_at	C8orf4	chromosome 8 open reading frame 4	-1.6533	0.0023
218544_s_at	RCL1	RNA terminal phosphate cyclase-like 1	-0.5789	0.0021
218552_at	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	-1.1167	0
218560_s_at	JMJD4	jumonji domain containing 4	-1.0397	0
218561_s_at	LYRM4	LYR motif containing 4	-0.459	0.0378
218570_at	KBTBD4	kelch repeat and BTB (POZ) domain containing 4	-0.3041	0.037
218583_s_at	DCUN1D1	DCN1; defective in cullin neddylation 1; domain containing 1 (S. cerevisiae)	-0.5363	0.001
218589_at	P2RY5	purinergic receptor P2Y; G-protein coupled; 5	-1.8022	0.0002
218591_s_at	NOL10	nucleolar protein 10	-0.1231	0.0146
218592_s_at	CECR5	cat eye syndrome chromosome region; candidate 5	-0.5565	0.0182
218600_at	LIMD2	LIM domain containing 2	-0.1979	0.0318
218605_at	TFB2M	transcription factor B2; mitochondrial	-0.6798	0.0006
218612_s_at	TSSC4	tumor suppressing subtransferable candidate 4	-0.2963	0.0162
218613_at	PSD3	pleckstrin and Sec7 domain containing 3	-1.4342	0.0489
218618_s_at	FNDC3B	fibronectin type III domain containing 3B	-0.5638	0.0332
218620_s_at	HEMK1	HemK methyltransferase family member 1	-0.6957	0.0214
218623_at	HMP19	HMP19 protein	-0.2743	0.0201
218627_at	DRAM	damage-regulated autophagy modulator	-0.9647	0.0162
218631_at	AVPI1	arginine vasopressin-induced 1	-2.8172	0
218638_s_at	SPON2	spondin 2; extracellular matrix protein	-2.7674	0

218644_at	PLEK2	pleckstrin 2	-3.4462	0.0001
218656_s_at	LHFP	lipoma HMGIC fusion partner	-1.584	0.002
218664_at	MECR	mitochondrial trans-2-enoyl-CoA reductase	-0.4599	0.0194
218665_at	FZD4	frizzled homolog 4 (Drosophila)	-1.4325	0.0006
218678_at	NES	nestin	-0.6232	0.03
218680_x_at	HYPK	Huntingtin interacting protein K	-0.5596	0.0012
218684_at	LRRC8D	leucine rich repeat containing 8 family; member D	-0.9284	0.0097
218688_at	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	-4.3836	0
218692_at	GOLSYN	Golgi-localized protein	-1.9298	0.0149
218696_at	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	-0.7125	0.0001
218698_at	APIP	APAF1 interacting protein	-0.6383	0.0196
218701_at	LACTB2	lactamase; beta 2	-1.019	0.01
218704_at	RNF43	ring finger protein 43	-0.9721	0.048
218706_s_at	GRAMD3	GRAM domain containing 3	-2.6685	0
218710_at	TTC27	tetratricopeptide repeat domain 27	-1.0387	0.0008
218730_s_at	OGN	osteoglycin	-3.2417	0
218732_at	PTRH2	peptidyl-tRNA hydrolase 2	-0.8612	0.011
218736_s_at	PALMD	palmdelphin	-1.5047	0.0088
218743_at	CHMP6	chromatin modifying protein 6	-0.279	0.0478
218744_s_at	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	-1.0089	0
218752_at	ZMAT5	zinc finger; matrin type 5	-0.4837	0.0284
218754_at	NOL9	nucleolar protein 9	-0.6768	0.006
218756_s_at	MGC4172	short-chain dehydrogenase/reductase	-0.8393	0.007
218760_at	COQ6	coenzyme Q6 homolog; monooxygenase (S. cerevisiae)	-0.8125	0.0045
218765_at	SIDT2	SID1 transmembrane family; member 2	-0.4855	0.0068
218773_s_at	MSRB2	methionine sulfoxide reductase B2	-0.5311	0.0019
218789_s_at	C11orf71	chromosome 11 open reading frame 71	-1.1184	0.0063
218792_s_at	BSPRY	B-box and SPRY domain containing	-0.2686	0.0176
218795_at	ACP6	acid phosphatase 6; lysophosphatidic	-0.8558	0.0205
218796_at	C20orf42	chromosome 20 open reading frame 42	-1.727	0.0018
218805_at	GIMAP5	GTPase; IMAP family member 5	-1.6634	0
218810_at	ZC3H12A	zinc finger CCCH-type containing 12A	-2.782	0
218814_s_at	C1orf75	chromosome 1 open reading frame 75	-0.1549	0.0304
218818_at	FHL3	four and a half LIM domains 3	-0.3839	0.0002
218820_at	C14orf132	chromosome 14 open reading frame 132	-1.643	0.0005
218828_at	PLSCR3	phospholipid scramblase 3	-0.3638	0.0257

218831_s_at	FCGRT	Fc fragment of IgG; receptor; transporter; alpha	-2.3732	0
218843_at	FNDC4	fibronectin type III domain containing 4	-3.0786	0
218844_at	FLJ20920	hypothetical protein FLJ20920	-1.7388	0
218845_at	DUSP22	dual specificity phosphatase 22	-0.5636	0.0455
218853_s_at	MOSPD1	motile sperm domain containing 1	-0.7479	0.0317
218854_at	DSE	dermatan sulfate epimerase	-1.6332	0
218858_at	DEPDC6	DEP domain containing 6	-2.2162	0.0003
218864_at	TNS1	tensin 1	-0.8429	0.0092
218865_at	MOSC1	MOCO sulphurase C-terminal domain containing 1	-0.5664	0.0005
218872_at	TESC	tescalcin	-2.6764	0
218878_s_at	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	-2.4468	0
218880_at	FOSL2	FOS-like antigen 2	-2.2196	0.0001
218881_s_at	FOSL2	FOS-like antigen 2	-1.8136	0
218901_at	PLSCR4	phospholipid scramblase 4	-1.2659	0.0147
218915_at	NF2	neurofibromin 2 (bilateral acoustic neuroma)	-0.6683	0.0092
218935_at	EHD3	EH-domain containing 3	-2.0816	0
218946_at	NFU1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	-0.842	0
218957_s_at	PAAF1	proteasomal ATPase-associated factor 1	-0.7191	0.0115
218970_s_at	CUTC	cutC copper transporter homolog (E. coli)	-0.5978	0.006
218972_at	TTC17	tetratricopeptide repeat domain 17	-0.8481	0.0205
218976_at	DNAJC12	DnaJ (Hsp40) homolog; subfamily C; member 12	-2.4387	0.0011
218980_at	FHOD3	formin homology 2 domain containing 3	-1.2756	0.0239
218983_at	C1RL	complement component 1; r subcomponent-like	-1.5683	0.002
218997_at	POLR1E	polymerase (RNA) I polypeptide E; 53kDa	-0.6459	0.0174
219008_at	C2orf43	chromosome 2 open reading frame 43	-0.494	0.0177
219011_at	PLEKHA4	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 4	-0.4463	0.0003
219015_s_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	-0.9506	0.0403
219016_at	FASTKD5	FAST kinase domains 5	-0.6369	0.0137
219021_at	RNF121	ring finger protein 121	-0.2788	0.0092
219044_at	THNSL2	threonine synthase-like 2 (S. cerevisiae)	-1.2088	0.0319
219046_s_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.3746	0.0004
219049_at	ChGn	chondroitin beta1;4 N-acetylgalactosaminyltransferase	-1.8035	0.0125
219058_x_at	TINAGL1	tubulointerstitial nephritis antigen-like 1	-0.3842	0.0066

219059_s_at	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	-2.2074	0.0132
219070_s_at	MOSPD3	motile sperm domain containing 3	-0.5762	0.0117
219076_s_at	PXMP2	peroxisomal membrane protein 2; 22kDa	-1.1256	0.0011
219087_at	ASPN	asporin	-2.4042	0.0004
219093_at	PID1	phosphotyrosine interaction domain containing 1	-3.0075	0.0001
219102_at	RCN3	reticulocalbin 3; EF-hand calcium binding domain	-0.2395	0.0448
219104_at	RNF141	ring finger protein 141	-1.3766	0
219107_at	BCAN	brevican	-0.2411	0.0051
219108_x_at	DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	-0.49	0.0361
219115_s_at	IL20RA	interleukin 20 receptor; alpha	-1.5108	0.0002
219126_at	PHF10	PHD finger protein 10	-1.7657	0.0001
219131_at	UBIAD1	UbiA prenyltransferase domain containing 1	-0.395	0.0072
219132_at	PELI2	pellino homolog 2 (Drosophila)	-1.3222	0.0003
219138_at	RPL14	ribosomal protein L14	-0.2772	0.0108
219140_s_at	RBP4	retinol binding protein 4; plasma	-3.5531	0
219144_at	DUSP26	dual specificity phosphatase 26 (putative)	-0.9121	0
219157_at	KLHL2	kelch-like 2; Mayven (Drosophila)	-0.8936	0.002
219169_s_at	TFB1M	transcription factor B1; mitochondrial	-0.6383	0.0328
219173_at	MYO15B	myosin XVB pseudogene	-0.3933	0.0061
219176_at	C2orf47	chromosome 2 open reading frame 47	-0.3762	0.0189
219179_at	DACT1	dapper; antagonist of beta-catenin; homolog 1 (Xenopus laevis)	-1.3356	0.0102
219183_s_at	PSCD4	pleckstrin homology; Sec7 and coiled-coil domains 4	-0.5687	0.0109
219192_at	UBAP2	ubiquitin associated protein 2	-0.71	0.002
219197_s_at	SCUBE2	signal peptide; CUB domain; EGF-like 2	-0.5097	0.0001
219202_at	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	-0.6495	0.0022
219204_s_at	SRR	serine racemase	-0.8719	0.0014
219205_at	SRR	serine racemase	-1.1529	0.001
219213_at	JAM2	junctional adhesion molecule 2	-2.1307	0.0025
219214_s_at	NT5C	5'; 3'-nucleotidase; cytosolic	-0.4372	0.0014
219217_at	NARS2	asparaginyl-tRNA synthetase 2; mitochondrial (putative)	-1.0602	0.0009
219220_x_at	MRPS22	mitochondrial ribosomal protein S22	-0.5698	0.0002
219222_at	RBKS	ribokinase	-1.5839	0.0009
219228_at	ZNF331	zinc finger protein 331	-3.4676	0
219238_at	PIGV	phosphatidylinositol glycan anchor biosynthesis; class V	-0.8574	0.0009
219241_x_at	SSH3	slingshot homolog 3 (Drosophila)	-0.3671	0.0035
219242_at	CEP63	centrosomal protein 63kDa	-0.6214	0.0079
219243_at	GIMAP4	GTPase; IMAP family member 4	-1.0576	0.0073

219244_s_at	MRPL46	mitochondrial ribosomal protein L46	-0.8996	0.0063
219254_at	FLJ22222	hypothetical protein FLJ22222	-0.3551	0.0364
219255_x_at	IL17RB	interleukin 17 receptor B	-0.1854	0.0034
219272_at	TRIM62	tripartite motif-containing 62	-0.7244	0.0011
219276_x_at	C9orf82	chromosome 9 open reading frame 82	-0.6145	0.0136
219279_at	DOCK10	dedicator of cytokinesis 10	-1.345	0.0219
219283_at	C1GALT1C1	C1GALT1-specific chaperone 1	-0.8456	0.0036
219284_at	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	-1.0835	0.0005
219286_s_at	RBM15	RNA binding motif protein 15	-0.327	0.0418
219298_at	ECHDC3	enoyl Coenzyme A hydratase domain containing 3	-3.5487	0
219304_s_at	PDGFD	platelet derived growth factor D	-2.88	0.0003
219314_s_at	ZNF219	zinc finger protein 219	-0.4707	0.0469
219315_s_at	C16orf30	chromosome 16 open reading frame 30	-1.6704	0
219316_s_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family; member 2	-2.875	0
219323_s_at			-0.1366	0.0381
219324_at	NOL12	TRIO and F-actin binding protein, nucleolar protein 12	-0.9469	0.0003
219325_s_at	ELAC1	elaC homolog 1 (E. coli)	-0.259	0.0046
219329_s_at	C2orf28	chromosome 2 open reading frame 28	-0.2558	0.004
219331_s_at	KLHDC8A	kelch domain containing 8A	-1.2324	0.025
219332_at	MICALL2	MICAL-like 2	-1.0104	0.0172
219333_s_at	CAPN10	calpain 10	-0.2493	0.0417
219334_s_at	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	-0.2401	0.035
219336_s_at	ASCC1	activating signal cointegrator 1 complex subunit 1	-1.019	0
219342_at	CASD1	CAS1 domain containing 1	-0.9471	0.0048
219343_at	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.1322	0.0001
219348_at	MDS032	uncharacterized hematopoietic stem/progenitor cells protein MDS032	-0.6166	0.0266
219358_s_at	CENTA2	centaurin; alpha 2	-1.8928	0
219367_s_at		CDNA: FLJ21027 fis; clone CAE07110	-0.509	0.0015
219370_at	RPRM	reprimo; TP53 dependent G2 arrest mediator candidate	-1.9982	0.0055
219371_s_at	KLF2	Kruppel-like factor 2 (lung)	-1.5278	0.0001
219373_at	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	-0.5801	0.0074
219377_at	FAM59A	family with sequence similarity 59; member A	-1.7543	0.0003
219379_x_at	ZNF358	zinc finger protein 358	-0.464	0.0277
219388_at	GRHL2	grainyhead-like 2 (Drosophila)	-0.1367	0.0375
219396_s_at	NEIL1	nei endonuclease VIII-like 1 (E. coli)	-1.3087	0.0002
219397_at	COQ10B	coenzyme Q10 homolog B (S. cerevisiae)	-0.3781	0.0194

219398_at	CIDEC	cell death-inducing DFFA-like effector c	-0.8376	0.0001
219403_s_at	HPSE	heparanase	-1.2717	0.0149
219404_at	EPS8L3	EPS8-like 3	-0.1733	0.0088
219413_at	ACBD4	acyl-Coenzyme A binding domain containing 4	-0.536	0.0003
219419_at	C18orf22	chromosome 18 open reading frame 22	-0.9484	0
219423_x_at	TNFRSF25	tumor necrosis factor receptor superfamily; member 25	-0.5869	0.008
219424_at	EBI3	Epstein-Barr virus induced gene 3	-0.6912	0.0001
219431_at	ARHGAP10	Rho GTPase activating protein 10	-0.8011	0
219436_s_at	EMCN	endomucin	-2.4203	0
219438_at	FAM77C	family with sequence similarity 77; member C	-2.9135	0
219440_at	RAI2	retinoic acid induced 2	-2.4841	0
219441_s_at	LRRK1	leucine-rich repeat kinase 1	-0.3161	0.0025
219473_at	GDAP2	ganglioside induced differentiation associated protein 2	-0.1667	0.03
219478_at	WFDC1	WAP four-disulfide core domain 1	-5.1569	0
219480_at	SNAI1	snail homolog 1 (Drosophila)	-0.6158	0.0001
219483_s_at	PORCN	porcupine homolog (Drosophila)	-1.514	0.0023
219488_at	A4GALT	alpha 1;4-galactosyltransferase (globotriaosylceramide synthase)	-0.3288	0.0051
219491_at	LRFN4	leucine rich repeat and fibronectin type III domain containing 4	-0.4684	0.0319
219492_at	CHIC2	cysteine-rich hydrophobic domain 2	-0.53	0.0408
219500_at	CLCF1	cardiotrophin-like cytokine factor 1	-0.3335	0.0008
219519_s_at	SIGLEC1	sialic acid binding Ig-like lectin 1; sialoadhesin	-2.1598	0.0003
219520_s_at	WWC3	WWC family member 3	-1.0889	0.0008
219521_at	B3GAT1	beta-1;3-glucuronyltransferase 1 (glucuronosyltransferase P)	-0.1524	0.0095
219525_at	SLC47A1	solute carrier family 47; member 1	-1.8239	0.0058
219534_x_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57; Kip2)	-3.1025	0
219543_at	PBLD	phenazine biosynthesis-like protein domain containing	-1.4943	0.0002
219545_at	KCTD14	potassium channel tetramerisation domain containing 14	-2.5505	0.0004
219547_at	COX15	COX15 homolog; cytochrome c oxidase assembly protein (yeast)	-0.3783	0.0447
219550_at	ROBO3	roundabout; axon guidance receptor; homolog 3 (Drosophila)	-0.7849	0
219561_at	COPZ2	coatomer protein complex; subunit zeta 2	-1.9229	0.0001
219563_at	C14orf139	chromosome 14 open reading frame 139	-1.5419	0.0037
219565_at	CYP20A1	cytochrome P450; family 20; subfamily A; polypeptide 1	-0.7332	0.0061
219570_at	C20orf23	chromosome 20 open reading frame 23	-1.1539	0.0003
219574_at	1-Mar	membrane-associated ring finger (C3HC4) 1	-0.7811	0.0396
219579_at	RAB3IL1	RAB3A interacting protein (rabin3)-like 1	-0.2559	0.0465

219582_at	OGFRL1	opioid growth factor receptor-like 1	-0.5026	0.0327
219587_at	TTC12	tetratricopeptide repeat domain 12	-0.4986	0.0206
219597_s_at	DUOX1	dual oxidase 1	-2.325	0
219600_s_at	TMEM50B	transmembrane protein 50B	-0.8378	0.0394
219603_s_at	ZNF226	zinc finger protein 226	-0.7091	0.0162
219607_s_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	-3.0925	0.0001
219609_at	WDR25	WD repeat domain 25	-0.4025	0.0002
219610_at	RGNEF	Rho-guanine nucleotide exchange factor	-2.0261	0
219615_s_at	KCNK5	potassium channel; subfamily K; member 5	-2.0334	0
219620_x_at	C9orf167	chromosome 9 open reading frame 167	-0.3427	0.0015
219622_at	RAB20	RAB20; member RAS oncogene family	-2.599	0
219636_s_at	ARMC9	armadillo repeat containing 9	-0.7255	0
219637_at	ARMC9	armadillo repeat containing 9	-1.5364	0.0001
219654_at	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member A	-1.4222	0.0036
219655_at	C7orf10	chromosome 7 open reading frame 10	-2.8292	0
219656_at	PCDH12	protocadherin 12	-0.8031	0.0001
219659_at	ATP8A2	ATPase; aminophospholipid transporter-like; Class I; type 8A; member 2	-0.5534	0.0009
219660_s_at	ATP8A2	ATPase; aminophospholipid transporter-like; Class I; type 8A; member 2	-0.2436	0.0053
219666_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-3.3321	0
219669_at	CD177	CD177 molecule	-0.163	0.0385
219680_at	NLRX1	NLR family member X1	-0.7189	0
219687_at	HHAT	hedgehog acyltransferase	-0.6942	0.0001
219704_at	YBX2	Y box binding protein 2	-0.2085	0.0392
219713_at	CARKL	carbohydrate kinase-like	-0.5751	0
219716_at	APOL6	apolipoprotein L; 6	-0.7081	0.0062
219718_at	FLJ10986	hypothetical protein FLJ10986	-0.8634	0.0008
219734_at	SIDT1	SID1 transmembrane family; member 1	-0.4759	0.0111
219737_s_at	PCDH9	protocadherin 9	-1.5024	0.0083
219738_s_at	PCDH9	protocadherin 9	-0.6453	0.0248
219741_x_at	ZNF552	zinc finger protein 552	-0.3024	0.0044
219761_at	CLEC1A	C-type lectin domain family 1; member A	-0.413	0.0101
219771_at	TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	-1.233	0.0022
219776_s_at			-0.1651	0.0418
219777_at	GIMAP6	GTPase; IMAP family member 6	-1.7754	0.0002
219778_at	ZFPM2	zinc finger protein; multitype 2	-1.4885	0.0175

219791_s_at	NBLA00301	putative protein product of Nbla00301	-0.6618	0.0078
219798_s_at	MEPCE	methylphosphate capping enzyme	-1.0518	0.0003
219806_s_at	C11orf75	chromosome 11 open reading frame 75	-1.2286	0.02
219815_at	GAL3ST4	galactose-3-O-sulfotransferase 4	-0.419	0.0093
219839_x_at	TCL6	T-cell leukemia/lymphoma 6	-0.1673	0.0254
219847_at	HDAC11	histone deacetylase 11	-0.2597	0.0028
219859_at	CLEC4E	C-type lectin domain family 4; member E	-0.1904	0.0002
219860_at	LY6G5C	lymphocyte antigen 6 complex; locus G5C	-0.1468	0.0163
219866_at	CLIC5	chloride intracellular channel 5	-0.2289	0.0208
219873_at	COLEC11	collectin sub-family member 11	-2.6301	0
219896_at	DRD1IP	dopamine receptor D1 interacting protein	-0.2421	0.0083
219902_at	BHMT2	betaine-homocysteine methyltransferase 2	-1.9087	0.0024
219912_s_at			-0.1263	0.0324
219920_s_at	GMPPB	GDP-mannose pyrophosphorylase B	-1.0449	0.0016
219932_at	SLC27A6	solute carrier family 27 (fatty acid transporter); member 6	-4.0209	0
219934_s_at	SULT1E1	sulfotransferase family 1E; estrogen-preferring; member 1	-1.0532	0
219939_s_at	CSDE1	cold shock domain containing E1; RNA-binding	-0.4119	0.0019
219943_s_at	FLJ11850	hypothetical protein FLJ11850	-0.1469	0.0143
219952_s_at	MCOLN1	mucolipin 1	-0.6734	0.0285
219955_at	L1TD1	LINE-1 type transposase domain containing 1	-0.145	0.001
219959_at	MOCOS	molybdenum cofactor sulfurase	-1.7891	0.0052
219970_at	GIPC2	GIPC PDZ domain containing family; member 2	-4.1034	0
219973_at	ARSJ	arylsulfatase family; member J	-0.5884	0.0354
219985_at	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	-1.6164	0.0004
219991_at	SLC2A9	solute carrier family 2 (facilitated glucose transporter); member 9	-0.3365	0.0058
219999_at	MAN2A2	mannosidase; alpha; class 2A; member 2	-0.6543	0.0164
220000_at	SIGLEC5	sialic acid binding Ig-like lectin 5	-0.2322	0.0026
220002_at	KIF26B	kinesin family member 26B	-0.275	0.0019
220005_at	P2RY13	purinergic receptor P2Y; G-protein coupled; 13	-1.2808	0.0002
220006_at	CCDC48	coiled-coil domain containing 48	-0.2181	0.004
220013_at	ABHD9	abhydrolase domain containing 9	-0.113	0.0284
220015_at	CASZ1	castor zinc finger 1	-0.2114	0.0372
220016_at	AHNAK	AHNAK nucleoprotein	-0.3477	0.0005
220025_at	TBR1	T-box; brain; 1	-0.119	0.0325
220031_at	OTUD7B	OTU domain containing 7B	-0.1697	0.0065
220034_at	IRAK3	interleukin-1 receptor-associated kinase 3	-0.359	0.0082

220037_s_at	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	-2.0004	0.0348
220046_s_at	CCNL1	cyclin L1	-0.6491	0.0093
220050_at	C9orf9	chromosome 9 open reading frame 9	-0.7344	0.0004
220053_at	GDF3	growth differentiation factor 3	-0.1545	0.0052
220061_at	FLJ20581	hypothetical protein FLJ20581	-0.6671	0.0013
220065_at	TNMD	tenomodulin	-0.164	0.0141
220076_at	ANKH	ankylosis; progressive homolog (mouse)	-0.2189	0.0086
220077_at	CCDC134	coiled-coil domain containing 134	-0.3347	0.0072
220078_at	USP48	ubiquitin specific peptidase 48	-0.5178	0.002
220079_s_at	USP48	ubiquitin specific peptidase 48	-1.0444	0
220088_at	C5AR1	complement component 5a receptor 1	-2.3728	0.0003
220092_s_at	ANTXR1	anthrax toxin receptor 1	-0.5928	0.0002
220093_at	ANTXR1	anthrax toxin receptor 1	-0.3729	0.0005
220097_s_at	TMEM104	transmembrane protein 104	-0.3634	0.0049
220108_at	GNA14	guanine nucleotide binding protein (G protein); alpha 14	-0.9609	0
220110_s_at	NXF3	nuclear RNA export factor 3	-0.2577	0
220116_at	KCNN2	potassium intermediate/small conductance calcium-activated channel; subfamily N; member 2	-3.2742	0.0001
220118_at	ZBTB32	zinc finger and BTB domain containing 32	-0.1516	0.0312
220136_s_at	CRYBA2	crystallin; beta A2	-0.1489	0.0077
220137_at	FLJ20674	hypothetical protein FLJ20674	-0.3453	0.0075
220140_s_at	SNX11	sorting nexin 11	-0.4743	0.006
220142_at	HAPLN2	hyaluronan and proteoglycan link protein 2	-0.1892	0.0271
220152_at	C10orf95	chromosome 10 open reading frame 95	-0.1643	0.0125
220153_at	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	-1.0424	0.0003
220162_s_at	CARD9	caspase recruitment domain family; member 9	-0.2462	0.0429
220165_at	FLJ20309	hypothetical protein FLJ20309	-0.1666	0.05
220170_at	FHL5	four and a half LIM domains 5	-0.8379	0
220180_at	CCDC68	coiled-coil domain containing 68	-1.6746	0
220187_at	STEAP4	STEAP family member 4	-1.5343	0.0052
220191_at	GKN1	gastrokine 1	-0.9288	0
220204_s_at	BMP8A	bone morphogenetic protein 8a	-0.1676	0.0485
220209_at	PYY2	peptide YY; 2 (seminalplasmin)	-1.2535	0
220211_at	FLJ13224	hypothetical protein FLJ13224	-0.1561	0.0083
220212_s_at	THADA	thyroid adenoma associated	-0.4147	0.0148
220217_x_at	SPANXC	SPANX family; member C	-0.2599	0.0079
220218_at	C9orf68	chromosome 9 open reading frame 68	-0.1649	0.0173
220248_x_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-0.4368	0.0066

220249_at	HYAL4	hyaluronoglucosaminidase 4	-0.1775	0.0061
220256_s_at	OXCT2	3-oxoacid CoA transferase 2	-0.3748	0.0001
220266_s_at	KLF4	Kruppel-like factor 4 (gut)	-2.8342	0
220287_at	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif; 9	-1.2831	0.0056
220290_at	AIM1L	absent in melanoma 1-like	-0.1566	0.0265
220297_at	BTBD7	BTB (POZ) domain containing 7	-0.2172	0.0039
220298_s_at	SPATA6	spermatogenesis associated 6	-0.5418	0.0182
220299_at	SPATA6	spermatogenesis associated 6	-0.5068	0.0098
220307_at	CD244	CD244 molecule; natural killer cell receptor 2B4	-0.1907	0.0202
220308_at	CCDC19	coiled-coil domain containing 19	-0.1726	0.0034
220309_at	TTC22	tetratricopeptide repeat domain 22	-0.119	0.0156
220318_at	EPN3	epsin 3	-0.8484	0.0002
220319_s_at	MYLIP	myosin regulatory light chain interacting protein	-1.3479	0.0017
220320_at	DOK3	docking protein 3	-0.1969	0.0005
220323_at	CNTD2	cyclin N-terminal domain containing 2	-0.2381	0.0011
220326_s_at	FLJ10357	hypothetical protein FLJ10357	-0.9118	0.028
220327_at	VGLL3	vestigial like 3 (Drosophila)	-0.5536	0
220330_s_at	SAMSN1	SAM domain; SH3 domain and nuclear localization signals 1	-1.6358	0.0068
220332_at	CLDN16	claudin 16	-0.1061	0.0074
220344_at	C11orf16	chromosome 11 open reading frame 16	-0.239	0.0086
220348_at	KLHL29	kelch-like 29 (Drosophila)	-0.3665	0
220351_at	CCRL1	chemokine (C-C motif) receptor-like 1	-0.2854	0.0401
220358_at	SNFT	Jun dimerization protein p21SNFT	-0.3883	0.0268
220370_s_at	USP36	ubiquitin specific peptidase 36	-1.0856	0.0007
220373_at	DCHS2	dachsous 2 (Drosophila)	-0.1868	0.0013
220383_at	ABCG5	ATP-binding cassette; sub-family G (WHITE); member 5 (sterolin 1)	-0.4726	0
220420_at	CPLX3	complexin 3, lectin; mannose-binding; 1 like	-0.1555	0.024
220421_at	BTNL8	butyrophilin-like 8, similar to Butyrophilin-like protein 8 precursor	-0.1906	0.0275
220424_at	NPHS2	nephrosis 2; idiopathic; steroid-resistant (podocin)	-0.1188	0.019
220431_at	TMPRSS11E	transmembrane protease; serine 11E, transmembrane protease; serine 11E2	-0.132	0.0204
220437_at	LOC55908	hepatocellular carcinoma-associated gene TD26	-0.193	0.0002
220439_at	RIN3	Ras and Rab interactor 3	-0.16	0.0167
220453_at	PQLC2	PQ loop repeat containing 2	-0.2042	0.0126
220454_s_at	SEMA6A	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6A	-2.2255	0
220478_at	APOL5	apolipoprotein L; 5	-0.1016	0.0489

220480_at	HAND2	heart and neural crest derivatives expressed 2	-0.1581	0.0248
220484_at	MCOLN3	mucolipin 3	-2.8949	0.001
220488_s_at	BCAS3	breast carcinoma amplified sequence 3	-0.6369	0.009
220490_at			-0.1994	0.0084
220501_at	ACTL7A	actin-like 7A	-0.1503	0.002
220505_at	C9orf53	chromosome 9 open reading frame 53	-0.1215	0.026
220507_s_at	UPB1	ureidopropionase; beta	-0.1806	0.0011
220514_at		PRO0943	-0.239	0.0035
220516_at	ZSCAN2	zinc finger and SCAN domain containing 2	-0.1107	0.0281
220526_s_at	MRPL20	mitochondrial ribosomal protein L20	-0.395	0.0134
220529_at	FLJ11710	hypothetical protein FLJ11710	-0.3414	0.0006
220531_at	FLJ14126	hypothetical protein FLJ14126	-0.4159	0
220538_at	ADM2	adrenomedullin 2	-0.1606	0.0281
220541_at	MMP26	matrix metallopeptidase 26	-0.1325	0.0323
220543_at	C21orf62	chromosome 21 open reading frame 62	-0.187	0.003
220547_s_at	FAM35A	family with sequence similarity 35; member A	-0.5607	0
220554_at	SLC22A7	solute carrier family 22 (organic anion transporter); member 7	-0.2503	0.0252
220556_at	ATP1B4	ATPase; (Na+)/K+ transporting; beta 4 polypeptide	-0.1636	0.0046
220557_s_at	PACS1	phosphofurin acidic cluster sorting protein 1	-0.1437	0.0214
220566_at	PIK3R5	phosphoinositide-3-kinase; regulatory subunit 5; p101	-0.195	0.0045
220569_at			-0.1569	0.0162
220573_at	KLK14	kallikrein-related peptidase 14	-0.2049	0.009
220576_at	PGAP1	GPI deacylase	-4.0807	0
220578_at	ADAMTSL4	ADAMTS-like 4	-0.1197	0.0121
220580_at	BICC1	bicaudal C homolog 1 (Drosophila)	-0.4162	0.0001
220598_at	CARD14	caspase recruitment domain family; member 14	-0.1292	0.0456
220612_at		Clone HQ0641 PRO0641	-1.811	0
220614_s_at	C6orf103	chromosome 6 open reading frame 103	-0.113	0.0231
220616_at			-0.1719	0.0111
220618_s_at	ZCWPW1	zinc finger; CW type with PWWP domain 1	-0.359	0.0009
220630_s_at	CHIA	chitinase; acidic	-0.1996	0.002
220635_at	PSORS1C2	psoriasis susceptibility 1 candidate 2	-0.2024	0.0104
220645_at	FAM55D	family with sequence similarity 55; member D	-0.2056	0.0132
220647_s_at	CHCHD8	coiled-coil-helix-coiled-coil-helix domain containing 8	-0.6259	0
220657_at	KLHL11	kelch-like 11 (Drosophila)	-0.1081	0.0439
220665_at	LUZP4	leucine zipper protein 4	-0.1133	0.041

220670_at			-0.1113	0.042
220677_s_at	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif; 8	-0.1505	0.0136
220681_at	C22orf26	chromosome 22 open reading frame 26	-0.1572	0.0431
220682_s_at			-0.1688	0.0282
220689_at			-0.1244	0.0459
220714_at	PRDM14	PR domain containing 14	-0.1461	0.0481
220722_s_at	SLC5A7	solute carrier family 5 (choline transporter); member 7	-0.2897	0
220732_at	DEPDC2	DEP domain containing 2	-0.1489	0.0216
220733_at	SLC26A1	solute carrier family 26 (sulfate transporter); member 1	-0.1839	0.0131
220736_at	SLC19A3	solute carrier family 19; member 3	-0.1622	0.0425
220742_s_at	NGLY1	N-glycanase 1	-0.7806	0.0001
220743_at			-0.1782	0.0267
220745_at	IL19	interleukin 19	-0.1344	0.0341
220751_s_at	C5orf4	chromosome 5 open reading frame 4	-1.3767	0.0027
220753_s_at	CRYL1	crystallin; lambda 1	-1.8276	0
220765_s_at	LIMS2	LIM and senescent cell antigen-like domains 2	-0.4473	0.0017
220767_at			-0.1255	0.0018
220777_at	KIF13A	kinesin family member 13A	-0.3944	0.0306
220784_s_at	UTS2	urotensin 2	-2.3835	0.0058
220786_s_at	SLC38A4	solute carrier family 38; member 4	-0.3468	0.0001
220795_s_at	BEGAIN	brain-enriched guanylate kinase-associated homolog (rat)	-0.3645	0.0004
220804_s_at	TP73	tumor protein p73	-0.1541	0.0247
220806_x_at	GNG13	guanine nucleotide binding protein (G protein); gamma 13	-0.1731	0.0046
220808_at	THEG	Theg homolog (mouse)	-0.1468	0.0077
220816_at	EDG7	endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 7	-0.2891	0.0013
220819_at	FRMD1	FERM domain containing 1	-0.1135	0.0266
220825_s_at	KIRREL	kin of IRRE like (Drosophila)	-0.2123	0.018
220834_at	MS4A12	membrane-spanning 4-domains; subfamily A; member 12	-0.1184	0.0357
220835_s_at	ZNF407	zinc finger protein 407	-0.147	0.0226
220848_x_at	OBP2A	odorant binding protein 2A	-0.1221	0.0427
220852_at	PRO1768	PRO1768 protein	-0.1401	0.0185
220858_at	SORBS2	sorbin and SH3 domain containing 2	-1.5457	0.0051
220863_at	MIP	major intrinsic protein of lens fiber	-0.1467	0.0126
220873_at		PRO0386	-0.1177	0.0405
220875_at			-0.15	0.0052
220881_at		PRO1787	-0.1121	0.0466
220886_at	GABRQ	gamma-aminobutyric acid (GABA) receptor; theta	-0.165	0.0048

220887_at	C14orf162	chromosome 14 open reading frame 162	-0.1537	0.0318
220918_at	C21orf96	chromosome 21 open reading frame 96	-0.3806	0.0137
220921_at	SPANXB1	SPANX family; member B1, SPANX family; member B2	-0.1385	0.0406
220924_s_at	SLC38A2	solute carrier family 38; member 2	-0.3767	0.0421
220943_s_at	C2orf56	chromosome 2 open reading frame 56	-0.4673	0.0239
220944_at	PGLYRP4	peptidoglycan recognition protein 4	-0.1837	0.0061
220960_x_at	RPL22	ribosomal protein L22	-0.2223	0.0037
220964_s_at	RAB1B	RAB1B; member RAS oncogene family	-0.4528	0.01
220965_s_at	RSHL1	radial spokehead-like 1	-0.2321	0.0151
220970_s_at	KRTAP2-4	keratin associated protein 2-4, similar to keratin associated protein 2-4	-0.1481	0.0035
220975_s_at	C1QTNF1	C1q and tumor necrosis factor related protein 1	-1.7247	0.0001
220976_s_at	KRTAP1-1	keratin associated protein 1-1, similar to keratin associated protein 1-1	-0.1155	0.0461
220979_s_at	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2;3-beta-galactosyl-1;3)-N-acetylgalactosaminide alpha-2;6-sialyltransferase 5	-3.6553	0
220984_s_at	SLCO5A1	solute carrier organic anion transporter family; member 5A1	-0.1242	0.0215
220990_s_at	MIRN21	microRNA 21, transmembrane protein 49	-0.544	0.0048
220998_s_at	UNC93B1	unc-93 homolog B1 (C. elegans)	-0.3809	0.0124
221001_at	C15orf49	chromosome 15 open reading frame 49	-0.1705	0.0089
221003_s_at	CAB39L	calcium binding protein 39-like	-0.7442	0
221005_s_at	PTDSS2	phosphatidylserine synthase 2	-0.3878	0.0092
221015_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	-0.3333	0.0063
221016_s_at	TCF7L1	transcription factor 7-like 1 (T-cell specific; HMG-box)	-0.3247	0.0324
221017_s_at	LRRC3	leucine rich repeat containing 3	-0.145	0.0037
221024_s_at	SLC2A10	solute carrier family 2 (facilitated glucose transporter); member 10	-1.5901	0.0328
221044_s_at	TRIM34	tripartite motif-containing 34, tripartite motif-containing 6 and tripartite motif-containing 34	-1.3156	0
221060_s_at	TLR4	toll-like receptor 4	-0.7344	0.0002
221061_at	PKD2L1	polycystic kidney disease 2-like 1	-0.1777	0.0024
221068_at	ANKRD25	ankyrin repeat domain 25	-0.173	0.0083
221072_at	C9orf31	chromosome 9 open reading frame 31	-0.1328	0.041
221074_at	NCR2	Natural cytotoxicity triggering receptor 2	-0.1543	0.0273
221081_s_at	DENND2D	DENN/MADD domain containing 2D	-0.8794	0.037
221083_at	KCNQ4	potassium voltage-gated channel; KQT-like subfamily; member 4	-0.3088	0.0046
221085_at	TNFSF15	tumor necrosis factor (ligand) superfamily; member 15	-0.1434	0.0176

221087_s_at	APOL3	apolipoprotein L; 3	-1.1409	0.0001
221096_s_at	TMCO6	transmembrane and coiled-coil domains 6	-0.7801	0.0027
221105_at			-0.1306	0.0056
221107_at	CHRNA9	cholinergic receptor; nicotinic; alpha 9	-0.1353	0.047
221108_at	LOC51233	hypothetical protein LOC51233	-0.1038	0.002
221114_at	AMBN	ameloblastin (enamel matrix protein)	-0.2301	0.0209
221119_at	FLJ20184	hypothetical protein FLJ20184	-0.195	0.0076
221127_s_at	RIG	regulated in glioma	-1.6952	0
221129_at	C17orf88	chromosome 17 open reading frame 88	-0.1463	0.0016
221131_at	A4GNT	alpha-1;4-N-acetylglucosaminyltransferase	-0.1247	0.0237
221151_at	PRDM9	PR domain containing 9	-0.1579	0.0277
221157_s_at	FBXO24	F-box protein 24	-0.1818	0.023
221160_s_at	CABP5	calcium binding protein 5	-0.1822	0.0002
221162_at	HHLA1	HERV-H LTR-associating 1	-0.3569	0.0003
221163_s_at	MLXIPL	MLX interacting protein-like	-0.7792	0.0078
221166_at	FGF23	fibroblast growth factor 23	-0.1741	0.0111
221186_at		CDNA FLJ12781 fis; clone NT2RP2001861	-0.2296	0.0017
221188_s_at	CIDEB	cell death-inducing DFFA-like effector b	-1.0785	0.0337
221207_s_at	NBEA	neurobeachin	-1.6202	0.0014
221229_s_at	FLJ20628	hypothetical protein FLJ20628	-0.776	0.0044
221235_s_at	LOC644617	Hypothetical LOC644617	-1.1174	0
221236_s_at	STMN4	stathmin-like 4	-0.2141	0.0002
221237_s_at	OSBP2	oxysterol binding protein 2	-0.3179	0.0046
221245_s_at	FZD5	frizzled homolog 5 (Drosophila)	-1.5399	0.0001
221246_x_at	TNS1	tensin 1	-0.4768	0.0003
221249_s_at	FAM117A	family with sequence similarity 117; member A	-0.6633	0.0094
221251_x_at	ZNHIT4	zinc finger; HIT type 4	-0.2559	0.0345
221256_s_at	HDHD3	haloacid dehalogenase-like hydrolase domain containing 3	-1.2968	0.0131
221263_s_at	SF3B5	splicing factor 3b; subunit 5; 10kDa	-0.4582	0.0009
221271_at	IL21	interleukin 21	-0.1067	0.0192
221272_s_at	C1orf21	chromosome 1 open reading frame 21	-1.1482	0.0106
221273_s_at	RNF208	ring finger protein 208	-0.367	0.0134
221278_at	HOXB8	homeobox B8	-0.1437	0.0007
221283_at	RUNX2	runt-related transcription factor 2	-0.1473	0.007
221292_at	PTCH2	patched homolog 2 (Drosophila)	-0.144	0.0108
221293_s_at	DEF6	differentially expressed in FDCP 6 homolog (mouse)	-0.1989	0.0179
221299_at	GPR173	G protein-coupled receptor 173	-0.1039	0.0329

221301_at	C6orf27	chromosome 6 open reading frame 27	-0.1295	0.0306
221310_at	FGF14	fibroblast growth factor 14	-0.2302	0
221313_at	GPR52	G protein-coupled receptor 52	-0.2619	0.0005
221318_at	NEUROD4	neurogenic differentiation 4	-0.1766	0.0339
221320_at	BCL2L10	BCL2-like 10 (apoptosis facilitator)	-0.2086	0.0016
221329_at	OR52A1	olfactory receptor; family 52; subfamily A; member 1	-0.1685	0.0029
221334_s_at	FOXP3	forkhead box P3	-0.1373	0.0344
221336_at	ATOH1	atonal homolog 1 (Drosophila)	-0.2255	0.0024
221338_at	LY6G6E	lymphocyte antigen 6 complex; locus G6E	-0.1658	0.001
221339_at	OR10C1	olfactory receptor; family 10; subfamily C; member 1	-0.1175	0.0162
221341_s_at	OR1D4	olfactory receptor; family 1; subfamily D; member 4, olfactory receptor; family 1; subfamily D; member 5	-0.1071	0.03
221342_at	C6orf25	chromosome 6 open reading frame 25	-0.206	0.0038
221345_at	FFAR2	free fatty acid receptor 2	-0.1694	0.0026
221347_at	CHRM5	cholinergic receptor; muscarinic 5	-0.2484	0.0072
221352_at	HUMBINDC	DNA binding protein for surfactant protein B	-0.126	0.035
221354_s_at	MCHR1	melanin-concentrating hormone receptor 1	-0.1638	0.001
221355_at	CHRNG	cholinergic receptor; nicotinic; gamma	-0.1477	0.0058
221357_at	CHRM4	cholinergic receptor; muscarinic 4	-0.1691	0.0092
221369_at	MTNR1A	melatonin receptor 1A	-0.1097	0.0201
221371_at	TNFSF18	tumor necrosis factor (ligand) superfamily; member 18	-0.1302	0.0488
221373_x_at	PSPN	persephin	-0.1303	0.0342
221374_at	FGF16	fibroblast growth factor 16	-0.174	0.0027
221375_at	OR1G1	olfactory receptor; family 1; subfamily G; member 1	-0.1432	0.0065
221378_at	CER1	cerberus 1; cysteine knot superfamily; homolog (Xenopus laevis)	-0.1368	0.0265
221379_at			-0.2111	0.004
221382_at			-0.1075	0.0305
221383_at	NMUR1	neuromedin U receptor 1	-0.1436	0.01
221384_at	UCP1	uncoupling protein 1 (mitochondrial; proton carrier)	-0.1961	0.0051
221385_s_at	FFAR3	G protein-coupled receptor 42, free fatty acid receptor 3, similar to Free fatty acid receptor 3 (G-protein coupled receptor 41)	-0.1577	0.0105
221389_at	PLA2G2E	phospholipase A2; group IIE	-0.2106	0.001
221390_s_at	MTMR8	myotubularin related protein 8	-0.2257	0.0159
221393_at	TAAR3	trace amine associated receptor 3	-0.1035	0.0116
221401_at	CACNG5	calcium channel; voltage-dependent; gamma subunit 5	-0.1806	0.0199

221402_at	OR1F1	olfactory receptor; family 1; subfamily F; member 1	-0.1179	0.046
221404_at	IL1F6	interleukin 1 family; member 6 (epsilon)	-0.1457	0.0302
221411_at	HOXD12	homeobox D12	-0.1414	0.0196
221416_at	PLA2G2F	phospholipase A2; group IIF	-0.1374	0.0091
221425_s_at	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-0.6828	0.0384
221432_s_at	SLC25A28	solute carrier family 25; member 28	-1.2487	0
221435_x_at	HYI	hydroxypyruvate isomerase homolog (E. coli)	-0.6371	0.0017
221437_s_at	MRPS15	mitochondrial ribosomal protein S15	-0.5641	0.0361
221439_at	RBBP9	retinoblastoma binding protein 9	-0.1307	0.0267
221442_at	MC3R	melanocortin 3 receptor	-0.1472	0.0011
221445_at	OR1A2	olfactory receptor; family 1; subfamily A; member 2	-0.1505	0.0307
221451_s_at	OR2W1	olfactory receptor; family 2; subfamily W; member 1	-0.1219	0.0235
221452_s_at	TMEM14B	transmembrane protein 14B	-0.9016	0.0002
221459_at	TAAR5	trace amine associated receptor 5	-0.2151	0.0019
221472_at	SERINC3	serine incorporator 3	-0.3215	0.0309
221474_at	MRLC2	myosin regulatory light chain MRLC2	-0.2156	0.0021
221486_at	ENSA	endosulfine alpha	-0.986	0.0003
221488_s_at	CUTA	cutA divalent cation tolerance homolog (E. coli)	-0.3844	0.0161
221490_at	UBAP1	ubiquitin associated protein 1	-0.9347	0
221491_x_at	hCG_1998957	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1, major histocompatibility complex; class II; DR beta 3, major histocompatibility complex; class II; DR beta 4, major histocompatibility complex; class II; DR beta 5	-2.2284	0.0035
221493_at	TSPYL1	TSPY-like 1	-0.6244	0
221496_s_at	TOB2	transducer of ERBB2; 2	-0.8131	0.0288
221512_at	C1orf160	chromosome 1 open reading frame 160	-0.4278	0.0376
221518_s_at	USP47	ubiquitin specific peptidase 47	-0.5406	0.0017
221541_at	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	-3.0853	0
221546_at	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	-0.1158	0.0302
221547_at	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	-0.447	0.0402
221559_s_at	MIS12	MIS12; MIND kinetochore complex component; homolog (yeast)	-0.3721	0.0196
221561_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-0.878	0.0069
221562_s_at	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	-0.4358	0.0227
221568_s_at	LIN7C	lin-7 homolog C (C. elegans)	-0.4599	0.0001

221581_s_at	LAT2	linker for activation of T cells family; member 2	-0.6671	0.0115
221585_at	CACNG4	calcium channel; voltage-dependent; gamma subunit 4	-0.1629	0.0211
221589_s_at	ALDH6A1	aldehyde dehydrogenase 6 family; member A1	-1.0928	0.0041
221599_at	C11orf67	chromosome 11 open reading frame 67	-1.0946	0
221600_s_at	C11orf67	chromosome 11 open reading frame 67	-1.159	0.0008
221605_s_at	PIPOX	pipecolic acid oxidase	-0.2749	0.028
221614_s_at	RPH3AL	rabphilin 3A-like (without C2 domains)	-1.4918	0
221622_s_at	TMEM126B	transmembrane protein 126B	-0.7114	0.0013
221636_s_at	MOSC2	MOCO sulphurase C-terminal domain containing 2	-0.8143	0.0499
221641_s_at	ACOT9	acyl-CoA thioesterase 9	-0.5147	0.009
221644_s_at	SLC45A2	solute carrier family 45; member 2	-0.1382	0.0047
221656_s_at	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	-0.7965	0
221662_s_at	SLC22A7	solute carrier family 22 (organic anion transporter); member 7	-0.2129	0.0028
221669_s_at	ACAD8	acyl-Coenzyme A dehydrogenase family; member 8	-1.3088	0.0001
221675_s_at	CHPT1	choline phosphotransferase 1	-0.7053	0.003
221678_at	ABHD6	abhydrolase domain containing 6	-0.1486	0.0316
221688_s_at	IMP3	IMP3; U3 small nucleolar ribonucleoprotein; homolog (yeast)	-0.6204	0.0033
221689_s_at	PIGP	phosphatidylinositol glycan anchor biosynthesis; class P	-0.7496	0.0018
221698_s_at	CLEC7A	C-type lectin domain family 7; member A	-1.9002	0.0005
221704_s_at	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	-2.6283	0
221714_s_at	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	-0.1488	0.0166
221717_at			-0.2237	0.0005
221719_s_at	LZTS1	leucine zipper; putative tumor suppressor 1	-0.2383	0.0096
221721_s_at	LZTS1	leucine zipper; putative tumor suppressor 1	-0.1032	0.0287
221725_at	WASF2	WAS protein family; member 2	-0.7346	0.0257
221731_x_at	VCAN	versican	-2.6689	0.0105
221740_x_at	LRRC37A2	CDNA clone IMAGE:4902949, Leucine rich repeat containing 37; member A2	-0.6236	0.0031
221747_at	TNS1	Tensin 1	-1.7138	0.0005
221748_s_at	TNS1	tensin 1	-1.2596	0.0026
221760_at	MAN1A1	mannosidase; alpha; class 1A; member 1	-1.8185	0.0002
221767_x_at	HDLBP	high density lipoprotein binding protein (vigilin)	-0.242	0.0319
221769_at	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	-0.5973	0.0073
221773_at	ELK3	ELK3; ETS-domain protein (SRF accessory protein 2)	-1.3751	0.0034

221775_x_at	RPL22	ribosomal protein L22	-0.2815	0.005
221787_at	C6orf120	chromosome 6 open reading frame 120	-0.6999	0.01
221788_at		CDNA FLJ11614 fis; clone HEMBA1004015	-1.3254	0.0003
221808_at	RAB9A	RAB9A; member RAS oncogene family	-0.6649	0.0251
221809_at	RANBP10	RAN binding protein 10	-0.9369	0.0192
221816_s_at	PHF11	PHD finger protein 11	-1.238	0.0001
221822_at	CCDC101	coiled-coil domain containing 101	-0.4169	0.0007
221824_s_at	8-Mar	membrane-associated ring finger (C3HC4) 8	-0.6881	0.0023
221831_at	LUZP1	leucine zipper protein 1	-0.6335	0.0001
221832_s_at	LUZP1	leucine zipper protein 1	-0.7353	0.0002
221839_s_at	UBAP2	ubiquitin associated protein 2	-0.5041	0.0224
221840_at	PTPRE	protein tyrosine phosphatase; receptor type; E	-1.5327	0.0156
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	-2.3871	0
221844_x_at		CDNA clone IMAGE:6208446	-0.3881	0.014
221846_s_at	CASKIN2	CASK interacting protein 2	-0.6934	0.0034
221847_at		Full-length cDNA clone CS0DE005YD08 of Placenta of Homo sapiens (human)	-0.5875	0.0098
221872_at	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	-1.982	0.0007
221885_at	DENND2A	DENN/MADD domain containing 2A	-0.3357	0
221900_at	COL8A2	collagen; type VIII; alpha 2	-0.313	0.0359
221904_at	FAM131A	family with sequence similarity 131; member A	-0.6985	0.0102
221907_at	C14orf172	chromosome 14 open reading frame 172	-0.3158	0.0066
221913_at	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	-0.2235	0.0097
221921_s_at	CADM3	cell adhesion molecule 3	-0.2639	0.0155
221928_at	ACACB	acetyl-Coenzyme A carboxylase beta	-0.5802	0.0186
221929_at	RBM12B	RNA binding motif protein 12B	-0.2257	0.0146
221930_at	PHF7	PHD finger protein 7	-0.1184	0.0146
221931_s_at	SEH1L	SEH1-like (S. cerevisiae)	-0.421	0.0207
221947_at			-0.1874	0.0097
221949_at	LOC222070	hypothetical protein LOC222070	-0.6151	0
221951_at	TMEM80	transmembrane protein 80	-1.3854	0
221979_at	TOPORS	Topoisomerase I binding; arginine/serine-rich	-1.1235	0.0001
221980_at	EMILIN2	Elastin microfibril interfacer 2	-0.1172	0.0444
221990_at	PAX8	paired box 8	-0.1891	0.0022
221995_s_at			-0.5245	0.0013
222002_at	C7orf26	Chromosome 7 open reading frame 26	-0.1004	0.0153
222005_s_at	GNG3	guanine nucleotide binding protein (G protein); gamma 3	-0.2858	0.0008

222015_at	CSNK1E	Casein kinase 1; epsilon	-0.407	0.0213
222043_at	CLU	clusterin	-1.1084	0.0166
222044_at	C20orf67	chromosome 20 open reading frame 67	-0.8658	0
222045_s_at	C20orf67	chromosome 20 open reading frame 67	-0.5553	0.0046
222049_s_at	RBP4	Retinol binding protein 4; plasma	-0.1581	0.0001
222064_s_at	AARSD1	alanyl-tRNA synthetase domain containing 1	-0.8008	0.0004
222065_s_at	FLII	flightless I homolog (Drosophila)	-0.334	0.0264
222066_at	EPB41L1	Erythrocyte membrane protein band 4.1-like 1	-0.2027	0.0226
222069_s_at			-0.1292	0.0396
222073_at	COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	-4.5202	0
222078_at		Transcribed locus	-0.1401	0.0464
222084_s_at	SBF1	SET binding factor 1	-0.1598	0.0083
222093_s_at	ZNHIT4	zinc finger; HIT type 4	-0.3104	0.02
222095_s_at	C1orf76	chromosome 1 open reading frame 76	-0.3586	0.0039
222100_at	CYP2E1	Cytochrome P450; family 2; subfamily E; polypeptide 1	-0.1847	0.0153
222116_s_at	TBC1D16	TBC1 domain family; member 16	-0.9888	0.0019
222125_s_at	PH-4	hypoxia-inducible factor prolyl 4-hydroxylase	-0.7639	0.0272
222148_s_at	RHOT1	ras homolog gene family; member T1	-0.3769	0.0156
222162_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif; 1	-2.7806	0
222171_s_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.4064	0
222192_s_at	C2orf43	chromosome 2 open reading frame 43	-0.5651	0.0235
222200_s_at	BSDC1	BSD domain containing 1	-0.3515	0.0077
222209_s_at	TMEM135	transmembrane protein 135	-0.8563	0.0347
222229_x_at	LOC392501	similar to 60S ribosomal protein L26	-0.3566	0.0001
222231_s_at	LRRC59	leucine rich repeat containing 59	-0.5294	0.0004
222234_s_at	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	-0.2403	0.0336
222243_s_at	TOB2	transducer of ERBB2; 2	-1.1886	0.0003
222256_s_at	PLA2G4B	phospholipase A2; group IVB (cytosolic)	-0.3731	0.0024
222261_at	KIAA1609	KIAA1609	-0.1041	0.0427
222268_x_at	MUC5B	mucin 5B; oligomeric mucus/gel-forming	-0.1323	0.0244
222279_at	RP3-377H14.5	hypothetical protein FLJ35429	-0.4456	0.017
222288_at		Transcribed locus; moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]	-1.6297	0.0056

222290_at	LOC730421	olfactory receptor; family 2; subfamily A; member 20 pseudogene, olfactory receptor; family 2; subfamily A; member 9 pseudogene, region containing olfactory receptor; family 2; subfamily A; member 9 pseudogene; olfactory receptor; family 2; subfamily A; member 20 pseudogene	-0.1917	0.0127
222294_s_at		CDNA clone IMAGE:5745639	-0.9517	0.0222
222297_x_at	LOC390612	similar to ribosomal protein L18	-0.1595	0.0255
222302_at			-1.0635	0.0004
222303_at			-2.0592	0.0004
222304_x_at	OR7E47P	olfactory receptor; family 7; subfamily E; member 47 pseudogene	-0.1996	0.0239
222321_at	AGTR2	angiotensin II receptor; type 2	-0.3373	0.0046
222327_x_at	OR7E156P	olfactory receptor; family 7; subfamily E; member 156 pseudogene	-0.3313	0.0007
222332_at			-0.1341	0.0448
222333_at	ALS2CL	ALS2 C-terminal like	-0.3649	0.0327
222334_at			-0.1268	0.0247
222351_at	PPP2R1B	protein phosphatase 2 (formerly 2A); regulatory subunit A; beta isoform	-0.554	0.0003
222355_at		Transcribed locus	-0.1182	0.037
222365_at		Transcribed locus	-0.2776	0.0012
222377_at	TBX10	T-box 10	-0.27	0.0103
222391_at	TMEM30A	transmembrane protein 30A	-0.3283	0.0495
222401_s_at	TMEM50A	transmembrane protein 50A	-0.5611	0.0044
222408_s_at	YPEL5	yippee-like 5 (Drosophila)	-0.4105	0.0153
222411_s_at	SSR3	signal sequence receptor; gamma (translocon-associated protein gamma)	-0.4217	0.0392
222425_s_at	POLDIP2	polymerase (DNA-directed); delta interacting protein 2	-0.8477	0
222426_at	MAPKAP1	mitogen-activated protein kinase associated protein 1	-0.5462	0.0236
222433_at	ENAH	enabled homolog (Drosophila)	-0.3814	0.0437
222436_s_at	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	-0.5381	0.0452
222438_at	MED4	mediator complex subunit 4	-0.9581	0.0002
222440_s_at	THRAP3	thyroid hormone receptor associated protein 3	-0.5438	0.0001
222447_at	METTL9	methyltransferase like 9	-0.7488	0.0287
222449_at	TMEPAI	transmembrane; prostate androgen induced RNA	-3.1447	0
222450_at	TMEPAI	transmembrane; prostate androgen induced RNA	-2.1465	0
222453_at	CYBRD1	cytochrome b reductase 1	-2.5998	0
222454_s_at	PARVA	parvin; alpha	-1.5371	0

222455_s_at	PARVA	parvin; alpha	-1.728	0
222457_s_at	LIMA1	LIM domain and actin binding 1	-1.0113	0.0401
222465_at	C15orf15	chromosome 15 open reading frame 15, similar to ribosomal protein L24-like	-0.298	0.0437
222468_at	KIAA0319L	KIAA0319-like	-0.3281	0.0128
222469_s_at	TOLLIP	toll interacting protein	-0.4673	0.0348
222474_s_at	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	-0.7642	0.0053
222478_at	VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	-1.1143	0.0045
222481_at	FXC1	fracture callus 1 homolog (rat)	-0.7886	0.0102
222486_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif; 1	-2.0448	0
222490_at	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	-1.149	0.0001
222494_at	FOXN3	forkhead box N3	-0.9025	0.0005
222495_at	C1orf119	chromosome 1 open reading frame 119, similar to K07F5.15	-0.4074	0.0188
222496_s_at	FLJ20273	RNA-binding protein	-0.6944	0.0366
222498_at	AZI2	5-azacytidine induced 2	-0.7282	0
222500_at	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	-1.1516	0.0002
222513_s_at	SORBS1	sorbin and SH3 domain containing 1	-0.9521	0.0004
222517_at	AP3M1	adaptor-related protein complex 3; mu 1 subunit	-1.0767	0.0026
222518_at	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	-0.575	0.0104
222520_s_at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	-0.6162	0
222521_x_at	NDUFC2	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 2; 14.5kDa	-0.3688	0.0091
222537_s_at	CDC42SE1	CDC42 small effector 1	-1.1868	0.0012
222541_at	RSF1	remodeling and spacing factor 1	-1.1252	0.0001
222546_s_at	EPS8L2	EPS8-like 2	-0.1537	0.0182
222549_at	CLDN1	Claudin 1	-1.6319	0.0252
222558_at	P15RS	hypothetical protein FLJ10656	-1.0086	0.0048
222559_s_at	P15RS	hypothetical protein FLJ10656	-1.2171	0.0005
222570_at	FREQ	frequenin homolog (Drosophila)	-0.8611	0.0001
222571_at	ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminyl-2;3-beta-galactosyl-1;3)-N-acetylgalactosaminide alpha-2;6-sialyltransferase 6	-0.6102	0.0001
222572_at	PPM2C	protein phosphatase 2C; magnesium-dependent; catalytic subunit	-1.0178	0.0009
222578_s_at	UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1	-0.7987	0.0126
222579_at	UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1	-0.7359	0.0075
222580_at	ZNF644	zinc finger protein 644	-0.4737	0.0215

222592_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5	-0.4068	0.031
222603_at	ERMP1	endoplasmic reticulum metallopeptidase 1	-1.6264	0.0005
222618_at	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	-0.4203	0.0062
222624_s_at	ZNF639	zinc finger protein 639	-0.7318	0.0013
222671_s_at	JMJD4	jumonji domain containing 4	-0.3955	0
222672_at	LYRM4	LYR motif containing 4	-0.4493	0.0248
222677_x_at			-0.2281	0.0045
222692_s_at	FNDC3B	fibronectin type III domain containing 3B	-1.3548	0.0005
222693_at	FNDC3B	fibronectin type III domain containing 3B	-0.9669	0.0064
222706_at	CCDC49	coiled-coil domain containing 49	-0.5474	0.0001
222709_at	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	-0.4847	0.0191
222710_at	GMPPB	GDP-mannose pyrophosphorylase B	-0.5701	0.0059
222711_s_at	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	-0.1862	0.0095
222714_s_at	LACTB2	lactamase; beta 2	-0.9096	0.0159
222717_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	-1.8654	0.0043
222722_at	OGN	osteoglycin	-5.2066	0
222730_s_at	ZDHHC2	zinc finger; DHHC-type containing 2	-1.8917	0.004
222731_at	ZDHHC2	zinc finger; DHHC-type containing 2	-2.2423	0.0008
222732_at	TRIM39	tripartite motif-containing 39	-0.3681	0.0299
222734_at	WARS2	tryptophanyl tRNA synthetase 2; mitochondrial	-1.13	0.008
222743_s_at	C11orf71	chromosome 11 open reading frame 71	-0.6373	0.0007
222746_s_at	BSPRY	B-box and SPRY domain containing	-0.2561	0.0102
222756_s_at	ARRB1	arrestin; beta 1	-0.6004	0.0013
222783_s_at	SMOC1	SPARC related modular calcium binding 1	-0.1988	0.0057
222784_at	SMOC1	SPARC related modular calcium binding 1	-0.3992	0.0003
222785_x_at	C11orf1	chromosome 11 open reading frame 1	-0.9753	0.0025
222803_at	PRTFDC1	phosphoribosyl transferase domain containing 1	-1.7494	0.0044
222808_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	-0.6632	0.0136
222818_at	OSBPL10	oxysterol binding protein-like 10	-0.1397	0.0279
222828_at	IL20RA	interleukin 20 receptor; alpha	-0.1996	0.014
222829_s_at	IL20RA	interleukin 20 receptor; alpha	-0.518	0.0016
222840_at	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-0.3719	0.0234
222857_s_at	KCNMB4	potassium large conductance calcium-activated channel; subfamily M; beta member 4	-2.1604	0.0249
222860_s_at	PDGFD	platelet derived growth factor D	-1.9751	0.0007
222865_x_at	C16orf30	chromosome 16 open reading frame 30	-0.171	0.0052

222866_s_at	FLVCR2	feline leukemia virus subgroup C cellular receptor family; member 2	-1.6518	0
222871_at	KLHDC8A	kelch domain containing 8A	-2.3333	0.0027
222876_s_at	CENTA2	centaurin; alpha 2	-1.8858	0
222877_at		CDNA: FLJ21027 fis; clone CAE07110	-1.7354	0.0011
222881_at	HPSE	heparanase	-0.8424	0
222885_at	EMCN	endomucin	-2.6498	0
222899_at	ITGA11	integrin; alpha 11	-0.3995	0.0104
222907_x_at	TMEM50B	transmembrane protein 50B	-0.8876	0.0028
222912_at	ARRB1	arrestin; beta 1	-1.1703	0.0002
222913_at	KLF3	Kruppel-like factor 3 (basic)	-0.3293	0.0015
222916_s_at	HDLBP	high density lipoprotein binding protein (vigilin)	-0.9496	0.0001
222924_at	SLMAP	sarcolemma associated protein	-0.3574	0.0364
222933_at	MORN1	MORN repeat containing 1	-0.1071	0.0465
222934_s_at	CLEC4E	C-type lectin domain family 4; member E	-0.6618	0.0161
222937_s_at	MMP28	matrix metallopeptidase 28	-0.1787	0.0314
222940_at	SULT1E1	sulfotransferase family 1E; estrogen-preferring; member 1	-1.1168	0
222967_at	SLC5A7	solute carrier family 5 (choline transporter); member 7	-1.24	0
222968_at			-0.3172	0.0346
222980_at	RAB10	RAB10; member RAS oncogene family	-0.3156	0.0033
222981_s_at	RAB10	RAB10; member RAS oncogene family	-0.6297	0.0046
222982_x_at	SLC38A2	solute carrier family 38; member 2	-0.3856	0.0097
222997_s_at	MRPS21	mitochondrial ribosomal protein S21	-0.5578	0.0003
223009_at	C11orf59	chromosome 11 open reading frame 59	-0.5169	0.0001
223015_at	EIF2A	eukaryotic translation initiation factor 2A; 65kDa	-0.4205	0.0019
223019_at	FAM129B	family with sequence similarity 129; member B	-1.0609	0.0228
223027_at	SNX9	sorting nexin 9	-1.0819	0
223030_at	TRAF7	TNF receptor-associated factor 7	-0.1215	0.0426
223033_s_at	SCYL1	SCY1-like 1 (S. cerevisiae)	-0.5232	0.0326
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter); member 1	-1.4087	0.0002
223058_at	FAM107B	family with sequence similarity 107; member B	-2.3592	0.0025
223059_s_at	FAM107B	family with sequence similarity 107; member B	-2.2423	0.0036
223063_at	C1orf198	chromosome 1 open reading frame 198	-0.5632	0.0059
223070_at	SELK	selenoprotein K	-0.7446	0.0001
223072_s_at	WBP1	WW domain binding protein 1	-0.4119	0.0029
223084_s_at	CCNDBP1	cyclin D-type binding-protein 1	-0.6601	0.0323
223085_at	RNF19A	ring finger protein 19A	-0.7891	0.0055

223092_at	ANKH	ankylosis; progressive homolog (mouse)	-1.3633	0.0032
223093_at	ANKH	ankylosis; progressive homolog (mouse)	-0.4697	0.0191
223103_at	STARD10	StAR-related lipid transfer (START) domain containing 10	-2.3587	0.0013
223104_at	JAGN1	jagunal homolog 1 (Drosophila)	-0.461	0.0419
223105_s_at	TMEM14B	transmembrane protein 14B, transmembrane protein 14C	-0.4456	0.0002
223106_at	TMEM14C	transmembrane protein 14C	-0.4513	0.0004
223113_at	TMEM138	transmembrane protein 138	-0.6948	0.0024
223115_at	MED17	mediator complex subunit 17	-0.2691	0.05
223117_s_at	USP47	ubiquitin specific peptidase 47	-0.6424	0.0035
223119_s_at	USP47	ubiquitin specific peptidase 47	-0.59	0.0115
223125_s_at	C1orf21	chromosome 1 open reading frame 21	-1.259	0.0183
223126_s_at	C1orf21	chromosome 1 open reading frame 21	-2.5205	0
223129_x_at	MYLIP	myosin regulatory light chain interacting protein	-1.5165	0.0003
223130_s_at	MYLIP	myosin regulatory light chain interacting protein	-1.8477	0.0001
223133_at	TMEM14B	transmembrane protein 14B	-0.7953	0
223155_at	HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	-0.4896	0.0006
223167_s_at	USP25	ubiquitin specific peptidase 25	-0.6483	0.0227
223170_at	LOC440181	hypothetical LOC440181, transmembrane protein 98	-1.6052	0.0034
223176_at	KCTD20	potassium channel tetramerisation domain containing 20	-1.2421	0.0025
223177_at	NT5DC1	5'-nucleotidase domain containing 1	-0.5608	0.0302
223191_at	C14orf112	chromosome 14 open reading frame 112	-0.3952	0.0147
223192_at	SLC25A28	solute carrier family 25; member 28	-1.1767	0
223204_at	C4orf18	chromosome 4 open reading frame 18	-0.5911	0.042
223205_s_at	L3MBTL2	l(3)mbt-like 2 (Drosophila)	-0.4326	0.028
223211_at	HACL1	2-hydroxyacyl-CoA lyase 1	-0.6514	0.0302
223217_s_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; zeta	-1.1042	0.02
223218_s_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; zeta	-2.5097	0.0001
223222_at	SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier); member 19	-2.2897	0
223227_at	BBS2	Bardet-Biedl syndrome 2	-0.6131	0.0129
223228_at	LDOC1L	leucine zipper; down-regulated in cancer 1-like	-0.731	0.0154
223230_at	PRPF38A	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	-0.6326	0.0019
223235_s_at	SMOC2	SPARC related modular calcium binding 2	-2.2794	0.0002
223238_s_at	PBRM1	polybromo 1	-0.457	0.042

223239_at	C14orf129	chromosome 14 open reading frame 129	-1.1044	0.0004
223264_at	MESDC1	mesoderm development candidate 1	-1.4587	0
223266_at	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 2	-0.865	0.0017
223267_at	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	-0.8507	0.0013
223268_at	C11orf54	chromosome 11 open reading frame 54	-1.6262	0
223269_at	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	-0.6835	0.0004
223277_at	TMEM103	transmembrane protein 103	-0.4038	0.0254
223280_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-2.6998	0
223299_at	SEC11C	SEC11 homolog C (S. cerevisiae)	-0.6208	0.0463
223306_at	EBPL	emopamil binding protein-like	-1.0607	0.0004
223309_x_at	PNPLA8	patatin-like phospholipase domain containing 8	-0.9753	0.0028
223310_x_at	PNPLA8	patatin-like phospholipase domain containing 8	-0.6874	0.0003
223311_s_at	MTA3	metastasis associated 1 family; member 3	-1.6298	0
223321_s_at	FGFRL1	fibroblast growth factor receptor-like 1	-1.1251	0.0171
223329_x_at	SUGT1	SGT1; suppressor of G2 allele of SKP1 (S. cerevisiae)	-0.5542	0.0103
223330_s_at	SUGT1	SGT1; suppressor of G2 allele of SKP1 (S. cerevisiae)	-1.0311	0.0028
223334_at	TMEM126A	transmembrane protein 126A	-0.7034	0.0084
223343_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	-2.6836	0.0001
223344_s_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	-2.342	0.0001
223350_x_at	LIN7C	lin-7 homolog C (C. elegans)	-0.7358	0
223370_at	PLEKHA3	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 3	-0.547	0.0038
223371_s_at	DNAJC4	DnaJ (Hsp40) homolog; subfamily C; member 4	-0.4055	0.0003
223375_at	TBC1D22B	TBC1 domain family; member 22B	-0.9031	0
223380_s_at	LATS2	LATS; large tumor suppressor; homolog 2 (Drosophila)	-1.0361	0.0007
223386_at	FAM118B	family with sequence similarity 118; member B	-0.6693	0.0355
223395_at	ABI3BP	ABI gene family; member 3 (NESH) binding protein	-2.2484	0.0114
223405_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	-0.8115	0.0252
223408_s_at			-0.7345	0
223409_at			-0.3736	0.0002
223410_s_at			-0.3307	0
223411_at	MIF4GD	MIF4G domain containing	-0.8874	0.0209
223418_x_at	ANKRD13C	ankyrin repeat domain 13C	-0.7583	0.0054

223426_s_at	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	-0.191	0.025
223430_at	SNF1LK2	SNF1-like kinase 2	-1.4022	0.0006
223432_at	OSBP2	oxysterol binding protein 2	-0.6668	0.0046
223442_at	NICN1	nicolin 1	-1.1699	0
223448_x_at	MRPS22	mitochondrial ribosomal protein S22	-0.6195	0.0002
223449_at	SEMA6A	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6A	-3.8915	0
223459_s_at	C1orf56	chromosome 1 open reading frame 56	-1.3428	0
223464_at	OSBPL5	oxysterol binding protein-like 5	-0.3805	0.0001
223467_at	RASD1	RAS; dexamethasone-induced 1	-2.7572	0
223468_s_at	RGMA	RGM domain family; member A	-0.5219	0
223480_s_at	MRPL47	mitochondrial ribosomal protein L47	-0.3157	0.0247
223482_at	TMEM120A	transmembrane protein 120A	-0.5781	0.0315
223486_at	GTPBP8	GTP-binding protein 8 (putative)	-0.6745	0.0117
223503_at	TMEM163	transmembrane protein 163	-1.4121	0.0197
223504_at	RBJ	rab and DnaJ domain containing	-0.5491	0.0474
223509_at	CLDN2	claudin 2	-0.4768	0
223516_s_at	C6orf49	chromosome 6 open reading frame 49	-0.3657	0.0398
223520_s_at	KIF13A	kinesin family member 13A	-0.3498	0.0001
223523_at	TMEM108	transmembrane protein 108	-1.3234	0.0032
223524_s_at	TMEM108	transmembrane protein 108	-2.288	0.0002
223527_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	-0.7838	0.0417
223529_at	SYT4	synaptotagmin IV	-0.6918	0.0127
223549_s_at	ESPN	espin	-0.2793	0.0131
223552_at	LRRC4	leucine rich repeat containing 4	-1.6698	0
223560_s_at	C2orf56	chromosome 2 open reading frame 56	-0.9195	0.0067
223576_at	C6orf203	chromosome 6 open reading frame 203	-0.5537	0.0099
223582_at	GPR98	G protein-coupled receptor 98	-4.3016	0.0001
223583_at	TNFAIP8L2	tumor necrosis factor; alpha-induced protein 8-like 2	-0.7237	0.0001
223587_s_at	AMN	amnionless homolog (mouse)	-0.1748	0.0007
223598_at	RAD23B	RAD23 homolog B (S. cerevisiae)	-0.6166	0.0181
223603_at	ZNF179	zinc finger protein 179	-0.2233	0.0001
223605_at	SLC25A18	solute carrier family 25 (mitochondrial carrier); member 18	-0.2841	0.0001
223608_at	EFCAB2	EF-hand calcium binding domain 2	-1.0888	0.0063
223611_s_at	LNX1	ligand of numb-protein X 1	-0.6181	0.0195
223615_at	ABI3	ABI gene family; member 3	-0.3633	0.0084
223620_at	GPR34	G protein-coupled receptor 34	-2.7171	0.0002
223622_s_at	HYI	hydroxypyruvate isomerase homolog (E. coli)	-0.7223	0.0011

223623_at	C2orf40	chromosome 2 open reading frame 40	-3.276	0
223624_at	ANUBL1	AN1; ubiquitin-like; homolog (Xenopus laevis)	-0.6209	0.007
223631_s_at	C19orf33	chromosome 19 open reading frame 33	-1.12	0
223637_s_at	C11orf56	chromosome 11 open reading frame 56	-0.5261	0.0054
223640_at	HCST	hematopoietic cell signal transducer	-0.7878	0.0248
223647_x_at	HSCB	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	-0.6257	0.0134
223652_at	AS3MT	arsenic (+3 oxidation state) methyltransferase, chromosome 10 open reading frame 32	-2.0687	0.0063
223657_at	C1orf90	chromosome 1 open reading frame 90	-1.1612	0.0001
223658_at	KCNK6	potassium channel; subfamily K; member 6	-0.274	0.0024
223659_at	TMPRSS13	transmembrane protease; serine 13	-0.1286	0.0101
223660_at	ADORA3	adenosine A3 receptor	-2.9715	0
223670_s_at	HEMGN	hemogen	-0.1524	0.0416
223681_s_at	INADL	InaD-like (Drosophila)	-1.1472	0.0017
223695_s_at	ARSD	arylsulfatase D	-0.6356	0.0205
223696_at	ARSD	arylsulfatase D	-1.1418	0.0002
223699_at	CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	-0.113	0.0187
223703_at	C10orf11	chromosome 10 open reading frame 11	-1.8782	0.0001
223710_at	CCL26	chemokine (C-C motif) ligand 26	-0.4117	0.0001
223721_s_at	DNAJC12	DnaJ (Hsp40) homolog; subfamily C; member 12	-2.9601	0
223722_at	DNAJC12	DnaJ (Hsp40) homolog; subfamily C; member 12	-2.5795	0
223727_at	KCNIP2	Kv channel interacting protein 2	-0.4392	0.0059
223745_at	FBXO31	F-box protein 31	-0.1326	0.0421
223752_at	CFC1	cripto; FRL-1; cryptic family 1	-0.1896	0.0008
223753_s_at	CFC1	cripto; FRL-1; cryptic family 1, similar to cryptic	-0.1724	0.0154
223754_at	MGC13057	hypothetical protein MGC13057	-0.5908	0
223757_at	DIO3OS	deiodinase; iodothyronine; type III opposite strand	-0.2953	0.0012
223767_at	GPR84	G protein-coupled receptor 84	-0.3521	0.0007
223769_x_at	HYI	hydroxypyruvate isomerase homolog (E. coli)	-0.7041	0.0004
223775_at	HHIP	hedgehog interacting protein	-0.3991	0.0122
223776_x_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	-0.536	0.0068
223778_at	KIF9	kinesin family member 9	-0.2021	0.0199
223800_s_at	LIMS3	LIM and senescent cell antigen-like domains 3	-1.9517	0
223801_s_at	APOL4	apolipoprotein L; 4	-0.2351	0.0066

223808_s_at	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3; 30kDa (NADH-coenzyme Q reductase), protein tyrosine phosphatase; mitochondrial 1	-1.0551	0
223811_s_at	C7orf20	chromosome 7 open reading frame 20	-0.5796	0.0362
223812_at	LOC51252	hypothetical protein LOC51252	-0.2049	0.037
223813_at	PRND	prion protein 2 (dublet)	-0.1057	0.0055
223828_s_at	LGALS12	lectin; galactoside-binding; soluble; 12 (galectin 12)	-0.2826	0.0003
223836_at	FGFBP2	fibroblast growth factor binding protein 2	-0.2418	0.0013
223843_at	SCARA3	scavenger receptor class A; member 3	-0.7132	0.0121
223845_at	LOC144305	hypothetical protein BC001437	-0.4074	0.0024
223873_s_at	VN1R3	vomeronasal 1 receptor 3	-0.1262	0.0045
223874_at	ARP11	actin-related Arp11	-1.8274	0
223876_at	SPATA16	spermatogenesis associated 16	-0.2245	0.0159
223881_at	ICA1L	islet cell autoantigen 1;69kDa-like	-0.1406	0.0093
223884_at	OPTC	opticin	-0.1764	0.0322
223887_at	GPR132	G protein-coupled receptor 132	-0.2396	0.0029
223895_s_at	EPN3	epsin 3	-1.387	0.0002
223899_at	PBRM1	polybromo 1	-0.1655	0.0164
223907_s_at	PINX1	PIN2-interacting protein 1	-0.3227	0.0492
223910_at	ERN2	endoplasmic reticulum to nucleus signaling 2	-0.2577	0.0072
223911_at	MGC2664	hypothetical protein MGC2664	-0.1296	0.0442
223919_at	P53AIP1	p53-regulated apoptosis-inducing protein 1	-0.219	0.0053
223922_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-2.15	0
223923_at	C21orf62	chromosome 21 open reading frame 62	-0.1139	0.0444
223938_at	C1orf49	chromosome 1 open reading frame 49	-0.1759	0.0173
223944_at	NLRP12	NLR family; pyrin domain containing 12	-0.1392	0.0383
223946_at	MED23	mediator complex subunit 23	-0.4241	0.0055
223951_at	C21orf116	chromosome 21 open reading frame 116	-0.1671	0.0409
223953_s_at	ZBTB37	zinc finger and BTB domain containing 37	-0.1704	0.0191
223955_at	EFCAB4B	EF-hand calcium binding domain 4B	-0.1058	0.01
223982_s_at	PNPLA8	patatin-like phospholipase domain containing 8	-0.8109	0
223986_x_at	DMRT2	doublesex and mab-3 related transcription factor 2	-0.1271	0.0155
223992_x_at	ZCWPW1	zinc finger; CW type with PWWP domain 1	-0.1762	0.008
224000_at	C2orf16	chromosome 2 open reading frame 16	-0.1822	0.0441
224007_at	HSFY1	heat shock transcription factor; Y linked 2, heat shock transcription factor; Y-linked 1	-0.1955	0.01

224011_at		CDNA clone IMAGE:3446313	-0.2135	0.0072
224019_at	SCD5	stearoyl-CoA desaturase 5	-0.1625	0.0034
224023_s_at	C3orf10	chromosome 3 open reading frame 10	-0.2375	0.0037
224042_at	UPB1	ureidopropionase; beta	-0.1032	0.0334
224051_at			-0.1434	0.0162
224054_at			-0.1673	0.0138
224061_at	INMT	indolethylamine N-methyltransferase	-4.6695	0
224066_s_at	HIPK2	homeodomain interacting protein kinase 2	-0.1235	0.0074
224074_at	VSX1	visual system homeobox 1	-0.2029	0.0003
224087_at			-0.1732	0.0376
224088_at	NMUR2	neuromedin U receptor 2	-0.1153	0.0242
224093_at	IFNK	interferon; kappa	-0.1299	0.0062
224108_at			-0.1107	0.0194
224112_at		Clone FLC0461 PRO2812	-0.131	0.0118
224117_at	LOC284912	hypothetical gene supported by BC001801	-0.1601	0.0253
224119_at		CDNA clone IMAGE:3139291	-0.1058	0.0415
224122_at			-0.1397	0.0411
224123_at	DKFZp434F142	hypothetical protein DKFZp434F142	-0.1232	0.0303
224129_s_at	HDPY-30	dpy-30-like protein	-0.3078	0.0124
224151_s_at	AK3	adenylate kinase 3	-0.6732	0.0012
224156_x_at	IL17RB	interleukin 17 receptor B	-0.2402	0.0028
224157_at	KAAG1	kidney associated antigen 1	-0.1532	0.0041
224160_s_at	ACAD9	acyl-Coenzyme A dehydrogenase family; member 9	-0.7005	0.0032
224174_at	TTTY11	testis-specific transcript; Y-linked 11	-0.1223	0.0179
224175_s_at	TRIM34	tripartite motif-containing 34, tripartite motif-containing 6 and tripartite motif-containing 34	-0.2685	0.0213
224178_s_at	SOX6	SRY (sex determining region Y)-box 6	-0.2088	0.001
224184_s_at	BOC	Boc homolog (mouse)	-0.7516	0
224197_s_at	C1QTNF1	C1q and tumor necrosis factor related protein 1	-0.75	0
224198_at	ELA1	elastase 1; pancreatic	-0.6685	0
224207_x_at	MMP28	matrix metallopeptidase 28	-0.3603	0.0016
224208_at	PLEKHA8	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 8	-0.1309	0.0198
224215_s_at	DLL1	delta-like 1 (Drosophila)	-1.4943	0.0039
224235_at			-0.2326	0.0034
224238_at			-0.2063	0.0045
224245_at	INGX	inhibitor of growth family; X-linked; pseudogene	-0.1496	0.0251
224256_at		Full length insert cDNA clone YB31B05	-0.185	0.0088

224261_at		PRO3098	-0.4996	0.0109
224273_at	C3orf20	chromosome 3 open reading frame 20	-0.2213	0.0013
224280_s_at	FAM54B	family with sequence similarity 54; member B	-0.5338	0.0111
224283_x_at	IL18BP	interleukin 18 binding protein	-0.2036	0.0038
224291_at	CACNG6	calcium channel; voltage-dependent; gamma subunit 6	-0.1056	0.0236
224309_s_at	SUGT1	SGT1; suppressor of G2 allele of SKP1 (S. cerevisiae)	-0.5799	0.0106
224324_at	MRO	maestro	-0.2181	0.0026
224330_s_at	MRPL27	mitochondrial ribosomal protein L27	-0.4332	0.0047
224336_s_at	DUSP16	dual specificity phosphatase 16	-0.9577	0.0302
224339_s_at	ANGPTL1	angiopoietin-like 1	-3.0973	0
224341_x_at	TLR4	toll-like receptor 4	-1.973	0
224346_at			-0.1622	0.0258
224348_s_at			-0.8511	0
224356_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-2.874	0
224357_s_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	-1.5645	0
224358_s_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	-1.4114	0.0001
224360_s_at	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	-0.125	0.0287
224361_s_at	IL17RB	interleukin 17 receptor B	-0.2117	0.0009
224379_at	FTHL17	ferritin; heavy polypeptide-like 17	-0.2275	0
224390_s_at	RGS8	regulator of G-protein signaling 8	-0.16	0.0068
224391_s_at	SIAE	sialic acid acetylesterase	-1.1284	0.0124
224393_s_at	CECR6	cat eye syndrome chromosome region; candidate 6	-0.2072	0.0126
224415_s_at	HINT2	histidine triad nucleotide binding protein 2	-0.7619	0.0072
224432_at	SH3GLB2	SH3-domain GRB2-like endophilin B2	-0.1532	0.0243
224443_at	C1orf97	chromosome 1 open reading frame 97	-0.7598	0.0258
224444_s_at	C1orf97	chromosome 1 open reading frame 97	-0.6141	0.0043
224445_s_at	ZFYVE21	zinc finger; FYVE domain containing 21	-0.7165	0.0137
224449_at	DDI2	DDI1; DNA-damage inducible 1; homolog 2 (S. cerevisiae)	-0.1418	0.0047
224450_s_at	RIOK1	RIO kinase 1 (yeast)	-0.4037	0.0194
224454_at	ETNK1	ethanolamine kinase 1	-0.1297	0.0309
224475_at			-0.1613	0.0131
224488_s_at	SPON1	spondin 1; extracellular matrix protein	-0.2691	0.0008
224500_s_at	MON1A	MON1 homolog A (yeast)	-0.4651	0.0418
224512_s_at	LSMD1	LSM domain containing 1	-0.549	0.0006
224522_s_at	DCAKD	dephospho-CoA kinase domain containing	-0.6279	0.0028
224523_s_at	C3orf26	chromosome 3 open reading frame 26	-0.5197	0.0086

224537_at	PCDHGC5	protocadherin gamma subfamily C; 5	-0.1093	0.0362
224538_s_at	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	-0.1556	0.0053
224543_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	-0.1708	0.0413
224548_at	HES7	hairy and enhancer of split 7 (Drosophila)	-0.2261	0.0361
224552_s_at	KCNK4	potassium channel; subfamily K; member 4	-0.1919	0.0004
224560_at	TIMP2	TIMP metallopeptidase inhibitor 2	-1.0918	0.0165
224573_at	MGC71993	similar to DNA segment; Chr 11; Brigham & Womens Genetics 0434 expressed	-0.3219	0.0024
224622_at	TBC1D14	TBC1 domain family; member 14	-0.4404	0.0109
224633_s_at	GPATCH4	G patch domain containing 4	-0.2117	0.0071
224635_s_at	BIRC6	baculoviral IAP repeat-containing 6 (apollon)	-0.4006	0.0171
224646_x_at	H19	H19; imprinted maternally expressed untranslated mRNA	-4.8514	0
224654_at	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	-0.3967	0.0409
224655_at	AK3	adenylate kinase 3	-0.5186	0
224657_at	ERRFI1	ERBB receptor feedback inhibitor 1	-1.6542	0.0003
224658_x_at	PACS1	phosphofurin acidic cluster sorting protein 1	-0.3803	0.0196
224659_at	SEPN1	selenoprotein N; 1	-0.5915	0.0011
224660_at	PIGY	phosphatidylinositol glycan anchor biosynthesis; class Y	-0.3135	0.009
224666_at	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	-0.7455	0.0054
224672_x_at	MESDC2	mesoderm development candidate 2	-0.4013	0.0014
224677_x_at	C11orf31	chromosome 11 open reading frame 31	-0.4138	0.0168
224679_at	MESDC2	mesoderm development candidate 2	-0.431	0.0411
224683_at	FBXO18	F-box protein; helicase; 18	-0.4633	0.0026
224694_at	ANTXR1	anthrax toxin receptor 1	-1.3392	0.002
224698_at	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	-0.4449	0.0069
224700_at	STT3B	STT3; subunit of the oligosaccharyltransferase complex; homolog B (S. cerevisiae)	-0.415	0.0103
224707_at	C5orf32	chromosome 5 open reading frame 32	-0.6966	0.0409
224710_at	RAB34	RAB34; member RAS oncogene family	-3.6311	0
224729_s_at	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	-0.7919	0.0007
224735_at	CYBASC3	cytochrome b; ascorbate dependent 3	-2.1209	0
224746_at	KIAA1522	KIAA1522	-0.8634	0.0194
224750_at	RNF185	ring finger protein 185	-0.4716	0.0305
224755_at	TM9SF3	transmembrane 9 superfamily member 3	-0.9806	0.0018

224764_at	ARHGAP21	Rho GTPase activating protein 21	-0.7791	0.0015
224780_at	RBM17	RNA binding motif protein 17	-0.6473	0.0179
224784_at	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 6	-0.8151	0.0001
224789_at	WDR40A	WD repeat domain 40A	-0.5405	0.0046
224799_at	NDFIP2	Nedd4 family interacting protein 2	-0.9061	0.0079
224801_at	NDFIP2	Nedd4 family interacting protein 2	-0.726	0.0478
224802_at	NDFIP2	Nedd4 family interacting protein 2	-1.0043	0.0049
224808_s_at	C7orf20	chromosome 7 open reading frame 20	-0.6463	0.0025
224809_x_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	-0.5139	0.0082
224811_at		CDNA FLJ30652 fis; clone DFNES2000011	-1.0207	0
224812_at	HIBADH	3-hydroxyisobutyrate dehydrogenase	-0.586	0.0051
224816_at	C7orf20	Chromosome 7 open reading frame 20	-1.17	0
224817_at	SH3PXD2A	SH3 and PX domains 2A	-1.42	0.0003
224820_at	FAM36A	family with sequence similarity 36; member A	-0.9877	0.0016
224821_at	ABHD14B	abhydrolase domain containing 14B	-1.1432	0.0056
224823_at	MYLK	myosin; light chain kinase	-3.3193	0
224826_at	RP5-1022P6.2	hypothetical protein KIAA1434	-0.9485	0.0184
224831_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	-0.448	0.0433
224833_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	-0.7991	0.0018
224840_at	FKBP5	FK506 binding protein 5	-0.8225	0.0391
224861_at	GNAQ	Guanine nucleotide binding protein (G protein); q polypeptide	-0.9397	0
224862_at	GNAQ	Guanine nucleotide binding protein (G protein); q polypeptide	-0.7582	0.0007
224865_at	MLSTD2	male sterility domain containing 2	-0.6231	0.0377
224871_at	FAM79A	family with sequence similarity 79; member A	-0.6344	0.0099
224887_at	GNPTG	N-acetylglucosamine-1-phosphate transferase; gamma subunit	-0.6114	0.0223
224900_at	ANKFY1	ankyrin repeat and FYVE domain containing 1	-0.5275	0.0143
224901_at	SCD5	stearoyl-CoA desaturase 5	-1.0111	0.0317
224906_at	TMEM16F	transmembrane protein 16F	-0.5528	0.0119
224912_at	TTC7A	tetratricopeptide repeat domain 7A	-0.918	0.0002
224916_at	TMEM173	transmembrane protein 173	-0.8937	0.0022
224918_x_at	MGST1	microsomal glutathione S-transferase 1	-1.9818	0.0436
224923_at	TTC7A	tetratricopeptide repeat domain 7A	-0.936	0
224924_at	TTC7A	tetratricopeptide repeat domain 7A	-0.4516	0.0001
224928_at	SETD7	SET domain containing (lysine methyltransferase) 7	-0.8088	0.0049
224929_at	TMEM173	transmembrane protein 173	-1.4946	0

224937_at	PTGFRN	prostaglandin F2 receptor negative regulator	-1.2177	0.0246
224940_s_at	PAPPA	pregnancy-associated plasma protein A; pappalysin 1	-1.8315	0.0069
224958_at	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	-0.5532	0.0108
224964_s_at	GNG2	guanine nucleotide binding protein (G protein); gamma 2	-1.9836	0.0013
224970_at	NFIA	nuclear factor I/A	-1.0771	0.0001
224975_at	NFIA	nuclear factor I/A	-1.1254	0
224976_at	NFIA	nuclear factor I/A	-1.2079	0.0041
224978_s_at	USP36	ubiquitin specific peptidase 36	-1.5984	0
224979_s_at	USP36	ubiquitin specific peptidase 36	-0.4938	0.0024
224989_at		Full-length cDNA clone CS0DE011YO20 of Placenta of Homo sapiens (human)	-0.844	0.0183
224990_at	C4orf34	chromosome 4 open reading frame 34	-0.874	0.001
224995_at	SPIRE1	spire homolog 1 (Drosophila)	-0.7206	0.0002
224997_x_at	H19	H19; imprinted maternally expressed untranslated mRNA	-4.2894	0
225003_at	MGC3205	MBC3205, hypothetical protein MGC3205	-0.5401	0.0338
225012_at	HDLBP	high density lipoprotein binding protein (vigilin)	-1.6507	0
225013_at	LZTS2	leucine zipper; putative tumor suppressor 2	-0.115	0.0198
225016_at	APCDD1	adenomatosis polyposis coli down-regulated 1	-2.0703	0.0174
225032_at	FNDC3B	fibronectin type III domain containing 3B	-0.6709	0.0003
225044_at	NT5C3L	5'-nucleotidase; cytosolic III-like	-0.5673	0.0401
225048_at	PHF10	PHD finger protein 10	-0.9248	0.0012
225055_at		Homo sapiens; clone IMAGE:3345917; mRNA	-0.4829	0.0458
225065_x_at	C17orf45	chromosome 17 open reading frame 45	-1.5016	0.0008
225069_at	PCYT1A	Phosphate cytidylyltransferase 1; choline; alpha	-0.5878	0.0062
225070_at	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	-0.81	0.0091
225083_at	GTF3C6	general transcription factor IIIC; polypeptide 6; alpha 35kDa	-0.3343	0.0033
225093_at	UTRN	utrophin	-0.7524	0.0007
225095_at	SPTLC2	Serine palmitoyltransferase; long chain base subunit 2	-0.5626	0.0404
225108_at	HEATR2	HEAT repeat containing 2	-1.5604	0.0015
225110_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-0.3513	0.0499
225121_at	TBC1D23	TBC1 domain family; member 23	-0.9103	0.0004
225122_at	RNF31	ring finger protein 31	-0.1802	0.0057
225124_at	PPP1R9B	protein phosphatase 1; regulatory (inhibitor) subunit 9B	-0.9048	0.002
225130_at	ZRANB1	zinc finger; RAN-binding domain containing 1	-1.5157	0.0003

225131_at	ZRANB1	zinc finger; RAN-binding domain containing 1	-1.7393	0
225132_at	FBXL3	F-box and leucine-rich repeat protein 3	-0.7765	0.0004
225138_at	ZRANB1	zinc finger; RAN-binding domain containing 1	-1.6644	0
225144_at	BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	-0.9705	0
225148_at	RPS19BP1	ribosomal protein S19 binding protein 1	-1.004	0.0022
225151_at	RTKN	rhotekin	-0.1289	0.034
225162_at	SH3D19	SH3 domain protein D19	-2.7992	0
225165_at	PPP1R1B	protein phosphatase 1; regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein; DARPP-32)	-0.5681	0.0024
225166_at	ARHGAP18	Rho GTPase activating protein 18	-1.9895	0
225171_at	ARHGAP18	Rho GTPase activating protein 18	-0.858	0.0012
225173_at	ARHGAP18	Rho GTPase activating protein 18	-0.9403	0.0129
225177_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)	-0.5064	0.0478
225182_at	TMEM50B	transmembrane protein 50B	-0.9654	0.0008
225185_at	MRAS	muscle RAS oncogene homolog	-1.978	0.0002
225186_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-0.7792	0.0001
225188_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-2.3751	0
225189_s_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-2.1005	0
225190_x_at	RPL35A	ribosomal protein L35a	-0.2768	0.0009
225206_s_at	MTRF1L	mitochondrial translational release factor 1-like	-0.5005	0.0037
225207_at	PDK4	pyruvate dehydrogenase kinase; isozyme 4	-0.8915	0.0316
225212_at	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier); member 25	-2.0204	0
225213_at	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	-0.5992	0.0115
225225_at	KRTAP4-7	Keratin associated protein 4-7	-0.4843	0.0201
225227_at		CDNA clone IMAGE:5299642	-0.6912	0.0416
225228_at	TMEM77	transmembrane protein 77	-0.7074	0.0036
225231_at	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	-1.0534	0.0006
225238_at	MSI2	musashi homolog 2 (Drosophila)	-1.0743	0.0069
225240_s_at	MSI2	musashi homolog 2 (Drosophila)	-0.8181	0.0034
225243_s_at	SLMAP	sarcolemma associated protein	-0.3897	0.0207
225244_at	C1orf142	chromosome 1 open reading frame 142	-1.0427	0
225255_at	MRPL35	mitochondrial ribosomal protein L35	-0.4932	0.0097
225258_at	FBLIM1	filamin binding LIM protein 1	-1.7133	0.0001
225262_at	FOSL2	FOS-like antigen 2	-1.8624	0

225263_at	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	-1.2203	0.0019
225264_at	RARS2	arginyl-tRNA synthetase 2; mitochondrial (putative)	-0.8531	0.0028
225272_at	SAT2	spermidine/spermine N1-acetyltransferase 2	-0.8043	0.0005
225273_at	WWC3	WWC family member 3	-0.9757	0.0031
225275_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	-2.4998	0.0014
225280_x_at	ARSD	arylsulfatase D	-0.7709	0.0018
225282_at	SMAP1L	stromal membrane-associated protein 1-like	-0.644	0.014
225284_at	DNAJC3	DnaJ (Hsp40) homolog; subfamily C; member 3, hypothetical protein LOC144871	-0.8212	0.0025
225286_at	ARSD	arylsulfatase D	-1.5023	0
225289_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	-0.6892	0.0043
225298_at	PNKD	paroxysmal nonkinesigenic dyskinesia	-1.2768	0
225302_at	TXNDC10	thioredoxin domain containing 10	-0.4437	0.0402
225303_at	KIRREL	kin of IRRE like (Drosophila)	-1.8133	0
225305_at	SLC25A29	solute carrier family 25; member 29	-1.0546	0.0002
225306_s_at	SLC25A29	solute carrier family 25; member 29	-1.2691	0.0001
225308_s_at	TANC1	tetratricopeptide repeat; ankyrin repeat and coiled-coil containing 1	-0.8768	0.0104
225311_at	IVD	isovaleryl Coenzyme A dehydrogenase	-1.0474	0.0044
225312_at	COMMD6	COMM domain containing 6	-0.7028	0
225325_at	FLJ20160	FLJ20160 protein	-0.9483	0.0367
225330_at	IGF1R	insulin-like growth factor 1 receptor	-1.1134	0.0176
225334_at	C10orf32	chromosome 10 open reading frame 32	-0.4197	0.0111
225338_at	ZYG11B	zyg-11 homolog B (C. elegans)	-0.456	0.0017
225344_at	NCOA7	nuclear receptor coactivator 7	-0.9871	0
225348_at	FUSIP1	FUS interacting protein (serine/arginine-rich) 1, similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein...	-0.9166	0.0248
225352_at	TLOC1	translocation protein 1	-0.4488	0.0243
225353_s_at	C1QC	complement component 1; q subcomponent; C chain	-1.8714	0.0005
225354_s_at	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	-0.6041	0.0174
225358_at	DNAJC19	DnaJ (Hsp40) homolog; subfamily C; member 19	-0.5537	0.037
225359_at	DNAJC19	DnaJ (Hsp40) homolog; subfamily C; member 19	-0.7359	0.0065

225363_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-0.4745	0.0217
225367_at	PGM2	phosphoglucomutase 2	-0.6226	0.034
225372_at	C10orf54	chromosome 10 open reading frame 54	-0.4706	0
225373_at	C10orf54	chromosome 10 open reading frame 54	-0.9746	0.0044
225375_at	C17orf32	chromosome 17 open reading frame 32	-0.7106	0.0022
225381_at	LOC399959	hypothetical gene supported by BX647608	-2.5982	0.0008
225390_s_at	KLF13	Kruppel-like factor 13	-1.1443	0.0102
225396_at		CDNA FLJ31794 fis; clone NT2RI2008808	-0.6955	0.0202
225404_at	C1orf212	chromosome 1 open reading frame 212	-0.9548	0.0002
225407_at	MBP	myelin basic protein	-0.6668	0.0113
225420_at	GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	-1.2166	0.0293
225424_at	GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	-1.4297	0.0142
225427_s_at	APOA1BP	apolipoprotein A-I binding protein	-0.559	0.0135
225435_at	SSR1	Signal sequence receptor; alpha (translocon-associated protein alpha)	-0.9221	0.025
225441_x_at	LSMD1	LSM domain containing 1	-0.4862	0.0019
225442_at	DDR2	Discoidin domain receptor family; member 2	-1.6955	0.0136
225448_at	NAPG	N-ethylmaleimide-sensitive factor attachment protein; gamma	-0.6922	0.0001
225464_at	FRMD6	FERM domain containing 6	-1.9546	0.0009
225475_at	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	-0.8881	0.0002
225479_at	LRRC58	leucine rich repeat containing 58	-1.1061	0
225481_at	FRMD6	FERM domain containing 6	-1.8332	0.0006
225491_at	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter); member 2	-3.4488	0
225494_at		Transcribed locus; strongly similar to XP_530050.1 hypothetical protein XP_530050 [Pan troglodytes]	-0.5089	0.0024
225504_at		MRNA; cDNA DKFZp686E0389 (from clone DKFZp686E0389)	-0.5991	0.0226
225511_at	GPRC5B	G protein-coupled receptor; family C; group 5; member B	-0.4554	0.0144
225512_at	ZBTB38	zinc finger and BTB domain containing 38	-0.7073	0.0002
225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter; y+ system); member 2	-1.4749	0.0149
225523_at	MRPL53	mitochondrial ribosomal protein L53	-0.658	0.0001
225524_at	ANTXR2	anthrax toxin receptor 2	-1.4118	0.007
225525_at	CTA-221G9.4	KIAA1671 protein	-0.7773	0.0155
225534_at	C8orf40	chromosome 8 open reading frame 40	-0.5087	0.0234

225539_at	ZNF295	zinc finger protein 295	-2.1293	0
225546_at	EEF2K	eukaryotic elongation factor-2 kinase	-0.543	0.0417
225550_at	C1orf71	chromosome 1 open reading frame 71	-0.5711	0.0251
225557_at	AXUD1	AXIN1 up-regulated 1	-2.3467	0
225564_at	SPATA13	spermatogenesis associated 13	-1.0348	0.0151
225566_at	NRP2	neuropilin 2	-1.3332	0.0016
225571_at	LIFR	leukemia inhibitory factor receptor alpha	-1.7642	0.0008
225574_at	RWDD4A	RWD domain containing 4A	-1.1563	0.0012
225575_at	LIFR	leukemia inhibitory factor receptor alpha	-2.4614	0.0002
225579_at	PQLC3	PQ loop repeat containing 3	-1.2894	0.0002
225591_at	FBXO25	F-box protein 25	-1.5751	0
225611_at			-1.0524	0.0141
225615_at	LOC126917	hypothetical protein LOC126917	-1.0271	0
225618_at	ARHGAP27	Rho GTPase activating protein 27	-0.2942	0.0353
225627_s_at	CACHD1	cache domain containing 1	-1.8938	0.002
225629_s_at	ZBTB4	zinc finger and BTB domain containing 4	-0.8849	0.0001
225632_s_at	ISY1	ISY1 splicing factor homolog (S. cerevisiae), RAB43; member RAS oncogene family	-0.2735	0.047
225641_at	MEF2D	myocyte enhancer factor 2D	-0.2934	0.036
225660_at	SEMA6A	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6A	-3.0882	0
225664_at	COL12A1	collagen; type XII; alpha 1	-2.7591	0
225678_at	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	-0.7899	0
225685_at		CDNA FLJ31353 fis; clone MESAN2000264	-1.531	0.0024
225688_s_at	PHLDB2	pleckstrin homology-like domain; family B; member 2	-2.0677	0.0002
225692_at	CAMTA1	calmodulin binding transcription activator 1	-0.3463	0.0252
225699_at	C7orf40	chromosome 7 open reading frame 40	-0.6629	0.0388
225714_s_at			-0.1324	0.0004
225720_at	SYNPO2	synaptopodin 2	-2.2956	0
225721_at	SYNPO2	synaptopodin 2	-1.5302	0.0009
225728_at	SORBS2	sorbin and SH3 domain containing 2	-2.3293	0.0013
225729_at	C6orf89	chromosome 6 open reading frame 89	-0.7705	0.0018
225762_x_at	LOC284801	hypothetical protein LOC284801	-0.4963	0.0046
225763_at	RCSD1	RCSD domain containing 1	-0.9834	0.009
225767_at			-2.4714	0.0002
225780_at	DDI2	DDI1; DNA-damage inducible 1; homolog 2 (S. cerevisiae), regulatory solute carrier protein; family 1; member 1	-1.3742	0

225783_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	-0.5208	0.0063
225785_at	REEP3	receptor accessory protein 3	-0.3686	0.0129
225787_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	-0.5205	0.0037
225789_at	CENTG3	centaurin; gamma 3	-0.6201	0.0158
225792_at	HOOK1	hook homolog 1 (Drosophila)	-1.1662	0.0171
225794_s_at	C22orf32	chromosome 22 open reading frame 32	-0.9218	0.0001
225795_at	C22orf32	chromosome 22 open reading frame 32	-0.947	0.0015
225796_at	PXK	PX domain containing serine/threonine kinase	-0.5088	0.0175
225798_at	JAZF1	JAZF zinc finger 1	-1.5228	0.0005
225800_at	JAZF1	JAZF zinc finger 1	-2.0575	0
225804_at	CYB5D2	cytochrome b5 domain containing 2	-1.0924	0.0001
225809_at	DKFZP564O0823	DKFZP564O0823 protein	-2.7836	0.0003
225810_at	MTMR10	myotubularin related protein 10	-0.8673	0.0007
225811_at		Transcribed locus	-1.0103	0
225817_at	CGNL1	cingulin-like 1	-2.3147	0.0112
225819_at	TBRG1	transforming growth factor beta regulator 1	-0.8516	0
225822_at	TMEM125	transmembrane protein 125	-0.2787	0
225831_at	LUZP1	leucine zipper protein 1	-1.2114	0
225835_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters); member 2	-0.7299	0.0338
225842_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-1.54	0.0308
225844_at	POLE4	polymerase (DNA-directed); epsilon 4 (p12 subunit)	-0.8985	0.0038
225845_at	ZBTB44	zinc finger and BTB domain containing 44	-0.4586	0.0047
225847_at	AADACL1	arylacetamide deacetylase-like 1	-1.6961	0.0001
225849_s_at	SFT2D1	SFT2 domain containing 1	-0.5331	0.0376
225855_at	EPB41L5	erythrocyte membrane protein band 4.1 like 5	-1.362	0.0001
225867_at	VASN	vasorin	-1.2374	0.0004
225869_s_at	UNC93B1	unc-93 homolog B1 (C. elegans)	-0.2853	0.0227
225872_at	SLC35F5	solute carrier family 35; member F5	-0.5728	0.0022
225884_s_at	GZF1	GDNF-inducible zinc finger protein 1	-1.3339	0
225886_at		Full-length cDNA clone CS0DF030YM05 of Fetal brain of Homo sapiens (human)	-0.6851	0.0063
225893_at		Clone TESTIS-724 mRNA sequence	-0.8134	0.0026
225894_at	SYNPO2	synaptopodin 2	-0.2988	0.0075
225895_at	SYNPO2	synaptopodin 2	-2.1506	0.0006
225901_at	PTPMT1	protein tyrosine phosphatase; mitochondrial 1	-1.1844	0
225908_at	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	-0.7497	0.0025

225910_at	HELZ	helicase with zinc finger	-0.5674	0.0349
225914_s_at	CAB39L	calcium binding protein 39-like	-2.5106	0
225915_at	CAB39L	calcium binding protein 39-like	-4.1423	0
225919_s_at	C9orf72	chromosome 9 open reading frame 72	-1.5176	0.0007
225923_at		CDNA FLJ41394 fis; clone BRCAN2026197	-1.2739	0.0014
225925_s_at	USP48	ubiquitin specific peptidase 48	-1.144	0
225926_at	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	-0.558	0.0121
225939_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3	-0.5195	0.0167
225940_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3	-0.853	0.0058
225941_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3	-1.0868	0.0043
225953_at	P15RS	hypothetical protein FLJ10656	-1.0365	0
225954_s_at	MIDN	midnolin	-0.78	0.0172
225955_at	LOC653506	meteorin; glial cell differentiation regulator-like, similar to meteorin; glial cell differentiation regulator-like	-1.4089	0.003
225966_at	C17orf89	chromosome 17 open reading frame 89	-0.1788	0.0318
225975_at	PCDH18	protocadherin 18	-1.511	0.02
225982_at	UBTF	upstream binding transcription factor; RNA polymerase I	-0.4406	0.0182
225987_at	STEAP4	STEAP family member 4	-4.0636	0
225990_at	BOC	Boc homolog (mouse)	-1.7804	0
225991_at	TMEM41A	transmembrane protein 41A	-0.5973	0.0434
225996_at	LONRF2	LON peptidase N-terminal domain and ring finger 2	-2.3161	0.0004
226008_at	NDNL2	necdin-like 2	-0.5806	0.0039
226011_at	CCDC12	coiled-coil domain containing 12	-0.6134	0.0006
226012_at	ANKRD11	ankyrin repeat domain 11	-0.9339	0.0001
226013_at	TRAK1	trafficking protein; kinesin binding 1	-0.5308	0.0176
226014_at	EIF3S5	Eukaryotic translation initiation factor 3; subunit 5 epsilon; 47kDa	-0.1048	0.0457
226018_at	C7orf41	chromosome 7 open reading frame 41	-0.5808	0.0138
226019_at	OMA1	OMA1 homolog; zinc metallopeptidase (S. cerevisiae)	-0.6157	0.0152
226020_s_at	DAB1	OMA1 homolog; zinc metallopeptidase (S. cerevisiae), disabled homolog 1 (Drosophila)	-0.6774	0.0442
226021_at	RDH10	retinol dehydrogenase 10 (all-trans)	-1.5732	0.0013
226024_at	COMMD1	copper metabolism (Murr1) domain containing 1	-0.6828	0
226026_at	DIRC2	disrupted in renal carcinoma 2	-0.9423	0.0005
226028_at	ROBO4	roundabout homolog 4; magic roundabout (Drosophila)	-0.6444	0.0183
226030_at	ACADSB	acyl-Coenzyme A dehydrogenase; short/branched chain	-2.4166	0
226038_at	LONRF1	LON peptidase N-terminal domain and ring finger 1	-0.6333	0.0131

226039_at	MGAT4A	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme A	-1.0753	0.0493
226047_at	MRVI1	murine retrovirus integration site 1 homolog	-1.2991	0.001
226051_at	SELM	selenoprotein M	-1.818	0.0019
226056_at	CDGAP	Cdc42 GTPase-activating protein	-0.3798	0.0054
226066_at	MITF	microphthalmia-associated transcription factor	-1.2122	0.0112
226068_at	SYK	spleen tyrosine kinase	-1.1159	0.0044
226073_at	LOC219854	hypothetical protein LOC219854	-1.0631	0.0012
226074_at	PPM1M	protein phosphatase 1M (PP2C domain containing)	-0.7813	0.0006
226089_at	LOC653256	RAB; member of RAS oncogene family-like 3, similar to RAB; member of RAS oncogene family-like 3	-0.6393	0.0439
226096_at	FNDC5	fibronectin type III domain containing 5	-3.7036	0
226097_at	FNDC5	fibronectin type III domain containing 5	-0.63	0
226099_at	ELL2	elongation factor; RNA polymerase II; 2	-2.4299	0.0001
226103_at	NEXN	nexilin (F actin binding protein)	-3.0119	0
226106_at	RNF141	ring finger protein 141	-0.8182	0
226112_at	SGCB	sarcoglycan; beta (43kDa dystrophin-associated glycoprotein)	-0.5932	0.0352
226119_at	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-0.5909	0.0013
226134_s_at		Transcribed locus	-0.9653	0.0004
226135_at	C6orf107	chromosome 6 open reading frame 107	-0.8798	0.0083
226139_at		Full length insert cDNA clone ZA04F06	-0.2308	0.0457
226148_at	ZBTB44	zinc finger and BTB domain containing 44	-0.2761	0.0409
226162_at	SLC30A6	solute carrier family 30 (zinc transporter); member 6	-0.1475	0.0042
226169_at	SBF2	SET binding factor 2	-0.4846	0.0174
226179_at	SLC25A37	solute carrier family 25; member 37	-0.5922	0.0453
226184_at	FMNL2	formin-like 2	-1.2011	0.0012
226188_at	HSPC159	galectin-related protein	-0.6047	0.0421
226190_at		Homo sapiens; clone IMAGE:4294444; mRNA	-0.7405	0.0036
226206_at	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	-0.7895	0.0368
226213_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-0.3596	0.0006
226214_at	MIR16	membrane interacting protein of RGS16	-0.5568	0.0129
226219_at	ARHGAP30	Rho GTPase activating protein 30	-1.0066	0.0179
226220_at	METTL9	Methyltransferase like 9	-0.4788	0.0043
226223_at		Transcribed locus	-1.7877	0.0012

226224_at	FOXK2	forkhead box K2	-1.7413	0
226229_s_at	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	-1.2696	0
226230_at	SMEK2	SMEK homolog 2; suppressor of mek1 (Dictyostelium)	-0.7843	0.0001
226231_at		Transcribed locus	-1.1283	0.0005
226236_at	LOC388789	hypothetical gene supported by AF147354	-0.3196	0.0406
226237_at		MRNA full length insert cDNA clone EUROIMAGE 1913076	-2.4037	0.0002
226238_at	MCEE	methylmalonyl CoA epimerase	-1.6046	0.0001
226239_at	TMEM150	transmembrane protein 150	-0.3274	0.0401
226243_at	LOC391356	similar to CG14903-PA	-0.9362	0
226245_at	KCTD1	potassium channel tetramerisation domain containing 1	-1.2401	0.0047
226246_at	KCTD1	potassium channel tetramerisation domain containing 1	-0.8843	0.0114
226250_at		CDNA FLJ34585 fis; clone KIDNE2008758	-0.6966	0.0304
226257_x_at	MRPS22	mitochondrial ribosomal protein S22	-0.5317	0.0004
226264_at	SUSD1	sushi domain containing 1	-0.7247	0.0098
226278_at	DKFZp313A2432	hypothetical protein DKFZp313A2432	-0.9953	0.0394
226280_at		CDNA FLJ43545 fis; clone PROST2011631	-1.1046	0.001
226281_at	DNER	delta/notch-like EGF repeat containing	-2.2868	0.0111
226282_at		Full length insert cDNA clone ZE03F06	-0.9912	0.0019
226296_s_at	MRPS15	mitochondrial ribosomal protein S15	-0.3183	0.0268
226297_at	HIPK3	Homeodomain interacting protein kinase 3	-0.6897	0.0001
226300_at	MED19	mediator complex subunit 19	-0.9894	0.0079
226302_at	ATP8B1	ATPase; Class I; type 8B; member 1	-1.3938	0.001
226303_at	PGM5	phosphoglucomutase 5	-1.843	0.004
226321_at	LYSMD3	LysM; putative peptidoglycan-binding; domain containing 3	-0.6283	0.0062
226326_at	PCGF5	polycomb group ring finger 5	-0.7919	0.0062
226342_at	SPTBN1	spectrin; beta; non-erythrocytic 1	-2.0546	0
226345_at	ARL5B	ADP-ribosylation factor-like 5B	-1.234	0.0081
226357_at	USP19	ubiquitin specific peptidase 19	-0.3555	0.0043
226360_at	ZNRF3	zinc and ring finger 3	-1.7731	0.0172
226370_at	KLHL15	kelch-like 15 (Drosophila)	-1.088	0.0018
226374_at		Full-length cDNA clone CS0DF012YG01 of Fetal brain of Homo sapiens (human)	-0.986	0.032
226380_at	PTPN21	protein tyrosine phosphatase; non-receptor type 21	-0.9674	0.0061
226381_at	PS1TP4	HBV preS1-transactivated protein 4	-0.7846	0.0004
226392_at		CDNA: FLJ21652 fis; clone COL08582	-0.3861	0.0257
226395_at	LOC286170	hypothetical protein LOC286170	-0.5439	0.0395

226396_at	CDK3	cyclin-dependent kinase 3	-0.4418	0.0251
226415_at	KIAA1576	KIAA1576 protein	-2.6057	0.0034
226417_at	RHOB	Ras homolog gene family; member B	-0.1483	0.0023
226431_at	ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 13	-1.4182	0.0003
226434_at	C7orf47	chromosome 7 open reading frame 47	-1.2293	0.0141
226435_at	PAPLN	papilin; proteoglycan-like sulfated glycoprotein	-1.6382	0
226436_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	-1.437	0.0158
226438_at		CDNA: FLJ21447 fis; clone COL04468	-1.7096	0.0028
226439_s_at	NBEA	neurobeachin	-1.4242	0.0065
226442_at	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	-0.1599	0.0128
226448_at	FAM89A	family with sequence similarity 89; member A	-1.8323	0.0004
226452_at	PDK1	pyruvate dehydrogenase kinase; isozyme 1	-1.2181	0.0042
226453_at	RNASEH2C	ribonuclease H2; subunit C	-0.5045	0.0132
226479_at	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	-1.4248	0
226482_s_at	F11R	F11 receptor	-2.702	0
226484_at	ZBTB47	zinc finger and BTB domain containing 47	-0.7078	0.0015
226500_at	ZBTB47	zinc finger and BTB domain containing 47	-0.2225	0.0186
226522_at	PODN	podocan	-0.5122	0.0003
226523_at	TAGLN	Transgelin	-0.9675	0
226535_at	ITGB6	integrin; beta 6	-0.1008	0.0167
226550_at		Homo sapiens; Similar to LOC169932; clone IMAGE:4499203; mRNA	-1.0503	0.0092
226553_at	TMPRSS2	transmembrane protease; serine 2	-0.2016	0.0021
226556_at		Homo sapiens; clone IMAGE:4294444; mRNA	-1.1657	0.0007
226561_at	LOC285086	hypothetical protein LOC285086	-0.7158	0.0384
226568_at	FAM102B	family with sequence similarity 102; member B	-0.9509	0.0403
226570_at	ATP1B3	ATPase; Na+/K+ transporting; beta 3 polypeptide	-0.9074	0
226578_s_at	DUSP1	Dual specificity phosphatase 1	-0.4232	0.0007
226591_at		CDNA FLJ33569 fis; clone BRAMY2010317	-1.2607	0.0392
226595_at	SNX21	sorting nexin family member 21	-0.7004	0
226610_at	PRR6	proline rich 6	-1.0936	0.0253
226611_s_at	PRR6	proline rich 6	-1.6123	0.0057
226616_s_at	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3; 10kDa	-0.6198	0.0191
226617_at	ARL5A	ADP-ribosylation factor-like 5A	-0.5631	0.0002
226620_x_at	DAZAP1	DAZ associated protein 1	-0.5755	0

226632_at	CYGB	cytoglobin	-0.8962	0.0101
226633_at	RAB8B	RAB8B; member RAS oncogene family	-0.5759	0.0041
226636_at	PLD1	phospholipase D1; phosphatidylcholine-specific	-2.1588	0
226645_at	KLF2	Kruppel-like factor 2 (lung)	-0.1363	0.0212
226646_at	KLF2	Kruppel-like factor 2 (lung)	-0.1778	0.0094
226647_at	TMEM25	transmembrane protein 25	-0.9445	0.0049
226652_at	USP3	ubiquitin specific peptidase 3	-0.654	0.0072
226657_at	MGC33894	transcript expressed during hematopoiesis 2	-0.3347	0.047
226660_at	RPS6KB1	ribosomal protein S6 kinase; 70kDa; polypeptide 1	-0.7192	0.0141
226665_at	AHSA2	AHA1; activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	-1.4249	0.0157
226680_at	IKZF5	IKAROS family zinc finger 5 (Pegasus)	-0.5145	0.0306
226682_at	LOC283666	hypothetical protein LOC283666	-1.0341	0.0308
226684_at	ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-0.8366	0.0001
226688_at	C3orf23	chromosome 3 open reading frame 23	-0.661	0.0089
226694_at	AKAP2	A kinase (PRKA) anchor protein 2, PALM2-AKAP2 protein	-0.8784	0.0321
226707_at	NAPRT1	nicotinate phosphoribosyltransferase domain containing 1	-1.7905	0.0007
226713_at	CCDC50	coiled-coil domain containing 50	-1.8235	0.0006
226718_at	AMIGO1	adhesion molecule with Ig-like domain 1	-1.513	0.0003
226719_at		CDNA FLJ34899 fis; clone NT2NE2018594	-1.0557	0
226722_at	FAM20C	family with sequence similarity 20; member C	-1.171	0.0037
226727_at	CISD3	CDGSH iron sulfur domain 3	-1.4653	0
226729_at	USP37	ubiquitin specific peptidase 37	-0.5601	0.0115
226730_s_at	USP37	ubiquitin specific peptidase 37	-1.0926	0.0047
226731_at	PELO	Pelota homolog (Drosophila)	-1.2112	0.0184
226735_at	TAPT1	transmembrane anterior posterior transformation 1	-1.0242	0.0001
226738_at	WDR81	WD repeat domain 81	-0.8588	0.002
226746_s_at	UBE4B	Ubiquitination factor E4B (UFD2 homolog; yeast)	-0.2882	0.0021
226750_at	LARP2	La ribonucleoprotein domain family; member 2	-1.0458	0.0015
226751_at	C2orf32	chromosome 2 open reading frame 32	-1.2692	0.0112
226765_at	SPTBN1	Spectrin; beta; non-erythrocytic 1	-0.9311	0
226769_at	FIBIN	fin bud initiation factor	-1.3626	0.0017
226774_at	FAM120B	family with sequence similarity 120B	-0.512	0.0308
226780_s_at	C7orf55	chromosome 7 open reading frame 55	-0.5849	0.0047
226781_at	C7orf55	chromosome 7 open reading frame 55	-0.4424	0.0382

226789_at	LOC647121	similar to embigin homolog	-3.392	0.0004
226790_at	MORN2	MORN repeat containing 2	-0.5524	0.0116
226798_at	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-0.3192	0.0047
226806_s_at			-1.229	0
226810_at		MRNA full length insert cDNA clone EUROIMAGE 1509279	-2.9208	0
226813_at	C1orf57	chromosome 1 open reading frame 57	-0.6913	0.011
226817_at	DSC2	desmocollin 2	-1.0988	0.0003
226818_at	MPEG1	macrophage expressed gene 1	-2.6123	0
226821_at		Full-length cDNA clone CS0DF029YD16 of Fetal brain of Homo sapiens (human)	-0.5577	0.0436
226833_at	CYB5D1	cytochrome b5 domain containing 1	-0.9748	0.0054
226834_at		Transcribed locus	-3.0664	0.0003
226836_at	SFT2D1	SFT2 domain containing 1	-0.1994	0.0074
226841_at	MPEG1	macrophage expressed gene 1	-2.4675	0
226846_at	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	-2.2172	0
226850_at	SUMF1	sulfatase modifying factor 1	-0.5456	0.0115
226852_at	MTA3	metastasis associated 1 family; member 3	-0.5754	0.0007
226865_at		MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	-1.0653	0.0176
226867_at	DENND4C	DENN/MADD domain containing 4C	-0.327	0.0349
226878_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	-1.6692	0.0025
226879_at	HVCN1	hydrogen voltage-gated channel 1	-0.8697	0.0006
226885_at		Transcribed locus	-1.2875	0.0123
226900_at	GABPB2	GA binding protein transcription factor; beta subunit 2	-0.1118	0.0251
226902_at		CDNA FLJ34165 fis; clone FCBBF3014770	-2.0687	0
226911_at	EGFLAM	EGF-like; fibronectin type III and laminin G domains	-1.108	0
226920_at	CSNK1A1	Casein kinase 1; alpha 1	-0.1731	0.0076
226922_at	RANBP2	RAN binding protein 2	-2.2631	0
226932_at		Transcribed locus	-1.968	0.0003
226940_at	FAM69B	Family with sequence similarity 69; member B	-0.1674	0.0094
226950_at	ACVRL1	activin A receptor type II-like 1	-0.9	0.0004
226956_at	MTMR3	myotubularin related protein 3	-0.5794	0.0038
226958_s_at	MED11	mediator complex subunit 11	-1.2584	0
226974_at		Full-length cDNA clone CS0DF038YD07 of Fetal brain of Homo sapiens (human)	-1.2814	0.0002
226982_at	ELL2	elongation factor; RNA polymerase II; 2	-3.0276	0
226993_at		CDNA FLJ46626 fis; clone TRACH2001612	-0.5932	0.0022
227002_at	FAM78A	family with sequence similarity 78; member A	-0.5753	0.0012

227009_at		MRNA; cDNA DKFZp667E0114 (from clone DKFZp667E0114)	-0.7722	0.0003
227011_at	ZNF672	Zinc finger protein 672	-0.1567	0.0496
227013_at	LATS2	LATS; large tumor suppressor; homolog 2 (Drosophila)	-1.3065	0.001
227020_at	YPEL2	yippee-like 2 (Drosophila)	-1.0676	0.0039
227024_s_at	MRPL55	Mitochondrial ribosomal protein L55	-0.1661	0.0148
227026_at	HSMPP8	M-phase phosphoprotein; mpp8	-0.4221	0.0376
227029_at	C14orf24	chromosome 14 open reading frame 24	-0.8662	0.0022
227043_at	LOC126075	hypothetical protein LOC126075	-1.3136	0
227047_x_at	ZBTB4	zinc finger and BTB domain containing 4	-0.689	0.0043
227050_at	ODZ3	Odz; odd Oz/ten-m homolog 3 (Drosophila)	-0.1575	0.0023
227052_at		Full-length cDNA clone CS0DE011YO20 of Placenta of Homo sapiens (human)	-0.7542	0.0014
227054_at	N6AMT2	N-6 adenine-specific DNA methyltransferase 2 (putative)	-0.6352	0.0107
227056_at	KIAA0141	KIAA0141	-0.7347	0.0318
227058_at	C13orf33	chromosome 13 open reading frame 33	-0.3198	0.0209
227060_at	RELT	RELT tumor necrosis factor receptor	-0.3309	0.0089
227063_at	C17orf61	chromosome 17 open reading frame 61	-0.8846	0.0007
227064_at	ANKRD40	ankyrin repeat domain 40	-0.7305	0.0003
227066_at	MOBKL2C	MOB1; Mps One Binder kinase activator-like 2C (yeast)	-0.6313	0.0001
227070_at	GLT8D2	glycosyltransferase 8 domain containing 2	-2.1731	0.0034
227073_at	MAP3K2	mitogen-activated protein kinase kinase kinase 2	-0.3652	0.0071
227080_at	ZNF697	zinc finger protein 697	-1.1461	0.0065
227081_at	DNALI1	dynein; axonemal; light intermediate chain 1	-1.9012	0
227086_at	LOC128977	hypothetical protein LOC128977	-0.2948	0.0295
227088_at	PDE5A	phosphodiesterase 5A; cGMP-specific	-1.5898	0.01
227093_at	USP36	Ubiquitin specific peptidase 36	-1.3315	0.0009
227095_at	LEPROT	leptin receptor overlapping transcript	-0.6568	0.0059
227099_s_at	LOC387763	hypothetical LOC387763	-2.2974	0
227110_at	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	-0.3837	0.033
227126_at		Transcribed locus	-1.6201	0.0007
227128_s_at	TACSTD2	Tumor-associated calcium signal transducer 2	-0.1109	0.0288
227131_at	MAP3K3	mitogen-activated protein kinase kinase kinase 3	-0.3844	0.0267
227138_at	CRTAP	cartilage associated protein	-0.3931	0.026
227142_at	PLEKHG5	pleckstrin homology domain containing; family G (with RhoGef domain) member 5	-0.4826	0.0001
227144_at	C22orf9	chromosome 22 open reading frame 9	-0.7379	0

227145_at	LOXL4	lysyl oxidase-like 4	-0.462	0.0008
227150_at	MTF1	metal-regulatory transcription factor 1	-1.1159	0
227151_at	SH3PX3	SH3 and PX domain containing 3	-0.8995	0
227154_at	IGSF21	immunoglobin superfamily; member 21	-0.6392	0.0127
227158_at	C14orf126	chromosome 14 open reading frame 126	-0.6877	0.0045
227159_at	GHDC	GH3 domain containing	-0.9741	0.0085
227167_s_at		Mesenchymal stem cell protein DSC96	-0.6536	0.0449
227173_s_at	BACH2	BTB and CNC homology 1; basic leucine zipper transcription factor 2	-0.1897	0.0465
227175_at	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	-0.1253	0.0089
227184_at			-0.8385	0.0048
227190_at	TMEM37	transmembrane protein 37	-1.0822	0.0016
227195_at	ZNF503	zinc finger protein 503	-1.5624	0.0056
227197_at	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	-0.8278	0.0179
227200_at			-0.6373	0.0193
227202_at	CNTN1	Contactin 1	-0.9093	0.0109
227209_at	CNTN1	Contactin 1	-1.5128	0.0003
227226_at	C6orf117	chromosome 6 open reading frame 117	-1.1208	0
227235_at		CDNA clone IMAGE:5302158	-1.5772	0.0043
227240_at	NGEF	neuronal guanine nucleotide exchange factor	-2.3775	0.0068
227250_at	KREMEN1	kringle containing transmembrane protein 1	-1.309	0
227265_at	FGL2	fibrinogen-like 2	-2.4521	0.0001
227268_at	LOC51136	PTD016 protein	-0.8759	0.0157
227271_at	FGF11	fibroblast growth factor 11	-2.2531	0.0021
227274_at		Transcribed locus; strongly similar to XP_524440.1 similar to Phospholipid hydroperoxide glutathione peroxidase; mitochondrial precursor (PHGPx) (GPX-4) [Pan troglodytes]	-0.4192	0.0068
227278_at			-0.5445	0.0103
227298_at	FLJ37798	hypothetical gene supported by AK095117	-0.3941	0.0387
227302_s_at	FLII	flightless I homolog (Drosophila), lethal giant larvae homolog 1 (Drosophila)	-0.1777	0.0022
227314_at	ITGA2	integrin; alpha 2 (CD49B; alpha 2 subunit of VLA-2 receptor)	-1.8495	0.0081
227317_at	LMCD1	LIM and cysteine-rich domains 1	-0.124	0.0254
227328_at	CAMTA1	Calmodulin binding transcription activator 1	-0.8055	0.0091
227338_at	LOC440983	hypothetical gene supported by BC066916	-0.292	0.028
227344_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)	-0.3103	0.0264

227345_at	TNFRSF10D	tumor necrosis factor receptor superfamily; member 10d; decoy with truncated death domain	-0.4531	0.0006
227351_at	C16orf52	chromosome 16 open reading frame 52	-0.7	0.0025
227353_at	TMC8	transmembrane channel-like 8	-0.5846	0.0102
227356_at		CDNA: FLJ22198 fis; clone HRC01218	-0.8899	0.0038
227366_at	RILP	Rab interacting lysosomal protein	-1.2387	0
227368_at		Transcribed locus; moderately similar to XP_001091208.1 hypothetical protein [Macaca mulatta]	-1.3831	0.016
227370_at	KIAA1946	KIAA1946	-2.2033	0.0006
227375_at	ANKRD13C	ankyrin repeat domain 13C	-0.778	0.0008
227379_at	MBOAT1	membrane bound O-acyltransferase domain containing 1	-0.5531	0.042
227380_x_at	C16orf13	Chromosome 16 open reading frame 13	-0.1283	0.0174
227381_at	CEECAM1	Cerebral endothelial cell adhesion molecule 1	-0.1476	0.0023
227386_s_at	TTMB	TTMB protein	-0.9891	0.01
227397_at	TPM2	tropomyosin 2 (beta)	-0.2705	0.0097
227399_at	VGLL3	vestigial like 3 (Drosophila)	-1.7128	0
227404_s_at	EGR1	Early growth response 1	-2.2171	0.0006
227407_at	TAPT1	transmembrane anterior posterior transformation 1	-0.8248	0.0098
227419_x_at	PLAC9	placenta-specific 9	-0.9134	0.0001
227433_at	KIAA2018	KIAA2018	-0.6805	0.0097
227436_at	OTUD7B	OTU domain containing 7B	-1.1157	0.0002
227443_at	C9orf150	chromosome 9 open reading frame 150	-2.213	0.0001
227444_at	ARMCX4	Armadillo repeat containing; X-linked 4	-1.5666	0.0072
227466_at	LOC285550	hypothetical protein LOC285550	-0.785	0.0006
227470_at	ZNF553	zinc finger protein 553	-0.7225	0.0002
227474_at	LOC654433	Hypothetical LOC654433	-1.4751	0.019
227478_at	LOC284262	hypothetical protein LOC284262	-1.9017	0
227480_at	SUSD2	sushi domain containing 2	-1.9781	0
227486_at	NT5E	5'-nucleotidase; ecto (CD73)	-0.298	0.002
227491_at		CDNA: FLJ22539 fis; clone HRC13227	-1.5473	0.0006
227502_at	KIAA1147	KIAA1147	-0.2685	0.0062
227506_at	SLC16A9	solute carrier family 16; member 9 (monocarboxylic acid transporter 9)	-3.8929	0
227516_at	SF3A1	splicing factor 3a; subunit 1; 120kDa	-0.5905	0.0081
227529_s_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-1.0621	0.0056
227530_at	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	-2.3014	0
227542_at	SOCS6	suppressor of cytokine signaling 6	-0.7093	0.0032

227546_x_at	AURKAIP1	aurora kinase A interacting protein 1, similar to Cyclin-L2 (Paneth cell-enhanced expression protein)	-0.2316	0.0323
227550_at	LOC143381	hypothetical protein LOC143381	-0.668	0
227557_at	SCARF2	scavenger receptor class F; member 2	-0.3275	0.0005
227561_at	DDR2	Discoidin domain receptor family; member 2	-1.3974	0.0232
227582_at	KLHDC9	kelch domain containing 9	-0.9767	0.0154
227588_s_at	C7orf20	Chromosome 7 open reading frame 20	-0.2261	0.0002
227591_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-0.431	0.001
227598_at	C7orf29	chromosome 7 open reading frame 29	-1.8712	0.0055
227599_at	C3orf59	chromosome 3 open reading frame 59	-1.168	0.0321
227613_at	ZNF331	zinc finger protein 331	-4.4878	0
227616_at	BCL9L	B-cell CLL/lymphoma 9-like	-0.7239	0.0088
227620_at	SLC44A1	solute carrier family 44; member 1	-1.1275	0.0024
227629_at	PRLR	Prolactin receptor	-2.585	0.01
227630_at		CDNA FLJ34250 fis; clone FCBBF4000529	-1.2548	0.0001
227635_at	LOC730111	hypothetical protein LOC730111	-0.1848	0.0134
227645_at	PIK3R5	phosphoinositide-3-kinase; regulatory subunit 5; p101	-0.7208	0.0004
227654_at	C20orf175	chromosome 20 open reading frame 175	-3.5156	0
227656_at	C6orf70	chromosome 6 open reading frame 70	-0.4431	0.0376
227657_at	RNF150	ring finger protein 150	-1.5323	0.0151
227660_at	ANTXR1	anthrax toxin receptor 1	-0.8181	0.0003
227662_at	SYNPO2	synaptopodin 2	-1.3167	0.0248
227667_at	CUEDC1	CUE domain containing 1	-0.6548	0.0006
227669_at	BRP44	brain protein 44	-1.089	0.0006
227676_at	FAM3D	family with sequence similarity 3; member D	-0.1762	0.0448
227681_at	ZFP36L2	Zinc finger protein 36; C3H type-like 2	-0.1669	0.0016
227693_at	WDR20	WD repeat domain 20	-0.8736	0.0002
227697_at	SOCS3	suppressor of cytokine signaling 3	-2.3451	0.0005
227702_at	CYP4X1	cytochrome P450; family 4; subfamily X; polypeptide 1	-1.5428	0
227703_s_at	SYTL4	synaptotagmin-like 4 (granuphilin-a)	-0.7881	0
227704_at	C19orf12	chromosome 19 open reading frame 12	-0.6453	0
227705_at	TCEAL7	transcription elongation factor A (SII)-like 7	-1.357	0.0023
227708_at	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	-1.5046	0
227710_s_at	LOC728913	Pp13759, Similar to Reticulocalbin-1 precursor	-0.3386	0.0164
227727_at	MRGPRF	MAS-related GPR; member F	-0.5169	0.0007
227730_at		CDNA clone IMAGE:40018609	-0.7338	0.0001

227731_at		CDNA FLJ11631 fis; clone HEMBA1004267	-0.938	0.0002
227735_s_at	C10orf99	chromosome 10 open reading frame 99	-0.1848	0.0305
227748_at	CCBL2	cysteine conjugate-beta lyase 2	-0.9564	0.0128
227749_at		Transcribed locus	-0.3082	0.02
227755_at		CDNA clone IMAGE:4077090	-1.895	0.0008
227758_at	RERG	RAS-like; estrogen-regulated; growth inhibitor	-2.122	0.0038
227761_at	MYO5A	myosin VA (heavy chain 12; myoxin)	-0.6091	0.0324
227771_at	LIFR	leukemia inhibitory factor receptor alpha	-1.083	0.0458
227777_at	C10orf18	chromosome 10 open reading frame 18	-0.8472	0.0104
227782_at	ZBTB7C	zinc finger and BTB domain containing 7C	-1.3794	0.0023
227783_at	CCDC57	coiled-coil domain containing 57, similar to coiled-coil domain containing 57	-0.281	0.0003
227788_at		CDNA FLJ34165 fis; clone FCBBF3014770	-1.3785	0
227791_at	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger); member 9	-0.8449	0.0139
227806_at	C16orf74	chromosome 16 open reading frame 74	-0.188	0.0206
227819_at	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	-0.1969	0.0176
227821_at	LGI4	leucine-rich repeat LGI family; member 4	-0.2371	0.0025
227826_s_at		CDNA clone IMAGE:4791597	-4.9033	0
227827_at		CDNA clone IMAGE:4791597	-4.7891	0
227838_at		CDNA FLJ12425 fis; clone MAMMA1003104	-2.3263	0.0005
227840_at	LOC130355	hypothetical protein LOC130355	-0.5986	0.0223
227850_x_at	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	-1.0228	0.0456
227855_at	FLJ10357	hypothetical protein FLJ10357	-0.7443	0.0275
227863_at	CTSD	cathepsin D	-3.0306	0.0001
227865_at	C9orf103	chromosome 9 open reading frame 103	-1.6113	0
227867_at	LOC129293	hypothetical protein LOC129293	-0.2484	0.0131
227874_at		MRNA; cDNA DKFZp586N0121 (from clone DKFZp586N0121)	-3.3745	0
227879_at	ALKBH7	AlkB; alkylation repair homolog 7 (E. coli)	-0.2369	0.0009
227881_s_at	C18orf17	Chromosome 18 open reading frame 17	-0.16	0.0105
227885_at	LOC400236	Hypothetical LOC400236	-0.2224	0.0294
227887_at	LOC400236	hypothetical LOC400236	-0.6721	0
227893_at	C9orf130	chromosome 9 open reading frame 130	-0.2916	0.0043
227899_at	VIT	vitrin	-0.2031	0.0168
227900_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-0.8845	0.0064

227925_at	FLJ39051	Hypothetical gene supported by AK096370	-2.3217	0
227932_at	ARIH2	ariadne homolog 2 (Drosophila)	-0.8333	0.0032
227935_s_at	PCGF5	polycomb group ring finger 5	-1.4567	0.0019
227947_at	PHACTR2	phosphatase and actin regulator 2	-1.2114	0.0034
227957_at	GSN	Gelsolin (amyloidosis; Finnish type)	-0.1133	0.0182
227958_s_at	GSN	Gelsolin (amyloidosis; Finnish type)	-0.121	0.0164
227962_at	ACOX1	acyl-Coenzyme A oxidase 1; palmitoyl	-1.4882	0.0004
227968_at	PDDC1	Parkinson disease 7 domain containing 1	-0.4534	0.0048
227969_at	LOC400960	hypothetical gene supported by BC040598	-0.5177	0.0001
227971_at	NRK	Nik related kinase	-2.3405	0.0181
227973_at	FLJ38973	hypothetical protein FLJ38973	-0.4447	0.011
227979_at		CDNA FLJ36727 fis; clone UTERU2012286	-0.7108	0.0393
227989_at	LTBP4	Latent transforming growth factor beta binding protein 4	-0.1822	0.0084
227995_at		MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	-1.3498	0.0003
227998_at	S100A16	S100 calcium binding protein A16	-2.8141	0
228000_at	ADC	arginine decarboxylase	-0.3182	0.0087
228002_at	GTPBP4	GTP binding protein 4, isopentenyl-diphosphate delta isomerase 2	-1.6356	0
228006_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-1.0696	0.0018
228015_s_at	TRIM8	Tripartite motif-containing 8	-0.1115	0.036
228019_s_at	MRPS18C	mitochondrial ribosomal protein S18C	-0.484	0.0061
228022_at	CCDC18	coiled-coil domain containing 18	-0.1241	0.0121
228025_s_at	PPP2R2C	protein phosphatase 2 (formerly 2A); regulatory subunit B; gamma isoform	-0.1392	0.0077
228037_at		CDNA clone IMAGE:5162874	-1.2549	0
228042_at	ADPRH	ADP-ribosylarginine hydrolase	-0.3636	0.0082
228045_at		MRNA; cDNA DKFZp451K063 (from clone DKFZp451K063)	-1.4443	0.0018
228048_at	C10orf41	chromosome 10 open reading frame 41	-0.2881	0.0142
228049_x_at		Transcribed locus; strongly similar to XP_001172939.1 hypothetical protein [Pan troglodytes]	-0.763	0.0126
228059_x_at	MRPS22	mitochondrial ribosomal protein S22	-0.5147	0.0001
228062_at	NAP1L5	nucleosome assembly protein 1-like 5	-2.4002	0.003
228063_s_at	NAP1L5	nucleosome assembly protein 1-like 5	-2.278	0.0039
228065_at	BCL9L	B-cell CLL/lymphoma 9-like	-0.5059	0.0108
228070_at		CDNA FLJ34250 fis; clone FCBBF4000529	-0.4247	0.0108
228071_at	GIMAP7	GTPase; IMAP family member 7	-1.3743	0.0008
228072_at	SYT12	synaptotagmin XII	-0.7622	0.0002

228075_x_at	TFB1M	transcription factor B1; mitochondrial	-0.6992	0.0255
228083_at	CACNA2D4	calcium channel; voltage-dependent; alpha 2/delta subunit 4	-0.5105	0.0094
228089_x_at	LOC374395	similar to RIKEN cDNA 1810059G22	-0.6086	0.0069
228092_at	CREM	cAMP responsive element modulator	-3.2275	0
228096_at	C1orf151	chromosome 1 open reading frame 151	-0.3868	0.0192
228097_at	MYLIP	myosin regulatory light chain interacting protein	-0.7139	0.002
228098_s_at	MYLIP	myosin regulatory light chain interacting protein	-1.7353	0.0012
228103_s_at	NRP2	Neuropilin 2	-0.1328	0.0119
228115_at		Full length insert cDNA clone ZE05E03	-2.0856	0
228127_at		CDNA FLJ41679 fis; clone HCASM2003212	-1.3831	0.0141
228128_x_at	PAPPA	pregnancy-associated plasma protein A; pappalysin 1	-2.0938	0.0023
228139_at	RIPK3	receptor-interacting serine-threonine kinase 3	-0.1662	0.0327
228142_at	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD)	-0.8721	0.0227
228143_at	CP	ceruloplasmin (ferroxidase)	-0.7753	0.0004
228159_at		CDNA FLJ38039 fis; clone CTONG2013934	-0.9024	0.0096
228178_s_at	HAS3	hyaluronan synthase 3	-0.1883	0.0128
228183_s_at	RPAIN	RPA interacting protein	-0.3702	0.039
228186_s_at	RSPO3	R-spondin 3 homolog (Xenopus laevis)	-5.1589	0
228188_at			-2.211	0
228193_s_at	C13orf15	Chromosome 13 open reading frame 15	-0.1353	0.0313
228195_at	MGC13057	hypothetical protein MGC13057	-0.6875	0.0214
228202_at	PLN	Phospholamban	-1.6163	0
228203_at	B3GNT1	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 1	-0.1489	0.0047
228204_at	PSMB4	Proteasome (prosome; macropain) subunit; beta type; 4	-0.7233	0.0138
228224_at	PRELP	proline/arginine-rich end leucine-rich repeat protein	-2.1775	0
228233_at	FREM1	FRAS1 related extracellular matrix 1	-0.6796	0
228249_at	C11orf74	chromosome 11 open reading frame 74	-0.7963	0.0003
228254_at		Transcribed locus	-0.7961	0.0011
228263_at	GRASP	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	-0.487	0.003
228264_at	PHACS	1-aminocyclopropane-1-carboxylate synthase	-0.9469	0.0003
228265_at		CDNA clone IMAGE:6214748	-0.1176	0.0208
228268_at	FMO2	flavin containing monooxygenase 2 (non-functional)	-6.2067	0
228275_at		CDNA FLJ32438 fis; clone SKMUS2001402	-0.5785	0.0349

228292_at		Transcribed locus; moderately similar to XP_001084705.1 similar to bile acid beta-glucosidase [Macaca mulatta]	-0.7989	0.0442
228294_s_at	ZNF775	Zinc finger protein 775	-0.1362	0.0144
228298_at	FAM113B	family with sequence similarity 113; member B	-1.9488	0.0072
228299_at	KCTD20	Potassium channel tetramerisation domain containing 20	-0.9418	0.0008
228314_at	LRRC8C	leucine rich repeat containing 8 family; member C	-1.0782	0.0034
228317_at	ZFAND5	Zinc finger; AN1-type domain 5	-0.1445	0.0188
228325_at	KIAA0146	KIAA0146	-2.7058	0
228332_s_at	C11orf31	chromosome 11 open reading frame 31	-0.4425	0.0012
228333_at		Full length insert cDNA clone YT94E02	-2.0216	0
228335_at	CLDN11	claudin 11 (oligodendrocyte transmembrane protein)	-2.5863	0
228349_at	KIAA1958	KIAA1958	-1.5829	0
228370_at	SNRPN	Small nuclear ribonucleoprotein polypeptide N	-1.9402	0.0035
228375_at	IGSF11	immunoglobulin superfamily; member 11	-2.4962	0
228376_at	GGTA1	glycoprotein; alpha-galactosyltransferase 1, similar to glycoprotein galactosyltransferase alpha 1; 3	-2.4467	0
228380_at		Transcribed locus	-0.5733	0.0006
228381_at	ATF7IP2	Activating transcription factor 7 interacting protein 2	-1.9881	0.0006
228383_at	PNPLA7	patatin-like phospholipase domain containing 7	-0.3748	0.0001
228384_s_at	C10orf33	chromosome 10 open reading frame 33	-1.3229	0
228391_at	CYP4V2	cytochrome P450; family 4; subfamily V; polypeptide 2	-1.5171	0.0208
228395_at	GLT8D1	Glycosyltransferase 8 domain containing 1	-0.5974	0
228396_at	PRKG1	protein kinase; cGMP-dependent; type I	-2.2005	0.0001
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-0.2241	0.0037
228407_at	SCUBE3	signal peptide; CUB domain; EGF-like 3	-2.8508	0
228409_at	KIAA1881	KIAA1881	-0.7321	0.0001
228411_at	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	-0.6667	0.0001
228420_at	PDCD2	programmed cell death 2	-0.6537	0
228421_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	-0.1004	0.0204
228425_at	LOC654433	hypothetical LOC654433	-1.1463	0.0377
228428_at	LOC729758	hypothetical protein LOC729758	-0.2127	0.0013
228436_at	KCNC4	potassium voltage-gated channel; Shaw-related subfamily; member 4	-0.3775	0
228444_at		Transcribed locus	-0.2043	0.0346
228448_at	MAP6	microtubule-associated protein 6	-1.2388	0.0003

228449_at		Transcribed locus; strongly similar to NP_694589.1 protein LOC150291 [Homo sapiens]	-0.2056	0.0149
228452_at	C17orf39	chromosome 17 open reading frame 39	-0.4317	0.0093
228456_s_at	LOC149832	hypothetical protein LOC149832	-0.6572	0.0076
228466_at	MGC29891	hypothetical protein MGC29891	-0.4127	0.0499
228469_at	PPID	Peptidylprolyl isomerase D (cyclophilin D)	-2.1576	0
228477_at	FLJ10154	hypothetical protein FLJ10154	-0.5526	0.0229
228479_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-1.3698	0
228482_at	CDRT4	CMT1A duplicated region transcript 4	-0.6941	0.0493
228488_at	TBC1D16	TBC1 domain family; member 16	-0.244	0.0496
228491_at	KRT19	Keratin 19	-0.1369	0.0066
228492_at	USP9Y	ubiquitin specific peptidase 9; Y-linked (fat facets-like; Drosophila)	-2.8581	0.0012
228494_at	PPP1R9A	protein phosphatase 1; regulatory (inhibitor) subunit 9A	-1.1003	0.0029
228496_s_at	CRIM1	Cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.0476	0.0087
228498_at		Transcribed locus; strongly similar to XP_531236.1 hypothetical protein XP_531236 [Pan troglodytes]	-1.3278	0.0005
228504_at		Transcribed locus	-4.5805	0
228508_at	MAML3	mastermind-like 3 (Drosophila)	-0.1232	0.0309
228523_at	NANOS1	nanos homolog 1 (Drosophila)	-3.6717	0
228524_at	ADCK5	aarF domain containing kinase 5	-0.6675	0.0002
228525_at		Transcribed locus; strongly similar to XP_512572.1 similar to low density lipoprotein receptor-related protein 3 [Pan troglodytes]	-0.4018	0.0392
228526_at	NANOS1	Nanos homolog 1 (Drosophila)	-0.2932	0.0008
228528_at		CDNA FLJ41270 fis; clone BRAMY2036387	-2.9181	0
228532_at	C1orf162	chromosome 1 open reading frame 162	-3.5684	0
228533_at			-0.1537	0.0132
228534_s_at			-0.1064	0.0391
228536_at	LOC90826	hypothetical protein BC004337	-2.9974	0
228540_at	QKI	quaking homolog; KH domain RNA binding (mouse)	-0.4001	0.0007
228543_at	CSRP2BP	CSRP2 binding protein	-0.5448	0.0343
228555_at	CAMK2D	Calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.3228	0.0005
228557_at	L3MBTL4	l(3)mbt-like 4 (Drosophila)	-0.7452	0
228560_at		Full length insert cDNA clone YY51E04	-0.5576	0.0095
228562_at		Transcribed locus	-0.5826	0.0462
228565_at	KIAA1804	mixed lineage kinase 4	-1.1225	0.0019
228568_at	Gcom1	GRINL1A combined protein	-1.6475	0.0043

228572_at	GRB2	growth factor receptor-bound protein 2	-0.389	0.0013
228573_at		Full-length cDNA clone CS0DD001YA12 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)	-1.7848	0.0004
228576_s_at	MXRA8	Matrix-remodelling associated 8	-0.1235	0.0038
228586_at	ENG	Endoglin (Osler-Rendu-Weber syndrome 1)	-0.1382	0.0035
228591_at	TNRC6C	Trinucleotide repeat containing 6C	-0.1279	0.0149
228593_at	LOC339483	hypothetical LOC339483	-0.7371	0.0001
228598_at	DPP10	dipeptidyl-peptidase 10	-1.771	0.0364
228599_at	MS4A1	membrane-spanning 4-domains; subfamily A; member 1	-0.149	0.0075
228603_at		Transcribed locus	-0.8153	0.0498
228612_at		CDNA clone IMAGE:5277380	-0.9089	0.0045
228615_at	LOC286161	hypothetical protein LOC286161	-1.1762	0
228618_at	PEAR1	platelet endothelial aggregation receptor 1	-1.1887	0
228622_s_at	DNAJC4	DnaJ (Hsp40) homolog; subfamily C; member 4	-0.9429	0
228634_s_at	CSDA	Cold shock domain protein A	-0.1271	0.0062
228635_at	PCDH10	protocadherin 10	-1.6903	0
228642_at	HOXA2	Homeobox A2	-2.5386	0
228661_s_at		CDNA FLJ11489 fis; clone HEMBA1001915	-1.343	0.0016
228665_at	CYYR1	cysteine/tyrosine-rich 1	-2.3053	0.0001
228670_at	TEP1	telomerase-associated protein 1	-0.992	0.0015
228673_s_at	EML4	Echinoderm microtubule associated protein like 4	-0.1747	0.0037
228678_at	FAM116B	family with sequence similarity 116; member B	-0.2276	0.0013
228689_at	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 11; 14.7kDa	-0.219	0.0306
228692_at		CDNA FLJ13569 fis; clone PLACE1008369	-0.5316	0.0056
228696_at	SLC45A3	solute carrier family 45; member 3	-0.5036	0.0001
228698_at	SOX7	SRY (sex determining region Y)-box 7	-0.9702	0.0483
228701_at	C8orf46	chromosome 8 open reading frame 46	-0.1827	0.0118
228716_at	THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	-2.5979	0
228726_at	SERPINB1	serpin peptidase inhibitor; clade B (ovalbumin); member 1	-1.272	0.0002
228727_at	ANXA11	annexin A11	-0.2608	0.0157
228730_s_at	SCRN2	secernin 2	-0.5262	0.0472
228731_at		CDNA clone IMAGE:5273964	-1.3084	0.0111
228732_at		CDNA clone IMAGE:5273964	-0.4244	0.0383
228733_at	PUSL1	pseudouridylate synthase-like 1	-0.6767	0.0025
228736_at	HEL308	DNA helicase HEL308	-0.7802	0.0194
228739_at	CYS1	cystin 1	-0.4345	0.0071

228746_s_at	CDV3	CDV3 homolog (mouse)	-1.0979	0.0042
228749_at	ZDBF2	zinc finger; DBF-type containing 2	-1.7411	0.0001
228754_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter; taurine); member 6	-1.5728	0
228763_at	CHMP4A	chromatin modifying protein 4A, magnesium-dependent phosphatase 1	-0.5456	0.0138
228771_at	ADRBK2	adrenergic; beta; receptor kinase 2	-1.8387	0.0002
228772_at	HNMT	histamine N-methyltransferase	-1.3891	0.0001
228775_at			-0.9011	0.0152
228777_at	KBTBD3	kelch repeat and BTB (POZ) domain containing 3	-0.5165	0.0007
228779_at	LOC440456	similar to pleckstrin homology domain containing; family M (with RUN domain) member 1; adapter protein 162, similar to similar to pleckstrin homology domain containing; family M (with RUN domain) member 1; adapter protein 162	-0.1946	0.0064
228780_at		MRNA; clone ICRFp507B0451	-0.1395	0.0286
228789_at	MTMR6	myotubularin related protein 6	-0.8947	0
228807_at			-0.4221	0.0018
228809_at	CXorf40A	chromosome X open reading frame 40A	-4.196	0
228811_at		Transcribed locus	-1.1372	0.0013
228812_at		Transcribed locus	-1.3297	0.0006
228813_at	HDAC4	histone deacetylase 4	-1.1021	0.0018
228826_at		Homo sapiens; clone IMAGE:5215917; mRNA	-0.4548	0.0092
228828_at		Homo sapiens; clone IMAGE:5215917; mRNA	-0.4045	0.0017
228834_at	TOB1	transducer of ERBB2; 1	-1.9046	0.0032
228840_at	AMOTL1	angiomotin like 1	-0.1514	0.05
228844_at	SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter); member 5	-0.8019	0.0153
228845_at	P76	hypothetical protein LOC196463	-1.0221	0.0153
228850_s_at			-3.0971	0.0001
228855_at	LOC729777	similar to Peroxisomal coenzyme A diphosphatase NUDT7 (Nucleoside diphosphate-linked moiety X motif 7) (Nudix motif 7)	-1.328	0.0269
228857_at	LOC285831	hypothetical protein LOC285831	-0.4765	0.0302
228870_at	FAM84B	family with sequence similarity 84; member B	-0.1109	0.0239
228871_at			-0.2918	0
228874_at	LOC653583	Similar to pleckstrin homology-like domain; family B; member 1	-0.1631	0.0179
228877_at	RGL3	ral guanine nucleotide dissociation stimulator-like 3	-1.0815	0.0295
228879_at			-0.8642	0.0085

228882_at	TUB	tubby homolog (mouse)	-1.6185	0.0016
228885_at	MAMDC2	MAM domain containing 2	-2.9308	0.0001
228888_at	STAC2	SH3 and cysteine rich domain 2	-0.3656	0.0191
228890_at	ATOH8	atonal homolog 8 (Drosophila)	-0.4149	0.0302
228892_at	SH3RF2	SH3 domain containing ring finger 2	-0.2102	0.0121
228893_at		CDNA clone IMAGE:30332316	-0.15	0.019
228896_at		Transcribed locus	-0.212	0.0027
228898_s_at	SMARCB1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily b; member 1	-0.3695	0.0012
228903_at	FLJ37464	hypothetical protein FLJ37464	-0.279	0.007
228915_at	DACH1	dachshund homolog 1 (Drosophila)	-2.4214	0.0053
228916_at	CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	-0.7269	0.0053
228918_at		CDNA FLJ32207 fis; clone PLACE6003204	-0.2191	0.0467
228922_at	SHF	Src homology 2 domain containing F	-1.0322	0
228924_s_at	UBE2J1	Ubiquitin-conjugating enzyme E2; J1 (UBC6 homolog; yeast)	-0.1935	0.0054
228937_at	C13orf31	chromosome 13 open reading frame 31	-1.643	0.0004
228939_at	OAF	OAF homolog (Drosophila)	-0.2286	0.0264
228943_at	MAP6	microtubule-associated protein 6	-1.1438	0.004
228947_x_at	C16orf30	chromosome 16 open reading frame 30	-0.2153	0.0005
228967_at	EIF1	Eukaryotic translation initiation factor 1	-0.8164	0.0003
228973_at	DLG2	discs; large homolog 2; chapsyn-110 (Drosophila)	-1.4792	0.0008
228976_at	ICOSLG	inducible T-cell co-stimulator ligand	-0.2583	0.0047
229005_at		CDNA: FLJ23331 fis; clone HEP12664	-0.1823	0.0364
229011_at		Transcribed locus	-0.6049	0.0015
229012_at	C9orf24	chromosome 9 open reading frame 24	-0.4213	0.0001
229014_at	FLJ42709	hypothetical gene supported by AK124699	-2.135	0.0002
229021_at		CDNA: FLJ23331 fis; clone HEP12664	-0.5531	0.0002
229023_at	SFT2D3	SFT2 domain containing 3	-0.2205	0.0167
229024_at		CDNA FLJ10151 fis; clone HEMBA1003402	-2.0559	0.0019
229031_at		CDNA FLJ25763 fis; clone TST06294	-0.4223	0.0144
229048_at		Full length insert cDNA clone ZD86A03	-0.1815	0.0144
229058_at	ANKRD16	ankyrin repeat domain 16	-0.3836	0.0497
229063_s_at	CCDC107	coiled-coil domain containing 107	-0.6274	0.0028
229076_s_at		Transcribed locus	-0.22	0.0362

229083_at		Full-length cDNA clone CS0DC006YB07 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	-1.0633	0.0005
229088_at			-0.746	0.0075
229091_s_at	CCNJ	cyclin J	-0.6089	0.0163
229092_at		Full length insert cDNA clone YX37E06	-0.6614	0.009
229098_s_at	C5orf24	Chromosome 5 open reading frame 24	-0.1211	0.0162
229101_at	LOC150166	Hypothetical protein LOC150166	-0.9562	0.0097
229106_at	DYNLL2	dynein; light chain; LC8-type 2	-1.6489	0
229110_at		CDNA clone IMAGE:4794876	-0.8619	0.0122
229113_s_at	C1orf86	chromosome 1 open reading frame 86	-1.2907	0
229116_at	CNKSR2	connector enhancer of kinase suppressor of Ras 2	-0.6498	0.0269
229119_s_at	ZSWIM7	zinc finger; SWIM-type containing 7	-1.7717	0.0001
229120_s_at	CDC42SE1	CDC42 small effector 1	-0.6637	0.0002
229121_at		CDNA FLJ44441 fis; clone UTERU2020242	-1.2686	0
229124_at	PROK1	prokineticin 1	-1.2409	0.0026
229125_at	ANKRD38	ankyrin repeat domain 38	-0.1883	0.0029
229127_at		CDNA FLJ31517 fis; clone NT2RI2000007	-2.8184	0.0003
229136_s_at		Transcribed locus	-0.2219	0.0215
229146_at	C7orf31	chromosome 7 open reading frame 31	-0.9782	0.0005
229149_at			-0.1952	0.0015
229151_at	SLC14A1	Solute carrier family 14 (urea transporter); member 1 (Kidd blood group)	-0.3591	0
229154_at	WNT10A	Wingless-type MMTV integration site family; member 10A	-0.1324	0.0186
229156_s_at		CDNA clone IMAGE:5274141	-0.2878	0.0057
229157_at		CDNA clone IMAGE:5274141	-0.3252	0.0003
229160_at	MUM1L1	melanoma associated antigen (mutated) 1-like 1	-2.8423	0
229164_s_at	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1	-0.5526	0.0039
229168_at	COL23A1	collagen; type XXIII; alpha 1	-0.1632	0.0064
229171_at	MGC16385	Hypothetical protein MGC16385	-0.1032	0.0096
229172_at	HSPA12B	heat shock 70kD protein 12B	-0.4802	0.0004
229175_at	SMYD4	SET and MYND domain containing 4	-2.0023	0
229176_at	ANKH	ankylosis; progressive homolog (mouse)	-0.1685	0.0095
229177_at	MGC45438	hypothetical protein MGC45438	-0.5392	0
229185_at		CDNA clone IMAGE:4829282	-0.1001	0.0486
229201_at		Full-length cDNA clone CS0DF014YC15 of Fetal brain of Homo sapiens (human)	-0.6114	0.0058
229204_at	HP1BP3	Heterochromatin protein 1; binding protein 3	-0.4504	0.0126

229210_at	RNASEH2B	ribonuclease H2; subunit B	-0.447	0.0008
229213_at		Transcribed locus	-0.3646	0
229221_at	CD44	CD44 molecule (Indian blood group)	-0.1107	0.0426
229230_at	OSTalpha	organic solute transporter alpha	-2.0661	0.0322
229239_x_at	SLCO4A1	Solute carrier organic anion transporter family; member 4A1	-0.1827	0.0071
229242_at		Transcribed locus	-0.7964	0.0093
229245_at	PLEKHA6	pleckstrin homology domain containing; family A member 6	-0.6449	0
229253_at	THEM4	thioesterase superfamily member 4	-1.1674	0
229258_at	KIF12	kinesin family member 12	-0.1287	0.0326
229265_at	SKI	v-ski sarcoma viral oncogene homolog (avian)	-1.3366	0.0002
229277_at		Beta-1 adrenergic receptor mRNA; 3' UTR	-0.1437	0.0067
229280_s_at	FLJ22536	hypothetical locus LOC401237	-1.8409	0.0013
229287_at	PCNX	pecanex homolog (Drosophila)	-1.0148	0.0021
229290_at	DAPL1	death associated protein-like 1	-5.8202	0
229295_at	LOC150166	hypothetical protein LOC150166	-1.1664	0.0001
229296_at		CDNA FLJ34873 fis; clone NT2NE2014950	-0.4028	0.006
229301_at			-0.1963	0.026
229308_at		Transcribed locus	-2.1364	0
229310_at	KLHL29	kelch-like 29 (Drosophila)	-3.6287	0
229313_at	TMEM16E	transmembrane protein 16E	-1.6744	0.0002
229319_at		CDNA FLJ34311 fis; clone FEBRA2008255	-1.1964	0.0008
229320_at	C2orf55	chromosome 2 open reading frame 55	-0.309	0.0104
229323_at	LOC387723	hypothetical LOC387723, hypothetical protein LOC651940	-1.0118	0
229326_at	TNFSF13	Tumor necrosis factor (ligand) superfamily; member 13	-0.2151	0.0003
229329_s_at	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	-0.1439	0.0135
229337_at	USP2	ubiquitin specific peptidase 2	-1.5238	0.0071
229348_at	UBIAD1	UbiA prenyltransferase domain containing 1	-0.8187	0
229367_s_at	GIMAP6	GTPase; IMAP family member 6	-1.0484	0.0121
229368_s_at	ZFAND5	Zinc finger; AN1-type domain 5	-0.2858	0
229375_at		Full-length cDNA clone CS0DC020YH17 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	-0.1645	0.0057
229377_at	GRTP1	growth hormone regulated TBC protein 1	-0.9752	0.0338
229378_at	STOX1	storkhead box 1	-1.2314	0
229379_at	AHDC1	AT hook; DNA binding motif; containing 1	-0.1008	0.0354
229383_at		CDNA FLJ34016 fis; clone FCBBF2002541	-0.9881	0.0091

229395_at	STX4	syntaxin 4	-0.5055	0.0091
229396_at	OVOL1	ovo-like 1(Drosophila)	-0.1283	0.0274
229402_at	SAMD13	sterile alpha motif domain containing 13	-1.0732	0.0001
229403_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 1	-0.1169	0.0252
229408_at	HDAC5	histone deacetylase 5	-0.1913	0.0167
229415_at	CYCS	cytochrome c; somatic	-1.2825	0.0027
229424_s_at	ARHGAP27	Rho GTPase activating protein 27	-0.1784	0.0354
229443_at	C6orf125	Chromosome 6 open reading frame 125	-0.1295	0.0037
229444_at	LOC729776	hypothetical protein LOC729776	-0.886	0.0207
229452_at	TMEM88	transmembrane protein 88	-1.1378	0
229458_s_at	GALK1	Galactokinase 1	-0.1665	0.0104
229461_x_at	NEGR1	neuronal growth regulator 1	-2.1615	0
229469_at	CTD-2267G17.3	X antigen family; member 2, X antigen family; member 2-like	-0.1879	0.0365
229471_s_at	SFRS2B	Splicing factor; arginine/serine-rich 2B	-0.1767	0.0109
229474_at	MICAL3	microtubule associated monoxygenase; calponin and LIM domain containing 3	-0.2976	0.0131
229476_s_at	THRSP	thyroid hormone responsive (SPOT14 homolog; rat)	-1.4331	0.0003
229477_at	THRSP	thyroid hormone responsive (SPOT14 homolog; rat)	-0.8351	0.0011
229480_at		MRNA; cDNA DKFZp686I18116 (from clone DKFZp686I18116)	-1.2226	0.0013
229486_s_at	TMEM132A	Transmembrane protein 132A	-0.2428	0.0134
229488_at	OTUD7B	OTU domain containing 7B	-0.3485	0.0355
229492_at	VANGL1	vang-like 1 (van gogh; Drosophila)	-0.7563	0.0018
229496_at	CLP1	CLP1; cleavage and polyadenylation factor I subunit; homolog (S. cerevisiae)	-0.2487	0.0012
229499_at	CAPN13	calpain 13	-0.1349	0.0222
229501_s_at	USP8	Ubiquitin specific peptidase 8	-0.425	0.0387
229503_at	SLC15A4	Solute carrier family 15; member 4	-0.1401	0.0216
229505_at	NAP1L4	Nucleosome assembly protein 1-like 4	-0.1324	0.0347
229508_at	U2AF2	U2 small nuclear RNA auxiliary factor 2	-0.1711	0.021
229510_at	NYD-SP21	MS4A13 protein	-0.6341	0.0003
229515_at	PAWR	PRKC; apoptosis; WT1; regulator	-0.8008	0.0007
229523_at	TTMA	Two transmembrane domain family member A	-2.0466	0
229525_at			-0.2181	0.0047
229526_at	AQP11	aquaporin 11	-1.3741	0.0113
229529_at	TCF21	transcription factor 21	-0.5544	0
229535_at	PTPMT1	protein tyrosine phosphatase; mitochondrial 1	-0.8363	0

229537_at		Transcribed locus; strongly similar to XP_513538.1 similar to LIM domain transcription factor LMO4 (LIM-only protein 4) (LMO-4) (Breast tumor autoantigen) [Pan troglodytes]	-0.1624	0.0197
229541_at			-0.274	0.0315
229542_at	C20orf85	chromosome 20 open reading frame 85	-0.1302	0.0042
229544_at		CDNA clone IMAGE:4791887, MRNA; cDNA DKFZp564C0762 (from clone DKFZp564C0762)	-0.8384	0.0299
229554_at		Transcribed locus	-3.7384	0
229563_s_at	RPL10A	ribosomal protein L10a	-0.1685	0.0108
229565_x_at	TBX3	T-box 3 (ulnar mammary syndrome)	-0.1924	0.0372
229580_at		Transcribed locus	-0.7892	0.0243
229582_at	C18orf37	chromosome 18 open reading frame 37	-0.6797	0.0029
229594_at	SPTY2D1	SPT2; Suppressor of Ty; domain containing 1 (S. cerevisiae)	-0.7735	0.0001
229596_at	AMDHD1	amidohydrolase domain containing 1	-4.0841	0
229598_at	COBLL1	COBL-like 1	-1.809	0
229604_at	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase)	-0.3628	0.0013
229619_at	FOLR2	Folate receptor 2 (fetal)	-0.2665	0.0041
229620_at	SEPP1	selenoprotein P; plasma; 1	-0.9707	0.0004
229623_at	FLJ12993	Hypothetical LOC441027	-2.2476	0.0001
229624_at		Transcribed locus	-0.4272	0.0012
229630_s_at	WTAP	Wilms tumor 1 associated protein	-0.4075	0.0142
229634_at	TMEM139	transmembrane protein 139	-0.2906	0.0016
229638_at	IRX3	iroquois homeobox 3	-2.2334	0.0001
229639_s_at	SLC19A1	Solute carrier family 19 (folate transporter); member 1	-0.1616	0.0258
229640_x_at		CDNA FLJ26856 fis; clone PRS08123	-0.6819	0.0016
229641_at		Transcribed locus	-1.9234	0.0257
229647_at			-0.7205	0.0238
229652_s_at	LOC400236	hypothetical LOC400236	-0.1004	0.0156
229657_at	THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	-1.7914	0
229668_at	LOC90393	hypothetical protein LOC90393	-1.0753	0
229670_at		5.5 kb mRNA upregulated in retinoic acid treated HL-60 neutrophilic cells	-1.1484	0
229678_at	LOC728431	Hypothetical protein LOC728431	-1.2851	0.0001
229683_s_at	KCTD15	Potassium channel tetramerisation domain containing 15	-0.1759	0.0021
229687_s_at		Full length insert cDNA clone ZD53C10	-0.3176	0.0049
229688_at		Full length insert cDNA clone ZD53C10	-0.1937	0.0161

229689_s_at		Transcribed locus	-0.7151	0.0004
229691_at		Full-length cDNA clone CS0DH005YI18 of T cells (Jurkat cell line) of Homo sapiens (human)	-0.2728	0.0336
229693_at	LOC388335	similar to RIKEN cDNA A730055C05 gene	-2.0313	0
229696_at		Transcribed locus	-0.5699	0
229699_at		CDNA FLJ45384 fis; clone BRHIP3021987	-1.44	0
229708_at	C9orf167	Chromosome 9 open reading frame 167	-0.122	0.0494
229709_at	ATP1B3	ATPase; Na+/K+ transporting; beta 3 polypeptide	-0.7907	0
229727_x_at	NLF2	nuclear localized factor 2	-0.1925	0.0402
229739_s_at	FAM116B	family with sequence similarity 116; member B	-0.3769	0.0047
229740_at	LOC643008	PP12104	-0.1994	0.0043
229753_at			-0.1024	0.0357
229755_x_at	DLL3	Delta-like 3 (Drosophila)	-0.1602	0.0335
229756_at		Transcribed locus; strongly similar to XP_515285.1 similar to inhibitor of DNA binding 2; inhibitor of differentiation 2; DNA-binding protein inhibitor ID2; helix-loop-helix protein ID2 [Pan troglodytes]	-0.7633	0.0006
229757_at		Transcribed locus	-0.4496	0.0448
229771_at	TMEM41A	Transmembrane protein 41A	-0.542	0
229779_at	COL4A4	collagen; type IV; alpha 4	-4.162	0
229780_at	MTSS1	Metastasis suppressor 1	-0.1996	0.0328
229783_at	LOC728163	hypothetical protein LOC728163	-0.1285	0.0457
229786_at		CDNA clone IMAGE:4819555	-0.5048	0
229797_at	MCOLN3	mucolipin 3	-2.4965	0.0048
229799_s_at	NCAM1	neural cell adhesion molecule 1	-0.2043	0.0004
229802_at		CDNA FLJ14388 fis; clone HEMBA1002716	-2.8194	0.0006
229806_at	QRICH1	Glutamine-rich 1	-0.2821	0
229807_s_at	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	-0.1443	0.0065
229810_at		Transcribed locus	-0.6057	0.0298
229812_at	USP48	ubiquitin specific peptidase 48	-2.2319	0
229813_x_at	DAZAP1	DAZ associated protein 1	-0.5892	0.0002
229820_at	LOC440993	hypothetical gene supported by AK128346	-0.2571	0.0197
229823_at		Transcribed locus	-1.6255	0.0144
229824_at		CDNA FLJ45325 fis; clone BRHIP3006717	-3.0076	0
229825_at	PLK3	Polo-like kinase 3 (Drosophila)	-0.1275	0.008
229826_at	LOC440957	similar to CG32736-PA	-0.9638	0.0413
229827_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.1708	0.004
229833_at		CDNA FLJ90099 fis; clone HEMBA1006016	-0.2857	0.0452

229840_at	IQSEC2	IQ motif and Sec7 domain 2	-0.5658	0.0041
229848_at	ZNF10	zinc finger protein 10	-0.9595	0.0032
229851_s_at	C11orf54	chromosome 11 open reading frame 54	-1.2672	0
229856_s_at	C1orf128	Chromosome 1 open reading frame 128	-0.1384	0.0135
229857_s_at	LOC644246	Hypothetical protein LOC644246	-0.15	0.0239
229865_at	FNDC3B	fibronectin type III domain containing 3B	-0.5604	0.016
229867_at	BTBD9	BTB (POZ) domain containing 9	-0.4527	0.0041
229874_x_at	LOC729604	hypothetical protein LOC729604	-0.6787	0.0391
229884_s_at	MRPL2	mitochondrial ribosomal protein L2	-0.7163	0.0255
229885_at		Transcribed locus	-0.7463	0.0023
229888_at	C12orf60	chromosome 12 open reading frame 60	-2.5925	0
229893_at	FRMD3	FERM domain containing 3	-1.7843	0
229894_s_at	RAB43	RAB43; member RAS oncogene family	-0.2375	0.0122
229898_at		Transcribed locus	-0.6556	0.0001
229902_at	FLT4	fms-related tyrosine kinase 4	-0.4835	0.009
229904_at		Homo sapiens; clone IMAGE:4186245; mRNA	-0.1282	0.024
229907_at		Homo sapiens; clone IMAGE:6176018; mRNA	-0.5188	0.0033
229910_at	SHE	Src homology 2 domain containing E	-2.1525	0
229922_at	GPRIN1	G protein regulated inducer of neurite outgrowth 1	-0.1847	0.0389
229923_at	ZDHHC21	zinc finger; DHHC-type containing 21	-0.151	0.0498
229928_at			-0.2057	0.0335
229931_at	ZNF775	Zinc finger protein 775	-0.1072	0.0481
229932_at	RNF181	Ring finger protein 181	-0.3094	0.0083
229934_at		Mir-223 transcript variant 1 mRNA; complete sequence	-0.5013	0.0074
229936_at	GFRA3	GDNF family receptor alpha 3	-0.3209	0.0028
229940_at	SETD3	SET domain containing 3	-0.544	0
229941_at	LOC730112	similar to CG18335-PA	-2.1321	0.0125
229942_at	BNC2	basonuclin 2	-0.3728	0.0315
229948_at		Transcribed locus; strongly similar to XP_001092008.1 similar to family with sequence similarity 98; member B isoform 1 [Macaca mulatta]	-1.5558	0
229950_s_at			-0.1388	0.0194
229954_at		Transcribed locus; strongly similar to XP_001082768.1 similar to choline dehydrogenase [Macaca mulatta]	-0.6322	0
229969_at	SEC63	SEC63 homolog (S. cerevisiae)	-1.069	0.0002
229973_at	C1orf173	chromosome 1 open reading frame 173	-1.0325	0

229974_at	EVC2	Ellis van Creveld syndrome 2 (limbin)	-0.3317	0.0003
229991_s_at	SYTL4	Synaptotagmin-like 4 (granuphilin-a)	-0.6874	0
229996_s_at	PCGF5	Polycomb group ring finger 5	-0.1907	0.0039
230009_at	FAM118B	family with sequence similarity 118; member B	-0.693	0.0015
230023_at	NSUN4	NOL1/NOP2/Sun domain family; member 4	-0.5545	0.0488
230025_at	GJC1	gap junction protein; chi 1; 31.9kDa	-0.3935	0.0009
230030_at	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	-0.3959	0.0062
230031_at	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein; 78kDa)	-1.4404	0.0003
230041_at		CDNA FLJ14057 fis; clone HEMBB1000337	-0.1837	0.0405
230045_at	CNTN2	contactin 2 (axonal)	-0.1156	0.0242
230048_at		Transcribed locus	-0.9536	0.0004
230051_at	C10orf47	chromosome 10 open reading frame 47	-0.258	0.002
230054_at	PRRT1	Proline-rich transmembrane protein 1	-0.3527	0.0258
230067_at	FAM124A	Family with sequence similarity 124A	-0.2265	0.0378
230080_at	HOXA4	Homeobox A4	-0.3441	0.0001
230081_at	PLCXD3	phosphatidylinositol-specific phospholipase C; X domain containing 3	-3.1341	0.0001
230083_at	USP53	ubiquitin specific peptidase 53	-3.2019	0
230087_at	PRIMA1	proline rich membrane anchor 1	-0.8992	0
230110_at	MCOLN2	mucolipin 2	-1.8812	0.0003
230117_at	VSTM2A	V-set and transmembrane domain containing 2A	-0.2927	0.0008
230130_at	SLIT2	Slit homolog 2 (Drosophila)	-3.5994	0.0003
230131_x_at	ARSD	arylsulfatase D	-0.6957	0.0007
230135_at		Homo sapiens; clone IMAGE:4690669; mRNA	-2.2822	0.0001
230138_at	FREQ	Frequenin homolog (Drosophila)	-0.1677	0.0092
230140_at	PTPN9	Protein tyrosine phosphatase; non-receptor type 9	-0.1028	0.0064
230154_at		Transcribed locus; strongly similar to XP_001106227.1 similar to WW domain-containing adapter with a coiled-coil region isoform 1 [Macaca mulatta]	-0.3756	0.0132
230156_x_at	CHD2	Chromodomain helicase DNA binding protein 2	-0.2327	0.0415
230159_at			-0.1432	0.0229
230163_at	LOC143381	Hypothetical protein LOC143381	-0.2545	0
230166_at	KIAA1958	KIAA1958	-0.8736	0.0071
230172_at	FAM14B	Family with sequence similarity 14; member B	-1.0377	0.0007
230176_at		Transcribed locus	-0.5306	0.0071
230178_s_at		CDNA FLJ38461 fis; clone FEBRA2020977	-1.3763	0

230184_at		CDNA FLJ39179 fis; clone OCBBF2004147	-0.1761	0.0102
230188_at	ICHTHYIN	ichthyin protein	-0.2561	0.0044
230189_x_at		Transcribed locus	-0.1742	0.037
230190_at	NDFIP2	Nedd4 family interacting protein 2	-0.1013	0.0093
230192_at	TRIM13	tripartite motif-containing 13	-0.5824	0.0478
230195_at		Hypothetical protein (ORF1); clone 00275	-0.155	0.0018
230196_x_at	ARHGAP23	Rho GTPase activating protein 23	-0.2125	0.036
230197_s_at	TPPP	Tubulin polymerization promoting protein	-0.1277	0.0407
230202_at	RELA	V-rel reticuloendotheliosis viral oncogene homolog A; nuclear factor of kappa light polypeptide gene enhancer in B-cells 3; p65 (avian)	-0.2543	0.0049
230203_at	FLJ46875	hypothetical LOC440918	-0.4135	0.034
230216_at	C12orf51	Chromosome 12 open reading frame 51	-0.2122	0.0018
230218_at	HIC1	hypermethylated in cancer 1	-1.103	0
230231_at	FGF14	fibroblast growth factor 14	-0.2368	0.0008
230233_at		Transcribed locus	-2.0995	0.0001
230234_at		Transcribed locus	-0.2253	0.0467
230239_at	ROCK1	Rho-associated; coiled-coil containing protein kinase 1	-0.3077	0.0085
230241_at		Transcribed locus	-1.2497	0.0015
230247_at		Transcribed locus	-0.1953	0.0413
230250_at	PTPRB	Protein tyrosine phosphatase; receptor type; B	-3.299	0
230251_at	C6orf176	Chromosome 6 open reading frame 176	-5.9406	0
230252_at	GPR92	G protein-coupled receptor 92	-1.0815	0
230253_at	SCUBE3	Signal peptide; CUB domain; EGF-like 3	-0.2024	0.0248
230260_s_at			-0.1156	0.0036
230262_at	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 3	-0.3008	0.0063
230268_at		Transcribed locus	-0.453	0
230269_at		Transcribed locus	-0.1436	0.0129
230274_s_at	NUP88	Nucleoporin 88kDa	-0.3308	0.0012
230276_at			-0.7761	0.0011
230279_at		CDNA FLJ37891 fis; clone BRTHA2003436	-0.214	0.0273
230288_at	FGF14	fibroblast growth factor 14	-0.3991	0.0005
230290_at	SCUBE3	signal peptide; CUB domain; EGF-like 3	-0.4739	0
230296_at	C16orf52	Chromosome 16 open reading frame 52	-0.5565	0.0049
230303_at	SYNPR	synaptoporin	-0.1189	0.0346
230305_at		Transcribed locus	-2.3985	0
230309_at		Transcribed locus	-1.8957	0.0007
230317_x_at	TMCO3	Transmembrane and coiled-coil domains 3	-0.131	0.0064

230320_at	TBRG1	transforming growth factor beta regulator 1	-0.4726	0.033
230321_at			-0.3508	0.0359
230322_at	NFAM1	NFAT activating protein with ITAM motif 1	-0.3417	0.0013
230326_s_at	C11orf73	chromosome 11 open reading frame 73	-0.3711	0.045
230333_at		Transcribed locus	-0.8551	0.046
230335_at	C9orf50	chromosome 9 open reading frame 50	-0.1881	0.0025
230349_at	XKRX	XK; Kell blood group complex subunit-related; X-linked	-0.2208	0.0136
230351_at	LOC283481	hypothetical protein LOC283481	-1.4455	0
230352_at	PRPS2	Phosphoribosyl pyrophosphate synthetase 2	-2.9322	0
230353_at	LOC284112	hypothetical protein LOC284112	-1.4796	0
230354_at		Transcribed locus	-0.4775	0
230358_at	ZER1	Zer-1 homolog (C. elegans)	-0.1483	0.0086
230360_at	GLDN	gliomedin	-1.6785	0.0039
230364_at	CHPT1	choline phosphotransferase 1	-1.0659	0.002
230371_at	HPS6	Hermansky-Pudlak syndrome 6	-0.1875	0.0071
230377_s_at	TBC1D2B	TBC1 domain family; member 2B	-0.1178	0.0285
230378_at	SCGB3A1	secretoglobin; family 3A; member 1	-0.1988	0.0216
230379_x_at	C2orf56	chromosome 2 open reading frame 56	-0.7836	0.0021
230380_at	THAP2	THAP domain containing; apoptosis associated protein 2	-4.8926	0
230385_at	LOC153277	hypothetical protein LOC153277	-0.3251	0.0045
230388_s_at	LOC644246	hypothetical protein LOC644246	-2.8717	0
230391_at	CD84	CD84 molecule	-1.2995	0.0097
230410_at	NRP2	Neuropilin 2	-0.1193	0.0286
230416_at		Transcribed locus	-1.1128	0.006
230422_at	FPRL2	formyl peptide receptor-like 2	-1.4555	0.0021
230433_at	LOC729970	hypothetical protein LOC729970	-1.1994	0.0209
230435_at	LOC375190	hypothetical LOC375190	-0.6501	0.0091
230443_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	-0.1849	0.0243
230449_x_at		Transcribed locus; weakly similar to XP_519878.1 similar to ubiquitin-conjugating enzyme E2 variant 1 isoform c; DNA-binding protein [Pan troglodytes]	-0.9139	0.012
230455_at	PPP1R9B	protein phosphatase 1; regulatory (inhibitor) subunit 9B	-0.149	0.0482
230459_s_at	SHB	Src homology 2 domain containing adaptor protein B	-0.1319	0.0088
230463_at		CDNA FLJ36891 fis; clone BRACE2000368	-0.7755	0
230467_at	TMEM52	transmembrane protein 52	-1.2294	0.0358
230468_s_at	C1orf56	Chromosome 1 open reading frame 56	-0.1802	0.0019
230470_at	DSCR9	Down syndrome critical region gene 9	-0.166	0.0112

230473_s_at	HMGB4	high-mobility group box 4	-0.1598	0.0488
230479_at		Transcribed locus	-0.8194	0.0019
230482_at	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2;3-beta-galactosyl-1;3)-N-acetylgalactosaminide alpha-2;6-sialyltransferase 5	-1.8006	0
230488_s_at	LOC138948	BPR	-0.3024	0.0007
230491_at		MRNA; cDNA DKFZp686J01116 (from clone DKFZp686J01116)	-0.6689	0.0336
230502_s_at	LOC149832	Hypothetical protein LOC149832	-0.2861	0.038
230510_at	HSPB9	heat shock protein; alpha-crystallin-related; B9	-0.1469	0.0101
230511_at	CREM	cAMP responsive element modulator	-3.7468	0
230512_x_at	TMEM165	Transmembrane protein 165	-0.1651	0.0234
230514_s_at	LYZL1	lysozyme-like 1, lysozyme-like 2	-0.127	0.0172
230515_at			-0.1252	0.0119
230517_at	tcag7.1196	similar to GLI-Kruppel family member HKR1	-0.1251	0.0276
230519_at	FAM124A	family with sequence similarity 124A	-0.2134	0.0212
230520_at	AIG1	androgen-induced 1	-0.241	0.0114
230523_at	QSOX1	quiescin Q6 sulfhydryl oxidase 1	-0.2281	0.0005
230529_at	HECA	headcase homolog (Drosophila)	-0.2355	0.0093
230530_at			-0.2265	0.0107
230544_at	RPS6KA4	Ribosomal protein S6 kinase; 90kDa; polypeptide 4	-0.1986	0.0071
230549_at	ELK4	ELK4; ETS-domain protein (SRF accessory protein 1)	-0.1114	0.0493
230550_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-2.4545	0
230553_at			-0.1663	0.005
230563_at	RASGEF1A	RasGEF domain family; member 1A	-1.1729	0.0355
230564_at	SIPA1L3	Signal-induced proliferation-associated 1 like 3	-0.1561	0.0035
230572_at	C4orf38	chromosome 4 open reading frame 38	-0.1022	0.0414
230574_at			-0.2172	0.0148
230577_at		Transcribed locus	-0.9512	0.0083
230589_at			-0.1212	0.0381
230595_at	LOC572558	hypothetical locus LOC572558	-3.2003	0
230608_at	C1orf182	chromosome 1 open reading frame 182	-0.2025	0.03
230611_at	SYPL2	synaptophysin-like 2	-0.8192	0.0082
230619_at	ARNT	aryl hydrocarbon receptor nuclear translocator	-0.7561	0.0019
230631_s_at		Full-length cDNA clone CS0DI051YA02 of Placenta Cot 25-normalized of Homo sapiens (human)	-0.1489	0.0429
230633_at	TMEM102	transmembrane protein 102	-0.4377	0
230642_at		Transcribed locus	-0.2243	0.0041

230643_at	WNT9A	wingless-type MMTV integration site family; member 9A	-0.5437	0.0004
230644_at	LRFN5	leucine rich repeat and fibronectin type III domain containing 5	-1.2586	0
230645_at	FRMD3	FERM domain containing 3	-2.344	0.0001
230648_at	LOC283663	hypothetical protein LOC283663	-0.1609	0.0183
230657_at		Transcribed locus	-1.7422	0
230658_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter; y+ system); member 2	-0.1175	0.0062
230665_at		CDNA FLJ40823 fis; clone TRACH2011093	-0.2714	0.0095
230670_at	IGSF10	immunoglobulin superfamily; member 10	-2.8156	0
230673_at	PKHD1L1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	-0.3513	0
230677_at	C14orf73	chromosome 14 open reading frame 73	-0.1594	0.0212
230680_at		Transcribed locus	-2.4973	0.0003
230691_at	STX1B	syntaxin 1B	-0.1828	0.0027
230699_at	PGLS	6-phosphogluconolactonase	-0.2518	0.0036
230700_at	RTN4RL1	reticulon 4 receptor-like 1	-0.4492	0.0024
230706_s_at	CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	-1.9648	0
230709_x_at	ZBTB7A	Zinc finger and BTB domain containing 7A	-0.2337	0.0042
230711_at		CDNA FLJ13510 fis; clone PLACE1005146	-0.2137	0.0244
230715_at	KIAA1729	KIAA1729 protein	-0.4554	0.0202
230716_at	LOC285733	hypothetical protein LOC285733	-0.252	0
230721_at	C16orf52	chromosome 16 open reading frame 52	-0.7782	0
230727_at	CISD3	CDGSH iron sulfur domain 3	-0.5517	0.0026
230729_at		Transcribed locus; strongly similar to XP_001115485.1 similar to exportin 1 isoform 1 [Macaca mulatta]	-0.5217	0.0027
230740_at			-0.9449	0
230743_at	LOC404266	hypothetical LOC404266	-0.182	0.0298
230744_at		Transcribed locus	-1.3862	0
230747_s_at	C18orf17	Chromosome 18 open reading frame 17	-2.3112	0
230749_s_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-0.1579	0.0167
230750_at		Transcribed locus	-0.2253	0.0033
230754_at	ZBTB38	zinc finger and BTB domain containing 38	-0.3947	0
230760_at	ZFY	Zinc finger protein; Y-linked	-0.8594	0.0182
230769_at	DENND2C	DENN/MADD domain containing 2C	-0.2011	0.0292
230774_at	ZADH1	zinc binding alcohol dehydrogenase; domain containing 1	-0.658	0.0067
230776_at		CDNA FLJ36181 fis; clone TESTI2026794	-0.1201	0.0232

230780_at	LOC730091	hypothetical protein LOC730091	-0.4562	0.0224
230781_at			-1.4537	0.0047
230782_at	LOC653381	similar to Sorbitol dehydrogenase (L-iditol 2-dehydrogenase)	-0.9856	0.0052
230788_at	GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	-0.1737	0.038
230790_x_at			-0.4959	0.0124
230810_at	JMJD4	jumonji domain containing 4	-0.2634	0.0007
230816_at	C9orf166	Chromosome 9 open reading frame 166	-0.2365	0.0001
230822_at	TMEM61	transmembrane protein 61	-0.8745	0
230831_at			-2.1984	0.0032
230833_at	ACRBP	acrosin binding protein	-0.2233	0.0244
230839_at	PRMT8	protein arginine methyltransferase 8	-0.1611	0.0073
230863_at	LRP2	low density lipoprotein-related protein 2	-0.1548	0.0356
230870_at	MUS81	MUS81 endonuclease homolog (S. cerevisiae)	-0.1467	0.0064
230871_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-0.7833	0.0198
230875_s_at	ATP11A	ATPase; Class VI; type 11A	-1.1607	0.0026
230877_at	IGHD	immunoglobulin heavy constant delta	-0.1388	0.0244
230894_s_at		Transcribed locus	-0.973	0.0007
230899_at	SETD4	SET domain containing 4	-0.1762	0.006
230911_at	SIX1	SIX homeobox 1	-0.1226	0.0294
230913_at		Full length insert cDNA clone ZE12B03	-1.5595	0.0074
230921_s_at		Transcribed locus	-0.24	0.029
230922_x_at	FUNDC2	FUN14 domain containing 2	-0.3506	0.0193
230923_at	FAM19A1	family with sequence similarity 19 (chemokine (C-C motif)-like); member A1	-0.1238	0.0397
230924_at	TTLL6	tubulin tyrosine ligase-like family; member 6	-0.1391	0.0378
230925_at	APBB1IP	amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	-1.2924	0.0052
230938_x_at	ATF5	activating transcription factor 5	-0.202	0.029
230939_at			-0.1778	0.0224
230950_at		Transcribed locus	-0.1248	0.0333
230958_s_at		Transcribed locus	-1.24	0.0004
230963_at	EMX2OS	empty spiracles homeobox 2 opposite strand	-0.1681	0.0103
230965_at	USP2	ubiquitin specific peptidase 2	-0.2419	0.0347
230977_at	NPM2	nucleophosmin/nucleoplasmin; 2	-0.8969	0
230979_at		Transcribed locus	-0.1299	0.0227

230980_x_at		Transcribed locus; strongly similar to XP_001101257.1 similar to sterol regulatory element-binding transcription factor 2 [Macaca mulatta]	-0.2322	0.0306
230985_at	C9orf131	chromosome 9 open reading frame 131	-0.2281	0.0336
230989_s_at	TSSK6	testis-specific serine kinase 6	-0.1666	0.0036
230999_at	FLJ39051	Hypothetical gene supported by AK096370	-1.3053	0.002
231000_at			-0.1378	0.0474
231001_at	FIBIN	fin bud initiation factor	-0.4272	0.0189
231002_s_at	RABEP1	Rabaptin; RAB GTPase binding effector protein 1	-0.4028	0.0002
231011_at	LARP2	La ribonucleoprotein domain family; member 2	-0.1995	0.0112
231016_s_at		Transcribed locus	-0.5292	0.0005
231017_at	STK11	serine/threonine kinase 11	-0.4684	0.0329
231019_x_at	STK11	Serine/threonine kinase 11	-0.4788	0.0001
231020_at			-0.1249	0.0379
231033_at		Full length insert cDNA clone YI40A07	-0.144	0.0006
231035_s_at		Transcribed locus	-0.4558	0.0063
231045_x_at	C11orf31	chromosome 11 open reading frame 31	-0.3936	0.0148
231050_at	HRASLS5	HRAS-like suppressor family; member 5	-0.4069	0
231058_at	FXYD4	FXYD domain containing ion transport regulator 4	-0.1172	0.0326
231066_s_at	CLCN4	Chloride channel 4	-0.1524	0.0156
231067_s_at		Transcribed locus	-0.6081	0.0003
231069_at		Transcribed locus	-1.1432	0.007
231072_at	MIDN	midnolin	-0.1122	0.0494
231073_at	C1orf168	chromosome 1 open reading frame 168	-0.122	0.0409
231078_at		Transcribed locus; strongly similar to XP_001106001.1 similar to mitochondrial solute carrier-like protein isoform 2 [Macaca mulatta]	-0.5098	0.002
231083_at			-0.1558	0.0102
231086_at		Transcribed locus; weakly similar to XP_001094263.1 beta-site APP-cleaving enzyme 1 isoform 5 [Macaca mulatta]	-0.4225	0.0036
231091_x_at		Transcribed locus	-0.1803	0.0066
231097_at		CDNA: FLJ22240 fis; clone HRC02512	-0.1578	0.0139
231098_at		Transcribed locus	-0.3516	0.0007
231110_at		Transcribed locus	-0.2819	0.0002
231118_at	ANKRD35	ankyrin repeat domain 35	-0.3607	0.0001
231121_at	HPS3	Hermansky-Pudlak syndrome 3	-0.2915	0.0301
231132_at	LOC348120	Hypothetical protein LOC348120	-0.166	0.0066
231136_at			-0.2742	0.0035

231137_at		Transcribed locus	-0.2595	0.0001
231140_at	TPPP2	tubulin polymerization-promoting protein family member 2	-0.1281	0.013
231141_at		CDNA clone IMAGE:4838568	-0.1694	0.0087
231148_at	IGFL2	IGF-like family member 2	-0.1343	0.0233
231157_at	TTLL11	tubulin tyrosine ligase-like family; member 11	-0.7383	0.0017
231159_at			-0.2003	0.0151
231163_at	C1orf111	chromosome 1 open reading frame 111	-0.148	0.0122
231174_s_at		Transcribed locus	-0.1229	0.0379
231181_at		Transcribed locus	-0.7286	0
231182_at	WIPF1	WAS/WASL interacting protein family; member 1	-0.2206	0.0198
231189_at	MGC40574	hypothetical protein MGC40574	-0.1828	0.0235
231195_at	KLRG2	killer cell lectin-like receptor subfamily G; member 2	-0.1611	0.0037
231209_at	C14orf73	chromosome 14 open reading frame 73	-0.2039	0.0037
231210_at	LOC283129	hypothetical protein LOC283129	-0.1484	0.048
231211_s_at	LOC541469	hypothetical protein LOC541469	-0.2032	0.0375
231213_at	PDE1A	phosphodiesterase 1A; calmodulin-dependent	-0.9105	0.0328
231216_at	TMEM179	Transmembrane protein 179	-0.1455	0.0387
231222_at		Transcribed locus	-0.1402	0.005
231231_at	FMNL3	Formin-like 3	-0.1532	0.0102
231240_at	DIO2	deiodinase; iodothyronine; type II	-1.1121	0
231244_at	CASD1	CAS1 domain containing 1	-0.1408	0.0032
231245_s_at			-0.2117	0.0103
231270_at	CA13	carbonic anhydrase XIII	-1.1292	0.0205
231275_at	FLJ42875	FLJ42875 protein	-0.1833	0.0021
231279_at	PATE	expressed in prostate and testis	-0.1791	0.0109
231280_at		Transcribed locus	-0.1616	0.0005
231311_at		CDNA FLJ11417 fis; clone HEMBA1000960	-0.5762	0.0346
231317_at		Transcribed locus	-0.1641	0.0295
231341_at	SLC35D3	solute carrier family 35; member D3	-0.205	0.0045
231343_at			-0.1323	0.0305
231354_at	LOC780529	hypothetical LOC780529	-0.1356	0.0261
231358_at		Transcribed locus	-0.3163	0.0207
231363_at	LELP1	late cornified envelope-like proline-rich 1	-0.2756	0.0055
231367_s_at	LOC647131	hypothetical LOC647131	-0.6832	0.0001
231371_at	TDRD10	tudor domain containing 10	-0.6386	0
231377_at	LOC158830	similar to Ab2-183	-0.1444	0.032
231378_at		Transcribed locus; moderately similar to XP_001095369.1 hypothetical protein [Macaca mulatta]	-0.2147	0.0156

231387_at		Transcribed locus	-0.2006	0.0143
231390_at	LOC730116	hypothetical protein LOC730116	-0.1028	0.0214
231398_at	SLC22A7	solute carrier family 22 (organic anion transporter); member 7	-0.1018	0.0476
231400_s_at		Transcribed locus	-0.1285	0.0137
231409_at		Transcribed locus	-0.1178	0.0149
231411_at	LHFP	Lipoma HMGIC fusion partner	-1.2034	0.0002
231418_at		Transcribed locus	-0.1286	0.0009
231423_s_at	ANKRD16	ankyrin repeat domain 16	-0.2445	0.0115
231424_at		MRNA; cDNA DKFZp564G223 (from clone DKFZp564G223)	-0.1543	0.0264
231427_at	LOC284648	hypothetical protein LOC284648	-0.1172	0.0357
231434_at	LOC728460	similar to zinc finger protein 474	-0.1581	0.0257
231445_at		Transcribed locus; strongly similar to XP_530274.1 hypothetical protein XP_530274 [Pan troglodytes]	-0.1301	0.0163
231452_at	HRASLS5	HRAS-like suppressor family; member 5	-0.2471	0.0013
231456_at		Transcribed locus	-0.1242	0.0279
231458_at		CDNA clone IMAGE:5266545	-0.1579	0.005
231462_at	LOC283953	Hypothetical LOC283953	-0.2054	0.006
231470_at	ZNF493	Zinc finger protein 493	-1.6318	0.0001
231473_at		Transcribed locus	-0.1402	0.0003
231482_at		MRNA; cDNA DKFZp781G0123 (from clone DKFZp781G0123)	-0.137	0.0356
231491_at	C21orf23	chromosome 21 open reading frame 23	-0.1015	0.0267
231492_at		Transcribed locus	-0.1387	0.0381
231496_at	FCAMR	Fc receptor; IgA; IgM; high affinity	-0.1276	0.012
231498_at		CDNA clone IMAGE:4827941	-0.1273	0.0195
231506_at		Transcribed locus	-0.107	0.034
231530_s_at	C11orf1	chromosome 11 open reading frame 1	-0.9796	0.0034
231538_at	C11orf1	Chromosome 11 open reading frame 1	-0.269	0.0052
231542_at		Homo sapiens; clone IMAGE:3464359; mRNA	-0.2169	0.0079
231545_at			-0.103	0.0341
231555_at		Transcribed locus	-0.2646	0
231566_at	C14orf148	chromosome 14 open reading frame 148	-0.1064	0.0354
231567_s_at	CCDC62	coiled-coil domain containing 62	-0.1724	0.0179

231568_at	CT47.7	cancer/testis CT47 family; member 1, cancer/testis CT47 family; member 10, cancer/testis CT47 family; member 11, cancer/testis CT47 family; member 2, cancer/testis CT47 family; member 3, cancer/testis CT47 family; member 4, cancer/testis CT47 family; member 5, cancer/testis CT47 family; member 6, cancer/testis CT47 family; member 7, cancer/testis CT47 family; member 8, cancer/testis CT47 family; member 9	-0.1863	0.0189
231571_at	LOC285827	hypothetical protein LOC285827	-0.1923	0.0227
231572_at	LOC136242	similar to RIKEN cDNA 1700016G05	-0.1819	0.0278
231574_at		Transcribed locus	-0.1267	0.0173
231579_s_at	TIMP2	TIMP metallopeptidase inhibitor 2	-1.0486	0.0218
231580_at	LOC729464	hypothetical protein LOC729464	-0.1455	0.0378
231589_at			-0.1811	0.0049
231593_at		Transcribed locus	-0.1349	0.0095
231595_at		CDNA clone MGC:40177 IMAGE:5167345	-0.359	0
231596_at		Transcribed locus	-0.1311	0.0237
231604_at		Transcribed locus	-0.2841	0.0064
231605_at		Transcribed locus	-0.1092	0.0234
231611_at		Transcribed locus; weakly similar to XP_001104477.1 hypothetical protein [Macaca mulatta]	-0.1771	0.0459
231619_at		Transcribed locus	-0.2165	0.031
231631_at		Transcribed locus	-0.1926	0.0015
231635_x_at	RNF31	Ring finger protein 31	-0.1427	0.0073
231639_at		CDNA clone IMAGE:5277868	-0.2429	0.0153
231644_at		Transcribed locus	-1.5071	0.008
231651_at		CDNA FLJ36110 fis; clone TESTI2021939	-0.1575	0.049
231652_at		Homo sapiens; clone IMAGE:5744200; mRNA	-0.1179	0.0357
231659_at	ST3GAL3	ST3 beta-galactoside alpha-2;3-sialyltransferase 3	-0.146	0.0353
231667_at	SLC39A5	solute carrier family 39 (metal ion transporter); member 5	-0.16	0.0322
231669_at	SEPP1	Selenoprotein P; plasma; 1	-0.2404	0.0159
231670_at			-0.1805	0.0068
231671_at	FGA	Fibrinogen alpha chain	-0.1469	0.0368
231681_x_at	HIST3H2A	Histone cluster 3; H2a	-0.1495	0.0002
231687_at		MRNA; cDNA DKFZp781F2222 (from clone DKFZp781F2222)	-0.1067	0.0101
231699_at	NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; alpha	-0.2427	0.0004
231700_at	GUCA1A	guanylate cyclase activator 1A (retina)	-0.1688	0.0159

231705_at	HRSP12	Heat-responsive protein 12	-0.1694	0.032
231706_s_at	EVX1	even-skipped homeobox 1	-0.164	0.0086
231707_at			-0.2127	0.0155
231722_at	CASP14	caspase 14; apoptosis-related cysteine peptidase	-0.2082	0.0004
231734_at	RBP2	retinol binding protein 2; cellular	-0.1206	0.0322
231735_s_at	PRO1073	PRO1073 protein	-0.6339	0.0081
231736_x_at	MGST1	microsomal glutathione S-transferase 1	-2.0238	0.0399
231746_at	MIXL1	Mix1 homeobox-like 1 (Xenopus laevis)	-0.2006	0.0035
231748_at	ULBP3	UL16 binding protein 3	-0.1124	0.0265
231751_at	ABCG8	ATP-binding cassette; sub-family G (WHITE); member 8 (sterolin 2)	-0.1156	0.0458
231752_at	NPBWR1	neuropeptides B/W receptor 1	-0.1799	0.0414
231756_at	ZP4	zona pellucida glycoprotein 4	-0.1079	0.0449
231766_s_at	COL12A1	collagen; type XII; alpha 1	-1.0214	0.0004
231769_at	FBXO6	F-box protein 6	-0.9191	0.044
231773_at	ANGPTL1	angiopoietin-like 1	-3.5791	0
231778_at	DLX3	distal-less homeobox 3	-0.1711	0.0257
231783_at	CHRM1	cholinergic receptor; muscarinic 1	-0.1454	0.0243
231785_at	NTF5	neurotrophin 5 (neurotrophin 4/5)	-0.1149	0.0423
231788_at	GPR92	G protein-coupled receptor 92	-0.176	0.0259
231790_at	DMGDH	dimethylglycine dehydrogenase	-0.4733	0.0298
231795_at	STON1	stonin 1	-0.1532	0.001
231796_at	EPHA8	EPH receptor A8	-0.2542	0.0034
231804_at	RXFP1	relaxin/insulin-like family peptide receptor 1	-2.7908	0
231807_at	KIAA1217	KIAA1217	-2.0259	0.0001
231817_at	USP53	ubiquitin specific peptidase 53	-2.8469	0
231835_at	C1orf93	chromosome 1 open reading frame 93	-1.8586	0.0001
231851_at	RAVER2	ribonucleoprotein; PTB-binding 2	-0.7411	0.0286
231857_s_at	AGBL5	ATP/GTP binding protein-like 5	-0.3876	0.0319
231867_at	ODZ2	odz; odd Oz/ten-m homolog 2 (Drosophila)	-0.7147	0.001
231873_at	BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	-0.8284	0.0052
231879_at	COL12A1	collagen; type XII; alpha 1	-0.6464	0.0025
231881_at	CALD1	caldesmon 1	-0.1777	0.002
231899_at	ZC3H12C	zinc finger CCCH-type containing 12C	-1.2681	0.0011
231910_at	NUDT14	Nudix (nucleoside diphosphate linked moiety X)-type motif 14	-0.1072	0.0181
231914_at	NUDT14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	-0.5783	0.0202
231919_at	DBT	dihydrolipoamide branched chain transacylase E2	-0.7813	0.0004
231923_at	FLJ12993	hypothetical LOC441027	-1.5493	0.0001

231930_at	ELMOD1	ELMO/CED-12 domain containing 1	-0.585	0.0029
231948_s_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	-0.4714	0.0078
231983_at	C1orf69	chromosome 1 open reading frame 69	-0.2985	0.0181
231984_at	MTAP	methylthioadenosine phosphorylase	-1.5367	0
231987_at	LOC728264	hypothetical protein LOC728264	-0.2869	0.0441
231995_at	C9orf82	chromosome 9 open reading frame 82	-0.5466	0.0211
232003_at	KIAA1183	KIAA1183 protein	-1.4325	0.0004
232006_at	STK35	Serine/threonine kinase 35	-0.1032	0.0102
232042_at	TTYH2	tweety homolog 2 (Drosophila)	-0.2415	0.0049
232068_s_at	TLR4	toll-like receptor 4	-1.1399	0
232073_at	PPFIA2	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 2	-0.2581	0.0298
232081_at		EST from clone 208499; full insert	-2.5643	0.0001
232088_x_at		CDNA clone IMAGE:4829494	-0.2535	0.041
232090_at		CDNA FLJ11481 fis; clone HEMBA1001803	-1.0212	0.0035
232093_at	LOC147650	hypothetical protein LOC147650, hypothetical protein LOC729781	-0.217	0.0024
232104_at	C1orf95	chromosome 1 open reading frame 95	-0.1417	0.0322
232110_at		CDNA FLJ12136 fis; clone MAMMA1000312	-0.1172	0.0126
232115_at	SLC39A3	solute carrier family 39 (zinc transporter); member 3	-0.1535	0.0261
232122_s_at	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	-3.1425	0.0009
232142_at		CDNA FLJ13973 fis; clone Y79AA1001555	-0.1131	0.0282
232153_at	SPEG	SPEG complex locus	-0.2451	0.0038
232170_at	S100A7A	S100 calcium binding protein A7A	-0.1067	0.0235
232172_at	LOC401577	hypothetical protein LOC401577	-0.3323	0
232175_at	ARF1	ADP-ribosylation factor 1	-0.3795	0.0136
232177_at		Homo sapiens; clone IMAGE:5415705	-0.2324	0.0027
232183_at	SERAC1	serine active site containing 1	-0.6548	0.0295
232185_at	C20orf132	chromosome 20 open reading frame 132	-0.2918	0
232187_at	PALMD	palmdelphin	-0.277	0.005
232189_at		CDNA: FLJ22806 fis; clone KAIA2845	-0.1472	0.0056
232191_at	C21orf105	chromosome 21 open reading frame 105	-0.1418	0.0015
232201_at	NKD2	naked cuticle homolog 2 (Drosophila)	-0.6304	0
232213_at	PELI1	Pellino homolog 1 (Drosophila)	-0.5545	0.0323
232220_at	S100A7A	S100 calcium binding protein A7A	-0.1863	0.0188
232227_at		HSPC324	-0.2243	0.0007
232241_at			-0.1889	0.0003

232243_at	MCPH1	microcephaly; primary autosomal recessive 1	-0.1445	0.0191
232245_at	SLC25A34	solute carrier family 25; member 34	-0.8862	0
232248_at		CDNA: FLJ22566 fis; clone HSI01980	-0.1643	0.0234
232250_at	KIAA1257	KIAA1257	-0.1212	0.01
232252_at	DUSP27	dual specificity phosphatase 27 (putative)	-0.2803	0
232259_s_at	LOC100009676	hypothetical LOC100009676	-0.2259	0.0188
232262_at	PIGL	phosphatidylinositol glycan anchor biosynthesis; class L	-0.6058	0.0001
232270_at	C9orf3	Chromosome 9 open reading frame 3	-1.1795	0
232280_at	SLC25A29	Solute carrier family 25; member 29	-0.3334	0.0018
232284_at	PSMD6	Proteasome (prosome; macropain) 26S subunit; non-ATPase; 6	-0.2261	0.0115
232287_at	PGBD3	piggyBac transposable element derived 3	-0.1663	0.0257
232291_at	MIRH1	microRNA host gene (non-protein coding) 1	-0.5059	0.0004
232292_at		CDNA FLJ13509 fis; clone PLACE1005108	-0.1903	0.0105
232304_at	PELI1	Pellino homolog 1 (Drosophila)	-0.9432	0.0202
232305_at	HMGCLL1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	-0.2014	0.0145
232310_at	LOC388889	hypothetical LOC388889	-0.2249	0.0005
232313_at	TMEM132C	transmembrane protein 132C	-0.647	0
232322_x_at	STARD10	StAR-related lipid transfer (START) domain containing 10	-2.0152	0.002
232325_at		MRNA full length insert cDNA clone EUROIMAGE 196784	-0.1001	0.0312
232326_at	C8orf56	chromosome 8 open reading frame 56	-0.1599	0.0024
232332_at	RP13-347D8.3	KIAA1210 protein	-2.3421	0
232336_at	ZSWIM5	zinc finger; SWIM-type containing 5	-1.0532	0.0077
232345_at	C18orf8	Chromosome 18 open reading frame 8	-0.5091	0.0002
232348_at	C18orf8	Chromosome 18 open reading frame 8	-0.8134	0
232349_x_at	IQWD1	IQ motif and WD repeats 1	-0.9326	0.0036
232354_at		CDNA FLJ12021 fis; clone HEMBB1001756	-0.5707	0.0271
232367_x_at	ZNF598	zinc finger protein 598	-0.2423	0.0436
232374_s_at			-0.1903	0.0247
232377_at	NXPH1	neurexophilin 1	-4.9585	0
232394_at		MRNA; cDNA DKFZp434L231 (from clone DKFZp434L231)	-0.1733	0.0326
232401_at	KCNS2	potassium voltage-gated channel; delayed-rectifier; subfamily S; member 2	-0.1296	0.0246
232419_at	TMEM132A	transmembrane protein 132A	-0.3184	0.0038
232422_at	RP11-151A6.2	hypothetical protein BC004360	-0.5146	0.0063
232433_at	KIAA1683	KIAA1683	-0.1617	0.0442
232434_at	DIRC3	disrupted in renal carcinoma 3	-0.2251	0.0184

232435_at	CXorf45	chromosome X open reading frame 45	-0.1879	0.0071
232443_at	LOC441052	hypothetical gene supported by AF131741	-0.167	0.0048
232456_at	C10orf71	chromosome 10 open reading frame 71	-0.1696	0.0192
232460_at		CDNA: FLJ22870 fis; clone KAT02506; highly similar to D84064 Homo sapiens mRNA for Hrs	-0.1217	0.0183
232472_at		CDNA FLJ12399 fis; clone MAMMA1002780	-0.8534	0.0173
232493_at		Transcribed locus	-0.48	0.0142
232499_at	ITPKB	inositol 1;4;5-trisphosphate 3-kinase B	-0.1473	0.0301
232520_s_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-0.4004	0.0043
232527_at		CDNA FLJ13309 fis; clone OVARC1001442	-1.2121	0
232539_at		MRNA; cDNA DKFZp761H1023 (from clone DKFZp761H1023)	-0.4204	0.006
232583_at		CDNA FLJ11435 fis; clone HEMBA1001208	-0.3777	0.0445
232589_at		CDNA FLJ11489 fis; clone HEMBA1001915	-0.5933	0.0446
232605_s_at	LOC646871	hypothetical LOC646871	-0.2352	0.0061
232617_at	CTSS	cathepsin S	-1.0282	0.0485
232618_at	CYorf15A	chromosome Y open reading frame 15A	-1.4837	0.0119
232620_at	LOC56964	hypothetical protein from EUROIMAGE 384293	-0.1582	0.0348
232623_at		CDNA: FLJ20888 fis; clone ADKA03289	-0.1911	0.01
232634_at	DKFZp566F0947	hypothetical gene DKFZp566F0947	-0.166	0.0334
232636_at	SLITRK4	SLIT and NTRK-like family; member 4	-4.3399	0
232655_at	UGT1A6	UDP glucuronosyltransferase 1 family; polypeptide A6	-0.1401	0.0063
232657_at		CDNA FLJ13400 fis; clone PLACE1001414	-0.1596	0.0034
232678_at	SLC2A9	solute carrier family 2 (facilitated glucose transporter); member 9	-0.2183	0.0032
232697_at	LRFN2	leucine rich repeat and fibronectin type III domain containing 2	-0.1346	0.0347
232698_at	BPIL1	bactericidal/permeability-increasing protein-like 1	-0.1929	0.005
232709_at		CDNA FLJ13427 fis; clone PLACE1002477	-0.2336	0.0482
232715_at		CDNA FLJ11544 fis; clone HEMBA1002826	-0.2126	0.0002
232719_at	BRUNOL4	bruno-like 4; RNA binding protein (Drosophila)	-0.1576	0.0042
232724_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-0.5267	0.0013
232725_s_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	-0.1645	0.0172
232726_at		CDNA: FLJ21303 fis; clone COL02107	-2.0804	0.0006
232743_at		MRNA; cDNA DKFZp761K1112 (from clone DKFZp761K1112)	-0.1422	0.0269
232750_at	TNS1	Tensin 1	-1.6725	0.0019

232763_at	TLN1	Talin 1	-0.346	0.0001
232765_x_at	LOC146429	hypothetical protein LOC146429	-0.1692	0.0095
232766_at	C20orf179	chromosome 20 open reading frame 179	-0.1313	0.0118
232776_at		CDNA FLJ11646 fis; clone HEMBA1004394	-0.7479	0.0177
232783_at		CDNA FLJ13625 fis; clone PLACE1011032	-0.1298	0.0293
232795_at		CDNA FLJ10145 fis; clone HEMBA1003322	-0.3464	0
232807_at	FAM131A	family with sequence similarity 131; member A	-0.1641	0.0415
232808_at		CDNA FLJ12293 fis; clone MAMMA1001815	-0.3893	0.0053
232811_x_at	PRICKLE1	Prickle homolog 1 (Drosophila)	-0.1935	0.0302
232820_s_at	FAM112A	family with sequence similarity 112; member A	-0.2072	0.0107
232821_at	FAM112A	family with sequence similarity 112; member A	-0.1431	0.0163
232831_at		CDNA FLJ11910 fis; clone HEMBB1000113	-0.3292	0
232835_at		Transcribed locus	-0.5888	0.0005
232837_at	KIF13A	kinesin family member 13A	-0.3296	0.0017
232856_at	LRRC55	Leucine rich repeat containing 55	-0.167	0.0167
232863_at	ZNF815	zinc finger protein 815	-0.1213	0.048
232887_at	hCG_1776018	HCG1776018	-0.1715	0.0103
232892_at	C20orf166	chromosome 20 open reading frame 166	-0.2471	0.0114
232899_at	FAM41C	family with sequence similarity 41; member C, ribosomal protein L23a pseudogene 7, similar to RPL23AP7 protein	-0.6413	0.0191
232902_s_at	RARS2	arginyl-tRNA synthetase 2; mitochondrial (putative)	-0.9525	0.0395
232926_x_at	ANKRD19	ankyrin repeat domain 19	-0.1116	0.027
232949_at		CDNA FLJ11873 fis; clone HEMBA1007066	-0.1814	0.017
232956_at		CDNA FLJ12293 fis; clone MAMMA1001815	-0.1168	0.0329
232983_s_at	SERGEF	secretion regulating guanine nucleotide exchange factor	-0.5249	0.0053
232992_at	C6orf64	Chromosome 6 open reading frame 64	-0.1762	0.0028
232994_s_at	RGNEF	Rho-guanine nucleotide exchange factor	-1.9547	0.0001
232995_at		CDNA: FLJ21725 fis; clone COLF1013	-0.2288	0.0204
233001_at	SAMD10	sterile alpha motif domain containing 10	-0.1289	0.0104
233031_at	ZEB2	zinc finger E-box binding homeobox 2	-0.347	0
233051_at	SLITRK2	SLIT and NTRK-like family; member 2	-0.2084	0.0107
233059_at		CDNA: FLJ22731 fis; clone HSI15841	-0.2028	0.0046
233060_at	ZMIZ1	zinc finger; MIZ-type containing 1	-0.1872	0.0169
233085_s_at	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	-1.1708	0.0248

233091_at	ATAD3B	ATPase family; AAA domain containing 3B	-0.1613	0.0399
233103_at		CDNA FLJ14109 fis; clone MAMMA1001322; moderately similar to B-CELL GROWTH FACTOR PRECURSOR	-0.1326	0.0413
233107_at		CDNA: FLJ23530 fis; clone LNG06055	-0.2011	0.0021
233109_at	COL12A1	Collagen; type XII; alpha 1	-0.5317	0.0005
233113_at	LOC730057	Hypothetical protein LOC730057	-0.1457	0.0164
233116_at		CDNA FLJ25090 fis; clone CBL08887	-0.7	0.0316
233119_at	FLJ14213	Hypothetical protein FLJ14213	-0.1154	0.0328
233121_at		CDNA FLJ12299 fis; clone MAMMA1001851	-0.574	0.0011
233127_at		CDNA FLJ12412 fis; clone MAMMA1003004	-4.076	0
233130_at		CDNA FLJ12202 fis; clone MAMMA1000908	-0.8878	0.0007
233131_at	C10orf80	chromosome 10 open reading frame 80	-0.2037	0.0014
233134_at	RPH3AL	rabphilin 3A-like (without C2 domains)	-0.1906	0
233136_at	PABPC5	poly(A) binding protein; cytoplasmic 5	-0.7138	0.0299
233150_at	GALNTL5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5	-0.1057	0.0295
233156_at	RNASEH2B	ribonuclease H2; subunit B	-0.1031	0.044
233158_at	KRT82	keratin 82	-0.1648	0.0366
233159_at	STARD13	START domain containing 13	-0.1063	0.0412
233166_at	DEFB126	defensin; beta 126	-0.2162	0.0008
233168_s_at	RP3-402G11.5	selenoprotein O	-0.6247	0.0126
233181_at		Full length insert cDNA clone ZD76B01	-0.1491	0.0288
233189_at		Clone 24974 mRNA sequence	-0.135	0.005
233200_at			-0.1775	0.0029
233204_at	FLJ11903	similar to hypothetical protein MGC40405	-0.1886	0.0187
233221_at	DEFB118	defensin; beta 118	-0.2276	0.0059
233223_at		CDNA FLJ20843 fis; clone ADKA01954	-1.0241	0.0034
233236_at	TSPAN16	tetraspanin 16	-0.1044	0.0333
233245_at	C6orf107	chromosome 6 open reading frame 107	-0.1997	0.0051
233247_x_at	ZDHHC21	zinc finger; DHHC-type containing 21	-0.1699	0.0028
233260_at		CDNA FLJ13528 fis; clone PLACE1006143	-0.1299	0.0164
233266_at		CDNA FLJ13844 fis; clone THYRO1000805	-0.1854	0.0257
233267_at	SELENBP1	Selenium binding protein 1	-0.1161	0.0322
233274_at		CDNA FLJ11615 fis; clone HEMBA1004024	-0.2968	0.0155

233285_at		CDNA FLJ13635 fis; clone PLACE1011143	-0.1191	0.045
233291_at		CDNA FLJ11962 fis; clone HEMBB1001047	-0.3772	0.028
233301_at	OXCT2	3-oxoacid CoA transferase 2	-0.1778	0
233317_at	CD9	CD9 molecule	-0.2337	0.0104
233335_at		MRNA; cDNA DKFZp586J1717 (from clone DKFZp586J1717)	-0.1265	0.028
233342_at	LOC90520	hypothetical protein LOC90520	-0.1106	0.0322
233365_at		CDNA FLJ12285 fis; clone MAMMA1001764	-1.0398	0.0101
233375_at	EFCAB2	EF-hand calcium binding domain 2	-1.0841	0.0021
233378_at	LOC731419	hypothetical protein LOC731419	-0.1427	0.0094
233387_s_at	PCNT	pericentrin (kendrin)	-0.1337	0.0423
233416_at		CDNA FLJ30762 fis; clone FEBRA2000575	-0.1739	0.0165
233442_at		CDNA FLJ12196 fis; clone MAMMA1000867	-1.291	0.0303
233460_at		Clone FLB3043	-0.1532	0.0065
233479_at		CDNA FLJ12362 fis; clone MAMMA1002360	-4.1426	0
233486_at	LOC729940	hypothetical protein LOC729940	-0.1755	0.0349
233506_at		Full length insert cDNA clone ZB81B12	-2.3039	0
233513_at		CDNA FLJ12999 fis; clone NT2RP3000324	-0.142	0.0381
233524_at	C9orf44	chromosome 9 open reading frame 44	-0.1588	0.0301
233531_at	SLC46A1	Solute carrier family 46; member 1	-0.1394	0.0296
233537_at	KRTAP3-1	keratin associated protein 3-1	-0.159	0.0034
233542_at		Clone IMAGE:241742; mRNA sequence	-0.1051	0.0121
233584_at			-0.18	0.0011
233585_at	SDK2	sidekick homolog 2 (chicken)	-0.1471	0.0492
233586_s_at	KLK12	kallikrein-related peptidase 12	-0.2266	0.0297
233589_x_at	C9orf167	chromosome 9 open reading frame 167	-0.2319	0.0022
233597_at	PNPLA5	patatin-like phospholipase domain containing 5	-0.1376	0.0022
233598_at	hCG_2045828	hCG2045828	-0.1552	0.0099
233601_at			-0.177	0.0342
233611_at		CDNA FLJ12106 fis; clone HEMBB1002702	-1.429	0.0034
233619_at			-0.1328	0.0228
233623_at		Clone FLB3107	-0.2589	0.0001
233634_at	MARVELD3	MARVEL domain containing 3	-0.1232	0.0412
233636_at	MIRH1	microRNA host gene (non-protein coding) 1	-0.1298	0.0123
233639_at	POMGNT1	protein O-linked mannose beta1;2-N-acetylglucosaminyltransferase	-0.1265	0.0349
233647_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	-1.0567	0.0017
233648_at		CDNA: FLJ23261 fis; clone COL05862	-2.4369	0

233650_at	CEP63	centrosomal protein 63kDa	-0.1725	0.0006
233657_at	OPN5	opsin 5	-0.1329	0.0149
233668_at		Clone IMAGE:113399 mRNA sequence	-0.1717	0.0003
233669_s_at	TRIM54	tripartite motif-containing 54	-0.3217	0.0001
233686_at	ASXL3	additional sex combs like 3 (Drosophila)	-0.1114	0.0194
233690_at		CDNA: FLJ23090 fis; clone LNG07119	-0.4575	0.0447
233691_at		CDNA: FLJ21706 fis; clone COL09945	-1.899	0
233695_s_at	CECR2	cat eye syndrome chromosome region; candidate 2	-0.1411	0.0099
233696_at		CDNA: FLJ21357 fis; clone COL02835	-0.2844	0.0036
233720_at	SORBS2	Sorbin and SH3 domain containing 2	-2.1405	0.0002
233725_at			-0.1269	0.0261
233731_at		MRNA; cDNA DKFZp564D123 (from clone DKFZp564D123)	-0.2183	0.0042
233734_s_at	OSBPL5	oxysterol binding protein-like 5	-0.3878	0.0007
233739_at		MRNA; cDNA DKFZp564M093 (from clone DKFZp564M093)	-0.1134	0.0184
233740_at	PRO1268	PRO1268 protein	-0.134	0.0071
233741_at	FTCD	formiminotransferase cyclodeaminase	-0.1563	0.0317
233746_x_at	HYPK	Huntingtin interacting protein K	-0.5042	0.0018
233749_at	MSN	Moesin	-0.1206	0.0377
233751_at	ZFHX3	zinc finger homeobox 3	-0.1071	0.0096
233767_at		CDNA FLJ12557 fis; clone NT2RM4000783	-0.1485	0.0238
233785_at	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif; 9	-0.1393	0.0083
233795_at	ODF3	outer dense fiber of sperm tails 3	-0.1909	0.0228
233798_at		CDNA FLJ10285 fis; clone HEMBB1001369	-0.1494	0.002
233806_at		CDNA FLJ10073 fis; clone HEMBA1001731	-0.1492	0.0266
233812_at			-0.1726	0.0296
233820_at		CDNA: FLJ22542 fis; clone HSI00196	-0.3824	0.0013
233843_at	ZBTB12	zinc finger and BTB domain containing 12	-0.1045	0.0211
233846_at	CCDC85A	coiled-coil domain containing 85A	-0.1879	0.0407
233855_at	LOC284017	hypothetical protein LOC284017	-0.1884	0.0009
233863_at	CASZ1	castor zinc finger 1	-0.1636	0.0063
233892_at	GRIN3B	glutamate receptor; ionotropic; N-methyl-D-aspartate 3B	-0.11	0.0416
233900_at		Expressed unknown mRNA	-0.1079	0.0335
233913_at	WFDC10A	WAP four-disulfide core domain 10A	-0.1727	0.0071
233920_at		CDNA FLJ12016 fis; clone HEMBB1001707	-0.1328	0.0205
233925_at		MRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724)	-0.135	0.0337

233930_at	DMRT3	doublesex and mab-3 related transcription factor 3	-0.1121	0.0301
233938_at	FLJ22675	hypothetical gene supported by AK026328	-0.5224	0.0011
233952_s_at	ZNF295	zinc finger protein 295	-1.9774	0
233962_at	C20orf120	chromosome 20 open reading frame 120	-0.1722	0.0378
233965_at	LOC255480	hypothetical protein LOC255480	-0.1282	0.0049
233966_at		CDNA: FLJ22271 fis; clone HRC03191	-0.1303	0.0195
233985_x_at	PPP1R9A	protein phosphatase 1; regulatory (inhibitor) subunit 9A	-0.2897	0.0482
233991_at		Clone 24894 mRNA sequence	-0.2041	0.0101
233994_at		Clone 24894 mRNA sequence	-1.112	0.0001
234009_at		CDNA FLJ13777 fis; clone PLACE4000392	-0.1597	0.009
234012_at		MRNA; chromosome 1 specific transcript KIAA0497	-0.1951	0.0089
234014_at		CDNA FLJ10003 fis; clone HEMBA1000050	-0.1676	0.0035
234018_s_at	SEL1L2	sel-1 suppressor of lin-12-like 2 (C. elegans)	-0.1723	0.0006
234024_at	CBLN4	cerebellin 4 precursor	-1.6538	0
234027_at	CCDC129	coiled-coil domain containing 129	-0.1353	0.0187
234044_at		CDNA: FLJ22608 fis; clone HSI04854	-0.1489	0.0044
234045_x_at	BHLHB4	basic helix-loop-helix domain containing; class B; 4	-0.1523	0.0103
234055_s_at	GZF1	GDNF-inducible zinc finger protein 1	-1.7299	0
234064_at		CDNA: FLJ21247 fis; clone COL01205	-0.1432	0.0069
234066_at	IL1RL1	Interleukin 1 receptor-like 1	-1.4732	0
234070_at		CDNA FLJ10289 fis; clone MAMMA1002319	-0.161	0.0002
234072_at	SEMA4A	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4A	-0.1294	0.0451
234077_at		CDNA FLJ11664 fis; clone HEMBA1004632	-0.2268	0.0283
234078_at	LOC730057	Hypothetical protein LOC730057	-0.2621	0.0131
234089_at		CDNA FLJ12210 fis; clone MAMMA1000968	-0.1525	0.0075
234102_at	RASL11B	RAS-like; family 11; member B	-0.102	0.0471
234109_x_at	ONECUT3	one cut homeobox 3	-0.1228	0.0437
234115_s_at	C6orf12	chromosome 6 open reading frame 12	-0.1599	0.0059
234116_at	CX40.1	connexin40.1	-0.2232	0.0068
234126_at		MRNA; cDNA DKFZp761M1112 (from clone DKFZp761M1112)	-0.1223	0.0072
234128_at		Clone HQ0670	-0.1552	0.0066
234138_at		CDNA FLJ13320 fis; clone OVARC1001611	-0.1371	0.0136
234143_at		CDNA FLJ24013 fis; clone LNG12005	-0.2828	0.002

234156_at		CDNA: FLJ23252 fis; clone COL04668	-0.2271	0.0102
234167_at	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	-0.1297	0.0019
234176_at		CDNA: FLJ21224 fis; clone COL00694	-0.1101	0.0493
234191_at	BCL2L14	BCL2-like 14 (apoptosis facilitator)	-0.1484	0.0392
234195_at		CDNA: FLJ22426 fis; clone HRC08780	-0.1199	0.0305
234206_at		CDNA: FLJ21271 fis; clone COL01751	-0.1767	0.0387
234232_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	-0.1781	0.0148
234233_s_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	-0.118	0.0191
234247_at		MRNA; cDNA DKFZp761D1723 (from clone DKFZp761D1723)	-0.1198	0.028
234264_at		MRNA partial cDNA sequence from cDNA selection; DCR1-8.0	-0.1192	0.0105
234271_at	OTOP2	otopetrin 2	-0.1142	0.0246
234273_at		MRNA; cDNA DKFZp434M031 (from clone DKFZp434M031)	-0.1922	0.0097
234284_at	GNG8	guanine nucleotide binding protein (G protein); gamma 8	-0.3678	0.0016
234285_at	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat), zinc finger and BTB domain containing 9	-0.2919	0.0064
234289_x_at			-0.1411	0.0273
234298_at	LOC652231	L1 protein	-0.1964	0.0059
234301_s_at		Neuroblastoma cDNA; clone:Nbla00136; full insert sequence	-0.1084	0.0111
234309_at	TTTY7	testis-specific transcript; Y-linked 7	-0.1095	0.0078
234310_s_at	SUSD2	sushi domain containing 2	-0.2973	0
234314_at	C20orf74	chromosome 20 open reading frame 74	-2.5974	0.0172
234318_x_at	NDOR1	NADPH dependent diflavin oxidoreductase 1	-0.1434	0.0211
234324_at	NHSL1	NHS-like 1	-0.1392	0.0156
234327_at		CDNA: FLJ22687 fis; clone HSI10991	-0.1752	0.0453
234329_at	CLIC5	chloride intracellular channel 5	-0.1178	0.0267
234338_s_at	ZBTB47	zinc finger and BTB domain containing 47	-0.1847	0.0333
234339_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.4453	0.0091
234353_at	C19orf15	chromosome 19 open reading frame 15	-0.1245	0.0346
234355_s_at	PTCHD2	patched domain containing 2	-0.1889	0.0036
234364_at	IGL@	Immunoglobulin lambda locus	-0.1647	0.0051
234376_at	MYCN	v-myc myelocytomatosis viral related oncogene; neuroblastoma derived (avian)	-0.124	0.0169
234388_at	LOC731848	hypothetical protein LOC731848	-0.1203	0.0221
234401_at		TCR V-alpha w31	-0.1749	0.0418
234407_s_at	TRPC7	transient receptor potential cation channel; subfamily C; member 7	-0.1097	0.0246

234408_at	IL17F	interleukin 17F	-0.1161	0.0366
234417_at		Mutant dystrophin	-0.2653	0.0003
234418_x_at	CD44	CD44 molecule (Indian blood group)	-0.154	0.0269
234422_at			-0.1905	0.0049
234427_at	TRA@	T cell receptor alpha chain (TRCAV2S1-N-AJ41-C) mRNA; anti-melanoma cytotoxic T lymphocyte clone MU-45; -63; -79, T cell receptor alpha locus	-0.1841	0.0045
234430_at	ANTXR1	Anthrax toxin receptor 1	-0.108	0.0181
234454_at			-0.1451	0.0133
234456_at	TRAPPC4	trafficking protein particle complex 4	-0.1205	0.016
234458_at	ANPEP	Alanyl (membrane) aminopeptidase (aminopeptidase N; aminopeptidase M; microsomal aminopeptidase; CD13; p150)	-0.1322	0.0174
234460_at			-0.1481	0.002
234463_at	LOC646701	similar to developmental pluripotency associated 5	-0.1693	0.0239
234466_at		MRNA; cDNA DKFZp547C074 (from clone DKFZp547C074)	-0.2295	0.02
234468_at	hCG_401283	hCG401283	-0.1869	0.0196
234477_at	IGHA1	immunoglobulin heavy constant alpha 1	-0.1221	0.0245
234482_at			-0.164	0.0121
234483_at	ACSS1	acyl-CoA synthetase short-chain family member 1	-0.1148	0.0143
234485_at	LOC340947	hypothetical protein LOC732107, similar to eukaryotic translation initiation factor 3; subunit 6 interacting protein	-0.242	0.0258
234498_at	LOC130951	Hypothetical protein BC014602	-0.1518	0.0211
234502_at		MRNA; cDNA DKFZp564D043 (from clone DKFZp564D043)	-0.1191	0.0277
234504_at	SPAG4L	sperm associated antigen 4-like	-0.1039	0.0373
234508_at			-0.2849	0.0059
234527_at			-0.1356	0.0053
234534_at		CDNA FLJ20100 fis; clone COL04648	-0.1101	0.0494
234553_at		CDNA FLJ20012 fis; clone ADKA03438	-0.1762	0.0006
234554_at	KCNK16	potassium channel; subfamily K; member 16	-0.1199	0.0075
234555_at		CDNA FLJ20083 fis; clone COL03440	-0.2416	0.0042
234556_at		MRNA; cDNA DKFZp434P2450 (from clone DKFZp434P2450)	-0.1573	0.0195
234561_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	-0.1319	0.0046
234566_at		MRNA; cDNA DKFZp761E11121 (from clone DKFZp761E11121)	-0.1042	0.0263
234568_at	SCAMP5	Secretory carrier membrane protein 5	-0.2612	0.0074
234575_at	ZNF71	zinc finger protein 71	-0.1455	0.0286

234576_at	ANPEP	Alanyl (membrane) aminopeptidase (aminopeptidase N; aminopeptidase M; microsomal aminopeptidase; CD13; p150)	-0.147	0.0011
234580_at	TMEM106A	Transmembrane protein 106A	-0.1749	0.0232
234591_at		CDNA: FLJ21261 fis; clone COL01461	-0.1775	0.0015
234594_at	C14orf85	chromosome 14 open reading frame 85	-0.161	0.0163
234600_at		CDNA: FLJ21209 fis; clone COL00396	-0.1276	0.0262
234627_at	FLJ21408	hypothetical gene supported by AK025061	-0.1207	0.0482
234670_at		CDNA: FLJ23600 fis; clone LNG15477	-0.1297	0.0138
234671_at	KRTAP4-2	keratin associated protein 4-2	-0.1665	0.0292
234679_at	KRTAP9-3	keratin associated protein 9-3	-0.1163	0.0135
234683_at	KRTAP4-15	keratin associated protein 4-15, keratin associated protein 4-6	-0.142	0.0185
234696_at	LOC138652	similar to testicular serine protease 2	-0.2326	0.0039
234705_at		CATX-1	-0.1377	0.011
234707_x_at	IGLV1-44	immunoglobulin lambda variable 1-44	-0.1456	0.0211
234722_x_at	OBP2A	odorant binding protein 2A, odorant binding protein 2B	-0.1237	0.0461
234742_at	SIRPG	Signal-regulatory protein gamma	-0.1699	0.0381
234743_at	LIMD1	LIM domains containing 1	-0.1121	0.0406
234745_at		Clone IMAGE:111995; mRNA sequence	-0.13	0.0185
234750_at	CACNG8	calcium channel; voltage-dependent; gamma subunit 8	-0.1155	0.0405
234754_at	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter); member 1	-0.1412	0.005
234757_at		CDNA FLJ38091 fis; clone CTONG2026770	-0.1201	0.0345
234766_at	OR8D2	olfactory receptor; family 8; subfamily D; member 2	-0.1396	0.0117
234770_at			-0.2186	0.0006
234773_x_at		MRNA; cDNA DKFZp434A0226 (from clone DKFZp434A0226)	-0.163	0.0024
234784_at			-0.1385	0.0029
234791_at	GSX1	GS homeobox 1	-0.1716	0.0251
234797_at			-0.128	0.0359
234798_x_at	C20orf66	chromosome 20 open reading frame 66	-0.1415	0.0048
234822_at		Pregnancy-induced hypertension syndrome-related protein (PIH1)	-0.1162	0.019
234828_at		MRNA; cDNA DKFZp434J0721 (from clone DKFZp434J0721)	-0.1895	0.0059
234829_at	C20orf57	chromosome 20 open reading frame 57	-0.1508	0.0105
234832_at	ANTXR1	Anthrax toxin receptor 1	-0.241	0.0002
234834_at			-0.1691	0.0052
234838_at		Pregnancy-induced hypertension syndrome-related protein (PIH1)	-0.1329	0.0265

234841_x_at	OBP2A	odorant binding protein 2A, odorant binding protein 2B	-0.1081	0.0388
234847_at	DKFZp434G179	hypothetical protein DKFZp434G179	-0.1328	0.0131
234851_at	IGL@	Immunoglobulin lambda locus	-0.1396	0.0328
234865_at	TRBC1	(1.3) mRNA for T-cell receptor beta chain, T cell receptor beta constant 1, T-cell receptor rearranged beta-chain V-region (V-D-J) mRNA; clone ph15	-0.1897	0.0016
234868_s_at	GFRA4	GDNF family receptor alpha 4	-0.1279	0.0432
234874_at	ATE1	arginyltransferase 1	-0.1205	0.0053
234876_at	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	-0.1374	0.0165
234877_x_at			-0.1769	0.0043
234878_at	ZC3H12B	zinc finger CCCH-type containing 12B	-0.1769	0.0294
234888_at	CACHD1	Cache domain containing 1	-0.1716	0.0293
234896_at			-0.1057	0.0369
234897_s_at	C6orf21	chromosome 6 open reading frame 21	-0.1131	0.0254
234898_at			-0.1613	0.0456
234904_x_at	ELAVL4	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 4 (Hu antigen D)	-0.1334	0.0074
234910_at	RASAL2	RAS protein activator like 2	-0.1683	0.0033
234936_s_at	KIAA1345	KIAA1345 protein	-0.7418	0.005
234943_at	CSNK1E	casein kinase 1; epsilon	-0.161	0.0383
234951_s_at	COL12A1	collagen; type XII; alpha 1	-0.1319	0.0151
234952_s_at	KIAA1542	CTD-binding SR-like protein rA9	-0.2302	0.0463
234961_at			-0.1039	0.027
234966_at	KLK15	kallikrein-related peptidase 15	-0.1317	0.0415
234971_x_at	PLCD3	phospholipase C; delta 3	-0.3755	0.0063
234974_at	GALM	Galactose mutarotase (aldose 1-epimerase)	-0.8929	0.0006
234980_at	TMEM56	transmembrane protein 56	-0.9467	0.041
234986_at	GCLM	glutamate-cysteine ligase; modifier subunit	-1.1195	0.0002
234994_at	KIAA1913	KIAA1913	-2.4214	0.0075
235001_at	DNAJA5	DnaJ homology subfamily A member 5	-0.1186	0.046
235010_at	LOC729013	hypothetical protein LOC729013	-1.3284	0.0038
235033_at	NPEPL1	Aminopeptidase-like 1	-0.5404	0.0477
235044_at	CYYR1	cysteine/tyrosine-rich 1	-2.6209	0.0001
235054_at	NUDT16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-0.7938	0.0087
235065_at		Full length insert cDNA clone ZE05E03	-1.5678	0.0003
235066_at	MAP4	microtubule-associated protein 4	-0.1217	0.0063
235072_s_at		Transcribed locus	-0.9319	0.0004
235076_at	CALCOCO2	calcium binding and coiled-coil domain 2	-1.0294	0

235086_at	THBS1	Thrombospondin 1	-2.0826	0
235090_at	ZNF710	Zinc finger protein 710	-0.1439	0.0093
235102_x_at		Transcribed locus	-0.4419	0.0358
235108_at		CDNA FLJ41679 fis; clone HCASM2003212	-1.9106	0.0038
235117_at	CHAC2	ChaC; cation transport regulator homolog 2 (E. coli)	-0.9817	0.0235
235127_at	PMP2	peripheral myelin protein 2	-0.146	0.005
235129_at	PPP1R1A	protein phosphatase 1; regulatory (inhibitor) subunit 1A	-0.2793	0.0018
235139_at	GNGT2	guanine nucleotide binding protein (G protein); gamma transducing activity polypeptide 2	-0.2353	0.0151
235175_at	GBP4	guanylate binding protein 4	-0.4226	0.0234
235192_at	TP53RK	TP53 regulating kinase	-0.4417	0.0289
235194_at	TPCN2	two pore segment channel 2	-0.2289	0.0019
235195_at	FBXW2	F-box and WD repeat domain containing 2	-1.0456	0.0032
235204_at	COX15	COX15 homolog; cytochrome c oxidase assembly protein (yeast)	-2.3272	0
235211_at		Transcribed locus	-0.6041	0.0001
235214_at	C1orf190	chromosome 1 open reading frame 190	-0.2115	0.0054
235225_at	SCN2B	sodium channel; voltage-gated; type II; beta	-0.2372	0
235242_at		CDNA FLJ41375 fis; clone BRCAN2007700	-0.9677	0.0183
235245_at	TMEM92	transmembrane protein 92	-0.1995	0.0054
235248_at	BTBD9	BTB (POZ) domain containing 9	-0.5294	0.0001
235256_s_at	GALM	galactose mutarotase (aldose 1-epimerase)	-1.3238	0.0001
235269_at	FAM83F	family with sequence similarity 83; member F	-0.1375	0.032
235276_at	EPSTI1	epithelial stromal interaction 1 (breast)	-0.9192	0.0161
235277_at	AMOTL1	angiomotin like 1	-0.2019	0.013
235279_at		CDNA FLJ25106 fis; clone CBR01467	-1.0383	0
235282_at		CDNA clone IMAGE:5206119	-0.4878	0.0294
235306_at	GIMAP8	GTPase; IMAP family member 8	-1.5697	0.0022
235307_at	LMTK2	lemur tyrosine kinase 2	-0.1202	0.0167
235309_at		CDNA clone IMAGE:4140029	-0.9584	0.0186
235313_at	NRAP	nebulin-related anchoring protein	-0.1475	0.0176
235333_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 6	-2.0228	0.0001
235335_at	ABCA9	ATP-binding cassette; sub-family A (ABC1); member 9	-0.2211	0.0025
235342_at	SPOCK3	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 3	-1.0146	0.0017
235349_at	FAM82A	family with sequence similarity 82; member A	-1.8953	0.0001
235359_at	LRRC33	leucine rich repeat containing 33	-0.5746	0.007
235360_at		CDNA clone IMAGE:30408657	-2.4837	0

235361_at		Transcribed locus	-0.2747	0.0069
235367_at	MYPN	myopalladin	-0.236	0.0005
235371_at	GLT8D4	glycosyltransferase 8 domain containing 4	-1.5775	0.0021
235381_at		Homo sapiens; clone IMAGE:3457110; mRNA	-0.573	0.0148
235392_at		Transcribed locus	-2.3319	0
235403_at		Transcribed locus	-0.1166	0.0357
235405_at	GSTA4	glutathione S-transferase A4	-1.4603	0.0098
235407_at		Transcribed locus	-0.8291	0.0002
235413_at	GGCX	gamma-glutamyl carboxylase	-0.8321	0.0001
235419_at		Transcribed locus	-1.365	0.0194
235421_at	MAP3K8	CDNA clone IMAGE:4689481, Mitogen-activated protein kinase kinase kinase 8	-1.1941	0.0059
235427_at		Transcribed locus	-1.9712	0
235434_at		CDNA FLJ30141 fis; clone BRACE2000148	-1.9365	0.0007
235450_at	FBXL4	F-box and leucine-rich repeat protein 4	-0.6857	0.0056
235454_at	HNRPA2B1	Heterogeneous nuclear ribonucleoprotein A2/B1	-0.1115	0.0123
235467_s_at	KCNC4	potassium voltage-gated channel; Shaw-related subfamily; member 4	-0.5298	0
235471_at	C10orf72	Chromosome 10 open reading frame 72	-1.5286	0.0148
235477_at		Transcribed locus	-0.177	0.0143
235492_at	RNF217	ring finger protein 217	-0.3795	0.024
235495_at	CCDC97	coiled-coil domain containing 97	-0.1459	0.0023
235499_at	ZNF775	Zinc finger protein 775	-0.2234	0.005
235514_at	SASP	skin aspartic protease	-0.1846	0.0254
235521_at	HOXA3	homeobox A3	-0.5324	0.0114
235523_at		Transcribed locus	-0.207	0.0007
235527_at	LOC284214	hypothetical protein LOC284214	-2.1247	0
235546_at	SPINT1	Serine peptidase inhibitor; Kunitz type 1	-0.1453	0.0359
235570_at		CDNA FLJ36544 fis; clone TRACH2006378	-2.7983	0
235578_at	ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	-0.1453	0.0032
235580_at	ZNF141	zinc finger protein 141	-2.6868	0
235583_at	ILDR1	immunoglobulin-like domain containing receptor 1	-0.3459	0.0006
235592_at		CDNA FLJ36210 fis; clone THYMU2000155	-2.1104	0.0012
235593_at	ZEB2	zinc finger E-box binding homeobox 2	-3.349	0
235603_at	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	-2.0073	0
235608_at		Transcribed locus	-0.2242	0.0295
235616_at	TSHZ2	teashirt zinc finger homeobox 2	-1.3825	0.0164

235630_at		Transcribed locus	-0.1972	0.027
235636_at		CDNA FLJ23896 fis; clone LNG15157	-0.1045	0.0302
235639_at		Transcribed locus	-0.527	0
235658_at		Transcribed locus	-0.2715	0.0157
235660_at		MRNA; cDNA DKFZp667E0114 (from clone DKFZp667E0114)	-0.4118	0.0094
235666_at	ITGA8	integrin; alpha 8	-2.293	0
235667_at	LOC643783	hypothetical LOC643783	-0.3853	0.003
235670_at		Transcribed locus	-1.0808	0
235672_at	MAP6	microtubule-associated protein 6	-0.4048	0.001
235703_at	PLB1	phospholipase B1	-0.2706	0.0194
235708_at	KLB	klotho beta	-0.1762	0.0181
235712_at	GAS5	Growth arrest-specific 5	-0.2366	0.0171
235724_at	ACSS1	Acyl-CoA synthetase short-chain family member 1	-0.2413	0.0092
235725_at		Transcribed locus	-0.9887	0
235739_at		Transcribed locus	-3.5922	0
235745_at	ERN1	endoplasmic reticulum to nucleus signaling 1	-4.1177	0
235746_s_at	PLA2R1	phospholipase A2 receptor 1; 180kDa	-0.8909	0.0001
235766_x_at		CDNA clone IMAGE:5745639	-1.009	0.0214
235768_at	SH3RF2	SH3 domain containing ring finger 2	-0.1191	0.0117
235769_at			-0.1281	0.0239
235772_at		Transcribed locus	-0.6475	0.0004
235782_at		Transcribed locus	-0.352	0.042
235791_x_at	CHD1	chromodomain helicase DNA binding protein 1	-1.263	0
235797_x_at	LOC727754	Similar to hemicentin 1	-0.1767	0.0343
235798_at			-0.833	0.0052
235806_at	CENTD3	centaurin; delta 3	-0.1044	0.014
235821_at		CDNA FLJ14388 fis; clone HEMBA1002716	-1.5072	0.0014
235827_at	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	-0.1187	0.0206
235830_at		Transcribed locus	-0.4047	0.0139
235834_at	CALD1	Caldesmon 1	-0.9579	0.0001
235837_at		Transcribed locus	-0.7932	0.0001
235838_at	NLGN2	Neuroligin 2	-0.1199	0.0255
235841_at		Full-length cDNA clone CS0DM006YA12 of Fetal liver of Homo sapiens (human)	-0.3422	0.0235
235848_x_at		Transcribed locus	-1.1227	0.0084
235855_at		Transcribed locus	-0.2197	0.0242
235867_at	GSTM3	glutathione S-transferase M3 (brain)	-1.0824	0.0162
235885_at	P2RY12	purinergic receptor P2Y; G-protein coupled; 12	-1.5626	0.0001

235887_at		Transcribed locus	-0.2968	0
235890_at		Transcribed locus	-0.6743	0.0002
235891_at			-0.3513	0.0054
235898_at		Transcribed locus; strongly similar to XP_515434.1 hypothetical protein XP_515434 [Pan troglodytes]	-0.3141	0.0001
235906_at	TAF10	TAF10 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 30kDa	-0.1219	0.0416
235928_at		Transcribed locus	-0.4448	0.0021
235933_at	RP11-93B14.6	hypothetical protein FLJ32154	-0.1986	0.0005
235936_at	LOC254559	hypothetical protein LOC254559	-0.2413	0.0104
235938_at		Transcribed locus	-0.5699	0.0058
235962_at		Transcribed locus	-0.607	0
235964_x_at		Full-length cDNA clone CS0DI067YM20 of Placenta Cot 25-normalized of Homo sapiens (human)	-0.5742	0.0342
235972_at	TMEM131	transmembrane protein 131	-0.1518	0.0427
235977_at	LONRF2	LON peptidase N-terminal domain and ring finger 2	-2.5528	0.0001
235978_at	FABP4	Fatty acid binding protein 4; adipocyte	-1.0238	0.0037
235979_at	C7	complement component 7	-3.0869	0
235980_at	PIK3CA	Phosphoinositide-3-kinase; catalytic; alpha polypeptide	-0.5001	0.0051
235981_at	C8orf22	chromosome 8 open reading frame 22	-0.1476	0.0017
235982_at	FCRL1	Fc receptor-like 1	-0.1558	0.002
235990_at		CDNA FLJ38836 fis; clone MESAN2002519; weakly similar to Mus musculus cell cycle checkpoint control protein Mrad9 gene	-0.2687	0.0349
235995_at			-0.1945	0.0034
236011_at	FOXK1	forkhead box K1	-0.1007	0.0248
236024_at	GPM6A	glycoprotein M6A	-0.2485	0.0002
236031_x_at	FREM1	FRAS1 related extracellular matrix 1	-0.2202	0.02
236035_at		Transcribed locus	-0.484	0
236038_at		Transcribed locus	-2.2533	0.0004
236040_at	XAGE3	X antigen family; member 3	-0.1518	0.0025
236052_at	LOC388610	hypothetical LOC388610	-0.1713	0.0105
236053_at		CDNA FLJ43003 fis; clone BRTHA2013262	-0.2117	0.0127
236054_at		Transcribed locus	-0.234	0.0161
236063_at		Transcribed locus	-0.1372	0.0063
236082_at	PHLDB3	pleckstrin homology-like domain; family B; member 3	-0.2948	0.0001
236084_at		Transcribed locus	-0.1791	0.0186
236086_at		Transcribed locus	-0.2031	0.0007

236118_at	LOC728473	hypothetical protein LOC728473	-1.928	0.0004
236123_at	ST7L	Suppression of tumorigenicity 7 like	-0.5047	0.0001
236132_at			-0.7465	0.0001
236137_at		Transcribed locus	-0.1553	0.0189
236140_at	GCLM	glutamate-cysteine ligase; modifier subunit	-0.6371	0.0035
236141_at	NBLA00301	putative protein product of Nbla00301	-0.7111	0.0135
236150_at	LOC123688	similar to RIKEN cDNA C630028N24 gene	-0.4037	0.0043
236154_at	QKI	Quaking homolog; KH domain RNA binding (mouse)	-0.3483	0.0253
236171_at	ATP2C2	ATPase; Ca++ transporting; type 2C; member 2	-0.1463	0.0318
236176_at	LOC645757	hypothetical LOC645757	-0.2271	0.0087
236183_at	DYNC1H1	dynein; cytoplasmic 1; heavy chain 1	-0.1027	0.0172
236184_at		Transcribed locus	-0.3106	0.008
236191_at		Transcribed locus	-0.2044	0.0185
236200_at	FAF1	Fas (TNFRSF6) associated factor 1	-0.1965	0.0071
236211_at		Transcribed locus	-0.1432	0.0018
236225_at	GGT6	gamma-glutamyltransferase 6 homolog (rat)	-0.1952	0.0094
236231_at		Transcribed locus	-0.2692	0.0051
236245_at	ODF3L1	outer dense fiber of sperm tails 3-like 1	-0.1582	0.0008
236247_at	NSUN4	NOL1/NOP2/Sun domain family; member 4	-1.0744	0
236260_at		Transcribed locus; moderately similar to XP_001104560.1 hypothetical protein [Macaca mulatta]	-0.1322	0.03
236273_at	NBPF1	neuroblastoma breakpoint family; member 1	-1.3393	0.0243
236277_at		Primary neuroblastoma cDNA; clone:Nbla04246; full insert sequence	-0.2428	0.0485
236303_at			-0.1274	0.012
236307_at		Transcribed locus	-0.9361	0
236308_at	VSTM2A	V-set and transmembrane domain containing 2A	-0.3204	0.0104
236313_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15; inhibits CDK4)	-0.9905	0.0222
236323_at		Transcribed locus	-0.173	0.0195
236335_at		CDNA clone IMAGE:5273964	-1.2551	0.0052
236340_at		Transcribed locus; strongly similar to XP_001146557.1 hypothetical protein [Pan troglodytes]	-0.1842	0.039
236344_at		Transcribed locus	-0.2112	0.0011
236345_at		Transcribed locus	-0.2112	0.0064
236350_at		Transcribed locus	-0.4179	0.0031
236358_at			-1.0188	0.0001
236359_at	SCN4B	sodium channel; voltage-gated; type IV; beta	-2.1062	0

236373_at		Transcribed locus	-0.1843	0.0311
236383_at		Transcribed locus	-2.0386	0.0015
236387_at		Transcribed locus	-0.1411	0.009
236394_at			-0.1497	0.0091
236396_at		Transcribed locus	-0.5055	0.0025
236401_at		Full-length cDNA clone CS0DI016YI23 of Placenta Cot 25-normalized of Homo sapiens (human)	-0.3093	0.003
236406_at	ZNF324B	Zinc finger protein 324B	-0.1631	0.0021
236434_at	PES1	pescadillo homolog 1; containing BRCT domain (zebrafish)	-0.1851	0.0072
236440_at		CDNA FLJ41325 fis; clone BRAMY2046871	-0.121	0.0318
236451_at		CDNA FLJ14635 fis; clone NT2RP2001196	-0.1641	0.0129
236452_at		Transcribed locus	-0.1528	0.0151
236455_at		Transcribed locus	-0.1743	0.0064
236475_at	MICAL2	Microtubule associated monoxygenase; calponin and LIM domain containing 2	-0.2455	0.0041
236479_at			-0.2049	0.006
236491_at	BCL2L10	BCL2-like 10 (apoptosis facilitator)	-0.2792	0.0228
236497_at	LOC729683	hypothetical protein LOC729683	-0.1451	0.0337
236504_x_at	C6orf52	chromosome 6 open reading frame 52	-0.2592	0.0094
236515_at		Transcribed locus; strongly similar to XP_529424.1 hypothetical protein XP_529424 [Pan troglodytes]	-0.8593	0
236516_at			-0.238	0.0054
236536_at	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	-0.307	0.0401
236541_at	ARSA	Arylsulfatase A	-0.3138	0.0002
236547_at			-0.2031	0.0041
236548_at	GIPC2	GIPC PDZ domain containing family; member 2	-3.8571	0
236554_x_at	TMC8	transmembrane channel-like 8	-0.1537	0.027
236573_at	MIB1	Mindbomb homolog 1 (Drosophila)	-0.179	0.0068
236575_at		CDNA clone IMAGE:4823793	-0.1323	0.0106
236583_at		Transcribed locus	-0.6769	0
236593_at		Transcribed locus; strongly similar to XP_001097428.1 similar to putative membrane-bound dipeptidase 2 [Macaca mulatta]	-0.1713	0.0498
236594_at	LLGL1	lethal giant larvae homolog 1 (Drosophila)	-0.5778	0.0001
236598_at		CDNA FLJ14635 fis; clone NT2RP2001196	-0.1147	0.0409
236600_at	SPG20	spastic paraplegia 20 (Troyer syndrome)	-2.3997	0

236601_at		Transcribed locus	-0.1366	0.0354
236628_at		Transcribed locus	-0.1501	0.0091
236629_at	C1orf69	chromosome 1 open reading frame 69	-0.6902	0.0002
236632_at	LOC646576	hypothetical LOC646576	-0.2662	0.0017
236640_at	LOC399959	Hypothetical gene supported by BX647608	-0.2546	0.0007
236644_at	RNF180	ring finger protein 180	-0.5278	0.0105
236647_at		Transcribed locus	-0.1261	0.0167
236656_s_at		Full length insert cDNA YI37C01	-1.6863	0.0001
236657_at		Full length insert cDNA YI37C01	-0.2863	0.0158
236663_at		Transcribed locus	-0.3352	0.0013
236669_at		(clone 33) macronuclear mRNA	-0.4638	0
236675_at		MSTP075 (MST075)	-0.2929	0.0001
236677_at	NGB	neuroglobin	-0.3473	0.0007
236686_at	MVK	mevalonate kinase (mevalonic aciduria)	-0.2618	0.0072
236690_at	RHBDD1	Rhomboid domain containing 1	-0.1833	0.0043
236694_at	CYorf15A	chromosome Y open reading frame 15A	-2.6105	0.001
236713_at	ACTR1A	ARP1 actin-related protein 1 homolog A; centractin alpha (yeast)	-0.1757	0.0271
236717_at	LOC165186	similar to RIKEN cDNA 4632412N22 gene	-0.4218	0.0001
236730_at	GIPC3	GIPC PDZ domain containing family; member 3	-0.1131	0.0353
236753_at	LOC154822	hypothetical protein LOC154822	-0.1704	0.0211
236760_at	AMMECR1	Alport syndrome; mental retardation; midface hypoplasia and elliptocytosis chromosomal region; gene 1	-0.1965	0.0336
236770_at	SUGT1L1	SGT1; suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	-0.274	0
236772_s_at		Transcribed locus	-0.805	0
236774_at		Transcribed locus	-0.1769	0.0055
236775_s_at		Transcribed locus	-0.1765	0.015
236781_at		Transcribed locus	-0.3781	0.0243
236784_s_at	LOC646808	Hypothetical LOC646808	-0.2849	0.022
236796_at	BACH2	BTB and CNC homology 1; basic leucine zipper transcription factor 2	-0.9598	0.001
236797_at		Transcribed locus	-0.279	0.0012
236798_at		CDNA FLJ32438 fis; clone SKMUS2001402	-0.6501	0.0365
236810_at		Transcribed locus; moderately similar to XP_001087864.1 integrin; beta 7 [Macaca mulatta]	-0.1166	0.0241
236812_at			-0.1756	0.0049
236823_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	-0.1065	0.0417
236836_at		CDNA FLJ46538 fis; clone THYMU3037827	-0.7244	0.009
236844_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-0.1434	0.0263

236889_at		Transcribed locus	-0.8699	0.0241
236893_at	LOC404266	Hypothetical LOC404266	-0.1347	0.0266
236901_at		Transcribed locus	-1.0809	0
236909_at	LOC129881	hypothetical LOC129881	-0.1354	0.0224
236922_at		CDNA FLJ38215 fis; clone FCBBF2000291	-0.4009	0.0285
236927_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	-0.3824	0.0001
236932_s_at	GATAD2A	GATA zinc finger domain containing 2A	-0.131	0.0025
236934_at		CDNA FLJ34654 fis; clone KIDNE2018294	-0.8785	0
236950_s_at	LOC157381	hypothetical protein LOC157381	-0.1273	0.0224
236959_s_at		Transcribed locus	-0.125	0.0391
236964_at		Transcribed locus	-0.1156	0.0444
236965_at	UBQLNL	ubiquilin-like	-0.2355	0.0159
236973_at		CDNA FLJ45218 fis; clone BRCAN2019653	-0.1142	0.0281
236975_at		Transcribed locus	-0.4099	0
236979_at	C1orf178	chromosome 1 open reading frame 178	-0.1363	0.0011
236988_x_at	ITGB2	integrin; beta 2 (complement component 3 receptor 3 and 4 subunit)	-0.2883	0.0004
236991_at		Transcribed locus	-0.1717	0.0115
236996_at		Transcribed locus	-0.1787	0.0116
237002_at	NCDN	Neurochondrin	-0.1142	0.0163
237004_at		Transcribed locus	-0.1618	0.0434
237016_at	C6orf128	chromosome 6 open reading frame 128	-0.5759	0.0345
237022_at			-0.1323	0.0065
237024_at	C3orf45	chromosome 3 open reading frame 45	-0.1351	0.0182
237025_at		Transcribed locus	-0.465	0.0004
237027_at			-0.1666	0.0285
237044_s_at			-0.482	0.0447
237052_x_at			-0.4088	0.0001
237055_at		Transcribed locus; weakly similar to XP_524364.2 zinc finger protein 649 [Pan troglodytes]	-0.1773	0.0271
237056_at	INSC	inscuteable homolog (Drosophila)	-0.1433	0.0014
237068_at		Transcribed locus	-0.1677	0.0016
237073_at			-0.3723	0.0019
237078_at		Transcribed locus	-0.1008	0.0035
237081_at		Transcribed locus	-1.0095	0.0003
237089_at			-0.1582	0.0072
237090_at		MRNA; cDNA DKFZp434I192 (from clone DKFZp434I192)	-0.1276	0.0498
237091_at			-0.1544	0.0147

237093_at			-0.1742	0.0192
237108_x_at	FLJ42875	FLJ42875 protein	-0.324	0.0008
237111_at			-0.2008	0.0102
237112_at			-0.4076	0.0005
237115_at		Transcribed locus; strongly similar to XP_530679.1 hypothetical protein XP_530679 [Pan troglodytes]	-0.1467	0.0159
237127_at		Transcribed locus	-0.7856	0
237128_at		Transcribed locus	-0.1521	0.0147
237146_at		Transcribed locus	-0.1503	0.0375
237154_at		Transcribed locus	-1.2604	0
237166_at		CDNA FLJ31536 fis; clone NT2RI2000689	-0.135	0.003
237167_at	KIAA1217	KIAA1217	-0.1545	0.0457
237170_at			-0.1392	0.0332
237172_at		Transcribed locus	-0.167	0.0063
237176_at		Transcribed locus	-0.2811	0.0215
237186_at		MRNA; cDNA DKFZp779F2345 (from clone DKFZp779F2345)	-3.2803	0
237190_at		CDNA FLJ38935 fis; clone NT2NE2014681	-0.2488	0.0008
237191_x_at		Transcribed locus	-0.1253	0.0048
237192_at		Full length insert cDNA clone ZD75H06	-0.14	0.0053
237204_at		Transcribed locus; weakly similar to XP_213396.4 similar to diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1 [Rattus norvegicus]	-1.6198	0
237235_at		Transcribed locus	-0.1208	0.0103
237236_x_at	LOC731789	similar to amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	-0.1577	0.0069
237237_at		Transcribed locus	-0.1792	0.0201
237252_at	THBD	thrombomodulin	-0.3101	0.0393
237254_at	SLC5A11	solute carrier family 5 (sodium/glucose cotransporter); member 11	-0.2708	0.0007
237255_at			-0.1873	0.0184
237262_at		Full length insert cDNA clone ZE05E03	-1.0625	0.001
237271_at	LOC154872	hypothetical LOC154872	-0.1381	0.0111
237274_at		Transcribed locus	-0.2402	0.0309
237279_at		Transcribed locus	-0.1535	0.0219
237280_at	TCTE1	t-complex-associated-testis-expressed 1	-0.1849	0.0028
237283_at		Transcribed locus	-0.2278	0.0123
237285_at	SORBS2	sorbin and SH3 domain containing 2	-0.8941	0.0001
237288_at	TGM7	transglutaminase 7	-0.1453	0.0192

237290_at		Transcribed locus	-0.4287	0.0135
237303_at		Transcribed locus	-0.1181	0.0243
237307_at		Transcribed locus	-0.2505	0.0014
237312_at	LOC731477	hypothetical protein LOC731477	-0.1586	0.0132
237313_at		Homo sapiens; clone IMAGE:5225774; mRNA	-1.103	0.0002
237329_at		Transcribed locus	-0.612	0
237342_at	TOLLIP	Toll interacting protein	-0.2635	0.0002
237345_at			-0.2398	0.0057
237349_at	TSHR	Thyroid stimulating hormone receptor	-0.1212	0.0432
237350_at	LOC143941	similar to CDNA sequence BC021608	-0.2287	0.0133
237351_at		CDNA clone IMAGE:5311297	-0.1318	0.0127
237355_at		Transcribed locus	-0.2458	0.0065
237358_at			-0.1805	0.0006
237359_at		Transcribed locus	-0.1392	0.0012
237360_at	ACTRT2	actin-related protein T2	-0.1794	0.0046
237366_at			-0.1269	0.0402
237378_at	FLJ46321	FLJ46321 protein	-0.2021	0.0259
237380_at	FBXO46	F-box protein 46	-0.207	0.0208
237394_at		Transcribed locus	-0.1336	0.0123
237395_at	CYP4Z1	cytochrome P450; family 4; subfamily Z; polypeptide 1	-0.1751	0.0002
237397_at		Full length insert cDNA YQ55F05	-0.2181	0.002
237400_at	ATP5S	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit s (factor B)	-0.7572	0.0473
237401_at	ACTN1	Actinin; alpha 1	-0.1852	0.0248
237403_at	GFI1B	growth factor independent 1B (potential regulator of CDKN1A; translocated in CML)	-0.1332	0.0297
237407_at	HS1BP3	HCLS1 binding protein 3	-0.2577	0.024
237408_at		CDNA FLJ38454 fis; clone FEBRA2019690	-0.5777	0
237413_at		Transcribed locus	-0.5311	0.0065
237420_at			-0.142	0.0155
237431_at	LOC731851	hypothetical protein LOC731851	-0.2258	0.001
237443_at			-0.1488	0.0021
237444_at		Transcribed locus	-0.4905	0.0005
237451_x_at		Transcribed locus	-0.9882	0
237453_at	ZNF529	Zinc finger protein 529	-0.1245	0.0098
237460_x_at	LOC283551	hypothetical protein LOC283551	-2.4227	0
237465_at	USP53	ubiquitin specific peptidase 53	-1.5722	0
237466_s_at	HHIP	hedgehog interacting protein	-0.7971	0.0011
237476_at		Transcribed locus	-0.2352	0.0096

237484_at	LOC440087	hypothetical gene supported by AK092637	-0.172	0.0156
237494_at		Transcribed locus	-0.251	0.0454
237496_at			-1.9517	0
237497_at		Transcribed locus	-0.2279	0.0083
237500_at		Transcribed locus	-0.1995	0.0095
237501_at		CDNA FLJ37024 fis; clone BRACE2010837	-0.1207	0.0117
237508_at			-0.1195	0.0094
237513_at	TRY1	trypsin X3	-0.159	0.011
237515_at	TMEM56	transmembrane protein 56	-1.5718	0.0002
237529_at		CDNA clone IMAGE:4825924	-0.1681	0.006
237536_at		CDNA clone IMAGE:4819956	-0.3366	0.0037
237547_at			-0.1221	0.0202
237550_at		Transcribed locus	-0.1056	0.0449
237584_at		Transcribed locus	-0.1283	0.0116
237590_at			-0.1693	0.008
237592_at	C6orf94	chromosome 6 open reading frame 94	-0.1184	0.0292
237595_at	LMX1A	LIM homeobox transcription factor 1; alpha	-0.1363	0.0347
237603_at	C1orf100	chromosome 1 open reading frame 100	-0.1659	0.0137
237604_at	BC038740	BC038740	-0.1721	0.0192
237610_at	LOC643194	hypothetical LOC643194	-0.1142	0.0328
237612_at		Transcribed locus	-0.19	0.0019
237617_at		Transcribed locus; moderately similar to XP_001085521.1 hypothetical protein [Macaca mulatta]	-0.1251	0.0012
237622_at		Transcribed locus	-1.0911	0.0009
237627_at		Transcribed locus	-0.2293	0.0146
237631_at		Transcribed locus	-0.1152	0.0344
237638_at			-0.1495	0.0052
237639_at	UNQ846	SRSR846	-0.1683	0.017
237643_at		Transcribed locus	-0.497	0
237656_at	WWC2	WW and C2 domain containing 2	-0.1134	0.0221
237657_at			-0.1367	0.0428
237661_at		Transcribed locus	-0.1262	0.0287
237674_at		Transcribed locus	-0.1174	0.0151
237676_at		Transcribed locus	-0.115	0.0443
237685_at	LOC339760	hypothetical LOC339760, hypothetical protein LOC651281	-0.1809	0.0005
237694_at		Transcribed locus	-0.1519	0.0095
237704_at		Transcribed locus	-0.1394	0.0187
237706_at	STXBP4	Syntaxin binding protein 4	-0.3629	0.0063
237714_at		Transcribed locus	-0.1885	0.0014

237718_at	EIF4E	eukaryotic translation initiation factor 4E	-0.693	0
237731_at	LOC154092	hypothetical protein LOC154092	-0.1329	0.0226
237734_s_at		CDNA clone IMAGE:5296164	-0.1526	0.0071
237738_at		CDNA clone IMAGE:5742524	-0.1361	0.0061
237740_at		Transcribed locus	-0.1765	0.0101
237742_at		Transcribed locus	-0.1442	0.0353
237744_at			-0.244	0.0028
237754_at		CDNA FLJ32805 fis; clone TESTI2002690	-0.1626	0.0018
237755_s_at	WDR16	WD repeat domain 16	-0.1081	0.0284
237757_at		Transcribed locus	-0.1267	0.027
237765_at	C14orf68	chromosome 14 open reading frame 68	-0.1289	0.0244
237780_at		Transcribed locus	-0.122	0.0434
237781_at	HORMAD2	HORMA domain containing 2	-0.1191	0.0235
237801_at			-0.161	0.0279
237811_at		Transcribed locus	-0.1197	0.0162
237818_at		Transcribed locus	-0.1938	0.0002
237822_at		Transcribed locus	-0.1205	0.0358
237824_at		Transcribed locus	-0.116	0.0346
237847_at	NTN1	Netrin 1	-0.1716	0.0175
237849_at		Transcribed locus	-2.3589	0
237855_at	ZNF777	zinc finger protein 777	-0.1937	0.0284
237861_at	LOC729556	hypothetical protein LOC729556	-0.153	0.0436
237881_at		Transcribed locus	-0.8928	0.0006
237887_at			-0.2618	0.001
237894_at	C3orf22	chromosome 3 open reading frame 22	-0.1034	0.043
237896_at	NODAL	nodal homolog (mouse)	-0.1096	0.0075
237900_at	KLHDC4	kelch domain containing 4	-0.2196	0.0001
237904_at		Transcribed locus	-0.5992	0
237914_s_at		Transcribed locus	-0.1393	0.015
237925_at		Transcribed locus	-0.1484	0.0138
237929_at	C17orf50	chromosome 17 open reading frame 50	-0.1079	0.0142
237935_at		Transcribed locus	-0.1677	0.0088
237940_s_at		Transcribed locus	-0.2157	0.0023
237960_at			-0.1285	0.0083
237970_at			-0.1396	0.039
237994_at		Transcribed locus	-0.132	0.0281
238003_at	HEPACAM	cancer susceptibility gene HEPN1, hepatocyte cell adhesion molecule	-0.224	0.0021

238007_at		Transcribed locus; moderately similar to XP_001099461.1 similar to pyrroline-5-carboxylate synthetase isoform 2 isoform 2 [Macaca mulatta]	-0.8471	0
238017_at	RDHE2	epidermal retinal dehydrogenase 2	-0.1284	0.0258
238018_at	hCG_1990170	hypothetical protein LOC285016	-1.6281	0.0197
238026_at	RPL35A	ribosomal protein L35a	-0.7798	0
238035_at	SP3	Sp3 transcription factor	-0.5453	0.0433
238036_at	SHE	Src homology 2 domain containing E	-0.8455	0
238041_at		Transcribed locus	-0.3985	0.0057
238048_at	CLASP2	Cytoplasmic linker associated protein 2	-0.1163	0.0073
238049_at	GRAMD3	GRAM domain containing 3	-1.1963	0
238050_at		Transcribed locus	-0.2762	0.0004
238053_at	DHRSX	dehydrogenase/reductase (SDR family) X-linked	-0.5739	0.0004
238062_at	LOC338328	high density lipoprotein-binding protein	-0.5928	0.0037
238067_at	TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	-1.5178	0.0003
238073_at			-0.3058	0.0205
238084_at	PCGF3	polycomb group ring finger 3	-0.6138	0.0001
238087_at	RTCD1	RNA terminal phosphate cyclase domain 1	-0.2314	0.0438
238088_at		CDNA clone IMAGE:5259414	-0.1841	0.008
238091_at		CDNA clone IMAGE:5200118	-2.4773	0
238092_at		Transcribed locus	-0.2941	0.0046
238095_at	GATA5	GATA binding protein 5	-0.3395	0.0002
238100_at	AAK1	AP2 associated kinase 1	-0.2236	0.0033
238102_s_at	LOC149478	Hypothetical protein LOC149478	-0.1672	0.0388
238106_at		Transcribed locus	-2.0054	0
238112_at	LOC283177	hypothetical protein LOC283177	-0.1595	0.0142
238121_at	GK5	glycerol kinase 5 (putative)	-1.7198	0
238134_at			-0.1351	0.0279
238152_at	MGC3032	hypothetical protein MGC3032	-0.1347	0.0169
238153_at	PDE6B	phosphodiesterase 6B; cGMP-specific; rod; beta (congenital stationary night blindness 3; autosomal dominant)	-0.1698	0.039
238157_at		Transcribed locus	-0.1335	0.0468
238165_at	PDZRN3	PDZ domain containing RING finger 3	-0.5135	0.0071
238169_at		Transcribed locus	-0.4712	0.0139
238178_at		Transcribed locus	-1.3997	0
238187_at	C2orf57	chromosome 2 open reading frame 57	-0.1968	0.0008
238197_at	GATA5	GATA binding protein 5	-0.8501	0.0002
238201_at		Transcribed locus	-0.2118	0.0013

238203_at			-0.1205	0.0086
238206_at		Transcribed locus	-2.9396	0
238215_at	SLC6A18	solute carrier family 6; member 18	-0.1864	0.0094
238222_at	GKN2	gastrokine 2	-0.1585	0.0124
238223_at		Transcribed locus	-0.1985	0.0016
238228_at			-0.4759	0.0059
238233_at		Transcribed locus	-0.1097	0.0243
238242_at		CDNA FLJ45493 fis; clone BRTHA2008598	-0.2237	0.0442
238249_at		Transcribed locus	-0.1848	0.0031
238250_at		Transcribed locus	-0.1353	0.0124
238255_at			-0.1678	0.0403
238275_at	HAP1	huntingtin-associated protein 1 (neuroan 1)	-0.1945	0.0094
238284_at		Transcribed locus; strongly similar to XP_001156258.1 hypothetical protein [Pan troglodytes]	-0.1125	0.04
238288_at		Transcribed locus	-0.1302	0.018
238300_s_at	DAZAP2	DAZ associated protein 2	-0.1744	0.0485
238310_at			-0.1693	0.0106
238319_at	LOC641912	hypothetical LOC644090, hypothetical protein LOC641912	-0.264	0.0006
238329_at	M-RIP	Myosin phosphatase-Rho interacting protein	-0.2908	0.003
238332_at	ANKRD29	ankyrin repeat domain 29	-1.5262	0.017
238338_at		Transcribed locus	-0.1144	0.0464
238351_x_at		Transcribed locus	-0.1954	0.0045
238352_s_at		Transcribed locus	-0.1369	0.0115
238389_s_at		Transcribed locus; moderately similar to XP_001093747.1 tumor protein p53 binding protein; 2 [Macaca mulatta]	-1.1809	0.0015
238397_at		Transcribed locus	-0.2331	0.0027
238399_x_at			-0.152	0.003
238415_at		Transcribed locus	-0.1676	0.0073
238419_at	PHLDB2	pleckstrin homology-like domain; family B; member 2	-0.2891	0.0054
238431_at		Transcribed locus	-1.0894	0.0009
238432_at	FLJ35776	hypothetical protein LOC649446	-2.2211	0
238440_at	CLYBL	citrate lyase beta like	-1.8182	0
238447_at	RBMS3	RNA binding motif; single stranded interacting protein	-1.9976	0.0008
238467_at		CDNA FLJ41419 fis; clone BRHIP2002339	-0.7787	0.0488
238472_at	FBXO9	F-box protein 9	-1.5716	0
238480_at	C18orf50	Chromosome 18 open reading frame 50	-2.6141	0.0001
238481_at	MGP	matrix Gla protein	-3.2941	0
238497_at	TMEM136	transmembrane protein 136	-1.0128	0.0017

238498_at		MRNA full length insert cDNA clone EUROIMAGE 1090207	-0.3355	0.0001
238506_at	LRRC58	leucine rich repeat containing 58	-0.9647	0.0001
238507_at		Transcribed locus	-0.268	0.0081
238512_at		Transcribed locus	-0.3316	0.0106
238516_at	BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	-0.5525	0.0021
238518_x_at	GLYCTK	glycerate kinase	-0.2241	0.0335
238519_at	DDI2	DDI1; DNA-damage inducible 1; homolog 2 (S. cerevisiae)	-0.9372	0.0008
238521_at		Transcribed locus	-3.3841	0.0001
238524_at			-0.2785	0.0487
238531_x_at		Transcribed locus; weakly similar to XP_001117086.1 similar to Olfactory receptor 10T2 (Olfactory receptor OR1-3) [Macaca mulatta]	-0.1598	0.0085
238544_at		Transcribed locus	-0.5095	0.0004
238554_at	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	-1.1086	0.0159
238568_s_at		Transcribed locus	-2.6596	0
238569_at	GABBR1	Gamma-aminobutyric acid (GABA) B receptor; 1	-1.0607	0
238572_at	MGC16211	hypothetical protein MGC16211	-0.3474	0
238573_at		Transcribed locus	-0.463	0.0105
238576_at		Homo sapiens; clone IMAGE:4414697; mRNA	-0.5856	0.0373
238577_s_at	TSHZ2	Teashirt zinc finger homeobox 2	-1.7502	0.0014
238597_at	ANKRD13C	Ankyrin repeat domain 13C	-0.4725	0.002
238624_at	NLK	Nemo-like kinase	-1.5245	0.0033
238629_x_at		Transcribed locus; weakly similar to XP_001117086.1 similar to Olfactory receptor 10T2 (Olfactory receptor OR1-3) [Macaca mulatta]	-0.1304	0.0355
238633_at	EPC1	Enhancer of polycomb homolog 1 (Drosophila)	-0.4925	0
238638_at	SLC37A2	solute carrier family 37 (glycerol-3-phosphate transporter); member 2	-2.5246	0
238639_x_at	LOC730496	hypothetical protein LOC730496	-0.2456	0.0015
238640_at		Transcribed locus	-0.4275	0
238641_at	FLJ43806	Hypothetical protein FLJ43806	-0.1536	0.008
238647_at	C14orf28	chromosome 14 open reading frame 28	-0.3427	0.0394
238648_at	FLJ42291	hypothetical LOC346547	-0.2085	0.0279
238659_at		CDNA FLJ36185 fis; clone TESTI2026936	-0.2168	0.007
238668_at		Transcribed locus	-1.0623	0.003
238674_at		Transcribed locus	-0.1131	0.0308
238682_at	CCDC96	coiled-coil domain containing 96	-0.559	0.0002
238709_at		CDNA FLJ38461 fis; clone FEBRA2020977	-0.1599	0.0277
238747_at		CDNA clone IMAGE:4796172	-0.1309	0.0129

238751_at		CDNA clone IMAGE:4791597	-3.6038	0
238753_at	FREQ	frequenin homolog (Drosophila)	-0.4864	0.0014
238758_at		Transcribed locus	-0.3454	0.0275
238762_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	-1.5658	0.0002
238776_x_at	OBSL1	Obscurin-like 1	-0.2025	0.0054
238780_s_at		MRNA; cDNA DKFZp779F2345 (from clone DKFZp779F2345)	-5.3413	0
238798_at	TAPT1	transmembrane anterior posterior transformation 1	-0.4141	0.0189
238824_at		CDNA FLJ30581 fis; clone BRAWH2007069	-0.5089	0.0154
238825_at	ACRC	acidic repeat containing	-1.5363	0.0177
238835_at		Transcribed locus	-6.0925	0
238846_at	TNFRSF11A	tumor necrosis factor receptor superfamily; member 11a; NFKB activator	-0.9063	0.0069
238872_at		CDNA FLJ43312 fis; clone NT2RI2012659	-0.1561	0.0022
238873_at		Transcribed locus	-0.3793	0
238904_at		MRNA; cDNA DKFZp547A0515 (from clone DKFZp547A0515)	-0.1757	0.035
238914_at		Transcribed locus	-0.2133	0.0004
238919_at		Full-length cDNA clone CS0DF024YN04 of Fetal brain of Homo sapiens (human)	-1.348	0.0093
238933_at	IRS1	Insulin receptor substrate 1	-2.7484	0
238935_at	RPS27L	ribosomal protein S27-like	-0.828	0.0074
238974_at	FLJ38973	hypothetical protein FLJ38973	-0.5168	0
238979_at		Transcribed locus; strongly similar to XP_507970.1 similar to Hermansky-Pudlak syndrome 1 protein isoform a; Hermansky-Pudlak syndrome gene; Hermansky-Pudlak syndrome type 1 [Pan troglodytes]	-0.1904	0.0064
238987_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1;4-galactosyltransferase; polypeptide 1	-1.8898	0
238989_at	C1GALT1C1	C1GALT1-specific chaperone 1	-1.0706	0
238998_x_at	OTUD1	OTU domain containing 1	-0.1611	0.0009
239001_at	MGST1	Microsomal glutathione S-transferase 1	-1.8068	0.0119
239009_at	KIAA0754	hypothetical LOC643314	-0.1159	0.032
239023_at		CDNA FLJ30352 fis; clone BRACE2007646	-0.2221	0.0094
239030_at			-0.1309	0.0155
239033_at		MRNA; cDNA DKFZp666M079 (from clone DKFZp666M079)	-1.6255	0.0017
239037_at	GNAS	GNAS complex locus	-0.11	0.0047
239045_at		Transcribed locus	-2.3691	0
239053_at	CIAO1	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	-0.2838	0.0298
239057_at	LMOD2	leiomodin 2 (cardiac)	-0.1313	0.0262

239058_at		Transcribed locus	-0.5368	0.0029
239059_at	DNAH1	dynein; axonemal; heavy chain 1	-0.1743	0.0012
239060_at		Transcribed locus	-0.2813	0.0161
239062_at		CDNA clone IMAGE:5286005	-0.1579	0.0038
239064_at		CDNA FLJ36582 fis; clone TRACH2013081	-0.2759	0.0061
239066_at		Transcribed locus	-1.9394	0.0015
239068_at	LOC285831	hypothetical protein LOC285831	-0.2208	0.0023
239085_at		Transcribed locus	-0.1704	0.0389
239089_at		Transcribed locus	-0.3692	0
239094_at	LOC730961	hypothetical protein LOC730961	-0.1767	0.033
239105_at		Transcribed locus	-3.5347	0
239118_at	KCNA2	potassium voltage-gated channel; shaker-related subfamily; member 2	-0.2034	0.0029
239119_at	DNAJC3	DnaJ (Hsp40) homolog; subfamily C; member 3	-0.1422	0.0367
239120_at		CDNA FLJ38312 fis; clone FCBBF3021506	-0.2135	0.0057
239138_at		CDNA clone IMAGE:4797099	-0.5039	0
239148_at	MARVELD3	MARVEL domain containing 3	-0.1308	0.0254
239161_at	FDX1	ferredoxin 1	-1.5415	0.0066
239172_x_at	MDFIC	MyoD family inhibitor domain containing	-0.1057	0.0388
239178_at	FGF9	fibroblast growth factor 9 (glia-activating factor)	-1.4537	0.0196
239183_at	ANGPTL1	angiopoietin-like 1	-2.7205	0
239185_at	ABCA9	ATP-binding cassette; sub-family A (ABC1); member 9	-0.2112	0.0013
239217_x_at	ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	-1.5766	0
239218_at		CDNA FLJ43039 fis; clone BRTHA3003023	-0.3473	0.0001
239221_at	GPR123	G protein-coupled receptor 123	-0.2545	0.0012
239232_at	MSI2	Musashi homolog 2 (Drosophila)	-1.0897	0.0008
239267_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	-0.1476	0.0295
239270_at	PLCXD3	phosphatidylinositol-specific phospholipase C; X domain containing 3	-2.6493	0.0005
239272_at	MMP28	matrix metallopeptidase 28	-0.2943	0.0065
239273_s_at	MMP28	matrix metallopeptidase 28	-0.2774	0.0013
239275_at	FRMPD2	FERM and PDZ domain containing 2, FERM and PDZ domain containing 2 like 1, FERM and PDZ domain containing 2 like 2	-0.1455	0.0009
239276_at		Transcribed locus	-0.1522	0.0076
239277_at			-0.5689	0.007
239283_at	TMED5	transmembrane emp24 protein transport domain containing 5	-1.2643	0
239294_at		Transcribed locus	-0.799	0.0144
239296_at		Transcribed locus	-1.2943	0.001

239299_at	DDI1	DDI1; DNA-damage inducible 1; homolog 1 (S. cerevisiae)	-0.1076	0.0211
239305_at		Transcribed locus	-0.3873	0.0001
239317_at	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	-0.1001	0.0328
239336_at	THBS1	Thrombospondin 1	-0.8486	0
239341_at			-0.2373	0.0025
239345_at	SLC19A3	solute carrier family 19; member 3	-0.1476	0.0461
239356_at		Clone IMAGE:1257951; mRNA sequence	-0.1579	0.0261
239369_at	LCN8	lipocalin 8	-0.1236	0.0183
239370_at		Full length insert cDNA clone ZE01A04	-0.1934	0.0044
239371_at		Transcribed locus	-0.3246	0.0001
239372_at		Transcribed locus	-0.1793	0.0212
239381_at	KLK7	kallikrein-related peptidase 7	-0.2142	0.0272
239412_at	IRF5	interferon regulatory factor 5	-0.6485	0.0264
239417_x_at	C6orf52	chromosome 6 open reading frame 52	-0.2762	0.0371
239421_at	FLJ35776	Hypothetical protein LOC649446	-0.2569	0.0023
239426_at	SLC2A8	Solute carrier family 2; (facilitated glucose transporter) member 8	-0.549	0.0303
239434_at			-0.2225	0.0041
239437_at		Transcribed locus	-1.2044	0
239440_at		Transcribed locus	-0.1221	0.0345
239451_at		CDNA FLJ26407 fis; clone HRT09288	-1.2583	0.0032
239452_at		Transcribed locus	-0.3318	0
239454_at	SCARF2	scavenger receptor class F; member 2	-0.1006	0.0296
239483_at	FLJ37035	FLJ37035 protein	-0.2047	0.0178
239499_at	DNAH2	dynein; axonemal; heavy chain 2	-0.1526	0.0276
239510_at	C1orf212	chromosome 1 open reading frame 212	-0.103	0.016
239517_at		Transcribed locus	-0.2091	0.0074
239518_at		Transcribed locus	-0.11	0.0334
239526_x_at	PTPN1	Protein tyrosine phosphatase; non-receptor type 1	-0.1862	0.0026
239528_at	PROM2	prominin 2	-0.1736	0.0112
239544_at		Transcribed locus	-0.3632	0.0002
239548_at	NEGR1	neuronal growth regulator 1	-0.2179	0.0002
239564_at		CDNA clone IMAGE:4824791	-0.1465	0.0033
239565_at		CDNA FLJ37010 fis; clone BRACE2009732	-0.3179	0.0034
239566_at		Transcribed locus	-0.1948	0.0004
239567_at		Transcribed locus	-0.8214	0.0009
239569_at	FLJ31485	hypothetical gene supported by AK056047; AK056281; AK123838	-0.1186	0.0065
239574_at		Transcribed locus	-0.2303	0.0336

239584_at		CDNA FLJ35805 fis; clone TESTI2005982	-0.6487	0
239595_at	GPX2	Glutathione peroxidase 2 (gastrointestinal)	-0.2523	0.0011
239603_x_at			-0.2675	0.0111
239604_at		Transcribed locus	-0.5438	0.001
239606_at		CDNA FLJ25345 fis; clone TST01118	-0.1127	0.0394
239617_at	SEC13	SEC13 homolog (S. cerevisiae)	-0.1591	0.0433
239618_at	SEC16B	SEC16 homolog B (S. cerevisiae)	-0.1224	0.0482
239626_x_at	TM9SF3	Transmembrane 9 superfamily member 3	-0.1749	0.0047
239627_at	TMED9	Transmembrane emp24 protein transport domain containing 9	-0.2243	0.0319
239652_at		Transcribed locus	-0.1308	0.0238
239676_x_at	LOC642031	hypothetical protein LOC642031	-0.102	0.0172
239677_at		Transcribed locus	-0.2438	0.0031
239683_at			-0.5105	0.0004
239686_at		Transcribed locus	-0.1897	0.0134
239704_at	RNF144B	ring finger 144B	-0.2011	0.0069
239708_at		Transcribed locus	-0.3915	0.0098
239725_at	PGAP1	GPI deacylase	-3.5593	0
239746_at	MESDC2	mesoderm development candidate 2	-0.1507	0.0063
239747_s_at		MRNA full length insert cDNA clone EUROIMAGE 381867	-0.1666	0.039
239749_at	FAF1	Fas (TNFRSF6) associated factor 1	-0.1255	0.05
239750_x_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A; 33kDa	-0.2114	0.0011
239763_at	PRDM11	PR domain containing 11	-0.5824	0
239772_x_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-0.3572	0.0004
239777_at	LOC283551	hypothetical protein LOC283551	-1.2439	0.0058
239782_at		Transcribed locus	-0.244	0.0048
239786_at		Transcribed locus	-0.1769	0.0033
239789_at	C11orf49	chromosome 11 open reading frame 49	-0.1475	0.0298
239791_at	LOC404266	Hypothetical LOC404266	-0.237	0.0008
239820_at	RNF7	Ring finger protein 7	-0.1251	0.0267
239821_at	FLJ30064	hypothetical protein LOC644975	-0.1213	0.0069
239822_at		CDNA clone IMAGE:4816129	-0.1163	0.0376
239828_at	FLJ25791	hypothetical protein FLJ25791	-0.1779	0.006
239845_at		Transcribed locus	-0.4067	0.0046
239849_at		Transcribed locus	-0.7078	0
239855_at	PPM1L	Protein phosphatase 1 (formerly 2C)-like	-0.1049	0.0068
239865_at		Transcribed locus	-0.1969	0.0012
239866_at		CDNA FLJ14392 fis; clone HEMBA1003166	-0.9916	0.0176

239875_at	LOC729207	hypothetical protein LOC729207	-0.1171	0.0444
239882_at		Non-coding transcript; polyA signal; clone 48-E/2.4Kb	-0.1028	0.0337
239891_x_at	RAB12	RAB12; member RAS oncogene family	-0.3336	0.0016
239898_x_at	ZNF286A	zinc finger protein 286A	-0.2159	0.0025
239899_at	RNF145	Ring finger protein 145	-0.1988	0.0017
239916_at	WDR16	WD repeat domain 16	-0.111	0.0116
239925_at		Transcribed locus; moderately similar to XP_001117448.1 hypothetical protein [Macaca mulatta]	-0.1476	0.0364
239932_at		Transcribed locus	-0.1686	0.0217
239940_at		Transcribed locus	-0.1507	0.0376
239959_x_at			-0.1451	0.0379
239961_at		Transcribed locus	-0.122	0.0491
239964_at	TCL6	T-cell leukemia/lymphoma 6	-0.1948	0.0009
239966_at		Transcribed locus	-0.2222	0.0478
239967_at		Transcribed locus	-0.1188	0.0191
239968_at	C21orf84	chromosome 21 open reading frame 84	-0.598	0
239975_at	HLA-DPB2	major histocompatibility complex; class II; DP beta 2 (pseudogene)	-0.8101	0.0068
239981_x_at	LOC728902	hypothetical protein LOC728902	-0.2083	0.0005
239984_at			-0.6309	0
239989_at		Transcribed locus	-0.2373	0.0251
239993_at	LOC390705	similar to protein phosphatase 2A 48 kDa regulatory subunit isoform 1; serine/threonine protein phosphatase 2A; 48kDa regulatory subunit; PP2A; subunit B; PR48 isoform; PP2A B subunit PR48; NY-REN-8 antigen	-0.15	0.0018
239998_at	C10orf53	chromosome 10 open reading frame 53	-0.2599	0.0003
239999_at	C21orf34	Chromosome 21 open reading frame 34	-1.1992	0.0194
240009_at		Transcribed locus	-0.1809	0.0061
240010_at		Transcribed locus	-0.1607	0.0073
240017_at	LOC400960	Hypothetical gene supported by BC040598	-0.147	0.017
240021_at		Transcribed locus	-0.2404	0.0009
240023_at		Transcribed locus	-0.1803	0.0178
240024_at	SEC14L2	SEC14-like 2 (S. cerevisiae)	-0.1356	0.0073
240030_at	COMMD6	COMM domain containing 6	-0.1733	0.0045
240035_at		Transcribed locus	-0.1392	0.0235
240038_at		Transcribed locus	-2.6024	0
240039_at	PLA2R1	phospholipase A2 receptor 1; 180kDa	-0.182	0.0086
240041_at	PTCHD1	patched domain containing 1	-0.1525	0.0067

240060_at		Full-length cDNA clone CS0DF025YK13 of Fetal brain of Homo sapiens (human)	-2.9245	0
240064_at		Transcribed locus; strongly similar to XP_529518.1 hypothetical protein XP_529518 [Pan troglodytes]	-0.2066	0.0382
240074_at		Transcribed locus	-0.2542	0.0175
240077_at		Transcribed locus	-0.1632	0.0035
240082_s_at	C17orf74	chromosome 17 open reading frame 74	-0.1732	0.0033
240085_at			-0.1847	0.0091
240108_at		Transcribed locus	-0.3497	0.0083
240110_at	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	-0.2064	0.001
240115_at		MRNA; cDNA DKFZp686I01132 (from clone DKFZp686I01132)	-0.2285	0.0051
240119_at	TEPP	testis/prostate/placenta-expressed protein	-0.4831	0.0002
240120_at		Transcribed locus	-2.4231	0.0003
240123_at		Transcribed locus	-0.1453	0.0078
240142_at		Transcribed locus; strongly similar to XP_001108111.1 similar to adipocyte-specific adhesion molecule [Macaca mulatta]	-0.2295	0.0066
240163_at	LOC283666	hypothetical protein LOC283666	-0.1463	0.0139
240169_at		Full length insert cDNA clone YO64F11	-0.1651	0.0405
240175_at		Transcribed locus	-0.4264	0.0006
240180_at		MRNA full length insert cDNA clone EUROIMAGE 1090207	-0.3816	0
240188_at			-1.1834	0.008
240203_at		Transcribed locus	-0.1408	0.0097
240217_s_at		Transcribed locus	-0.1696	0.0108
240219_at		MRNA; cDNA DKFZp313E1940 (from clone DKFZp313E1940)	-0.1459	0.0048
240220_at		Transcribed locus	-0.1253	0.0129
240227_at	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	-0.1483	0.0419
240245_at			-1.3866	0.0031
240257_at	SYNJ2	synaptojanin 2	-0.1652	0.0287
240272_at	KRT223P	keratin 223 pseudogene	-0.1113	0.0051
240274_at			-0.2375	0.0041
240281_at		Transcribed locus	-0.1256	0.0127
240283_at			-0.2058	0.0137
240287_at	LOC730249	similar to Immune-responsive protein 1	-0.1416	0.0347
240293_at	LOC283152	hypothetical protein LOC283152	-0.1659	0.004
240312_at	LOC389895	similar to CG4768-PA	-2.9751	0
240323_at		Transcribed locus	-0.1262	0.0149

240329_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.2366	0.0009
240333_at		Transcribed locus	-0.2599	0.0002
240334_at			-0.1312	0.009
240337_at	RHOA	Ras homolog gene family; member A	-0.1038	0.0237
240340_at	SPATA3	spermatogenesis associated 3	-0.2005	0.0017
240343_at		Transcribed locus	-0.1287	0.0258
240346_at	LOC644222	hypothetical LOC644222	-0.1187	0.0093
240360_at	BRD4	bromodomain containing 4	-0.1262	0.0437
240372_at		Transcribed locus	-0.3013	0.0006
240374_at			-0.1209	0.0313
240380_at	hCG_1813624	hCG1813624	-0.1043	0.0497
240384_at		Transcribed locus; strongly similar to XP_511070.1 similar to Nedd-4-like E3 ubiquitin-protein ligase WWP2 (WW domain-containing protein 2) (Atropin-1 interacting protein 2) (AIP2) [Pan troglodytes]	-0.1432	0.0206
240385_at			-2.1363	0
240387_at	STS-1	Cbl-interacting protein Sts-1	-0.1725	0.04
240398_at		Transcribed locus	-0.2782	0.0458
240402_at	KIRREL3	kin of IRRE like 3 (Drosophila)	-0.1809	0.0276
240404_at		Transcribed locus	-0.1528	0.0154
240409_at	SUGT1L1	SGT1; suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)	-0.2592	0.0003
240410_at		Transcribed locus	-0.2124	0.0234
240412_s_at	FLJ40243	hypothetical protein FLJ40243	-0.1377	0.0369
240430_at	KCMF1	potassium channel modulatory factor 1	-0.2239	0.0198
240437_at			-0.9247	0
240455_at		Transcribed locus	-0.2424	0.036
240459_at	YTHDC1	YTH domain containing 1	-0.1969	0.0311
240465_at	C4orf32	chromosome 4 open reading frame 32	-0.1546	0.0126
240471_at			-0.1269	0.012
240473_at			-0.1702	0.0141
240476_at		Transcribed locus	-0.1202	0.0188
240481_at		Transcribed locus	-0.1475	0.0428
240486_at	HELZ	Helicase with zinc finger	-0.1933	0.0417
240495_at		CDNA clone IMAGE:5266735	-0.1625	0.0294
240496_at		Transcribed locus	-0.2472	0.0204
240508_at			-0.2137	0.0083
240519_at		Transcribed locus; strongly similar to XP_001143029.1 hypothetical protein [Pan troglodytes]	-0.1395	0.0202
240527_at			-0.2712	0.0156
240532_at	SLC32A1	solute carrier family 32 (GABA vesicular transporter); member 1	-0.1208	0.0205

240534_at		Transcribed locus	-0.128	0.0045
240560_at			-0.1318	0.0214
240576_at	MGC51025	hypothetical protein MGC51025, zinc finger protein 286A	-0.1495	0.0217
240582_x_at		Transcribed locus	-0.255	0.013
240588_at			-0.1678	0.0008
240590_at	LOC348761	hypothetical protein LOC348761	-0.1174	0.0217
240598_at			-0.1496	0.0375
240623_at		Transcribed locus	-0.1543	0.0149
240629_at		Transcribed locus	-0.4871	0
240630_at		Transcribed locus	-0.2545	0.0045
240632_at			-0.1523	0.0173
240633_at	DOK7	docking protein 7	-0.171	0.0092
240643_at	TTBK1	tau tubulin kinase 1	-0.1275	0.0012
240644_at		Transcribed locus	-0.2409	0.0093
240645_at			-0.1113	0.0232
240648_at		Transcribed locus; strongly similar to XP_530233.1 hypothetical protein XP_530233 [Pan troglodytes]	-0.2594	0.0015
240650_at	CACNA1E	Calcium channel; voltage-dependent; R type; alpha 1E subunit	-0.1465	0.0105
240651_at		Transcribed locus	-1.9386	0.0003
240652_at			-0.335	0.028
240661_at	LOC284475	hypothetical protein LOC284475	-0.1071	0.0427
240672_at			-0.1616	0.0287
240679_at		Transcribed locus	-0.1489	0.0041
240682_at	BEYLA	hypothetical LOC497634	-0.1873	0.0026
240683_at			-0.1288	0.0204
240689_at	LOC283677	hypothetical LOC283677	-0.2136	0.0036
240693_at		Transcribed locus	-0.1373	0.0213
240694_at		Transcribed locus	-0.1553	0.0043
240695_at			-0.151	0.0139
240696_at		Transcribed locus	-0.1427	0.0104
240707_at		Transcribed locus	-0.1493	0.0023
240722_at		Transcribed locus	-0.1462	0.0197
240740_at		Transcribed locus	-0.1578	0.0101
240743_at			-0.1089	0.0151
240744_at	CPA5	carboxypeptidase A5	-0.1311	0.037
240747_at		Transcribed locus	-0.1093	0.0273
240752_at	PCGF2	Polycomb group ring finger 2	-0.2106	0.0026
240753_at		Transcribed locus	-0.1141	0.0332
240756_at		CDNA FLJ34247 fis; clone FCBBF4000192	-0.3287	0

240767_x_at	VPS13A	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	-0.1388	0.0425
240781_x_at		CDNA FLJ38454 fis; clone FEBRA2019690	-0.239	0.003
240783_at		Transcribed locus	-0.1556	0.046
240785_at		Transcribed locus	-0.1772	0.0043
240786_at	NOTCH4	Notch homolog 4 (Drosophila)	-0.1889	0.0129
240792_at			-0.1939	0.0451
240794_at	NPAS4	Neuronal PAS domain protein 4	-0.1633	0.0102
240795_at		CDNA clone IMAGE:5288566	-0.1891	0.048
240804_at			-0.1706	0.0341
240818_at		Transcribed locus; moderately similar to XP_001101446.1 similar to ovochymase 1 [Macaca mulatta]	-0.1105	0.0338
240821_at		Transcribed locus	-0.2163	0.0477
240822_at	TDP1	Tyrosyl-DNA phosphodiesterase 1	-0.142	0.0152
240826_at		Transcribed locus	-0.1568	0.0076
240827_at		Homo sapiens; clone IMAGE:4498705; mRNA	-0.1404	0.0272
240831_at		Transcribed locus	-0.189	0.0185
240837_at	FNDC7	fibronectin type III domain containing 7	-0.1778	0.004
240849_at			-0.194	0.0118
240852_at			-0.1019	0.0121
240853_at			-0.2284	0.0112
240860_at		Transcribed locus	-0.1573	0.0008
240862_at	RASGRP4	RAS guanyl releasing protein 4	-0.1238	0.0038
240863_at	CYP19A1	cytochrome P450; family 19; subfamily A; polypeptide 1	-0.4711	0
240871_at	C9orf128	chromosome 9 open reading frame 128	-0.1353	0.0222
240891_at	FSTL1	Follistatin-like 1	-0.3358	0.0002
240892_at		Transcribed locus	-0.2698	0.0063
240894_at		Transcribed locus	-0.1092	0.0495
240896_at			-0.1164	0.0006
240897_at		Transcribed locus	-0.2137	0.0017
240903_at		Transcribed locus	-0.2142	0.0022
240913_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-0.1493	0.0413
240916_x_at			-0.1346	0.0379
240920_at		Transcribed locus	-0.1444	0.0408
240923_at		Transcribed locus	-0.1777	0.0013
240925_at		Transcribed locus	-0.1607	0.0155
240929_at			-0.4885	0.0042
240937_at	LOC389662	similar to septin 10 isoform 1	-0.1118	0.027

240944_at		CDNA clone IMAGE:5532261	-0.1079	0.0025
240948_at		Transcribed locus	-0.697	0
240954_at		Transcribed locus	-0.1419	0.0215
240977_at			-0.1118	0.0169
240999_at	LOC401351	hypothetical gene supported by BC040831	-0.1415	0.0484
241003_at			-0.1273	0.0302
241017_at	TBC1D8	TBC1 domain family; member 8 (with GRAM domain)	-0.4931	0.0005
241030_at			-0.1156	0.0247
241042_at			-0.1252	0.0066
241045_at			-0.2373	0.0152
241046_at		Transcribed locus	-0.1598	0.0127
241051_at			-0.1546	0.0417
241054_at		Transcribed locus	-0.2055	0.0231
241057_x_at			-0.1894	0.0205
241059_at		Transcribed locus	-0.1095	0.0356
241067_at		Transcribed locus	-0.1282	0.0493
241087_at			-0.1664	0.0204
241088_at		Transcribed locus	-0.1001	0.0278
241112_at			-0.231	0.0018
241114_s_at		Transcribed locus	-0.8425	0
241119_at			-0.1784	0.0032
241129_at		Transcribed locus	-0.1232	0.018
241137_at	DPCR1	diffuse panbronchiolitis critical region 1	-0.1023	0.0305
241143_at		Transcribed locus	-0.1354	0.0243
241145_at			-0.1002	0.0159
241155_at			-0.1417	0.003
241160_at		Transcribed locus	-0.1057	0.0103
241175_at		Transcribed locus	-0.269	0.0001
241178_at			-0.1644	0.0275
241181_x_at		Transcribed locus	-0.1004	0.0498
241187_at		Transcribed locus	-0.2074	0.0337
241189_at			-0.2218	0.0086
241193_at	ETS2	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	-0.1622	0.0097
241196_at	LOC728777	hypothetical protein LOC728777	-0.1643	0.0083
241212_at		Transcribed locus	-0.1268	0.0039
241213_x_at		Transcribed locus	-0.366	0.0015
241215_at		Transcribed locus	-0.7242	0.0084
241230_at			-0.1635	0.0087
241240_at		Transcribed locus	-0.137	0.032
241243_at		Transcribed locus	-0.1672	0.0428

241248_at			-0.1317	0.0163
241258_at		Transcribed locus	-0.1667	0.0013
241276_at			-0.2216	0.0243
241279_at			-0.1199	0.0225
241280_at	ALDOB	Aldolase B; fructose-bisphosphate	-0.1263	0.0431
241282_at		Transcribed locus	-0.1409	0.0344
241288_at			-0.16	0.002
241295_at		Transcribed locus	-0.1303	0.0088
241299_at		Transcribed locus	-0.2714	0.0049
241302_at		Transcribed locus	-3.0599	0
241308_at	LOC729589	hypothetical protein LOC729589	-0.1422	0.001
241323_at		Transcribed locus	-0.1167	0.0242
241326_at	AK7	adenylate kinase 7	-0.1416	0.0375
241332_at		Transcribed locus	-0.1012	0.0156
241337_at	LOC728347	Hypothetical protein LOC728347	-0.131	0.0337
241349_at		Transcribed locus	-0.1473	0.0039
241359_at		CDNA FLJ20031 fis; clone ADSU02180	-1.7957	0.0007
241363_at	FLJ20433	hypothetical protein FLJ20433	-0.3	0
241364_at	TMEM57	transmembrane protein 57	-1.2488	0
241368_at	LSDP5	lipid storage droplet protein 5	-0.2435	0.0364
241373_at		Transcribed locus	-0.481	0.0001
241378_at	MIB2	Mindbomb homolog 2 (Drosophila)	-0.18	0.0148
241384_x_at	GK5	glycerol kinase 5 (putative)	-0.6534	0
241395_at	NIT1	Nitrilase 1	-1.097	0
241396_at	NEDD4L	neural precursor cell expressed; developmentally down-regulated 4-like	-1.2631	0
241398_at	MPPED1	Metallophosphoesterase domain containing 1	-0.1266	0.0292
241416_at		Transcribed locus	-0.764	0.0067
241428_x_at	TCEA2	transcription elongation factor A (SII); 2	-0.3401	0.0192
241442_at		Transcribed locus	-0.2401	0.0004
241451_s_at		Homo sapiens; clone IMAGE:4523945; mRNA	-0.153	0.0352
241459_at		Transcribed locus	-0.9225	0.015
241477_at	NEIL1	nei endonuclease VIII-like 1 (E. coli)	-0.2972	0.0046
241486_at	HGSNAT	Heparan-alpha-glucosaminide N-acetyltransferase	-0.2877	0.0437
241493_at		Transcribed locus	-0.235	0.0046
241504_at		Transcribed locus; moderately similar to XP_001111131.1 hypothetical protein [Macaca mulatta]	-0.203	0.001
241511_at			-0.1365	0.0092
241516_at			-0.1208	0.0303

241521_at		Transcribed locus	-0.2173	0.0028
241523_at			-0.1766	0.0021
241536_at		Full length insert cDNA YO61A08	-0.1178	0.0178
241540_at			-0.3455	0.0017
241552_at		AA02 pseudogene mRNA; partial sequence	-0.2053	0.0132
241561_at		Transcribed locus	-0.3134	0.026
241566_at			-0.1087	0.0089
241568_at		Transcribed locus	-0.1603	0.0458
241580_at	KIAA1729	KIAA1729 protein	-0.3135	0.002
241582_at		Transcribed locus	-0.1422	0.0072
241587_at		Transcribed locus	-0.1054	0.0282
241591_at			-0.1281	0.0002
241594_at	LOC643449	hypothetical LOC643449	-0.1088	0.021
241597_at			-0.2042	0.0001
241602_at	ZNF582	zinc finger protein 582	-0.619	0.0006
241603_at	ATP11A	ATPase; Class VI; type 11A	-0.1012	0.0465
241605_at	TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	-0.1361	0.0007
241610_x_at		Transcribed locus	-0.2846	0.001
241615_x_at		Transcribed locus	-0.2451	0.0001
241640_at	BCAP29	B-cell receptor-associated protein 29	-0.3274	0.0413
241648_at		Transcribed locus	-0.1005	0.0326
241677_x_at			-0.1999	0.0088
241679_at			-0.618	0.0004
241684_at		Transcribed locus	-0.194	0.0002
241703_at	RPIB9	Rap2-binding protein 9	-1.0922	0.0303
241721_at		CDNA FLJ37844 fis; clone BRSSN2012622	-0.8134	0.0156
241739_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-1.0822	0.0166
241740_at		Transcribed locus	-2.081	0
241743_at		CDNA FLJ31091 fis; clone IMR321000155; highly similar to 60S RIBOSOMAL PROTEIN L35A	-0.1743	0.0476
241764_at			-0.1161	0.0249
241771_at	RIMBP2	RIMS binding protein 2	-0.1298	0.0275
241789_at		CDNA FLJ36544 fis; clone TRACH2006378	-1.9106	0
241791_at	TTN	titin	-0.2263	0.0163
241801_at	PGAP1	GPI deacylase	-2.5902	0
241824_at		Transcribed locus	-2.1108	0.0003
241835_at		CDNA clone IMAGE:4822225	-0.7326	0.025
241839_at		Transcribed locus	-0.2129	0.0308
241841_at		Transcribed locus	-0.28	0.0053

241842_x_at	C19orf45	chromosome 19 open reading frame 45	-0.2142	0.0431
241855_s_at			-0.1581	0.0257
241859_at		Transcribed locus	-0.276	0.001
241862_x_at	C19orf45	chromosome 19 open reading frame 45	-0.3049	0.0013
241864_x_at		Transcribed locus	-0.6299	0.0008
241878_at		Transcribed locus	-0.2149	0.0063
241894_at	VMO1	vitelline membrane outer layer 1 homolog (chicken)	-0.1855	0.0278
241896_at			-0.1349	0.0037
241907_at		Full length insert cDNA clone YR58A05	-0.1891	0.0418
241919_x_at	WDR31	WD repeat domain 31	-0.2179	0.0088
241922_at			-0.171	0.0452
241939_at	IQGAP3	IQ motif containing GTPase activating protein 3	-0.1748	0.0026
241945_at			-0.14	0.0406
241949_at	ACOT6	acyl-CoA thioesterase 6	-0.1654	0.0066
241952_at	SLC16A11	Solute carrier family 16; member 11 (monocarboxylic acid transporter 11)	-0.2391	0.0105
241962_at		Transcribed locus	-0.3734	0.0003
241980_at	MAP6	microtubule-associated protein 6	-0.1529	0.0049
241991_at		Transcribed locus	-1.0709	0.0077
242004_x_at		Transcribed locus	-0.1631	0.0011
242032_at		Transcribed locus	-0.1554	0.0226
242033_at	RNF180	ring finger protein 180	-1.0231	0.0005
242048_at	PFDN6	prefoldin subunit 6	-0.2055	0.0372
242071_x_at	ITGA8	integrin; alpha 8	-0.2906	0.0123
242086_at	SPATA6	spermatogenesis associated 6	-1.3399	0
242090_x_at		Transcribed locus	-0.1094	0.0211
242093_at	SYTL5	synaptotagmin-like 5	-4.0107	0
242123_at	PAQR7	progestin and adipoQ receptor family member VII	-0.6904	0
242125_at		CDNA FLJ36209 fis; clone THYMU2000022	-0.4035	0.0024
242137_at		CDNA FLJ36544 fis; clone TRACH2006378	-0.4784	0.0387
242151_at		Transcribed locus	-0.1647	0.0152
242177_at		Transcribed locus	-0.1399	0.0334
242185_at	SFRS12	Splicing factor; arginine/serine-rich 12	-0.2346	0.0023
242205_at		Transcribed locus	-0.3136	0.0021
242220_at	SPTBN1	spectrin; beta; non-erythrocytic 1	-0.2739	0
242226_at		Clone IMAGp998D064417Q2 mRNA sequence	-0.1802	0.0342
242230_at	ATXN1	ataxin 1	-0.2525	0.0403
242255_at	WDR37	WD repeat domain 37	-2.0467	0

242262_x_at		CDNA clone IMAGE:5272066	-0.1663	0.0118
242263_at	TMED5	transmembrane emp24 protein transport domain containing 5	-1.2894	0.0007
242267_x_at		Transcribed locus	-0.1213	0.0359
242278_at		Transcribed locus	-0.1234	0.0308
242281_at			-0.4886	0.0487
242285_at		Transcribed locus	-0.1369	0.0114
242300_at		Ubiquitin B (UBB) mRNA; 3' UTR and genetic suppressor element	-1.3624	0.0024
242304_at	WIBG	within bgcn homolog (Drosophila)	-1.1365	0.0018
242315_at		Transcribed locus	-0.2471	0.0182
242317_at		Transcribed locus	-1.1852	0.0012
242319_at	DGKG	diacylglycerol kinase; gamma 90kDa	-0.1092	0.037
242320_at		Homo sapiens; clone IMAGE:4769230; mRNA	-0.6512	0.0181
242332_at	LOC283904	hypothetical protein LOC283904	-0.2907	0.0018
242340_at		Transcribed locus	-0.2578	0
242341_x_at	GLYCTK	glycerate kinase	-0.187	0.0225
242342_at		CDNA FLJ40823 fis; clone TRACH2011093	-0.8107	0.0013
242344_at	GABRB2	gamma-aminobutyric acid (GABA) A receptor; beta 2	-2.429	0
242363_at		Full-length cDNA clone CS0DF025YA01 of Fetal brain of Homo sapiens (human)	-0.9199	0.0439
242365_at		Transcribed locus	-0.1491	0.0222
242367_at			-0.1556	0.0158
242382_at		Homo sapiens; clone IMAGE:5539086; mRNA	-0.1236	0.0154
242386_x_at			-0.2376	0.0052
242399_at			-0.181	0.0242
242411_at	ARL10	ADP-ribosylation factor-like 10	-0.1299	0.0215
242419_at		Transcribed locus; strongly similar to XP_530243.1 hypothetical protein XP_530243 [Pan troglodytes]	-0.1309	0.0109
242435_at	PDE4A	Phosphodiesterase 4A; cAMP-specific (phosphodiesterase E2 dunce homolog; Drosophila)	-0.2367	0.003
242454_at		Transcribed locus	-0.1936	0.0158
242461_at			-0.4161	0.0192
242464_at		Transcribed locus	-0.1032	0.0327
242489_at		Transcribed locus	-0.2842	0.002
242495_at			-0.1153	0.0288
242496_at		CDNA FLJ23728 fis; clone HEP14243	-0.656	0.0005
242501_at		Transcribed locus	-0.1962	0.007
242505_at		Transcribed locus	-0.2438	0.0137
242515_x_at	C11orf17	chromosome 11 open reading frame 17	-0.6811	0.0095

242524_at	CBLN4	cerebellin 4 precursor	-3.4275	0
242528_at	HOXA4	Homeobox A4	-0.278	0.0001
242541_at	ABCA9	ATP-binding cassette; sub-family A (ABC1); member 9	-0.4878	0.0001
242545_at	TTLL11	tubulin tyrosine ligase-like family; member 11	-0.4155	0.0001
242548_x_at	ANKRD37	ankyrin repeat domain 37	-0.1756	0.0127
242551_at			-1.2638	0.001
242553_at	ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	-0.4042	0.0272
242566_at	VASH1	Vasohibin 1	-0.1943	0.0159
242581_at	MAP3K15	Mitogen-activated protein kinase kinase kinase 15	-0.4635	0
242582_at		Transcribed locus	-0.1182	0.0293
242600_at	FRMD3	FERM domain containing 3	-0.3613	0.0081
242632_at	FGD2	FYVE; RhoGEF and PH domain containing 2	-0.1194	0.0149
242638_at		CDNA FLJ27401 fis; clone WMC03071	-0.1561	0.004
242642_at			-0.8208	0
242651_at		Transcribed locus	-0.8916	0
242657_at		Transcribed locus	-0.5585	0.0006
242661_x_at	ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 12	-0.1263	0.0281
242676_at		Transcribed locus	-0.1359	0.0178
242680_at		Transcribed locus	-5.6818	0
242686_at	STARD13	StAR-related lipid transfer (START) domain containing 13	-0.1928	0.0065
242712_x_at	RANBP2	RAN binding protein 2, RANBP2-like and GRIP domain containing 1, RANBP2-like and GRIP domain containing 2, RANBP2-like and GRIP domain containing 3, RANBP2-like and GRIP domain containing 4, RANBP2-like and GRIP domain containing 5, RANBP2-like and GRIP domain containing 6, RANBP2-like and GRIP domain containing 7, RANBP2-like and GRIP domain containing 8	-2.4851	0
242714_at			-0.8838	0
242716_at	SLC30A1	solute carrier family 30 (zinc transporter); member 1	-0.1536	0.0008
242720_at	ITIH4	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	-0.5383	0.0024
242731_x_at		Transcribed locus	-0.1963	0.0141
242736_at			-0.5039	0.0006
242747_at			-0.2489	0.0023
242751_at		Transcribed locus	-1.1464	0.0075

242754_at		Transcribed locus; strongly similar to XP_001101513.1 similar to ribosomal protein S12 [Macaca mulatta]	-0.1332	0.0354
242763_at			-0.232	0.0001
242779_at		Transcribed locus	-0.272	0.0012
242794_at	MAML3	mastermind-like 3 (Drosophila)	-1.3301	0.0273
242803_at		Transcribed locus	-0.268	0.0082
242809_at	IL1RL1	Interleukin 1 receptor-like 1	-2.6653	0
242814_at	SERPINB9	serpin peptidase inhibitor; clade B (ovalbumin); member 9	-2.8322	0.0001
242821_at	C9orf93	chromosome 9 open reading frame 93	-0.1332	0.0304
242832_at	PER1	period homolog 1 (Drosophila)	-0.2782	0
242835_s_at	LOC728730	Hypothetical protein LOC728730	-0.2475	0.0199
242836_at		Transcribed locus	-5.3061	0
242845_at		MRNA; cDNA DKFZp564B213 (from clone DKFZp564B213)	-0.1622	0.0113
242846_at		Transcribed locus	-0.408	0.0052
242868_at		Transcribed locus	-1.2281	0.0268
242871_at	PAQR5	progestin and adipoQ receptor family member V	-2.1463	0.005
242901_at		MRNA; cDNA DKFZp686G24244 (from clone DKFZp686G24244)	-0.1275	0.0499
242905_at	PNO1	partner of NOB1 homolog (S. cerevisiae)	-0.8391	0.0013
242907_at			-1.8348	0.0044
242931_at			-1.6592	0.0087
242938_s_at	FOXK2	forkhead box K2	-0.5515	0.0127
242941_x_at	TBX1	T-box 1	-0.168	0.0009
242960_at		Transcribed locus	-0.4517	0
242978_x_at		Transcribed locus	-0.4422	0.0025
242987_x_at		Transcribed locus	-0.1535	0.0182
242992_at	ZNF551	Zinc finger protein 551	-0.1361	0.0154
242994_at		Transcribed locus; strongly similar to XP_001105075.1 similar to nardilysin (N-arginine dibasic convertase) [Macaca mulatta]	-0.1797	0.0209
243010_at	MSI2	musashi homolog 2 (Drosophila)	-2.0023	0.0001
243012_at		Transcribed locus	-0.4293	0.0015
243022_at		Transcribed locus	-0.104	0.0477
243034_at		Transcribed locus	-0.2716	0
243039_at			-2.349	0
243041_s_at		Transcribed locus	-0.6959	0.0032
243050_at		Transcribed locus	-0.1776	0.0269
243052_at	MOBKL2C	MOB1; Mps One Binder kinase activator-like 2C (yeast)	-0.1601	0.0197
243053_x_at		CDNA clone IMAGE:5274492	-0.1684	0.0459
243056_at	C12orf60	Chromosome 12 open reading frame 60	-1.4316	0

243066_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	-0.1226	0.0436
243083_at	LOC401351	hypothetical gene supported by BC040831	-0.1081	0.0323
243085_at			-0.1263	0.049
243087_at	WDR63	WD repeat domain 63	-2.6057	0.0002
243095_at		Transcribed locus	-0.1751	0.0125
243096_at		Transcribed locus	-0.1892	0
243099_at	NFAM1	NFAT activating protein with ITAM motif 1	-0.3242	0.0035
243104_at		Transcribed locus	-0.1656	0.0461
243107_at			-0.1452	0.0333
243120_at			-0.1521	0.0452
243123_at		Transcribed locus	-0.1548	0.0152
243129_at			-1.5418	0
243137_at		Transcribed locus	-0.1204	0.0052
243138_at		Transcribed locus	-0.1593	0.0097
243151_at	ANKRD42	Ankyrin repeat domain 42	-0.1687	0.001
243157_at		Transcribed locus	-0.1231	0.0148
243176_at		CDNA FLJ30090 fis; clone BNGH41000015	-1.1135	0.0001
243177_at			-0.1794	0.0097
243185_at		Full-length cDNA clone CS0DL010YP06 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human)	-0.1768	0.021
243201_at	HNRPH2	Heterogeneous nuclear ribonucleoprotein H2 (H')	-0.3295	0.0212
243202_at	FAM102B	Family with sequence similarity 102; member B	-0.1505	0.0153
243208_x_at	MGC33407	hypothetical protein MGC33407	-0.21	0.0053
243213_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	-0.6387	0
243225_at	LOC283481	hypothetical protein LOC283481	-0.6121	0
243242_at		Transcribed locus	-0.1221	0.0221
243256_at	MKNK1	MAP kinase interacting serine/threonine kinase 1	-1.1872	0.0008
243258_at	KIAA0664	KIAA0664	-0.2294	0.0292
243259_at		Transcribed locus	-0.3339	0.0019
243261_at	LOC154822	hypothetical protein LOC154822	-0.2149	0.0139
243269_s_at	C9orf144	chromosome 9 open reading frame 144	-0.2424	0.0023
243291_at		Transcribed locus	-0.2098	0.0119
243296_at	PBEF1	Pre-B-cell colony enhancing factor 1	-2.0322	0.0009
243307_at		Transcribed locus	-0.1384	0.0239
243311_at	RP5-1103G7.6	defensin; beta 32	-0.1453	0.0338
243320_at			-0.1363	0.0193

243328_at		Transcribed locus; strongly similar to XP_531234.1 hypothetical protein XP_531234 [Pan troglodytes]	-0.1157	0.0332
243344_at		Homo sapiens; clone IMAGE:5194137; mRNA	-0.1679	0.01
243349_at	KIAA1324	KIAA1324	-0.1202	0.008
243357_at	NEGR1	neuronal growth regulator 1	-0.9131	0
243372_at	HSPD1	heat shock 60kDa protein 1 (chaperonin), similar to 60 kDa heat shock protein; mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60)	-1.0199	0.0261
243383_at		Transcribed locus	-0.2328	0.0031
243394_at			-0.1702	0.0446
243395_at		Transcribed locus	-2.6894	0
243399_at		Transcribed locus; strongly similar to XP_515434.1 hypothetical protein XP_515434 [Pan troglodytes]	-0.2214	0.0016
243402_at	LOC643406	hypothetical protein LOC643406	-0.1927	0.0162
243406_at	LOC440268	hypothetical LOC440268	-0.1986	0.0004
243408_at		Transcribed locus	-0.1323	0.0402
243415_at			-0.1458	0.004
243418_at			-0.1702	0.0208
243425_at		Transcribed locus	-0.1925	0.0068
243429_at		Transcribed locus	-0.1499	0.0209
243451_at		Transcribed locus	-0.1374	0.0113
243452_at	LOC646778	hypothetical LOC646778	-0.2871	0.0015
243459_x_at			-0.1301	0.0497
243467_at		CDNA FLJ46553 fis; clone THYMU3038879	-0.1138	0.0089
243472_at		Transcribed locus	-0.1452	0.0318
243493_at		Transcribed locus	-0.1409	0.0019
243508_at	C20orf196	chromosome 20 open reading frame 196	-0.1915	0.0096
243526_at	WDR86	WD repeat domain 86	-0.3961	0
243531_at	ORAOV1	oral cancer overexpressed 1	-0.2834	0.0012
243544_at	ADH1B	Alcohol dehydrogenase IB (class I); beta polypeptide	-0.1209	0.0152
243553_x_at		Transcribed locus	-0.2129	0.0104
243564_at		CDNA FLJ43039 fis; clone BRTHA3003023	-0.1177	0.0386
243570_at			-0.3649	0.0066
243575_at	MAST4	microtubule associated serine/threonine kinase family member 4	-0.1829	0.0107
243579_at	MSI2	musashi homolog 2 (Drosophila)	-2.1729	0

243580_at	GNA14	guanine nucleotide binding protein (G protein); alpha 14	-0.2736	0
243596_at		Transcribed locus	-0.1353	0.01
243607_at		Transcribed locus	-0.1054	0.0354
243614_s_at	PRODH2	proline dehydrogenase (oxidase) 2	-0.25	0.0058
243615_at		Transcribed locus	-0.1263	0.0303
243616_at		Transcribed locus	-0.1367	0.037
243622_at	LOC145694	hypothetical protein LOC145694	-0.1575	0.0035
243634_at		Full-length cDNA clone CS0DE011YO20 of Placenta of Homo sapiens (human)	-0.8303	0.0026
243642_x_at			-0.1102	0.0228
243653_at	SHROOM3	Shroom family member 3	-0.2049	0.0033
243659_at		CDNA FLJ36210 fis; clone THYMU2000155	-1.3285	0
243669_s_at	PRAP1	proline-rich acidic protein 1	-0.2436	0.0017
243680_at		Transcribed locus; strongly similar to XP_001152474.1 hypothetical protein [Pan troglodytes]	-0.2782	0.0279
243697_at		Transcribed locus	-0.1846	0.0033
243698_at		Transcribed locus	-0.2017	0.0055
243700_x_at	FAM47A	family with sequence similarity 47; member A	-0.1146	0.0108
243717_at	EPHA10	EPH receptor A10	-0.1069	0.0241
243719_at	STK19	serine/threonine kinase 19	-0.732	0
243721_at		Transcribed locus; strongly similar to XP_001171836.1 hypothetical protein [Pan troglodytes]	-0.1355	0.0048
243724_at		Transcribed locus	-0.3608	0.0004
243725_at		Transcribed locus	-0.1112	0.0091
243726_at		Transcribed locus	-0.1642	0.0152
243732_at		Transcribed locus	-0.1183	0.0277
243740_at		Transcribed locus	-0.1877	0.0431
243741_at		Transcribed locus	-0.1136	0.023
243744_at	LOC348751	Hypothetical protein LOC348751	-0.1059	0.0319
243757_at		Transcribed locus	-0.1343	0.0247
243769_at			-0.1364	0.0401
243778_at		Transcribed locus	-0.1169	0.0186
243782_at		Transcribed locus	-0.2284	0.0019
243783_at		CDNA FLJ36183 fis; clone TESTI2026854	-0.1328	0.0484
243803_at	LOC643037	hypothetical LOC643037	-0.1005	0.0275
243809_at	HEL308	DNA helicase HEL308	-0.4532	0.0023
243814_at	ZMYND8	Zinc finger; MYND-type containing 8	-0.2848	0.003
243825_at	BCL6B	B-cell CLL/lymphoma 6; member B (zinc finger protein)	-0.1731	0.015
243831_at		Transcribed locus	-0.1277	0.0175

243837_x_at		Transcribed locus	-0.1144	0.0195
243842_at		Transcribed locus	-0.461	0.0062
243843_at	CG018	hypothetical gene CG018	-0.2709	0.0072
243845_at	HSPD1	Heat shock 60kDa protein 1 (chaperonin)	-0.2072	0.003
243847_at		Transcribed locus	-0.1723	0.003
243848_at		Transcribed locus	-0.1826	0.0091
243879_at		CDNA FLJ36891 fis; clone BRACE2000368	-0.4094	0
243881_at		CDNA FLJ45325 fis; clone BRHIP3006717	-0.2218	0.0366
243883_at	MMP15	matrix metallopeptidase 15 (membrane-inserted)	-0.1404	0.0232
243884_at	C13orf26	chromosome 13 open reading frame 26	-0.1523	0.0009
243900_at	WDR38	WD repeat domain 38	-0.1681	0.0035
243941_at		Transcribed locus	-0.1241	0.0242
243943_x_at	C6orf52	chromosome 6 open reading frame 52	-0.3012	0.0177
243944_at			-0.1921	0.0045
243947_s_at		Transcribed locus	-0.3202	0.0019
243951_at	ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	-3.1225	0
243955_at		Transcribed locus	-0.1636	0.027
243978_at	C20orf175	chromosome 20 open reading frame 175	-0.1527	0.0134
243979_at		Transcribed locus	-0.1175	0.0195
243990_at		Transcribed locus	-0.166	0.0011
243994_at	LOC730168	hypothetical protein LOC730168	-0.1164	0.0149
244012_x_at			-0.2657	0.0226
244023_at	SYK	spleen tyrosine kinase	-0.4336	0.006
244025_at			-0.3721	0.0057
244026_at		Transcribed locus	-2.3764	0
244050_at	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	-3.1056	0
244057_s_at	C10orf72	chromosome 10 open reading frame 72	-0.5312	0.0463
244064_at		Transcribed locus	-0.1463	0.0314
244079_at		Transcribed locus; strongly similar to XP_001104786.1 hypothetical protein [Macaca mulatta]	-0.1271	0.0081
244088_at		Transcribed locus	-0.1444	0.045
244089_at	MYC	V-myc myelocytomatosis viral oncogene homolog (avian)	-0.2365	0.0019
244095_at			-0.1613	0.0474
244103_at	C1orf55	chromosome 1 open reading frame 55	-0.4184	0.0428
244108_at	SYNPO2	synaptopodin 2	-0.2793	0.0028
244109_at	WDR38	WD repeat domain 38	-0.1509	0.0021
244120_at	LOC340178	hypothetical protein LOC340178	-0.1619	0.0134

244123_at		Transcribed locus	-0.1461	0.0288
244126_at	PEX11G	peroxisomal biogenesis factor 11 gamma	-0.517	0.0001
244136_at		CDNA clone IMAGE:5272580	-0.1884	0.0061
244141_at		Full length insert cDNA clone ZC19C04	-0.1064	0.0146
244147_at		Transcribed locus	-0.2364	0
244152_at		Transcribed locus	-0.1399	0.0286
244166_at	APLN	Apelin; AGTRL1 ligand	-1.9518	0.0001
244176_at	LOC401913	hypothetical LOC401913	-0.1807	0.006
244191_at	RPLP1	Ribosomal protein; large; P1	-0.1895	0.0322
244192_x_at			-0.1492	0.0117
244199_at	TWF1	Twinfilin; actin-binding protein; homolog 1 (Drosophila)	-0.2578	0.0047
244209_at	LOC282992	hypothetical protein LOC282992	-0.1943	0.0209
244215_at		Transcribed locus	-0.2223	0.0039
244218_at			-0.23	0.0009
244229_at	PARVG	Parvin; gamma	-0.1349	0.0127
244231_at	LOC149684	hypothetical protein LOC149684	-0.3261	0
244232_at			-0.1483	0.0022
244239_at		Full length insert cDNA YN63H06	-0.3792	0.0155
244251_at	LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-0.256	0.0498
244264_at	KLRG2	killer cell lectin-like receptor subfamily G; member 2	-0.205	0.0064
244266_at	AKR1C2	Aldo-keto reductase family 1; member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase; type III)	-0.1492	0.0036
244294_at		CDNA FLJ26260 fis; clone DMC05193	-0.3739	0.0087
244320_at	NHLRC2	NHL repeat containing 2	-0.2315	0.011
244321_at	PGAP1	GPI deacylase	-2.5441	0
244329_at			-0.1633	0.0296
244339_at		Transcribed locus	-0.1276	0.0052
244361_at	LOC728981	hypothetical protein LOC728981	-0.1087	0.0053
244368_x_at		MRNA; cDNA DKFZp451K063 (from clone DKFZp451K063)	-0.296	0.0031
244379_at			-0.1815	0.0225
244381_at		Transcribed locus	-0.1534	0.0042
244388_at		Transcribed locus	-0.1623	0.0011
244394_at		Transcribed locus	-0.1677	0.0073
244408_at		Transcribed locus	-0.1932	0.0195
244410_at	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	-0.1431	0.0127
244430_at	LOC201164	Similar to CG12314 gene product	-0.1131	0.0328
244432_at		Transcribed locus	-0.1336	0.0205

244434_at			-0.8765	0.0008
244446_at		CDNA clone IMAGE:5266114	-0.1178	0.0273
244448_at	TMEM17	Transmembrane protein 17	-0.135	0.0064
244453_at	ANKRD53	ankyrin repeat domain 53	-0.3182	0.0002
244467_at	C22:CTA-250D10.9	transmembrane protein 46-like	-2.8791	0.0002
244489_at			-0.347	0.0005
244494_at	ZDHHC1	Zinc finger; DHHC-type containing 1	-0.227	0.0246
244499_at	CCDC131	coiled-coil domain containing 131	-0.9589	0
244524_at		Transcribed locus	-0.2437	0.0299
244533_at			-0.6582	0.0122
244537_at			-0.272	0.0171
244543_s_at		Homo sapiens; clone IMAGE:3910487; mRNA	-0.1699	0.0054
244545_at		CDNA clone IMAGE:5296106	-0.134	0.0252
244549_at	FEZ2	Fasciculation and elongation protein zeta 2 (zygin II)	-0.1876	0.0054
244555_at		Transcribed locus; moderately similar to XP_001093747.1 tumor protein p53 binding protein; 2 [Macaca mulatta]	-0.3997	0.0011
244556_at	LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-0.2501	0.0018
244562_s_at			-0.1858	0.0017
244564_at	FLJ37638	Hypothetical gene supported by AK094957	-0.1708	0.0119
244571_s_at	TTC12	Tetratricopeptide repeat domain 12	-0.1865	0.0489
244572_at	KY	kyphoscoliosis peptidase	-0.7132	0.0004
244573_at		MRNA full length insert cDNA clone EUROIMAGE 200247	-0.1711	0.0189
244576_at		Transcribed locus	-0.1298	0.0467
244578_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-0.1821	0.006
244582_at		Transcribed locus	-0.1026	0.0181
244591_x_at	RNF207	Ring finger protein 207	-0.2302	0.0474
244598_at		Full length insert cDNA clone ZD66F04	-0.3244	0.008
244600_at		Transcribed locus; strongly similar to XP_001157267.1 hypothetical protein [Pan troglodytes]	-0.1378	0.0367
244617_at	GPR26	G protein-coupled receptor 26	-0.2376	0.0138
244626_at			-0.1375	0.0036
244627_at	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	-2.7187	0
244629_s_at			-0.1902	0.0157
244645_at		Transcribed locus	-0.1188	0.0263
244652_at		Transcribed locus	-0.1572	0.035
244653_at	SETD7	SET domain containing (lysine methyltransferase) 7	-0.1702	0.042

244661_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-1.3972	0.0002
244672_at	WDR1	WD repeat domain 1	-0.169	0.0153
244677_at		Transcribed locus	-1.4045	0.001
244681_at	C3orf46	chromosome 3 open reading frame 46	-0.1515	0.0144
244701_at		CDNA FLJ33712 fis; clone BRAWH2008255	-0.2027	0.0091
244713_at		Transcribed locus	-0.1645	0.017
244717_x_at	SV2B	synaptic vesicle glycoprotein 2B	-0.185	0.0038
244720_at			-0.1094	0.0219
244739_at		Transcribed locus	-0.6701	0.0014
244745_at	RERG	RAS-like; estrogen-regulated; growth inhibitor	-2.1106	0.0082
244746_at	SEMA6D	Sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	-0.1495	0.0348
244759_x_at	RNF207	Ring finger protein 207	-0.21	0.0008
244763_at	MTRF1	mitochondrial translational release factor 1	-0.3762	0.0037
244779_at		CDNA FLJ34038 fis; clone FCBBF2005645	-2.1285	0.0001
244787_at		Full-length cDNA clone CS0DF030YH04 of Fetal brain of Homo sapiens (human)	-0.7167	0.0001
244798_at		Transcribed locus; moderately similar to XP_001099403.1 hypothetical protein [Macaca mulatta]	-0.1135	0.0293
244800_x_at			-0.1585	0.0216
244807_at	C17orf45	Chromosome 17 open reading frame 45	-0.141	0.0319
244815_at		Transcribed locus	-0.2116	0.0026
244824_at		Transcribed locus; strongly similar to XP_001151354.1 hypothetical protein isoform 1 [Pan troglodytes]	-0.1423	0.0338
244827_at			-0.1588	0.0149
244828_x_at	LOC92345	hypothetical protein BC008207	-0.8482	0.001
244840_x_at	DOCK4	dedicator of cytokinesis 4	-0.4595	0.0189
244847_at		Transcribed locus	-0.2578	0.0219
244855_at		Transcribed locus	-0.9721	0
244860_at		Transcribed locus	-0.3817	0.0364
244867_at		Transcribed locus	-0.1639	0.0024
244868_at		Transcribed locus	-0.6962	0.0001
244870_at	TES	testis derived transcript (3 LIM domains)	-0.2012	0.0078
244880_at		Transcribed locus	-0.1623	0.0275
244890_at			-0.2175	0.0023
31799_at		Clone 24627 mRNA sequence	-0.983	0
31837_at	TMEM112B	transmembrane protein 112B	-0.4448	0.0385
31874_at	GAS2L1	growth arrest-specific 2 like 1	-1.0318	0.0147

32811_at	MYO1C	myosin IC	-0.5886	0.0306
33197_at	MYO7A	myosin VIIA	-2.4226	0
33494_at	ETFDH	electron-transferring-flavoprotein dehydrogenase	-1.1858	0.0002
336_at	TBXA2R	thromboxane A2 receptor	-1.2288	0.0269
33767_at	NEFH	neurofilament; heavy polypeptide 200kDa	-1.7365	0.0126
33778_at	TBC1D22A	TBC1 domain family; member 22A	-0.7496	0.0029
34206_at	CENTD2	centaurin; delta 2	-0.7735	0.0001
34846_at	CAMK2B	Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-0.1568	0.0205
35265_at	FXR2	fragile X mental retardation; autosomal homolog 2	-0.4097	0.0159
35685_at	RING1	ring finger protein 1	-0.4006	0.0222
36129_at	SGSM2	small G protein signaling modulator 2	-0.9275	0.0096
36553_at	ASMTL	acetylserotonin O-methyltransferase-like	-0.8483	0.008
36554_at	ASMTL	acetylserotonin O-methyltransferase-like	-1.1913	0.0074
36564_at	RNF19B	ring finger protein 19B	-1.7107	0
36566_at	CTNS	cystinosis; nephropathic	-0.7267	0.0022
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	-2.8389	0.0001
36829_at	PER1	period homolog 1 (Drosophila)	-1.713	0
36830_at	MIPEP	mitochondrial intermediate peptidase	-0.6159	0.0234
37012_at	CAPZB	capping protein (actin filament) muscle Z-line; beta	-0.309	0.0033
37022_at	PRELP	proline/arginine-rich end leucine-rich repeat protein	-1.2854	0
37384_at	PPM1F	protein phosphatase 1F (PP2C domain containing)	-0.6529	0.0007
37965_at	PARVB	parvin; beta	-1.2881	0.0011
37966_at	PARVB	parvin; beta	-0.8231	0.0135
38037_at	HBEGF	heparin-binding EGF-like growth factor	-0.6649	0.011
38157_at	DOM3Z	dom-3 homolog Z (C. elegans)	-1.6063	0.0004
38241_at	BTN3A3	butyrophilin; subfamily 3; member A3	-0.7221	0.0442
38340_at	HIP1R	huntingtin interacting protein 1 related, similar to huntingtin interacting protein 1 related	-1.6663	0
38487_at	STAB1	stabilin 1	-3.308	0
38918_at	SOX13	SRY (sex determining region Y)-box 13	-0.5621	0.0072
38964_r_at	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	-0.521	0.0042
39817_s_at	C6orf108	chromosome 6 open reading frame 108	-1.3328	0
39835_at	SBF1	SET binding factor 1	-0.791	0.0069
40612_at	DOPEY1	dopey family member 1	-0.3139	0.001
40665_at	FMO3	flavin containing monooxygenase 3	-4.5933	0

40687_at	GJA4	gap junction protein; alpha 4; 37kDa	-0.7701	0.0016
40837_at	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog; Drosophila)	-1.8601	0
41047_at	C9orf16	chromosome 9 open reading frame 16	-0.6458	0.0319
41386_i_at	JMJD3	jumonji domain containing 3	-0.7659	0.0123
41387_r_at	JMJD3	jumonji domain containing 3	-0.3798	0.0006
41553_at	OSGIN2	Oxidative stress induced growth inhibitor family member 2	-0.1506	0.0012
43427_at	ACACB	acetyl-Coenzyme A carboxylase beta	-0.6879	0.0408
44673_at	SIGLEC1	sialic acid binding Ig-like lectin 1; sialoadhesin	-1.4085	0.0004
44702_at	SYDE1	synapse defective 1; Rho GTPase; homolog 1 (C. elegans)	-0.5124	0.0156
46256_at	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3	-0.5649	0.0128
46270_at	UBAP1	ubiquitin associated protein 1	-0.8754	0
46665_at	SEMA4C	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4C	-0.6315	0.0117
48030_i_at	C5orf4	chromosome 5 open reading frame 4	-0.7825	0.0004
48031_r_at	C5orf4	chromosome 5 open reading frame 4	-0.7839	0.0034
48106_at	FLJ20489	hypothetical protein FLJ20489	-0.8393	0.0417
48117_at	CCDC101	coiled-coil domain containing 101	-0.4255	0.0024
49327_at	SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	-0.2255	0.0428
49452_at	ACACB	acetyl-Coenzyme A carboxylase beta	-0.7473	0.0343
49878_at	PEX16	peroxisomal biogenesis factor 16	-0.3369	0.0175
50400_at	PAOX	polyamine oxidase (exo-N4-amino)	-0.2936	0.0132
51146_at	PIGV	phosphatidylinositol glycan anchor biosynthesis; class V	-0.7413	0.0001
51192_at	SSH3	slingshot homolog 3 (Drosophila)	-0.2806	0.0426
51774_s_at	LOC222070	hypothetical protein LOC222070	-0.8263	0.0024
52078_at	C1orf160	chromosome 1 open reading frame 160	-0.3635	0.0403
52159_at	HEMK1	HemK methyltransferase family member 1	-0.6098	0.0134
52741_at	C14orf172	chromosome 14 open reading frame 172	-0.3008	0.0028
53071_s_at	FLJ22222	hypothetical protein FLJ22222	-0.9442	0.0063
53912_at	SNX11	sorting nexin 11	-0.2095	0.0381
53968_at	INTS5	integrator complex subunit 5	-0.3671	0.0367
53987_at	RANBP10	RAN binding protein 10	-0.6162	0.0467
53991_at	DENND2A	DENN/MADD domain containing 2A	-0.2793	0.0041
54632_at	THADA	thyroid adenoma associated	-0.4802	0.0308
55616_at	PERLD1	per1-like domain containing 1	-0.3752	0.023
56197_at	PLSCR3	phospholipid scramblase 3	-0.5299	0.0109

56256_at	SIDT2	SID1 transmembrane family; member 2	-0.7382	0.0309
57540_at	RBKS	ribokinase	-1.8819	0.0006
58308_at	TRIM62	tripartite motif-containing 62	-0.81	0.0003
58780_s_at	FLJ10357	hypothetical protein FLJ10357	-0.6743	0.0264
58900_at	LOC222070	hypothetical protein LOC222070	-0.6438	0.0031
58916_at	KCTD14	potassium channel tetramerisation domain containing 14	-2.9154	0.0004
59375_at	MYO15B	myosin XVB pseudogene	-0.4155	0.0252
59705_at	SCLY	selenocysteine lyase	-0.2436	0.0006
60474_at	C20orf42	chromosome 20 open reading frame 42	-1.5853	0.0028
61297_at	CASKIN2	CASK interacting protein 2	-0.8421	0.0071
63305_at	PKNOX2	PBX/knotted 1 homeobox 2	-0.4787	0.0001
64064_at	GIMAP5	GTPase; IMAP family member 5	-1.1464	0
64438_at	FLJ22222	hypothetical protein FLJ22222	-0.2504	0.0215
65630_at	TMEM80	transmembrane protein 80	-1.088	0
78383_at	TOPORS	Topoisomerase I binding; arginine/serine-rich	-0.7482	0.0001
89948_at	C20orf67	chromosome 20 open reading frame 67	-0.4792	0
89977_at	FLJ20581	hypothetical protein FLJ20581	-0.6776	0.0041
AFFX-M27830_3_at			-0.1413	0.0073
AFFX-ThrX-3_at			-0.1172	0.0006
AFFX-r2-Bs-phe-5_at			-0.1177	0.0237
AFFX-r2-Bs-thr-5_s_at			-0.1284	0.0078
AFFX-r2-Bs-thr-M_s_at			-0.1761	0.0005

*For the difference in expression

Supplemental Table 4. Biological processes Significantly ($P<0.05$) changed in tumors from ACC patients with high *MET* expression relative to tumors with low *MET* expression (dataset GSE10927) as presented in Figure 2a.

	BIOLOGICAL PROCESS	CANCER HALLMARK*	Z SCORE	P-VALUE
1	Pyrimidine nucleotide metabolic process	1, 10	1.499438242	0.04288499
2	Negative regulation of progression through mitotic cell cycle	1,2	-1.543647742	0.029661017
3	Nucleotide metabolic process	1, 10	1.548759866	0.044534413
4	Activation of NF-kappaB-inducing kinase	1, 2, 5, 6, 7, 9, 10	1.586722687	0.011650485
5	MAPKKK cascade	1, 5, 6, 7, 9	1.612826018	0.015180266
6	Centrosome organization and biogenesis	1	1.675998689	0.009960159
7	Activation of MAPK activity	1, 2, 5, 6, 7, 9	1.711905776	0.003992016
8	Cell death	9	-1.534593	0.018072289
9	Focal adhesion formation	6	1.487977151	0.039840637
10	Cytoskeleton organization and biogenesis	6	1.526306096	0.014403292
11	Bone resorption	6	1.603841653	0.025225225
12	Cell fate determination	4	-1.595906386	0.031180401
13	Telomere maintenance	4	1.74593275	0.009140768
14	Regulation of angiogenesis	7	-1.550155228	0.042769857
15	Electron transport	10	1.395095008	0.035885167
16	Mitochondrial electron transport; NADH to ubiquinone	10	1.546833289	0.039215686
17	Proton transport	10	1.58760142	0.035087719
18	ATP synthesis coupled proton transport	10	1.746648657	0.007692308
19	Very-long-chain fatty acid metabolic process	10	1.790811372	0.004016064
20	Nucleotide-excision repair	8	-1.521036899	0.024793388
21	DNA catabolic process	11	1.573891525	0.022494888
22	Chondroitin sulfate biosynthetic process	11	1.570318173	0.03649635
23	Prostaglandin biosynthetic process	11	1.627218291	0.034749035
24	Regulation of DNA recombination	11	1.575376444	0.037848606
25	Mesodermal cell fate determination	11	-1.879388652	0.002070393
26	Tissue development	11	-1.616216646	0.018329939
27	Adrenal gland development	11	-1.711306937	0.006147541
28	Adult behavior	11	1.531725059	0.028747433
29	B cell receptor signaling pathway	11	1.681609165	0.021696252
30	Brown fat cell differentiation	11	1.657664146	0.005988024
31	Cellular defense response	11	1.819418382	0.016494845
32	Clathrin cage assembly	11	1.528170616	0.032520325
33	Cobalamin transport	11	1.537551673	0.025490196
34	Collagen fibril organization	11	-1.569978901	0.041575492

35	Embryonic limb morphogenesis	11	-1.628136141	0.013015184
36	Histone methylation	11	-1.664856993	0.014198783
37	Immune response	11	1.651209711	0.029680365
38	Leukocyte adhesion	11	1.585713858	0.03030303
39	Lipid glycosylation	11	1.521583405	0.033826638
40	Lymph node development	11	1.845834239	0
41	Melanocyte differentiation	11	1.672639818	0.021653543
42	Membrane organization and biogenesis	11	-1.605267216	0.010775862
43	Mesoderm formation	11	-1.555068684	0.044303797
44	Metanephros development	11	-2.017658478	0
45	Midbrain development	11	-1.621103083	0.025193798
46	Muscle cell differentiation	11	-1.723137357	0.002159827
47	Myoblast fusion	11	1.530277549	0.030737705
48	N-glycan processing	11	1.567483984	0.046601942
49	Negative regulation of follicle-stimulating hormone secretion	11	-1.560491868	0.026262626
50	Negative regulation of transcription	11	-1.414760592	0.048
51	Neuron recognition	11	-1.598478784	0.035789474
52	Pathogenesis	11	1.552054324	0.040685225
53	Phagocytosis; engulfment	11	1.631471838	0.002008032
54	Phosphoenolpyruvate-dependent sugar phosphotransferase system	11	-1.639881228	0.008752735
55	Post-Golgi vesicle-mediated transport	11	1.734607659	0.008438819
56	Proximal/distal pattern formation	11	-1.513014572	0.045364892
57	Receptor-mediated endocytosis	11	1.575458839	0.027944112
58	Signal complex assembly	11	1.668547312	0.004237288
59	Skeletal development	11	-1.500785369	0.040772532
60	Sphingomyelin metabolic process	11	1.529533146	0.038387716
61	T-helper 1 type immune response	11	1.642101531	0.036121673
62	Unsaturated fatty acid biosynthetic process	11	-1.481707191	0.047131148
63	Vesicle-mediated transport	11	1.478172666	0.034482759

* The cancer hallmarks that each biological process may be related to are as follows: 1 = sustained proliferation; 2 = evasion of growth suppression; 3 = escape from immune surveillance; 4 = replicative immortality; 5 = tumor inflammation; 6 = metastasis and invasion; 7 = tumor angiogenesis; 8 = genomic instability and mutation; 9 = resistance to cell death; 10 = deregulating cellular energetics (energy metabolism); 11 = no relation to a cancer hallmark.

Supplemental Table 5. Genes significantly (*P* ≤ 0.05, absolute value of log ratio > 0.1) changed in tumors from ACC patients with high *MET* expression compared to those with low *MET* expression (dataset GSE10927).

PROBE	GENE SYMBOL	GENE NAME	FOLD CHANGE (LOG RATIO)	*P*-VALUE*
1053_at	RFC2	replication factor C (activator 1) 2; 40kDa	0.7609	0.0197
1552276_a_at	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	0.1835	0.0082
1552291_at	PIGX	phosphatidylinositol glycan anchor biosynthesis; class X	0.5513	0.0291
1552302_at	LOC728772	similar to transmembrane protein 106A, transmembrane protein 106A	0.4852	0.0452
1552315_at	GIMAP1	GTPase; IMAP family member 1	0.2057	0.0271
1552316_a_at	GIMAP1	GTPase; IMAP family member 1	1.0108	0.0219
1552330_at	MGC16385	hypothetical protein MGC16385	1.1341	0.0379
1552373_s_at	C4orf33	chromosome 4 open reading frame 33	0.3728	0.0013
1552381_at	SRrp35	serine-arginine repressor protein (35 kDa)	0.293	0.0349
1552386_at	C5orf29	chromosome 5 open reading frame 29	0.3527	0.0098
1552389_at	C8orf47	chromosome 8 open reading frame 47	0.4816	0.0425
1552390_a_at	C8orf47	chromosome 8 open reading frame 47	1.1017	0.0428
1552398_a_at	CLEC12A	C-type lectin domain family 12; member A	0.206	0.0413
1552400_a_at	C15orf27	chromosome 15 open reading frame 27	0.841	0.0296
1552430_at	WDR17	WD repeat domain 17	0.4173	0.0345
1552470_a_at	ABHD11	abhydrolase domain containing 11	0.4954	0.0063
1552484_at	SMCR8	Smith-Magenis syndrome chromosome region; candidate 8	0.1364	0.0364
1552485_at	LACTB	lactamase; beta	1.1511	0.0427
1552486_s_at	LACTB	lactamase; beta	1.3269	0.0135
1552553_a_at	NLRC4	NLR family; CARD domain containing 4	0.3826	0.0422
1552557_a_at	ZDHHC15	zinc finger; DHHC-type containing 15	0.516	0.0405
1552573_s_at	MIPOL1	mirror-image polydactyly 1	0.4642	0.0316
1552584_at	IL12RB1	interleukin 12 receptor; beta 1	0.4521	0.0278
1552612_at	CDC42SE2	CDC42 small effector 2	0.6359	0.0484
1552651_a_at	RFFL	ring finger and FYVE-like domain containing 1	0.2428	0.0487
1552671_a_at	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger); member 7	0.5016	0.0011
1552691_at	ARL11	ADP-ribosylation factor-like 11	0.2974	0.0274
1552696_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	0.6391	0.0047
1552758_at	HDAC9	histone deacetylase 9	0.1505	0.0375
1552806_a_at	SIGLEC10	sialic acid binding Ig-like lectin 10	0.2043	0.0205
1552868_at	C19orf23	chromosome 19 open reading frame 23	0.2104	0.0072
1552902_a_at	FOXP2	forkhead box P2	0.167	0.0415
1552964_at	C10orf93	chromosome 10 open reading frame 93	0.1091	0.0243
1552980_at	HAS3	hyaluronan synthase 3	0.2215	0.0077
1553031_at	GPR115	G protein-coupled receptor 115	0.4651	0.0008
1553055_a_at	SLFN5	schlafen family member 5	0.6394	0.0091
1553105_s_at	DSG2	desmoglein 2	1.3277	0.0096
1553158_at	C3orf34	chromosome 3 open reading frame 34	0.477	0.014
1553172_at	ZNF777	zinc finger protein 777	0.4416	0.0179
1553204_at	C20orf200	chromosome 20 open reading frame 200	0.1491	0.0219
1553207_at	ARL10	ADP-ribosylation factor-like 10	0.1367	0.0205
1553239_at	FAM124A	family with sequence similarity 124A	0.1643	0.0368
1553269_at	ZNF718	zinc finger protein 718	1.3112	0.0212
1553297_a_at	CSF3R	colony stimulating factor 3 receptor (granulocyte)	0.6878	0.017
1553321_a_at	SULT1C4	sulfotransferase family; cytosolic; 1C; member 4	0.1652	0.0053
1553351_at	OTUD7A	OTU domain containing 7A	0.2478	0.0362
1553395_a_at	CD200R1	CD200 receptor 1	0.229	0.0026
1553409_at	ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif; 20	0.1185	0.0324
1553533_at	JPH1	junctophilin 1	0.166	0.0234
1553622_a_at	FSIP1	fibrous sheath interacting protein 1	0.1093	0.0475

1553635_s_at	TCTEX1D1	Tctex1 domain containing 1	0.2331	0.0253
1553646_at	HDX	highly divergent homeobox	0.5584	0.0046
1553655_at	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	0.1198	0.0135
1553681_a_at	PRF1	perforin 1 (pore forming protein)	0.3312	0.0127
1553743_at	FAM119A	family with sequence similarity 119; member A	0.6938	0.0492
1553752_at	C20orf165	chromosome 20 open reading frame 165	0.1282	0.0442
1553778_at	WBSCR27	Williams Beuren syndrome chromosome region 27	0.2655	0.0238
1553785_at	RASGEF1B	RasGEF domain family; member 1B	0.1669	0.0352
1553815_a_at			0.5066	0.0122
1553835_a_at	FLJ35880	hypothetical protein FLJ35880	0.2427	0.0096
1553876_at	SAMD3	sterile alpha motif domain containing 3	0.1129	0.0165
1553978_at	MEF2B	myocyte enhancer factor 2B	0.9034	0.0257
1553987_at	C12orf47	chromosome 12 open reading frame 47	0.9626	0.0073
1553994_at	NT5E	5'-nucleotidase; ecto (CD73)	1.1665	0.0058
1553995_a_at	NT5E	5'-nucleotidase; ecto (CD73)	0.8174	0.0141
1553997_a_at	ASPHD1	aspartate beta-hydroxylase domain containing 1	1.3672	0.0356
1554050_at	SMPDL3B	sphingomyelin phosphodiesterase; acid-like 3B	0.2739	0.0199
1554077_a_at	TMEM53	transmembrane protein 53	1.1765	0.0293
1554093_a_at	SNAPC5	small nuclear RNA activating complex; polypeptide 5; 19kDa	0.7153	0.0101
1554119_at	C16orf57	chromosome 16 open reading frame 57	0.1884	0.0107
1554157_a_at	WFDC8	WAP four-disulfide core domain 8	0.1077	0.0467
1554171_at	ZMYM3	zinc finger; MYM-type 3	0.5468	0.0234
1554172_a_at	ZMYM3	zinc finger; MYM-type 3	0.4253	0.0246
1554175_at	CD300LB	CD300 molecule-like family member b	0.1656	0.0271
1554206_at	TMLHE	trimethyllysine hydroxylase; epsilon	0.3176	0.0266
1554214_at			0.1451	0.032
1554240_a_at	ITGAL	integrin; alpha L (antigen CD11A (p180); lymphocyte function-associated antigen 1; alpha polypeptide)	0.9059	0.0112
1554258_a_at	DNAJC5B	DnaJ (Hsp40) homolog; subfamily C; member 5 beta	0.3563	0.018
1554279_a_at	CXorf34	chromosome X open reading frame 34	0.4921	0.0021
1554285_at	HAVCR2	hepatitis A virus cellular receptor 2	0.2537	0.037
1554317_s_at	C14orf172	chromosome 14 open reading frame 172	0.3187	0.006
1554331_a_at	LRRC18	leucine rich repeat containing 18	0.1552	0.0134
1554335_at	PSCD4	pleckstrin homology; Sec7 and coiled-coil domains 4	0.1955	0.0035
1554371_at	PKD1L2	polycystic kidney disease 1-like 2	0.6615	0.0102
1554406_a_at	CLEC7A	C-type lectin domain family 7; member A	0.4507	0.0367
1554414_a_at	OSGIN2	oxidative stress induced growth inhibitor family member 2	0.8236	0.0447
1554447_at	LOC554203	hypothetical LOC554203	0.8725	0.0167
1554481_a_at	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1; RH-linked)	0.2315	0.0004
1554508_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	0.3183	0.0232
1554519_at	CD80	CD80 molecule	0.2109	0.0225
1554531_at	TTC12	tetratricopeptide repeat domain 12	0.129	0.0284
1554536_at	DPYD	dihydropyrimidine dehydrogenase	0.1701	0.0401
1554537_at	TMEM126B	transmembrane protein 126B	0.2183	0.0083
1554580_a_at	WWP2	WW domain containing E3 ubiquitin protein ligase 2	0.1324	0.0283
1554652_s_at	MAST4	microtubule associated serine/threonine kinase family member 4	0.2248	0.0374
1554689_a_at	NLGN4X	neuroligin 4; X-linked	0.2015	0.0387
1554702_at	NALCN	sodium leak channel; non-selective	0.1212	0.0133
1554728_at	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger); member 1 (antiporter; Na+/H+; amiloride sensitive)	0.128	0.0374
1554730_at	MCTP1	multiple C2 domains; transmembrane 1	0.2596	0.0001
1554741_s_at	FGF7	fibroblast growth factor 7 (keratinocyte growth factor), keratinocyte growth factor-like protein 1, keratinocyte growth factor-like protein 2	1.0659	0.0238
1554841_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0.6492	0.0002
1554899_s_at	FCER1G	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	2.1423	0.0058

1554930_a_at	FUT8	fucosyltransferase 8 (alpha (1;6) fucosyltransferase)	1.1586	0.0036
1555097_a_at	PTGFR	prostaglandin F receptor (FP)	0.6937	0.0369
1555118_at	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	0.1609	0.008
1555120_at	CD96	CD96 molecule	0.1681	0.0282
1555220_a_at	AKR1CL2	aldo-keto reductase family 1; member C-like 2	0.7045	0.0411
1555236_a_at	PGC	progastricsin (pepsinogen C)	0.1388	0.0431
1555255_a_at	HISPPD2A	histidine acid phosphatase domain containing 2A	0.6855	0.0154
1555292_at	FAM40B	family with sequence similarity 40; member B	0.5431	0.0483
1555349_a_at	ITGB2	integrin; beta 2 (complement component 3 receptor 3 and 4 subunit)	1.3521	0.0165
1555419_a_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	0.8165	0.0342
1555426_a_at	OTUD5	OTU domain containing 5	0.5025	0.0156
1555441_at	UBE1L2	ubiquitin-activating enzyme E1-like 2	0.2416	0.0397
1555464_at	IFIH1	interferon induced with helicase C domain 1	0.2689	0.0218
1555610_at	AGK	acylglycerol kinase	0.1201	0.0191
1555613_a_at	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	0.2604	0.0492
1555628_a_at	HAVCR2	hepatitis A virus cellular receptor 2	0.1805	0.0393
1555638_a_at	SAMSN1	SAM domain; SH3 domain and nuclear localization signals 1	0.5818	0.0151
1555691_a_at	KLRC4	killer cell lectin-like receptor subfamily C; member 4, killer cell lectin-like receptor subfamily K; member 1	0.2645	0.0226
1555722_at	SCAMPER	sphingolipid Ca2+ release mediating protein of endoplasmic reticulum	0.1908	0.0067
1555728_a_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	1.5553	0.0347
1555734_x_at	AP1S3	adaptor-related protein complex 1; sigma 3 subunit	0.1826	0.0119
1555745_a_at	LYZ	lysozyme (renal amyloidosis)	1.585	0.0148
1555756_a_at	CLEC7A	C-type lectin domain family 7; member A	1.252	0.0049
1555764_s_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	0.6468	0.0051
1555779_a_at	CD79A	CD79a molecule; immunoglobulin-associated alpha	0.1808	0.013
1555784_s_at	IRAK1	interleukin-1 receptor-associated kinase 1	0.5911	0.0115
1555800_at	ZNF533	zinc finger protein 533	1.4054	0.003
1555801_s_at	ZNF533	zinc finger protein 533	1.9056	0.0029
1555852_at			2.1496	0.0003
1555862_s_at	MICALL2	MICAL-like 2	0.2607	0.0335
1555883_s_at	SPIN3	spindlin family; member 3	0.6849	0.0165
1555902_at	ARMCX5	armadillo repeat containing; X-linked 5	0.5795	0.0073
1555910_at	PTCD2	pentatricopeptide repeat domain 2	0.8025	0.0079
1555961_a_at	HINT1	histidine triad nucleotide binding protein 1	0.3404	0.019
1556026_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	0.3186	0.0271
1556042_s_at	LOC338799	hypothetical locus LOC338799	0.5349	0.0016
1556129_at	LOC642533	hypothetical LOC642533	0.4159	0.0144
1556134_a_at	B3GNT5	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 5	0.3117	0.018
1556167_at	LOC339766	hypothetical protein LOC339766	0.1791	0.0133
1556168_s_at	LOC339766	hypothetical protein LOC339766	0.1148	0.0047
1556182_x_at	hCG_20426	hCG20426	0.3226	0.0188
1556285_s_at	PPA2	pyrophosphatase (inorganic) 2	1.0776	0.0165
1556321_a_at		MRNA full length insert cDNA clone EUROIMAGE 283668	0.2539	0.0136
1556323_at	CUGBP2	CUG triplet repeat; RNA binding protein 2	0.2358	0.0254
1556336_at	RBMX	RNA binding motif protein; X-linked	0.6972	0.042
1556385_at		CDNA FLJ39926 fis; clone SPLEN2021157	0.2308	0.0223
1556397_at		CDNA FLJ37122 fis; clone BRACE2022448	0.1394	0.0175
1556588_at	C15orf37	chromosome 15 open reading frame 37	0.4809	0.0239
1556638_at	LOC284530	hypothetical protein LOC284530	0.1195	0.0481
1556667_at	LOC348751	hypothetical protein LOC348751	0.5574	0.0131
1556698_a_at	GPRIN3	GPRIN family member 3	0.3234	0.0073
1556739_at	FLJ35785	hypothetical protein FLJ35785, similar to golgi autoantigen; golgin subfamily a; 8A	0.1228	0.0153
1556766_at	ERICH1	Glutamate-rich 1	0.1095	0.0461
1556771_a_at	BC038740	BC038740	0.2245	0.003

1556967_at	ZDHHC14	zinc finger; DHHC-type containing 14	0.1268	0.0462
1557078_at	SLFN5	schlafen family member 5	1.1294	0.0005
1557105_a_at		MRNA; cDNA DKFZp686P1116 (from clone DKFZp686P1116)	0.2219	0.0259
1557119_a_at	ZNF575	zinc finger protein 575	0.4182	0.002
1557195_at		MRNA; cDNA DKFZp547B198 (from clone DKFZp547B198)	0.2874	0.0427
1557263_s_at		CDNA FLJ35536 fis; clone SPLEN2002451	0.3044	0.0344
1557383_a_at		CDNA FLJ38112 fis; clone D3OST2002272	0.761	0.0466
1557518_a_at		Full length insert cDNA clone YB25F11	0.1654	0.0013
1557567_a_at	LOC148987	hypothetical protein LOC148987	0.1346	0.0492
1557626_at		CDNA FLJ39805 fis; clone SPLEN2007951	0.7282	0.0121
1557914_s_at		CDNA FLJ13785 fis; clone PLACE4000612	0.1843	0.0315
1558000_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.1817	0.0207
1558105_a_at		Homo sapiens; Similar to LOC169932; clone IMAGE:4499203; mRNA	0.8939	0.0242
1558177_at	C14orf83	chromosome 14 open reading frame 83	0.2287	0.0356
1558195_at	LOC283404	hypothetical protein LOC283404	0.3299	0.0173
1558334_a_at	C22orf15	chromosome 22 open reading frame 15	0.1522	0.0109
1558368_s_at	C1orf187	chromosome 1 open reading frame 187	0.1452	0.0332
1558484_s_at	LRRC27	leucine rich repeat containing 27	0.134	0.0474
1558522_at		Homo sapiens; clone IMAGE:3459334; mRNA	1.3508	0.0012
1558523_at	C6orf60	chromosome 6 open reading frame 60	0.299	0.0387
1558527_at		CDNA clone IMAGE:5259766	0.639	0.0332
1558529_s_at		Homo sapiens; clone IMAGE:4778855	0.5424	0.035
1558546_at	DNASE1	deoxyribonuclease I	0.1536	0.0108
1558662_s_at	BANK1	B-cell scaffold protein with ankyrin repeats 1	0.9347	0.0383
1558770_a_at	C17orf38	chromosome 17 open reading frame 38	0.1924	0.008
1558785_a_at	RGS5	Regulator of G-protein signalling 5	0.1686	0.0139
1558847_at		CDNA FLJ34734 fis; clone MESAN2006971	0.1592	0.037
1558857_at		CDNA clone IMAGE:4818155	0.1103	0.047
1558964_at	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	0.1623	0.0306
1559020_a_at		CDNA FLJ14081 fis; clone HEMBB1002280	0.4738	0.0007
1559062_at		Homo sapiens; clone IMAGE:5730164; mRNA	0.2572	0.0133
1559140_at	FAM87A	family with sequence similarity 87; member A	0.4761	0.0026
1559141_s_at	FAM87A	family with sequence similarity 87; member A	0.674	0.0049
1559205_s_at		Homo sapiens; clone IMAGE:5745627; mRNA	0.1763	0.0139
1559263_s_at	PPIL4	peptidylprolyl isomerase (cyclophilin)-like 4, zinc finger CCCH-type containing 12D	0.519	0.0275
1559297_at	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	0.1471	0.0091
1559333_at		Homo sapiens; clone IMAGE:5206016; mRNA	0.5109	0.0155
1559399_s_at	ZCCHC10	zinc finger; CCHC domain containing 10	1.0595	0.0271
1559402_a_at	C1orf61	chromosome 1 open reading frame 61	0.1402	0.0183
1559502_s_at	LRRC25	leucine rich repeat containing 25	1.5698	0.0141
1559584_a_at	C16orf54	chromosome 16 open reading frame 54, similar to chromosome 16 open reading frame 54	0.7509	0.0469
1559645_at		Non-coding RNA HANC	0.242	0.013
1559777_at		CDNA FLJ32866 fis; clone TESTI2003718	0.1327	0.0269
1560071_a_at			0.4627	0.0304
1560435_at		CDNA FLJ36444 fis; clone THYMU2012902	0.1363	0.0089
1560457_x_at	LSDP5	Lipid storage droplet protein 5	0.1267	0.0295
1560472_at	LOC338588	hypothetical protein LOC338588	0.1298	0.0139
1560488_at	FLJ45224	FLJ45224 protein	0.173	0.0154
1560565_at		Homo sapiens; clone IMAGE:5170127; mRNA	0.1513	0.0035
1560618_at		Homo sapiens; clone IMAGE:5186867; mRNA	0.1174	0.0425
1560706_at		MRNA; cDNA DKFZp667N1617 (from clone DKFZp667N1617)	0.1683	0.0356
1560727_at	HEATR4	HEAT repeat containing 4	0.1395	0.0311
1561004_at		Full length insert cDNA clone YY74A01	0.1374	0.0072
1561062_a_at		CDNA clone IMAGE:5287572	0.1403	0.0353
1561400_at		CDNA clone IMAGE:5297865	0.1583	0.0298

1561414_at	LOC401497	similar to PRO2738	0.148	0.0197
1561459_at		CDNA clone IMAGE:4837993	0.1239	0.0367
1561523_at	CCDC65	coiled-coil domain containing 65	0.1217	0.016
1561666_a_at	KIAA1908	KIAA1908 protein	0.2764	0.0209
1561700_at		CDNA clone IMAGE:4830876	0.1186	0.0362
1561795_at		Homo sapiens; clone IMAGE:4276820; mRNA	0.1034	0.0391
1561860_at		CDNA clone IMAGE:4796386	0.1007	0.0155
1561871_at		Homo sapiens; clone IMAGE:4300626; mRNA	0.1261	0.0435
1562084_at		CDNA clone IMAGE:5288020	0.1435	0.0484
1562211_a_at	ZNF491	zinc finger protein 491	0.1516	0.0187
1562264_at	LOC339685	hypothetical protein LOC339685	0.1819	0.0144
1562289_at		MRNA; cDNA DKFZp434N0220 (from clone DKFZp434N0220)	0.3211	0.0263
1562463_at		Homo sapiens; clone IMAGE:3921647; mRNA	0.1352	0.0329
1562568_at	LOC400541	hypothetical gene supported by AK096066	0.1515	0.0037
1562577_at		Homo sapiens; clone IMAGE:4546564; mRNA	0.2248	0.0019
1562736_at	LHX9	LIM homeobox 9	0.1377	0.0329
1562741_at	UBXD2	UBX domain containing 2	0.1715	0.0091
1562896_at	KIAA1856	KIAA1856 protein	0.227	0.0107
1562934_at		Homo sapiens; clone IMAGE:5519753; mRNA	0.1865	0.0078
1562966_at	KIAA1217	KIAA1217	0.2136	0.0155
1563086_at		CDNA clone IMAGE:5526877	0.1375	0.0373
1563111_a_at	PIGX	phosphatidylinositol glycan anchor biosynthesis; class X	1.1944	0.0007
1563160_at	F11	coagulation factor XI (plasma thromboplastin antecedent)	0.1342	0.0149
1563165_at		CDNA clone IMAGE:3638910	0.2002	0.006
1563178_at		Homo sapiens; clone IMAGE:5538207; mRNA	0.1152	0.0443
1563182_at		CDNA clone IMAGE:4796641	0.2216	0.0454
1563253_s_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0.1034	0.0437
1563318_s_at	MAGIX	MAGI family member; X-linked	0.22	0.026
1563385_at	D21S2091E	D21S2091E	0.1184	0.0438
1563445_x_at	CTSLL3	cathepsin L-like 3	0.2779	0.0441
1563473_at		MRNA; cDNA DKFZp761L0320 (from clone DKFZp761L0320)	0.2353	0.0319
1563528_at	LOC91149	hypothetical protein LOC91149	0.1215	0.0154
1563796_s_at	EARS2	glutamyl-tRNA synthetase 2; mitochondrial (putative)	0.6983	0.0489
1563839_at	TBC1D7	TBC1 domain family; member 7	0.126	0.0069
1563840_at			0.1405	0.0488
1564138_at	FBXW12	F-box and WD repeat domain containing 12	0.1059	0.0479
1564202_at		CDNA FLJ38820 fis; clone LIVER2008473	0.102	0.011
1564310_a_at	PARP15	poly (ADP-ribose) polymerase family; member 15	0.1476	0.0407
1564331_at	LOC162993	hypothetical protein LOC162993	0.2336	0.0022
1564469_at	LMOD3	leiomodin 3 (fetal)	0.2588	0.0002
1564475_s_at	LOC728723	hypothetical protein LOC728723	0.2437	0.0382
1564595_at		Homo sapiens; clone IMAGE:5745181; mRNA	0.1041	0.0442
1564637_a_at	FAM98B	family with sequence similarity 98; member B	0.6604	0.0049
1564662_at	LOC285346	hypothetical protein LOC285346	0.2064	0.0053
1564837_at	LOC151760	hypothetical LOC151760	0.3853	0.0382
1564886_at		MRNA; cDNA DKFZp547M115 (from clone DKFZp547M115)	0.1828	0.0375
1564907_s_at	LOC727839	matrin 3, similar to Matrin-3 (Nuclear scaffold protein P130/MAT3), small nucleolar RNA host gene (non-protein coding) 4	0.2513	0.0052
1564931_at		MRNA; cDNA DKFZp667G014 (from clone DKFZp667G014)	0.1481	0.0312
1565150_at		EST from clone 76558; 5' end	0.3342	0.0156
1565579_at		CDNA clone IMAGE:3689276	0.2217	0.023
1565627_a_at		Full length insert cDNA clone ZD55G10	0.1843	0.0309
1565656_x_at		CDNA FLJ36440 fis; clone THYMU2012565	0.1281	0.0306
1565752_at	FGD2	FYVE; RhoGEF and PH domain containing 2	0.3881	0.0149
1565754_x_at	FGD2	FYVE; RhoGEF and PH domain containing 2	0.4458	0.0222

1565759_at	RPL13	Ribosomal protein L13	0.1968	0.0258
1565868_at	CD44	CD44 molecule (Indian blood group)	0.1713	0.0207
1566101_at	TTLL5	Tubulin tyrosine ligase-like family; member 5	0.1446	0.0161
1566302_at	PPP1R11	protein phosphatase 1; regulatory (inhibitor) subunit 11	0.1572	0.0229
1566437_at	LOC283475	Hypothetical protein LOC283475	0.1003	0.0278
1566504_at		CDNA clone IMAGE:5265199	0.1308	0.0487
1566555_at	FLJ90757	hypothetical protein LOC440465	0.1083	0.0363
1566680_at		CDNA FLJ37017 fis; clone BRACE2010642	0.1025	0.0286
1566700_at	VRK3	vaccinia related kinase 3	0.1376	0.0005
1566772_at		MRNA; cDNA DKFZp547L1918 (from clone DKFZp547L1918)	0.316	0.0229
1566844_at	PER4	period 4 pseudogene	0.1147	0.0421
1566984_at	LOC651250	hypothetical protein LOC651250, hypothetical protein LOC729074	0.1596	0.0407
1567080_s_at	CLN6	ceroid-lipofuscinosis; neuronal 6; late infantile; variant	0.8995	0.009
1567379_at		Partial mRNA; ID band56	0.1479	0.0098
1567623_at	ABLIM2	Actin binding LIM protein family; member 2	0.1795	0.0271
1567628_at	CD74	CD74 molecule; major histocompatibility complex; class II invariant chain	1.9159	0.01
1568191_at			0.1966	0.0127
1568592_at	TRIM69	tripartite motif-containing 69	1.501	0.001
1568593_a_at	NUDT16P	nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene	0.4563	0.0213
1568646_x_at	ZNF208	zinc finger protein 208	0.1435	0.0434
1568743_at	ATP10A	ATPase; Class V; type 10A	0.1687	0.0108
1568830_at	IRAK3	Interleukin-1 receptor-associated kinase 3	0.1291	0.0352
1568931_at		CDNA clone IMAGE:4799464	0.3099	0.0146
1569039_s_at	ZNF677	zinc finger protein 677	0.6632	0.0401
1569289_at	BIVM	Basic; immunoglobulin-like variable motif containing	0.1418	0.0134
1569393_at	MGC15885	hypothetical protein MGC15885	0.1586	0.0031
1569403_at		CDNA clone IMAGE:4706427	1.532	0.0052
1569640_s_at	KIAA1706	KIAA1706 protein	0.1581	0.0408
1569660_at		Pp13439	0.2122	0.0001
1569689_s_at	LOC730017	similar to gamma-aminobutyric acid (GABA) A receptor; beta 3	0.1414	0.0254
1569765_at		CDNA clone IMAGE:4812570	0.219	0.0019
1569792_a_at	MGC50559	hypothetical protein MGC50559	0.4705	0.0137
1569846_at		CDNA clone IMAGE:4838270	0.1732	0.0465
1569867_at	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.653	0.0078
1569868_s_at	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.7538	0.0355
1569898_a_at		CDNA clone IMAGE:5259766	1.0739	0.0003
1569986_x_at	TNNT3	troponin T type 3 (skeletal; fast)	0.4565	0.022
1569995_at	LOC152586	similar to RIKEN cDNA 4933434I20	0.194	0.0047
1570100_at		Homo sapiens; clone IMAGE:4780054; mRNA	0.1032	0.0223
1570125_at		Homo sapiens; clone IMAGE:5229457; mRNA	0.3122	0.0037
1570234_at		Homo sapiens; clone IMAGE:5169759; mRNA	0.1323	0.0192
1570239_a_at	MIST	mast cell immunoreceptor signal transducer	0.1907	0.0393
1570301_at		CDNA clone IMAGE:4696931	0.2298	0.0319
1570330_at		Homo sapiens; clone IMAGE:4151631; mRNA	0.1529	0.0284
1570375_at		Homo sapiens; clone IMAGE:4475530; mRNA	0.1534	0.028
1570410_at	CYGB	cytoglobin	0.1146	0.0303
1570490_at		CDNA clone IMAGE:4248504	0.1101	0.0233
1570523_s_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	1.0363	0.0057
1598_g_at	GAS6	growth arrest-specific 6	0.9307	0.0478
200046_at	DAD1	defender against cell death 1	0.4546	0.0265
200093_s_at	HINT1	histidine triad nucleotide binding protein 1	0.4586	0.0165
200600_at	MSN	moesin	0.9341	0.0469
200609_s_at	WDR1	WD repeat domain 1	0.5496	0.0207
200628_s_at	WARS	tryptophanyl-tRNA synthetase	1.2684	0.0063
200629_at	WARS	tryptophanyl-tRNA synthetase	1.3775	0.0066
200655_s_at	CALM1	calmodulin 1 (phosphorylase kinase; delta)	0.4555	0.0115

200657_at	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator); member 5	0.7344	0.0074
200659_s_at	PHB	prohibitin	0.5773	0.0121
200668_s_at	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog; yeast), ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog; yeast)	0.2858	0.0448
200678_x_at	GRN	granulin	0.743	0.0169
200690_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.9543	0.0434
200691_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.4647	0.0205
200692_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.5755	0.035
200704_at	LITAF	lipopolysaccharide-induced TNF factor	0.5961	0.0125
200724_at	RPL10	ribosomal protein L10	0.2323	0.0023
200725_x_at	RPL10	ribosomal protein L10	0.2114	0.0355
200742_s_at	TPP1	tripeptidyl peptidase I	1.0111	0.0093
200743_s_at	TPP1	tripeptidyl peptidase I	0.6727	0.009
200790_at	ODC1	ornithine decarboxylase 1	0.9756	0.0498
200801_x_at	ACTB	actin; beta	0.1045	0.0241
200808_s_at	ZYX	zyxin	1.6631	0.0012
200824_at	GSTP1	glutathione S-transferase pi	1.8919	0.0124
200830_at	PSMD2	proteasome (prosome; macropain) 26S subunit; non-ATPase; 2	0.2597	0.0362
200852_x_at	GNB2	guanine nucleotide binding protein (G protein); beta polypeptide 2	0.4077	0.0269
200883_at	UQCRC2	ubiquinol-cytochrome c reductase core protein II	0.6989	0.0169
200893_at	SFRS10	splicing factor; arginine/serine-rich 10 (transformer 2 homolog; Drosophila)	0.1453	0.0247
200904_at	HLA-E	major histocompatibility complex; class I; E	1.1664	0.0105
200905_x_at	HLA-E	major histocompatibility complex; class I; E	0.869	0.0057
200915_x_at	KTN1	kinectin 1 (kinesin receptor)	0.2579	0.0363
200933_x_at	RPS4X	ribosomal protein S4; X-linked	0.1524	0.041
200954_at	ATP6V0C	ATPase; H+ transporting; lysosomal 16kDa; V0 subunit c	0.5907	0.0253
200961_at	SEPHS2	selenophosphate synthetase 2	0.739	0.0177
201023_at	TAF7	TAF7 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 55kDa	0.4358	0.0426
201035_s_at	HADH	hydroxyacyl-Coenzyme A dehydrogenase	0.7072	0.0352
201038_s_at	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family; member A	0.5071	0.0441
201068_s_at	PSMC2	proteasome (prosome; macropain) 26S subunit; ATPase; 2	0.2491	0.0474
201079_at	SYNGR2	synaptogyrin 2	0.9481	0.0278
201089_at	ATP6V1B2	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B2	0.9626	0.0014
201132_at	HNRPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	0.6657	0.0055
201134_x_at	COX7C	cytochrome c oxidase subunit VIIc	0.3111	0.0278
201136_at	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	0.6758	0.0184
201137_s_at	HLA-DPB1	major histocompatibility complex; class II; DP beta 1	1.7782	0.0153
201140_s_at	RAB5C	RAB5C; member RAS oncogene family	0.4595	0.0476
201156_s_at	RAB5C	RAB5C; member RAS oncogene family	0.8915	0.0132
201197_at	AMD1	adenosylmethionine decarboxylase 1	0.4218	0.0021
201200_at	CREG1	cellular repressor of E1A-stimulated genes 1	0.7398	0.0128
201212_at	LGMN	legumain	0.8585	0.0448
201237_at	CAPZA2	capping protein (actin filament) muscle Z-line; alpha 2	0.633	0.0113
201238_s_at	CAPZA2	capping protein (actin filament) muscle Z-line; alpha 2	0.5556	0.0087
201264_at	COPE	coatomer protein complex; subunit epsilon	0.413	0.0426
201266_at	TXNRD1	thioredoxin reductase 1	0.586	0.0296
201274_at	PSMA5	proteasome (prosome; macropain) subunit; alpha type; 5	0.6803	0.0422
201282_at	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0.8725	0.0064
201311_s_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	1.0176	0.0027
201312_s_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	0.6209	0.0025
201317_s_at	PSMA2	proteasome (prosome; macropain) subunit; alpha type; 2	0.3871	0.0492

201349_at	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger); member 3 regulator 1	1.8496	0.018
201361_at	TMEM109	transmembrane protein 109	0.6135	0.016
201364_s_at	OAZ2	ornithine decarboxylase antizyme 2	0.9501	0.0152
201365_at	OAZ2	ornithine decarboxylase antizyme 2	0.5847	0.0078
201381_x_at	CACYBP	calcyclin binding protein	0.4023	0.0417
201391_at	TRAP1	TNF receptor-associated protein 1	0.6264	0.0374
201412_at	LRP10	low density lipoprotein receptor-related protein 10	0.3965	0.0199
201422_at	IFI30	interferon; gamma-inducible protein 30	1.4598	0.0317
201430_s_at	DPYSL3	dihydropyrimidinase-like 3	0.7054	0.0096
201431_s_at	DPYSL3	dihydropyrimidinase-like 3	1.5575	0.0147
201434_at	TTC1	tetratricopeptide repeat domain 1	1.0279	0.0208
201435_s_at	EIF4E	eukaryotic translation initiation factor 4E	0.8421	0.0122
201440_at	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	0.493	0.0233
201453_x_at	RHEB	Ras homolog enriched in brain	0.2525	0.0464
201472_at	VBP1	von Hippel-Lindau binding protein 1	0.6493	0.0063
201479_at	DKC1	dyskeratosis congenita 1; dyskerin	0.5431	0.031
201491_at	AHSA1	AHA1; activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	0.4998	0.0468
201526_at	ARF5	ADP-ribosylation factor 5	0.5045	0.0056
201527_at	ATP6V1F	ATPase; H+ transporting; lysosomal 14kDa; V1 subunit F	0.4152	0.0266
201532_at	PSMA3	proteasome (prosome; macropain) subunit; alpha type; 3	0.6707	0.0146
201562_s_at	LOC653381	similar to Sorbitol dehydrogenase (L-iditol 2-dehydrogenase), sorbitol dehydrogenase	1.0022	0.0178
201573_s_at	ETF1	eukaryotic translation termination factor 1	0.6895	0.0184
201575_at	SNW1	SNW domain containing 1	0.304	0.0201
201581_at	TXNDC13	thioredoxin domain containing 13	0.752	0.0158
201605_x_at	CNN2	calponin 2	0.5295	0.0263
201607_at	PWP1	PWP1 homolog (S. cerevisiae)	0.6403	0.0276
201646_at	SCARB2	scavenger receptor class B; member 2	0.8371	0.033
201695_s_at	NP	nucleoside phosphorylase	1.8609	0.001
201705_at	PSMD7	proteasome (prosome; macropain) 26S subunit; non-ATPase; 7	0.3297	0.0452
201743_at	CD14	CD14 molecule	1.6027	0.0451
201756_at	RPA2	replication protein A2; 32kDa	0.7197	0.0287
201765_s_at	HEXA	hexosaminidase A (alpha polypeptide)	0.7301	0.0162
201769_at	CLINT1	clathrin interactor 1	0.5738	0.0084
201801_s_at	SLC29A1	solute carrier family 29 (nucleoside transporters); member 1	2.0087	0.0092
201802_at	SLC29A1	solute carrier family 29 (nucleoside transporters); member 1	1.1594	0.0084
201812_s_at	LOC201725	hypothetical protein LOC201725, translocase of outer mitochondrial membrane 7 homolog (yeast)	0.3369	0.0419
201831_s_at	VDP	vesicle docking protein p115	0.8717	0.011
201832_s_at	VDP	vesicle docking protein p115	0.496	0.0039
201840_at	NEDD8	neural precursor cell expressed; developmentally down-regulated 8	0.3655	0.0169
201857_at	ZFR	zinc finger RNA binding protein	0.2192	0.0453
201880_at	ARIH1	Ariadne homolog; ubiquitin-conjugating enzyme E2 binding protein; 1 (Drosophila)	0.4796	0.0467
201891_s_at	B2M	beta-2-microglobulin	0.2972	0.0054
201895_at	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	0.6255	0.0168
201898_s_at	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.6582	0.0094
201899_s_at	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.7077	0.0008
201903_at	UQCRC1	ubiquinol-cytochrome c reductase core protein I	0.399	0.0317
201905_s_at	CTDSPL	CTD (carboxy-terminal domain; RNA polymerase II; polypeptide A) small phosphatase-like	0.3518	0.0284
201931_at	ETFA	electron-transfer-flavoprotein; alpha polypeptide (glutaric aciduria II)	0.5184	0.0143
201972_at	ATP6V1A	ATPase; H+ transporting; lysosomal 70kDa; V1 subunit A	0.3965	0.0193

201974_s_at	C7orf28A	chromosome 7 open reading frame 28A, chromosome 7 open reading frame 28B, similar to CG14980-PB	0.1157	0.0416
202009_at	TWF2	twinfilin; actin-binding protein; homolog 2 (Drosophila)	0.7684	0.001
202032_s_at	MAN2A2	mannosidase; alpha; class 2A; member 2	0.689	0.0325
202063_s_at	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	0.3124	0.0037
202069_s_at	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	1.2765	0.021
202070_s_at	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	1.1269	0.0444
202071_at	SDC4	syndecan 4	1.3543	0.0309
202077_at	NDUFAB1	NADH dehydrogenase (ubiquinone) 1; alpha/beta subcomplex; 1; 8kDa	0.4802	0.0025
202078_at	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	0.4641	0.036
202085_at	TJP2	tight junction protein 2 (zona occludens 2)	1.1331	0.031
202087_s_at	CTSL1	cathepsin L1	0.4098	0.0155
202090_s_at	TMEM54	transmembrane protein 54, ubiquinol-cytochrome c reductase; 6.4kDa subunit	0.3476	0.0199
202105_at	IGBP1	immunoglobulin (CD79A) binding protein 1	0.561	0.0431
202110_at	COX7B	cytochrome c oxidase subunit VIIb	0.6052	0.0039
202113_s_at	SNX2	sorting nexin 2	0.8103	0.0416
202114_at	SNX2	sorting nexin 2	0.4886	0.015
202177_at	GAS6	growth arrest-specific 6	0.7733	0.0104
202201_at	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	1.2976	0.01
202209_at	LSM3	LSM3 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.5586	0.034
202266_at	TTRAP	TRAF and TNF receptor associated protein	0.3912	0.034
202267_at	LAMC2	laminin; gamma 2	0.2	0.0395
202276_at	SHFM1	split hand/foot malformation (ectrodactyly) type 1	0.3118	0.018
202279_at	C14orf2	chromosome 14 open reading frame 2	0.6809	0.0375
202298_at	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 1; 7.5kDa	0.5958	0.0016
202307_s_at	TAP1	transporter 1; ATP-binding cassette; sub-family B (MDR/TAP)	1.4557	0.0112
202329_at	CSK	c-src tyrosine kinase	0.7759	0.001
202345_s_at	FABP5	fatty acid binding protein 5 (psoriasis-associated), similar to Fatty acid-binding protein; epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	1.9987	0.002
202357_s_at	CFB	complement factor B	1.0102	0.0411
202382_s_at	GNPDA1	glucosamine-6-phosphate deaminase 1	0.9234	0.0094
202387_at	BAG1	BCL2-associated athanogene	0.7276	0.0236
202395_at	NSF	N-ethylmaleimide-sensitive factor	0.4661	0.0443
202430_s_at	PLSCR1	phospholipid scramblase 1	0.9022	0.0313
202471_s_at	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma	0.571	0.0275
202504_at	TRIM29	tripartite motif-containing 29	0.1863	0.0351
202511_s_at	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	0.5821	0.0343
202517_at	CRMP1	collapsin response mediator protein 1	1.7957	0.0104
202518_at	BCL7B	B-cell CLL/lymphoma 7B	1.0076	0.0013
202531_at	IRF1	interferon regulatory factor 1	1.2884	0.0093
202535_at	FADD	Fas (TNFRSF6)-associated via death domain	0.6063	0.0243
202536_at	CHMP2B	chromatin modifying protein 2B	0.8543	0.0147
202541_at	SCYE1	small inducible cytokine subfamily E; member 1 (endothelial monocyte-activating)	0.6463	0.0012
202591_s_at	SSBP1	single-stranded DNA binding protein 1	0.4601	0.0147
202592_at	BLOC1S1	biogenesis of lysosome-related organelles complex-1; subunit 1	0.6741	0.0229
202601_s_at	HTATSF1	HIV-1 Tat specific factor 1	0.7624	0.0167
202602_s_at	HTATSF1	HIV-1 Tat specific factor 1	0.4958	0.0268
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	1.5517	0.0055
202626_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	1.8978	0.0035
202667_s_at	SLC39A7	solute carrier family 39 (zinc transporter); member 7	0.3811	0.0463

202677_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.6755	0.0185
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily; member 10	0.967	0.0097
202688_at	TNFSF10	tumor necrosis factor (ligand) superfamily; member 10	0.9517	0.0219
202693_s_at	STK17A	serine/threonine kinase 17a	1.0949	0.0268
202694_at	STK17A	serine/threonine kinase 17a	0.9085	0.0186
202695_s_at	STK17A	serine/threonine kinase 17a	1.6233	0.0201
202702_at	TRIM26	tripartite motif-containing 26	0.5733	0.0084
202713_s_at	KIAA0391	KIAA0391	0.7825	0.0043
202716_at	PTPN1	protein tyrosine phosphatase; non-receptor type 1	0.6647	0.0223
202720_at	TES	testis derived transcript (3 LIM domains)	1.5386	0.0479
202750_s_at	TFIP11	tuftelin interacting protein 11	0.5437	0.0341
202751_at	TFIP11	tuftelin interacting protein 11	0.3027	0.0094
202753_at	PSMD6	proteasome (prosome; macropain) 26S subunit; non-ATPase; 6	0.5274	0.0136
202758_s_at	RFXANK	regulatory factor X-associated ankyrin-containing protein	0.5614	0.0264
202787_s_at	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	1.1338	0.0378
202788_at	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	1.3903	0.0133
202803_s_at	ITGB2	integrin; beta 2 (complement component 3 receptor 3 and 4 subunit)	1.5226	0.0382
202829_s_at	SYBL1	synaptobrevin-like 1	0.7146	0.0083
202833_s_at	SERPINA1	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 1	1.8061	0.0023
202838_at	FUCA1	fucosidase; alpha-L- 1; tissue	0.94	0.0334
202848_s_at	GRK6	G protein-coupled receptor kinase 6	0.38	0.0393
202852_s_at	FLJ11506	hypothetical protein FLJ11506	0.5632	0.027
202872_at	ATP6V1C1	ATPase; H+ transporting; lysosomal 42kDa; V1 subunit C1	0.5333	0.0287
202874_s_at	ATP6V1C1	ATPase; H+ transporting; lysosomal 42kDa; V1 subunit C1	0.5545	0.0237
202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A); regulatory subunit A; beta isoform	1.1165	0.0429
202895_s_at	SIRPA	signal-regulatory protein alpha	0.4071	0.0236
202896_s_at	SIRPA	signal-regulatory protein alpha	1.0136	0.0285
202897_at	SIRPA	signal-regulatory protein alpha	1.0279	0.0346
202904_s_at	LSM5	LSM5 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.9379	0.0364
202905_x_at	NBN	nibrin	0.8661	0.0143
202906_s_at	NBN	nibrin	0.3919	0.028
202907_s_at	NBN	nibrin	0.7515	0.0045
202921_s_at	ANK2	ankyrin 2; neuronal	0.4749	0.0384
202953_at	C1QB	complement component 1; q subcomponent; B chain	1.9306	0.0108
202957_at	HCLS1	hematopoietic cell-specific Lyn substrate 1	1.5502	0.0297
202958_at	PTPN9	protein tyrosine phosphatase; non-receptor type 9	0.5001	0.0475
202974_at	MPP1	membrane protein; palmitoylated 1; 55kDa	1.2444	0.0021
202982_s_at	ACOT1	acyl-CoA thioesterase 1, acyl-CoA thioesterase 2	1.8477	0
202985_s_at	BAG5	BCL2-associated athanogene 5	0.5254	0.0367
202996_at	POLD4	polymerase (DNA-directed); delta 4	0.4251	0.0475
203016_s_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	1.3035	0.028
203017_s_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	1.0541	0.0439
203018_s_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.6667	0.031
203019_x_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.4853	0.0292
203041_s_at	LAMP2	lysosomal-associated membrane protein 2	1.0108	0.0227
203042_at	LAMP2	lysosomal-associated membrane protein 2	0.7472	0.0222
203047_at	STK10	serine/threonine kinase 10	0.8892	0.0038
203051_at	BAHD1	bromo adjacent homology domain containing 1	0.922	0.001
203072_at	LOC390588	myosin IE, similar to CDK105 protein	0.517	0.0409
203097_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.615	0.0105
203104_at	CSF1R	colony stimulating factor 1 receptor; formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	2.0244	0.0024

203108_at	GPRC5A	G protein-coupled receptor; family C; group 5; member A	1.4019	0.0416
203123_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	1.2644	0.0147
203124_s_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	0.9391	0.013
203125_x_at	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters); member 2	0.8493	0.0133
203142_s_at	AP3B1	adaptor-related protein complex 3; beta 1 subunit	0.7876	0.0253
203143_s_at	KIAA0040	KIAA0040	0.7628	0.0021
203144_s_at	KIAA0040	KIAA0040	0.3081	0.0172
203151_at	MAP1A	microtubule-associated protein 1A	1.2138	0.0311
203200_s_at	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0.8155	0.0061
203207_s_at	MTFR1	mitochondrial fission regulator 1	0.8099	0.0461
203218_at	MAPK9	mitogen-activated protein kinase 9	0.8108	0.0343
203234_at	UPP1	uridine phosphorylase 1	1.0411	0.0313
203236_s_at	LGALS9	lectin; galactoside-binding; soluble; 9 (galectin 9)	1.0006	0.0164
203253_s_at	HISPPD1	histidine acid phosphatase domain containing 1	0.4682	0.04
203262_s_at	FAM50A	family with sequence similarity 50; member A	0.541	0.0493
203267_s_at	DRG2	developmentally regulated GTP binding protein 2	0.2962	0.0422
203268_s_at	DRG2	developmentally regulated GTP binding protein 2	0.2842	0.043
203272_s_at	TUSC2	tumor suppressor candidate 2	0.7629	0.0291
203274_at	F8A1	coagulation factor VIII-associated (intronic transcript) 1	0.6829	0.0329
203290_at	HLA-DQA1	major histocompatibility complex; class II; DQ alpha 1	2.9528	0.0015
203291_at	CNOT4	CCR4-NOT transcription complex; subunit 4	0.6326	0.0236
203300_x_at	AP1S2	adaptor-related protein complex 1; sigma 2 subunit	1.0122	0.003
203302_at	DCK	deoxycytidine kinase	0.6374	0.02
203305_at	F13A1	coagulation factor XIII; A1 polypeptide	1.4166	0.0455
203314_at	GTPBP6	GTP binding protein 6 (putative)	0.5974	0.0394
203320_at	SH2B3	SH2B adaptor protein 3	0.881	0.0175
203339_at	SLC25A12	solute carrier family 25 (mitochondrial carrier; Aralar); member 12	1.1052	0.0067
203342_at	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	1.0382	0.0142
203365_s_at	MMP15	matrix metallopeptidase 15 (membrane-inserted)	1.0689	0.0167
203388_at	ARRB2	arrestin; beta 2	1.1382	0.0036
203406_at	MFAP1	microfibrillar-associated protein 1	0.9483	0.0046
203407_at	PPL	periplakin	1.5691	0.024
203413_at	NELL2	NEL-like 2 (chicken)	0.4905	0.0005
203416_at	CD53	CD53 molecule	1.7608	0.0218
203454_s_at	ATOX1	ATX1 antioxidant protein 1 homolog (yeast)	0.6232	0.0157
203457_at	STX7	syntaxin 7	0.6522	0.0044
203470_s_at	PLEK	pleckstrin	0.6669	0.034
203471_s_at	PLEK	pleckstrin	1.2275	0.0198
203472_s_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	0.5013	0.0006
203473_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	1.8711	0.0021
203478_at	NDUFC1	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 1; 6kDa	0.2205	0.0369
203485_at	RTN1	reticulon 1	1.693	0.0154
203502_at	BPGM	2;3-bisphosphoglycerate mutase	1.0947	0.0009
203510_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	3.9422	0
203514_at	MAP3K3	mitogen-activated protein kinase kinase kinase 3	0.5419	0.0426
203518_at	LYST	lysosomal trafficking regulator	0.9794	0.0039
203527_s_at	APC	adenomatosis polyposis coli	0.5627	0.0238
203547_at	CD4	CD4 molecule	1.0724	0.0046
203557_s_at	PCBD1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	1.0523	0.0155
203561_at	FCGR2A	Fc fragment of IgG; low affinity IIa; receptor (CD32)	1.1815	0.021
203565_s_at	MNAT1	menage a trois homolog 1; cyclin H assembly factor (Xenopus laevis)	0.8291	0.045

203570_at	LOXL1	lysyl oxidase-like 1	1.112	0.0478
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	2.7748	0.0068
203591_s_at	CSF3R	colony stimulating factor 3 receptor (granulocyte)	0.2385	0.0333
203606_at	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6; 13kDa (NADH-coenzyme Q reductase)	0.4931	0.0389
203609_s_at	ALDH5A1	aldehyde dehydrogenase 5 family; member A1 (succinate-semialdehyde dehydrogenase)	0.1459	0.0476
203635_at	DSCR3	Down syndrome critical region gene 3	0.9588	0.0088
203644_s_at	MON1B	MON1 homolog B (yeast)	0.7523	0.0013
203661_s_at	TMOD1	tropomodulin 1	1.4404	0.0208
203662_s_at	TMOD1	tropomodulin 1	1.6492	0.0131
203663_s_at	COX5A	cytochrome c oxidase subunit Va	0.5334	0.0019
203667_at	TBCA	tubulin folding cofactor A	0.257	0.0321
203678_at	MTMR15	myotubularin related protein 15	0.4603	0.0495
203688_at	PKD2	polycystic kidney disease 2 (autosomal dominant)	0.6842	0.0461
203692_s_at	E2F3	E2F transcription factor 3	0.9523	0.0052
203695_s_at	DFNA5	deafness; autosomal dominant 5	2.7494	0.0143
203696_s_at	RFC2	replication factor C (activator 1) 2; 40kDa	0.9511	0.0335
203707_at	ZNF263	zinc finger protein 263	0.7508	0.0435
203730_s_at	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	0.6652	0.0399
203731_s_at	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	0.3544	0.0232
203733_at	DEXI	dexamethasone-induced transcript	0.934	0.0361
203738_at	C5orf22	chromosome 5 open reading frame 22	0.7676	0.0332
203745_at	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	0.9139	0.0398
203746_s_at	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	1.0674	0.0161
203760_s_at	SLA	Src-like-adaptor	0.5873	0.021
203761_at	SLA	Src-like-adaptor	1.3751	0.0279
203767_s_at	STS	steroid sulfatase (microsomal); isozyme S	1.6419	0.0049
203768_s_at	STS	steroid sulfatase (microsomal); isozyme S	0.6278	0.0005
203769_s_at	STS	steroid sulfatase (microsomal); isozyme S	0.7866	0.0212
203770_s_at	STS	steroid sulfatase (microsomal); isozyme S	0.2327	0.0389
203771_s_at	BLVRA	biliverdin reductase A	0.7188	0.0141
203776_at	GPKOW	G patch domain and KOW motifs	0.9226	0.0105
203879_at	PIK3CD	phosphoinositide-3-kinase; catalytic; delta polypeptide	1.6509	0.0065
203888_at	THBD	thrombomodulin	0.8295	0.0319
203893_at	TAF9	TAF9 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 32kDa	0.4875	0.0041
203912_s_at	DNASE1L1	deoxyribonuclease I-like 1	1.2542	0.0064
203915_at	CXCL9	chemokine (C-X-C motif) ligand 9	1.6581	0.0189
203922_s_at	CYBB	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	0.711	0.0026
203923_s_at	CYBB	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	1.9602	0.0014
203925_at	GCLM	glutamate-cysteine ligase; modifier subunit	1.2333	0.0148
203927_at	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; epsilon	0.6692	0.0038
203932_at	HLA-DMB	major histocompatibility complex; class II; DM beta	1.3709	0.0187
203939_at	NT5E	5'-nucleotidase; ecto (CD73)	0.8798	0.0286
203974_at	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	1.3191	0.0119
203977_at	TAZ	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.3837	0.0157
203988_s_at	FUT8	fucosyltransferase 8 (alpha (1;6) fucosyltransferase)	1.2487	0.0187
204006_s_at	FCGR3A	Fc fragment of IgG; low affinity IIIa; receptor (CD16a), Fc fragment of IgG; low affinity IIIb; receptor (CD16b)	0.8847	0.0143
204007_at	FCGR3B	Fc fragment of IgG; low affinity IIIb; receptor (CD16b)	0.4706	0.0321
204012_s_at	LCMT2	leucine carboxyl methyltransferase 2	0.7931	0.0324
204024_at	OSGIN2	oxidative stress induced growth inhibitor family member 2	0.5643	0.035
204034_at	ETHE1	ethylmalonic encephalopathy 1	1.5759	0.0029
204035_at	SCG2	secretogranin II (chromogranin C)	2.185	0.0214
204039_at	CEBPA	CCAAT/enhancer binding protein (C/EBP); alpha	1.7927	0.0083

204043_at	TCN2	transcobalamin II; macrocytic anemia	0.9097	0.0126
204045_at	TCEAL1	transcription elongation factor A (SII)-like 1	0.7777	0.0063
204057_at	IRF8	interferon regulatory factor 8	1.3188	0.0057
204061_at	PRKX	protein kinase; X-linked	0.607	0.0153
204070_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	1.5449	0.017
204093_at	CCNH	cyclin H	0.7132	0.0253
204096_s_at	ELL	elongation factor RNA polymerase II	0.2222	0.0044
204097_s_at	RBMX2	RNA binding motif protein; X-linked 2	0.805	0.0121
204098_at	RBMX2	RNA binding motif protein; X-linked 2	0.65	0.0218
204101_at	MTM1	myotubularin 1	0.8461	0.0002
204116_at	IL2RG	interleukin 2 receptor; gamma (severe combined immunodeficiency)	0.9746	0.0024
204118_at	CD48	CD48 molecule	1.2975	0.0206
204119_s_at	ADK	adenosine kinase	1.3567	0.0018
204120_s_at	ADK	adenosine kinase	0.6831	0.0195
204122_at	TYROBP	TYRO protein tyrosine kinase binding protein	1.6776	0.0162
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	2.6428	0.0009
204161_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	1.4249	0.0006
204174_at	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	1.6767	0.0213
204175_at	ZNF593	zinc finger protein 593	0.7021	0.0416
204185_x_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	0.5307	0.0089
204186_s_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	0.855	0.0144
204192_at	CD37	CD37 molecule	0.6802	0.0336
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP); gamma	1.0293	0.0231
204215_at	C7orf23	chromosome 7 open reading frame 23	1.2068	0.0067
204219_s_at	PSMC1	proteasome (prosome; macropain) 26S subunit; ATPase; 1	0.538	0.0098
204220_at	GMFG	glia maturation factor; gamma	0.9817	0.0455
204224_s_at	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	1.3197	0.0413
204227_s_at	TK2	thymidine kinase 2; mitochondrial	0.8263	0.032
204232_at	FCER1G	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	1.7403	0.0163
204236_at	FLI1	Friend leukemia virus integration 1	0.7235	0.0452
204247_s_at	CDK5	cyclin-dependent kinase 5	1.057	0.0029
204265_s_at	GPSM3	G-protein signaling modulator 3 (AGS3-like; C. elegans)	1.0836	0.0076
204279_at	PSMB9	proteasome (prosome; macropain) subunit; beta type; 9 (large multifunctional peptidase 2)	2.0361	0.0089
204300_at	PET112L	PET112-like (yeast)	0.7827	0.0371
204319_s_at	RGS10	regulator of G-protein signaling 10	1.7183	0.0065
204321_at	NEO1	neogenin homolog 1 (chicken)	0.86	0.0307
204331_s_at	MRPS12	mitochondrial ribosomal protein S12	0.6701	0.0452
204332_s_at	AGA	aspartylglucosaminidase	1.3312	0.0123
204333_s_at	AGA	aspartylglucosaminidase	1.7032	0.0039
204336_s_at	RGS19	regulator of G-protein signaling 19	1.0741	0.018
204340_at	TMEM187	transmembrane protein 187	0.9293	0.0092
204343_at	ABCA3	ATP-binding cassette; sub-family A (ABC1); member 3	1.0081	0.0203
204353_s_at	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	1.0939	0.0039
204354_at	POT1	POT1 protection of telomeres 1 homolog (S. pombe)	0.6504	0.0021
204357_s_at	LIMK1	LIM domain kinase 1	0.3672	0.0303
204393_s_at	ACPP	acid phosphatase; prostate	1.2276	0.0076
204405_x_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	0.6117	0.009
204408_at	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	1.0792	0.0139
204436_at	PLEKHQ1	pleckstrin homology domain containing; family Q member 1	0.9843	0.0225
204439_at	IFI44L	interferon-induced protein 44-like	2.0201	0.0493
204470_at	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity; alpha)	0.295	0.0236
204493_at	BID	BH3 interacting domain death agonist	0.6679	0.0486
204495_s_at	C15orf39	chromosome 15 open reading frame 39	0.5395	0.0371

204513_s_at	ELMO1	engulfment and cell motility 1	1.0019	0.0143
204532_x_at	UGT1A4	UDP glucuronosyltransferase 1 family; polypeptide A4	1.7102	0.0219
204533_at	CXCL10	chemokine (C-X-C motif) ligand 10	1.8326	0.005
204536_s_at			0.146	0.0358
204546_at	KIAA0513	KIAA0513	1.3042	0.0157
204549_at	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase epsilon	0.2854	0.0359
204552_at		CDNA FLJ34214 fis; clone FCBBF3021807	0.9459	0.0191
204554_at	PPP1R3D	protein phosphatase 1; regulatory (inhibitor) subunit 3D	1.2089	0.0006
204563_at	SELL	selectin L (lymphocyte adhesion molecule 1)	0.9566	0.0239
204565_at	THEM2	thioesterase superfamily member 2	0.6923	0.0159
204571_x_at	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting; 4 (parvulin)	0.7293	0.0024
204587_at	SLC25A14	solute carrier family 25 (mitochondrial carrier; brain); member 14	1.0838	0.0023
204604_at	PFTK1	PFTAIRE protein kinase 1	1.7671	0.001
204618_s_at	GABPB2	GA binding protein transcription factor; beta subunit 2	0.4888	0.0129
204625_s_at	ITGB3	integrin; beta 3 (platelet glycoprotein IIIa; antigen CD61)	0.1192	0.0305
204643_s_at	ENOX2	ecto-NOX disulfide-thiol exchanger 2	1.0207	0.0026
204670_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1	1.8206	0.02
204674_at	LRMP	lymphoid-restricted membrane protein	0.4351	0.0199
204676_at	TMEM186	transmembrane protein 186	0.6596	0.0199
204701_s_at	STOML1	stomatin (EPB72)-like 1	1.3031	0.0038
204766_s_at	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.8017	0.0341
204770_at	TAP2	transporter 2; ATP-binding cassette; sub-family B (MDR/TAP)	0.6239	0.0154
204774_at	EVI2A	ecotropic viral integration site 2A	1.4799	0.0025
204777_s_at	MAL	mal; T-cell differentiation protein	0.2215	0.0273
204789_at	FMNL1	formin-like 1	0.5097	0.0352
204796_at	EML1	echinoderm microtubule associated protein like 1	1.668	0.0065
204797_s_at	EML1	echinoderm microtubule associated protein like 1	1.8299	0.0113
204802_at	RRAD	Ras-related associated with diabetes	2.1511	0.0105
204803_s_at	RRAD	Ras-related associated with diabetes	1.1629	0.0178
204806_x_at	HLA-F	major histocompatibility complex; class I; F	0.8549	0.0014
204819_at	FGD1	FYVE; RhoGEF and PH domain containing 1 (faciogenital dysplasia)	1.0571	0.0314
204826_at	CCNF	cyclin F	0.3323	0.0265
204827_s_at	CCNF	cyclin F	0.2689	0.0135
204829_s_at	FOLR2	folate receptor 2 (fetal)	1.1413	0.02
204834_at	FGL2	fibrinogen-like 2	1.4701	0.0016
204838_s_at	MLH3	mutL homolog 3 (E. coli)	1.5477	0.018
204871_at	MTERF	mitochondrial transcription termination factor	0.7482	0.0291
204883_s_at	HUS1	HUS1 checkpoint homolog (S. pombe)	0.7558	0.0254
204890_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.277	0.0187
204891_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.9692	0.0257
204907_s_at	BCL3	B-cell CLL/lymphoma 3	0.2776	0.0182
204909_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	0.2715	0.0123
204912_at	IL10RA	interleukin 10 receptor; alpha	1.5497	0.0136
204923_at	CXorf9	chromosome X open reading frame 9	1.0893	0.0125
204928_s_at	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family); member 3	1.5168	0
204951_at	RHOH	ras homolog gene family; member H	0.2756	0.0162
204960_at	CORO1B	coronin; actin binding protein; 1B, protein tyrosine phosphatase; receptor type; C-associated protein	0.4439	0.0482
204961_s_at	NCF1	neutrophil cytosolic factor 1; (chronic granulomatous disease; autosomal 1), neutrophil cytosolic factor 1B pseudogene, neutrophil cytosolic factor 1C pseudogene	0.4176	0.0128
204976_s_at	AMMECR1	Alport syndrome; mental retardation; midface hypoplasia and elliptocytosis chromosomal region; gene 1	1.1049	0.0431
204979_s_at	SH3BGR	SH3 domain binding glutamic acid-rich protein	1.1273	0.0238

204983_s_at	GPC4	glypican 4	1.0209	0.0094
204984_at	GPC4	glypican 4	1.29	0.0457
204989_s_at	ITGB4	integrin; beta 4	0.196	0.0158
204990_s_at	ITGB4	integrin; beta 4	0.2791	0.0051
204994_at	MX2	myxovirus (influenza virus) resistance 2 (mouse)	1.4468	0.0214
205003_at	DOCK4	dedicator of cytokinesis 4	1.436	0.0105
205008_s_at	CIB2	calcium and integrin binding family member 2	1.3453	0.006
205036_at	LSM6	LSM6 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.4304	0.0271
205038_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)	0.2448	0.0225
205039_s_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)	0.3066	0.0092
205047_s_at	ASNS	asparagine synthetase	0.9389	0.0247
205061_s_at	EXOSC9	exosome component 9	0.5762	0.0009
205068_s_at	ARHGAP26	Rho GTPase activating protein 26	0.5107	0.0195
205072_s_at	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.5185	0.013
205074_at	SLC22A5	solute carrier family 22 (organic cation transporter); member 5	1.0108	0.0433
205098_at	CCR1	chemokine (C-C motif) receptor 1	1.3493	0.0429
205099_s_at	CCR1	chemokine (C-C motif) receptor 1	0.9422	0.0392
205115_s_at	RBM19	RNA binding motif protein 19	1.2916	0.01
205140_at	FPGT	fucose-1-phosphate guanylyltransferase	0.7398	0.0315
205147_x_at	NCF4	neutrophil cytosolic factor 4; 40kDa	0.6516	0.0244
205159_at	CSF2RB	colony stimulating factor 2 receptor; beta; low-affinity (granulocyte-macrophage)	1.195	0.0164
205173_x_at	CD58	CD58 molecule	1.5554	0.0244
205213_at	CENTB1	centaurin; beta 1	0.4991	0.0242
205217_at	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	0.9947	0.0103
205238_at	CXorf34	chromosome X open reading frame 34	1.1025	0.0351
205242_at	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	1.5414	0.023
205248_at	DOPEY2	dopey family member 2	0.6577	0.0077
205252_at	ZNF174	zinc finger protein 174	0.3199	0.034
205262_at	KCNH2	potassium voltage-gated channel; subfamily H (eag-related); member 2	1.8654	0.0314
205269_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	1.1308	0.0432
205270_s_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	1.1509	0.0095
205279_s_at	GLRB	glycine receptor; beta	1.8197	0.0004
205280_at	GLRB	glycine receptor; beta	2.1461	0.0018
205285_s_at	FYB	FYN binding protein (FYB-120/130)	0.3308	0.0266
205291_at	IL2RB	interleukin 2 receptor; beta	0.8403	0.0013
205312_at	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	0.2439	0.0248
205326_at	RAMP3	receptor (G protein-coupled) activity modifying protein 3	0.9931	0.045
205352_at	SERPINI1	serpin peptidase inhibitor; clade I (neuroserpin); member 1	2.2456	0.0011
205397_x_at	SMAD3	SMAD family member 3	0.4131	0.0019
205412_at	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	0.6165	0.0239
205414_s_at	RICH2	Rho-type GTPase-activating protein RICH2	0.4856	0.0308
205429_s_at	MPP6	membrane protein; palmitoylated 6 (MAGUK p55 subfamily member 6)	2.0341	0.0006
205450_at	PHKA1	phosphorylase kinase; alpha 1 (muscle)	0.7283	0.0366
205452_at	PIGB	phosphatidylinositol glycan anchor biosynthesis; class B	1.1885	0.0015
205488_at	GZMA	granzyme A (granzyme 1; cytotoxic T-lymphocyte-associated serine esterase 3)	1.6642	0.0053
205495_s_at	GNLY	granulysin	1.1517	0.0115
205504_at	BTK	Bruton agammaglobulinemia tyrosine kinase	0.3604	0.0298
205512_s_at	AIFM1	apoptosis-inducing factor; mitochondrion-associated; 1	1.2584	0.0101

205540_s_at	RRAGB	Ras-related GTP binding B	0.9484	0.0364
205542_at	STEAP1	six transmembrane epithelial antigen of the prostate 1	1.5581	0.0264
205543_at	HSPA4L	heat shock 70kDa protein 4-like	1.0036	0.0148
205544_s_at	CR2	complement component (3d/Epstein Barr virus) receptor 2	0.2983	0.014
205555_s_at	MSX2	msh homeobox 2	0.2213	0.0391
205569_at	LAMP3	lysosomal-associated membrane protein 3	1.0479	0.0051
205583_s_at	CXorf45	chromosome X open reading frame 45	0.9058	0.034
205584_at	CXorf45	chromosome X open reading frame 45	0.7837	0.0282
205618_at	PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	1.3926	0.0081
205621_at	ALKBH1	alkB; alkylation repair homolog 1 (E. coli)	0.606	0.0323
205639_at	AOAH	acyloxyacyl hydrolase (neutrophil)	0.8976	0.0145
205659_at	HDAC9	histone deacetylase 9	1.422	0.0037
205663_at	PCBP3	poly(rC) binding protein 3	0.4737	0.0243
205671_s_at	HLA-DOB	major histocompatibility complex; class II; DO beta	0.2821	0.018
205682_x_at	APOM	apolipoprotein M	0.2496	0.0476
205685_at	CD86	CD86 molecule	0.6245	0.0471
205686_s_at	CD86	CD86 molecule	0.8536	0.0137
205690_s_at	BUD31	BUD31 homolog (S. cerevisiae)	0.487	0.0394
205696_s_at	GFRA1	GDNF family receptor alpha 1	0.2245	0.0027
205708_s_at	TRPM2	transient receptor potential cation channel; subfamily M; member 2	0.4228	0.0488
205718_at	ITGB7	integrin; beta 7	0.3264	0.0322
205761_s_at	DUS4L	dihydrouridine synthase 4-like (S. cerevisiae)	0.8193	0.0331
205768_s_at	SLC27A2	solute carrier family 27 (fatty acid transporter); member 2	2.2681	0.0103
205769_at	SLC27A2	solute carrier family 27 (fatty acid transporter); member 2	2.2057	0.0051
205778_at	KLK7	kallikrein-related peptidase 7	0.1187	0.0316
205781_at	C16orf7	chromosome 16 open reading frame 7	0.3746	0.0199
205786_s_at	ITGAM	integrin; alpha M (complement component 3 receptor 3 subunit)	0.936	0.0372
205789_at	CD1D	CD1d molecule	0.5782	0.021
205798_at	IL7R	interleukin 7 receptor	2.2523	0.0091
205821_at	KLRK1	killer cell lectin-like receptor subfamily K; member 1	1.0732	0.0038
205831_at	CD2	CD2 molecule	1.2578	0.0138
205833_s_at	PART1	prostate androgen-regulated transcript 1	0.195	0.0369
205859_at	LY86	lymphocyte antigen 86	1.5788	0.0063
205890_s_at	UBD	ubiquitin D	1.1188	0.0348
205896_at	SLC22A4	solute carrier family 22 (organic cation transporter); member 4	0.9332	0.0187
205898_at	CX3CR1	chemokine (C-X3-C motif) receptor 1	1.8944	0.0137
205920_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter; taurine); member 6	0.9814	0.0197
205921_s_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter; taurine); member 6	0.2683	0.0475
205931_s_at	CREB5	cAMP responsive element binding protein 5	0.5434	0.0238
205934_at	PLCL1	phospholipase C-like 1	1.1389	0.0167
205937_at	CGREF1	cell growth regulator with EF-hand domain 1	0.2243	0.0429
205965_at	BATF	basic leucine zipper transcription factor; ATF-like	0.2097	0.0456
205984_at	CRHBP	corticotropin releasing hormone binding protein	0.9374	0.0213
205987_at	CD1C	CD1c molecule	0.4977	0.0164
205988_at	CD84	CD84 molecule	1.0333	0.0071
205997_at	ADAM28	ADAM metallopeptidase domain 28	0.5773	0.0124
206006_s_at	KIAA1009	KIAA1009	0.3061	0.0436
206011_at	CASP1	caspase 1; apoptosis-related cysteine peptidase (interleukin 1; beta; convertase)	1.2631	0.0124
206049_at	SELP	selectin P (granule membrane protein 140kDa; antigen CD62)	1.0928	0.0126
206052_s_at	SLBP	stem-loop (histone) binding protein	0.4819	0.0239
206060_s_at	PTPN22	protein tyrosine phosphatase; non-receptor type 22 (lymphoid)	0.4346	0.0195
206062_at	GUCA1A	guanylate cyclase activator 1A (retina)	0.1131	0.0402
206068_s_at	ACADL	acyl-Coenzyme A dehydrogenase; long chain	2.3728	0.0245

206069_s_at	ACADL	acyl-Coenzyme A dehydrogenase; long chain	2.5481	0.0094
206074_s_at	HMGA1	high mobility group AT-hook 1	1.2445	0.0301
206076_at	LRRC23	leucine rich repeat containing 23	0.7194	0.0335
206082_at	HCP5	HLA complex P5	2.2324	0.0001
206087_x_at	HFE	hemochromatosis	0.7695	0.0261
206090_s_at	DISC1	disrupted in schizophrenia 1	0.6382	0.037
206094_x_at	UGT1A1	UDP glucuronosyltransferase 1 family; polypeptide A1, UDP glucuronosyltransferase 1 family; polypeptide A10, UDP glucuronosyltransferase 1 family; polypeptide A3, UDP glucuronosyltransferase 1 family; polypeptide A4, UDP glucuronosyltransferase 1 family; polypeptide A5, UDP glucuronosyltransferase 1 family; polypeptide A6, UDP glucuronosyltransferase 1 family; polypeptide A7, UDP glucuronosyltransferase 1 family; polypeptide A8, UDP glucuronosyltransferase 1 family; polypeptide A9	1.3962	0.0387
206118_at	STAT4	signal transducer and activator of transcription 4	0.5904	0.001
206120_at	CD33	CD33 molecule	0.4446	0.0112
206129_s_at	ARSB	arylsulfatase B	0.3645	0.0237
206150_at	CD27	CD27 molecule	0.3412	0.0199
206170_at	ADRB2	adrenergic; beta-2-; receptor; surface	0.3898	0.0035
206181_at	SLAMF1	signaling lymphocytic activation molecule family member 1	0.1799	0.0315
206219_s_at	VAV1	vav 1 guanine nucleotide exchange factor	0.2595	0.0237
206227_at	CILP	cartilage intermediate layer protein; nucleotide pyrophosphohydrolase	0.2427	0.0168
206247_at	MICB	MHC class I polypeptide-related sequence B	2.4218	0.0044
206256_at	CPN1	carboxypeptidase N; polypeptide 1	0.1623	0.0323
206260_at	TGM4	transglutaminase 4 (prostate)	0.2289	0.0079
206299_at	TMEM28	transmembrane protein 28	1.0663	0.0262
206306_at	RYR3	ryanodine receptor 3	0.9851	0.043
206313_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	0.3407	0.0123
206337_at	CCR7	chemokine (C-C motif) receptor 7	0.2921	0.0272
206342_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	1.3066	0.0412
206346_at	PRLR	prolactin receptor	1.6174	0.0495
206347_at	PDK3	pyruvate dehydrogenase kinase; isozyme 3	0.1987	0.0204
206366_x_at	XCL2	chemokine (C motif) ligand 2	0.9009	0.0004
206407_s_at	CCL13	chemokine (C-C motif) ligand 13	0.3552	0.0155
206410_at	NR0B2	nuclear receptor subfamily 0; group B; member 2	2.1452	0.0224
206420_at	IGSF6	immunoglobulin superfamily; member 6	1.3457	0.0134
206441_s_at	COMMD4	COMM domain containing 4	0.8529	0.0007
206449_s_at	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	0.4133	0.0377
206468_s_at	KIAA0859	KIAA0859	1.0938	0.0103
206480_at	LTC4S	leukotriene C4 synthase	0.3406	0.0221
206512_at	ZRSR1	zinc finger (CCCH type); RNA-binding motif and serine/arginine rich 1	0.3641	0.0289
206513_at	AIM2	absent in melanoma 2	0.4306	0.0113
206538_at	MRAS	muscle RAS oncogene homolog	0.5667	0.0407
206553_at	OAS2	2'-5'-oligoadenylate synthetase 2; 69/71kDa	0.2346	0.0345
206554_x_at	SETMAR	SET domain and mariner transposase fusion gene	1.0718	0.0004
206584_at	LY96	lymphocyte antigen 96	3.2463	0.0016
206589_at	GFI1	growth factor independent 1	0.1644	0.0471
206600_s_at	SLC16A5	solute carrier family 16; member 5 (monocarboxylic acid transporter 6)	0.7198	0.0331
206602_s_at	HOXD3	homeobox D3	0.1111	0.0427
206617_s_at	RENBP	renin binding protein	1.2306	0.0242
206649_s_at	TFE3	transcription factor binding to IGHM enhancer 3	0.6988	0.0441
206656_s_at	C20orf3	chromosome 20 open reading frame 3	0.3905	0.0469
206666_at	GZMK	granzyme K (granzyme 3; tryptase II)	0.9397	0.0203
206680_at	CD5L	CD5 molecule-like	0.2328	0.0165
206682_at	CLEC10A	C-type lectin domain family 10; member A	0.7487	0.0136
206715_at	TFEC	transcription factor EC	1.1831	0.0177

206733_at	TULP2	tubby like protein 2	0.1176	0.037
206739_at	HOXC5	homeobox C5	0.557	0.0251
206746_at	BFSP1	beaded filament structural protein 1; filensin	0.4949	0.0079
206756_at	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	0.6464	0.025
206761_at	CD96	CD96 molecule	0.4083	0.0107
206783_at	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1; Kaposi sarcoma oncogene)	0.1644	0.0087
206785_s_at	KLRC1	killer cell lectin-like receptor subfamily C; member 1, killer cell lectin-like receptor subfamily C; member 2	0.754	0.0021
206838_at	TBX19	T-box 19	0.3266	0.0167
206842_at	KCND1	potassium voltage-gated channel; Shal-related subfamily; member 1	0.2542	0.0248
206850_at	RASL10A	RAS-like; family 10; member A	0.5259	0.007
206860_s_at	FLJ20323	hypothetical protein FLJ20323	0.8216	0.006
206891_at	ACTN3	actinin; alpha 3	0.2111	0.0037
206914_at	CRTAM	cytotoxic and regulatory T cell molecule	0.2499	0.0484
206923_at	PRKCA	protein kinase C; alpha	0.2783	0.0268
206925_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 4	0.1244	0.0484
206978_at	CCR2	chemokine (C-C motif) receptor 2, similar to C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2) (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CD192 antigen)	0.7384	0.0338
206987_x_at	FGF18	fibroblast growth factor 18	0.181	0.0024
206991_s_at	CCR5	chemokine (C-C motif) receptor 5	0.8697	0.0085
207037_at	TNFRSF11A	tumor necrosis factor receptor superfamily; member 11a; NFKB activator	0.138	0.0076
207072_at	IL18RAP	interleukin 18 receptor accessory protein	0.3675	0.0029
207075_at	NLRP3	NLR family; pyrin domain containing 3	0.2761	0.0195
207085_x_at	CSF2RA	colony stimulating factor 2 receptor; alpha; low-affinity (granulocyte-macrophage)	0.3738	0.0028
207098_s_at	MFN1	mitofusin 1	0.8496	0.0295
207124_s_at	GNB5	guanine nucleotide binding protein (G protein); beta 5	1.0329	0.0498
207126_x_at	UGT1A4	UDP glucuronosyltransferase 1 family; polypeptide A4	1.7394	0.0207
207138_at	PHF2	PHD finger protein 2	0.1207	0.0338
207144_s_at	CITED1	Cbp/p300-interacting transactivator; with Glu/Asp-rich carboxy-terminal domain; 1	0.542	0.0176
207156_at	HIST1H2AG	histone cluster 1; H2ag	1.2073	0.0137
207206_s_at	ALOX12	arachidonate 12-lipoxygenase	0.1649	0.0132
207222_at	PLA2G10	phospholipase A2; group X	0.1286	0.0291
207224_s_at	SIGLEC7	sialic acid binding Ig-like lectin 7	0.8302	0.0279
207233_s_at	MITF	microphthalmia-associated transcription factor	1.2487	0.0208
207238_s_at	PTPRC	protein tyrosine phosphatase; receptor type; C	1.5057	0.0024
207255_at	LEPR	leptin receptor	0.1254	0.0107
207277_at	CD209	CD209 molecule	0.8101	0.0235
207312_at	PHKG1	phosphorylase kinase; gamma 1 (muscle)	0.6877	0.0424
207335_x_at	ATP5I	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit E, major facilitator superfamily domain containing 7	0.4159	0.0365
207338_s_at	ZNF200	zinc finger protein 200	0.7164	0.0161
207339_s_at	LTB	lymphotoxin beta (TNF superfamily; member 3)	0.4527	0.0246
207351_s_at	SH2D2A	SH2 domain protein 2A	0.2014	0.047
207362_at	SLC30A4	solute carrier family 30 (zinc transporter); member 4	0.2111	0.0263
207375_s_at	IL15RA	interleukin 15 receptor; alpha	1.0639	0.0166
207383_s_at	RHBDL1	rhomboid; veinlet-like 1 (Drosophila)	0.2248	0.0371
207386_at	CYP7B1	cytochrome P450; family 7; subfamily B; polypeptide 1	0.8911	0.0408
207396_s_at	ALG3	asparagine-linked glycosylation 3 homolog (S. cerevisiae; alpha-1;3-mannosyltransferase)	0.4991	0.034
207419_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family; small GTP binding protein Rac2)	0.5772	0.0322
207438_s_at	SNUPN	snurportin 1	0.8157	0.0005

207439_s_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter); member A2	1.058	0.0019
207440_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter); member A2	0.8071	0.0096
207446_at	TLR6	toll-like receptor 6	0.364	0.0122
207455_at	P2RY1	purinergic receptor P2Y; G-protein coupled; 1	0.1805	0.0495
207496_at	MS4A2	membrane-spanning 4-domains; subfamily A; member 2 (Fc fragment of IgE; high affinity I; receptor for; beta polypeptide)	0.1663	0.0217
207540_s_at	SYK	spleen tyrosine kinase	0.5486	0.0262
207551_s_at	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	0.638	0.0376
207610_s_at	EMR2	egf-like module containing; mucin-like; hormone receptor-like 2	0.6336	0.0295
207623_at	ABCF2	ATP-binding cassette; sub-family F (GCN20); member 2	0.3389	0.0001
207649_at	KRT37	keratin 37	0.123	0.0134
207658_s_at	FOXG1	forkhead box G1	0.4946	0.0475
207677_s_at	NCF4	neutrophil cytosolic factor 4; 40kDa	0.6977	0.0365
207681_at	CXCR3	chemokine (C-X-C motif) receptor 3	0.2155	0.0073
207695_s_at	IGSF1	immunoglobulin superfamily; member 1	0.3227	0.0063
207707_s_at	SEC13	SEC13 homolog (S. cerevisiae)	0.9122	0.0041
207721_x_at	HINT1	histidine triad nucleotide binding protein 1	0.3863	0.0191
207723_s_at	KLRC3	killer cell lectin-like receptor subfamily C; member 3	0.1608	0.0151
207735_at	RNF125	ring finger protein 125	0.6015	0.0075
207741_x_at	TPSAB1	tryptase alpha/beta 1, tryptase beta 2	0.541	0.0098
207765_s_at	KIAA1539	KIAA1539	0.6433	0.03
207795_s_at	KLRD1	killer cell lectin-like receptor subfamily D; member 1	0.3204	0.004
207796_x_at	KLRD1	killer cell lectin-like receptor subfamily D; member 1	0.2857	0.0005
207800_at	AKAP5	A kinase (PRKA) anchor protein 5	0.1374	0.0081
207805_s_at	PSMD9	proteasome (prosome; macropain) 26S subunit; non-ATPase; 9	0.4967	0.0287
207808_s_at	PROS1	protein S (alpha)	1.4655	0.0235
207840_at	CD160	CD160 molecule	0.272	0.0354
207871_s_at	ST7	suppression of tumorigenicity 7	0.8961	0.0479
207880_at	ADAM11	ADAM metallopeptidase domain 11	0.1543	0.0285
207895_at	NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	0.232	0.0205
207908_at	KRT2	keratin 2 (epidermal ichthyosis bullosa of Siemens)	0.1428	0.023
207911_s_at	TGM5	transglutaminase 5	0.2394	0.0261
207922_s_at	LOC730744	macrophage erythroblast attacher, similar to macrophage erythroblast attacher	0.4439	0.0273
207935_s_at	KRT13	keratin 13	0.1407	0.0353
207939_x_at	RNPS1	RNA binding protein S1; serine-rich domain	0.3514	0.0183
207949_s_at	ICA1	islet cell autoantigen 1; 69kDa	0.3033	0.0295
207960_at			0.141	0.0378
208018_s_at	HCK	hemopoietic cell kinase	1.4272	0.0101
208037_s_at	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	0.1495	0.0389
208052_x_at	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	0.2179	0.0291
208062_s_at	NRG2	neuregulin 2	0.263	0.0404
208071_s_at	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	0.3018	0.0066
208091_s_at	ECOP	EGFR-coamplified and overexpressed protein	0.6255	0.0321
208117_s_at	LAS1L	LAS1-like (S. cerevisiae)	1.0141	0.0381
208121_s_at	PTPRO	protein tyrosine phosphatase; receptor type; O	1.0612	0.0369
208130_s_at	TBXAS1	thromboxane A synthase 1 (platelet; cytochrome P450; family 5; subfamily A)	0.6454	0.0012
208146_s_at	CPVL	carboxypeptidase; vitellogenic-like	1.4288	0.0437
208179_x_at	KIR2DL3	killer cell immunoglobulin-like receptor; two domains; long cytoplasmic tail; 3, killer cell immunoglobulin-like receptor; two domains; short cytoplasmic tail; 5	0.1859	0.0251
208241_at	NRG1	neuregulin 1	0.3852	0.0375
208306_x_at	HLA-DRB1	Major histocompatibility complex; class II; DR beta 1	1.7299	0.0233
208315_x_at	TRAF3	TNF receptor-associated factor 3	0.2693	0.0158
208318_s_at	XYLB	xylulokinase homolog (H. influenzae)	0.19	0.0043

208319_s_at	RBM3	RNA binding motif (RNP1; RRM) protein 3	1.0866	0.004
208335_s_at	DARC	Duffy blood group; chemokine receptor	1.2653	0.0223
208370_s_at	RCAN1	regulator of calcineurin 1	0.8663	0.043
208373_s_at	P2RY6	pyrimidinergic receptor P2Y; G-protein coupled; 6	0.369	0.004
208447_s_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	1.4642	0.0217
208450_at	LGALS2	lectin; galactoside-binding; soluble; 2	0.4663	0.0044
208473_s_at	GP2	glycoprotein 2 (zymogen granule membrane)	0.1465	0.0103
208486_at	DRD5	dopamine receptor D5	0.1887	0.0391
208509_s_at	OR7A17	olfactory receptor; family 7; subfamily A; member 17	0.1003	0.0214
208594_x_at	LILRA6	leukocyte immunoglobulin-like receptor; subfamily A (with TM domain); member 6	0.2757	0.0016
208596_s_at	UGT1A1	UDP glucuronosyltransferase 1 family; polypeptide A1, UDP glucuronosyltransferase 1 family; polypeptide A10, UDP glucuronosyltransferase 1 family; polypeptide A3, UDP glucuronosyltransferase 1 family; polypeptide A4, UDP glucuronosyltransferase 1 family; polypeptide A5, UDP glucuronosyltransferase 1 family; polypeptide A6, UDP glucuronosyltransferase 1 family; polypeptide A7, UDP glucuronosyltransferase 1 family; polypeptide A8, UDP glucuronosyltransferase 1 family; polypeptide A9	1.7583	0.031
208598_s_at	HUWE1	HECT; UBA and WWE domain containing 1	0.5922	0.012
208640_at	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family; small GTP binding protein Rac1)	0.1431	0.0483
208658_at	PDIA4	protein disulfide isomerase family A; member 4	0.6297	0.0362
208693_s_at	GARS	glycyl-tRNA synthetase	0.5734	0.0214
208705_s_at	EIF5	eukaryotic translation initiation factor 5	0.5184	0.0242
208706_s_at	EIF5	eukaryotic translation initiation factor 5	0.6385	0.0209
208708_x_at	EIF5	eukaryotic translation initiation factor 5	1.0299	0.0339
208714_at	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1; 51kDa	0.3958	0.0379
208729_x_at	HLA-B	major histocompatibility complex; class I; B	0.9755	0.0013
208736_at	ARPC3	actin related protein 2/3 complex; subunit 3; 21kDa	0.4002	0.0253
208749_x_at	FLOT1	flotillin 1	0.3648	0.0449
208785_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	0.5995	0.0387
208786_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	0.5057	0.0286
208787_at	MRPL3	mitochondrial ribosomal protein L3	0.4019	0.0027
208812_x_at	HLA-C	major histocompatibility complex; class I; C, similar to major histocompatibility complex; class I; C	0.5207	0.0042
208826_x_at	HINT1	histidine triad nucleotide binding protein 1	0.3682	0.0343
208827_at	PSMB6	proteasome (prosome; macropain) subunit; beta type; 6	0.4978	0.0084
208837_at	TMED3	transmembrane emp24 protein transport domain containing 3	1.0335	0.0097
208847_s_at	ADH5	alcohol dehydrogenase 5 (class III); chi polypeptide	0.3278	0.042
208848_at	ADH5	alcohol dehydrogenase 5 (class III); chi polypeptide	0.6258	0.0277
208885_at	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	1.3823	0.0007
208894_at	HLA-DRA	major histocompatibility complex; class II; DR alpha	2.4115	0.0047
208898_at	ATP6V1D	ATPase; H+ transporting; lysosomal 34kDa; V1 subunit D	0.6371	0.0019
208899_x_at	ATP6V1D	ATPase; H+ transporting; lysosomal 34kDa; V1 subunit D	0.7871	0.009
208909_at	UQCRFS1	ubiquinol-cytochrome c reductase; Rieske iron-sulfur polypeptide 1	0.3681	0.0415
208921_s_at	SRI	sorcin	0.7858	0.0008
208923_at	CYFIP1	cytoplasmic FMR1 interacting protein 1	0.5743	0.0122
208968_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.5331	0.0472
209015_s_at	DNAJB6	DnaJ (Hsp40) homolog; subfamily B; member 6	1.1792	0.0088
209036_s_at	MDH2	malate dehydrogenase 2; NAD (mitochondrial)	0.3835	0.0435
209040_s_at	PSMB8	proteasome (prosome; macropain) subunit; beta type; 8 (large multifunctional peptidase 7)	2.3702	0
209054_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.7066	0.0215
209066_x_at	UQCRB	ubiquinol-cytochrome c reductase binding protein	0.3039	0.0274
209083_at	CORO1A	coronin; actin binding protein; 1A	1.1076	0.0185

209104_s_at	NOLA2	nucleolar protein family A; member 2 (H/ACA small nucleolar RNPs)	0.5414	0.0452
209132_s_at	COMMD4	COMM domain containing 4	1.1283	0.0001
209133_s_at	COMMD4	COMM domain containing 4	0.1728	0.0238
209140_x_at	HLA-B	major histocompatibility complex; class I; B	0.636	0.0009
209171_at	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	0.6534	0.0158
209211_at	KLF5	Kruppel-like factor 5 (intestinal)	0.571	0.0365
209216_at	WDR45	WD repeat domain 45	0.7634	0.0201
209217_s_at	WDR45	WD repeat domain 45	0.8322	0.0134
209232_s_at	DCTN5	dynactin 5 (p25)	0.496	0.0395
209239_at	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	1.028	0.0045
209260_at	SFN	stratifin	0.1637	0.032
209269_s_at	SYK	spleen tyrosine kinase	0.2508	0.0101
209275_s_at	CLN3	ceroid-lipofuscinosis; neuronal 3; juvenile (Batten; Spielmeyer-Vogt disease)	0.8282	0.0445
209303_at	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4; 18kDa (NADH-coenzyme Q reductase)	0.5802	0.0238
209312_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1	2.0573	0.0182
209326_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter); member A2	0.9344	0.0114
209331_s_at	MAX	MYC associated factor X	0.6699	0.0067
209349_at	RAD50	RAD50 homolog (S. cerevisiae)	0.8683	0.0232
209370_s_at	SH3BP2	SH3-domain binding protein 2	0.2576	0.0476
209371_s_at	SH3BP2	SH3-domain binding protein 2	0.1998	0.0031
209373_at	MALL	mal; T-cell differentiation protein-like	0.8891	0.0111
209374_s_at	IGHM	immunoglobulin heavy constant mu	1.7305	0.0239
209394_at	ASMTL	acetylserotonin O-methyltransferase-like	0.9162	0.0147
209395_at	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	2.6391	0.0036
209396_s_at	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	2.2317	0.0039
209405_s_at	FAM3A	family with sequence similarity 3; member A	0.7601	0.038
209411_s_at	GGA3	golgi associated; gamma adaptin ear containing; ARF binding protein 3	0.7127	0.0471
209414_at	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	0.3601	0.0318
209440_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.8608	0.0118
209444_at	RAP1GDS1	RAP1; GTP-GDP dissociation stimulator 1	0.9004	0.0444
209449_at	LSM2	LSM2 homolog; U6 small nuclear RNA associated (S. cerevisiae)	0.7509	0.022
209450_at	OSGEP	O-sialoglycoprotein endopeptidase	1.1689	0.0009
209452_s_at	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	0.5994	0.0157
209479_at	CCDC28A	coiled-coil domain containing 28A	0.4886	0.0289
209482_at	POP7	processing of precursor 7; ribonuclease P/MRP subunit (S. cerevisiae)	0.5879	0.0115
209492_x_at	ATP5I	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit E	0.3878	0.0434
209493_at	PDZD2	PDZ domain containing 2	0.8186	0.0163
209499_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	0.6104	0.045
209500_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	0.7449	0.0446
209505_at	NR2F1	Nuclear receptor subfamily 2; group F; member 1	1.568	0.0083
209506_s_at	NR2F1	nuclear receptor subfamily 2; group F; member 1	0.9277	0.0329
209514_s_at	RAB27A	RAB27A; member RAS oncogene family	1.9823	0.0017
209515_s_at	RAB27A	RAB27A; member RAS oncogene family	1.2046	0.0342
209536_s_at	EHD4	EH-domain containing 4	1.137	0.0212
209542_x_at	IGF1	insulin-like growth factor 1 (somatomedin C)	0.4231	0.0412
209544_at	RIPK2	receptor-interacting serine-threonine kinase 2	0.5194	0.0016

209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	0.9846	0.0151
209563_x_at	CALM1	calmodulin 1 (phosphorylase kinase; delta)	0.4231	0.0089
209565_at	RNF113A	ring finger protein 113A	0.7421	0.0407
209580_s_at	MBD4	methyl-CpG binding domain protein 4	0.6529	0.0027
209619_at	CD74	CD74 molecule; major histocompatibility complex; class II invariant chain	1.5719	0.0216
209620_s_at	ABCB7	ATP-binding cassette; sub-family B (MDR/TAP); member 7	0.6554	0.0423
209626_s_at	OSBPL3	oxysterol binding protein-like 3	0.9632	0.0052
209627_s_at	OSBPL3	oxysterol binding protein-like 3	1.2043	0.0176
209633_at	PPP2R3A	protein phosphatase 2 (formerly 2A); regulatory subunit B''; alpha	0.9108	0.0228
209654_at	KIAA0947	KIAA0947 protein	0.8507	0.0115
209665_at	CYB561D2	cytochrome b-561 domain containing 2	0.8429	0.0073
209670_at	TRAC	T cell receptor alpha constant	0.8304	0.0312
209671_x_at	TRA@	T cell receptor alpha constant, T cell receptor alpha locus	0.7577	0.0072
209690_s_at	DOK4	docking protein 4	0.216	0.0247
209696_at	FBP1	fructose-1;6-bisphosphatase 1	1.1522	0.0042
209734_at	NCKAP1L	NCK-associated protein 1-like	0.9672	0.0076
209759_s_at	DCI	dodecenoyl-Coenzyme A delta isomerase (3;2 trans-enoyl-Coenzyme A isomerase)	0.6047	0.0274
209762_x_at	SP110	SP110 nuclear body protein	0.9307	0.0458
209790_s_at	CASP6	caspase 6; apoptosis-related cysteine peptidase	1.262	0.0009
209823_x_at	HLA-DQB1	major histocompatibility complex; class II; DQ beta 1	2.3978	0.0105
209827_s_at	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.5569	0.0055
209828_s_at	IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.1993	0.0337
209831_x_at	DNASE2	deoxyribonuclease II; lysosomal	0.6358	0.0229
209836_x_at	BOLA2	bolA homolog 2 (E. coli), bolA homolog 2B (E. coli)	0.6347	0.0147
209877_at	SNCG	synuclein; gamma (breast cancer-specific protein 1)	2.2257	0.0232
209879_at	SELPLG	selectin P ligand	1.3316	0.0055
209901_x_at	AIF1	allograft inflammatory factor 1	2.1457	0.0017
209906_at	C3AR1	complement component 3a receptor 1	1.3567	0.0329
209929_s_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase gamma	0.7127	0.0141
209943_at	FBXL4	F-box and leucine-rich repeat protein 4	0.6841	0.0211
209960_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	1.3314	0.0355
209970_x_at	CASP1	caspase 1; apoptosis-related cysteine peptidase (interleukin 1; beta; convertase)	1.4525	0.0274
209995_s_at	TCL1A	T-cell leukemia/lymphoma 1A	0.1909	0.0049
210016_at	MYT1L	myelin transcription factor 1-like	0.1018	0.0448
210024_s_at	UBE2E3	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog; yeast)	0.3869	0.0405
210031_at	CD247	CD247 molecule	0.4114	0.0187
210045_at	IDH2	isocitrate dehydrogenase 2 (NADP+); mitochondrial	0.7618	0.0332
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+); mitochondrial	1.4871	0.0241
210051_at	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	0.3761	0.0179
210061_at	ZNF589	zinc finger protein 589	0.2968	0.0315
210062_s_at	ZNF589	zinc finger protein 589	0.625	0.0033
210072_at	CCL19	chemokine (C-C motif) ligand 19	1.3382	0.035
210075_at	2-Mar	membrane-associated ring finger (C3HC4) 2	0.8782	0.0043
210112_at	HPS1	Hermansky-Pudlak syndrome 1	0.4608	0.0179
210116_at	SH2D1A	SH2 domain protein 1A; Duncan's disease (lymphoproliferative syndrome)	0.2776	0.0217
210127_at	RAB6B	RAB6B; member RAS oncogene family	0.4498	0.0449
210140_at	CST7	cystatin F (leukocystatin)	0.6115	0.0083
210145_at	PLA2G4A	phospholipase A2; group IVA (cytosolic; calcium-dependent)	0.7849	0.0385
210146_x_at	LILRB2	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 2	0.9204	0.0367
210150_s_at	LAMA5	laminin; alpha 5	1.1181	0.0078

210152_at	LILRB4	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 4	0.5955	0.0125
210162_s_at	NFATC1	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 1	0.2767	0.0134
210163_at	CXCL11	chemokine (C-X-C motif) ligand 11	0.3694	0.0211
210164_at	GZMB	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	1.6923	0.0112
210166_at	TLR5	toll-like receptor 5	0.832	0.0155
210174_at	NR5A2	nuclear receptor subfamily 5; group A; member 2	1.1292	0.0482
210176_at	TLR1	toll-like receptor 1	1.0216	0.0117
210184_at	ITGAX	integrin; alpha X (complement component 3 receptor 4 subunit)	0.6965	0.0421
210212_x_at	MTCP1	mature T-cell proliferation 1	0.7768	0.0382
210222_s_at	RTN1	reticulon 1	0.6621	0.032
210223_s_at	MR1	major histocompatibility complex; class I-related	1.0794	0.0289
210224_at	MR1	major histocompatibility complex; class I-related	0.5579	0.0243
210242_x_at	ST20	suppressor of tumorigenicity 20	0.351	0.0294
210255_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	0.2491	0.0013
210260_s_at	TNFAIP8	tumor necrosis factor; alpha-induced protein 8	1.4824	0.0429
210279_at	GPR18	G protein-coupled receptor 18	0.2914	0.0378
210288_at	KLRG1	killer cell lectin-like receptor subfamily G; member 1	0.2541	0.0026
210292_s_at	PCDH11X	protocadherin 11 X-linked, protocadherin 11 Y-linked	0.1059	0.0435
210305_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	0.2294	0.0315
210314_x_at	TNFSF12-TNFSF13	tumor necrosis factor (ligand) superfamily; member 12-member 13, tumor necrosis factor (ligand) superfamily; member 13	1.1857	0.0261
210315_at	SYN2	synapsin II	0.7366	0.0153
210319_x_at	MSX2	msh homeobox 2	0.5676	0.0135
210340_s_at	CSF2RA	colony stimulating factor 2 receptor; alpha; low-affinity (granulocyte-macrophage)	0.1855	0.0474
210345_s_at	DNAH9	dynein; axonemal; heavy chain 9	0.1173	0.0471
210354_at	IFNG	interferon; gamma	0.2213	0.0258
210356_x_at	MS4A1	membrane-spanning 4-domains; subfamily A; member 1	0.1445	0.0069
210367_s_at	PTGES	prostaglandin E synthase	0.8518	0.0323
210385_s_at	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	1.0249	0.0096
210447_at	GLUD2	glutamate dehydrogenase 2	1.161	0.0027
210450_at	LOC90925	hypothetical protein LOC90925	0.2231	0.0195
210476_s_at	PRLR	prolactin receptor	0.8465	0.0346
210482_x_at	MAP2K5	mitogen-activated protein kinase kinase 5	0.6113	0.0208
210514_x_at	HLA-G	HLA-G histocompatibility antigen; class I; G	0.5563	0.0118
210532_s_at	C14orf2	chromosome 14 open reading frame 2	0.376	0.0048
210533_at	MSH4	mutS homolog 4 (E. coli)	0.2788	0.03
210542_s_at	SLCO3A1	solute carrier organic anion transporter family; member 3A1	0.6618	0.0048
210548_at	CCL23	chemokine (C-C motif) ligand 23	0.1797	0.0122
210551_s_at	ASMT	acetylserotonin O-methyltransferase	0.3344	0.0284
210569_s_at	SIGLEC9	sialic acid binding Ig-like lectin 9	0.2255	0.0246
210570_x_at	MAPK9	mitogen-activated protein kinase 9	1.1159	0.0267
210572_at	PCDHA2	protocadherin alpha 2	0.4031	0.013
210582_s_at	LIMK2	LIM domain kinase 2	0.3983	0.0162
210584_s_at	CTA-126B4.3	CGI-96 protein, polymerase (DNA-directed); delta interacting protein 3, similar to CGI-96	0.2053	0.0062
210606_x_at	KLRD1	killer cell lectin-like receptor subfamily D; member 1	0.3685	0.0013
210621_s_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1.0645	0.0127
210629_x_at	LST1	leukocyte specific transcript 1	0.8234	0.0108
210644_s_at	LAIR1	leukocyte-associated immunoglobulin-like receptor 1	1.3066	0.0202

210674_s_at	PCDHA1	protocadherin alpha 1, protocadherin alpha 10, protocadherin alpha 11, protocadherin alpha 12, protocadherin alpha 13, protocadherin alpha 2, protocadherin alpha 3, protocadherin alpha 4, protocadherin alpha 5, protocadherin alpha 6, protocadherin alpha 7, protocadherin alpha 8, protocadherin alpha 9, protocadherin alpha subfamily C; 1, protocadherin alpha subfamily C; 2	2.2042	0.0477
210745_at	ONECUT1	one cut homeobox 1	0.1198	0.0346
210753_s_at	EPHB1	EPH receptor B1	1.2721	0.029
210754_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	1.4789	0.0014
210802_s_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	0.9441	0.0468
210813_s_at	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.5957	0.0173
210819_x_at	DIO2	deiodinase; iodothyronine; type II	0.1472	0.0203
210849_s_at	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	0.6304	0.0136
210859_x_at	CLN3	ceroid-lipofuscinosis; neuronal 3; juvenile (Batten; Spielmeyer-Vogt disease)	0.7425	0.0462
210871_x_at	SSX2IP	synovial sarcoma; X breakpoint 2 interacting protein	0.4911	0.039
210873_x_at	APOBEC3A	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 3A	0.6493	0.0171
210889_s_at	FCGR2B	Fc fragment of IgG; low affinity IIb; receptor (CD32), Fc fragment of IgG; low affinity IIc; receptor for (CD32)	1.1143	0.0233
210895_s_at	CD86	CD86 molecule	1.4034	0.0064
210907_s_at	PDCD10	programmed cell death 10	0.5828	0.0269
210915_x_at	TRBC1	T cell receptor beta constant 1, T cell receptor beta variable 19	1.6805	0.0074
210926_at	FKSG30	kappa-actin	0.3866	0.0062
210951_x_at	RAB27A	RAB27A; member RAS oncogene family	1.9367	0.0026
210959_s_at	SRD5A1	steroid-5-alpha-reductase; alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.2598	0.0141
210972_x_at	TRA@	T cell receptor alpha constant, T cell receptor alpha joining 17, T cell receptor alpha locus, T cell receptor alpha variable 20, T cell receptor delta variable 2	0.583	0.0424
210982_s_at	HLA-DRA	major histocompatibility complex; class II; DR alpha	2.5873	0.0088
210992_x_at	FCGR2C	Fc fragment of IgG; low affinity IIc; receptor for (CD32)	0.467	0.0215
210993_s_at	SMAD1	SMAD family member 1	1.0793	0.0091
210997_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	1.5371	0.0336
211005_at	LAT	linker for activation of T cells	0.4912	0.0022
211029_x_at	FGF18	fibroblast growth factor 18	0.2316	0.0017
211071_s_at	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 11	1.9906	0.031
211138_s_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0.6321	0.0104
211144_x_at	TARP	T cell receptor gamma constant 2, T cell receptor gamma variable 9, TCR gamma alternate reading frame protein	0.3621	0.0118
211153_s_at	TNFSF11	tumor necrosis factor (ligand) superfamily; member 11	0.1616	0.0085
211192_s_at	CD84	CD84 molecule	0.2715	0.0061
211241_at	ANXA2P3	annexin A2 pseudogene 3	0.2788	0.0422
211250_s_at	SH3BP2	SH3-domain binding protein 2	0.3519	0.0023
211267_at	HESX1	HESX homeobox 1	0.239	0.0466
211284_s_at	GRN	granulin	0.981	0.0174
211286_x_at	CSF2RA	colony stimulating factor 2 receptor; alpha; low-affinity (granulocyte-macrophage)	0.3783	0.015
211287_x_at	CSF2RA	colony stimulating factor 2 receptor; alpha; low-affinity (granulocyte-macrophage)	0.1492	0.0478
211327_x_at	HFE	hemochromatosis	0.2668	0.0071
211328_x_at	HFE	hemochromatosis	0.2288	0.0125
211329_x_at	HFE	hemochromatosis	0.3876	0.0005
211331_x_at	HFE	hemochromatosis	0.2161	0.0113

211333_s_at	FASLG	Fas ligand (TNF superfamily; member 6)	0.1176	0.0198
211339_s_at	ITK	IL2-inducible T-cell kinase	0.5755	0.015
211366_x_at	CASP1	caspase 1; apoptosis-related cysteine peptidase (interleukin 1; beta; convertase)	1.3572	0.0178
211367_s_at	CASP1	caspase 1; apoptosis-related cysteine peptidase (interleukin 1; beta; convertase)	1.1344	0.0078
211368_s_at	CASP1	caspase 1; apoptosis-related cysteine peptidase (interleukin 1; beta; convertase)	1.564	0.0123
211370_s_at	MAP2K5	mitogen-activated protein kinase kinase 5	0.7508	0.0341
211382_s_at	TACC2	transforming; acidic coiled-coil containing protein 2	0.7156	0.0486
211392_s_at	PATZ1	POZ (BTB) and AT hook containing zinc finger 1	0.2443	0.0422
211395_x_at	FCGR2C	Fc fragment of IgG; low affinity IIc; receptor for (CD32)	0.6456	0.0376
211417_x_at	GGT1	gamma-glutamyltransferase 1	0.2645	0.035
211429_s_at	SERPINA1	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 1	1.8118	0.0038
211430_s_at	IGH@	immunoglobulin heavy constant gamma 1 (G1m marker), immunoglobulin heavy constant gamma 2 (G2m marker), immunoglobulin heavy constant gamma 3 (G3m marker), immunoglobulin heavy constant mu, immunoglobulin heavy locus, immunoglobulin heavy variable 4-31	2.327	0.0228
211447_s_at	PDE4A	phosphodiesterase 4A; cAMP-specific (phosphodiesterase E2 dunce homolog; Drosophila)	0.3531	0.0099
211475_s_at	BAG1	BCL2-associated athanogene	0.784	0.0254
211485_s_at	FGF18	fibroblast growth factor 18	0.1374	0.0417
211502_s_at	PFTK1	PFTAIRE protein kinase 1	0.2434	0.0066
211528_x_at	HLA-G	HLA-G histocompatibility antigen; class I; G	0.5917	0.0065
211529_x_at	HLA-G	HLA-G histocompatibility antigen; class I; G	0.7323	0.004
211530_x_at	HLA-G	HLA-G histocompatibility antigen; class I; G	0.4323	0.0096
211557_x_at	SLCO2B1	solute carrier organic anion transporter family; member 2B1	0.508	0.0043
211581_x_at	LST1	leukocyte specific transcript 1	0.8982	0.0197
211582_x_at	LST1	leukocyte specific transcript 1	1.0899	0.0092
211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	1.0119	0.0082
211599_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.6598	0.0044
211644_x_at	GJB6	gap junction protein; beta 6, immunoglobulin kappa constant, netrin 2-like (chicken)	1.3891	0.0461
211645_x_at		Immunoglobulin kappa light chain (IGKV) mRNA variable region; joining region; and constant region	1.1898	0.0397
211656_x_at	HLA-DQB1	major histocompatibility complex; class II; DQ beta 1	1.6926	0.0335
211661_x_at	PTAFR	platelet-activating factor receptor	0.5216	0.0008
211663_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	0.4542	0.0479
211668_s_at	PLAU	plasminogen activator; urokinase	0.4119	0.0404
211704_s_at	SPIN2A	spindlin family; member 2A, spindlin family; member 2B	0.9888	0.003
211724_x_at	FLJ20323	hypothetical protein FLJ20323	0.7914	0.0064
211741_x_at	PSG3	pregnancy specific beta-1-glycoprotein 3	0.2094	0.0362
211742_s_at	EVI2B	ecotropic viral integration site 2B	1.6954	0.001
211744_s_at	CD58	CD58 molecule	1.5515	0.0196
211748_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	1.242	0.0313
211752_s_at	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7; 20kDa (NADH-coenzyme Q reductase)	0.7824	0.0292
211794_at	FYB	FYN binding protein (FYB-120/130)	0.6215	0.0025
211795_s_at	FYB	FYN binding protein (FYB-120/130)	1.0944	0.0079
211796_s_at	TRBC1	T cell receptor beta constant 1, T cell receptor beta variable 19, T cell receptor beta variable 3-1, T cell receptor beta variable 5-4, T cell receptor beta variable 7-2	1.5371	0.0103
211799_x_at	HLA-C	major histocompatibility complex; class I; C	1.2623	0.0013
211815_s_at	GGA3	golgi associated; gamma adaptin ear containing; ARF binding protein 3	0.2011	0.0204
211855_s_at	SLC25A14	solute carrier family 25 (mitochondrial carrier; brain); member 14	1.1642	0.0022
211863_x_at	HFE	hemochromatosis	0.1934	0.0399

211864_s_at	FER1L3	fer-1-like 3; myoferlin (C. elegans)	1.5669	0.0207
211870_s_at	PCDHA3	protocadherin alpha 3	0.3365	0.0139
211871_x_at	GNB5	guanine nucleotide binding protein (G protein); beta 5	0.4263	0.025
211876_x_at	PCDHGA10	protocadherin gamma subfamily A; 10, protocadherin gamma subfamily A; 11, protocadherin gamma subfamily A; 12, protocadherin gamma subfamily A; 3, protocadherin gamma subfamily A; 5, protocadherin gamma subfamily A; 6	0.8688	0.0094
211880_x_at	PCDHGA1	protocadherin gamma subfamily A; 1	0.3088	0.0309
211881_x_at	IGLJ3	immunoglobulin lambda joining 3	0.6761	0.0471
211887_x_at	MSR1	macrophage scavenger receptor 1	0.18	0.0301
211888_x_at	CASP10	caspase 10; apoptosis-related cysteine peptidase	0.1937	0.039
211898_s_at	EPHB1	EPH receptor B1	0.5804	0.0069
211902_x_at	TRA@	T cell receptor alpha locus	0.4332	0.0261
211911_x_at	HLA-B	major histocompatibility complex; class I; B	0.9341	0.0032
211917_s_at	PRLR	prolactin receptor	1.3384	0.0406
211960_s_at	RAB7A	RAB7A; member RAS oncogene family	0.5109	0.042
211984_at	CALM1	calmodulin 1 (phosphorylase kinase; delta)	0.7241	0.0074
211985_s_at	CALM1	calmodulin 1 (phosphorylase kinase; delta)	0.8223	0.0372
211990_at	HLA-DPA1	major histocompatibility complex; class II; DP alpha 1	1.3451	0.0307
211991_s_at	HLA-DPA1	major histocompatibility complex; class II; DP alpha 1	2.4281	0.0075
212010_s_at	CDV3	CDV3 homolog (mouse)	0.2407	0.0396
212018_s_at	RSL1D1	ribosomal L1 domain containing 1	0.5549	0.0246
212129_at	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	0.5583	0.0155
212133_at	NIPA2	Non imprinted in Prader-Willi/Angelman syndrome 2	0.7981	0.0363
212156_at	VPS39	vacuolar protein sorting 39 homolog (S. cerevisiae)	0.6451	0.016
212187_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	1.1648	0.0473
212223_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	1.0316	0.0329
212243_at	Gcom1	GRINL1A combined protein, glutamate receptor; ionotropic; N-methyl D-aspartate-like 1A	0.5601	0.012
212244_at	Gcom1	GRINL1A combined protein, glutamate receptor; ionotropic; N-methyl D-aspartate-like 1A	0.3962	0.0418
212308_at	CLASP2	cytoplasmic linker associated protein 2	0.7305	0.0186
212311_at	KIAA0746	KIAA0746 protein	2.3481	0.0014
212314_at	KIAA0746	KIAA0746 protein	2.8414	0.0109
212317_at	TNPO3	transportin 3	0.4986	0.0234
212340_at	YIPF6	Yip1 domain family; member 6	1.1926	0.0061
212341_at	YIPF6	Yip1 domain family; member 6	0.669	0.0223
212342_at	YIPF6	Yip1 domain family; member 6	1.2047	0.0037
212343_at	YIPF6	Yip1 domain family; member 6	0.9845	0.0292
212347_x_at	MXD4	MAX dimerization protein 4	1.0666	0.0224
212373_at	FEM1B	fem-1 homolog b (C. elegans)	0.7304	0.0457
212390_at	LOC727893	phosphodiesterase 4D interacting protein (myomegalin), similar to phosphodiesterase 4D interacting protein isoform 1	0.5272	0.0093
212405_s_at	KIAA0859	KIAA0859	0.7623	0.0113
212407_at	KIAA0859	KIAA0859	1.2811	0.0007
212418_at	ELF1	E74-like factor 1 (ets domain transcription factor)	0.7528	0.0277
212437_at	CENPB	centromere protein B; 80kDa	0.5265	0.0311
212459_x_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	0.5778	0.0164
212465_at	SETD3	SET domain containing 3	0.4971	0.0014
212499_s_at	C14orf32	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae), chromosome 14 open reading frame 32	0.4029	0.0355
212587_s_at	PTPRC	protein tyrosine phosphatase; receptor type; C	1.4029	0.0154
212588_at	PTPRC	protein tyrosine phosphatase; receptor type; C	2.0469	0.0047
212600_s_at	UQCRC2	ubiquinol-cytochrome c reductase core protein II	0.4443	0.0325
212631_at	STX7	Syntaxin 7	1.2281	0.001
212632_at	STX7	Syntaxin 7	0.9543	0.0126
212640_at	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member b	0.6648	0.0352
212660_at	PHF15	PHD finger protein 15	1.3795	0.029

212665_at	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	0.8505	0.0139
212671_s_at	HLA-DQA1	major histocompatibility complex; class II; DQ alpha 1, major histocompatibility complex; class II; DQ alpha 2, similar to HLA class II histocompatibility antigen; DQ(1) alpha chain precursor (DC-4 alpha chain)	3.5726	0.0003
212673_at	METAP1	methionyl aminopeptidase 1	0.8971	0.0013
212688_at	PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	0.7229	0.0435
212699_at	SCAMP5	secretory carrier membrane protein 5	1.4839	0.0093
212701_at		Clone 23962 mRNA sequence	0.7413	0.0039
212728_at	DLG3	discs; large homolog 3 (neuroendocrine-dlg; Drosophila)	0.6315	0.0324
212733_at	KIAA0226	KIAA0226	0.8968	0.0111
212786_at	CLEC16A	C-type lectin domain family 16; member A	0.612	0.0335
212798_s_at	ANKMY2	ankyrin repeat and MYND domain containing 2	0.777	0.0169
212814_at	KIAA0828	adenosylhomocysteinase 3	0.7954	0.0236
212820_at	DMXL2	Dmx-like 2	1.0083	0.0058
212829_at	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase; type II; alpha	1.9908	0
212841_s_at	PPFIBP2	PTPRF interacting protein; binding protein 2 (liprin beta 2)	0.9609	0.0271
212845_at	SAMD4A	sterile alpha motif domain containing 4A	1.2995	0.0032
212849_at	AXIN1	axin 1	0.5379	0.0036
212850_s_at	LRP4	low density lipoprotein receptor-related protein 4	0.8918	0.0155
212857_x_at	SUB1	SUB1 homolog (S. cerevisiae)	0.3092	0.0095
212862_at	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.9459	0.0124
212864_at	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.8612	0.0199
212920_at			0.5232	0.0057
212942_s_at	KIAA1199	KIAA1199	0.5423	0.0317
212959_s_at	GNPTAB	N-acetylglucosamine-1-phosphate transferase; alpha and beta subunits	1.4976	0.0156
212961_x_at	CXorf40B	chromosome X open reading frame 40B	1.1671	0.0027
212970_at		Full-length cDNA clone CS0DC015YK09 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	0.7211	0.0323
212972_x_at		Full-length cDNA clone CS0DC015YK09 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	0.176	0.0397
212985_at		Full-length cDNA clone CS0DC015YK09 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	1.0104	0.0084
213010_at	PRKCDBP	protein kinase C; delta binding protein	0.8476	0.0386
213012_at	NEDD4	neural precursor cell expressed; developmentally down-regulated 4	1.2632	0.0003
213056_at	FRMD4B	FERM domain containing 4B	1.3861	0.0094
213060_s_at	CHI3L2	chitinase 3-like 2	0.3336	0.0041
213073_at	ZFYVE26	zinc finger; FYVE domain containing 26	0.646	0.0172
213094_at	GPR126	G protein-coupled receptor 126	0.2955	0.0049
213095_x_at	AIF1	allograft inflammatory factor 1	1.7455	0.0014
213112_s_at	SQSTM1	sequestosome 1	1.296	0.0225
213114_at			0.2502	0.0201
213115_at	ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	1.3257	0.0044
213160_at	DOCK2	dedicator of cytokinesis 2	1.0422	0.0175
213188_s_at	MINA	MYC induced nuclear antigen	0.6388	0.0066
213189_at	MINA	MYC induced nuclear antigen	0.92	0.0368
213193_x_at	TRBC1	T cell receptor beta constant 1, T cell receptor beta variable 19	1.3934	0.0158
213203_at	SNAPC5	small nuclear RNA activating complex; polypeptide 5; 19kDa	0.5575	0.0357
213246_at	C14orf109	chromosome 14 open reading frame 109	0.6544	0.0369
213247_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	1.0068	0.0377
213282_at		CDNA FLJ39590 fis; clone SKNMC1000079	0.8553	0.026

213289_at		CDNA FLJ39590 fis; clone SKNMC1000079	0.957	0.0224
213315_x_at	CXorf40A	chromosome X open reading frame 40A	1.1798	0.0036
213317_at	CLIC5	chloride intracellular channel 5	0.6468	0.0275
213333_at	MDH2	malate dehydrogenase 2; NAD (mitochondrial)	0.9152	0.0334
213363_at		Homo sapiens; clone IMAGE:5244869; mRNA	0.4181	0.0328
213372_at	PAQR3	progestin and adipoQ receptor family member III	1.4942	0.0006
213379_at	COQ2	coenzyme Q2 homolog; prenyltransferase (yeast)	0.8133	0.0182
213415_at	CLIC2	chloride intracellular channel 2	1.8886	0.0048
213416_at	ITGA4	integrin; alpha 4 (antigen CD49D; alpha 4 subunit of VLA-4 receptor)	1.6762	0.0142
213419_at	APBB2	amyloid beta (A4) precursor protein-binding; family B; member 2 (Fe65-like)	0.5705	0.0011
213448_at		CDNA FLJ31688 fis; clone NT2RI2005520	0.5088	0.0388
213497_at	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	0.4717	0.0481
213498_at	CREB3L1	cAMP responsive element binding protein 3-like 1	0.1593	0.0169
213511_s_at	MTMR1	myotubularin related protein 1	0.6762	0.0474
213527_s_at	ZNF688	zinc finger protein 688	0.9972	0.0186
213529_at	ZNF688	zinc finger protein 688	0.379	0.0293
213535_s_at	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog; yeast)	0.4474	0.0153
213539_at	CD3D	CD3d molecule; delta (CD3-TCR complex)	0.9216	0.027
213546_at	DKFZp586I1420	hypothetical protein DKFZp586I1420	1.2187	0.0073
213566_at	RNASE6	ribonuclease; RNase A family; k6	2.1073	0.0054
213587_s_at	ATP6V0E2	ATPase; H+ transporting V0 subunit e2	1.7595	0.0086
213601_at	SLIT1	slit homolog 1 (Drosophila)	0.2337	0.0348
213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family; small GTP binding protein Rac2)	1.7639	0.0223
213618_at	CENTD1	centaurin; delta 1	1.3543	0.0047
213648_at	EXOSC7	exosome component 7	0.4871	0.0391
213667_at	SRCAP	Snf2-related CBP activator protein	0.3876	0.0087
213669_at	FCHO1	FCH domain only 1	0.6106	0.0214
213670_x_at	NSUN5B	NOL1/NOP2/Sun domain family; member 5B	0.82	0.0371
213689_x_at	FAM69A	family with sequence similarity 69; member A	1.3521	0.0206
213695_at	PON3	paraoxonase 3	0.6805	0.021
213712_at	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2; SUR4/Elo3; yeast)-like 2	0.5604	0.0216
213724_s_at	PDK2	pyruvate dehydrogenase kinase; isozyme 2	0.5949	0.0163
213733_at	MYO1F	myosin IF	0.8983	0.0445
213759_at	ARL4C	ADP-ribosylation factor-like 4C	0.1068	0.0403
213765_at	MFAP5	microfibrillar associated protein 5	0.284	0.0262
213778_x_at	ZNF276	zinc finger protein 276	0.3401	0.0324
213780_at	TCHH	trichohyalin	0.1994	0.0362
213795_s_at	PTPRA	protein tyrosine phosphatase; receptor type; A	0.8063	0.0111
213807_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.4607	0.0001
213816_s_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	0.223	0.0094
213820_s_at	STARD5	StAR-related lipid transfer (START) domain containing 5	0.5303	0.006
213824_at	OLIG2	oligodendrocyte lineage transcription factor 2	0.1222	0.0165
213830_at	TRA@	T cell receptor alpha locus	0.3168	0.0092
213835_x_at	GTPBP3	GTP binding protein 3 (mitochondrial)	0.3113	0.0396
213846_at	COX7C	cytochrome c oxidase subunit VIIc	0.7282	0.0267
213915_at	NKG7	natural killer cell group 7 sequence	0.9199	0.0019
213923_at	RAP2B	RAP2B; member of RAS oncogene family	1.0682	0.0171
213932_x_at	HLA-A	major histocompatibility complex; class I; A	0.3201	0.0144
213937_s_at	FTSJ1	FtsJ homolog 1 (E. coli)	0.6067	0.042
213975_s_at	LYZ	lysozyme (renal amyloidosis)	2.1947	0.0082
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	1.0923	0.0277
214000_s_at	RGS10	Regulator of G-protein signalling 10	0.1541	0.0439
214015_at	SOCS7	suppressor of cytokine signaling 7	0.162	0.0246
214045_at	LIAS	lipoic acid synthetase	1.1167	0.0211
214049_x_at	CD7	CD7 molecule	0.3677	0.003
214054_at	DOK2	docking protein 2; 56kDa	0.6799	0.0133

214058_at	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1; lung carcinoma derived (avian)	0.2655	0.039
214066_x_at	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	0.4203	0.0293
214084_x_at	LOC648998	neutrophil cytosolic factor 1; (chronic granulomatous disease; autosomal 1), neutrophil cytosolic factor 1B pseudogene, neutrophil cytosolic factor 1C pseudogene, similar to Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein) (NOXO2)	0.5037	0.0136
214100_x_at	NSUN5B	NOL1/NOP2/Sun domain family; member 5B	0.7165	0.0436
214108_at	MAX	MYC associated factor X	0.2017	0.0165
214112_s_at	CXorf40A	chromosome X open reading frame 40A, chromosome X open reading frame 40B	1.0298	0.0077
214147_at	C1orf175	chromosome 1 open reading frame 175	0.3076	0.0242
214151_s_at	CCPG1	cell cycle progression 1	1.3069	0.0437
214162_at	LOC284244	hypothetical protein LOC284244	0.2239	0.0188
214164_x_at	CA12	carbonic anhydrase XII	1.3282	0.0241
214175_x_at	PDLIM4	PDZ and LIM domain 4	0.5932	0.0436
214181_x_at	LST1	leukocyte specific transcript 1	1.0305	0.018
214186_s_at	3.8-1	MHC class I mRNA fragment 3.8-1	0.6042	0.0198
214205_x_at	GLRX3	glutaredoxin 3	0.2965	0.0349
214218_s_at	XIST	X (inactive)-specific transcript	3.2755	0.0378
214224_s_at	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting; 4 (parvulin)	0.68	0.0047
214253_s_at	DTNB	dystrobrevin; beta	0.273	0.0118
214264_s_at	C14orf143	chromosome 14 open reading frame 143	0.8848	0.0191
214272_at	CYLD	cylindromatosis (turban tumor syndrome)	0.5367	0.0152
214396_s_at	MBD2	methyl-CpG binding domain protein 2	0.1464	0.0031
214411_x_at	CTRB2	chymotrypsinogen B2	1.1727	0.05
214446_at	ELL2	elongation factor; RNA polymerase II; 2	0.5634	0.0156
214447_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	0.2044	0.0219
214448_x_at	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; beta	0.3083	0.023
214455_at	HIST1H2BC	histone cluster 1; H2bc, histone cluster 1; H2bg	0.8831	0.0346
214459_x_at	HLA-C	major histocompatibility complex; class I; C	0.5895	0.0019
214467_at	GPR65	G protein-coupled receptor 65	0.5833	0.0238
214469_at	HIST1H2AE	histone cluster 1; H2ae	1.0073	0.0451
214470_at	KLRB1	killer cell lectin-like receptor subfamily B; member 1	0.6388	0.0074
214482_at	ZBTB25	zinc finger and BTB domain containing 25	0.4123	0.0213
214483_s_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	0.8282	0.038
214498_at	ASIP	agouti signaling protein; nonagouti homolog (mouse)	0.1574	0.0263
214511_x_at	FCGR1B	Fc fragment of IgG; high affinity Ib; receptor (CD64)	1.5253	0.0087
214518_at	PDHA2	pyruvate dehydrogenase (lipoamide) alpha 2	0.1558	0.0049
214525_x_at	MLH3	mutL homolog 3 (E. coli)	0.8454	0.0011
214551_s_at	CD7	CD7 molecule	0.2846	0.045
214560_at	FPRL2	formyl peptide receptor-like 2	0.4632	0.0103
214567_s_at	XCL1	chemokine (C motif) ligand 1, chemokine (C motif) ligand 2	0.9001	0.0058
214574_x_at	LST1	leukocyte specific transcript 1	1.0822	0.0063
214617_at	PRF1	perforin 1 (pore forming protein)	0.9468	0.0075
214625_s_at	MINK1	misshapen-like kinase 1 (zebrafish)	0.2824	0.0491
214647_s_at	HFE	hemochromatosis	0.6177	0.0047
214669_x_at	IGKC	Immunoglobulin kappa constant	1.5135	0.0368
214681_at	GK	glycerol kinase	0.8983	0.0052
214691_x_at	FAM63B	family with sequence similarity 63; member B	0.5868	0.024
214703_s_at	MAN2B2	mannosidase; alpha; class 2B; member 2	0.945	0.0054
214719_at	SLC46A3	solute carrier family 46; member 3	1.3914	0.0461
214745_at	PLCH1	phospholipase C; eta 1	0.2087	0.0302
214749_s_at	ARMCX6	armadillo repeat containing; X-linked 6	0.5522	0.0124

214763_at	ACOT11	acyl-CoA thioesterase 11	0.644	0.0125
214765_s_at	ASAHL	N-acylsphingosine amidohydrolase (acid ceramidase)-like	1.3698	0.0133
214770_at	MSR1	macrophage scavenger receptor 1	1.5012	0.0096
214830_at	SLC38A6	solute carrier family 38; member 6	1.3432	0.0023
214835_s_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	0.4752	0.0333
214836_x_at	IGKC	immunoglobulin kappa constant, immunoglobulin kappa variable 1-5	1.2069	0.0287
214844_s_at	DOK5	docking protein 5	1.6264	0.0306
214847_s_at	GPSM3	G-protein signaling modulator 3 (AGS3-like; C. elegans)	0.2592	0.007
214860_at	SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger); member 7	0.1809	0.0281
214876_s_at	TUBGCP5	tubulin; gamma complex associated protein 5	1.0609	0.001
214896_at		MRNA full length insert cDNA clone EUROIMAGE 29222	1.556	0.0198
214923_at	ATP6V1D	ATPase; H+ transporting; lysosomal 34kDa; V1 subunit D	0.2869	0.0052
214992_s_at	DNASE2	deoxyribonuclease II; lysosomal	0.8714	0.0213
215051_x_at	AIF1	allograft inflammatory factor 1	1.9688	0.0014
215121_x_at	IGL@	immunoglobulin lambda locus, immunoglobulin lambda variable 2-14, immunoglobulin lambda variable 3-25, immunoglobulin lambda variable 4-3	1.6863	0.0425
215125_s_at	UGT1A1	UDP glucuronosyltransferase 1 family; polypeptide A1, UDP glucuronosyltransferase 1 family; polypeptide A10, UDP glucuronosyltransferase 1 family; polypeptide A3, UDP glucuronosyltransferase 1 family; polypeptide A4, UDP glucuronosyltransferase 1 family; polypeptide A5, UDP glucuronosyltransferase 1 family; polypeptide A6, UDP glucuronosyltransferase 1 family; polypeptide A7, UDP glucuronosyltransferase 1 family; polypeptide A8, UDP glucuronosyltransferase 1 family; polypeptide A9	1.7444	0.0403
215176_x_at	NTN2L	Netrin 2-like (chicken)	1.6776	0.0322
215193_x_at	HLA-DRB1	hypothetical protein LOC730415, major histocompatibility complex; class II; DR beta 1, major histocompatibility complex; class II; DR beta 3	2.0533	0.022
215210_s_at	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex), dihydrolipoamide S-succinyltransferase pseudogene (E2 component of 2-oxo-glutarate complex)	0.6933	0.0436
215261_at		Clone 23578 mRNA sequence	0.1564	0.0194
215263_at	ZXDA	zinc finger; X-linked; duplicated A, zinc finger; X-linked; duplicated B	0.434	0.0156
215313_x_at	HLA-A	major histocompatibility complex; class I; A	0.413	0.0067
215315_at	ZNF549	zinc finger protein 549	0.1625	0.028
215325_x_at	C19orf26	chromosome 19 open reading frame 26	0.1649	0.0161
215332_s_at	CD8B	CD8b molecule	0.1594	0.0499
215343_at	CCDC88C	coiled-coil domain containing 88C	0.1705	0.0392
215362_at		Clone 23738 mRNA sequence	0.1226	0.0193
215379_x_at	IGL@	immunoglobulin lambda joining 3, immunoglobulin lambda locus, immunoglobulin lambda variable 2-14, immunoglobulin lambda variable 3-25	1.7439	0.0374
215380_s_at	C7orf24	chromosome 7 open reading frame 24	0.4622	0.0184
215494_at		Apoptotic-related protein PCAR	0.105	0.0465
215495_s_at	SAMD4A	sterile alpha motif domain containing 4A	0.3338	0.0136
215565_at	DTNB	dystrobrevin; beta	0.2334	0.027
215602_at	FGD2	FYVE; RhoGEF and PH domain containing 2	0.1898	0.0056
215633_x_at	LST1	leukocyte specific transcript 1	0.9607	0.0104
215660_s_at	MAST2	microtubule associated serine/threonine kinase 2	0.2877	0.0191
215663_at	MBNL1	muscleblind-like (Drosophila)	0.1304	0.0149
215666_at	HLA-DRB4	major histocompatibility complex; class II; DR beta 4	0.1541	0.0233
215706_x_at	ZYX	zyxin	1.4202	0.0019
215732_s_at	DTX2	deltex homolog 2 (Drosophila)	0.3207	0.0202
215771_x_at	RET	ret proto-oncogene	0.3356	0.0166

215772_x_at	SUCLG2	succinate-CoA ligase; GDP-forming; beta subunit	0.5735	0.0155
215779_s_at	HIST1H2BG	histone cluster 1; H2bg	1.1522	0.0302
215784_at	CD1E	CD1e molecule	0.1784	0.017
215806_x_at	TARP	T cell receptor gamma constant 2, T cell receptor gamma variable 9, TCR gamma alternate reading frame protein	0.3596	0.0358
215843_s_at	TLL2	tolloid-like 2	0.2045	0.0082
215884_s_at	UBQLN2	ubiquilin 2	0.531	0.0103
215894_at	PTGDR	prostaglandin D2 receptor (DP)	1.174	0.027
215903_s_at	MAST2	microtubule associated serine/threonine kinase 2	0.5414	0.0492
215961_at	F12	coagulation factor XII (Hageman factor)	0.1256	0.0386
215967_s_at	LY9	lymphocyte antigen 9	0.2674	0.031
216013_at	ZXDB	zinc finger; X-linked; duplicated B	0.2404	0.0047
216014_s_at	ZXDA	zinc finger; X-linked; duplicated A, zinc finger; X-linked; duplicated B	0.153	0.0338
216020_at	IFIH1	Interferon induced with helicase C domain 1	0.1409	0.0452
216041_x_at	GRN	granulin	0.8537	0.0147
216044_x_at	FAM69A	family with sequence similarity 69; member A	1.2736	0.0191
216058_s_at	CYP2C19	cytochrome P450; family 2; subfamily C; polypeptide 19	0.1093	0.0077
216064_s_at	AGA	aspartylglucosaminidase	1.726	0.0013
216102_at	PHLDB1	pleckstrin homology-like domain; family B; member 1	0.1139	0.031
216162_at	SBNO1	Strawberry notch homolog 1 (Drosophila)	0.1128	0.0444
216191_s_at	TRA@	T cell receptor alpha locus, T cell receptor delta locus	0.2161	0.0379
216203_at	SPTLC2	serine palmitoyltransferase; long chain base subunit 2	0.1493	0.033
216207_x_at	IGKV1D-13	immunoglobulin kappa variable 1D-13	1.1906	0.0418
216231_s_at	B2M	beta-2-microglobulin	0.4803	0.0002
216250_s_at	LPXN	leupaxin	1.1437	0.0485
216323_x_at	TUBA3D	tubulin; alpha 3d	0.2353	0.0219
216352_x_at	PCDHGA3	protocadherin gamma subfamily A; 3	1.0192	0.0015
216365_x_at	CPVL	carboxypeptidase; vitellogenic-like, immunoglobulin lambda locus	0.1176	0.0496
216430_x_at		Clone CPRF1-T2 immunoglobulin lambda chain VJ region; (IGL)	0.2133	0.0232
216440_at	ERC1	ELKS/RAB6-interacting/CAST family member 1	0.2007	0.0062
216526_x_at	HLA-C	major histocompatibility complex; class I; C	0.5528	0.0048
216532_x_at	LOC728344	similar to Thioredoxin-like protein 2 (PKC-interacting cousin of thioredoxin) (PKC-theta-interacting protein) (PKCq-interacting protein)	0.3749	0.0486
216548_x_at	HMG4L	high-mobility group (nonhistone chromosomal) protein 4-like	1.0492	0.0062
216564_at			0.1395	0.0184
216629_at	SRRM2	Serine/arginine repetitive matrix 2	0.2352	0.0213
216661_x_at	CYP2C9	Cytochrome P450; family 2; subfamily C; polypeptide 9	0.1438	0.0281
216667_at	LOC643332	ribonuclease; RNase A family; 2 (liver; eosinophil-derived neurotoxin), similar to Nonsecretory ribonuclease precursor (Ribonuclease US) (Eosinophil-derived neurotoxin) (RNase UpI-2) (Ribonuclease 2) (RNase 2)	0.1183	0.0349
216690_at	OR7C1	olfactory receptor; family 7; subfamily C; member 1	0.2276	0.0156
216731_s_at		CDNA FLJ13628 fis; clone PLACE1011054	0.1809	0.041
216750_at	APBB2	amyloid beta (A4) precursor protein-binding; family B; member 2 (Fe65-like)	0.1238	0.0276
216807_at	KIAA1751	KIAA1751	0.1682	0.0459
216841_s_at	SOD2	superoxide dismutase 2; mitochondrial	0.8736	0.0496
216845_x_at	TNRC21	trinucleotide repeat containing 21	0.1263	0.045
216862_s_at	MTCP1	mature T-cell proliferation 1	0.6089	0.0442
216880_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	0.1185	0.0317
216919_at	TP53I11	tumor protein p53 inducible protein 11	0.145	0.0133
216920_s_at	TARP	T cell receptor gamma constant 2, T cell receptor gamma variable 9, TCR gamma alternate reading frame protein	0.6119	0.0145
216942_s_at	CD58	CD58 molecule	1.4566	0.0253
216950_s_at	FCGR1A	Fc fragment of IgG; high affinity Ia; receptor (CD64)	1.1475	0.0257

216981_x_at	SPN	sialophorin (leukosialin; CD43)	0.1666	0.0422
217000_at	KRT18P50	keratin 18 pseudogene 50	0.2085	0.0264
217007_s_at	ADAM15	ADAM metallopeptidase domain 15	0.2242	0.0265
217022_s_at	IGHA1	immunoglobulin heavy constant alpha 1, immunoglobulin heavy constant alpha 2 (A2m marker)	1.7431	0.0433
217023_x_at	TPSAB1	tryptase alpha/beta 1, tryptase beta 2	0.7157	0.0468
217043_s_at	MFN1	mitofusin 1	0.7907	0.0151
217048_at	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	0.1877	0.004
217078_s_at	CD300A	CD300a molecule	0.3544	0.0302
217106_x_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	0.5988	0.0123
217107_at	LOC442257	similar to 40S ribosomal protein S4; Y isoform 2	0.257	0.0175
217125_at			0.69	0.0316
217135_x_at			0.1903	0.0376
217143_s_at	TRA@	T cell receptor alpha locus, T cell receptor delta locus	0.4525	0.003
217157_x_at		Immunoglobulin kappa chain; V-region (SPK.3)	0.3343	0.0258
217168_s_at	HERPUD1	homocysteine-inducible; endoplasmic reticulum stress-inducible; ubiquitin-like domain member 1	0.5282	0.0267
217216_x_at	MLH3	mutL homolog 3 (E. coli)	0.8218	0.0335
217235_x_at		Immunoglobulin (mAb56) light chain V region mRNA; partial sequence	0.3792	0.0252
217239_x_at	CPVL	Carboxypeptidase; vitellogenic-like, Immunoglobulin heavy chain; partial; clone VH3-7	0.1451	0.0165
217249_x_at			0.3477	0.0277
217258_x_at	IVD	Isovaleryl Coenzyme A dehydrogenase	0.3753	0.0446
217281_x_at	IL8	Interleukin 8	0.4251	0.0218
217299_s_at	NBN	nibrin	0.5854	0.0198
217305_s_at	SAC	testicular soluble adenylyl cyclase	0.144	0.007
217307_at			0.2401	0.0081
217329_x_at			0.6398	0.0011
217334_at	OR2J3	olfactory receptor; family 2; subfamily J; member 3	0.1713	0.0027
217349_s_at	LMO6	LIM domain only 6	0.4968	0.003
217354_s_at	HPS1	Hermansky-Pudlak syndrome 1, similar to Hermansky-Pudlak syndrome 1 protein isoform b	0.3231	0.0004
217362_x_at	HLA-DRB6	major histocompatibility complex; class II; DR beta 6 (pseudogene)	0.9165	0.0063
217372_at			0.1029	0.0047
217374_x_at	TRGV5	T cell receptor gamma variable 5	0.1203	0.0222
217379_at	LOC442171	similar to ribosomal protein L10	0.4146	0.0188
217436_x_at	LOC730399	hypothetical protein LOC730399, hypothetical protein LOC731974	0.9482	0.0046
217450_at			0.1055	0.0157
217456_x_at	HLA-E	major histocompatibility complex; class I; E	0.5549	0.0063
217475_s_at	LIMK2	LIM domain kinase 2	0.2522	0.0019
217478_s_at	HLA-DMA	major histocompatibility complex; class II; DM alpha	2.6126	0.0015
217484_at	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	0.2199	0.0064
217491_x_at	COX7C	cytochrome c oxidase subunit VIIc	0.3582	0.0191
217502_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	0.9265	0.0431
217511_at	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	0.3164	0.0259
217520_x_at	LOC731884	Similar to programmed cell death 6 interacting protein	0.7924	0.0473
217559_at	RPL10L	ribosomal protein L10-like	0.242	0.0161
217606_at		MRNA; cDNA DKFZp686P24158 (from clone DKFZp686P24158)	0.5071	0.0436
217618_x_at	HUS1	HUS1 checkpoint homolog (S. pombe)	0.4795	0.003
217621_at			0.144	0.0473
217629_at		Transcribed locus	0.1263	0.0202
217685_at	SLC16A3	Solute carrier family 16; member 3 (monocarboxylic acid transporter 4)	0.1479	0.0359
217727_x_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.2895	0.0385

217773_s_at	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 4; 9kDa	0.4661	0.0057
217784_at	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	0.8799	0.0277
217785_s_at	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	1.2703	0.0245
217790_s_at	SSR3	signal sequence receptor; gamma (translocon-associated protein gamma)	0.7477	0.0081
217809_at	BZW2	basic leucine zipper and W2 domains 2	0.9626	0.007
217827_s_at	SPG21	spastic paraplegia 21 (autosomal recessive; Mast syndrome)	0.4458	0.0268
217835_x_at	C20orf24	chromosome 20 open reading frame 24	0.6696	0.0015
217838_s_at	EVL	Enah/Vasp-like	0.9222	0.0151
217865_at	RNF130	ring finger protein 130	0.949	0.0224
217933_s_at	LAP3	leucine aminopeptidase 3	0.7073	0.0037
217956_s_at	ENOPH1	enolase-phosphatase 1	0.3405	0.0459
217957_at	C16orf80	chromosome 16 open reading frame 80	0.722	0.0077
217961_at	SLC25A38	solute carrier family 25; member 38	0.5941	0.0324
217962_at	NOLA3	nucleolar protein family A; member 3 (H/ACA small nucleolar RNPs)	0.7615	0
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	0.2692	0.0363
217972_at	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	0.4986	0.0292
217976_s_at	DYNC1LI1	dynein; cytoplasmic 1; light intermediate chain 1	0.7242	0.0171
217977_at	SEPX1	selenoprotein X; 1	1.0181	0.0121
217979_at	TSPAN13	Tetraspanin 13	0.6025	0.0232
217990_at	GMPR2	guanosine monophosphate reductase 2	0.882	0.007
217993_s_at	MAT2B	methionine adenosyltransferase II; beta	0.6277	0.0027
217995_at	SQRDL	sulfide quinone reductase-like (yeast)	1.8107	0.006
218023_s_at	FAM53C	family with sequence similarity 53; member C	0.8263	0.0048
218027_at	MRPL15	mitochondrial ribosomal protein L15	0.7397	0.0036
218034_at	FIS1	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	0.4932	0.025
218042_at	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	0.3704	0.0353
218059_at	ZNF706	zinc finger protein 706	0.4388	0.0318
218069_at	XTP3TPA	XTP3-transactivated protein A	1.0018	0.0005
218076_s_at	ARHGAP17	Rho GTPase activating protein 17	0.7206	0.0038
218081_at	C20orf27	chromosome 20 open reading frame 27	0.4789	0.0237
218086_at	NPDC1	neural proliferation; differentiation and control; 1	1.062	0.0455
218094_s_at	C20orf169-DBNDD2	C20orf169-DBNDD2 readthrough transcript, dysbindin (dystrobrevin binding protein 1) domain containing 2	1.3224	0.0058
218109_s_at	MFSD1	major facilitator superfamily domain containing 1	0.6135	0.0034
218112_at	MRPS34	mitochondrial ribosomal protein S34	0.6795	0.0113
218131_s_at	GATAD2A	GATA zinc finger domain containing 2A	0.7003	0.0127
218138_at	MKKS	McKusick-Kaufman syndrome	0.9246	0.0039
218143_s_at	SCAMP2	secretory carrier membrane protein 2	0.6627	0.0139
218161_s_at	CLN6	ceroid-lipofuscinosis; neuronal 6; late infantile; variant	0.6866	0.0033
218163_at	MCTS1	malignant T cell amplified sequence 1	0.791	0.0097
218200_s_at	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 2; 8kDa	0.4923	0.0021
218201_at	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 2; 8kDa	0.6169	0.0066
218219_s_at	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	0.7339	0.0487
218230_at	ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)	0.4467	0.0245
218232_at	C1QA	complement component 1; q subcomponent; A chain	1.5955	0.0228
218246_at	C1orf166	chromosome 1 open reading frame 166	0.587	0.0215
218248_at	FAM111A	family with sequence similarity 111; member A	0.7091	0.0324
218256_s_at	NUP54	nucleoporin 54kDa	0.4865	0.0237
218267_at	CINP	cyclin-dependent kinase 2-interacting protein	0.3721	0.0081
218282_at	EDEM2	ER degradation enhancer; mannosidase alpha-like 2	0.6786	0.0206
218317_x_at	GIYD1	GIY-YIG domain containing 1, GIY-YIG domain containing 2	0.7125	0.036

218320_s_at	NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 11; 17.3kDa	0.4962	0.0253
218329_at	PRDM4	PR domain containing 4	1.0194	0.0176
218347_at	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	0.7564	0.0184
218351_at	COMMD8	COMM domain containing 8	0.819	0.0066
218354_at	TRAPPC2L	trafficking protein particle complex 2-like	0.7381	0.0425
218356_at	FTSJ2	FtsJ homolog 2 (E. coli)	0.4286	0.0349
218384_at	CARHSP1	calcium regulated heat stable protein 1; 24kDa	1.1341	0.0081
218395_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	0.4727	0.0281
218408_at	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	0.8293	0.0012
218417_s_at	FLJ20489	hypothetical protein FLJ20489	1.1736	0.0164
218485_s_at	SLC35C1	solute carrier family 35; member C1	0.2086	0.0449
218495_at	UXT	ubiquitously-expressed transcript	0.6614	0.0138
218506_x_at	N-PAC	cytokine-like nuclear factor n-pac	0.4781	0.0346
218513_at	FLJ11184	hypothetical protein FLJ11184	0.431	0.0434
218526_s_at	RANGRF	RAN guanine nucleotide release factor	0.5695	0.0168
218534_s_at	AGGF1	angiogenic factor with G patch and FHA domains 1	0.7701	0.0149
218540_at	THTPA	thiamine triphosphatase	0.6009	0.0353
218543_s_at	PARP12	poly (ADP-ribose) polymerase family; member 12	1.4546	0.0029
218544_s_at	RCL1	RNA terminal phosphate cyclase-like 1	0.4965	0.0315
218557_at	NIT2	nitrilase family; member 2	0.7804	0.0041
218571_s_at	CHMP4A	chromatin modifying protein 4A	0.5406	0.014
218572_at	CHMP4A	chromatin modifying protein 4A	0.6462	0.0112
218580_x_at	AURKAIP1	aurora kinase A interacting protein 1, similar to Cyclin-L2 (Paneth cell-enhanced expression protein)	0.4646	0.045
218583_s_at	DCUN1D1	DCN1; defective in cullin neddylation 1; domain containing 1 (S. cerevisiae)	0.5167	0.0032
218598_at	RINT1	RAD50 interactor 1	0.649	0.0387
218606_at	ZDHHC7	zinc finger; DHHC-type containing 7	0.677	0.0051
218607_s_at	SDAD1	SDA1 domain containing 1	0.7229	0.0191
218609_s_at	NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	0.8312	0.0021
218616_at	INTS12	integrator complex subunit 12	0.469	0.0195
218619_s_at	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.6627	0.019
218654_s_at	MRPS33	mitochondrial ribosomal protein S33	0.5788	0.0179
218660_at	DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	0.7527	0.0456
218668_s_at	RAP2C	RAP2C; member of RAS oncogene family	0.4971	0.0184
218669_at	RAP2C	RAP2C; member of RAS oncogene family	0.4342	0.0451
218670_at	PUS1	pseudouridylate synthase 1	0.5983	0.0357
218701_at	LACTB2	lactamase; beta 2	1.1529	0.0183
218703_at	SEC22A	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	0.3299	0.0484
218708_at	NXT1	NTF2-like export factor 1	0.6262	0.008
218719_s_at	GINS3	GINS complex subunit 3 (Psf3 homolog)	1.078	0.0179
218722_s_at	CCDC51	coiled-coil domain containing 51	0.5164	0.0243
218731_s_at	LOC727901	similar to von Willebrand factor A domain-related protein isoform 1, von Willebrand factor A domain containing 1	0.7741	0.0222
218733_at	MSL2L1	male-specific lethal 2-like 1 (Drosophila)	0.6672	0.0345
218739_at	ABHD5	abhydrolase domain containing 5	0.604	0.0486
218746_at	TAPBPL	TAP binding protein-like	1.1033	0.004
218747_s_at	TAPBPL	TAP binding protein-like	1.2642	0.0019
218757_s_at	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	0.9128	0.0464
218764_at	PRKCH	protein kinase C; eta	1.4555	0.0467
218797_s_at	LOC644124	similar to NAD-dependent deacetylase sirtuin-7 (SIR2-like protein 7), sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	0.6481	0.0216
218800_at	SRD5A2L	steroid 5 alpha-reductase 2-like	0.3472	0.0124
218802_at	CCDC109B	coiled-coil domain containing 109B	1.8512	0.0012
218805_at	GIMAP5	GTPase; IMAP family member 5	0.9113	0.0176

218806_s_at	VAV3	vav 3 guanine nucleotide exchange factor	0.2965	0.002
218807_at	VAV3	vav 3 guanine nucleotide exchange factor	0.7367	0.0132
218816_at	LRRC1	leucine rich repeat containing 1	0.6584	0.0327
218821_at	NPEPL1	aminopeptidase-like 1	0.5123	0.0068
218822_s_at	NPEPL1	aminopeptidase-like 1	0.4688	0.0037
218841_at	ASB8	ankyrin repeat and SOCS box-containing 8	0.687	0.0374
218853_s_at	MOSPD1	motile sperm domain containing 1	0.8091	0.0465
218854_at	DSE	dermatan sulfate epimerase	0.9342	0.0092
218860_at	NOC4L	nucleolar complex associated 4 homolog (S. cerevisiae)	0.4471	0.0346
218868_at	ACTR3B	ARP3 actin-related protein 3 homolog B (yeast)	0.5308	0.0432
218870_at	ARHGAP15	Rho GTPase activating protein 15	1.3131	0.0344
218903_s_at	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B	0.9285	0.0163
218910_at	TMEM16K	transmembrane protein 16K	0.7808	0.0432
218912_at	GCC1	GRIP and coiled-coil domain containing 1	1.2809	0.0014
218926_at	MYNN	myoneurin	0.458	0.0489
218927_s_at	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	0.6838	0.0204
218933_at	SPATA5L1	spermatogenesis associated 5-like 1	0.846	0.0007
218937_at	ZNF434	zinc finger protein 434	0.9582	0.0005
218956_s_at	PTCD1	pentatricopeptide repeat domain 1	0.5307	0.0403
218958_at	C19orf60	chromosome 19 open reading frame 60	0.5276	0.0491
218968_s_at	ZFP64	zinc finger protein 64 homolog (mouse)	0.7658	0.022
218971_s_at	WDR91	WD repeat domain 91	1.1194	0.002
218973_at	EFTUD1	elongation factor Tu GTP binding domain containing 1	1.5608	0.0002
218982_s_at	MRPS17	mitochondrial ribosomal protein S17	0.6829	0.0149
218986_s_at	FLJ20035	hypothetical protein FLJ20035	1.1544	0.0078
218987_at	ATF7IP	activating transcription factor 7 interacting protein	0.9675	0.0379
218989_x_at	SLC30A5	solute carrier family 30 (zinc transporter); member 5	0.4046	0.0435
218992_at	C9orf46	chromosome 9 open reading frame 46	1.0444	0.0102
218999_at	TMEM140	transmembrane protein 140	1.7768	0.0014
219010_at	C1orf106	chromosome 1 open reading frame 106	0.3174	0.0094
219014_at	PLAC8	placenta-specific 8	1.0218	0.0352
219015_s_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	1.6185	0.0052
219047_s_at	ZNF668	zinc finger protein 668	0.4132	0.0378
219061_s_at	LAGE3	L antigen family; member 3	1.4161	0.0003
219066_at	PPCDC	phosphopantothenoylcysteine decarboxylase	1.4549	0.0007
219072_at	BCL7C	B-cell CLL/lymphoma 7C	0.6871	0.007
219083_at	SHQ1	SHQ1 homolog (S. cerevisiae)	0.921	0.006
219088_s_at	ZNF576	zinc finger protein 576	0.8639	0.008
219089_s_at	ZNF576	zinc finger protein 576	0.9666	0.0011
219091_s_at	MMRN2	multimerin 2	1.2108	0.0168
219106_s_at	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	0.1597	0.0422
219110_at	NOLA1	nucleolar protein family A; member 1 (H/ACA small nucleolar RNPs)	0.4997	0.0081
219143_s_at	RPP25	ribonuclease P/MRP 25kDa subunit	1.4369	0.0095
219149_x_at	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	0.3986	0.0236
219159_s_at	SLAMF7	SLAM family member 7	0.3134	0.0461
219183_s_at	PSCD4	pleckstrin homology; Sec7 and coiled-coil domains 4	0.7139	0.0188
219191_s_at	BIN2	bridging integrator 2	0.5882	0.0041
219200_at	FASTKD3	FAST kinase domains 3	0.778	0.0336
219207_at	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	0.5046	0.0076
219210_s_at	RAB8B	RAB8B; member RAS oncogene family	0.8726	0.0095
219211_at	LOC727996	similar to ubiquitin specific peptidase 18, ubiquitin specific peptidase 18	1.1524	0.0173
219229_at	SLCO3A1	solute carrier organic anion transporter family; member 3A1	1.666	0
219235_s_at	PHACTR4	phosphatase and actin regulator 4	0.654	0.033
219243_at	GIMAP4	GTPase; IMAP family member 4	0.8419	0.0298
219247_s_at	ZDHHC14	zinc finger; DHHC-type containing 14	0.8006	0.0244
219252_s_at	GEMIN8	gem (nuclear organelle) associated protein 8	0.603	0.0222

219258_at	TIPIN	TIMELESS interacting protein	1.1318	0.0021
219261_at	C7orf26	chromosome 7 open reading frame 26	0.529	0.0025
219270_at	CHAC1	ChaC; cation transport regulator homolog 1 (E. coli)	0.3896	0.037
219283_at	C1GALT1C1	C1GALT1-specific chaperone 1	0.8997	0.0191
219288_at	C3orf14	chromosome 3 open reading frame 14	1.8973	0.0136
219291_at	DTWD1	DTW domain containing 1	0.5473	0.0161
219297_at	WDR44	WD repeat domain 44	0.6343	0.0297
219321_at	MPP5	membrane protein; palmitoylated 5 (MAGUK p55 subfamily member 5)	0.9862	0.0081
219334_s_at	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	0.2846	0.0125
219335_at	ARMCX5	armadillo repeat containing; X-linked 5	1.2972	0.0156
219354_at	KLHL26	kelch-like 26 (Drosophila)	0.8	0.0127
219356_s_at	CHMP5	chromatin modifying protein 5	0.5134	0.0333
219384_s_at	ADAT1	adenosine deaminase; tRNA-specific 1	0.8234	0.0186
219385_at	SLAMF8	SLAM family member 8	0.9196	0.0069
219386_s_at	SLAMF8	SLAM family member 8	1.4248	0.0222
219405_at	TRIM68	tripartite motif-containing 68	0.8347	0.0283
219414_at	CLSTN2	calsyntenin 2	0.291	0.0428
219427_at	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	0.7421	0.0046
219439_at	C1GALT1	core 1 synthase; glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase; 1	1.5229	0.0007
219449_s_at	TMEM70	transmembrane protein 70	0.7562	0.017
219456_s_at	RIN3	Ras and Rab interactor 3	0.48	0.0093
219457_s_at	RIN3	Ras and Rab interactor 3	1.1152	0.0014
219462_at	TMEM53	transmembrane protein 53	1.1493	0.0064
219481_at	TTC13	tetratricopeptide repeat domain 13	0.5069	0.0462
219485_s_at	PSMD10	proteasome (prosome; macropain) 26S subunit; non-ATPase; 10	0.5121	0.019
219505_at	CECR1	cat eye syndrome chromosome region; candidate 1	2.462	0.0091
219508_at	GCNT3	glucosaminyl (N-acetyl) transferase 3; mucin type	1.4939	0.0126
219526_at	C14orf169	chromosome 14 open reading frame 169	0.9007	0.0152
219529_at	CLIC3	chloride intracellular channel 3	0.299	0.0359
219538_at	WDR5B	WD repeat domain 5B	1.287	0.0102
219540_at	ZNF267	zinc finger protein 267	1.01	0.0033
219546_at	BMP2K	BMP2 inducible kinase	0.9629	0.0158
219564_at	KCNJ16	potassium inwardly-rectifying channel; subfamily J; member 16	0.8723	0.0157
219568_x_at	SOX18	SRY (sex determining region Y)-box 18	0.2888	0.0257
219574_at	1-Mar	membrane-associated ring finger (C3HC4) 1	1.2487	0.0065
219575_s_at	COG8	component of oligomeric golgi complex 8, peptide deformylase (mitochondrial)	0.7182	0.0076
219582_at	OGFRL1	opioid growth factor receptor-like 1	0.5238	0.0306
219593_at	SLC15A3	solute carrier family 15; member 3	1.1173	0.0447
219607_s_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	1.845	0.0296
219609_at	WDR25	WD repeat domain 25	0.3021	0.0221
219618_at	IRAK4	interleukin-1 receptor-associated kinase 4	0.5551	0.0498
219623_at	ACTR5	ARP5 actin-related protein 5 homolog (yeast)	0.6206	0.021
219647_at	POPDC2	popeye domain containing 2	0.2839	0.0475
219649_at	ALG6	asparagine-linked glycosylation 6 homolog (S. cerevisiae; alpha-1;3-glucosyltransferase)	0.9098	0.0196
219654_at	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member A	0.9826	0.0297
219661_at	RANBP17	RAN binding protein 17	0.5363	0.033
219666_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	2.297	0.0023
219673_at	MCM9	minichromosome maintenance complex component 9	0.7717	0.0085
219675_s_at	UXS1	UDP-glucuronate decarboxylase 1	1.309	0.008
219709_x_at	C16orf24	chromosome 16 open reading frame 24	0.7705	0.0283
219715_s_at	TDP1	tyrosyl-DNA phosphodiesterase 1	0.7151	0.0028
219716_at	APOL6	apolipoprotein L; 6	0.5316	0.026
219725_at	TREM2	triggering receptor expressed on myeloid cells 2	1.4761	0.0313

219760_at	LIN7B	lin-7 homolog B (C. elegans)	0.6608	0.006
219777_at	GIMAP6	GTPase; IMAP family member 6	1.0674	0.0268
219784_at	FBXO31	F-box protein 31	0.3658	0.0365
219788_at	PILRA	paired immunoglobin-like type 2 receptor alpha	0.2676	0.0072
219797_at	MGAT4A	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme A	0.4878	0.001
219798_s_at	MEPCE	methylphosphate capping enzyme	0.7069	0.0326
219800_s_at	THNSL1	threonine synthase-like 1 (S. cerevisiae)	0.3859	0.0217
219806_s_at	C11orf75	chromosome 11 open reading frame 75	1.3944	0.0241
219815_at	GAL3ST4	galactose-3-O-sulfotransferase 4	0.4568	0.014
219821_s_at	GFOD1	glucose-fructose oxidoreductase domain containing 1	0.7702	0.018
219837_s_at	CYTL1	cytokine-like 1	0.7525	0.0053
219864_s_at	RCAN3	RCAN family member 3	0.1539	0.0215
219866_at	CLIC5	chloride intracellular channel 5	0.2956	0.0195
219882_at	TTLL7	tubulin tyrosine ligase-like family; member 7	0.4891	0.0433
219892_at	TM6SF1	transmembrane 6 superfamily member 1	0.8238	0.0136
219902_at	BHMT2	betaine-homocysteine methyltransferase 2	1.8095	0.026
219921_s_at	DOCK5	dedicator of cytokinesis 5	0.6492	0.0161
219926_at	POPDC3	popeye domain containing 3	1.061	0.0114
219946_x_at	MYH14	myosin; heavy chain 14	0.3624	0.035
219968_at	ZNF589	zinc finger protein 589	0.7	0.0293
219994_at	APBB1IP	amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	0.2182	0.0151
219999_at	MAN2A2	mannosidase; alpha; class 2A; member 2	0.7644	0.0316
220005_at	P2RY13	purinergic receptor P2Y; G-protein coupled; 13	1.0284	0.0003
220021_at	TMC7	transmembrane channel-like 7	0.221	0.0256
220032_at	FLJ21986	hypothetical protein FLJ21986	0.7909	0.0286
220033_at			0.5548	0.0207
220052_s_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	0.7194	0.0001
220055_at	ZNF287	zinc finger protein 287	0.2517	0.037
220059_at	STAP1	signal transducing adaptor family member 1	0.1675	0.0143
220067_at	SPTBN5	spectrin; beta; non-erythrocytic 5	0.1406	0.0393
220103_s_at	MRPS18C	mitochondrial ribosomal protein S18C	0.202	0.0088
220108_at	GNA14	guanine nucleotide binding protein (G protein); alpha 14	0.5128	0.0313
220122_at	MCTP1	multiple C2 domains; transmembrane 1	1.6298	0.0028
220136_s_at	CRYBA2	crystallin; beta A2	0.1216	0.0292
220146_at	TLR7	toll-like receptor 7	1.0139	0.012
220150_s_at	C6orf60	chromosome 6 open reading frame 60	0.9941	0.0064
220162_s_at	CARD9	caspase recruitment domain family; member 9	0.3202	0.0366
220173_at	C14orf45	chromosome 14 open reading frame 45	0.5083	0.0318
220183_s_at	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0.9214	0.0109
220189_s_at	MGAT4B	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme B	1.0418	0.0499
220229_s_at	AP4E1	adaptor-related protein complex 4; epsilon 1 subunit	0.1458	0.0226
220258_s_at	WDR79	WD repeat domain 79	0.2503	0.0399
220261_s_at	ZDHHC4	zinc finger; DHHC-type containing 4	0.7538	0.0279
220307_at	CD244	CD244 molecule; natural killer cell receptor 2B4	0.2244	0.0125
220330_s_at	SAMSN1	SAM domain; SH3 domain and nuclear localization signals 1	1.542	0.0127
220358_at	SNFT	Jun dimerization protein p21SNFT	0.5854	0.0134
220364_at	FLJ11235	hypothetical protein FLJ11235	0.3559	0.0096
220416_at	ATP8B4	ATPase; Class I; type 8B; member 4	0.9085	0.0077
220440_at	LGALS13	lectin; galactoside-binding; soluble; 13 (galectin 13)	0.1244	0.0209
220448_at	KCNK12	potassium channel; subfamily K; member 12	1.2644	0.0339
220470_at	BET1L	blocked early in transport 1 homolog (S. cerevisiae)-like	0.2378	0.0394
220474_at	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier); member 21	0.281	0.0385
220491_at	HAMP	hepcidin antimicrobial peptide	0.7295	0.0358
220535_at	FAM90A1	family with sequence similarity 90; member A1	0.2445	0.0002
220569_at			0.1242	0.0482
220588_at	BCAS4	breast carcinoma amplified sequence 4	0.4269	0.0279

220643_s_at	FAIM	Fas apoptotic inhibitory molecule	1.1095	0.0047
220741_s_at	PPA2	pyrophosphatase (inorganic) 2	0.6021	0.0081
220753_s_at	CRYL1	crystallin; lambda 1	1.0957	0.0099
220756_s_at	GPR172B	G protein-coupled receptor 172B	0.2129	0.0034
220789_s_at	TBRG4	transforming growth factor beta regulator 4	0.5	0.0058
220815_at	CTNNA3	catenin (cadherin-associated protein); alpha 3	0.1123	0.0171
220832_at	TLR8	toll-like receptor 8	0.2195	0.0041
220929_at	GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	0.1557	0.0146
220953_s_at	MTMR12	myotubularin related protein 12	0.3378	0.0108
220961_s_at	TBRG4	transforming growth factor beta regulator 4	0.4907	0.042
220980_s_at	ADPGK	ADP-dependent glucokinase	0.584	0.0022
220987_s_at	C11orf17	NUAK family; SNF1-like kinase; 2, chromosome 11 open reading frame 17	0.8557	0.0313
220994_s_at	STXBP6	syntaxin binding protein 6 (amisyn)	1.1342	0.0075
221019_s_at	COLEC12	collectin sub-family member 12	1.6903	0.0421
221021_s_at	CTNNBL1	catenin; beta like 1	0.3316	0.0458
221022_s_at	PMFBP1	polyamine modulated factor 1 binding protein 1	0.1692	0.0375
221027_s_at	PLA2G12A	phospholipase A2; group XIIA	1.0275	0.0154
221029_s_at	WNT5B	wingless-type MMTV integration site family; member 5B	0.732	0.0299
221036_s_at	APH1B	anterior pharynx defective 1 homolog B (C. elegans)	0.7255	0.037
221041_s_at	SLC17A5	solute carrier family 17 (anion/sugar transporter); member 5	1.6496	0.0063
221098_x_at	UTP14A	UTP14; U3 small nucleolar ribonucleoprotein; homolog A (yeast)	0.264	0.0011
221122_at	HRASLS2	HRAS-like suppressor 2	0.3467	0.0029
221135_s_at	ASTE1	asteroid homolog 1 (Drosophila)	1.0881	0.008
221156_x_at	CCPG1	cell cycle progression 1	0.8277	0.0096
221181_at	LOC642452	hypothetical LOC642452, hypothetical protein LOC651791	0.5293	0.0132
221218_s_at	TPK1	thiamin pyrophosphokinase 1	2.724	0
221223_x_at	CISH	cytokine inducible SH2-containing protein	0.6823	0.0199
221224_s_at	DCAKD	dephospho-CoA kinase domain containing	0.181	0.0058
221227_x_at	COQ3	coenzyme Q3 homolog; methyltransferase (S. cerevisiae)	0.4757	0.0122
221232_s_at	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	0.2548	0.0434
221238_at	NSBP1	nucleosomal binding protein 1	0.4017	0.0375
221241_s_at	BCL2L14	BCL2-like 14 (apoptosis facilitator)	0.1157	0.0326
221265_s_at	C15orf44	chromosome 15 open reading frame 44	0.6184	0.0024
221297_at	GPRC5D	G protein-coupled receptor; family C; group 5; member D	0.119	0.0467
221304_at	UGT1A10	UDP glucuronosyltransferase 1 family; polypeptide A10	0.1681	0.0246
221314_at	GDF9	growth differentiation factor 9	0.2463	0.0205
221319_at	PCDHB8	protocadherin beta 8	0.2026	0.0293
221320_at	BCL2L10	BCL2-like 10 (apoptosis facilitator)	0.1626	0.035
221345_at	FFAR2	free fatty acid receptor 2	0.1339	0.0342
221410_x_at	PCDHB3	protocadherin beta 3	0.3822	0.0092
221413_at	KCNAB3	potassium voltage-gated channel; shaker-related subfamily; beta member 3	0.119	0.0151
221434_s_at	C14orf156	chromosome 14 open reading frame 156	0.6783	0.0147
221466_at	P2RY4	pyrimidinergic receptor P2Y; G-protein coupled; 4	0.1189	0.0141
221511_x_at	CCPG1	cell cycle progression 1	1.4109	0.0082
221513_s_at	UTP14A	UTP14; U3 small nucleolar ribonucleoprotein; homolog A (yeast), UTP14; U3 small nucleolar ribonucleoprotein; homolog C (yeast)	1.1039	0.0071
221514_at	UTP14A	UTP14; U3 small nucleolar ribonucleoprotein; homolog A (yeast)	1.3054	0.0008
221535_at	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	1.0146	0.0037
221536_s_at	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	1.1698	0
221578_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	0.1822	0.0265
221581_s_at	LAT2	linker for activation of T cells family; member 2	0.7581	0.002
221601_s_at	FAIM3	Fas apoptotic inhibitory molecule 3	0.5266	0.0363
221602_s_at	FAIM3	Fas apoptotic inhibitory molecule 3	0.1588	0.0379

221606_s_at	NSBP1	nucleosomal binding protein 1	1.3623	0.0271
221620_s_at	APOO	apolipoprotein O	1.2057	0.0016
221623_at	BCAN	brevican	0.1006	0.0489
221628_s_at	N-PAC	cytokine-like nuclear factor n-pac	0.4332	0.0183
221651_x_at	IGKC	immunoglobulin kappa constant, immunoglobulin kappa variable 1-5, immunoglobulin kappa variable 2-24	1.9826	0.0268
221671_x_at	IGKC	immunoglobulin kappa constant, immunoglobulin kappa variable 1-5, immunoglobulin kappa variable 2-24	2.0525	0.0216
221698_s_at	CLEC7A	C-type lectin domain family 7; member A	1.3466	0.0158
221702_s_at	TM2D3	TM2 domain containing 3	0.6065	0.0474
221722_x_at	LZTS1	leucine zipper; putative tumor suppressor 1	0.1411	0.0156
221728_x_at	XIST	X (inactive)-specific transcript	3.1659	0.047
221746_at	UBL4A	ubiquitin-like 4A	0.7152	0
221756_at	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	1.3152	0.0261
221757_at	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	1.2027	0.0023
221776_s_at	BRD7	bromodomain containing 7	0.706	0.003
221787_at	C6orf120	chromosome 6 open reading frame 120	0.7026	0.0415
221861_at		MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	0.7097	0.0075
221866_at	TFEB	transcription factor EB	0.3287	0.0464
221875_x_at	HLA-F	major histocompatibility complex; class I; F	0.8772	0.0024
221880_s_at	LOC400451	hypothetical gene supported by AK075564; BC060873	0.337	0.0403
221893_s_at	ADCK2	aarF domain containing kinase 2	1.3432	0.0004
221894_at	ADCK2	aarF domain containing kinase 2	0.5014	0.0094
221903_s_at	CYLD	cylindromatosis (turban tumor syndrome)	0.8161	0.0129
221907_at	C14orf172	chromosome 14 open reading frame 172	0.2851	0.048
221927_s_at	ABHD11	abhydrolase domain containing 11	0.9586	0.0325
221933_at	NLGN4X	neuroligin 4; X-linked	1.2755	0.0175
221940_at	RPUSD2	RNA pseudouridylate synthase domain containing 2	0.4086	0.0188
221978_at	HLA-F	major histocompatibility complex; class I; F	0.7088	0.0298
222011_s_at	TCP1	t-complex 1	0.7094	0.0342
222061_at	CD58	CD58 molecule	0.2409	0.0069
222111_at		CDNA clone IMAGE:4794011	1.1024	0.0052
222115_x_at	N-PAC	cytokine-like nuclear factor n-pac	0.3552	0.0293
222129_at	FAM134A	Family with sequence similarity 134; member A	0.6429	0.0169
222130_s_at	FTSJ2	FtsJ homolog 2 (E. coli)	0.6325	0.008
222143_s_at	MTMR14	myotubularin related protein 14	0.8847	0.0011
222156_x_at	CCPG1	cell cycle progression 1	1.4522	0.0015
222163_s_at	SPATA5L1	spermatogenesis associated 5-like 1	0.9053	0.0092
222173_s_at	TBC1D2	TBC1 domain family; member 2	0.4262	0.0231
222218_s_at	PILRA	paired immunoglobin-like type 2 receptor alpha	0.6189	0.0461
222225_at	FLJ45055	60S ribosomal pseudogene	0.2821	0.0378
222269_at	APOOL	apolipoprotein O-like	0.6488	0.0058
222271_at			0.3291	0.0016
222277_at	PCOTH	prostate collagen triple helix	0.256	0.0211
222294_s_at		CDNA clone IMAGE:5745639	1.1759	0.0296
222296_at		Homo sapiens; clone IMAGE:3921647; mRNA	0.9764	0.0221
222460_s_at	NIP30	NEFA-interacting nuclear protein NIP30	0.4581	0.0433
222465_at	C15orf15	chromosome 15 open reading frame 15, similar to ribosomal protein L24-like	0.4616	0.0104
222498_at	AZI2	5-azacytidine induced 2	0.4582	0.0047
222500_at	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	0.7869	0.0102
222503_s_at	WDR41	WD repeat domain 41	0.7016	0.0429
222512_at	NUB1	negative regulator of ubiquitin-like proteins 1	0.6082	0.0196
222526_at	GATAD2A	GATA zinc finger domain containing 2A	0.8489	0.0027
222530_s_at	MKKS	McKusick-Kaufman syndrome	0.8173	0.0036
222561_at	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	0.8585	0.0268
222582_at	PRKAG2	protein kinase; AMP-activated; gamma 2 non-catalytic subunit	0.6309	0.0093
222592_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5	0.4741	0.0423
222615_s_at	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	0.8629	0.0101

222631_at	PI4K2B	phosphatidylinositol 4-kinase type 2 beta	0.973	0.0096
222636_at	MED28	mediator complex subunit 28	0.6427	0.05
222647_at	SLC35C1	solute carrier family 35; member C1	0.331	0.0461
222652_s_at	N-PAC	cytokine-like nuclear factor n-pac	0.9871	0.0012
222659_at	IPO11	importin 11	0.7288	0.0414
222682_s_at	C5orf3	chromosome 5 open reading frame 3	0.9237	0.0113
222701_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	1.257	0.0097
222714_s_at	LACTB2	lactamase; beta 2	0.9805	0.0316
222723_at	LOC727901	similar to von Willebrand factor A domain-related protein isoform 1	0.3041	0.0063
222741_s_at	C6orf64	chromosome 6 open reading frame 64	0.8092	0.037
222744_s_at	TMLHE	trimethyllysine hydroxylase; epsilon	0.6713	0.0493
222750_s_at	SRD5A2L	steroid 5 alpha-reductase 2-like	1.7091	0.0028
222753_s_at	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0.9045	0.0137
222754_at	TRNT1	tRNA nucleotidyl transferase; CCA-adding; 1	0.6562	0.0219
222756_s_at	ARRB1	arrestin; beta 1	0.7207	0.0035
222783_s_at	SMOC1	SPARC related modular calcium binding 1	0.1621	0.0498
222786_at	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	0.7145	0.003
222799_at	WDR91	WD repeat domain 91	0.6513	0.0002
222808_at	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	0.926	0.0048
222815_at	RNF12	ring finger protein 12	1.0104	0.019
222817_at	HSD3B7	hydroxy-delta-5-steroid dehydrogenase; 3 beta- and steroid delta-isomerase 7	1.3892	0.0401
222838_at	SLAMF7	SLAM family member 7	0.9673	0.0454
222858_s_at	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	0.269	0.0082
222859_s_at	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	0.342	0.0041
222868_s_at	IL18BP	interleukin 18 binding protein	1.1713	0.0051
222876_s_at	CENTA2	centaurin; alpha 2	0.7156	0.0315
222886_at			0.1845	0.0284
222903_s_at	CPEB1	cytoplasmic polyadenylation element binding protein 1	0.2125	0.0189
222912_at	ARRB1	arrestin; beta 1	0.9671	0.0153
222952_s_at	TLR7	toll-like receptor 7	0.1469	0.0321
222996_s_at	CXXC5	CXXC finger 5	1.8279	0.043
223004_s_at	C3orf1	chromosome 3 open reading frame 1	0.4374	0.0184
223037_at	PDZD11	PDZ domain containing 11	0.8778	0.0032
223041_at	CD99L2	CD99 molecule-like 2	0.9487	0.0328
223043_at	TMEM85	transmembrane protein 85	0.528	0.0408
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter); member 1	0.8202	0.0489
223060_at	C14orf119	chromosome 14 open reading frame 119	0.584	0.0263
223065_s_at	STARD3NL	STARD3 N-terminal like	0.4626	0.0222
223076_s_at	NSUN2	NOL1/NOP2/Sun domain family; member 2	0.4434	0.0462
223084_s_at	CCNDBP1	cyclin D-type binding-protein 1	0.8351	0.0368
223087_at	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	0.6555	0.0285
223094_s_at	ANKH	ankylosis; progressive homolog (mouse)	0.4239	0.047
223112_s_at	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 10; 22kDa	0.6282	0.0042
223162_s_at	KIAA1147	KIAA1147	0.6939	0.0343
223174_at	BTBD10	BTB (POZ) domain containing 10	0.5526	0.035
223179_at	YPEL3	yippee-like 3 (Drosophila)	0.8801	0.0334
223191_at	C14orf112	chromosome 14 open reading frame 112	0.6268	0.0001
223197_s_at	SMARCAD1	SWI/SNF-related; matrix-associated actin-dependent regulator of chromatin; subfamily a; containing DEAD/H box 1	0.7349	0.0071
223200_s_at	LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	0.6906	0.0367
223210_at	CHURC1	churchill domain containing 1	0.6246	0.0134
223215_s_at	C14orf100	chromosome 14 open reading frame 100	0.5504	0.0061
223220_s_at	PARP9	poly (ADP-ribose) polymerase family; member 9	1.3998	0.0027

223221_at	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	0.6816	0.0374
223222_at	SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier); member 19	0.8646	0.0032
223241_at	SNX8	sorting nexin 8	0.6992	0.0459
223244_s_at	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 12	0.2477	0.0345
223247_at	MED10	mediator complex subunit 10	0.9117	0.0229
223278_at	GJB2	gap junction protein; beta 2; 26kDa	0.5513	0.0351
223280_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	2.3078	0.0002
223286_at	C17orf81	chromosome 17 open reading frame 81	0.6224	0.0381
223298_s_at	NT5C3	5'-nucleotidase; cytosolic III	0.6665	0.0083
223299_at	SEC11C	SEC11 homolog C (S. cerevisiae)	0.9887	0.0149
223325_at	TXNDC11	thioredoxin domain containing 11	0.5998	0.0081
223343_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	1.7602	0.0153
223344_s_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	1.6647	0.0047
223345_at	HDAC8	histone deacetylase 8	0.8526	0.0174
223346_at	VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	0.9781	0.0027
223358_s_at		CDNA FLJ33024 fis; clone THYMU1000532; moderately similar to HIGH-AFFINITY CAMP-SPECIFIC 3';5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)	0.8638	0.0065
223363_at	PSMG3	proteasome (prosome; macropain) assembly chaperone 3	0.7103	0.0016
223364_s_at	DHX37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	0.4843	0.029
223367_at	WBSCR18	Williams Beuren syndrome chromosome region 18	0.8352	0.0337
223373_s_at	PLA2G12A	phospholipase A2; group XIIA	1.6132	0.0028
223376_s_at	BRI3	brain protein I3	0.6028	0.0154
223377_x_at	CISH	cytokine inducible SH2-containing protein	0.896	0.0147
223382_s_at	ZNRF1	zinc and ring finger 1	0.9296	0.0027
223383_at	ZNRF1	zinc and ring finger 1	1.3778	0.0017
223396_at	TMEM60	transmembrane protein 60	0.3913	0.047
223397_s_at	NIP7	nuclear import 7 homolog (S. cerevisiae)	0.6425	0.0403
223405_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0.875	0.0449
223414_s_at	LYAR	Ly1 antibody reactive homolog (mouse)	0.2908	0.0363
223420_at	DNAJC14	DnaJ (Hsp40) homolog; subfamily C; member 14	0.7239	0.001
223435_s_at	PCDHA1	protocadherin alpha 1, protocadherin alpha 10, protocadherin alpha 11, protocadherin alpha 12, protocadherin alpha 13, protocadherin alpha 2, protocadherin alpha 3, protocadherin alpha 4, protocadherin alpha 5, protocadherin alpha 6, protocadherin alpha 7, protocadherin alpha 8, protocadherin alpha 9, protocadherin alpha subfamily C; 1, protocadherin alpha subfamily C; 2	2.6323	0.0216
223439_at	NKAP	NFKB activating protein	1.0048	0.0025
223441_at	SLC17A5	solute carrier family 17 (anion/sugar transporter); member 5	1.4819	0.0016
223445_at	DTNBP1	dystrobrevin binding protein 1	0.6253	0.0073
223484_at	C15orf48	chromosome 15 open reading frame 48	1.8154	0.044
223515_s_at	COQ3	coenzyme Q3 homolog; methyltransferase (S. cerevisiae)	0.7089	0.023
223518_at	DFFA	DNA fragmentation factor; 45kDa; alpha polypeptide	0.6191	0.0182
223541_at	HAS3	hyaluronan synthase 3	0.1547	0.0093
223551_at	PKIB	protein kinase (cAMP-dependent; catalytic) inhibitor beta	2.5302	0.0003
223565_at	MGC29506	hypothetical protein MGC29506	0.4858	0.0417
223573_s_at	PPP2R2C	protein phosphatase 2 (formerly 2A); regulatory subunit B; gamma isoform	0.6977	0.0099
223574_x_at	PPP2R2C	protein phosphatase 2 (formerly 2A); regulatory subunit B; gamma isoform	2.1023	0.0099
223580_at	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2	1.2559	0.0003
223583_at	TNFAIP8L2	tumor necrosis factor; alpha-induced protein 8-like 2	0.4535	0.0118

223596_at	SLC12A6	solute carrier family 12 (potassium/chloride transporters); member 6	0.3772	0.0252
223610_at	SEMA5B	sema domain; seven thrombospondin repeats (type 1 and type 1-like); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 5B	0.2174	0.0481
223615_at	ABI3	ABI gene family; member 3	0.3381	0.0393
223620_at	GPR34	G protein-coupled receptor 34	2.2456	0.0003
223636_at	ZMYND12	zinc finger; MYND-type containing 12	0.6372	0.01
223640_at	HCST	hematopoietic cell signal transducer	1.2724	0.005
223659_at	TMPRSS13	transmembrane protease; serine 13	0.1321	0.0137
223673_at	RFX4	regulatory factor X; 4 (influences HLA class II expression)	0.2252	0.0496
223677_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	0.9653	0.0063
223686_at	TPK1	thiamin pyrophosphokinase 1	1.7822	0
223688_s_at	LY6K	lymphocyte antigen 6 complex; locus K	0.2636	0.0275
223700_at	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	1.4063	0.0179
223709_s_at	WNT10A	wingless-type MMTV integration site family; member 10A	0.1397	0.0479
223720_at	SPINK7	serine peptidase inhibitor; Kazal type 7 (putative)	0.3084	0.0051
223728_at	MGC16385	hypothetical protein MGC16385	0.9859	0.001
223743_s_at	MRPL4	mitochondrial ribosomal protein L4	0.754	0.0189
223750_s_at	TLR10	toll-like receptor 10	0.1796	0.0098
223767_at	GPR84	G protein-coupled receptor 84	0.2323	0.0087
223776_x_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	0.8497	0.0002
223786_at	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	2.3996	0.0016
223809_at	RGS18	regulator of G-protein signaling 18	0.7789	0.0097
223833_at	WDR55	WD repeat domain 55	0.3585	0.0194
223834_at	CD274	CD274 molecule	0.1943	0.0232
223856_at	AKR1CL2	aldo-keto reductase family 1; member C-like 2	0.5347	0.0478
223857_x_at	TMEM85	transmembrane protein 85	0.4961	0.0432
223866_at	ARMC2	armadillo repeat containing 2	0.25	0.0032
223880_x_at	C20orf24	chromosome 20 open reading frame 24	0.671	0.0018
223889_at			0.15	0.005
223909_s_at	HDAC8	histone deacetylase 8	0.7173	0.0056
223922_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	1.8945	0.0005
223964_x_at			0.6102	0.0247
224009_x_at	DHRS9	dehydrogenase/reductase (SDR family) member 9	0.5515	0.0251
224015_s_at	MRPS25	mitochondrial ribosomal protein S25	0.8075	0.0035
224037_at			0.1579	0.049
224121_x_at	PLEKHB2	pleckstrin homology domain containing; family B (evectins) member 2	0.1016	0.0455
224160_s_at	ACAD9	acyl-Coenzyme A dehydrogenase family; member 9	0.5965	0.0419
224187_x_at	HSPA8	heat shock 70kDa protein 8, similar to heat shock protein 8	0.4223	0.027
224190_x_at	NOD1	nucleotide-binding oligomerization domain containing 1	0.2395	0.0246
224236_s_at			0.1567	0.0048
224238_at			0.1659	0.0331
224302_s_at	MRPS36	mitochondrial ribosomal protein S36	0.5339	0.0274
224303_x_at	NIN	ninein (GSK3B interacting protein)	0.5174	0.009
224304_x_at	NIN	ninein (GSK3B interacting protein)	0.754	0.0102
224356_x_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	2.3993	0.0004
224357_s_at	MS4A4A	membrane-spanning 4-domains; subfamily A; member 4	1.081	0.0118
224358_s_at	MS4A7	membrane-spanning 4-domains; subfamily A; member 7	0.8304	0.0122
224376_s_at	C20orf24	chromosome 20 open reading frame 24	0.8587	0.0049
224404_s_at	FCRL5	Fc receptor-like 5	0.2312	0.0439
224407_s_at	RP6-213H19.1	serine/threonine protein kinase MST4	0.6115	0.0319
224451_x_at	ARHGAP9	Rho GTPase activating protein 9	1.4058	0.0071
224452_s_at	MGC12966	hypothetical protein LOC84792	0.5193	0.0026
224455_s_at	ADPGK	ADP-dependent glucokinase	0.7008	0.0315

224476_s_at	MESP1	mesoderm posterior 1 homolog (mouse)	0.9399	0.0011
224478_s_at	C7orf50	chromosome 7 open reading frame 50	1.2957	0.0078
224480_s_at	MAG1	lung cancer metastasis-associated protein	1.5622	0.0012
224486_s_at	C15orf41	chromosome 15 open reading frame 41	0.4438	0.0428
224500_s_at	MON1A	MON1 homolog A (yeast)	0.8599	0.0038
224531_at	GPR61	G protein-coupled receptor 61	0.1261	0.0444
224539_s_at	PCDHAC2	protocadherin alpha subfamily C; 2	0.4037	0.0101
224573_at	MGC71993	similar to DNA segment; Chr 11; Brigham & Womens Genetics 0434 expressed	0.3015	0.0338
224586_x_at	SUB1	SUB1 homolog (S. cerevisiae)	0.2744	0.0314
224594_x_at	ACTB	actin; beta	0.1238	0.0198
224608_s_at	VPS25	vacuolar protein sorting 25 homolog (S. cerevisiae)	0.4957	0.0103
224661_at	PIGY	phosphatidylinositol glycan anchor biosynthesis; class Y	0.5107	0.0405
224669_at	SYS1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	0.9423	0.0439
224675_at	MESDC2	mesoderm development candidate 2	0.5739	0.0269
224679_at	MESDC2	mesoderm development candidate 2	0.5766	0.0438
224701_at	PARP14	poly (ADP-ribose) polymerase family; member 14	0.9235	0.0437
224707_at	C5orf32	chromosome 5 open reading frame 32	1.1693	0.0102
224709_s_at	CDC42SE2	CDC42 small effector 2	0.6225	0.0184
224732_at	CTF8	chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	0.8279	0.0005
224756_s_at	BAT5	HLA-B associated transcript 5	0.4847	0.0415
224779_s_at	FAM96A	family with sequence similarity 96; member A	0.459	0.0157
224809_x_at	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	0.6946	0.0026
224813_at	WASL	Wiskott-Aldrich syndrome-like	0.3125	0.0394
224816_at	C7orf20	Chromosome 7 open reading frame 20	0.1932	0.0124
224819_at	TCEAL8	transcription elongation factor A (SII)-like 8	1.1115	0.0008
224821_at	ABHD14B	abhydrolase domain containing 14B	1.1789	0.0353
224846_at	SHKBP1	SH3KBP1 binding protein 1	0.4952	0.0102
224869_s_at	MRPS25	mitochondrial ribosomal protein S25	0.856	0.0009
224880_at	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	0.5286	0.0345
224883_at	PLDN	pallidin homolog (mouse)	0.8322	0.0315
224890_s_at	LOC389541	similar to CG14977-PA	0.6861	0.0234
224892_at	PLDN	pallidin homolog (mouse)	0.5094	0.0293
224899_s_at	LOC728866	implantation-associated protein, similar to implantation-associated protein	0.4929	0.0436
224927_at	KIAA1949	KIAA1949	0.9817	0.0067
225002_s_at	SUMF2	sulfatase modifying factor 2	0.961	0.0025
225003_at	MGC3205	MBC3205, hypothetical protein MGC3205	0.7473	0.0323
225014_at	LOC389203	hypothetical gene supported by BC032431	0.8526	0.0327
225019_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	0.6815	0.0413
225049_at	BLOC1S2	biogenesis of lysosome-related organelles complex-1; subunit 2	0.5302	0.0259
225051_at	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1; RH-linked)	0.9109	0.0122
225092_at	RABEP1	rabaptin; RAB GTPase binding effector protein 1	0.7465	0.016
225104_at	ZNF598	zinc finger protein 598	0.5635	0.0299
225125_at	TMEM32	transmembrane protein 32	0.8059	0.0273
225145_at	NCOA5	nuclear receptor coactivator 5	0.7461	0.0185
225194_at	PLRG1	pleiotropic regulator 1 (PRL1 homolog; Arabidopsis)	0.3999	0.0454
225196_s_at	MRPS26	mitochondrial ribosomal protein S26	0.4436	0.0267
225204_at	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	0.6624	0.0364
225213_at	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	0.7633	0.0047
225228_at	TMEM77	transmembrane protein 77	0.6639	0.0365
225232_at	MTMR12	myotubularin related protein 12	1.1535	0.0002
225252_at	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	0.7221	0.0114
225253_s_at	METTL2A	methyltransferase like 2A, methyltransferase like 2B	0.6745	0.0472
225259_at	RAB6B	RAB6B; member RAS oncogene family	0.7718	0.0382
225270_at	NEO1	neogenin homolog 1 (chicken)	0.8729	0.0378

225305_at	SLC25A29	solute carrier family 25; member 29	0.7823	0.0261
225313_at	C20orf177	chromosome 20 open reading frame 177	1.2952	0.0058
225353_s_at	C1QC	complement component 1; q subcomponent; C chain	1.4218	0.0283
225357_s_at	INOC1	INO80 complex homolog 1 (S. cerevisiae)	0.4383	0.0095
225394_s_at	ZCRB1	zinc finger CCHC-type and RNA binding motif 1	0.4873	0.0358
225397_at	CCDC32	coiled-coil domain containing 32	0.9289	0.0185
225415_at	DTX3L	deltex 3-like (Drosophila)	0.7358	0.0224
225432_s_at	CSRP2BP	CSRP2 binding protein	0.906	0.0164
225447_at	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.9284	0.0342
225538_at	ZCCHC9	zinc finger; CCHC domain containing 9	0.836	0.0334
225545_at	EEF2K	eukaryotic elongation factor-2 kinase	0.8481	0.0359
225546_at	EEF2K	eukaryotic elongation factor-2 kinase	0.7138	0.0318
225552_x_at	AURKAIP1	aurora kinase A interacting protein 1, similar to Cyclin-L2 (Paneth cell-enhanced expression protein)	0.4617	0.035
225556_at	LOC203547	hypothetical protein LOC203547	0.7948	0.0009
225558_at	GIT2	G protein-coupled receptor kinase interactor 2	0.5921	0.0456
225559_at	C3orf19	chromosome 3 open reading frame 19	0.3863	0.0162
225583_at	UXS1	UDP-glucuronate decarboxylase 1	0.9572	0.0205
225601_at	HMGB3	high-mobility group box 3	1.7452	0.0045
225619_at	SLAIN1	SLAIN motif family; member 1	1.6193	0.0227
225622_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	0.5863	0.0237
225623_at	KIAA1737	KIAA1737	0.7517	0.0181
225626_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	1.397	0.0084
225630_at	KIAA1706	KIAA1706 protein	0.715	0.0005
225631_at	KIAA1706	KIAA1706 protein	0.5961	0.0036
225651_at	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog; yeast)	1.8204	0.0103
225653_at	LOC644617	Hypothetical LOC644617	0.1913	0.0474
225670_at	LOC134145	hypothetical protein LOC134145	0.953	0.0167
225701_at	AKNA	AT-hook transcription factor	0.8205	0.0312
225719_s_at	MRPL55	mitochondrial ribosomal protein L55	0.4464	0.0406
225734_at	FBXO22	F-box protein 22	0.6559	0.0207
225743_at	RPUSD3	RNA pseudouridylate synthase domain containing 3	0.7578	0.0422
225752_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	1.3612	0.0266
225763_at	RCSD1	RCSD domain containing 1	1.0234	0.0073
225769_at	COG6	component of oligomeric golgi complex 6	0.7082	0.0224
225775_at	TSPAN33	tetraspanin 33	1.1308	0.0006
225810_at	MTMR10	myotubularin related protein 10	0.836	0.0037
225832_s_at	DAGLB	diacylglycerol lipase; beta	0.6983	0.0382
225843_at	ZFYVE19	zinc finger; FYVE domain containing 19	0.6344	0.0199
225848_at	ZNF746	zinc finger protein 746	0.6461	0.0129
225853_at	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	0.7017	0.0005
225921_at	NIN	ninein (GSK3B interacting protein)	1.5074	0.0006
225922_at	KIAA1450	KIAA1450 protein	0.6777	0.0059
225926_at	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	0.8401	0.002
225940_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3	0.8127	0.0274
225941_at	EIF4E3	eukaryotic translation initiation factor 4E family member 3	0.9405	0.0318
225943_at	NLN	neurolysin (metallopeptidase M3 family)	0.7687	0.0379
225944_at	NLN	neurolysin (metallopeptidase M3 family)	1.5659	0.0102
225948_at	C14orf153	chromosome 14 open reading frame 153	0.8863	0.0064
225959_s_at	ZNRF1	zinc and ring finger 1	1.2376	0.0066
225973_at	TAP2	transporter 2; ATP-binding cassette; sub-family B (MDR/TAP)	1.4383	0.0169
225993_at	EARS2	glutamyl-tRNA synthetase 2; mitochondrial (putative)	0.6524	0.0423
226004_at	CABLES2	Cdk5 and Abl enzyme substrate 2	0.8418	0.0199
226026_at	DIRC2	disrupted in renal carcinoma 2	0.8536	0.0057

226037_s_at	LOC728198	TAF9B RNA polymerase II; TATA box binding protein (TBP)-associated factor; 31kDa, similar to transcription associated factor 9B	1.0516	0.0092
226039_at	MGAT4A	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme A	2.3076	0
226044_at	TDP1	tyrosyl-DNA phosphodiesterase 1	0.3675	0.0486
226066_at	MITF	microphthalmia-associated transcription factor	1.5812	0.0039
226068_at	SYK	spleen tyrosine kinase	1.0717	0.0302
226071_at	ADAMTSL4	ADAMTS-like 4	0.607	0.0457
226075_at	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	0.9258	0.0165
226083_at	TMEM70	transmembrane protein 70	0.5607	0.0005
226092_at	MPP5	membrane protein; palmitoylated 5 (MAGUK p55 subfamily member 5)	0.7857	0.0157
226099_at	ELL2	elongation factor; RNA polymerase II; 2	1.6817	0.0097
226107_at		CDNA FLJ13495 fis; clone PLACE1004425, Full-length cDNA clone CS0DI084YF13 of Placenta Cot 25-normalized of Homo sapiens (human)	0.5214	0.0257
226108_at	NHN1	conserved nuclear protein NHN1	0.6256	0.0284
226135_at	C6orf107	chromosome 6 open reading frame 107	0.9543	0.0116
226141_at	DKFZp761B107	hypothetical protein DKFZp761B107	0.4569	0.0484
226152_at	TTC7B	tetratricopeptide repeat domain 7B	0.8621	0.0059
226172_at	USP42	Ubiquitin specific peptidase 42	0.1291	0.0127
226180_at	WDR36	WD repeat domain 36	0.9822	0.0011
226182_s_at	WISP3	WNT1 inducible signaling pathway protein 3	0.109	0.0378
226195_at	C14orf179	chromosome 14 open reading frame 179	0.4986	0.0059
226196_s_at	C14orf179	chromosome 14 open reading frame 179	0.6274	0.0071
226218_at	IL7R	interleukin 7 receptor	2.5295	0.0037
226219_at	ARHGAP30	Rho GTPase activating protein 30	1.1728	0.0099
226241_s_at	MRPL52	mitochondrial ribosomal protein L52	0.7258	0.0027
226248_s_at	KIAA1324	KIAA1324	0.555	0.0017
226261_at	ZNRF2	zinc and ring finger 2	1.0787	0.0016
226272_at	RCAN3	RCAN family member 3	1.4182	0.0107
226276_at	TMEM167	transmembrane protein 167	0.7071	0.0296
226321_at	LYSMD3	LysM; putative peptidoglycan-binding; domain containing 3	0.762	0.0107
226354_at	LACTB	lactamase; beta	0.8747	0.015
226369_at	LOC338799	hypothetical locus LOC338799	0.4263	0.0178
226378_s_at	C19orf25	chromosome 19 open reading frame 25	0.7139	0.0453
226393_at	CYP2U1	cytochrome P450; family 2; subfamily U; polypeptide 1	1.2934	0.0126
226410_at	LOC348180	hypothetical protein LOC348180	0.5881	0.009
226421_at	AMMECR1	Alport syndrome; mental retardation; midface hypoplasia and elliptocytosis chromosomal region; gene 1	1.3433	0.0182
226423_at	PAQR8	progestin and adipoQ receptor family member VIII	0.9451	0.0485
226440_at	DUSP22	dual specificity phosphatase 22	0.8513	0.0343
226449_at	CCDC100	coiled-coil domain containing 100	0.6942	0.003
226459_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	1.4467	0.0232
226460_at	KIAA1450	KIAA1450 protein	0.6256	0.0112
226462_at	STXBP6	syntaxin binding protein 6 (amisyn)	0.6567	0.0116
226466_s_at	FAM58A	family with sequence similarity 58; member A	0.7297	0.0054
226474_at	NLRC5	NLR family; CARD domain containing 5	1.88	0.0064
226476_s_at	VPRBP	Vpr (HIV-1) binding protein	0.4992	0.0214
226499_at	NRARP	Notch-regulated ankyrin repeat protein	0.6518	0.0222
226519_s_at	AGXT2L2	alanine-glyoxylate aminotransferase 2-like 2	0.9424	0.0087
226524_at	C3orf38	chromosome 3 open reading frame 38	0.7307	0.0485
226560_at		Transcribed locus	2.4056	0.0264
226568_at	FAM102B	family with sequence similarity 102; member B	1.2831	0.0217
226579_at		Transcribed locus; weakly similar to XP_001053793.1 hypothetical protein [Rattus norvegicus]	0.7172	0.0239
226580_at	BRMS1L	breast cancer metastasis-suppressor 1-like	0.6966	0.0255
226584_s_at	FAM110A	family with sequence similarity 110; member A	0.3249	0.0117

226596_x_at	LOC729852	hypothetical protein LOC729852	0.8756	0.0198
226627_at	8-Sep	septin 8	0.5294	0.0186
226640_at	DAGLB	diacylglycerol lipase; beta	0.6168	0.0187
226642_s_at	NUDCD2	NudC domain containing 2	0.8481	0.0447
226650_at	ZFAND2A	zinc finger; AN1-type domain 2A	0.8631	0.0494
226659_at	DEF6	differentially expressed in FDCP 6 homolog (mouse)	0.4285	0.0164
226671_at	LAMP2	Lysosomal-associated membrane protein 2	1.0995	0.0272
226683_at	SNAG1	Sorting nexin associated golgi protein 1	0.9392	0.0078
226686_at	CISD2	CDGSH iron sulfur domain 2	0.5695	0.0482
226688_at	C3orf23	chromosome 3 open reading frame 23	0.7611	0.0145
226701_at	GJA5	gap junction protein; alpha 5; 40kDa	0.4329	0.0196
226722_at	FAM20C	family with sequence similarity 20; member C	1.0712	0.0215
226725_at	SLFN5	Schlafen family member 5	1.155	0.0085
226727_at	CISD3	CDGSH iron sulfur domain 3	0.6776	0.0314
226736_at	CHURC1	churchill domain containing 1	1.1201	0.0199
226741_at	SLC12A6	solute carrier family 12 (potassium/chloride transporters); member 6	0.9266	0.0007
226750_at	LARP2	La ribonucleoprotein domain family; member 2	0.9595	0.0109
226782_at	SLC25A30	solute carrier family 25; member 30	0.8365	0.0241
226785_at	ATP11C	ATPase; Class VI; type 11C	1.4215	0.0023
226787_at	ZNF18	zinc finger protein 18	0.8054	0.0165
226789_at	LOC647121	similar to embigin homolog	2.9813	0.007
226793_at	LOC283267	hypothetical protein LOC283267	0.5257	0.0373
226796_at	LOC116236	hypothetical protein LOC116236	0.7983	0.0065
226804_at	FAM20A	family with sequence similarity 20; member A	0.6204	0.0304
226810_at		MRNA full length insert cDNA clone EUROIMAGE 1509279	1.3842	0.029
226811_at	FAM46C	family with sequence similarity 46; member C	1.3202	0.0233
226815_at	C3orf31	chromosome 3 open reading frame 31	0.7091	0.0108
226817_at	DSC2	desmocollin 2	0.7262	0.0356
226818_at	MPEG1	macrophage expressed gene 1	1.629	0.0121
226823_at	PHACTR4	phosphatase and actin regulator 4	0.6636	0.0138
226836_at	SFT2D1	SFT2 domain containing 1	0.2136	0.0078
226841_at	MPEG1	macrophage expressed gene 1	1.3154	0.0281
226853_at	BMP2K	BMP2 inducible kinase	1.4231	0.0064
226860_at	TMEM19	transmembrane protein 19	0.8832	0.0479
226869_at	MEGF6	multiple EGF-like-domains 6	0.1682	0.0371
226873_at		CDNA clone IMAGE:4794011	0.6163	0.0317
226874_at	KLHL8	kelch-like 8 (Drosophila)	0.6592	0.0356
226878_at	HLA-DOA	major histocompatibility complex; class II; DO alpha	1.5237	0.0022
226881_at	GRPEL2	GrpE-like 2; mitochondrial (E. coli)	0.6256	0.035
226907_at	PPP1R14C	protein phosphatase 1; regulatory (inhibitor) subunit 14C	0.3773	0.0176
226912_at	ZDHHC23	zinc finger; DHHC-type containing 23	1.4101	0.0013
226938_at	WDR21A	WD repeat domain 21A	0.8627	0.0225
226947_at	GUSBL2	glucuronidase; beta-like 2	0.6255	0.0161
226952_at	EAF1	ELL associated factor 1	1.0812	0.0009
226953_at	DARC	Duffy blood group; chemokine receptor	0.1295	0.0493
226970_at	FBXO33	F-box protein 33	0.8621	0.0116
226983_at	ZNF777	zinc finger protein 777	0.3483	0.0338
226988_s_at	MYH14	myosin; heavy chain 14	0.5105	0.0174
226989_at	RGMB	RGM domain family; member B	0.9297	0.0322
227001_at	NPAL2	NIPA-like domain containing 2	1.2067	0.0402
227002_at	FAM78A	family with sequence similarity 78; member A	0.4757	0.005
227030_at		Full length insert cDNA clone YY82H04	0.4025	0.0065
227038_at	SGMS2	sphingomyelin synthase 2	2.0304	0.0044
227043_at	LOC126075	hypothetical protein LOC126075	0.5309	0.0233
227100_at	B3GALTL	beta 1;3-galactosyltransferase-like	0.5683	0.0391
227133_at	CXorf39	chromosome X open reading frame 39	1.123	0.0164
227135_at	ASAHL	N-acylsphingosine amidohydrolase (acid ceramidase)-like	1.4591	0.0218
227143_s_at	BID	BH3 interacting domain death agonist	0.6916	0.0346

227153_at	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	1.3266	0.0031
227168_at	MIAT	myocardial infarction associated transcript (non-protein coding)	0.7585	0.0425
227172_at	TMEM116	transmembrane protein 116	0.7525	0.0232
227178_at	CUGBP2	CUG triplet repeat; RNA binding protein 2	0.8593	0.0288
227180_at	ELOVL7	ELOVL family member 7; elongation of long chain fatty acids (yeast)	2.2101	0.0073
227184_at			0.7004	0.0177
227193_at		CDNA FLJ37631 fis; clone BRCOC2015944	1.1306	0.0066
227201_at	LOC643837	hypothetical protein LOC643837	0.4253	0.0028
227232_at	EVL	Enah/Vasp-like	0.4237	0.0407
227246_at	PLRG1	pleiotropic regulator 1 (PRL1 homolog; Arabidopsis)	0.805	0.0173
227262_at	HAPLN3	hyaluronan and proteoglycan link protein 3	0.2164	0.0403
227265_at	FGL2	fibrinogen-like 2	1.9719	0.001
227266_s_at	FYB	FYN binding protein (FYB-120/130)	1.654	0.0015
227272_at	C15orf52	chromosome 15 open reading frame 52	0.9927	0.0049
227280_s_at	CCNYL1	Cyclin Y-like 1	0.6887	0.0344
227294_at	ZNF689	zinc finger protein 689	0.7417	0.0254
227298_at	FLJ37798	hypothetical gene supported by AK095117	0.4128	0.0092
227304_at	SMCR8	Smith-Magenis syndrome chromosome region; candidate 8	0.5967	0.0247
227321_at	GATS	opposite strand transcription unit to STAG3	0.3144	0.0447
227335_at	DIDO1	death inducer-obliterator 1	1.0235	0.0104
227340_s_at	RGMB	RGM domain family; member B	0.7043	0.0115
227344_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)	0.4862	0.0038
227345_at	TNFRSF10D	tumor necrosis factor receptor superfamily; member 10d; decoy with truncated death domain	0.3692	0.0106
227346_at	IKZF1	IKAROS family zinc finger 1 (Ikaros)	1.072	0.0202
227353_at	TMC8	transmembrane channel-like 8	0.5951	0.0462
227354_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	0.5148	0.0304
227367_at	SLCO3A1	solute carrier organic anion transporter family; member 3A1	1.0862	0.0002
227396_at	PTPRJ	protein tyrosine phosphatase; receptor type; J	1.5985	0.0028
227413_at	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	0.4828	0.0372
227416_s_at	ZCRB1	zinc finger CCHC-type and RNA binding motif 1	0.5019	0.0216
227429_at	EFCAB4A	EF-hand calcium binding domain 4A	0.3639	0.0302
227445_at	ZNF689	zinc finger protein 689	0.9539	0.0244
227447_at	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	0.582	0.0067
227458_at			0.5095	0.0153
227459_at		CDNA FLJ32348 fis; clone PROST2007200	0.3261	0.0319
227460_at	C3orf63	Chromosome 3 open reading frame 63	0.1983	0.0136
227463_at	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0.2238	0.0481
227467_at	RDH10	retinol dehydrogenase 10 (all-trans)	1.119	0.0199
227482_at	ADCK1	aarF domain containing kinase 1	0.5659	0.0181
227521_at	FBXO33	F-box protein 33	0.8714	0.0304
227540_at	EEFSEC	eukaryotic elongation factor; selenocysteine-tRNA-specific	0.4492	0.0158
227559_at			0.96	0.0207
227575_s_at	C14orf102	chromosome 14 open reading frame 102	0.6199	0.0101
227580_s_at	DKFZP434B0335	DKFZP434B0335 protein	0.5195	0.0093
227586_at	TMEM170	transmembrane protein 170	0.6958	0.0081
227611_at	TARSL2	threonyl-tRNA synthetase-like 2	1.1147	0.0088
227628_at	LOC493869	similar to RIKEN cDNA 2310016C16	1.1106	0.0416
227633_at	RHEB	Ras homolog enriched in brain	0.6695	0.0025
227645_at	PIK3R5	phosphoinositide-3-kinase; regulatory subunit 5; p101	0.5197	0.0261
227699_at	C14orf149	chromosome 14 open reading frame 149	1.0379	0
227705_at	TCEAL7	transcription elongation factor A (SII)-like 7	0.9899	0.0436
227726_at	RNF166	ring finger protein 166	0.4593	0.0335

227741_at	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member b	0.8905	0.0384
227749_at		Transcribed locus	0.3405	0.0353
227767_at	CSNK1G3	casein kinase 1; gamma 3	0.5457	0.0306
227791_at	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger); member 9	1.072	0.0083
227798_at	SMAD1	SMAD family member 1	0.7877	0.0186
227841_at	CEMP1	Cementum protein 1	0.6575	0.0153
227844_at	FMNL3	formin-like 3	0.2681	0.0356
227846_at	GPR176	G protein-coupled receptor 176	0.6417	0.0032
227867_at	LOC129293	hypothetical protein LOC129293	0.2595	0.037
227869_at	FAM104B	Family with sequence similarity 104; member B	0.4571	0.0379
227871_at	CHM	choroideremia (Rab escort protein 1)	0.9315	0.0154
227897_at	RAP2B	RAP2B; member of RAS oncogene family	1.3659	0.0047
227941_at	LOC339803	hypothetical protein LOC339803	0.9956	0.0331
227949_at	PHACTR3	phosphatase and actin regulator 3	0.3859	0.0487
227966_s_at	CCDC74A	coiled-coil domain containing 74A, coiled-coil domain containing 74B	1.1049	0.0459
227967_at	TUBGCP5	tubulin; gamma complex associated protein 5	0.717	0.0073
228005_at	ZXDB	zinc finger; X-linked; duplicated B	1.3159	0.0023
228010_at	PPP2R2C	protein phosphatase 2 (formerly 2A); regulatory subunit B; gamma isoform	3.0405	0.0118
228019_s_at	MRPS18C	mitochondrial ribosomal protein S18C	0.6267	0.004
228027_at	GPRASP2	G protein-coupled receptor associated sorting protein 2	0.9712	0.0047
228031_at	C20orf121	chromosome 20 open reading frame 121	0.7233	0.0083
228042_at	ADPRH	ADP-ribosylarginine hydrolase	0.4025	0.0071
228050_at	UTP15	UTP15; U3 small nucleolar ribonucleoprotein; homolog (S. cerevisiae)	0.5131	0.007
228067_at	C2orf55	chromosome 2 open reading frame 55	1.1028	0.0434
228080_at	LAYN	layilin	1.1076	0.0276
228094_at	AMICA1	adhesion molecule; interacts with CXADR antigen 1	0.9275	0.0405
228108_at		CDNA clone IMAGE:5263177	1.5145	0.0457
228109_at	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	0.7456	0.0057
228118_x_at	C16orf13	Chromosome 16 open reading frame 13	0.1436	0.0072
228146_at	C17orf51	chromosome 17 open reading frame 51	0.3932	0.0003
228167_at	KLHL6	kelch-like 6 (Drosophila)	0.6416	0.0325
228190_at	ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae), Ctr9; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	0.8487	0.0011
228200_at		CDNA FLJ14756 fis; clone NT2RP3003193; moderately similar to ZINC FINGER PROTEIN 135	0.7603	0.0353
228231_at		MRNA; cDNA DKFZp761E1721 (from clone DKFZp761E1721)	0.3988	0.0301
228234_at	TICAM2	toll-like receptor adaptor molecule 2	0.9051	0.0346
228243_at		Transcribed locus	1.2788	0.0088
228274_at	SDSL	serine dehydratase-like	0.9442	0.0288
228283_at	MGC61571	hypothetical protein MGC61571	0.5406	0.0209
228289_at		Transcribed locus	0.5465	0.01
228293_at	DEPDC7	DEP domain containing 7	0.7287	0.0154
228301_x_at	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 10; 22kDa	0.4457	0.0201
228346_at		Transcribed locus	1.4391	0.0313
228353_x_at	STS-1	Cbl-interacting protein Sts-1	0.2006	0.0071
228355_s_at	NDUFA12L	NDUFA12-like	0.8309	0.0203
228359_at	STS-1	Cbl-interacting protein Sts-1	0.2521	0.0014
228363_at	BIRC4	baculoviral IAP repeat-containing 4	0.522	0.0445
228372_at	C10orf128	chromosome 10 open reading frame 128	1.5534	0.0005
228373_at	C16orf72	chromosome 16 open reading frame 72	0.5686	0.0444
228375_at	IGSF11	immunoglobulin superfamily; member 11	1.5981	0.0054
228376_at	GGTA1	glycoprotein; alpha-galactosyltransferase 1, similar to glycoprotein galactosyltransferase alpha 1; 3	1.4027	0.0141

228382_at	FAM105B	family with sequence similarity 105; member B	0.4736	0.0012
228394_at	STK10	serine/threonine kinase 10	0.5611	0.0001
228421_s_at	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	0.1194	0.0299
228444_at		Transcribed locus	0.2704	0.0282
228532_at	C1orf162	chromosome 1 open reading frame 162	1.4404	0.0302
228544_s_at	CSRP2BP	CSRP2 binding protein	0.5443	0.0187
228557_at	L3MBTL4	l(3)mbt-like 4 (Drosophila)	0.3778	0.0174
228570_at	BTBD11	BTB (POZ) domain containing 11	1.8849	0.036
228591_at	TNRC6C	Trinucleotide repeat containing 6C	0.1221	0.0446
228600_x_at	C7orf46	chromosome 7 open reading frame 46	1.0587	0.0024
228716_at	THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	2.0132	0.0091
228745_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing; beta	1.1515	0.0051
228775_at			0.9873	0.0429
228809_at	CXorf40A	chromosome X open reading frame 40A	1.022	0.0172
228855_at	LOC729777	similar to Peroxisomal coenzyme A diphosphatase NUDT7 (Nucleoside diphosphate-linked moiety X motif 7) (Nudix motif 7)	2.369	0.0009
228869_at		Transcribed locus	0.7842	0.0268
228951_at		Transcribed locus	0.8846	0.0093
229012_at	C9orf24	chromosome 9 open reading frame 24	0.2477	0.0384
229013_at	LOC145783	hypothetical protein LOC145783	0.4642	0.0064
229014_at	FLJ42709	hypothetical gene supported by AK124699	1.9202	0.0035
229019_at	ZNF533	zinc finger protein 533	1.8524	0.0291
229026_at	CDC42SE2	CDC42 small effector 2	1.9303	0.006
229037_at	TRIM69	Tripartite motif-containing 69	0.1733	0.0316
229055_at	GPR68	G protein-coupled receptor 68	0.3795	0.0181
229064_s_at	RCAN3	RCAN family member 3	0.3797	0.0202
229068_at	CCT5	chaperonin containing TCP1; subunit 5 (epsilon)	1.0716	0.0472
229094_at	LOC401431	hypothetical gene LOC401431	0.5087	0.0001
229109_s_at	BLVRA	Biliverdin reductase A	0.1759	0.0318
229121_at		CDNA FLJ44441 fis; clone UTERU2020242	0.7587	0.004
229125_at	ANKRD38	ankyrin repeat domain 38	0.2049	0.0025
229132_at	MINA	MYC induced nuclear antigen	0.1967	0.0117
229134_at	VANGL1	vang-like 1 (van gogh; Drosophila)	0.4798	0.0001
229139_at	JPH1	junctophilin 1	1.7014	0.0122
229156_s_at		CDNA clone IMAGE:5274141	0.2642	0.0165
229157_at		CDNA clone IMAGE:5274141	0.2219	0.0276
229174_at	C3orf38	chromosome 3 open reading frame 38	0.591	0.0251
229181_s_at	CEP27	centrosomal protein 27kDa	0.8206	0.0053
229208_at	CEP27	centrosomal protein 27kDa	0.6423	0.0211
229228_at	CREB5	cAMP responsive element binding protein 5	0.752	0.0406
229242_at		Transcribed locus	0.3584	0.0165
229276_at	IGSF9	immunoglobulin superfamily; member 9	0.2664	0.041
229277_at		Beta-1 adrenergic receptor mRNA; 3' UTR	0.1749	0.0028
229284_at	MAT2B	Methionine adenosyltransferase II; beta	0.1492	0.0013
229356_x_at	INOC1	INO80 complex homolog 1 (S. cerevisiae)	0.6466	0.0067
229363_at		CDNA FLJ32121 fis; clone PEBLM1000083	0.5878	0.0163
229367_s_at	GIMAP6	GTPase; IMAP family member 6	0.6826	0.0325
229383_at		CDNA FLJ34016 fis; clone FCBBF2002541	1.3012	0.0015
229390_at	FAM26F	family with sequence similarity 26; member F	1.7491	0.0247
229391_s_at	FAM26F	family with sequence similarity 26; member F	1.34	0.0197
229426_at	COX5A	cytochrome c oxidase subunit Va	0.7758	0.0083
229431_at	RFXAP	regulatory factor X-associated protein	0.4909	0.043
229485_x_at	LOC152573	hypothetical protein BC012029	2.9288	0.0008
229491_at	NHEDC2	Na+/H+ exchanger domain containing 2	0.8008	0.0499
229492_at	VANGL1	vang-like 1 (van gogh; Drosophila)	0.8493	0.0044
229506_at		CDNA clone IMAGE:5263177	0.8965	0.0478
229512_at		CDNA FLJ43676 fis; clone SYNOV4009129	1.5804	0.0038
229534_at	ACOT4	acyl-CoA thioesterase 4	0.421	0.0358

229537_at		Transcribed locus; strongly similar to XP_513538.1 similar to LIM domain transcription factor LMO4 (LIM-only protein 4) (LMO-4) (Breast tumor autoantigen) [Pan troglodytes]	0.1565	0.008
229543_at	FAM26F	Family with sequence similarity 26; member F	0.5245	0.0233
229560_at	TLR8	toll-like receptor 8	1.5985	0.0053
229569_at		CDNA clone IMAGE:5263455	0.2756	0.0441
229580_at		Transcribed locus	0.6945	0.021
229595_at	CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	0.7225	0.0417
229597_s_at	WDFY4	WDFY family member 4	0.3807	0.0261
229603_at	BBS12	Bardet-Biedl syndrome 12	1.0561	0.0023
229605_at	LOC606495	hypothetical protein LOC606495	0.3188	0.0148
229625_at	GBP5	guanylate binding protein 5	0.5477	0.0114
229629_at		Transcribed locus	0.2488	0.0043
229635_at		CDNA clone IMAGE:4800262	0.7762	0.0136
229657_at	THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	0.8795	0.0426
229681_at			0.2162	0.0416
229691_at		Full-length cDNA clone CS0DH005YI18 of T cells (Jurkat cell line) of Homo sapiens (human)	0.3482	0.0315
229713_at		Transcribed locus; strongly similar to XP_001145575.1 hypothetical protein [Pan troglodytes]	1.3162	0.0004
229743_at	ZNF438	zinc finger protein 438	0.4592	0.0181
229776_at	SLCO3A1	solute carrier organic anion transporter family; member 3A1	0.5997	0.0002
229801_at	C10orf47	chromosome 10 open reading frame 47	0.4485	0.0446
229803_s_at		Transcribed locus	0.8191	0.0418
229811_at		Transcribed locus; strongly similar to XP_001088798.1 adhesion regulating molecule 1 isoform 1 [Macaca mulatta]	0.45	0.0113
229815_at		CDNA clone IMAGE:4814828	1.124	0.023
229831_at	CNTN3	contactin 3 (plasmacytoma associated)	1.377	0.0345
229842_at			0.1326	0.0021
229844_at		Transcribed locus	0.5182	0.0125
229864_at	TMEM103	Transmembrane protein 103	0.4771	0.0156
229900_at	CD109	CD109 molecule	0.3844	0.041
229905_at	RAP1GDS1	RAP1; GTP-GDP dissociation stimulator 1	0.8402	0.0341
229906_at	ARMC7	armadillo repeat containing 7	0.2871	0.0084
229925_at	SLC6A17	solute carrier family 6; member 17	0.8553	0.0408
229929_at	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	0.3472	0.0152
229934_at		Mir-223 transcript variant 1 mRNA; complete sequence	0.2152	0.0263
229937_x_at	LILRB1	Leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 1	1.1665	0.0106
229940_at	SETD3	SET domain containing 3	0.2556	0.0474
229962_at	LRRC37A3	leucine rich repeat containing 37; member A3	0.6678	0.0499
229968_at		Transcribed locus	1.161	0.0003
229971_at	GPR114	G protein-coupled receptor 114	0.1765	0.0101
229984_at		Transcribed locus	0.8391	0.0021
229997_at	VANGL1	vang-like 1 (van gogh; Drosophila)	0.6247	0.0369
230059_at	DEAF1	Deformed epidermal autoregulatory factor 1 (Drosophila)	0.1462	0.048
230062_at	KIAA1666	KIAA1666 protein, similar to Peripheral-type benzodiazepine receptor-associated protein 1 (PRAX-1) (Peripheral benzodiazepine receptor-interacting protein) (PBR-IP) (RIM-binding protein 1) (RIM-BP1)	0.2631	0.0182
230067_at	FAM124A	Family with sequence similarity 124A	0.3412	0.0069
230083_at	USP53	ubiquitin specific peptidase 53	1.127	0.0466
230121_at	C1orf133	chromosome 1 open reading frame 133	0.3258	0.0112
230157_at	CDH24	cadherin-like 24	0.2752	0.0125
230233_at		Transcribed locus	1.1538	0.0493
230243_at	RG9MTD2	RNA (guanine-9-) methyltransferase domain containing 2	0.5805	0.0303

230261_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 4	0.8216	0.0183
230263_s_at	DOCK5	dedicator of cytokinesis 5	2.4486	0.0042
230264_s_at	AP1S2	adaptor-related protein complex 1; sigma 2 subunit	0.9512	0.0007
230300_at		CDNA FLJ42315 fis; clone TRACH2019661	0.9177	0.0412
230301_at		Transcribed locus	0.4768	0.028
230309_at		Transcribed locus	1.5535	0.0271
230329_s_at	NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	1.1299	0.032
230334_at		CDNA clone IMAGE:40078968	0.2535	0.036
230335_at	C9orf50	chromosome 9 open reading frame 50	0.1506	0.0329
230376_at		Transcribed locus	0.4951	0.0328
230383_x_at		Transcribed locus	1.5202	0.0072
230391_at	CD84	CD84 molecule	1.4762	0.0084
230399_at		Transcribed locus	0.8858	0.0098
230405_at	LOC441108	hypothetical gene supported by AK128882	0.6787	0.0229
230413_s_at	AP1S2	Adaptor-related protein complex 1; sigma 2 subunit	0.4559	0.0262
230422_at	FPRL2	formyl peptide receptor-like 2	1.2418	0.0176
230444_at		Transcribed locus	0.1624	0.0195
230486_at		Transcribed locus	0.3717	0.0147
230499_at		Transcribed locus	0.4008	0.0478
230526_at		CDNA clone IMAGE:5286005	0.16	0.0499
230542_at	ZNF597	zinc finger protein 597	0.3182	0.0087
230550_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	1.67	0.0021
230557_at	XRRA1	X-ray radiation resistance associated 1	0.221	0.0398
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	2.1556	0.0098
230566_at	C22orf27	chromosome 22 open reading frame 27	0.2645	0.0195
230606_at	GJC1	Gap junction protein; chi 1; 31.9kDa	1.0486	0.0029
230632_at		Full-length cDNA clone CS0DI051YA02 of Placenta Cot 25-normalized of Homo sapiens (human)	0.1648	0.0308
230642_at		Transcribed locus	0.1326	0.0355
230753_at	LOC197135	hypothetical LOC197135	0.2788	0.0355
230773_at		Transcribed locus	0.2276	0.01
230792_at	FAAH2	fatty acid amide hydrolase 2	1.4782	0.0078
230823_at			0.1967	0.0289
230830_at	OSTbeta	organic solute transporter beta	0.339	0.0125
230849_at	KCNA1	potassium voltage-gated channel; shaker-related subfamily; member 1 (episodic ataxia with myokymia)	0.1246	0.0253
230860_at		Transcribed locus	0.568	0.0129
230866_at	CYSLTR1	cysteinyl leukotriene receptor 1	0.3294	0.0128
230888_at	WDR91	WD repeat domain 91	0.7633	0.0248
230914_at	HNF4A	hepatocyte nuclear factor 4; alpha	0.4101	0.0303
230983_at	FAM129C	family with sequence similarity 129; member C	0.2121	0.0126
231011_at	LARP2	La ribonucleoprotein domain family; member 2	0.2123	0.0034
231082_at	IGL@	Immunoglobulin lambda locus	0.1541	0.0321
231093_at	FCRL3	Fc receptor-like 3	0.1898	0.0108
231100_at	RRAD	Ras-related associated with diabetes	0.2266	0.0045
231104_at	TDRD5	tudor domain containing 5	0.2894	0.0436
231120_x_at	PKIB	protein kinase (cAMP-dependent; catalytic) inhibitor beta	1.0156	0.0009
231145_at		Transcribed locus	0.2083	0.0056
231184_at	DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	0.1343	0.0221
231226_at	LOC728142	hypothetical protein LOC728142	0.1658	0.0432
231236_at	ZFP57	zinc finger protein 57 homolog (mouse)	0.2282	0.0386
231283_at	MGAT4A	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme A	0.414	0.0001
231376_at	UPP2	uridine phosphorylase 2	0.1272	0.0185
231377_at	LOC158830	similar to Ab2-183	0.1288	0.0349
231382_at	FGF18	Fibroblast growth factor 18	0.4935	0
231491_at	C21orf23	chromosome 21 open reading frame 23	0.1198	0.0039
231514_at	C1orf94	chromosome 1 open reading frame 94	0.3981	0.0259
231528_at		CDNA FLJ30460 fis; clone BRACE2009434	0.569	0.0041

231603_at	RNASE11	ribonuclease; RNase A family; 11 (non-active)	0.8281	0.0005
231655_x_at			0.129	0.0365
231727_s_at	MIF4GD	MIF4G domain containing	1.1156	0.0178
231747_at	CYSLTR1	cysteinyl leukotriene receptor 1	0.4325	0.0097
231769_at	FBXO6	F-box protein 6	1.4221	0.0145
231776_at	EOMES	eomesodermin homolog (Xenopus laevis)	0.8053	0.0025
231780_at	GBGT1	globoside alpha-1;3-N-acetylgalactosaminyltransferase 1	1.1619	0.0465
231790_at	DMGDH	dimethylglycine dehydrogenase	0.6855	0.0123
231817_at	USP53	ubiquitin specific peptidase 53	1.4318	0.0166
231824_at	LARP2	La ribonucleoprotein domain family; member 2	0.5683	0.0044
231849_at	KRT80	keratin 80	2.0722	0.0023
231871_at	GPR180	G protein-coupled receptor 180	0.5497	0.0438
231912_s_at	DKFZP434B 0335	DKFZP434B0335 protein	0.5531	0.0049
231913_s_at	BRCC3	BRCA1/BRCA2-containing complex; subunit 3	1.1249	0.028
231929_at	IKZF2	IKAROS family zinc finger 2 (Helios)	1.1544	0.0385
232024_at	GIMAP2	GTPase; IMAP family member 2	1.4677	0.0206
232036_at	KLC1	Kinesin light chain 1	0.358	0.0148
232067_at	C6orf168	chromosome 6 open reading frame 168	0.6279	0.0033
232068_s_at	TLR4	toll-like receptor 4	0.3597	0.0313
232072_at			0.308	0.0133
232154_at	LOC199800	hypothetical protein LOC199800	0.4767	0.001
232197_x_at	ARSB	arylsulfatase B	0.3194	0.0261
232209_x_at	HM13	histocompatibility (minor) 13	0.3649	0.043
232311_at	B2M	Beta-2-microglobulin	0.5171	0.0055
232364_at	FBXO11	F-box protein 11	0.1329	0.0429
232378_at	SLC5A9	solute carrier family 5 (sodium/glucose cotransporter); member 9	0.1985	0.0468
232383_at	TFEC	transcription factor EC	0.4344	0.0078
232403_at	SPG11	spastic paraplegia 11 (autosomal recessive)	0.2881	0.019
232434_at	DIRC3	disrupted in renal carcinoma 3	0.2454	0.0358
232504_at			0.2447	0.0038
232513_x_at	C20orf107	chromosome 20 open reading frame 107	0.1009	0.0487
232543_x_at	ARHGAP9	Rho GTPase activating protein 9	0.8966	0.0104
232574_at	XYLT1	xylosyltransferase I	0.1284	0.0342
232667_at		CDNA FLJ13690 fis; clone PLACE2000097	0.2473	0.0036
232687_at		CDNA FLJ33091 fis; clone TRACH2000660	0.5344	0.0023
232724_at	MS4A6A	membrane-spanning 4-domains; subfamily A; member 6A	0.4413	0.0081
232785_at	RGAG1	retrotransposon gag domain containing 1	0.2738	0.0096
232792_at	TRIM69	tripartite motif-containing 69	0.647	0.0199
232798_at	DNAJC5B	DnaJ (Hsp40) homolog; subfamily C; member 5 beta	0.3559	0.0207
232821_at	FAM112A	family with sequence similarity 112; member A	0.1444	0.0143
232827_at		Clone L50 polyadenylated HERV LTR sequence and flanking cellular sequence; mRNA	0.6809	0.0294
232959_at	LOC645513	similar to septin 7	0.1873	0.0391
232977_x_at	MYH14	myosin; heavy chain 14	0.55	0.0044
232986_at	ZNF233	zinc finger protein 233	0.3125	0.0215
233052_at	DNAH8	dynein; axonemal; heavy chain 8	0.1462	0.0101
233146_at	KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1	0.2012	0.0346
233216_at	ZDHHC21	zinc finger; DHHC-type containing 21	0.2095	0.0147
233218_at		CDNA FLJ12177 fis; clone MAMMA1000720	0.1281	0.0325
233220_at	GRIN3A	glutamate receptor; ionotropic; N-methyl-D-aspartate 3A	0.1186	0.0162
233256_at		CDNA: FLJ21297 fis; clone COL02035	0.118	0.0485
233334_x_at	GIYD1	GIY-YIG domain containing 1, GIY-YIG domain containing 2, sulfotransferase family; cytosolic; 1A; phenol-preferring; member 3, sulfotransferase family; cytosolic; 1A; phenol-preferring; member 4	0.5846	0.0296
233491_at			0.2038	0.0029
233510_s_at	PARVG	parvin; gamma	0.5414	0.0094
233520_s_at	CMYA5	cardiomyopathy associated 5	0.2199	0.0088
233557_s_at	MON1B	MON1 homolog B (yeast)	0.7854	0.0042

233592_at	ANKRD18A	ankyrin repeat domain 18A, ankyrin repeat domain 19, hypothetical LOC643133	0.1359	0.0476
233612_at		CDNA FLJ12420 fis; clone MAMMA1003049	0.1284	0.0394
233725_at			0.189	0.0009
233744_at		Uncharacterized gastric protein ZG33P	0.1829	0.0404
233809_at	HYPK	Huntingtin interacting protein K	0.2558	0.0231
233825_s_at	CD99L2	CD99 molecule-like 2	1.0894	0.0337
233857_s_at	ASB2	ankyrin repeat and SOCS box-containing 2	0.2584	0.0014
233864_s_at	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.3308	0.0368
233969_at	IGL@	Immunoglobulin lambda light chain, Immunoglobulin lambda locus	0.151	0.0019
234072_at	SEMA4A	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4A	0.1398	0.0233
234100_at		CDNA FLJ13402 fis; clone PLACE1001456	0.1141	0.0137
234147_at	LOC286059	hypothetical protein LOC286059	0.1007	0.0474
234165_at	PTGDR	prostaglandin D2 receptor (DP)	0.7209	0.0248
234269_at		CDNA FLJ20012 fis; clone ADKA03438	0.1602	0.0158
234273_at		MRNA; cDNA DKFZp434M031 (from clone DKFZp434M031)	0.1477	0.0231
234290_x_at	MYH14	myosin; heavy chain 14	0.5064	0.0169
234294_x_at	GATAD2A	GATA zinc finger domain containing 2A	0.7901	0.0029
234295_at	DBR1	debranching enzyme homolog 1 (S. cerevisiae)	0.731	0.0056
234304_s_at	IPO11	importin 11	0.8442	0.0316
234305_s_at	MLZE	melanoma-derived leucine zipper; extra-nuclear factor	0.2721	0.0063
234336_s_at	TTLL9	tubulin tyrosine ligase-like family; member 9	0.1427	0.0024
234349_at	SSPO	SCO-spondin homolog (Bos taurus)	0.1471	0.0458
234362_s_at	CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.1704	0.0392
234386_s_at	C15orf49	chromosome 15 open reading frame 49	0.1043	0.0493
234434_at		MRNA; cDNA DKFZp434F0535 (from clone DKFZp434F0535)	0.1287	0.0425
234446_at		MRNA; cDNA DKFZp434O0212 (from clone DKFZp434O0212)	0.2116	0.012
234460_at			0.1231	0.0407
234471_s_at	NCOA5	nuclear receptor coactivator 5	0.4325	0.0357
234561_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	0.1097	0.0196
234631_at	KRTAP4-8	keratin associated protein 4-8	0.1595	0.027
234653_at	LOC649898	Similar to NACHT-; LRR- and PYD-containing protein 2 (PYRIN-containing APAF1-like protein 2) (Nucleotide-binding site protein 1)	0.2047	0.0183
234657_at		CDNA: FLJ23521 fis; clone LNG04928	0.1494	0.0216
234770_at			0.1083	0.0401
234797_at			0.1567	0.0106
234903_at	OR2B3	olfactory receptor; family 2; subfamily B; member 3	0.1023	0.0282
234956_at	LOC93444	hypothetical protein LOC93444	0.1814	0.0284
234986_at	GCLM	glutamate-cysteine ligase; modifier subunit	0.8805	0.0074
235096_at	LEO1	Leo1; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	0.5338	0.0329
235133_at		Homo sapiens; clone IMAGE:5787583; mRNA	0.3215	0.0441
235175_at	GBP4	guanylate binding protein 4	0.5109	0.01
235199_at	RNF125	ring finger protein 125	0.8902	0
235229_at		Transcribed locus; weakly similar to XP_001117086.1 similar to Olfactory receptor 10T2 (Olfactory receptor OR1-3) [Macaca mulatta]	0.3213	0.0469
235249_at	RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	0.1366	0.0295
235296_at	EIF5A2	eukaryotic translation initiation factor 5A2	0.9924	0.0104
235299_at		Transcribed locus	1.0651	0.0359
235346_at	FUNDC1	FUN14 domain containing 1	0.7308	0.0238
235353_at	KIAA0746	KIAA0746 protein	0.3488	0.0136
235385_at		CDNA FLJ34016 fis; clone FCBBF2002541	1.0627	0.0069
235396_at	C22orf25	chromosome 22 open reading frame 25	0.7	0.0004

235397_at	LOC285908	hypothetical protein LOC285908	0.2031	0.0312
235403_at		Transcribed locus	0.1509	0.0089
235437_at		Transcribed locus	0.2053	0.0253
235458_at	HAVCR2	hepatitis A virus cellular receptor 2	1.2875	0.0076
235517_at	C4orf28	chromosome 4 open reading frame 28	0.2896	0.0336
235523_at		Transcribed locus	0.1374	0.0344
235552_at	KIAA1627	KIAA1627 protein	0.4439	0.044
235565_at	ZNF425	Zinc finger protein 425	0.125	0.0081
235651_at			0.2333	0.0236
235661_at		Transcribed locus	0.3067	0.0487
235667_at	LOC643783	hypothetical LOC643783	0.4817	0.0015
235675_at	DHFRL1	dihydrofolate reductase-like 1	0.6992	0.0037
235689_at	MTFMT	mitochondrial methionyl-tRNA formyltransferase	0.851	0.0259
235696_at		CDNA clone IMAGE:4837650	1.4486	0.0122
235733_at		Transcribed locus	0.7472	0.0067
235736_at		Homo sapiens; clone IMAGE:5167600; mRNA	0.7531	0.0034
235740_at		Transcribed locus	1.139	0.0052
235751_s_at	VMO1	vitelline membrane outer layer 1 homolog (chicken)	0.638	0.0299
235754_at	HFE	hemochromatosis	0.5259	0.0324
235756_at		CDNA FLJ26187 fis; clone ADG04782	0.4225	0.0014
235766_x_at		CDNA clone IMAGE:5745639	1.3687	0.0134
235770_at	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	0.5279	0.0239
235812_at	TMEM188	transmembrane protein 188	0.5007	0.0488
235857_at	KCTD11	potassium channel tetramerisation domain containing 11	0.4465	0.047
235864_at	MPP5	Membrane protein; palmitoylated 5 (MAGUK p55 subfamily member 5)	0.5492	0.0015
235870_at	LOC339524	hypothetical protein LOC339524	0.1411	0.0427
235900_at	SPNS3	spinster homolog 3 (Drosophila)	0.3038	0.012
235939_at		CDNA FLJ36815 fis; clone ASTRO2003740	0.6118	0.0203
235981_at	C8orf22	chromosome 8 open reading frame 22	0.1182	0.0333
236001_at	LOC400573	hypothetical gene supported by BC015790; BC041634	0.2185	0.0115
236018_at			0.2925	0.0373
236029_at	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	0.4675	0.0242
236085_at	CAPSL	calcyphosine-like	0.2369	0.0171
236086_at		Transcribed locus	0.1334	0.0291
236125_at		CDNA FLJ31332 fis; clone MAMGL1000096	0.3642	0.0316
236140_at	GCLM	glutamate-cysteine ligase; modifier subunit	0.5	0.0442
236141_at	NBLA00301	putative protein product of Nbla00301	0.1435	0.0205
236148_at		Full length insert cDNA clone YA80A03	0.2334	0.0314
236150_at	LOC123688	similar to RIKEN cDNA C630028N24 gene	0.3439	0.0448
236165_at	MSL3L1	male-specific lethal 3-like 1 (Drosophila)	0.19	0.0365
236190_at	XYLT1	Xylosyltransferase I	0.8847	0.0465
236193_at	HIST1H2BC	histone cluster 1; H2bc	0.8709	0.0257
236219_at	TMEM20	transmembrane protein 20	0.3644	0.0274
236228_at		Clone pp7583 unknown mRNA	0.2406	0.0151
236262_at	MMRN2	multimerin 2	1.4808	0.0378
236280_at		Transcribed locus	0.3684	0.006
236283_x_at	PAK2	p21 (CDKN1A)-activated kinase 2	0.3842	0.0423
236295_s_at	NLRC3	NLR family; CARD domain containing 3	0.4826	0.0054
236347_at	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	0.5935	0.0114
236398_s_at		Homo sapiens; clone IMAGE:3896086; mRNA	0.2294	0.0494
236407_at	KCNE1	potassium voltage-gated channel; Isk-related family; member 1	0.1403	0.0425
236434_at	PES1	pescadillo homolog 1; containing BRCT domain (zebrafish)	0.201	0.0038
236442_at	DPF3	D4; zinc and double PHD fingers; family 3	0.556	0.0288
236445_at	LOC731986	similar to cytochrome P450 monooxygenase CYP2T1	0.1675	0.0383
236464_at		Transcribed locus	0.1933	0.002
236506_at		Transcribed locus	0.7035	0.0016
236527_at		Transcribed locus	0.7144	0.0435

236539_at	PTPN22	protein tyrosine phosphatase; non-receptor type 22 (lymphoid)	0.3112	0.0213
236595_at			0.2132	0.0213
236627_at		Transcribed locus	0.1876	0.0136
236721_at	ALKBH1	alkB; alkylation repair homolog 1 (E. coli)	0.3634	0.0177
236787_at		CDNA FLJ35091 fis; clone PLACE6005786	0.3125	0.0344
236835_at	LOC645431	hypothetical protein LOC645431	0.3434	0.0116
236891_at			0.1631	0.0041
236921_at		Transcribed locus	0.997	0.0328
236927_at	SVEP1	sushi; von Willebrand factor type A; EGF and pentraxin domain containing 1	0.2401	0.0414
236954_at	BOLL	bol; boule-like (Drosophila)	0.2106	0.0028
236987_at			0.1624	0.0252
236995_x_at	TFEC	transcription factor EC	0.2691	0.0244
237003_at	BEST3	bestrophin 3	0.3908	0.0039
237083_at		Transcribed locus	0.6627	0.0237
237115_at		Transcribed locus; strongly similar to XP_530679.1 hypothetical protein XP_530679 [Pan troglodytes]	0.1769	0.0127
237117_at	LOC727930	similar to CG10275-PA	0.1852	0.0158
237133_at		Transcribed locus	0.1345	0.0052
237201_at		Transcribed locus	0.218	0.0011
237240_at		Transcribed locus	0.202	0.0104
237276_at	NASP	Nuclear autoantigenic sperm protein (histone-binding)	0.1609	0.0368
237293_at		Transcribed locus	0.1786	0.0408
237320_at	FAM137B	family with sequence similarity 137; member B	0.2127	0.0423
237339_at	hCG_25653	hCG25653	0.182	0.0099
237354_at	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.1181	0.0318
237363_at	C9orf68	chromosome 9 open reading frame 68	0.2008	0.0342
237372_at		Transcribed locus	0.3201	0.0182
237423_at	RSPO4	R-spondin family; member 4	0.1456	0.0357
237440_at		Transcribed locus	0.308	0.0132
237486_at		Transcribed locus	0.1269	0.0426
237595_at	LMX1A	LIM homeobox transcription factor 1; alpha	0.1408	0.0169
237638_at			0.1051	0.0448
237690_at	GPR115	G protein-coupled receptor 115	0.6125	0.003
237694_at		Transcribed locus	0.1345	0.0243
237710_at		Transcribed locus	0.1652	0.0455
237712_at		Transcribed locus; strongly similar to XP_001142191.1 hypothetical protein [Pan troglodytes]	0.1731	0.033
237722_at	FLI1	Friend leukemia virus integration 1	0.1329	0.0339
237759_at	CD48	CD48 molecule	0.4937	0.0127
237807_at	SPATA12	spermatogenesis associated 12	0.2631	0.0306
237814_at		Transcribed locus	0.2181	0.0008
237837_at		Transcribed locus	0.1398	0.0423
237967_at	HAL	Histidine ammonia-lyase	0.1194	0.0255
238002_at	GOLIM4	golgi integral membrane protein 4	0.4947	0.0253
238005_s_at		Transcribed locus	1.117	0.0107
238045_at	TMEM65	transmembrane protein 65	0.2894	0.0215
238053_at	DHRSX	dehydrogenase/reductase (SDR family) X-linked	0.4495	0.0285
238078_at		Transcribed locus	0.268	0.0406
238088_at		CDNA clone IMAGE:5259414	0.151	0.0179
238142_at		CDNA FLJ37584 fis; clone BRCOC2004950	1.1428	0.0029
238143_at	LOC646627	phospholipase inhibitor	0.1078	0.0196
238171_at	SLC25A30	solute carrier family 25; member 30	0.1419	0.0123
238187_at	C2orf57	chromosome 2 open reading frame 57	0.1234	0.0497
238190_at	TUFM	Tu translation elongation factor; mitochondrial	0.4284	0.0337
238195_at		Full length insert cDNA YI09H09	0.1096	0.0404
238250_at		Transcribed locus	0.1495	0.0137
238376_at		CDNA FLJ30967 fis; clone HEART2000309; weakly similar to PTB-ASSOCIATED SPLICING FACTOR	0.9192	0.0042
238430_x_at	SLFN5	schlafen family member 5	1.2237	0.0215

238451_at	MPP7	membrane protein; palmitoylated 7 (MAGUK p55 subfamily member 7)	0.8099	0.0303
238462_at	STS-1	Cbl-interacting protein Sts-1	0.3459	0.0113
238465_at	C5orf35	chromosome 5 open reading frame 35	1.1744	0.011
238466_at		CDNA FLJ33443 fis; clone BRALZ1000103	1.4335	0.0151
238467_at		CDNA FLJ41419 fis; clone BRHIP2002339	1.187	0.0152
238518_x_at	GLYCTK	glycerate kinase	0.259	0.0382
238533_at	EPHA7	EPH receptor A7	0.3531	0.0192
238567_at	SGPP2	sphingosine-1-phosphate phosphotase 2	1.392	0.0269
238581_at	GBP5	guanylate binding protein 5	0.4262	0.0093
238587_at	STS-1	Cbl-interacting protein Sts-1	0.2814	0.033
238606_at	ZNF747	zinc finger protein 747	0.5707	0.0341
238622_at	RAP2B	RAP2B; member of RAS oncogene family	0.4933	0.0124
238668_at		Transcribed locus	0.9616	0.0172
238681_at	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	1.1184	0.0461
238692_at	BTBD11	BTB (POZ) domain containing 11	1.2424	0.025
238725_at			0.9604	0.0499
238821_at	CSTF2	Cleavage stimulation factor; 3' pre-RNA; subunit 2; 64kDa	0.4307	0.0084
238846_at	TNFRSF11A	tumor necrosis factor receptor superfamily; member 11a; NFKB activator	0.7585	0.0143
238923_at	SPOP	speckle-type POZ protein	0.353	0.0232
238948_at	TM9SF1	Transmembrane 9 superfamily member 1	0.3481	0.0466
238976_at			0.1205	0.0113
239021_at		Transcribed locus; moderately similar to XP_530714.1 hypothetical protein XP_530714 [Pan troglodytes]	0.2925	0.0311
239053_at	CIAO1	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	0.3123	0.0462
239072_at	LOC647121	similar to embigin homolog	0.885	0.0136
239098_at	KCNRG	potassium channel regulator	0.2026	0.0101
239155_at	LOC653108	similar to coxsackie virus and adenovirus receptor precursor	0.596	0.014
239196_at	ANKRD22	ankyrin repeat domain 22	0.3844	0.033
239205_s_at	CR1	complement component (3b/4b) receptor 1 (Knops blood group), complement component (3b/4b) receptor 1-like, similar to complement component (3b/4b) receptor 1 isoform F precursor	0.4383	0.0186
239231_at		CDNA FLJ41910 fis; clone PEBLM2007834	0.7909	0.0164
239287_at		Transcribed locus	0.5444	0.0486
239294_at		Transcribed locus	0.9986	0.0094
239302_s_at		MRNA; cDNA DKFZp686P18215 (from clone DKFZp686P18215)	0.7334	0.0142
239319_at	LOC728342	Hypothetical protein LOC728342	0.3919	0.0337
239328_at		CDNA FLJ35362 fis; clone SKMUS2000330	0.1626	0.042
239342_at	DGKZ	diacylglycerol kinase; zeta 104kDa	0.2104	0.0464
239374_at	TRIM65	Tripartite motif-containing 65	0.1143	0.0406
239424_at			0.1141	0.0213
239431_at	TICAM2	toll-like receptor adaptor molecule 2	0.7231	0.0055
239529_at	C5orf20	chromosome 5 open reading frame 20	0.1686	0.0276
239537_at	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 2	0.3958	0.0419
239583_x_at	PLAC7	placenta-specific 7	0.176	0.0318
239594_at	LOC145837	hypothetical protein LOC145837	0.2122	0.0088
239606_at		CDNA FLJ25345 fis; clone TST01118	0.1299	0.0207
239624_at	LOC730259	hypothetical protein LOC730259	2.2689	0.0027
239648_at	DCUN1D3	DCN1; defective in cullin neddylation 1; domain containing 3 (S. cerevisiae)	0.7109	0.008
239652_at		Transcribed locus	0.1804	0.0067
239706_x_at	PLAC7	Placenta-specific 7	0.1744	0.0249
239719_at	CD109	CD109 molecule	0.1553	0.035
239777_at	LOC283551	hypothetical protein LOC283551	1.1913	0.0285

239781_at	hCG_1815504	hCG1815504	0.1604	0.0214
239822_at		CDNA clone IMAGE:4816129	0.1565	0.0052
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.9837	0.0023
239854_at	LOC644186	hypothetical protein LOC644186	0.5108	0.0268
239888_at			1.1375	0.001
239915_at	LOC285944	hypothetical protein LOC285944	0.392	0.0388
239982_at		CDNA clone IMAGE:4831215	0.152	0.0247
240013_at		Transcribed locus	0.2436	0.0144
240015_at		Transcribed locus	0.2522	0.0265
240017_at	LOC400960	Hypothetical gene supported by BC040598	0.1605	0.0447
240064_at		Transcribed locus; strongly similar to XP_529518.1 hypothetical protein XP_529518 [Pan troglodytes]	0.3646	0.0003
240106_at	GNPTAB	N-acetylglucosamine-1-phosphate transferase; alpha and beta subunits	0.4443	0.0088
240162_at		CDNA clone IMAGE:4830758	0.1473	0.0383
240173_at		Transcribed locus	0.4577	0.0151
240196_at		Transcribed locus	0.1576	0.0443
240266_at		Transcribed locus	0.1219	0.0322
240333_at		Transcribed locus	0.1548	0.0496
240342_at	TRIM61	tripartite motif-containing 61	0.5111	0.0098
240379_at		Transcribed locus	0.1392	0.0464
240411_at	FLJ40243	hypothetical protein FLJ40243	0.1258	0.0085
240413_at	PYHIN1	pyrin and HIN domain family; member 1	0.2257	0.0035
240523_at		Homo sapiens; Similar to LOC161538; clone IMAGE:5199550; mRNA	0.589	0.0001
240533_at			0.1747	0.0091
240555_at			0.1395	0.0326
240559_at	C19orf41	chromosome 19 open reading frame 41	0.4817	0.0457
240561_at		CDNA FLJ38120 fis; clone D3OST3000195	0.1912	0.0199
240603_s_at	EXOD1	exonuclease domain containing 1	0.1209	0.0359
240663_at		Transcribed locus	0.1111	0.0341
240747_at		Transcribed locus	0.155	0.0041
240844_at		Transcribed locus	0.11	0.0389
240854_x_at			0.2115	0.0472
240857_at	DNAH9	dynein; axonemal; heavy chain 9	0.3736	0.0458
240935_at			0.1072	0.0133
240938_at		CDNA FLJ25790 fis; clone TST06909	0.1109	0.0414
240987_at			0.1138	0.0377
241085_at		CDNA FLJ42607 fis; clone BRACE3012806; weakly similar to Homo sapiens adrenergic; alpha-1A-; receptor (ADRA1A)	0.2227	0.0147
241087_at			0.1875	0.0346
241183_at			0.1148	0.0262
241281_at			0.1437	0.0384
241297_at			0.2028	0.0007
241353_s_at		Transcribed locus; strongly similar to XP_531081.2 hypothetical protein [Pan troglodytes]	0.7483	0.0058
241456_at		CDNA FLJ30785 fis; clone FEBRA2000901	0.5972	0.0228
241570_at			0.1773	0.0327
241582_at		Transcribed locus	0.1092	0.0437
241602_at	ZNF582	zinc finger protein 582	0.4539	0.0431
241635_at		Transcribed locus	0.2285	0.0144
241657_at		Transcribed locus	0.1079	0.0421
241714_at			0.1328	0.0426
241759_at	MGC5566	Hypothetical protein MGC5566	0.1403	0.0181
241803_s_at			1.1426	0.0081
241810_at			0.1457	0.0311
241840_at		Transcribed locus	0.5069	0.006
241858_at		CDNA FLJ44346 fis; clone TRACH3005808; highly similar to Homo sapiens p150	0.3985	0.0221
241864_x_at		Transcribed locus	0.5644	0.0107

241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	0.2033	0.0135
241899_at	LOC553103	hypothetical LOC553103	0.2658	0.0044
241959_at	ANAPC10	anaphase promoting complex subunit 10, similar to Anaphase-promoting complex subunit 10 (APC10) (Cyclosome subunit 10)	0.8662	0.0075
241981_at	FAM20A	family with sequence similarity 20; member A	0.4467	0.0124
242153_at		Transcribed locus	0.3843	0.0016
242158_at	PAPOLB	poly(A) polymerase beta (testis specific)	0.1427	0.0022
242281_at			0.7438	0.0072
242288_s_at	EMILIN2	elastin microfibril interfacer 2	0.1694	0.046
242295_at	FLJ32955	hypothetical protein FLJ32955	0.1336	0.0173
242323_at		Full-length cDNA clone CS0DF027YF17 of Fetal brain of Homo sapiens (human)	0.9153	0.0315
242367_at			0.1063	0.0451
242375_x_at			0.385	0.0112
242382_at		Homo sapiens; clone IMAGE:5539086; mRNA	0.1336	0.0239
242399_at			0.1597	0.0268
242401_x_at		Transcribed locus	0.1184	0.0089
242412_at		Transcribed locus	0.185	0.0013
242434_at		CDNA FLJ31093 fis; clone IMR321000161	0.2589	0.0275
242596_at		Transcribed locus; weakly similar to XP_001129408.1 hypothetical protein [Homo sapiens]	0.1879	0.0156
242648_at	KLHL8	kelch-like 8 (Drosophila)	0.6888	0.0203
242682_at			0.106	0.0217
242683_at	FLJ38028	hypothetical gene supported by AK095347	0.1355	0.041
242698_at	AKAP14	A kinase (PRKA) anchor protein 14	0.1343	0.0389
242702_at	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	0.323	0.0145
242714_at			0.3081	0.0315
242760_x_at	PIGB	phosphatidylinositol glycan anchor biosynthesis; class B	0.8671	0.0056
242882_at	RNF207	ring finger protein 207	0.2434	0.0441
242925_at	RNF148	ring finger protein 148	0.6404	0.0475
242945_at	FAM20A	family with sequence similarity 20; member A	0.4695	0.0168
242961_x_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.2199	0.0192
242963_at	SGMS2	sphingomyelin synthase 2	0.496	0.0111
242998_at	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	1.1937	0.0325
243017_at		Transcribed locus	0.6905	0.0253
243018_at		Transcribed locus; moderately similar to XP_945958.1 hypothetical protein XP_945958 [Homo sapiens]	0.3147	0.0356
243024_at	ZNF394	Zinc finger protein 394	0.3196	0.0194
243049_at			0.1672	0.0446
243099_at	NFAM1	NFAT activating protein with ITAM motif 1	0.1976	0.0344
243107_at			0.1513	0.0457
243130_at		Transcribed locus	0.3471	0.0244
243141_at	SGMS2	sphingomyelin synthase 2	0.4401	0.0008
243278_at		Transcribed locus	1.2043	0.0301
243309_at	FLJ27352	hypothetical LOC145788	0.9617	0.0155
243357_at	NEGR1	neuronal growth regulator 1	0.1754	0.0073
243366_s_at		Transcribed locus	1.4313	0.0256
243444_at			0.826	0.0002
243477_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	0.3207	0.003
243521_at		Transcribed locus	1.0506	0.0009
243680_at		Transcribed locus; strongly similar to XP_001152474.1 hypothetical protein [Pan troglodytes]	0.3573	0.0066
243698_at		Transcribed locus	0.2047	0.027
243702_at		Full length insert cDNA clone YZ94H06	0.4277	0.0377
243742_at		Transcribed locus; strongly similar to XP_001135681.1 hypothetical protein [Pan troglodytes]	0.3246	0.0014
243762_at		CDNA clone IMAGE:5298708, Prostate-specific P775P mRNA sequence	0.209	0.0442
243824_at		Homo sapiens; clone IMAGE:5213378; mRNA	0.4057	0.0396
243894_at	SLC41A2	solute carrier family 41; member 2	1.4136	0.0127
243934_at		Transcribed locus	0.2049	0.0307

243994_at	LOC730168	hypothetical protein LOC730168	0.1271	0.0181
243999_at	SLFN5	schlafen family member 5	0.5313	0.0049
244123_at		Transcribed locus	0.16	0.0318
244170_at		CDNA FLJ37366 fis; clone BRAMY2024416	1.0796	0.0404
244200_at		Transcribed locus	0.1322	0.0351
244246_at	MIPOL1	mirror-image polydactyly 1	0.8791	0.0327
244280_at		Homo sapiens; clone IMAGE:5583725; mRNA	0.1732	0.0129
244293_at		Transcribed locus	0.4103	0.0429
244352_at	CD84	CD84 molecule	0.8838	0.019
244413_at	CLECL1	C-type lectin-like 1	0.5493	0.0013
244434_at			0.3369	0.0135
244445_at		Transcribed locus	0.1253	0.0328
244485_at		Transcribed locus	0.7294	0.0466
244514_at		Transcribed locus	0.2218	0.0275
244561_at		Homo sapiens; Similar to LOC169932; clone IMAGE:4499203; mRNA	0.5901	0.0025
244572_at	KY	kyphoscoliosis peptidase	0.3514	0.0127
244641_at	C7orf30	chromosome 7 open reading frame 30	0.5504	0.0039
244653_at	SETD7	SET domain containing (lysine methyltransferase) 7	0.2317	0.0229
244680_at	GLRB	glycine receptor; beta	1.1752	0.0006
244684_at		Transcribed locus	0.2019	0.0162
244688_at		Transcribed locus	0.1728	0.0091
244705_at		CDNA FLJ33356 fis; clone BRACE2005160	0.6928	0.0248
244710_at	LRGUK	leucine-rich repeats and guanylate kinase domain containing	0.232	0.0003
244748_at		Transcribed locus	0.1227	0.0266
244749_at		Homo sapiens; clone IMAGE:5218412; mRNA	0.4119	0.0028
244752_at	ZNF438	zinc finger protein 438	0.1897	0.0185
244802_at	GLUD1	glutamate dehydrogenase 1	1.0444	0.0164
244805_at		Transcribed locus	0.1131	0.0434
31846_at	RHOD	ras homolog gene family; member D	0.4025	0.0111
32042_at	ENOX2	ecto-NOX disulfide-thiol exchanger 2	0.7949	0.0261
33736_at	STOML1	stomatin (EPB72)-like 1	1.4495	0.0119
35974_at	LRMP	lymphoid-restricted membrane protein	0.4192	0.0226
36004_at	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase gamma	0.6487	0.0281
36553_at	ASMTL	acetylserotonin O-methyltransferase-like	0.7718	0.0326
36554_at	ASMTL	acetylserotonin O-methyltransferase-like	1.0802	0.0308
36920_at	MTM1	myotubularin 1	1.4518	0.0001
36994_at	ATP6V0C	ATPase; H+ transporting; lysosomal 16kDa; V0 subunit c	0.4543	0.0232
37145_at	GNLY	granulysin	1.1253	0.0099
37170_at	BMP2K	BMP2 inducible kinase	0.5482	0.019
37278_at	TAZ	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.6441	0.0017
37943_at	ZFYVE26	zinc finger; FYVE domain containing 26	0.6185	0.0062
37953_s_at	ACCN2	amiloride-sensitive cation channel 2; neuronal	0.2122	0.0265
38043_at	FAM3A	family with sequence similarity 3; member A	1.1646	0.0114
38241_at	BTN3A3	butyrophilin; subfamily 3; member A3	0.8794	0.0446
38766_at	SRCAP	Snf2-related CBP activator protein	0.3805	0.0024
40148_at	APBB2	amyloid beta (A4) precursor protein-binding; family B; member 2 (Fe65-like)	0.511	0.0009
40420_at	STK10	serine/threonine kinase 10	1.1377	0.0174
40465_at	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	0.6075	0.0138
43511_s_at		MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	0.7938	0.0343
44120_at	ADCK2	aarF domain containing kinase 2	0.9869	0.0008
44673_at	SIGLEC1	sialic acid binding Ig-like lectin 1; sialoadhesin	1.0205	0.0249
46167_at	C1orf175	chromosome 1 open reading frame 175, tetratricopeptide repeat domain 4	0.6982	0.0374
47083_at	C7orf26	chromosome 7 open reading frame 26	0.6197	0.0056
48106_at	FLJ20489	hypothetical protein FLJ20489	1.2166	0.0205

49111_at		MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	0.5754	0.0164
49306_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	0.4404	0.0198
49485_at	PRDM4	PR domain containing 4	0.8307	0.0331
50221_at	TFEB	transcription factor EB	1.1842	0.0035
50314_i_at	C20orf27	chromosome 20 open reading frame 27	0.8574	0.0112
51158_at	LOC400451	hypothetical gene supported by AK075564; BC060873	0.4911	0.0299
51200_at	C19orf60	chromosome 19 open reading frame 60	0.4592	0.0458
59644_at	BMP2K	BMP2 inducible kinase	1.1432	0.0152
60471_at	RIN3	Ras and Rab interactor 3	1.7283	0.0034
63009_at	SHQ1	SHQ1 homolog (S. cerevisiae)	0.7046	0.0128
64064_at	GIMAP5	GTPase; IMAP family member 5	0.7401	0.0119
64432_at	C12orf47	chromosome 12 open reading frame 47	0.6198	0.0365
71933_at	WNT6	wingless-type MMTV integration site family; member 6	0.1666	0.0032
90610_at	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	0.8622	0.0077
AFFX-HSAC07/X00351_3_at	ACTB	actin; beta	0.1085	0.0285
1552256_a_at	SCARB1	scavenger receptor class B; member 1	-0.8186	0.0227
1552347_at	CRYZL1	crystallin; zeta (quinone reductase)-like 1	-0.8593	0.0138
1552461_at	FAM46D	family with sequence similarity 46; member D	-0.1447	0.0057
1552588_a_at			-0.1364	0.0152
1552592_at	MMP21	matrix metallopeptidase 21	-0.1289	0.037
1552793_at	C8orf31	chromosome 8 open reading frame 31	-1.5972	0.0185
1552829_at			-0.2647	0.0357
1552910_at	SIGLEC11	sialic acid binding Ig-like lectin 11	-2.7414	0.0069
1552911_at	SIGLEC11	sialic acid binding Ig-like lectin 11	-1.9231	0.0132
1553022_at	ZIM3	zinc finger; imprinted 3	-0.114	0.0305
1553131_a_at	GATA4	GATA binding protein 4	-0.8951	0.0469
1553227_s_at	BRWD1	bromodomain and WD repeat domain containing 1	-0.9081	0.0089
1553346_a_at	TNRC6A	trinucleotide repeat containing 6A	-0.2426	0.0201
1553349_at	ARID2	AT rich interactive domain 2 (ARID; RFX-like)	-0.9683	0.041
1553356_at		PRO0902	-0.1314	0.0064
1553387_at	ATM	ataxia telangiectasia mutated	-0.2642	0.0066
1553458_at	C10orf72	chromosome 10 open reading frame 72	-0.4755	0.0043
1553504_at	MRGPRX4	MAS-related GPR; member X4	-0.1406	0.0249
1553602_at	MUCL1	mucin-like 1	-2.6255	0.0367
1553603_s_at	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	-1.4318	0.0181
1553686_at	C18orf25	chromosome 18 open reading frame 25	-0.1526	0.0153
1553749_at	FAM76B	family with sequence similarity 76; member B	-0.2514	0.0497
1553909_x_at	C10orf6	chromosome 10 open reading frame 6	-0.7	0.0447
1553920_at	C9orf84	chromosome 9 open reading frame 84	-1.3331	0.007
1553991_s_at	FLJ20674	hypothetical protein FLJ20674	-0.3461	0.018
1554106_at	ALS2CR16	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 16	-1.3909	0.017
1554178_a_at	FAM126B	family with sequence similarity 126; member B	-0.9539	0.006
1554319_at	RPS6KA5	ribosomal protein S6 kinase; 90kDa; polypeptide 5	-0.1364	0.0055
1554512_a_at	CCDC123	coiled-coil domain containing 123	-0.3646	0.0396
1554579_a_at	MYO18B	myosin XVIIIB	-0.1909	0.0418
1554638_at	ZFYVE16	zinc finger; FYVE domain containing 16	-1.0635	0.0267
1554733_at	MGC24125	hypothetical protein MGC24125	-2.0282	0.0067
1554771_at		CDNA clone IMAGE:4300887	-0.4707	0.0484
1554889_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-0.4472	0.0069
1554907_a_at	HYDIN	hydrocephalus inducing homolog (mouse), hydrocephalus inducing homolog 2 (mouse)	-0.1395	0.034
1554994_at	RAG1	recombination activating gene 1	-0.119	0.0167
1555025_at	TMEM26	transmembrane protein 26	-0.1569	0.0307
1555088_x_at	STAT5B	signal transducer and activator of transcription 5B	-0.2458	0.0342
1555117_at			-0.1522	0.0284
1555125_at	C21orf66	chromosome 21 open reading frame 66	-0.7246	0.0387
1555131_a_at	PER3	period homolog 3 (Drosophila)	-0.212	0.0491

1555146_at	ATF2	activating transcription factor 2	-0.4386	0.0087
1555245_s_at	RP1L1	retinitis pigmentosa 1-like 1	-0.1793	0
1555322_at		PP2672	-0.1223	0.0308
1555336_a_at	ITGA9	integrin; alpha 9	-0.5501	0.0098
1555514_a_at	PIAS2	protein inhibitor of activated STAT; 2	-0.693	0.0364
1555568_at	MGC22265	hypothetical protein MGC22265	-0.1717	0.0309
1555624_a_at	SSH1	slingshot homolog 1 (Drosophila)	-0.2391	0.0181
1555685_at	H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	-0.1867	0.0129
1555723_at		OK/SW-cl.79	-0.2868	0.0012
1555926_a_at		CDNA FLJ30680 fis; clone FCBBF2000123	-0.3218	0.0197
1555950_a_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-1.7924	0.0097
1555997_s_at	IGFBP5	insulin-like growth factor binding protein 5	-0.4169	0.0092
1556035_s_at	ZNF207	zinc finger protein 207	-1.4436	0.0103
1556049_at	RTN4	reticulon 4	-1.0748	0.0481
1556054_at		Full length insert cDNA clone ZD45C02	-1.1131	0.0106
1556060_a_at	KIAA1702	KIAA1702 protein	-1.1417	0.0043
1556105_at		CDNA FLJ41020 fis; clone UTERU2019163	-1.2023	0.0117
1556125_at	GPATCH2	G patch domain containing 2	-0.2575	0.041
1556277_a_at	PAPD4	PAP associated domain containing 4	-0.9744	0.0423
1556338_at		CDNA FLJ39845 fis; clone SPLEN2014452	-0.9303	0.0317
1556352_at		CDNA FLJ30440 fis; clone BRACE2009185	-0.8806	0.0098
1556364_at	LOC730057	Hypothetical protein LOC730057	-1.8661	0.0043
1556432_at		CDNA FLJ35329 fis; clone PROST2013873	-0.3788	0.0079
1556493_a_at	JMJD2C	jumonji domain containing 2C	-0.9029	0.0229
1556543_at		Full length insert cDNA clone YW18F01	-0.9294	0.0244
1556560_a_at	TSSK3	CDNA FLJ36415 fis; clone THYMU2010917, Testis-specific serine kinase 3	-0.2265	0.0226
1556568_a_at		Clone C4E 5.3 (CAC)n/(GTG)n repeat-containing mRNA	-2.5086	0.0024
1556582_at		CDNA FLJ25946 fis; clone JTH14258	-0.7024	0.0439
1556589_at		CDNA FLJ25645 fis; clone SYN00113	-2.1607	0.0012
1556590_s_at		CDNA FLJ25645 fis; clone SYN00113	-2.5236	0.0012
1556622_s_at		Full length insert cDNA clone YP97D11	-0.1189	0.0153
1556650_at		CDNA FLJ13011 fis; clone NT2RP3000561	-0.5508	0.0161
1556659_at		CDNA FLJ33647 fis; clone BRAMY2024374	-0.527	0.0196
1556682_s_at		Full length insert cDNA clone ZD73H04	-0.4634	0.0152
1556683_x_at		Full length insert cDNA clone ZD73H04	-0.3934	0.0064
1556689_a_at	WNT4	wingless-type MMTV integration site family; member 4	-0.3547	0.0242
1556715_at	PRPSAP1	Phosphoribosyl pyrophosphate synthetase-associated protein 1	-0.6383	0.0363
1556775_at		CDNA clone IMAGE:5271366	-0.2587	0.0142
1556787_s_at			-0.1996	0.0108
1556894_at	NT5DC2	5'-nucleotidase domain containing 2	-0.2489	0.0339
1556925_at	SMC3	Structural maintenance of chromosomes 3	-0.3274	0.0357
1556933_at		Full length insert cDNA clone YP43E01	-0.1729	0.0147
1556964_s_at		CDNA FLJ34002 fis; clone FCBBF1000206	-0.1443	0.0431
1556984_at		Full length insert cDNA clone YU27A09	-0.2448	0.0337
1557050_at	HOXA2	Homeobox A2	-0.4252	0.0337
1557094_at	LOC653110	hypothetical LOC653110, hypothetical protein LOC728449	-0.1166	0.0271
1557192_at	C1orf136	chromosome 1 open reading frame 136	-0.5783	0.02
1557223_at	SDHALP2	succinate dehydrogenase complex; subunit A; flavoprotein pseudogene 2	-0.4239	0.0493
1557224_at		CDNA FLJ30981 fis; clone HHDPC2000258	-0.8544	0.0245
1557239_at		Full length insert cDNA clone YW25E05	-1.6287	0.0036
1557240_a_at		Full length insert cDNA clone YW25E05	-1.7058	0.0059
1557246_at	KIDINS220	kinase D-interacting substrate of 220 kDa	-1.6555	0.0031
1557252_at		CDNA FLJ36213 fis; clone THYMU2000671	-0.9479	0.0015
1557289_s_at	GTF2IRD2	GTF2I repeat domain containing 2	-0.2259	0.0456
1557315_a_at		CDNA FLJ39920 fis; clone SPLEN2020166	-0.2762	0.0243
1557326_at		CDNA clone IMAGE:5301138	-1.2094	0.0198

1557339_at		Homo sapiens; clone IMAGE:5190399; mRNA	-0.119	0.0493
1557352_at	SQLE	Squalene epoxidase	-2.171	0.009
1557360_at	LRPPRC	leucine-rich PPR-motif containing	-1.1542	0.0475
1557403_s_at		CDNA FLJ36685 fis; clone UTERU2008018	-0.384	0.0065
1557437_a_at		CDNA clone IMAGE:5288367	-0.536	0.0176
1557502_at	PCCB	Propionyl Coenzyme A carboxylase; beta polypeptide	-0.1023	0.0084
1557506_a_at		Full length insert cDNA YH97B03	-0.1547	0.0257
1557543_at		MRNA; cDNA DKFZp313P2412 (from clone DKFZp313P2412)	-0.7199	0.0338
1557637_at		CDNA clone IMAGE:5267718	-0.3159	0.0027
1557683_at		CDNA FLJ14065 fis; clone HEMBB1000917	-0.1845	0.0247
1557685_at	C4orf38	chromosome 4 open reading frame 38	-0.5531	0.0165
1557689_at		CDNA FLJ11951 fis; clone HEMBB1000827	-0.9839	0.0114
1557690_x_at		CDNA FLJ11951 fis; clone HEMBB1000827	-0.9107	0.0136
1557699_x_at		Homo sapiens; clone IMAGE:4043992; mRNA	-0.4205	0.0046
1557706_at	ZHX2	zinc fingers and homeoboxes 2	-0.4656	0.0118
1557707_at		UV-B repressed sequence; HUR 8	-0.3803	0.046
1557719_at	PIP5K3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase; type III	-0.2824	0.0405
1557737_s_at	NKTR	natural killer-tumor recognition sequence	-0.5972	0.0375
1557751_at		CDNA FLJ32996 fis; clone THYMU1000142	-0.6556	0.011
1557805_at		Full length insert cDNA clone YT85B06	-0.6097	0.0297
1557818_x_at		HSPC103	-0.1238	0.0175
1557830_at		CDNA FLJ10112 fis; clone HEMBA1002750	-0.9112	0.0307
1557832_at		CDNA FLJ20833 fis; clone ADKA02957	-0.1514	0.0103
1557837_a_at	ELMOD2	ELMO/CED-12 domain containing 2	-0.1204	0.0427
1557895_at	FLJ35934	FLJ35934 protein	-0.417	0.0494
1557945_at	TCTE3	T-complex-associated-testis-expressed 3	-0.985	0.0445
1558109_x_at	LOC283788	hypothetical protein LOC283788	-0.2446	0.0361
1558142_at	TNRC6B	trinucleotide repeat containing 6B	-0.9952	0.0337
1558163_at	PEX13	Peroxisome biogenesis factor 13	-0.3346	0.0061
1558164_s_at	PEX13	Peroxisome biogenesis factor 13	-1.1308	0.0059
1558247_s_at	LOC126147	hypothetical protein BC018697	-0.1332	0.0114
1558348_at		CDNA FLJ33447 fis; clone BRAMY1000098	-0.4211	0.0452
1558385_at			-0.5265	0.0401
1558414_at	C9orf4	chromosome 9 open reading frame 4	-0.4626	0.0251
1558430_at		CDNA FLJ36648 fis; clone UTERU1000138	-0.2284	0.0441
1558476_at	C1orf165	Chromosome 1 open reading frame 165	-0.234	0.0229
1558512_at		CDNA FLJ33400 fis; clone BRACE2009828	-0.6685	0.0124
1558586_at	ZNF33B	zinc finger protein 33B	-0.3866	0.0247
1558600_a_at		CDNA FLJ37778 fis; clone BRHIP2026557	-0.3442	0.0172
1558631_at	PPARA	peroxisome proliferator-activated receptor alpha	-0.4942	0.0499
1558695_at		Full length insert cDNA clone YR58H12	-2.1174	0.003
1558787_a_at		CDNA FLJ43445 fis; clone OCBBF2031366	-0.14	0.008
1558815_at	SORBS2	sorbin and SH3 domain containing 2	-1.87	0.0035
1558822_at		Full length insert cDNA clone YP59C02	-0.7476	0.0263
1558849_at	LOC284276	hypothetical protein LOC284276	-0.2409	0.048
1558893_a_at	CCDC67	coiled-coil domain containing 67	-0.139	0.0466
1558900_at		CDNA FLJ11322 fis; clone PLACE1010329	-0.1423	0.0281
1558969_a_at	RPL32P3	ribosomal protein L32 pseudogene 3	-0.2921	0.0087
1559026_at		CDNA clone IMAGE:5295490	-0.1964	0.0467
1559038_at	2-Sep	septin 2	-1.2085	0.0256
1559039_at	DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	-0.4519	0.0278
1559109_a_at		CDNA FLJ32270 fis; clone PROST1000527	-0.1277	0.036
1559114_a_at	CXCR7	Chemokine (C-X-C motif) receptor 7	-0.1909	0.0195
1559117_at		CDNA FLJ34664 fis; clone LIVER2000592	-2.7933	0.0008
1559127_x_at	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	-0.2349	0.0002
1559128_at	HSDL2	hydroxysteroid dehydrogenase like 2	-1.0571	0.0004
1559156_at		MRNA; cDNA DKFZp686B1142 (from clone DKFZp686B1142)	-1.0221	0.0223
1559206_at	PSEN1	presenilin 1 (Alzheimer disease 3)	-0.12	0.0359

1559249_at	ATXN1	ataxin 1	-0.4557	0.0067
1559296_at	LOC730057	Hypothetical protein LOC730057	-0.6334	0.0065
1559331_x_at		CDNA FLJ25030 fis; clone CBL02631	-0.1575	0.0328
1559340_at	C9orf148	chromosome 9 open reading frame 148	-0.1041	0.0444
1559384_at		Transcribed locus	-0.1546	0.0152
1559391_s_at		Partial mRNA; ID EE2-8E	-1.5242	0.0087
1559403_at		Homo sapiens; clone IMAGE:5768746; mRNA	-0.1527	0.0407
1559421_at			-0.237	0.0182
1559491_at		MRNA; cDNA DKFZp761L149 (from clone DKFZp761L149)	-0.865	0.0047
1559529_at	PTK2	PTK2 protein tyrosine kinase 2	-1.5122	0.0008
1559544_s_at		CDNA clone IMAGE:5787947	-0.1878	0.0174
1559550_s_at		MRNA; cDNA DKFZp434C0326 (from clone DKFZp434C0326)	-0.6958	0.0467
1559600_at		MRNA; cDNA DKFZp547G2314 (from clone DKFZp547G2314)	-0.3399	0.0496
1559723_s_at		CDNA clone IMAGE:4830182	-0.4859	0.0125
1559820_at	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	-0.6135	0.0296
1559895_x_at			-0.1602	0.0236
1559910_at		MRNA full length insert cDNA clone EUROIMAGE 85905	-1.5169	0.0019
1559945_at	RUVBL2	RuvB-like 2 (E. coli)	-0.1264	0.0358
1559957_a_at	LOC642852	hypothetical LOC642852	-1.085	0.0371
1559987_at		Homo sapiens; clone IMAGE:5585678; mRNA	-0.2636	0.0219
1560026_at		CDNA clone IMAGE:5285703	-0.5164	0.0267
1560042_at	FAM82A	family with sequence similarity 82; member A	-1.3326	0.0194
1560048_at		CDNA FLJ30026 fis; clone 3NB692001123	-0.3778	0.0472
1560069_at	LOC389072	hypothetical protein LOC389072	-0.6753	0.035
1560112_at	WDFY2	WD repeat and FYVE domain containing 2	-0.9929	0.0172
1560133_at	TNRC15	trinucleotide repeat containing 15	-0.7718	0.0406
1560137_at		CDNA FLJ32278 fis; clone PROST2000143	-0.4927	0.0435
1560172_at	INTS10	integrator complex subunit 10	-0.2544	0.0319
1560259_at		Homo sapiens; clone IMAGE:4612205; mRNA	-2.0585	0.0004
1560274_at	WTAP	Wilms tumor 1 associated protein	-0.2647	0.0458
1560322_at	RBMS3	RNA binding motif; single stranded interacting protein	-0.1641	0.0301
1560340_s_at	LOC441212	retinitis pigmentosa 9 pseudogene	-0.2149	0.0061
1560342_at		CDNA clone IMAGE:5275043	-1.1927	0.0091
1560359_at	PELO	Pelota homolog (Drosophila)	-1.7575	0.0163
1560372_at		CDNA FLJ34680 fis; clone LIVER2003524	-0.148	0.03
1560373_a_at		CDNA FLJ34680 fis; clone LIVER2003524	-0.1527	0.0413
1560402_at	GAS5	growth arrest-specific 5	-0.2842	0.0266
1560429_at		Transcribed locus	-0.1324	0.0142
1560474_at		Homo sapiens; clone IMAGE:4294221; mRNA	-0.2378	0.0143
1560486_at	STXBP3	syntaxin binding protein 3	-0.2072	0.018
1560554_a_at	C1orf145	chromosome 1 open reading frame 145	-0.251	0.049
1560689_s_at	AKT2	V-akt murine thymoma viral oncogene homolog 2	-0.5725	0.0406
1560712_at	TMPRSS11B	transmembrane protease; serine 11B	-0.1178	0.0431
1560717_at		Homo sapiens; clone IMAGE:5164889; mRNA	-0.1515	0.0153
1560734_at			-0.1229	0.0346
1560813_at		Homo sapiens; clone IMAGE:4043849; mRNA	-1.9069	0.0031
1560846_at		CDNA clone IMAGE:4248996	-0.1474	0.0341
1560859_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	-0.2329	0.0237
1560910_at	PPIL6	Peptidylprolyl isomerase (cyclophilin)-like 6	-0.1457	0.0286
1560973_a_at		Full length insert cDNA clone ZD78G02	-0.2612	0.0155
1560986_a_at		Full length insert cDNA clone YW21C01	-0.63	0.0049
1560997_at		Full length insert cDNA clone YW24A03	-0.1073	0.0387
1560998_x_at		Full length insert cDNA clone YW24A03	-0.1098	0.0158
1561002_at		Clone IMAGE:111722 mRNA sequence	-0.2906	0.0022
1561121_at		Full length insert cDNA clone ZD64C04	-0.2167	0.0208
1561139_at		Full length insert cDNA clone ZD67D12	-0.6586	0.0462

1561153_at		Full length insert cDNA YP99H09	-0.4967	0.0019
1561167_at		Full length insert cDNA clone YA75A09	-1.4086	0.0075
1561240_at		MRNA; cDNA DKFZp434C122 (from clone DKFZp434C122)	-0.1315	0.0066
1561316_at	GABRB3	Gamma-aminobutyric acid (GABA) A receptor; beta 3	-0.1484	0.0081
1561365_at	NRP1	Neuropilin 1	-0.1491	0.0355
1561527_at		CDNA clone IMAGE:5271697	-0.1293	0.042
1561584_at		CDNA clone IMAGE:4824588	-0.1676	0.0065
1561640_at		Homo sapiens; clone IMAGE:4182761; mRNA	-0.7675	0.0027
1561657_at		Full length insert cDNA clone YZ55H04	-1.3117	0.0271
1561682_at		CDNA clone IMAGE:4836898	-0.1506	0.0324
1561739_at		MRNA; cDNA DKFZp667P184 (from clone DKFZp667P184)	-0.1131	0.0123
1561867_at		Full length insert cDNA clone YR85B05	-0.2745	0.0484
1561965_at	SNRPB2	Small nuclear ribonucleoprotein polypeptide B''	-0.3019	0.0209
1562062_at	KIAA1245	CLIP-190-like, KIAA1245, hypothetical protein LOC728895, neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 3, neuroblastoma breakpoint family; member 8, neuroblastoma breakpoint family; member 9	-0.8544	0.0212
1562063_x_at	KIAA1245	CLIP-190-like, KIAA1245, hypothetical protein LOC728895, neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 3, neuroblastoma breakpoint family; member 8, neuroblastoma breakpoint family; member 9	-0.9134	0.0111
1562142_at	SKIV2L2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-0.2916	0.0038
1562161_at		Full length insert cDNA clone YR48C03	-0.1364	0.04
1562235_s_at		Transcribed locus	-1.9884	0.0008
1562236_at	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	-0.3242	0.0248
1562238_at	USPL1	ubiquitin specific peptidase like 1	-0.3771	0.0179
1562280_at		CDNA clone IMAGE:5267748	-0.4577	0.0286
1562301_at	C8orf34	chromosome 8 open reading frame 34	-0.1892	0.0319
1562313_at	BCORL2	BCL6 co-repressor-like 2	-0.1055	0.0363
1562321_at	PDK4	pyruvate dehydrogenase kinase; isozyme 4	-2.9903	0.0077
1562342_at		MRNA; cDNA DKFZp667G1416 (from clone DKFZp667G1416)	-0.3667	0.0334
1562428_at	LOC654780	SFPQ	-0.191	0.0042
1562453_at		MRNA; cDNA DKFZp686F1318 (from clone DKFZp686F1318)	-0.1249	0.0339
1562454_at		MRNA; cDNA DKFZp313B1634 (from clone DKFZp313B1634)	-0.2186	0.0286
1562497_at		CDNA FLJ38224 fis; clone FCBBF2003395	-1.1969	0.0059
1562528_at		Homo sapiens; clone IMAGE:5747561; mRNA	-2.4915	0.0001
1562529_s_at		Homo sapiens; clone IMAGE:5747561; mRNA	-2.6607	0.001
1562579_at		CDNA clone IMAGE:5285194	-0.1241	0.0292
1562648_at	CCDC88A	Coiled-coil domain containing 88A	-0.6977	0.0021
1562650_at	FRYL	FRY-like	-0.2329	0.0162
1562684_at		MRNA; cDNA DKFZp586H0718 (from clone DKFZp586H0718)	-0.7979	0.0233
1562752_at		CDNA clone IMAGE:4801412	-0.1289	0.0211
1562780_at		CDNA clone IMAGE:5285536	-0.1207	0.047
1562849_at		CDNA FLJ37115 fis; clone BRACE2022158	-0.1973	0.0126
1562863_at		Homo sapiens; clone IMAGE:4289218; mRNA	-0.3465	0.0184
1562947_x_at		Homo sapiens; clone IMAGE:3503939; mRNA	-0.2905	0.0284
1562948_at		Homo sapiens; clone IMAGE:5722724; mRNA	-0.9313	0.0018
1562991_at	ZNF292	zinc finger protein 292	-0.1785	0.0018

1563026_at		CDNA clone IMAGE:4723122	-0.2465	0.0037
1563035_x_at	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.1111	0.0247
1563055_at		CDNA clone IMAGE:5312112	-0.1521	0.0125
1563166_at		CDNA clone IMAGE:4272661	-0.2547	0.0033
1563332_at		Homo sapiens; clone IMAGE:4697589; mRNA	-0.1552	0.011
1563364_at		Homo sapiens; clone IMAGE:4272847; mRNA	-0.9397	0.0415
1563396_x_at		Homo sapiens; clone IMAGE:4281761; mRNA	-0.2084	0.0047
1563398_at		Homo sapiens; clone IMAGE:4248696; mRNA	-0.1416	0.0148
1563471_at	KIAA1632	KIAA1632	-0.2737	0.0385
1563482_at		MRNA; cDNA DKFZp451M0319 (from clone DKFZp451M0319)	-0.1711	0.0499
1563483_at	FAM91A2	family with sequence similarity 91; member A2	-0.3404	0.0287
1563503_at			-0.1134	0.0098
1563505_at	DUSP16	Dual specificity phosphatase 16	-0.776	0.0102
1563776_at		CDNA clone IMAGE:4837134	-0.1944	0.0496
1563906_at	SOBP	sine oculis binding protein homolog (Drosophila)	-0.6474	0.0318
1563933_a_at	PLD5	phospholipase D family; member 5	-2.7551	0.0241
1563985_at			-0.1411	0.0441
1564151_at		CDNA FLJ25521 fis; clone CBR06845	-0.1843	0.0211
1564248_at		UG0651E06	-0.5428	0.0396
1564315_at	C8orf49	chromosome 8 open reading frame 49	-0.2117	0.0198
1564318_at	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A; 155kDa	-0.2018	0.0193
1564334_at		MRNA; cDNA DKFZp434C1427 (from clone DKFZp434C1427)	-0.1617	0.0074
1564378_a_at		CDNA: FLJ21448 fis; clone COL04473	-0.7255	0.0479
1564387_at	DOPEY1	dopey family member 1	-0.1219	0.0409
1564424_at		CDNA clone IMAGE:4689616	-1.2782	0.0123
1564627_at	DNAJC13	DnaJ (Hsp40) homolog; subfamily C; member 13	-0.1295	0.0341
1564665_at		CDNA: FLJ22725 fis; clone HSI14917	-0.2817	0.0217
1564733_at		Homo sapiens; clone IMAGE:3933170; mRNA	-1.3377	0.0005
1564950_at		CDNA clone IMAGE:4052341	-0.206	0.0007
1564972_x_at	SETDB2	SET domain; bifurcated 2	-0.1636	0.0436
1565034_s_at	AFF3	AF4/FMR2 family; member 3, myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila)	-1.0589	0.0353
1565149_at	DYNC2H1	dynein; cytoplasmic 2; heavy chain 1	-0.8318	0.0062
1565265_at		Trapped 3' terminal exon; clone C2D9	-0.1296	0.0455
1565620_at	CTGLF1	Centaurin; gamma-like family; member 1	-0.6541	0.0225
1565635_at		CDNA: FLJ20875 fis; clone ADKA02835	-0.1041	0.0457
1565703_at	SMAD4	SMAD family member 4	-1.1123	0.0041
1565705_x_at		CDNA: FLJ21395 fis; clone COL03557	-0.2205	0.0485
1565804_at		CDNA: FLJ21508 fis; clone COL05723	-0.3088	0.0238
1565806_at	FLJ37035	FLJ37035 protein	-0.1638	0.0069
1565811_at		CDNA clone IMAGE:5278245	-0.3185	0.0251
1565875_at		Full length insert cDNA clone YP86C01	-0.1425	0.036
1565876_x_at		Full length insert cDNA clone YP86C01	-0.2115	0.0015
1565881_at		CDNA FLJ12064 fis; clone HEMBB1002232	-0.3853	0.0201
1565898_at	METT5D1	Methyltransferase 5 domain containing 1	-0.2534	0.0147
1565975_at		CDNA FLJ23646 fis; clone COL03258	-0.6694	0.0222
1566079_at	LOC647190	similar to 40S ribosomal protein S16	-1.6455	0.0006
1566129_at	LIMS1	LIM and senescent cell antigen-like domains 1	-0.5212	0.0149
1566251_at	SH3GLP3	CDNA clone IMAGE:4182839, SH3-domain GRB2-like pseudogene 3	-0.1464	0.0103
1566284_at		PA4=candidate oncogene {3' region} [human; HEN-16; HEN-16T transformed endocervical cell lines; mRNA Partial; 315 nt]	-0.3013	0.0306
1566442_at			-1.0278	0.0228
1566468_at		MRNA; cDNA DKFZp547E1510 (from clone DKFZp547E1510)	-0.1407	0.0353
1566507_a_at	FBXO9	F-box protein 9	-0.4791	0.0453
1566511_at	FBXO9	F-box protein 9	-0.1559	0.0066
1566515_at	CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	-0.1779	0.0247

1566543_at		CDNA FLJ40975 fis; clone UTERU2013502	-0.1604	0.0053
1566778_at		CDNA clone IMAGE:5294798	-0.1218	0.0106
1566787_at		CDNA clone IMAGE:4796529	-0.1382	0.0171
1566851_at	TRIM42	tripartite motif-containing 42	-0.1544	0.0018
1566880_at		MRNA; cDNA DKFZp667L198 (from clone DKFZp667L198)	-0.721	0.0281
1566887_x_at		Multiple myeloma susceptibility mRNA sequence	-0.4249	0.0189
1566889_at	THADA	Thyroid adenoma associated	-0.1536	0.0304
1566924_at		CDNA: FLJ20971 fis; clone ADSU01565	-0.1199	0.0214
1567031_at	ZNF160	zinc finger protein 160	-0.1558	0.0013
1567222_x_at	ELOVL5	ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast)	-0.1508	0.0138
1567443_x_at	PSEN1	presenilin 1 (Alzheimer disease 3)	-0.1433	0.0176
1567687_at	CECR9	cat eye syndrome chromosome region; candidate 9	-0.1069	0.0147
1567856_x_at		Kox26 mRNA for zinc finger protein; partial	-0.1158	0.0163
1568696_at	ARMETL1	arginine-rich; mutated in early stage tumors-like 1	-0.1823	0.0413
1568801_at	C15orf44	chromosome 15 open reading frame 44	-0.2644	0.0175
1568834_s_at	CCDC90B	coiled-coil domain containing 90B	-1.4047	0.0078
1568857_a_at	NBR2	Neighbor of BRCA1 gene 2	-0.4561	0.0366
1568898_at		Homo sapiens; clone IMAGE:3921535; mRNA	-0.1299	0
1569021_at	PIK3C2A	phosphoinositide-3-kinase; class 2; alpha polypeptide	-0.2231	0.0316
1569041_at		CDNA clone IMAGE:5262215	-0.7987	0.0227
1569076_a_at	FLJ16287	FLJ16287 protein	-1.2735	0.0317
1569077_x_at	FLJ16287	FLJ16287 protein	-1.6015	0.0095
1569142_at	TRIM13	tripartite motif-containing 13	-0.4838	0.0331
1569190_at	SCLT1	sodium channel and clathrin linker 1	-0.2976	0.0282
1569193_at		CDNA clone IMAGE:4821290	-0.1092	0.0392
1569201_a_at		Homo sapiens; clone IMAGE:3454421; mRNA	-0.7603	0.0284
1569243_at		CDNA clone IMAGE:4792470	-0.2172	0.0192
1569253_at	INTS4	integrator complex subunit 4	-0.3538	0.0193
1569320_at	GPBP1L1	GC-rich promoter binding protein 1-like 1	-1.1787	0.0273
1569331_at		CDNA clone IMAGE:3923329	-0.1245	0.0116
1569342_at	GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)	-0.1947	0.0357
1569354_at	NSUN6	NOL1/NOP2/Sun domain family; member 6	-0.3699	0.0307
1569375_at		CDNA clone IMAGE:4297546	-0.1455	0.0317
1569377_at	TMEM67	transmembrane protein 67	-0.9493	0.005
1569411_at	TMEM67	transmembrane protein 67	-0.162	0.0112
1569450_at	CAPZA2	capping protein (actin filament) muscle Z-line; alpha 2	-0.2106	0.0188
1569538_at		Clone FLB8310 PRO2225	-0.4049	0.0428
1569540_at			-2.5974	0.0007
1569601_at		CDNA clone IMAGE:3935451	-0.4921	0.0119
1569630_a_at	RUFY2	RUN and FYVE domain containing 2	-0.1955	0.0089
1569652_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 3	-1.7757	0.003
1569701_at	PER3	Period homolog 3 (Drosophila)	-0.4178	0.0414
1569770_x_at			-0.2103	0.0102
1569781_at	LOC285423	hypothetical gene supported by BC031092	-0.1602	0.0051
1569794_at		CDNA clone IMAGE:4824066	-0.2199	0.0127
1569796_s_at	ATRNL1	attractin-like 1	-0.926	0.0288
1569813_at	STRN	striatin; calmodulin binding protein	-0.2215	0.009
1569871_at	LOC650392	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human), Hypothetical protein LOC650392	-1.2475	0.0214
1569872_a_at	LOC650392	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human), Hypothetical protein LOC650392	-2.8631	0.0073
1569900_at	FLJ16124	FLJ16124 protein	-0.1253	0.0497
1569962_at		Homo sapiens; clone IMAGE:4850403; mRNA	-0.1399	0.0301
1569975_at		CDNA clone IMAGE:5301641	-0.1006	0.0074
1569990_at	NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	-0.1114	0.0188

1569998_at	MMD2	monocyte to macrophage differentiation-associated 2	-0.1643	0.019
1570048_at	DPH4	DPH4; JJJ3 homolog (S. cerevisiae)	-0.2997	0.0059
1570160_at		CDNA clone IMAGE:4799031	-0.1761	0.0357
1570173_at	INTS7	integrator complex subunit 7	-0.3316	0.0307
1570190_at	LSAMP	Limbic system-associated membrane protein	-0.1392	0.0285
1570259_at	LIMS1	LIM and senescent cell antigen-like domains 1	-0.7883	0.0088
1570409_x_at		Clone pp9953 unknown mRNA	-0.1466	0.0104
1570411_at		Clone pp7683 unknown mRNA	-0.1534	0.0425
1570412_at		Pp10394	-0.729	0.0168
1570415_at	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	-0.1973	0.0408
1570441_at	NAPB	N-ethylmaleimide-sensitive factor attachment protein; beta	-0.8568	0.023
1570571_at	CCDC91	Coiled-coil domain containing 91	-1.0438	0.0179
1570578_at		CDNA clone IMAGE:5274593	-0.2501	0.0239
1570588_at		Homo sapiens; clone IMAGE:4703872; mRNA	-0.4456	0.0344
200038_s_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2523	0.0422
200094_s_at	EEF2	eukaryotic translation elongation factor 2	-0.2968	0.0205
200601_at	ACTN4	actinin; alpha 4	-0.4216	0.0208
200630_x_at	SET	SET translocation (myeloid leukemia-associated)	-0.4385	0.0068
200631_s_at	SET	SET translocation (myeloid leukemia-associated)	-0.4275	0.0212
200635_s_at	PTPRF	protein tyrosine phosphatase; receptor type; F	-1.1986	0.0059
200636_s_at	PTPRF	protein tyrosine phosphatase; receptor type; F	-1.6202	0.0071
200644_at	MARCKSL1	MARCKS-like 1	-0.9511	0.0438
200733_s_at	PTP4A1	protein tyrosine phosphatase type IVA; member 1	-0.4605	0.0358
200747_s_at	NUMA1	nuclear mitotic apparatus protein 1	-0.9137	0.013
200762_at	DPYSL2	dihydropyrimidinase-like 2	-0.8321	0.0277
200774_at	FAM120A	family with sequence similarity 120A	-0.1955	0.0498
200789_at	ECH1	enoyl Coenzyme A hydratase 1; peroxisomal	-0.5323	0.0436
200807_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.1883	0.0209
200831_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-2.0949	0.0361
200862_at	DHCR24	24-dehydrocholesterol reductase	-0.9975	0.0016
200911_s_at	TACC1	transforming; acidic coiled-coil containing protein 1	-0.5798	0.0275
200940_s_at	RERE	arginine-glutamic acid dipeptide (RE) repeats	-0.8322	0.0297
200962_at	RPL31	ribosomal protein L31	-1.5835	0.0021
201061_s_at	STOM	stomatin	-0.4327	0.0498
201070_x_at	SF3B1	splicing factor 3b; subunit 1; 155kDa	-0.8704	0.039
201071_x_at	SF3B1	splicing factor 3b; subunit 1; 155kDa	-0.3405	0.0326
201103_x_at	LOC728980	hypothetical protein LOC728980, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 15, neuroblastoma breakpoint family; member 16, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 8	-0.4207	0.0176
201147_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy; pseudoinflammatory)	-2.2727	0.0172
201148_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy; pseudoinflammatory)	-2.1708	0.0111
201149_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy; pseudoinflammatory)	-2.4858	0.0085
201150_s_at	TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy; pseudoinflammatory)	-2.1202	0.0022
201166_s_at	PUM1	pumilio homolog 1 (Drosophila)	-0.3192	0.0191
201207_at	TNFAIP1	tumor necrosis factor; alpha-induced protein 1 (endothelial)	-0.6102	0.0292
201217_x_at	RPL3	ribosomal protein L3	-0.2655	0.0035
201246_s_at	OTUB1	OTU domain; ubiquitin aldehyde binding 1	-0.3205	0.0453
201247_at	SREBF2	sterol regulatory element binding transcription factor 2	-1.1517	0.0117
201248_s_at	SREBF2	sterol regulatory element binding transcription factor 2	-1.0351	0.0275
201261_x_at	BGN	biglycan	-1.0026	0.043
201262_s_at	BGN	biglycan	-0.892	0.0443

201278_at	DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	-1.4029	0.0139
201279_s_at	DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	-1.6454	0.019
201280_s_at	DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	-1.383	0.0296
201294_s_at	WSB1	WD repeat and SOCS box-containing 1	-1.2455	0.0448
201295_s_at			-1.4978	0.0332
201310_s_at	C5orf13	chromosome 5 open reading frame 13	-0.8807	0.0105
201334_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	-0.4348	0.0202
201341_at	ENC1	ectodermal-neural cortex (with BTB-like domain)	-1.6637	0.029
201353_s_at	BAZ2A	bromodomain adjacent to zinc finger domain; 2A	-0.5126	0.0238
201362_at	IVNS1ABP	influenza virus NS1A binding protein	-0.7184	0.0381
201372_s_at	CUL3	cullin 3	-0.3169	0.0121
201377_at	UBAP2L	ubiquitin associated protein 2-like	-0.8011	0.023
201446_s_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-1.1533	0.0296
201448_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-0.6274	0.0381
201450_s_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-0.9188	0.0187
201458_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.5953	0.0347
201505_at	LAMB1	laminin; beta 1	-1.4301	0.0135
201540_at	FHL1	four and a half LIM domains 1	-1.3574	0.0261
201564_s_at	FSCN1	fascin homolog 1; actin-bundling protein (Strongylocentrotus purpuratus)	-1.3594	0.0421
201598_s_at	INPPL1	inositol polyphosphate phosphatase-like 1	-0.4455	0.0405
201623_s_at	DARS	aspartyl-tRNA synthetase	-0.431	0.0068
201624_at	DARS	aspartyl-tRNA synthetase	-0.6452	0.0127
201634_s_at	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	-0.5896	0.0373
201655_s_at	HSPG2	heparan sulfate proteoglycan 2	-0.7861	0.0162
201800_s_at	OSBP	oxysterol binding protein	-0.3161	0.0266
201810_s_at	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-1.0678	0.0412
201819_at	SCARB1	scavenger receptor class B; member 1	-1.1481	0.0242
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	-0.7522	0.0137
201875_s_at	LOC644387	myelin protein zero-like 1, similar to myelin protein zero-like 1 isoform a	-0.5783	0.0247
201893_x_at	DCN	decorin	-2.7527	0.0366
201910_at	FARP1	FERM; RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-1.6324	0.0434
201916_s_at	SEC63	SEC63 homolog (S. cerevisiae)	-0.3092	0.0207
201925_s_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-1.6629	0.0187
201926_s_at	CD55	CD55 molecule; decay accelerating factor for complement (Cromer blood group)	-1.8534	0.0093
201957_at	PPP1R12B	protein phosphatase 1; regulatory (inhibitor) subunit 12B	-0.5273	0.0134
201991_s_at	KIF5B	kinesin family member 5B	-0.4652	0.0017
202022_at	ALDOC	aldolase C; fructose-bisphosphate	-2.3962	0.0097
202068_s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	-1.3547	0.0294
202082_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-1.2221	0.0002
202083_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-1.1378	0.004
202084_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	-0.8543	0.0017
202124_s_at	TRAK2	trafficking protein; kinesin binding 2	-0.7333	0.0377
202127_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.8449	0.0267
202130_at	RIOK3	RIO kinase 3 (yeast)	-0.9022	0.0021
202132_at	WWTR1	WW domain containing transcription regulator 1	-1.0083	0.0056
202133_at	WWTR1	WW domain containing transcription regulator 1	-0.8018	0.0023
202173_s_at	VEZF1	vascular endothelial zinc finger 1	-0.5856	0.0035
202218_s_at	FADS2	fatty acid desaturase 2	-0.8537	0.0323
202308_at	SREBF1	sterol regulatory element binding transcription factor 1	-1.4199	0.0063
202314_at	CYP51A1	cytochrome P450; family 51; subfamily A; polypeptide 1	-0.6612	0.0374
202432_at	PPP3CB	protein phosphatase 3 (formerly 2B); catalytic subunit; beta isoform	-0.3722	0.0179

202452_at	ZER1	zer-1 homolog (C. elegans)	-0.4555	0.0296
202465_at	PCOLCE	procollagen C-endopeptidase enhancer	-2.5473	0.0151
202468_s_at	CTNNAL1	catenin (cadherin-associated protein); alpha-like 1	-1.0119	0.0124
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	-1.5861	0.0238
202479_s_at	TRIB2	tribbles homolog 2 (Drosophila)	-1.4005	0.0184
202492_at	ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	-1.1528	0.0011
202501_at	MAPRE2	microtubule-associated protein; RP/EB family; member 2	-0.8817	0.0039
202554_s_at	GSTM3	glutathione S-transferase M3 (brain)	-1.779	0.0064
202563_at	C14orf1	chromosome 14 open reading frame 1	-0.2677	0.0287
202573_at	CSNK1G2	casein kinase 1; gamma 2	-0.3062	0.0109
202575_at	CRABP2	cellular retinoic acid binding protein 2	-1.6243	0.0267
202627_s_at	SERPINE1	serpin peptidase inhibitor; clade E (nexin; plasminogen activator inhibitor type 1); member 1	-2.1344	0.0228
202628_s_at	SERPINE1	serpin peptidase inhibitor; clade E (nexin; plasminogen activator inhibitor type 1); member 1	-1.6947	0.0462
202651_at	LPGAT1	lysophosphatidylglycerol acyltransferase 1	-1.1384	0.0159
202679_at	NPC1	Niemann-Pick disease; type C1	-0.9789	0.0266
202683_s_at	RNMT	RNA (guanine-7-) methyltransferase	-0.5247	0.0083
202704_at	TOB1	transducer of ERBB2; 1	-0.5716	0.0305
202718_at	IGFBP2	insulin-like growth factor binding protein 2; 36kDa	-1.5872	0.0225
202728_s_at	LTBP1	latent transforming growth factor beta binding protein 1	-1.0049	0.0247
202757_at	RP13-122B23.3	cofactor of BRCA1	-0.4928	0.0169
202795_x_at	TRIOBP	TRIO and F-actin binding protein	-0.5897	0.0139
202817_s_at	SS18	synovial sarcoma translocation; chromosome 18	-1.1431	0.0095
202861_at	PER1	period homolog 1 (Drosophila)	-0.937	0.0284
202912_at	ADM	adrenomedullin	-1.7112	0.019
202932_at	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	-0.6702	0.037
202933_s_at	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	-0.5199	0.0192
203005_at	LTBR	lymphotoxin beta receptor (TNFR superfamily; member 3)	-0.8156	0.0442
203026_at	ZBTB5	zinc finger and BTB domain containing 5	-0.7268	0.0206
203058_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.8466	0.0217
203060_s_at	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.7826	0.022
203067_at	PDHX	pyruvate dehydrogenase complex; component X	-0.6423	0.0335
203080_s_at	BAZ2B	bromodomain adjacent to zinc finger domain; 2B	-1.0107	0.0206
203088_at	FBLN5	fibulin 5	-1.5251	0.0118
203169_at	KIAA0258	KIAA0258	-0.3063	0.0092
203192_at	ABCB6	ATP-binding cassette; sub-family B (MDR/TAP); member 6	-1.4358	0.0422
203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2;3-sialyltransferase 5	-1.1928	0.0391
203221_at	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	-1.0081	0.0029
203229_s_at	CLK2	CDC-like kinase 2	-0.7447	0.0299
203232_s_at	ATXN1	ataxin 1	-1.1276	0.0102
203245_s_at	FLJ35348	FLJ35348	-0.9408	0.0129
203247_s_at	ZNF24	zinc finger protein 24	-0.6128	0.0006
203255_at	FBXO11	F-box protein 11	-0.9998	0.0081
203278_s_at	PHF21A	PHD finger protein 21A	-0.8821	0.0106
203297_s_at	JARID2	jumonji; AT rich interactive domain 2	-0.8122	0.0155
203306_s_at	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter); member A1	-0.4838	0.0438
203318_s_at	ZNF148	zinc finger protein 148	-0.7836	0.0011
203319_s_at	ZNF148	zinc finger protein 148	-0.8172	0.0103
203321_s_at	ADNP2	ADNP homeobox 2	-0.6796	0.0229
203341_at	CEBPZ	CCAAT/enhancer binding protein zeta	-0.4623	0.0221
203348_s_at	ETV5	ets variant gene 5 (ets-related molecule)	-1.5517	0.017
203354_s_at	PSD3	pleckstrin and Sec7 domain containing 3	-1.9726	0.015
203355_s_at	PSD3	pleckstrin and Sec7 domain containing 3	-1.8088	0.0357
203394_s_at	HES1	hairy and enhancer of split 1; (Drosophila)	-1.4218	0.0019
203395_s_at	HES1	hairy and enhancer of split 1; (Drosophila)	-0.9071	0.0065
203424_s_at	IGFBP5	insulin-like growth factor binding protein 5	-1.2952	0.0339

203425_s_at	IGFBP5	insulin-like growth factor binding protein 5	-0.4751	0.0334
203450_at	CBY1	chibby homolog 1 (Drosophila)	-0.593	0.0357
203494_s_at	CEP57	centrosomal protein 57kDa	-0.6087	0.0225
203505_at	ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	-0.886	0.046
203545_at	ALG8	asparagine-linked glycosylation 8 homolog (S. cerevisiae; alpha-1;3-glucosyltransferase)	-0.5101	0.0259
203560_at	GGH	gamma-glutamyl hydrolase (conjugase; folylpolygammaglutamyl hydrolase)	-1.3121	0.0214
203604_at	ZNF516	zinc finger protein 516	-0.8064	0.0008
203646_at	FDX1	ferredoxin 1	-1.0004	0.0093
203647_s_at	FDX1	ferredoxin 1	-1.1274	0.0056
203680_at	PRKAR2B	protein kinase; cAMP-dependent; regulatory; type II; beta	-1.4523	0.0378
203753_at	TCF4	transcription factor 4	-0.8049	0.0238
203759_at	ST3GAL4	ST3 beta-galactoside alpha-2;3-sialyltransferase 4	-0.8422	0.0076
203794_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	-0.9139	0.0187
203799_at	CD302	CD302 molecule	-1.531	0.0173
203825_at	BRD3	bromodomain containing 3	-1.0913	0.0005
203835_at	LRRC32	leucine rich repeat containing 32	-1.001	0.033
203846_at	TRIM32	tripartite motif-containing 32	-0.8601	0.0345
203955_at	KIAA0649	KIAA0649	-0.5771	0.028
203959_s_at	ZBTB40	zinc finger and BTB domain containing 40	-0.5909	0.0446
203971_at	SLC31A1	solute carrier family 31 (copper transporters); member 1	-0.9838	0.0358
204028_s_at	RABGAP1	RAB GTPase activating protein 1	-0.5081	0.0447
204040_at	RNF144A	ring finger protein 144A	-1.3553	0.0008
204042_at	WASF3	WAS protein family; member 3	-1.5852	0.0347
204049_s_at	PHACTR2	phosphatase and actin regulator 2	-1.2673	0.0385
204077_x_at	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	-0.3504	0.035
204082_at	PBX3	pre-B-cell leukemia homeobox 3	-1.2477	0.0158
204094_s_at	TSC22D2	TSC22 domain family; member 2	-0.7208	0.0093
204102_s_at	EEF2	eukaryotic translation elongation factor 2	-0.2457	0.0407
204106_at	TESK1	testis-specific kinase 1	-1.0463	0.0086
204134_at	PDE2A	phosphodiesterase 2A; cGMP-stimulated	-3.1639	0.0016
204143_s_at	ENOSF1	enolase superfamily member 1	-0.7292	0.0382
204182_s_at	ZBTB43	zinc finger and BTB domain containing 43	-0.886	0.0327
204233_s_at	CHKA	choline kinase alpha	-1.1469	0.0005
204266_s_at	CHKA	choline kinase alpha, similar to choline kinase alpha isoform a	-1.2971	0.0004
204288_s_at	SORBS2	sorbin and SH3 domain containing 2	-2.0803	0.0152
204323_x_at	NF1	neurofibromin 1 (neurofibromatosis; von Recklinghausen disease; Watson disease)	-0.3197	0.0247
204461_x_at	RAD1	RAD1 homolog (S. pombe)	-0.5615	0.0353
204569_at	ICK	intestinal cell (MAK-like) kinase	-1.0788	0.0324
204595_s_at	STC1	stanniocalcin 1	-1.8765	0.0411
204688_at	SGCE	sarcoglycan; epsilon	-1.6329	0.0422
204706_at	INPP5E	inositol polyphosphate-5-phosphatase; 72 kDa	-0.5739	0.0411
204711_at	KIAA0753	KIAA0753	-0.5378	0.0426
204731_at	TGFBR3	transforming growth factor; beta receptor III	-1.4186	0.0382
204760_s_at	NR1D1	nuclear receptor subfamily 1; group D; member 1, thyroid hormone receptor; alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog; avian)	-1.7556	0.0009
204771_s_at	TTF1	transcription termination factor; RNA polymerase I	-0.7138	0.0063
204790_at	SMAD7	SMAD family member 7	-0.9167	0.0389
204842_x_at	PRKAR2A	protein kinase; cAMP-dependent; regulatory; type II; alpha	-0.3154	0.036
204881_s_at	UGCG	UDP-glucose ceramide glucosyltransferase	-1.767	0.0002
204894_s_at	AOC3	amine oxidase; copper containing 3 (vascular adhesion protein 1)	-2.4254	0.0109
204915_s_at	SOX11	SRY (sex determining region Y)-box 11	-0.1576	0.0246
204917_s_at	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 3	-1.0636	0.0175
204948_s_at	FST	follistatin	-1.4119	0.0496
204955_at	SRPX	sushi-repeat-containing protein; X-linked	-2.2573	0.021

205002_at	AHDC1	AT hook; DNA binding motif; containing 1	-0.9774	0.0263
205032_at	ITGA2	integrin; alpha 2 (CD49B; alpha 2 subunit of VLA-2 receptor)	-1.4207	0.0163
205174_s_at	QPCT	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	-1.5703	0.0318
205181_at	ZNF193	zinc finger protein 193	-1.1523	0.0138
205253_at	PBX1	pre-B-cell leukemia homeobox 1	-1.5762	0.0142
205381_at	LRRC17	leucine rich repeat containing 17	-2.0217	0.0394
205383_s_at	ZBTB20	zinc finger and BTB domain containing 20	-1.1469	0.0161
205409_at	FOSL2	FOS-like antigen 2	-0.6273	0.016
205434_s_at	AAK1	AP2 associated kinase 1	-0.5527	0.0316
205459_s_at	NPAS2	neuronal PAS domain protein 2	-0.5687	0.0269
205460_at	NPAS2	neuronal PAS domain protein 2	-0.4902	0.0299
205471_s_at	DACH1	dachshund homolog 1 (Drosophila)	-1.9519	0.0456
205472_s_at	DACH1	dachshund homolog 1 (Drosophila)	-1.497	0.0072
205492_s_at	DPYSL4	dihydropyrimidinase-like 4	-0.6372	0.0357
205493_s_at	DPYSL4	dihydropyrimidinase-like 4	-2.4688	0.0087
205516_x_at	CIZ1	CDKN1A interacting zinc finger protein 1	-0.7836	0.0302
205517_at	GATA4	GATA binding protein 4	-1.6954	0.0095
205585_at	ETV6	ets variant gene 6 (TEL oncogene)	-0.4524	0.0063
205593_s_at	PDE9A	phosphodiesterase 9A	-0.9473	0.0341
205594_at	ZNF652	zinc finger protein 652	-1.2018	0.0157
205597_at	SLC44A4	solute carrier family 44; member 4	-1.2337	0.0104
205655_at	MDM4	Mdm4; transformed 3T3 cell double minute 4; p53 binding protein (mouse)	-0.3132	0.0346
205706_s_at	ANKRD26	ankyrin repeat domain 26	-0.4641	0.0148
205735_s_at	AFF3	AF4/FMR2 family; member 3	-0.3261	0.0435
205771_s_at	AKAP7	A kinase (PRKA) anchor protein 7	-1.1601	0.0263
205780_at	BIK	BCL2-interacting killer (apoptosis-inducing)	-1.2444	0.0436
205917_at	ZNF264	zinc finger protein 264	-0.9701	0.0415
206009_at	ITGA9	integrin; alpha 9	-1.1686	0.0024
206091_at	MATN3	matrilin 3	-1.324	0.0491
206093_x_at	TNXB	tenascin XB	-1.9806	0.0039
206114_at	EPHA4	EPH receptor A4	-1.4194	0.0204
206172_at	IL13RA2	interleukin 13 receptor; alpha 2	-2.7176	0.0362
206245_s_at	IVNS1ABP	influenza virus NS1A binding protein	-0.668	0.0361
206249_at	MAP3K13	mitogen-activated protein kinase kinase kinase 13	-0.9003	0.0042
206251_s_at	AVPR1A	arginine vasopressin receptor 1A	-0.21	0.0029
206292_s_at	SULT2A1	sulfotransferase family; cytosolic; 2A; dehydroepiandrosterone (DHEA)-preferring; member 1	-2.2848	0.0113
206294_at	HSD3B2	hydroxy-delta-5-steroid dehydrogenase; 3 beta- and steroid delta-isomerase 2	-4.3946	0.0002
206307_s_at	FOXD1	forkhead box D1	-2.2543	0.0139
206548_at	hCG_1776259	hypothetical protein FLJ23556	-1.0302	0.0249
206686_at	PDK1	pyruvate dehydrogenase kinase; isozyme 1	-0.935	0.031
206755_at	CYP2B6	cytochrome P450; family 2; subfamily B; polypeptide 6	-0.1147	0.05
206767_at	RBMS3	RNA binding motif; single stranded interacting protein	-0.7097	0.0336
206848_at	HOXA7	homeobox A7	-2.3073	0.0006
206874_s_at	SLK	STE20-like kinase (yeast)	-0.6901	0.0265
206927_s_at	GUCY1A2	guanylate cyclase 1; soluble; alpha 2	-0.1869	0.0386
206929_s_at	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	-0.8834	0.0237
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	-1.4809	0.0185
207043_s_at	SLC6A9	solute carrier family 6 (neurotransmitter transporter; glycine); member 9	-0.8187	0.0226
207143_at	CDK6	cyclin-dependent kinase 6	-0.2552	0.0476
207190_at	ZZEF1	zinc finger; ZZ-type with EF-hand domain 1	-0.5969	0.0348
207263_x_at	VEZT	vezatin; adherens junctions transmembrane protein	-0.4236	0.0206
207283_at	RPL23AP13	ribosomal protein L23a pseudogene 13	-0.8518	0.0063
207292_s_at	MAPK7	mitogen-activated protein kinase 7	-0.5817	0.0078
207305_s_at	KIAA1012	KIAA1012	-0.4293	0.0236
207345_at	FST	follistatin	-0.7228	0.048
207365_x_at	USP34	ubiquitin specific peptidase 34	-0.6747	0.0239

207401_at	PROX1	prospero homeobox 1	-1.1713	0.0179
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily; member 4 (tax-transcriptionally activated glycoprotein 1; 34kDa)	-2.1316	0.0422
207464_at	AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-0.2228	0.0073
207470_at	DKFZp566H 0824	hypothetical protein DKFZp566H0824	-0.1394	0.0077
207471_at			-0.1172	0.0474
207492_at	NGLY1	N-glycanase 1	-0.5854	0.0461
207606_s_at	ARHGAP12	Rho GTPase activating protein 12	-0.8951	0.0189
207711_at	C20orf117	chromosome 20 open reading frame 117	-0.7395	0.0395
207737_at			-0.2142	0.001
207750_at	EPS15L2	epidermal growth factor receptor pathway substrate 15-like 2	-0.1541	0.0008
207819_s_at	ABCB4	ATP-binding cassette; sub-family B (MDR/TAP); member 4	-3.3743	0.0182
207836_s_at	RBPMS	RNA binding protein with multiple splicing	-1.1966	0.0399
207837_at	RBPMS	RNA binding protein with multiple splicing	-0.2327	0.0226
207953_at	RP5-886K2.1	neuronal thread protein AD7c-NTP	-0.3297	0.0092
207954_at	GATA2	GATA binding protein 2	-0.1058	0.0325
207981_s_at	ESRRG	estrogen-related receptor gamma	-1.8399	0.0362
208143_s_at	FAM12A	family with sequence similarity 12; member A	-0.1375	0.0254
208154_at	LOC51336	mesenchymal stem cell protein DSCD28	-0.3097	0.0389
208185_x_at			-0.1748	0.0394
208216_at	DLX4	distal-less homeobox 4	-0.2579	0.0144
208238_x_at			-0.2458	0.0392
208300_at	PTPRH	protein tyrosine phosphatase; receptor type; H	-0.9366	0.038
208324_at			-0.165	0.0418
208491_s_at	PGM5	phosphoglucomutase 5	-1.2238	0.0185
208606_s_at	WNT4	wingless-type MMTV integration site family; member 4	-2.9669	0.0083
208609_s_at	TNXA	tenascin XA pseudogene, tenascin XB	-2.1933	0.013
208611_s_at	SPTAN1	spectrin; alpha; non-erythrocytic 1 (alpha-fodrin)	-0.7115	0.0287
208619_at	DDB1	damage-specific DNA binding protein 1; 127kDa	-0.3536	0.0321
208720_s_at	RBM39	RNA binding motif protein 39	-0.2713	0.043
208794_s_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-0.804	0.0094
208820_at	PTK2	PTK2 protein tyrosine kinase 2	-0.4904	0.0023
208953_at	LARP5	La ribonucleoprotein domain family; member 5	-0.688	0.0361
208958_at	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	-0.7468	0.0255
208962_s_at	FADS1	fatty acid desaturase 1	-1.8056	0.0091
208963_x_at	FADS1	fatty acid desaturase 1	-1.7026	0.0142
208964_s_at	FADS1	fatty acid desaturase 1	-1.4101	0.0415
208990_s_at	HNRPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	-0.3372	0.0219
209081_s_at	COL18A1	collagen; type XVIII; alpha 1	-1.9915	0.0038
209082_s_at	COL18A1	collagen; type XVIII; alpha 1	-1.448	0.0115
209236_at	SLC23A2	solute carrier family 23 (nucleobase transporters); member 2	-1.2616	0.0186
209250_at	DEGS1	degenerative spermatocyte homolog 1; lipid desaturase (Drosophila)	-0.6275	0.0209
209390_at	TSC1	tuberous sclerosis 1	-0.812	0.0027
209430_at	BTAF1	BTAF1 RNA polymerase II; B-TFIID transcription factor-associated; 170kDa (Mot1 homolog; S. cerevisiae)	-0.5367	0.0242
209439_s_at	PHKA2	phosphorylase kinase; alpha 2 (liver)	-1.3286	0.0229
209487_at	RBPMS	RNA binding protein with multiple splicing	-1.3425	0.0316
209512_at	HSDL2	hydroxysteroid dehydrogenase like 2	-1.0057	0.0183
209513_s_at	HSDL2	hydroxysteroid dehydrogenase like 2	-0.9124	0.0006
209518_at	SMARCD1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily d; member 1	-0.3647	0.0331
209522_s_at	CRAT	carnitine acetyltransferase	-0.8125	0.0046
209547_s_at	SF4	splicing factor 4	-0.2798	0.0287
209630_s_at	FBXW2	F-box and WD repeat domain containing 2	-0.6468	0.002
209651_at	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-2.1427	0.0028

209705_at	MTF2	metal response element binding transcription factor 2	-0.7278	0.0168
209750_at	NR1D2	nuclear receptor subfamily 1; group D; member 2	-1.245	0.0396
209824_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-1.1331	0.0241
209866_s_at	LPHN3	latrophilin 3	-2.5079	0.024
209867_s_at	LPHN3	latrophilin 3	-2.0789	0.0361
209908_s_at	TGFB2	transforming growth factor; beta 2	-0.2229	0.0137
209909_s_at	TGFB2	transforming growth factor; beta 2	-1.1801	0.0306
209939_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	-0.6242	0.0401
209959_at	NR4A3	nuclear receptor subfamily 4; group A; member 3	-2.2948	0.025
209974_s_at	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.4837	0.0172
209982_s_at	NRXN2	neurexin 2	-1.4217	0.0185
209983_s_at	NRXN2	neurexin 2	-0.6012	0.0229
209993_at	ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	-1.7299	0.027
209994_s_at	ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1, ATP-binding cassette; sub-family B (MDR/TAP); member 4	-1.9161	0.0124
210094_s_at	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	-0.9677	0.0056
210132_at	EFNA3	ephrin-A3	-1.2565	0.0307
210210_at	MPZL1	myelin protein zero-like 1	-0.4404	0.0191
210214_s_at	BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	-0.5144	0.049
210231_x_at	SET	SET translocation (myeloid leukemia-associated)	-0.5388	0.0063
210261_at	KCNK2	potassium channel; subfamily K; member 2	-1.6229	0.0274
210276_s_at	TRIOBP	TRIO and F-actin binding protein	-1.0911	0.0122
210281_s_at	ZMYM2	zinc finger; MYM-type 2	-0.9597	0.0301
210282_at	ZMYM2	zinc finger; MYM-type 2	-0.9929	0.0239
210299_s_at	FHL1	four and a half LIM domains 1	-0.9377	0.0322
210303_at	MAB21L2	mab-21-like 2 (C. elegans)	-0.1648	0.0289
210333_at	NR5A1	nuclear receptor subfamily 5; group A; member 1	-0.9089	0.0361
210426_x_at	RORA	RAR-related orphan receptor A	-1.8853	0.0058
210436_at	CCT8	chaperonin containing TCP1; subunit 8 (theta)	-0.1157	0.0498
210479_s_at	RORA	RAR-related orphan receptor A	-2.0771	0.0056
210539_at	TTLL5	tubulin tyrosine ligase-like family; member 5	-0.2411	0.0027
210588_x_at	HNRPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	-0.3771	0.0469
210618_at	RAP1GAP	RAP1 GTPase activating protein	-0.163	0.0223
210623_at	LOC51035	SAPK substrate protein 1	-0.2952	0.0027
210678_s_at	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase; beta)	-0.331	0.0483
210679_x_at			-0.5268	0.0372
210757_x_at	DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	-1.4972	0.0141
210762_s_at	DLC1	deleted in liver cancer 1	-1.7001	0.0186
210933_s_at	FSCN1	fascin homolog 1; actin-bundling protein (Strongylocentrotus purpuratus)	-1.1098	0.024
210946_at	PPAP2A	phosphatidic acid phosphatase type 2A	-0.5662	0.0496
210954_s_at	TSC22D2	TSC22 domain family; member 2	-0.3157	0.0294
210964_s_at	GYG2	glycogenin 2	-0.2243	0.0457
210969_at	PKN2	protein kinase N2	-0.2482	0.0453
210971_s_at	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-0.8226	0.0408
211073_x_at	RPL3	ribosomal protein L3	-0.278	0.0046
211083_s_at	MAP3K13	mitogen-activated protein kinase kinase kinase 13	-0.3435	0.0236
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	-1.354	0.0423
211148_s_at	ANGPT2	angiopoietin 2	-1.2618	0.0311
211202_s_at	JARID1B	jumonji; AT rich interactive domain 1B	-0.9138	0.0435
211277_x_at	APP	amyloid beta (A4) precursor protein (peptidase nexin-II; Alzheimer disease)	-0.4452	0.0408
211304_x_at	KCNJ5	potassium inwardly-rectifying channel; subfamily J; member 5	-0.2226	0.0297
211373_s_at	PSEN2	presenilin 2 (Alzheimer disease 4)	-0.7771	0.038
211411_at		LDLR-FUT fusion protein (LDLR-FUT)	-0.1504	0.0443

211509_s_at	RTN4	reticulon 4	-0.1908	0.0175
211556_at	MAPRE2	microtubule-associated protein; RP/EB family; member 2	-0.1157	0.0143
211651_s_at	LAMB1	laminin; beta 1	-1.619	0.0182
211929_at	HNRPA3	heterogeneous nuclear ribonucleoprotein A3	-0.5318	0.0263
211930_at	HNRPA3	heterogeneous nuclear ribonucleoprotein A3	-0.5828	0.0164
211940_x_at	H3F3A	H3 histone; family 3A, H3 histone; family 3A pseudogene, similar to H3 histone; family 3B	-0.2573	0.0415
211958_at	IGFBP5	insulin-like growth factor binding protein 5	-1.0127	0.0129
211959_at	IGFBP5	insulin-like growth factor binding protein 5	-2.3125	0.0046
211975_at	ZNF289	zinc finger protein 289; ID1 regulated	-0.9671	0.0086
212039_x_at	RPL3	ribosomal protein L3	-0.2704	0.0109
212065_s_at	USP34	ubiquitin specific peptidase 34	-1.2883	0.0223
212066_s_at	USP34	ubiquitin specific peptidase 34	-0.8566	0.0209
212068_s_at	KIAA0515	KIAA0515	-0.8274	0.0155
212069_s_at	KIAA0515	KIAA0515	-0.9198	0.0029
212089_at	LMNA	lamin A/C	-0.6881	0.033
212094_at	PEG10	paternally expressed 10	-1.8198	0.0227
212099_at	RHOB	ras homolog gene family; member B	-0.6711	0.0107
212104_s_at	RBM9	RNA binding motif protein 9	-0.9903	0.0201
212115_at	HN1L	hematological and neurological expressed 1-like	-0.722	0.0031
212131_at	LSM14A	LSM14A; SCD6 homolog A (S. cerevisiae)	-0.7176	0.0033
212148_at	PBX1	pre-B-cell leukemia homeobox 1	-1.1798	0.0164
212151_at	PBX1	pre-B-cell leukemia homeobox 1	-1.3568	0.0106
212152_x_at	ARID1A	AT rich interactive domain 1A (SWI-like)	-0.521	0.0046
212153_at	POGZ	pogo transposable element with ZNF domain	-0.8866	0.0181
212182_at	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4, nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	-0.2213	0.0428
212186_at	ACACA	acetyl-Coenzyme A carboxylase alpha	-0.7104	0.022
212215_at	PREPL	prolyl endopeptidase-like	-0.3759	0.0075
212218_s_at	FASN	fatty acid synthase	-1.6039	0.0417
212232_at	FNBP4	formin binding protein 4	-0.663	0.0476
212270_x_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2517	0.0243
212276_at	LPIN1	lipin 1	-0.7801	0.0408
212279_at	TMEM97	transmembrane protein 97	-1.3357	0.0169
212281_s_at	TMEM97	transmembrane protein 97	-1.4403	0.0234
212282_at	TMEM97	transmembrane protein 97	-1.3557	0.0311
212289_at	ANKRD12	ankyrin repeat domain 12	-0.6838	0.0184
212298_at	NRP1	neuropilin 1	-0.913	0.0234
212336_at	EPB41L1	erythrocyte membrane protein band 4.1-like 1	-1.4037	0.0107
212339_at	EPB41L1	erythrocyte membrane protein band 4.1-like 1	-1.1551	0.0381
212359_s_at	KIAA0913	KIAA0913	-0.5344	0.0343
212366_at	ZNF292	zinc finger protein 292	-0.6718	0.0231
212368_at	ZNF292	zinc finger protein 292	-1.0112	0.0009
212428_at	KIAA0368	KIAA0368	-0.6341	0.0262
212468_at	SPAG9	sperm associated antigen 9	-0.709	0.0447
212492_s_at	JMJD2B	jumonji domain containing 2B	-1.6151	0.0006
212495_at	JMJD2B	jumonji domain containing 2B	-1.1404	0.0085
212496_s_at	JMJD2B	jumonji domain containing 2B	-1.1675	0.0046
212509_s_at	MXRA7	matrix-remodelling associated 7	-0.4236	0.0242
212517_at	ATRN	attractin	-0.6278	0.0314
212520_s_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-0.9486	0.0046
212534_at		CDNA FLJ11904 fis; clone HEMBB1000048	-0.5747	0.0028
212537_x_at	C18orf32	chromosome 18 open reading frame 32, hCG22804, hCG39912, ribosomal protein L17	-0.2406	0.0305
212547_at	FLJ35348	FLJ35348	-1.1133	0.0027
212557_at	ZNF451	zinc finger protein 451	-0.4656	0.0134
212622_at	TMEM41B	transmembrane protein 41B	-0.6185	0.0488
212650_at	EHBP1	EH domain binding protein 1	-1.0451	0.014
212653_s_at	EHBP1	EH domain binding protein 1	-0.7969	0.0459

212664_at	TUBB4	tubulin; beta 4	-2.0245	0.0108
212667_at	SPARC	secreted protein; acidic; cysteine-rich (osteonectin)	-1.0505	0.0189
212689_s_at	JMJD1A	jumonji domain containing 1A	-0.9052	0.0063
212690_at	DDHD2	DDHD domain containing 2	-0.6705	0.0468
212719_at	PHLPP	PH domain and leucine rich repeat protein phosphatase	-1.0394	0.0418
212752_at	CLASP1	cytoplasmic linker associated protein 1	-0.582	0.0249
212759_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific; HMG-box)	-0.7207	0.0168
212761_at	TCF7L2	transcription factor 7-like 2 (T-cell specific; HMG-box)	-0.5234	0.0425
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific; HMG-box)	-1.1495	0.0013
212775_at	OBSL1	obscurin-like 1	-1.7507	0.0134
212776_s_at	OBSL1	obscurin-like 1	-1.8207	0.0311
212793_at	DAAM2	dishevelled associated activator of morphogenesis 2	-2.8034	0.0085
212802_s_at	GAPVD1	GTPase activating protein and VPS9 domains 1	-0.6756	0.0034
212840_at	UBXD7	UBX domain containing 7	-1.0414	0.002
212852_s_at	TROVE2	TROVE domain family; member 2	-0.5414	0.0289
212854_x_at	NBPF10	neuroblastoma breakpoint family; member 10	-0.6083	0.0131
212875_s_at	C21orf25	chromosome 21 open reading frame 25	-1.6912	0.0015
212928_at	TSPYL4	TSPY-like 4	-0.6971	0.0101
212950_at	GPR116	G protein-coupled receptor 116	-1.0172	0.0356
212977_at	CXCR7	chemokine (C-X-C motif) receptor 7	-2.4608	0.0243
212980_at	USP34	ubiquitin specific peptidase 34	-0.912	0.0401
213015_at		ARTC1 mRNA; complete sequence	-1.0087	0.0398
213016_at		ARTC1 mRNA; complete sequence	-0.8003	0.0465
213048_s_at			-0.5717	0.0029
213052_at	PRKAR2A	Protein kinase; cAMP-dependent; regulatory; type II; alpha	-0.5098	0.0286
213154_s_at	BICD2	bicaudal D homolog 2 (Drosophila)	-0.4045	0.0413
213156_at		Homo sapiens; clone IMAGE:4214654; mRNA	-1.0474	0.0428
213158_at		Homo sapiens; clone IMAGE:4214654; mRNA	-1.0934	0.0328
213161_at	C9orf97	chromosome 9 open reading frame 97	-0.6061	0.0255
213197_at	ASTN1	astrotactin 1	-2.3391	0.0153
213248_at	LOC730101	similar to heterogeneous nuclear ribonucleoprotein A/B	-1.628	0.0205
213254_at	TNRC6B	trinucleotide repeat containing 6B	-0.3058	0.039
213310_at	EIF2C2	Eukaryotic translation initiation factor 2C; 2	-0.951	0.0437
213345_at	NFATC4	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 4	-0.6861	0.026
213381_at	C10orf72	Chromosome 10 open reading frame 72	-1.8045	0.0041
213387_at	ATAD2B	ATPase family; AAA domain containing 2B	-0.998	0.0344
213451_x_at	TNXB	tenascin XB	-2.0983	0.0025
213459_at	RPL37A	ribosomal protein L37a	-1.5333	0.0225
213462_at	NPAS2	neuronal PAS domain protein 2	-1.3926	0.0381
213478_at	KIAA1026	kazrin	-2.6897	0.0011
213488_at	SNED1	sushi; nidogen and EGF-like domains 1	-1.626	0.0094
213489_at	MAPRE2	Microtubule-associated protein; RP/EB family; member 2	-0.9185	0.0216
213531_s_at	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	-0.4887	0.0451
213570_at	EIF4E2	eukaryotic translation initiation factor 4E family member 2	-0.6422	0.026
213575_at	TRA2A	transformer-2 alpha	-0.7745	0.0259
213577_at	SQLE	squalene epoxidase	-1.8157	0.0404
213593_s_at	TRA2A	transformer-2 alpha	-1.3731	0.0021
213612_x_at	LOC728980	hypothetical protein LOC728980, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 15, neuroblastoma breakpoint family; member 16, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 8	-0.3922	0.0125
213619_at	HNRPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)	-0.3197	0.026
213649_at	SFRS7	splicing factor; arginine/serine-rich 7; 35kDa	-0.867	0.0427
213686_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	-1.3523	0.0189
213720_s_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-0.9531	0.0059
213744_at	ATRNL1	attractin-like 1	-1.0501	0.009
213745_at	ATRNL1	attractin-like 1	-1.636	0.0095

213771_at	IRF2BP1	interferon regulatory factor 2 binding protein 1	-0.4169	0.043
213785_at	IPO9	importin 9	-0.6728	0.0239
213792_s_at	INSR	insulin receptor	-0.9952	0.0497
213852_at	RBM8A	RNA binding motif protein 8A	-0.6191	0.0365
213904_at		Clone 23555 mRNA sequence	-2.7925	0.001
213931_at	ID2	inhibitor of DNA binding 2; dominant negative helix-loop-helix protein, inhibitor of DNA binding 2B; dominant negative helix-loop-helix protein	-1.742	0.0281
213936_x_at	SFTPB	surfactant; pulmonary-associated protein B	-0.2489	0.0193
213941_x_at	RPS7	ribosomal protein S7	-0.241	0.0388
213956_at	CEP350	centrosomal protein 350kDa	-0.7107	0.0288
213967_at	RALYL	RALY RNA binding protein-like	-2.3168	0.0446
213977_s_at	CIZ1	CDKN1A interacting zinc finger protein 1	-0.7644	0.0301
214016_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-0.6142	0.0475
214077_x_at	MEIS3P1	Meis homeobox 3 pseudogene 1	-1.3715	0.0031
214102_at	CENTD1	centaurin; delta 1	-0.9572	0.0356
214153_at	ELOVL5	ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast)	-0.6428	0.0103
214198_s_at	DGCR2	DiGeorge syndrome critical region gene 2	-0.4448	0.0219
214283_at	TMEM97	transmembrane protein 97	-1.9491	0.0248
214291_at	hCG_2004593	hCG2004593, hCG39912, hypothetical LOC643863, ribosomal protein L17, similar to 60S ribosomal protein L17 (L23), similar to 60S ribosomal protein L17 (L23) (Amino acid starvation-induced protein) (ASI)	-1.1955	0.0152
214305_s_at	SF3B1	splicing factor 3b; subunit 1; 155kDa	-0.7655	0.0464
214319_at	FRY	furry homolog (Drosophila)	-0.3842	0.0256
214341_at	THTPA	Thiamine triphosphatase	-0.1543	0.0216
214356_s_at	KIAA0368	KIAA0368	-0.6287	0.0163
214375_at	LOC729222	PTPRF interacting protein; binding protein 1 (liprin beta 1), similar to PTPRF interacting protein binding protein 1 isoform 1	-1.5384	0.0263
214388_at		BRCA2 region; mRNA sequence CG011	-0.1027	0.0333
214422_at	LOC131185	RAD23 homolog B (S. cerevisiae), similar to UV excision repair protein RAD23 homolog B (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	-0.6339	0.0202
214428_x_at	C4A	complement component 4A (Rodgers blood group), complement component 4B (Childo blood group)	-1.3491	0.0252
214477_at	MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 1	-0.1103	0.0234
214593_at	PIAS2	protein inhibitor of activated STAT; 2	-0.2393	0.013
214594_x_at	ATP8B1	ATPase; Class I; type 8B; member 1	-0.4789	0.049
214626_s_at	GANAB	glucosidase; alpha; neutral AB	-0.4816	0.0246
214660_at	PELO	Pelota homolog (Drosophila)	-1.8706	0.0088
214663_at	RIPK5	receptor interacting protein kinase 5	-0.8117	0.0279
214683_s_at	CLK1	CDC-like kinase 1	-0.5886	0.0169
214698_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	-0.235	0.0275
214704_at	TCF25	transcription factor 25 (basic helix-loop-helix)	-0.2187	0.0333
214707_x_at	ALMS1	Alstrom syndrome 1	-0.4521	0.0181
214728_x_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-0.8651	0.0119
214734_at	EXPH5	exophilin 5	-0.5319	0.0403
214785_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	-1.077	0.002
214797_s_at	PCTK3	PCTAIRE protein kinase 3	-0.5663	0.038
214843_s_at	USP33	ubiquitin specific peptidase 33	-0.5201	0.0397
214852_x_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	-0.2908	0.0105
214861_at	JMJD2C	jumonji domain containing 2C	-0.8724	0.0048
214917_at	PRKAA1	protein kinase; AMP-activated; alpha 1 catalytic subunit	-0.8767	0.0451
214918_at	HNRPM	heterogeneous nuclear ribonucleoprotein M	-0.5536	0.019
214948_s_at	TMF1	TATA element modulatory factor 1	-1.1372	0.0179
214949_at		CDNA FLJ31919 fis; clone NT2RP7004964	-0.9717	0.0232
214956_at	AAK1	AP2 associated kinase 1	-0.3184	0.0023

214978_s_at	PPFIA4	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 4	-0.7804	0.0464
214985_at		Clone 24739 mRNA sequence	-0.2439	0.0302
215012_at	ZNF451	zinc finger protein 451	-1.5103	0.0065
215018_at	KIAA1731	KIAA1731	-0.2041	0.0309
215046_at	FLJ23861	hypothetical protein FLJ23861	-0.7587	0.039
215063_x_at	LRRC40	leucine rich repeat containing 40	-0.1974	0.0373
215066_at	PTPRF	protein tyrosine phosphatase; receptor type; F	-0.3393	0.015
215067_x_at	PRDX2	peroxiredoxin 2	-0.5877	0.0381
215069_at	NMT2	N-myristoyltransferase 2	-0.2714	0.0228
215070_x_at	RABGAP1	RAB GTPase activating protein 1	-0.3807	0.0239
215116_s_at	DNM1	dynamin 1	-1.3395	0.0239
215138_s_at	KIAA1026	kazrin	-0.8634	0.0172
215143_at	DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	-1.6074	0.0166
215162_at	GARNL1	GTPase activating Rap/RanGAP domain-like 1	-0.3622	0.0204
215164_at		MRNA; cDNA DKFZp564I083 (from clone DKFZp564I083)	-0.8313	0.0351
215179_x_at	PGF	Placental growth factor; vascular endothelial growth factor-related protein	-0.3244	0.0476
215190_at	EIF3M	eukaryotic translation initiation factor 3; subunit M	-0.9012	0.01
215204_at		CDNA FLJ14090 fis; clone MAMMA1000264	-0.8779	0.0114
215206_at		CDNA: FLJ21490 fis; clone COL05464	-0.8931	0.0136
215284_at		Clone 24407 mRNA sequence	-0.2858	0.0123
215296_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	-0.6502	0.0339
215308_at	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen; 70kDa)	-0.232	0.0194
215321_at	RPIB9	Rap2-binding protein 9	-1.6499	0.0054
215350_at	SYNE1	spectrin repeat containing; nuclear envelope 1	-0.4478	0.0438
215372_x_at		CDNA FLJ12002 fis; clone HEMBB1001536	-0.3068	0.0403
215373_x_at	FLJ12151	hypothetical protein FLJ12151	-0.4219	0.033
215377_at	CTBP2	C-terminal binding protein 2	-0.2263	0.0269
215383_x_at	SPG21	spastic paraplegia 21 (autosomal recessive; Mast syndrome)	-0.2196	0.0225
215385_at		CDNA FLJ12411 fis; clone MAMMA1002964	-1.3293	0.004
215398_at		Clone 23821 mRNA sequence	-0.6386	0.0315
215404_x_at	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2; Pfeiffer syndrome)	-0.4271	0.006
215435_at		CDNA FLJ11921 fis; clone HEMBB1000318	-1.1151	0.0161
215436_at	HSDL2	Hydroxysteroid dehydrogenase like 2	-0.9141	0.0009
215457_at		Clone 24438 mRNA sequence	-0.3453	0.0035
215528_at		MRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)	-0.7773	0.0105
215556_at		CDNA FLJ13712 fis; clone PLACE2000394	-0.1756	0.0109
215558_at	UBR2	Ubiquitin protein ligase E3 component n-recognin 2	-0.4181	0.0128
215573_at	CAT	Catalase	-0.3607	0.019
215586_at		CDNA FLJ14111 fis; clone MAMMA1001630	-0.5741	0.0491
215588_x_at	RIOK3	RIO kinase 3 (yeast)	-0.7	0.0169
215595_x_at		CDNA FLJ13856 fis; clone THYRO1000988	-0.1977	0.0212
215597_x_at		CDNA FLJ11353 fis; clone HEMBA1000042	-0.254	0.0352
215604_x_at		CDNA FLJ13721 fis; clone PLACE2000450	-0.3649	0.0303
215605_at	NCOA2	Nuclear receptor coactivator 2	-0.7096	0.0368
215616_s_at	JMJD2B	jumonji domain containing 2B	-0.5513	0.0017
215620_at	RREB1	ras responsive element binding protein 1	-0.3384	0.015
215628_x_at		MRNA; cDNA DKFZp564M193 (from clone DKFZp564M193)	-0.3068	0.0225
215635_at		MRNA full length insert cDNA clone EUROIMAGE 239714	-0.7319	0.0259
215665_at	HSD3B2	hydroxy-delta-5-steroid dehydrogenase; 3 beta- and steroid delta-isomerase 2, similar to 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I (3Beta-HSD I) (Trophoblast antigen FDO161G)	-1.6518	0.043
215674_at	KIAA1659	KIAA1659 protein	-0.1622	0.0425

215714_s_at	SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	-1.1906	0.0402
215786_at		CDNA FLJ12108 fis; clone MAMMA1000009	-1.1025	0.0158
215802_at		CDNA FLJ20137 fis; clone COL07137	-0.579	0.01
215814_at	DST	Dystonin	-0.1159	0.0404
215828_at		MRNA; cDNA DKFZp547C126 (from clone DKFZp547C126)	-1.1829	0.009
215834_x_at	SCARB1	scavenger receptor class B; member 1	-1.3772	0.0188
215854_at		CDNA FLJ11844 fis; clone HEMBA1006665	-0.3886	0.0475
215874_at		CDNA: FLJ23167 fis; clone LNG09902	-0.238	0.0398
215888_at	PDS5B	Androgen-induced proliferation inhibitor	-1.3633	0.0176
215926_x_at	SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	-0.3713	0.0308
215940_at			-0.1027	0.0251
215963_x_at	LOC642741	similar to ribosomal protein L3 isoform a	-0.2838	0.0138
215978_x_at	LOC152719	hypothetical protein LOC152719	-0.4852	0.0297
215985_at	HCG8	HLA complex group 8	-0.5823	0.0298
216006_at		Clone 24694 mRNA sequence	-0.3943	0.0478
216028_at	DKFZP564C 152	DKFZP564C152 protein	-1.6539	0.0224
216035_x_at	TCF7L2	transcription factor 7-like 2 (T-cell specific; HMG-box)	-0.7153	0.027
216037_x_at	TCF7L2	transcription factor 7-like 2 (T-cell specific; HMG-box)	-0.5635	0.016
216066_at	ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	-0.1922	0.0032
216067_at		CDNA FLJ11624 fis; clone HEMBA1004193	-0.2048	0.0328
216086_at	SV2C	synaptic vesicle glycoprotein 2C	-1.7839	0.018
216093_at		MRNA; cDNA DKFZp566E103 (from clone DKFZp566E103)	-0.703	0.0213
216113_at	ABI2	Abl interactor 2	-0.4197	0.0075
216147_at		MRNA; cDNA DKFZp761L23121 (from clone DKFZp761L23121)	-0.3341	0.0214
216153_x_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	-0.2309	0.0194
216165_at	GARNL3	GTPase activating Rap/RanGAP domain-like 3	-0.2976	0.019
216210_x_at	TRIOBP	TRIO and F-actin binding protein	-0.4616	0.0348
216229_x_at	HCG2P7	HLA complex group 2 pseudogene 7	-0.3163	0.0428
216278_at		MRNA full length insert cDNA clone EUROIMAGE 73337	-0.6264	0.0326
216333_x_at	TNXB	tenascin XB	-1.9115	0.0058
216339_s_at	TNXA	tenascin XA pseudogene, tenascin XB	-1.7251	0.0284
216436_at	PIK3R4	Phosphoinositide-3-kinase; regulatory subunit 4; p150	-0.1208	0.0476
216452_at	TRPM3	transient receptor potential cation channel; subfamily M; member 3	-0.7312	0.0233
216459_x_at	TIGD1L	tigger transposable element derived 1-like	-0.2538	0.006
216494_at	LOC645468	similar to IGF-II mRNA-binding protein 3, similar to insulin-like growth factor 2 mRNA binding protein 3	-0.1107	0.0289
216550_x_at	ANKRD12	ankyrin repeat domain 12	-0.5093	0.031
216563_at	ANKRD12	Ankyrin repeat domain 12	-0.4953	0.0446
216595_at		MRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)	-0.1502	0.0168
216621_at		MRNA; cDNA DKFZp566F1224 (from clone DKFZp566F1224)	-0.3427	0.036
216657_at	ATXN3	ataxin 3	-0.1993	0.0093
216682_s_at	FAM48A	family with sequence similarity 48; member A	-0.8057	0.0437
216695_s_at	TNKS	tankyrase; TRF1-interacting ankyrin-related ADP-ribose polymerase	-0.2125	0.0224
216756_at		CDNA: FLJ21342 fis; clone COL02673	-0.3383	0.038
216819_at	LOC391076	similar to 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type II (3Beta-HSD II)	-0.1667	0.0492
216979_at	NR4A3	nuclear receptor subfamily 4; group A; member 3	-0.8461	0.0195
216983_s_at	ZNF224	zinc finger protein 224	-0.5021	0.0242
217042_at	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	-0.5856	0.0242
217059_at	MUC7	mucin 7; secreted	-0.1193	0.0364
217100_s_at	UBXD7	UBX domain containing 7	-0.9285	0.0279
217152_at		CDNA FLJ14074 fis; clone HEMBB1001869	-0.5845	0.0006

217164_at			-1.0564	0.006
217208_s_at	DLG1	discs; large homolog 1 (Drosophila)	-1.2907	0.0167
217321_x_at	ATXN3	Ataxin 3	-0.1814	0.0115
217322_x_at			-0.2779	0.0388
217437_s_at	TACC1	transforming; acidic coiled-coil containing protein 1	-0.8032	0.0491
217446_x_at		MRNA; cDNA DKFZp434M054 (from clone DKFZp434M054)	-0.2651	0.022
217482_at		CDNA FLJ11925 fis; clone HEMBB1000354	-0.5484	0.0448
217494_s_at	PTENP1	phosphatase and tensin homolog (mutated in multiple advanced cancers 1); pseudogene 1	-0.1428	0.04
217506_at	LOC400642	Hypothetical gene supported by BC041875; BX648984	-1.1885	0.0305
217554_at		Transcribed locus	-0.4324	0.0041
217578_at		Transcribed locus	-0.1488	0.0088
217579_x_at		Transcribed locus	-0.4648	0.0114
217591_at		Transcribed locus	-0.9583	0.0351
217617_at		Transcribed locus	-2.2695	0.0006
217649_at	LOC732229	Similar to Zinc finger A20 domain-containing protein 2 (Zinc finger protein 216)	-1.1181	0.0151
217659_at			-0.4729	0.0301
217662_x_at		Transcribed locus	-0.2679	0.0206
217671_at		Transcribed locus	-0.7764	0.01
217679_x_at			-0.5145	0.0295
217715_x_at			-0.3006	0.0075
217719_at	EIF3EIP	eukaryotic translation initiation factor 3; subunit E interacting protein	-0.4983	0.0152
217804_s_at	ILF3	interleukin enhancer binding factor 3; 90kDa	-0.4716	0.018
217807_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.415	0.0081
217808_s_at	MAPKAP1	mitogen-activated protein kinase associated protein 1	-0.7796	0.0167
217820_s_at	ENAH	enabled homolog (Drosophila)	-0.7126	0.0072
217833_at	SYNCRIP	synaptotagmin binding; cytoplasmic RNA interacting protein	-0.5837	0.0294
217841_s_at	PPME1	protein phosphatase methylesterase 1	-0.513	0.0396
217885_at	IPO9	importin 9	-0.8467	0.0164
217894_at	KCTD3	potassium channel tetramerisation domain containing 3	-0.8873	0.0054
217996_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-2.2808	0.0345
217997_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-2.0299	0.0479
217999_s_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-1.7543	0.0475
218000_s_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-1.1531	0.0254
218064_s_at	AKAP8L	A kinase (PRKA) anchor protein 8-like	-0.8534	0.0278
218132_s_at	TSEN34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	-0.4046	0.0193
218236_s_at	PRKD3	protein kinase D3	-1.2052	0.05
218240_at	NKIRAS2	NFKB inhibitor interacting Ras-like 2	-0.5367	0.0083
218242_s_at	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-0.7022	0.0167
218258_at	POLR1D	polymerase (RNA) I polypeptide D; 16kDa	-0.8674	0.0052
218263_s_at	ZBED5	zinc finger; BED-type containing 5	-0.4226	0.018
218274_s_at	ANKZF1	ankyrin repeat and zinc finger domain containing 1	-0.8908	0.0015
218311_at	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	-0.6731	0.0301
218323_at	RHOT1	ras homolog gene family; member T1	-0.4165	0.0312
218427_at	SDCCAG3	serologically defined colon cancer antigen 3	-0.4	0.0312
218428_s_at	REV1	REV1 homolog (S. cerevisiae)	-0.7486	0.0218
218434_s_at	AACS	acetoacetyl-CoA synthetase	-1.1966	0.0039
218471_s_at	BBS1	Bardet-Biedl syndrome 1	-0.6822	0.02
218476_at	POMT1	protein-O-mannosyltransferase 1	-0.687	0.0046
218546_at	C1orf115	chromosome 1 open reading frame 115	-1.8222	0.0379
218565_at	C9orf114	chromosome 9 open reading frame 114	-0.576	0.0189
218613_at	PSD3	pleckstrin and Sec7 domain containing 3	-2.2516	0.0138
218618_s_at	FNDC3B	fibronectin type III domain containing 3B	-0.6264	0.0412
218625_at	NRN1	neuritin 1	-3.2848	0.0019
218636_s_at	MAN1B1	mannosidase; alpha; class 1B; member 1	-0.7748	0.0108
218767_at	REXO4	REX4; RNA exonuclease 4 homolog (S. cerevisiae)	-0.3444	0.0463
218880_at	FOSL2	FOS-like antigen 2	-1.2515	0.0427

218881_s_at	FOSL2	FOS-like antigen 2	-0.7313	0.0101
218906_x_at	KLC2	kinesin light chain 2	-0.3866	0.0427
218957_s_at	PAAF1	proteasomal ATPase-associated factor 1	-0.79	0.0171
218979_at	RMI1	RMI1; RecQ mediated genome instability 1; homolog (S. cerevisiae)	-0.7152	0.0304
219093_at	PID1	phosphotyrosine interaction domain containing 1	-1.9632	0.0212
219116_s_at	DCUN1D2	DCN1; defective in cullin neddylation 1; domain containing 2 (S. cerevisiae)	-0.6867	0.0212
219152_at	PODXL2	podocalyxin-like 2	-0.2257	0.0049
219165_at	PDLIM2	PDZ and LIM domain 2 (mystique)	-1.1579	0.026
219169_s_at	TFB1M	transcription factor B1; mitochondrial	-0.9582	0.0037
219312_s_at	ZBTB10	zinc finger and BTB domain containing 10	-0.8761	0.0368
219317_at	POLI	polymerase (DNA directed) iota	-0.963	0.0264
219353_at	NHLRC2	NHL repeat containing 2	-0.7253	0.0038
219380_x_at	POLH	polymerase (DNA directed); eta	-0.3249	0.0273
219407_s_at	LAMC3	laminin; gamma 3	-2.0492	0.0294
219492_at	CHIC2	cysteine-rich hydrophobic domain 2	-0.6522	0.0398
219532_at	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2; SUR4/Elo3; yeast)-like 4	-1.7014	0.0216
219625_s_at	COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	-0.724	0.0047
219657_s_at	KLF3	Kruppel-like factor 3 (basic)	-0.8454	0.022
219670_at	C1orf165	chromosome 1 open reading frame 165	-1.2529	0.0159
219779_at	ZFHX4	zinc finger homeobox 4	-2.2943	0.0114
219794_at	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	-0.1546	0.0379
219825_at	CYP26B1	cytochrome P450; family 26; subfamily B; polypeptide 1	-1.7965	0.026
219844_at	C10orf118	chromosome 10 open reading frame 118	-0.2687	0.0429
219950_s_at	TIAM2	T-cell lymphoma invasion and metastasis 2	-0.1171	0.0102
219998_at	HSPC159	galectin-related protein	-0.9864	0.025
220102_at	FOXL2	forkhead box L2	-1.2867	0.0323
220175_s_at	CBWD1	COBW domain containing 1, COBW domain containing 2, COBW domain containing 3, COBW domain containing 5, COBW domain containing 6, COBW domain containing 7	-0.5053	0.0224
220195_at	MBD5	methyl-CpG binding domain protein 5	-1.063	0.0017
220221_at	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	-0.4974	0.0204
220328_at	PHC3	polyhomeotic homolog 3 (Drosophila)	-0.2144	0.0305
220338_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-0.4632	0.0393
220400_at	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	-0.2353	0.0083
220459_at	MCM3APAS	minichromosome maintenance complex component 3 associated protein antisense	-1.3442	0.0322
220467_at	FLJ21272	hypothetical protein FLJ21272	-1.3251	0.0202
220512_at	DLC1	deleted in liver cancer 1	-1.2946	0.0499
220533_at			-0.4706	0.044
220581_at	C6orf97	chromosome 6 open reading frame 97	-1.0848	0.0164
220612_at		Clone HQ0641 PRO0641	-0.2906	0.0327
220660_at	C9orf27	chromosome 9 open reading frame 27	-0.1228	0.0427
220670_at			-0.1405	0.0459
220694_at	DDEF1IT1	DDEF1 intronic transcript 1	-0.6985	0.0011
220702_at			-0.8463	0.0125
220711_at			-0.344	0.0261
220720_x_at	FAM128B	family with sequence similarity 128; member B	-0.6391	0.0066
220728_at			-0.8819	0.0017
220774_at	DYM	dymeclin	-0.4115	0.0175
220796_x_at	SLC35E1	solute carrier family 35; member E1	-0.4735	0.0257
220803_at	STAMBPL1	STAM binding protein-like 1	-0.3159	0.0013
220858_at	SORBS2	sorbin and SH3 domain containing 2	-1.4552	0.0302
220906_at			-0.6478	0.0213
220925_at	MAK10	MAK10 homolog; amino-acid N-acetyltransferase subunit; (S. cerevisiae)	-0.559	0.0452
220952_s_at	PLEKHA5	pleckstrin homology domain containing; family A member 5	-0.9652	0.0445

220975_s_at	C1QTNF1	C1q and tumor necrosis factor related protein 1	-1.1907	0.0195
221004_s_at	ITM2C	integral membrane protein 2C	-1.0397	0.0426
221009_s_at	ANGPTL4	angiopoietin-like 4	-1.2304	0.0271
221039_s_at	DDEF1	development and differentiation enhancing factor 1	-0.8157	0.0093
221208_s_at	C11orf61	chromosome 11 open reading frame 61	-0.6353	0.0245
221274_s_at	LMAN2L	lectin; mannose-binding 2-like	-0.7052	0.0013
221391_at	TAS2R14	taste receptor; type 2; member 14	-0.1693	0.0294
221395_at	TAS2R13	taste receptor; type 2; member 13	-0.1254	0.0041
221478_at	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	-0.5151	0.0368
221516_s_at	SMCR7L	Smith-Magenis syndrome chromosome region; candidate 7-like	-0.7357	0.0476
221592_at	TBC1D8	TBC1 domain family; member 8 (with GRAM domain)	-0.2407	0.0048
221599_at	C11orf67	chromosome 11 open reading frame 67	-0.7829	0.0109
221600_s_at	C11orf67	chromosome 11 open reading frame 67	-0.9752	0.0301
221616_s_at	TAF9B	TAF9B RNA polymerase II; TATA box binding protein (TBP)-associated factor; 31kDa	-0.8015	0.0377
221617_at	TAF9B	TAF9B RNA polymerase II; TATA box binding protein (TBP)-associated factor; 31kDa	-1.117	0.0158
221663_x_at	HRH3	histamine receptor H3	-0.2424	0.043
221743_at	CUGBP1	CUG triplet repeat; RNA binding protein 1	-0.4571	0.0049
221744_at	WDR68	WD repeat domain 68	-0.5966	0.0244
221747_at	TNS1	Tensin 1	-1.002	0.0438
221748_s_at	TNS1	tensin 1	-0.9874	0.0252
221751_at	SLC2A3P1	Solute carrier family 2 (facilitated glucose transporter); member 3 pseudogene 1	-0.5027	0.0254
221763_at	JMJD1C	jumonji domain containing 1C	-0.7416	0.0141
221765_at	UGCG	UDP-glucose ceramide glucosyltransferase	-2.4197	0.0018
221806_s_at	SETD5	SET domain containing 5	-0.5204	0.0482
221842_s_at	ZNF131	zinc finger protein 131	-0.3343	0.0443
221860_at	HNRNPL	heterogeneous nuclear ribonucleoprotein L	-0.9306	0.0105
221958_s_at	GPR177	G protein-coupled receptor 177	-1.2407	0.0123
222034_at	GNB2L1	Guanine nucleotide binding protein (G protein); beta polypeptide 2-like 1	-0.9788	0.0447
222066_at	EPB41L1	Erythrocyte membrane protein band 4.1-like 1	-0.2307	0.0043
222099_s_at	LSM14A	LSM14A; SCD6 homolog A (S. cerevisiae)	-0.6236	0.002
222128_at	NSUN6	NOL1/NOP2/Sun domain family; member 6	-1.0473	0.0034
222133_s_at	PHF20L1	PHD finger protein 20-like 1	-0.9969	0.0146
222146_s_at	TCF4	transcription factor 4	-1.0272	0.0277
222160_at	AKAP8L	A kinase (PRKA) anchor protein 8-like	-0.4021	0.0098
222167_at		CDNA FLJ11774 fis; clone HEMBA1005884	-0.7403	0.0164
222180_at		CDNA FLJ14122 fis; clone MAMMA1002033	-0.522	0.0372
222207_x_at	LOC389517	Williams Beuren syndrome chromosome region 19 pseudogene	-0.174	0.0256
222209_s_at	TMEM135	transmembrane protein 135	-1.2646	0.023
222214_at		CDNA: FLJ21335 fis; clone COL02546	-1.1366	0.0177
222244_s_at	TUG1	taurine upregulated gene 1	-0.4255	0.0343
222245_s_at	FER1L4	fer-1-like 4 (C. elegans)	-1.121	0.0468
222258_s_at	SH3BP4	SH3-domain binding protein 4	-1.6167	0.0117
222266_at	C19orf2	Chromosome 19 open reading frame 2	-0.7778	0.0213
222270_at	SMEK2	SMEK homolog 2; suppressor of mek1 (Dictyostelium)	-0.5762	0.0042
222286_at	SNAPC3	small nuclear RNA activating complex; polypeptide 3; 50kDa	-0.7918	0.0181
222297_x_at	LOC390612	similar to ribosomal protein L18	-0.202	0.0128
222306_at		Transcribed locus	-0.4096	0.0092
222310_at	SFRS15	splicing factor; arginine/serine-rich 15	-1.1308	0.0164
222311_s_at	SFRS15	splicing factor; arginine/serine-rich 15	-0.8897	0.0169
222320_at		Transcribed locus	-1.0901	0.0087
222357_at	ZBTB20	zinc finger and BTB domain containing 20	-1.4412	0.0052
222372_at		Transcribed locus	-1.3038	0.0097
222375_at		Transcribed locus	-0.6723	0.014
222426_at	MAPKAP1	mitogen-activated protein kinase associated protein 1	-0.8223	0.0068
222433_at	ENAH	enabled homolog (Drosophila)	-0.6599	0.0078

222434_at	ENAH	enabled homolog (Drosophila)	-0.9334	0.0262
222544_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	-0.8882	0.0107
222557_at	STMN3	stathmin-like 3	-1.2912	0.0497
222565_s_at	PRKD3	protein kinase D3	-1.4026	0.0286
222589_at	NLK	nemo-like kinase	-0.9827	0.0174
222628_s_at	REV1	REV1 homolog (S. cerevisiae)	-1.0157	0.0061
222629_at	REV1	REV1 homolog (S. cerevisiae)	-1.0276	0.0369
222654_at	IMPAD1	inositol monophosphatase domain containing 1	-0.6561	0.0496
222655_s_at	IMPAD1	inositol monophosphatase domain containing 1	-0.2368	0.0182
222667_s_at	ASH1L	ash1 (absent; small; or homeotic)-like (Drosophila)	-0.8004	0.0053
222670_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	-0.9282	0.0446
222694_at	MGC2752	hypothetical protein MGC2752	-0.5825	0.0405
222696_at	AXIN2	axin 2 (conductin; axil)	-1.7715	0.0051
222700_at	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	-0.7677	0.0252
222708_s_at	STX17	syntaxin 17	-1.1169	0.0004
222715_s_at	AP1GBP1	AP1 gamma subunit binding protein 1	-0.8903	0.0338
222759_at	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.511	0.0035
222760_at	ZNF703	zinc finger protein 703	-0.9182	0.0494
222790_s_at	RSBN1	round spermatid basic protein 1	-0.4582	0.0389
222791_at	RSBN1	round spermatid basic protein 1	-0.6706	0.0268
222807_at	C11orf30	chromosome 11 open reading frame 30	-0.7405	0.0231
222823_at	IPPK	inositol 1;3;4;5;6-pentakisphosphate 2-kinase	-0.173	0.0495
222873_s_at	EHMT1	euchromatic histone-lysine N-methyltransferase 1	-0.669	0.0443
222917_s_at	TBX3	T-box 3 (ulnar mammary syndrome)	-1.0771	0.0253
222988_s_at	TMEM9	transmembrane protein 9	-0.9102	0.0097
223129_x_at	MYLIP	myosin regulatory light chain interacting protein	-0.9746	0.0498
223169_s_at	RHOU	ras homolog gene family; member U	-2.0895	0.0307
223170_at	LOC440181	hypothetical LOC440181, transmembrane protein 98	-1.2722	0.0481
223190_s_at	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog; Drosophila)	-0.533	0.0234
223207_x_at	PHPT1	phosphohistidine phosphatase 1	-0.5357	0.0038
223226_x_at	SSBP4	single stranded DNA binding protein 4	-0.792	0.0125
223311_s_at	MTA3	metastasis associated 1 family; member 3	-0.7576	0.0219
223333_s_at	ANGPTL4	angiopoietin-like 4	-1.2123	0.0252
223434_at	GBP3	guanylate binding protein 3	-1.2873	0.0272
223437_at	PPARA	peroxisome proliferator-activated receptor alpha	-1.1969	0.0315
223466_x_at	COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	-0.7118	0.005
223498_at	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	-0.2272	0.0223
223559_s_at	C9orf80	chromosome 9 open reading frame 80	-0.5392	0.0263
223577_x_at	PRO1073	PRO1073 protein	-0.8457	0.0169
223598_at	RAD23B	RAD23 homolog B (S. cerevisiae)	-0.7085	0.0196
223612_s_at	LNX1	ligand of numb-protein X 1	-0.1414	0.0066
223619_x_at	PECR	peroxisomal trans-2-enoyl-CoA reductase	-0.3064	0.0098
223638_at	NBPF3	neuroblastoma breakpoint family; member 3	-0.8953	0.0271
223641_at		CDNA FLJ36838 fis; clone ASTRO2011426	-0.867	0.0102
223662_x_at	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	-0.2968	0.0368
223679_at	CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	-1.7974	0.0022
223698_at	SLC25A36	solute carrier family 25; member 36	-0.3263	0.0397
223703_at	C10orf11	chromosome 10 open reading frame 11	-1.7552	0.0018
223764_x_at	NIPSNAP3B	nipsnap homolog 3B (C. elegans)	-1.1844	0.034
223796_at	CNTNAP3	contactin associated protein-like 3, contactin associated protein-like 3B, similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-1.2776	0.0296
223797_at	PRO2852	hypothetical protein PRO2852	-0.9813	0.0238
223802_s_at	RBBP6	retinoblastoma binding protein 6	-0.7476	0.0234
223818_s_at	RSF1	remodeling and spacing factor 1	-0.5994	0.0217
223877_at	C1QTNF7	C1q and tumor necrosis factor related protein 7	-0.1309	0.0408
223878_at	INPP4B	inositol polyphosphate-4-phosphatase; type II; 105kDa	-0.1338	0.0342
223915_at	BCOR	BCL6 co-repressor	-0.8568	0.0147

223966_at	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog; yeast), ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog; yeast)	-0.2431	0.0088
224014_at	ZNF160	zinc finger protein 160	-0.4279	0.0185
224029_x_at	SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	-0.184	0.0289
224044_at	RHOT1	ras homolog gene family; member T1	-0.6279	0.0037
224050_s_at			-0.1245	0.012
224106_at			-0.5943	0.0053
224126_at	SLC10A7	solute carrier family 10 (sodium/bile acid cotransporter family); member 7	-0.1238	0.0493
224176_s_at	AXIN2	axin 2 (conductin; axil)	-0.304	0.0327
224276_at	ZNF33A	zinc finger protein 33A	-0.1341	0.0428
224277_at	MOP-1	MOP-1	-0.148	0.006
224320_s_at	MCM8	minichromosome maintenance complex component 8	-0.5908	0.0311
224454_at	ETNK1	ethanolamine kinase 1	-0.1359	0.0431
224569_s_at	IRF2BP2	interferon regulatory factor 2 binding protein 2	-0.6007	0.0444
224609_at	SLC44A2	solute carrier family 44; member 2	-1.0718	0.034
224621_at	MAPK1	mitogen-activated protein kinase 1	-0.571	0.0213
224624_at	LRRC8A	leucine rich repeat containing 8 family; member A	-0.489	0.0408
224651_at	CCNY	cyclin Y	-0.6695	0.0152
224662_at	KIF5B	kinesin family member 5B	-0.3043	0.0476
224667_x_at	C10orf104	chromosome 10 open reading frame 104	-0.296	0.0356
224720_at	MIB1	mindbomb homolog 1 (Drosophila)	-0.6446	0.0487
224725_at	MIB1	mindbomb homolog 1 (Drosophila)	-0.7698	0.0426
224755_at	TM9SF3	transmembrane 9 superfamily member 3	-0.973	0.0127
224760_at	SP1	Sp1 transcription factor	-0.5636	0.0258
224763_at	RPL37	Ribosomal protein L37	-1.0575	0.0288
224771_at	NAV1	neuron navigator 1	-0.8727	0.0362
224784_at	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 6	-0.5265	0.0259
224790_at	DDEF1	development and differentiation enhancing factor 1	-0.7222	0.0357
224796_at	DDEF1	development and differentiation enhancing factor 1	-0.6594	0.0127
224814_at	DPP7	dipeptidyl-peptidase 7	-0.8572	0.0026
224820_at	FAM36A	family with sequence similarity 36; member A	-0.9258	0.0253
224847_at	CDK6	cyclin-dependent kinase 6	-1.6004	0.0358
224848_at	CDK6	cyclin-dependent kinase 6	-1.8266	0.0162
224851_at	CDK6	cyclin-dependent kinase 6	-2.2481	0.0054
224872_at	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	-0.734	0.0016
224897_at	WDR26	WD repeat domain 26	-0.645	0.0207
224933_s_at	JMJD1C	jumonji domain containing 1C	-1.1325	0.0043
224937_at	PTGFRN	prostaglandin F2 receptor negative regulator	-1.3708	0.0419
224967_at	UGCG	UDP-glucose ceramide glucosyltransferase	-1.5671	0.0005
224998_at	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	-1.0483	0.0086
225009_at	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	-1.3014	0.0031
225032_at	FNDC3B	fibronectin type III domain containing 3B	-0.4787	0.0358
225098_at	ABI2	abl interactor 2	-0.8298	0.0025
225112_at	ABI2	abl interactor 2	-0.7237	0.0016
225126_at	MRRF	mitochondrial ribosome recycling factor	-0.7466	0.0236
225138_at	ZRANB1	zinc finger; RAN-binding domain containing 1	-0.6666	0.0377
225171_at	ARHGAP18	Rho GTPase activating protein 18	-0.8015	0.025
225175_s_at	SLC44A2	solute carrier family 44; member 2	-0.848	0.0146
225193_at	KIAA1967	KIAA1967	-0.8572	0.0228
225197_at		MRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818)	-0.8846	0.0409
225217_s_at	BRPF3	bromodomain and PHD finger containing; 3	-1.8699	0.0357
225233_at	MSI2	musashi homolog 2 (Drosophila)	-0.4529	0.0085
225237_s_at	MSI2	musashi homolog 2 (Drosophila)	-1.2229	0.0003
225240_s_at	MSI2	musashi homolog 2 (Drosophila)	-1.1945	0
225256_at		CDNA FLJ41369 fis; clone BRCAN2006117	-0.4935	0.041
225266_at	ZNF652	zinc finger protein 652	-0.7682	0.001
225275_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	-2.2756	0.0152

225371_at	GLE1L	GLE1 RNA export mediator-like (yeast)	-0.766	0.013
225385_s_at	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	-0.4523	0.0203
225393_at	GATAD2B	GATA zinc finger domain containing 2B	-0.5047	0.0132
225406_at	TWSG1	twisted gastrulation homolog 1 (Drosophila)	-0.9624	0.0108
225420_at	GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	-1.8463	0.0077
225422_at	CDC26	cell division cycle 26 homolog (S. cerevisiae)	-0.5574	0.0499
225424_at	GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	-2.2443	0.0021
225461_at	EHMT1	euchromatic histone-lysine N-methyltransferase 1	-1.0693	0.0044
225466_at	FLJ36874	FLJ36874 protein	-0.5688	0.0371
225473_at	C20orf117	chromosome 20 open reading frame 117	-0.6942	0.0328
225496_s_at	SYTL2	synaptotagmin-like 2	-2.2437	0.0274
225504_at		MRNA; cDNA DKFZp686E0389 (from clone DKFZp686E0389)	-0.6986	0.0495
225522_at	AAK1	AP2 associated kinase 1	-0.5091	0.0156
225544_at	TBX3	T-box 3 (ulnar mammary syndrome)	-1.2909	0.0435
225565_at		CDNA FLJ34215 fis; clone FCBBF3021985	-0.4597	0.0294
225569_at	EIF2C2	Eukaryotic translation initiation factor 2C; 2	-1.024	0.0211
225570_at	SLC41A1	solute carrier family 41; member 1	-1.2477	0.0061
225571_at	LIFR	leukemia inhibitory factor receptor alpha	-1.7324	0.0103
225575_at	LIFR	leukemia inhibitory factor receptor alpha	-1.9125	0.0174
225586_at	WDR85	WD repeat domain 85	-0.5235	0.0324
225594_at	CREBZF	CREB/ATF bZIP transcription factor	-1.2246	0.0117
225595_at	CREBZF	CREB/ATF bZIP transcription factor	-0.8359	0.042
225652_at		CDNA FLJ37981 fis; clone CTONG2010566	-1.1733	0.007
225677_at	BCAP29	B-cell receptor-associated protein 29	-0.6121	0.0493
225703_at	KIAA1545	KIAA1545 protein	-0.672	0.0267
225717_at	KIAA1715	KIAA1715	-0.8052	0.0331
225729_at	C6orf89	chromosome 6 open reading frame 89	-0.624	0.0361
225740_x_at	MDM4	Mdm4; transformed 3T3 cell double minute 4; p53 binding protein (mouse)	-0.7362	0.0175
225745_at	LRP6	low density lipoprotein receptor-related protein 6	-0.9533	0.0125
225817_at	CGNL1	cingulin-like 1	-2.4362	0.0385
225842_at	PHLDA1	pleckstrin homology-like domain; family A; member 1	-2.0256	0.0359
225845_at	ZBTB44	zinc finger and BTB domain containing 44	-0.517	0.0159
225889_at	AEBP2	AE binding protein 2	-0.6303	0.0147
225896_at		CDNA FLJ34018 fis; clone FCBBF2002801	-0.4432	0.0407
225898_at	WDR54	WD repeat domain 54	-1.6007	0.0152
225918_at	LOC146346	hypothetical protein LOC146346	-0.8441	0.0119
225992_at	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 10	-0.7764	0.0344
226010_at	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier); member 23	-0.9761	0.0222
226102_at		Full-length cDNA clone CS0DF010YE22 of Fetal brain of Homo sapiens (human)	-1.1103	0.044
226110_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-0.6686	0.0123
226129_at	FAM83H	family with sequence similarity 83; member H	-1.174	0.0337
226134_s_at		Transcribed locus	-1.053	0.0001
226143_at	RAI1	retinoic acid induced 1	-0.5106	0.0268
226148_at	ZBTB44	zinc finger and BTB domain containing 44	-0.4391	0.0085
226169_at	SBF2	SET binding factor 2	-0.6684	0.0171
226190_at		Homo sapiens; clone IMAGE:4294444; mRNA	-0.7639	0.0158
226201_at		MRNA; cDNA DKFZp586P1823 (from clone DKFZp586P1823)	-0.9822	0.0042
226207_at	FLJ39378	hypothetical protein FLJ39378	-0.8274	0.0307
226222_at	KIAA1432	KIAA1432	-0.4885	0.008
226245_at	KCTD1	potassium channel tetramerisation domain containing 1	-1.1551	0.0261
226250_at		CDNA FLJ34585 fis; clone KIDNE2008758	-0.8791	0.0478
226252_at		CDNA FLJ34585 fis; clone KIDNE2008758	-1.1503	0.0205
226275_at	MXD1	MAX dimerization protein 1	-1.0288	0.0183
226277_at		CDNA FLJ43397 fis; clone OCBBF2009788	-0.3768	0.0089
226285_at	CAPRIN1	cell cycle associated protein 1	-0.6961	0.0292

226291_at	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	-1.1936	0.0321
226303_at	PGM5	phosphoglucomutase 5	-1.7116	0.0366
226326_at	PCGF5	polycomb group ring finger 5	-0.8221	0.0373
226327_at	ZNF507	zinc finger protein 507	-0.7061	0.013
226347_at			-1.157	0.0037
226348_at			-1.3134	0.0107
226377_at		Transcribed locus	-0.8497	0.0203
226381_at	PS1TP4	HBV preS1-transactivated protein 4	-0.6305	0.026
226383_at	C11orf46	chromosome 11 open reading frame 46	-0.4742	0.0356
226390_at	STARD4	StAR-related lipid transfer (START) domain containing 4	-1.4471	0.0428
226398_s_at	C10orf4	chromosome 10 open reading frame 4	-0.6382	0.0298
226412_at	SFRS18	splicing factor; arginine/serine-rich 18	-0.9788	0.0008
226427_s_at	B3GALT6	UDP-Gal:betaGal beta 1;3-galactosyltransferase polypeptide 6	-0.1283	0.0254
226431_at	ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 13	-1.2351	0.0105
226446_at	HES6	hairy and enhancer of split 6 (Drosophila)	-2.6216	0.0092
226452_at	PDK1	pyruvate dehydrogenase kinase; isozyme 1	-1.2645	0.0089
226465_s_at	SON	SON DNA binding protein	-0.4413	0.0196
226470_at	GGTL3	gamma-glutamyltransferase-like 3	-0.9605	0.0335
226485_at		CDNA FLJ37658 fis; clone BRHIP2010593	-1.1384	0.0088
226503_at	RIF1	RAP1 interacting factor homolog (yeast)	-0.9304	0.0099
226512_at	ZMYM2	zinc finger; MYM-type 2	-0.8332	0.033
226520_at		Primary neuroblastoma cDNA; clone:Nbla11485	-0.7734	0.0249
226555_at	FLJ20309	hypothetical protein FLJ20309	-0.6736	0.0345
226563_at	SMAD2	SMAD family member 2	-1.4749	0.0045
226575_at	ZNF462	zinc finger protein 462	-0.5918	0.0251
226590_at	ZNF618	zinc finger protein 618	-1.184	0.0016
226592_at	ZNF618	zinc finger protein 618	-1.6061	0.0001
226625_at			-1.2918	0.0479
226639_at	SFT2D3	SFT2 domain containing 3	-0.7115	0.0261
226662_at		Full-length cDNA clone CS0DB009YL20 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	-0.7507	0.0476
226676_at	ZNF521	zinc finger protein 521	-1.431	0.0402
226679_at	SLC26A11	solute carrier family 26; member 11	-0.7235	0.0237
226682_at	LOC283666	hypothetical protein LOC283666	-1.8387	0.0047
226687_at	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-0.7401	0.0361
226729_at	USP37	ubiquitin specific peptidase 37	-0.5506	0.0194
226731_at	PELO	Pelota homolog (Drosophila)	-1.9448	0.0026
226740_x_at	LOC728980	hypothetical protein LOC728980, hypothetical protein LOC730476, neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 10, neuroblastoma breakpoint family; member 11, neuroblastoma breakpoint family; member 14, neuroblastoma breakpoint family; member 15, neuroblastoma breakpoint family; member 16, neuroblastoma breakpoint family; member 20, neuroblastoma breakpoint family; member 8	-0.4621	0.0097
226753_at	FAM76B	family with sequence similarity 76; member B	-0.9345	0.0076
226765_at	SPTBN1	Spectrin; beta; non-erythrocytic 1	-0.4738	0.0429
226797_at		MRNA; cDNA DKFZp434G0972 (from clone DKFZp434G0972)	-0.7435	0.0293
226828_s_at	HEYL	hairy/enhancer-of-split related with YRPW motif-like	-0.8627	0.0166
226866_at	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-0.9616	0.0393
226895_at	NFIC	Nuclear factor I/C (CCAAT-binding transcription factor)	-0.5669	0.0092
226913_s_at	SOX8	SRY (sex determining region Y)-box 8	-2.3771	0.0152
226945_at	RHBDD1	rhomboid domain containing 1	-0.7324	0.0359
226969_at	LOC149448	5-methyltetrahydrofolate-homocysteine methyltransferase, hypothetical protein LOC149448	-1.0799	0.0023
226978_at	PPARA	peroxisome proliferator-activated receptor alpha	-1.016	0.047

226995_at	C21orf86	Chromosome 21 open reading frame 86	-1.0867	0.032
227082_at		MRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	-1.4085	0.0272
227088_at	PDE5A	phosphodiesterase 5A; cGMP-specific	-1.972	0.0083
227121_at		MRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	-1.1394	0.0216
227146_at	QSOX2	quiescin Q6 sulfhydryl oxidase 2	-0.9949	0.0408
227162_at	ZBTB26	zinc finger and BTB domain containing 26	-0.7611	0.0155
227164_at	SFRS1	splicing factor; arginine/serine-rich 1 (splicing factor 2; alternate splicing factor)	-0.6788	0.0293
227195_at	ZNF503	zinc finger protein 503	-1.8705	0.0077
227198_at	AFF3	AF4/FMR2 family; member 3	-3.4336	0.0066
227223_at	LOC643167	RNA binding motif protein 39, similar to RNA-binding region-containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1)	-1.0499	0.049
227227_at		CDNA FLJ32605 fis; clone STOMA1000175	-0.8317	0.0292
227285_at	C1orf51	chromosome 1 open reading frame 51	-1.1051	0.0356
227297_at	ITGA9	integrin; alpha 9	-2.0544	0.0043
227314_at	ITGA2	integrin; alpha 2 (CD49B; alpha 2 subunit of VLA-2 receptor)	-2.2113	0.0132
227337_at	ANKRD37	ankyrin repeat domain 37	-1.4999	0.0176
227368_at		Transcribed locus; moderately similar to XP_001091208.1 hypothetical protein [Macaca mulatta]	-1.9199	0.0086
227378_x_at	C16orf13	chromosome 16 open reading frame 13	-0.8925	0.0287
227383_at	LOC727820	hypothetical protein LOC727820	-1.2476	0.0067
227400_at	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	-1.1985	0.0081
227422_at			-0.7989	0.0312
227432_s_at		Transcribed locus; weakly similar to XP_512323.2 insulin receptor; partial [Pan troglodytes]	-0.8371	0.019
227449_at	EPHA4	EPH receptor A4	-1.8614	0.0282
227489_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	-0.825	0.0335
227501_at		Transcribed locus	-1.4078	0.0443
227573_s_at	OBSL1	obscurin-like 1	-0.562	0.0451
227574_at	OBSL1	obscurin-like 1	-1.0088	0.0169
227585_at			-0.6545	0.0205
227603_at		CDNA FLJ41385 fis; clone BRCAN2022191	-0.6297	0.0299
227621_at	WTAP	Wilms tumor 1 associated protein	-0.5698	0.0359
227622_at	PCF11	PCF11; cleavage and polyadenylation factor subunit; homolog (S. cerevisiae)	-0.864	0.007
227648_at	C22orf32	chromosome 22 open reading frame 32	-0.3006	0.0396
227751_at	PDCD5	Programmed cell death 5	-0.9549	0.0075
227771_at	LIFR	leukemia inhibitory factor receptor alpha	-1.6808	0.0202
227793_at			-0.9291	0.0221
227856_at	C4orf32	chromosome 4 open reading frame 32	-1.1206	0.0464
227872_at	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A; 155kDa	-0.3779	0.0331
227884_at	TAF15	TAF15 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 68kDa	-1.1584	0.0393
227939_s_at	TRA2A	Transformer-2 alpha	-0.1203	0.009
227971_at	NRK	Nik related kinase	-3.0402	0.0094
227973_at	FLJ38973	hypothetical protein FLJ38973	-0.4665	0.0296
227984_at	LOC650392	Hypothetical protein LOC650392	-2.7044	0.0083
227987_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	-1.1815	0.0076
227988_s_at	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	-1.082	0.0014
227996_at	FARP1	FERM; RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-2.0409	0.0344
228007_at	C6orf204	chromosome 6 open reading frame 204	-0.832	0.0048
228020_at	PTCD3	Pentatricopeptide repeat domain 3	-0.7941	0.039
228040_at	LOC728903	family with sequence similarity 88; member B, hypothetical protein LOC728903	-1.2766	0.0184
228075_x_at	TFB1M	transcription factor B1; mitochondrial	-0.8911	0.0089

228091_at		Full-length cDNA clone CS0DB009YL20 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	-0.8753	0.0091
228098_s_at	MYLIP	myosin regulatory light chain interacting protein	-1.4476	0.0331
228105_at		Transcribed locus	-1.2308	0.0235
228116_at		Clone IMAGE:120162 mRNA sequence	-1.6202	0.0311
228119_at	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	-0.2672	0.029
228121_at	TGFB2	transforming growth factor; beta 2	-1.9827	0.0057
228125_at		MRNA; cDNA DKFZp686P1116 (from clone DKFZp686P1116)	-0.6096	0.0358
228127_at		CDNA FLJ41679 fis; clone HCASM2003212	-1.5106	0.0221
228148_at	ZNF584	zinc finger protein 584	-0.5146	0.0269
228156_at		Homo sapiens; clone IMAGE:4346533; mRNA	-1.3125	0.0027
228157_at	ZNF207	zinc finger protein 207	-1.1683	0.0415
228171_s_at	PLEKHG4	pleckstrin homology domain containing; family G (with RhoGef domain) member 4	-2.1452	0.0042
228173_at	GNAS	GNAS complex locus	-0.9854	0.0188
228180_at		Transcribed locus	-1.4401	0.0027
228181_at	SLC30A1	solute carrier family 30 (zinc transporter); member 1	-1.5223	0.0419
228240_at		Full-length cDNA clone CS0DM002YA18 of Fetal liver of Homo sapiens (human)	-1.0136	0.0103
228248_at	RICTOR	rapamycin-insensitive companion of mTOR	-0.7035	0.0022
228278_at	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	-0.474	0.0038
228284_at	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	-1.5313	0.0068
228454_at	LCOR	ligand dependent nuclear receptor corepressor	-0.9559	0.0028
228479_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-0.7055	0.0345
228480_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A; 33kDa	-1.7342	0.0066
228512_at	PTCD3	Pentatricopeptide repeat domain 3	-0.7953	0.0232
228515_at	LOC90784	hypothetical protein LOC90784	-0.9605	0.0186
228527_s_at	SLC25A37	Solute carrier family 25; member 37	-0.2423	0.0157
228545_at	ZNF148	zinc finger protein 148	-0.6707	0.0154
228553_at	ENAH	Enabled homolog (Drosophila)	-0.1158	0.0045
228554_at		MRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)	-2.1009	0.0136
228562_at		Transcribed locus	-1.1246	0.003
228566_at	P15RS	Hypothetical protein FLJ10656	-1.1548	0.0133
228590_at	PTCD3	Pentatricopeptide repeat domain 3	-0.7447	0.0083
228605_at		CDNA FLJ30010 fis; clone 3NB692000154	-1.0176	0.0101
228642_at	HOXA2	Homeobox A2	-1.2664	0.023
228650_at		CDNA FLJ38469 fis; clone FEBRA2021892	-0.4148	0.0428
228656_at	PROX1	Prospero homeobox 1	-2.0298	0.001
228673_s_at	EML4	Echinoderm microtubule associated protein like 4	-0.1244	0.0395
228740_at		CDNA clone IMAGE:5276765	-1.8975	0.0249
228834_at	TOB1	transducer of ERBB2; 1	-1.8732	0.021
228839_s_at	LOC439994	hypothetical LOC642361, hypothetical gene supported by AF064843; AK025716	-0.658	0.0185
228879_at			-1.0287	0.0086
228906_at	CXXC6	CXXC finger 6	-1.2523	0.0247
228908_s_at	C21orf86	Chromosome 21 open reading frame 86	-1.0997	0.0295
228909_at	C21orf86	Chromosome 21 open reading frame 86	-1.1065	0.0137
228915_at	DACH1	dachshund homolog 1 (Drosophila)	-2.244	0.0274
228927_at	ZNF397	zinc finger protein 397	-0.8431	0.0049
228931_at	COQ4	coenzyme Q4 homolog (S. cerevisiae)	-1.1066	0.0221
228933_at	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	-1.3094	0.0176
228940_at	LOC727762	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 4; 15kDa	-0.7234	0.0437
228948_at	EPHA4	EPH receptor A4	-1.2577	0.036

228988_at	ZNF711	zinc finger protein 711	-2.3289	0.048
229015_at	LOC286367	FP944	-1.032	0.0084
229016_s_at	TRERF1	transcriptional regulating factor 1	-0.2766	0.0424
229036_at	TNRC6B	trinucleotide repeat containing 6B	-0.3723	0.0349
229063_s_at	CCDC107	coiled-coil domain containing 107	-0.5942	0.0149
229141_at	WDR33	WD repeat domain 33	-0.7871	0.0201
229144_at		Transcribed locus	-2.1547	0.0043
229145_at	C10orf104	chromosome 10 open reading frame 104	-0.8492	0.0131
229187_at	ZNF542	CDNA FLJ45377 fis; clone BRHIP3019956, Zinc finger protein 542	-0.2532	0.0399
229193_at		CDNA FLJ33355 fis; clone BRACE2005151	-0.954	0.0049
229194_at	PCGF5	polycomb group ring finger 5	-0.8738	0.0398
229198_at	USP35	ubiquitin specific peptidase 35	-1.0262	0.0303
229269_x_at	LOC646044	similar to single stranded DNA binding protein 4 isoform a, single stranded DNA binding protein 4	-0.7577	0.0151
229272_at	FNBP4	formin binding protein 4	-1.5417	0.0009
229325_at	ZZZ3	zinc finger; ZZ-type containing 3	-0.6974	0.0463
229371_at		MRNA; cDNA DKFZp666B189 (from clone DKFZp666B189)	-0.8764	0.0126
229376_at			-1.5153	0.0058
229425_at		Transcribed locus	-0.4302	0.0024
229447_x_at	NBPF11	neuroblastoma breakpoint family; member 11	-0.4706	0.0154
229460_at		CDNA FLJ37917 fis; clone CTONG1000137	-1.0278	0.0069
229462_at			-0.1172	0.0383
229481_at	LOC283859	hypothetical protein LOC283859	-0.3751	0.0325
229516_at	WDR31	WD repeat domain 31	-0.4762	0.0075
229571_at		Transcribed locus	-0.2647	0.012
229576_s_at	TBX3	T-box 3 (ulnar mammary syndrome)	-1.533	0.0191
229626_at	LOC387856	similar to expressed sequence AI836003	-1.5269	0.0067
229627_at	KIAA1529	KIAA1529	-0.2002	0.0219
229628_s_at	KIAA1529	KIAA1529	-0.4422	0.0151
229638_at	IRX3	iroquois homeobox 3	-1.5673	0.0322
229656_s_at	FLJ42562	similar to echinoderm microtubule associated protein like 5	-2.3422	0.0033
229705_at		Transcribed locus	-1.093	0.0169
229710_at		Transcribed locus	-0.6514	0.0218
229736_at	TMEM86B	transmembrane protein 86B	-0.371	0.0035
229741_at	MGC3260	Hypothetical protein MGC3260	-0.4995	0.0324
229765_at		Transcribed locus	-1.1827	0.002
229799_s_at	NCAM1	neural cell adhesion molecule 1	-0.1371	0.0271
229841_at		Transcribed locus	-0.5833	0.0165
229879_at		Transcribed locus	-1.5396	0.0461
229897_at	ZNF641	Zinc finger protein 641	-0.997	0.0445
229909_at	B4GALNT3	beta-1;4-N-acetyl-galactosaminyl transferase 3	-0.8919	0.0398
229911_at	TPM2	tropomyosin 2 (beta)	-0.3203	0.0176
229953_x_at	LCA5	Leber congenital amaurosis 5	-0.4477	0.0083
229982_at	QSER1	glutamine and serine rich 1	-0.7652	0.0333
230007_at	JMJD1C	jumonji domain containing 1C	-0.1262	0.0455
230058_at	SDCCAG3	serologically defined colon cancer antigen 3	-0.5958	0.0181
230082_at		Transcribed locus; weakly similar to XP_001088736.1 similar to NEDD8-conjugating enzyme [Macaca mulatta]	-1.067	0.0059
230097_at	GART	Phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	-1.4384	0.0114
230099_at		Transcribed locus	-1.5722	0.0043
230102_at	ETV5	Ets variant gene 5 (ets-related molecule)	-1.1905	0.015
230133_at	RC3H2	ring finger and CCCH-type zinc finger domains 2	-0.5038	0.032
230134_s_at	RC3H2	ring finger and CCCH-type zinc finger domains 2	-0.3795	0.0477
230186_at	TMEM136	transmembrane protein 136	-0.3957	0.0342
230200_at	NSUN6	NOL1/NOP2/Sun domain family; member 6	-0.8857	0.0045
230229_at	DLG1	Discs; large homolog 1 (Drosophila)	-1.6575	0.0382
230293_at		MSTP088 (MST088)	-0.1626	0.04

230297_x_at	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat), zinc finger and BTB domain containing 9	-0.2304	0.0365
230332_at	ZCCHC7	Zinc finger; CCHC domain containing 7	-1.1972	0.0151
230337_at	SOS1	son of sevenless homolog 1 (Drosophila)	-0.7471	0.046
230375_at	SFRS18	splicing factor; arginine/serine-rich 18	-0.9375	0.0279
230409_at		Transcribed locus	-0.1448	0.0277
230424_at	C5orf13	chromosome 5 open reading frame 13	-1.8068	0.0115
230435_at	LOC375190	hypothetical LOC375190	-0.6663	0.0172
230440_at	ZNF469	zinc finger protein 469	-1.0077	0.0146
230491_at		MRNA; cDNA DKFZp686J01116 (from clone DKFZp686J01116)	-0.8092	0.0116
230528_s_at	MGC2752	hypothetical protein MGC2752	-0.7344	0.0029
230595_at	LOC572558	hypothetical locus LOC572558	-1.5628	0.0309
230688_at		Clone IMAGE:238558; mRNA sequence	-0.9827	0.0413
230710_at		CDNA FLJ41489 fis; clone BRTHA2004582	-1.8012	0.0134
230712_at	LOC730258	neuroblastoma breakpoint family; member 1, neuroblastoma breakpoint family; member 15, neuroblastoma breakpoint family; member 3, neuroblastoma breakpoint family; member 8, region containing neuroblastoma breakpoint family; member 8; neuroblastoma breakpoint family; member 10	-1.7689	0.0005
230715_at	KIAA1729	KIAA1729 protein	-0.4949	0.0105
230739_at	C18orf19	chromosome 18 open reading frame 19	-1.1231	0.0114
230746_s_at	STC1	Stanniocalcin 1	-2.1452	0.0181
230764_at		CDNA FLJ30669 fis; clone FCBBF1000684	-1.1906	0.0397
230779_at	TNRC6B	trinucleotide repeat containing 6B	-0.9116	0.044
230821_at	ZNF148	zinc finger protein 148	-0.7708	0.0427
230827_at		Transcribed locus; strongly similar to XP_001099397.1 similar to HBxAg transactivated protein 2 isoform 5 [Macaca mulatta]	-0.1546	0.0049
230868_at		Transcribed locus	-0.6985	0.0145
230882_at	FLJ34048	hypothetical protein FLJ34048	-0.7375	0.0203
230886_at		Transcribed locus	-1.2212	0.0027
230894_s_at		Transcribed locus	-0.9291	0.0026
230904_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	-0.7704	0.0093
230998_at		Transcribed locus	-1.0213	0.0357
231024_at	LOC572558	hypothetical locus LOC572558	-1.1711	0.0387
231040_at		CDNA FLJ43172 fis; clone FCBBF3007242	-2.489	0.0108
231075_x_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-0.8399	0.0032
231173_at	LOC642732	pyridine nucleotide-disulphide oxidoreductase domain 1, similar to CG10721-PA	-0.448	0.0167
231205_at			-1.8581	0.0013
231220_at	BRUNOL4	bruno-like 4; RNA binding protein (Drosophila)	-0.2948	0.0459
231235_at	NKTR	natural killer-tumor recognition sequence	-0.63	0.0371
231252_at	FLJ23861	hypothetical protein FLJ23861	-1.0486	0.01
231439_at		Full length insert cDNA clone ZD76G03	-0.1725	0.0499
231449_at		Transcribed locus	-0.3194	0.0377
231468_at			-0.4952	0.0435
231486_x_at			-0.1605	0.0133
231495_at		Transcribed locus	-0.2077	0.0307
231502_at		Transcribed locus	-0.9215	0.0055
231545_at			-0.1322	0.0163
231552_at		Transcribed locus	-1.0765	0.0046
231585_at	VPS13A	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	-0.1864	0.0291
231716_at	RC3H2	ring finger and CCCH-type zinc finger domains 2	-0.6847	0.0011
231818_x_at		MRNA; cDNA DKFZp666B189 (from clone DKFZp666B189)	-0.2961	0.0203
231827_at		Full length insert cDNA clone ZE04G11	-0.3604	0.0485
231836_at	HKR1	GLI-Kruppel family member HKR1	-0.3882	0.0395
231848_x_at	ZNF207	zinc finger protein 207	-0.9541	0.0296
231882_at	FLJ39632	hypothetical LOC642477	-1.8155	0.0284

231952_at	LOC731450	hypothetical protein LOC731450	-1.222	0.0157
231960_at	BRWD1	bromodomain and WD repeat domain containing 1	-0.7964	0.0203
232012_at	CAPN1	calpain 1; (mu/I) large subunit	-0.6361	0.021
232020_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	-0.6354	0.0459
232026_at	HERC4	hect domain and RLD 4	-0.4534	0.0442
232048_at	FAM76B	family with sequence similarity 76; member B	-0.5553	0.0182
232058_at		CDNA FLJ13694 fis; clone PLACE2000115	-1.7144	0.0021
232071_at	MRPL19	Mitochondrial ribosomal protein L19	-0.9031	0.0077
232112_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-0.4093	0.0477
232125_at		CDNA FLJ12166 fis; clone MAMMA1000616	-0.9697	0.0403
232138_at	MBNL2	Muscleblind-like 2 (Drosophila)	-1.4673	0.0325
232144_at		CDNA FLJ11405 fis; clone HEMBA1000769	-1.8416	0.0011
232145_at	LOC388969	hypothetical LOC388969	-0.8849	0.0266
232163_at	WDR19	WD repeat domain 19	-0.372	0.0324
232174_at		CDNA: FLJ21635 fis; clone COL08233; highly similar to AF131819 Homo sapiens clone 24838 mRNA sequence	-1.5815	0.0064
232180_at	UGP2	UDP-glucose pyrophosphorylase 2	-1.0573	0.0232
232183_at	SERAC1	serine active site containing 1	-0.7789	0.0415
232216_at	YME1L1	YME1-like 1 (S. cerevisiae)	-0.9884	0.0311
232264_at		CDNA FLJ12142 fis; clone MAMMA1000356	-1.1249	0.0237
232286_at		CDNA FLJ12187 fis; clone MAMMA1000831	-1.8069	0.0248
232312_at	SAPS3	SAPS domain family; member 3	-0.8825	0.0421
232356_at		CDNA FLJ13539 fis; clone PLACE1006640	-0.8703	0.0393
232363_at		CDNA: FLJ20863 fis; clone ADKA01804	-0.6432	0.0214
232365_at	SIAH1	seven in absentia homolog 1 (Drosophila)	-0.407	0.0025
232369_at		Clone IMAGE:119716; mRNA sequence	-1.4985	0.0355
232371_at	7-Mar	Membrane-associated ring finger (C3HC4) 7	-0.8086	0.0137
232376_at	PCCA	Propionyl Coenzyme A carboxylase; alpha polypeptide	-0.4356	0.0071
232392_at	SFRS3	Splicing factor; arginine/serine-rich 3	-1.3136	0.0238
232393_at	ZNF462	zinc finger protein 462	-0.3243	0.0046
232410_at		MRNA differentially expressed from human RPE cell in differential display experiment	-0.3286	0.0118
232440_at	ZDHHC13	Zinc finger; DHHC-type containing 13	-0.4038	0.0493
232441_at	KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	-1.0872	0.0234
232454_at		MRNA; cDNA DKFZp586N2224 (from clone DKFZp586N2224)	-0.2158	0.0447
232455_x_at	LOC340085	hypothetical protein LOC340085	-0.3091	0.0325
232465_at		CDNA FLJ11687 fis; clone HEMBA1004960	-0.3358	0.0146
232472_at		CDNA FLJ12399 fis; clone MAMMA1002780	-1.1172	0.0053
232477_at			-0.1338	0.0212
232478_at		CDNA clone IMAGE:4815026	-1.6294	0.004
232480_at	FLJ27365	FLJ27365 protein	-0.266	0.0392
232516_x_at	YY1AP1	YY1 associated protein 1	-0.2646	0.0152
232522_at		CDNA FLJ33679 fis; clone BRAWH2002352	-0.7673	0.0189
232576_at		CDNA FLJ11519 fis; clone HEMBA1002348	-0.568	0.0168
232582_at		CDNA FLJ12128 fis; clone MAMMA1000175	-0.6013	0.0403
232599_at	EXOC6	exocyst complex component 6	-0.5144	0.0035
232615_at		CDNA: FLJ22765 fis; clone KAIA1180	-1.157	0.0204
232626_at		CDNA FLJ14143 fis; clone MAMMA1002892	-0.6956	0.0001
232628_at		CDNA FLJ13464 fis; clone PLACE1003478	-1.2024	0.0492
232637_at	2-Sep	Septin 2	-0.6118	0.0389
232681_at		CDNA: FLJ23242 fis; clone COL01514	-0.5969	0.0454
232685_at		CDNA: FLJ21564 fis; clone COL06452	-0.5873	0.0122
232704_s_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	-0.439	0.0255
232705_at	LRRFIP2	Leucine rich repeat (in FLII) interacting protein 2	-0.1899	0.0299
232744_x_at		CDNA FLJ11681 fis; clone HEMBA1004865	-1.0826	0.0189
232750_at	TNS1	Tensin 1	-1.276	0.0231
232754_at		CDNA FLJ11563 fis; clone HEMBA1003202	-0.1243	0.038
232757_at		CDNA FLJ12372 fis; clone MAMMA1002446	-0.6887	0.0049
232759_at			-1.0647	0.0127

232773_at		CDNA: FLJ21440 fis; clone COL04389	-1.4598	0.0122
232776_at		CDNA FLJ11646 fis; clone HEMBA1004394	-0.7511	0.0218
232783_at		CDNA FLJ13625 fis; clone PLACE1011032	-0.2056	0.0035
232788_at		CDNA FLJ11366 fis; clone HEMBA1000282	-0.4694	0.0143
232795_at		CDNA FLJ10145 fis; clone HEMBA1003322	-0.2082	0.0015
232803_at	FLJ31958	hypothetical protein FLJ31958	-0.4557	0.0007
232814_x_at	C14orf153	Chromosome 14 open reading frame 153	-0.3552	0.0465
232824_at		CDNA FLJ10182 fis; clone HEMBA1004246	-0.4198	0.0028
232826_at		CDNA FLJ11400 fis; clone HEMBA1000673	-0.3638	0.0239
232835_at		Transcribed locus	-0.4056	0.0305
232852_at		CDNA FLJ26156 fis; clone ADG01420, CDNA FLJ26775 fis; clone PRS03610, CDNA: FLJ21326 fis; clone COL02445	-1.4406	0.0221
232858_at		CDNA FLJ11927 fis; clone HEMBB1000402	-0.2761	0.0125
232885_at	LOC92482	hypothetical protein LOC92482	-0.4533	0.0096
232898_at	DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	-3.305	0.0001
232901_at	RARS2	arginyl-tRNA synthetase 2; mitochondrial (putative)	-0.4845	0.0088
232914_s_at	SYTL2	synaptotagmin-like 2	-2.1902	0.0459
232919_at	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	-0.378	0.0028
232929_at		CDNA FLJ13240 fis; clone OVARC1000496	-0.7376	0.0177
232948_at		CDNA FLJ12111 fis; clone MAMMA1000025	-0.3549	0.0097
232952_at		CDNA FLJ11942 fis; clone HEMBB1000652	-0.3547	0.031
232962_x_at		CDNA FLJ34323 fis; clone FEBRA2008866	-0.2113	0.0204
232978_at		Clone IMAGE:27725; mRNA sequence	-1.2438	0.0052
232980_at		CDNA FLJ11854 fis; clone HEMBA1006767	-0.3034	0.0438
232982_at	AP1GBP1	AP1 gamma subunit binding protein 1	-0.115	0.0308
233003_at		CDNA FLJ11942 fis; clone HEMBB1000652	-0.8278	0.0028
233019_at	CNOT7	CCR4-NOT transcription complex; subunit 7	-0.833	0.0169
233035_at		CDNA FLJ12023 fis; clone HEMBB1001785	-0.4601	0.0427
233038_at		CDNA: FLJ22776 fis; clone KAIA1582	-0.238	0.0089
233040_at	PLEKHA5	pleckstrin homology domain containing; family A member 5	-0.4439	0.0059
233041_x_at		CDNA: FLJ21356 fis; clone COL02831	-0.3234	0.0273
233055_at		CDNA FLJ11510 fis; clone HEMBA1002185	-1.9582	0.0025
233068_at		CDNA FLJ13202 fis; clone NT2RP3004503	-0.6046	0.05
233079_at	MERTK	c-mer proto-oncogene tyrosine kinase	-1.1035	0.0163
233089_at	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	-0.5016	0.0372
233097_x_at		CDNA FLJ11133 fis; clone PLACE1006357	-0.2731	0.008
233101_at	MTMR9	myotubularin related protein 9	-0.5517	0.0148
233106_at	C14orf82	chromosome 14 open reading frame 82	-0.4524	0.0421
233113_at	LOC730057	Hypothetical protein LOC730057	-0.17	0.0092
233120_at		CDNA FLJ13845 fis; clone THYRO1000815	-0.1221	0.0436
233121_at		CDNA FLJ12299 fis; clone MAMMA1001851	-0.3299	0.02
233159_at	STARD13	START domain containing 13	-0.1204	0.0376
233173_x_at	GTF3C5	general transcription factor IIIC; polypeptide 5; 63kDa	-1.0573	0.0039
233191_at	RUFY2	RUN and FYVE domain containing 2	-0.2266	0.035
233196_at		CDNA FLJ11777 fis; clone HEMBA1005909	-0.845	0.0264
233212_at		CDNA FLJ41104 fis; clone BLADE2006607	-0.1672	0.0237
233214_at		CDNA FLJ11900 fis; clone HEMBA1007341	-0.7603	0.0197
233225_at		CDNA FLJ36087 fis; clone TESTI2020283	-0.52	0.0153
233228_at		CDNA: FLJ21229 fis; clone COL00740	-0.7117	0.0203
233239_at		CDNA: FLJ21229 fis; clone COL00740	-0.2814	0.0486
233248_at		CDNA FLJ11966 fis; clone HEMBB1001114	-0.4024	0.0064
233249_at	LOC730200	Hypothetical protein LOC730200	-1.9046	0.0411
233254_x_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-0.7788	0.0115
233257_at		CDNA FLJ12368 fis; clone MAMMA1002417	-2.2313	0.0007
233265_at		CDNA FLJ12203 fis; clone MAMMA1000914	-0.62	0.0198
233271_at		CDNA FLJ11709 fis; clone HEMBA1005133	-0.9117	0.0295
233273_at		CDNA FLJ12010 fis; clone HEMBB1001635	-1.1567	0.0177

233276_at		CDNA FLJ11923 fis; clone HEMBB1000341	-2.2158	0.0009
233288_at	ATR	ataxia telangiectasia and Rad3 related	-0.5358	0.0041
233290_at		CDNA FLJ11451 fis; clone HEMBA1001433	-0.4673	0.0137
233296_x_at		CDNA FLJ12131 fis; clone MAMMA1000254	-0.5403	0.0384
233300_at		CDNA FLJ11548 fis; clone HEMBA1002944	-1.2505	0.0004
233314_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-1.114	0.0288
233315_at		CDNA: FLJ21294 fis; clone COL01981	-0.4959	0.0212
233323_at		CDNA: FLJ21320 fis; clone COL02324	-0.5734	0.0439
233335_at		MRNA; cDNA DKFZp586J1717 (from clone DKFZp586J1717)	-0.1447	0.0336
233336_at	LOC142893	hypothetical protein LOC142893	-0.6272	0.0175
233358_at	FLJ14311	hypothetical gene FLJ14311	-0.1386	0.0482
233367_at		CDNA FLJ11566 fis; clone HEMBA1003273	-0.6224	0.0206
233374_at		CDNA: FLJ21297 fis; clone COL02035	-0.2634	0.0063
233412_x_at		CDNA FLJ11849 fis; clone HEMBA1006709	-0.2145	0.0091
233417_at		CDNA FLJ11625 fis; clone HEMBA1004200	-0.7269	0.0062
233425_at	ZCCHC2	zinc finger; CCHC domain containing 2	-0.4716	0.0218
233427_x_at		CDNA FLJ13808 fis; clone THYRO1000253	-0.2382	0.0429
233440_at		CDNA FLJ12367 fis; clone MAMMA1002413	-0.7874	0.0109
233442_at		CDNA FLJ12196 fis; clone MAMMA1000867	-1.5099	0.0226
233449_at		CDNA FLJ11377 fis; clone HEMBA1000442	-1.5138	0.0258
233468_at		CDNA FLJ13434 fis; clone PLACE1002578	-0.1439	0.003
233487_s_at	LRRC8A	leucine rich repeat containing 8 family; member A	-0.4635	0.022
233504_at	C9orf84	chromosome 9 open reading frame 84	-4.6403	0
233509_at	HERC4	hect domain and RLD 4	-0.1459	0.0101
233519_at		Clone 23637 mRNA sequence	-0.3625	0.0332
233539_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	-1.034	0.016
233570_at		IMAGE:512024 clone; mRNA	-0.4146	0.0297
233579_at		CDNA: FLJ22749 fis; clone KAIA0458	-0.2544	0.0136
233595_at	USP34	ubiquitin specific peptidase 34	-1.6506	0.0063
233608_at		CDNA FLJ11929 fis; clone HEMBB1000434	-0.8137	0.0061
233626_at		CDNA: FLJ20927 fis; clone ADSE01007	-0.4599	0.0152
233664_at		CDNA: FLJ22803 fis; clone KAIA2685	-0.48	0.0123
233700_at		CDNA: FLJ21638 fis; clone COL08269	-0.286	0.0224
233713_at		CDNA FLJ12119 fis; clone MAMMA1000092	-1.8931	0.0186
233720_at	SORBS2	Sorbin and SH3 domain containing 2	-1.7783	0.0056
233752_s_at	ZFHX3	zinc finger homeobox 3	-0.1365	0.0443
233753_at	SFRS15	splicing factor; arginine/serine-rich 15	-0.2538	0.0113
233775_x_at		CDNA FLJ13242 fis; clone OVARC1000578	-0.435	0.0297
233788_at		CDNA FLJ11617 fis; clone HEMBA1004045	-0.2341	0.0008
233794_at		CDNA FLJ10176 fis; clone HEMBA1004074	-0.1271	0.0368
233824_at		CDNA: FLJ21428 fis; clone COL04203	-0.6973	0.0103
233836_at	TNRC6A	trinucleotide repeat containing 6A	-0.3884	0.0022
233874_at	SLAIN2	SLAIN motif family; member 2	-0.5502	0.0065
233914_s_at	SBF2	SET binding factor 2	-0.8469	0.0135
233994_at		Clone 24894 mRNA sequence	-0.4963	0.0305
234032_at		PRO1550	-1.3331	0.0118
234034_at		MRNA; cDNA DKFZp761F052 (from clone DKFZp761F052)	-1.9984	0.0428
234042_at	TAS2R45	taste receptor; type 2; member 45	-0.6451	0.0108
234043_at		CDNA FLJ11920 fis; clone HEMBB1000312	-0.4351	0.0068
234078_at	LOC730057	Hypothetical protein LOC730057	-0.2675	0.036
234093_at	ZNF326	zinc finger protein 326	-0.1579	0.0169
234098_at	SOBP	Sine oculis binding protein homolog (Drosophila)	-0.7956	0.0493
234105_at		CDNA FLJ11473 fis; clone HEMBA1001712	-0.7727	0.027
234122_at		MRNA; cDNA DKFZp761B0823 (from clone DKFZp761B0823)	-0.2562	0.0118
234145_at	PBX3	pre-B-cell leukemia homeobox 3	-0.1395	0.0181
234159_at		CDNA: FLJ21529 fis; clone COL05981	-0.2426	0.0447

234162_at		CDNA: FLJ22641 fis; clone HSI06942	-0.1804	0.0427
234164_at		CDNA: FLJ22006 fis; clone HEP06915	-0.2131	0.0331
234211_at		CDNA: FLJ21436 fis; clone COL04279	-0.4057	0.0078
234227_at		CDNA: FLJ21166 fis; clone CAS10851	-0.1139	0.0418
234245_at		MRNA; cDNA DKFZp761M2223 (from clone DKFZp761M2223)	-1.0679	0.0284
234247_at		MRNA; cDNA DKFZp761D1723 (from clone DKFZp761D1723)	-0.1271	0.0365
234275_at		MRNA; cDNA DKFZp586A131 (from clone DKFZp586A131)	-0.1666	0.0475
234278_at			-0.7697	0.0141
234312_s_at	ACSS2	acyl-CoA synthetase short-chain family member 2	-1.1564	0.0415
234314_at	C20orf74	chromosome 20 open reading frame 74	-3.206	0.0206
234326_at		CDNA: FLJ21248 fis; clone COL01235	-0.3568	0.0204
234335_s_at	FAM84A	Family with sequence similarity 84; member A	-0.1743	0.0125
234339_s_at	GLTSCR2	glioma tumor suppressor candidate region gene 2	-0.4939	0.0292
234360_at			-0.232	0.0415
234445_at	C6orf12	chromosome 6 open reading frame 12	-0.4086	0.0151
234459_at	PPHLN1	periphilin 1	-0.326	0.0419
234489_at		CDNA FLJ11818 fis; clone HEMBA1006424	-0.3209	0.001
234544_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	-0.1529	0.0292
234548_at		MRNA; cDNA DKFZp586J1824 (from clone DKFZp586J1824)	-0.1194	0.0282
234565_x_at		CDNA FLJ20846 fis; clone ADKA01802	-0.2301	0.0248
234589_at	TMEM106A	Transmembrane protein 106A	-0.1393	0.0125
234601_x_at		CDNA: FLJ22732 fis; clone HSI15880	-0.137	0.0357
234650_at		CDNA: FLJ21254 fis; clone COL01317	-0.8751	0.0246
234652_at		NTera2D1 cell line mRNA containing L1 retroposon; clone P1	-0.1314	0.0467
234677_at		MRNA; cDNA DKFZp547K042 (from clone DKFZp547K042)	-0.1481	0.0094
234949_at	C20orf80	Chromosome 20 open reading frame 80	-0.7494	0.012
234967_at	IL6ST	interleukin 6 signal transducer (gp130; oncostatin M receptor)	-0.1332	0.0007
235013_at	SLC31A1	solute carrier family 31 (copper transporters); member 1	-0.7744	0.0335
235021_at	KIAA2026	KIAA2026	-0.3671	0.0107
235031_at		CDNA FLJ34195 fis; clone FCBBF3019320	-0.559	0.0252
235078_at		Transcribed locus	-1.2498	0.0138
235105_at		MRNA; cDNA DKFZp686F09227 (from clone DKFZp686F09227)	-0.1246	0.0363
235107_at		Transcribed locus	-1.1122	0.0336
235108_at		CDNA FLJ41679 fis; clone HCASM2003212	-1.6332	0.0471
235112_at		Homo sapiens; Similar to RIKEN cDNA E130308A19 gene; clone IMAGE:6198463; mRNA	-1.9479	0.0008
235132_at	LOC254128	hypothetical protein LOC254128	-0.6791	0.0254
235138_at		Transcribed locus	-1.0929	0.0213
235182_at	C20orf82	chromosome 20 open reading frame 82	-3.469	0.0051
235190_at		Transcribed locus	-1.263	0.0036
235205_at	LOC346887	similar to solute carrier family 16 (monocarboxylic acid transporters); member 14	-1.7626	0.0236
235226_at	CDC2L6	cell division cycle 2-like 6 (CDK8-like)	-0.9745	0.0098
235287_at	CDK6	cyclin-dependent kinase 6	-0.8247	0.0254
235308_at	ZBTB20	zinc finger and BTB domain containing 20	-0.9725	0.018
235328_at	PLXNC1	Plexin C1	-0.6112	0.0059
235374_at	MDH1	Malate dehydrogenase 1; NAD (soluble)	-1.0317	0.0028
235381_at		Homo sapiens; clone IMAGE:3457110; mRNA	-0.7321	0.0094
235392_at		Transcribed locus	-1.6558	0.0032
235471_at	C10orf72	Chromosome 10 open reading frame 72	-1.6349	0.0293
235477_at		Transcribed locus	-0.2215	0.0153
235484_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-0.8603	0.0474
235493_at		Transcribed locus	-1.2145	0.0061

235501_at		Clone IMAGE:609899; mRNA sequence	-2.0822	0.0403
235526_at	SOX6	SRY (sex determining region Y)-box 6	-1.0155	0.0059
235538_at		CDNA FLJ30718 fis; clone FCBBF2001675	-2.2169	0.0004
235540_at	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	-0.2483	0.048
235560_at		MRNA; cDNA DKFZp547A0515 (from clone DKFZp547A0515)	-0.3792	0.0397
235562_at	LOC285382	hypothetical gene supported by AK091454	-0.3173	0.0281
235567_at	LOC283666	Hypothetical protein LOC283666	-2.195	0.0011
235577_at	ZNF652	Zinc finger protein 652	-0.6397	0.0121
235589_s_at		Transcribed locus	-1.2194	0.0098
235600_at		Transcribed locus	-1.6091	0.0353
235612_at		Transcribed locus	-0.8682	0.0114
235613_at		Transcribed locus	-1.0895	0.0109
235618_at	ZNF507	zinc finger protein 507	-0.7803	0.0019
235652_at		CDNA FLJ37623 fis; clone BRCOC2014013	-1.2397	0.0313
235662_at		Transcribed locus	-0.5872	0.0164
235679_at		CDNA FLJ42928 fis; clone BRSSN2007076	-0.5741	0.0199
235693_at		Transcribed locus	-1.1769	0.0232
235716_at		Transcribed locus	-0.7458	0.0331
235721_at	DTX3	deltex 3 homolog (Drosophila)	-1.66	0.0055
235743_at			-1.0812	0.0159
235745_at	ERN1	endoplasmic reticulum to nucleus signaling 1	-1.8559	0.0136
235758_at	PNMA6A	paraneoplastic antigen like 6A	-0.975	0.0392
235762_at	TAS2R14	taste receptor; type 2; member 14	-0.763	0.0201
235763_at	SLC44A5	solute carrier family 44; member 5	-1.9992	0.0456
235792_x_at	PIK3C2A	phosphoinositide-3-kinase; class 2; alpha polypeptide	-0.4665	0.0289
235796_at		Transcribed locus	-0.5655	0.0302
235803_at		Transcribed locus	-1.1568	0.0117
235805_at		Transcribed locus	-1.7631	0.0072
235825_at		Transcribed locus; strongly similar to XP_001145544.1 hypothetical protein [Pan troglodytes]	-0.3857	0.0496
235874_at	PRSS35	protease; serine; 35	-0.7343	0.0295
235895_at		Transcribed locus	-0.2316	0.0325
235927_at			-1.1222	0.0151
235959_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	-1.2129	0.0136
235968_at	CENTG2	centaurin; gamma 2	-0.218	0.0235
235977_at	LONRF2	LON peptidase N-terminal domain and ring finger 2	-1.7128	0.028
235989_at		Transcribed locus	-0.8248	0.013
236006_s_at	AKAP10	A kinase (PRKA) anchor protein 10	-0.8129	0.0063
236007_at	AKAP10	A kinase (PRKA) anchor protein 10	-0.9327	0.0113
236009_at		Transcribed locus	-0.3766	0.0333
236062_at		Transcribed locus	-0.3025	0.0137
236066_at		Transcribed locus	-0.4139	0.0415
236067_at		Transcribed locus	-1.5541	0.0029
236118_at	LOC728473	hypothetical protein LOC728473	-1.3682	0.0437
236134_at	WDR68	WD repeat domain 68	-0.6924	0.0166
236139_at		Transcribed locus	-0.2982	0.0469
236168_at		Transcribed locus	-0.4725	0.0067
236194_at		Transcribed locus; moderately similar to NP_001018860.1 protein LOC401398 [Homo sapiens]	-0.6477	0.049
236210_at		Transcribed locus	-0.6906	0.0008
236216_at		MRNA; cDNA DKFZp313B2312 (from clone DKFZp313B2312)	-0.4728	0.0371
236241_at	MED31	mediator complex subunit 31	-0.9825	0.0098
236244_at	HNRPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	-0.4811	0.0184
236246_x_at	LOC653160	Hypothetical protein LOC653160	-0.1359	0.0338
236266_at	LOC283666	Hypothetical protein LOC283666	-1.5802	0.0131
236273_at	NBPF1	neuroblastoma breakpoint family; member 1	-1.9837	0.0062
236302_at	PPM1E	protein phosphatase 1E (PP2C domain containing)	-0.9944	0.0289
236355_s_at		Transcribed locus	-0.902	0.0381

236368_at	KIAA0368	KIAA0368	-1.0022	0.014
236370_at		Transcribed locus	-1.1976	0.0178
236404_at		Transcribed locus	-0.783	0.041
236415_at	MGC24039	hypothetical protein MGC24039	-0.1494	0.0383
236432_at		Transcribed locus	-0.1386	0.0421
236435_at			-1.1687	0.0054
236438_at		Transcribed locus	-0.1658	0.0057
236451_at		CDNA FLJ14635 fis; clone NT2RP2001196	-0.1421	0.0487
236472_at		Transcribed locus	-0.9103	0.0027
236480_at		CDNA FLJ41489 fis; clone BRTHA2004582	-1.2695	0.0391
236483_at		Transcribed locus	-0.1893	0.0267
236492_at	PPP2R2A	protein phosphatase 2 (formerly 2A); regulatory subunit B; alpha isoform	-1.1838	0.0228
236528_at		Transcribed locus	-0.6141	0.0048
236533_at	DDEF1	development and differentiation enhancing factor 1	-0.4498	0.0296
236545_at		Transcribed locus	-1.6675	0.0025
236669_at		(clone 33) macronuclear mRNA	-0.2192	0.043
236681_at	HOXD13	homeobox D13	-0.4237	0.0028
236699_at		CDNA FLJ90129 fis; clone HEMBB1000309	-1.8281	0.0123
236715_x_at	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	-0.333	0.0462
236752_at		Transcribed locus	-0.8395	0.0364
236755_at		Transcribed locus	-0.3584	0.0248
236780_at		Transcribed locus	-0.3364	0.0496
236799_at		Transcribed locus	-0.1206	0.0274
236814_at	MDM4	Mdm4; transformed 3T3 cell double minute 4; p53 binding protein (mouse)	-0.9998	0.0017
236839_at		Transcribed locus	-0.2131	0.0393
236841_at	FAM39DP	Family with sequence similarity 39; member D pseudogene	-1.1092	0.0004
236850_at	CAPRIN1	Cell cycle associated protein 1	-0.1255	0.0433
236879_at		Transcribed locus	-0.5416	0.0357
236887_at	KIN	KIN; antigenic determinant of recA protein homolog (mouse)	-0.45	0.016
236915_at			-1.5969	0.043
236948_x_at	SFRS11	Splicing factor; arginine/serine-rich 11	-0.2656	0.0287
236978_at		Transcribed locus	-0.9258	0.0218
237001_at		Transcribed locus	-0.4131	0.0139
237025_at		Transcribed locus	-0.4602	0.0028
237040_at	CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	-0.4508	0.0217
237044_s_at			-0.6796	0.0253
237051_at		Transcribed locus	-0.7113	0.0244
237067_at			-0.2667	0.0335
237081_at		Transcribed locus	-0.6215	0.0486
237084_at		CDNA FLJ41316 fis; clone BRAMY2043314	-0.5494	0.0123
237107_at	PRKRA	protein kinase; interferon-inducible double stranded RNA dependent activator, protein kinase; interferon-inducible double stranded RNA dependent activator pseudogene 1	-0.7538	0.0153
237114_at		Transcribed locus	-0.1891	0.0045
237136_at		Transcribed locus	-0.1275	0.0465
237180_at	PSME4	Proteasome (prosome; macropain) activator subunit 4	-1.2744	0.0082
237218_at			-0.4069	0.0201
237261_at			-0.6435	0.033
237285_at	SORBS2	sorbin and SH3 domain containing 2	-0.5647	0.0321
237305_at		Transcribed locus	-1.6952	0.022
237310_at		Transcribed locus	-0.975	0.0016
237330_at		Transcribed locus	-1.1229	0.0091
237346_at	TGDS	TDP-glucose 4;6-dehydratase	-0.3279	0.0116
237377_at		Transcribed locus	-0.2698	0.0189
237384_x_at		CDNA clone IMAGE:5262496	-0.1394	0.0445
237398_at		Transcribed locus	-0.7315	0.0054
237418_at	CDK5RAP2	CDK5 regulatory subunit associated protein 2	-0.5778	0.0041

237456_at		Transcribed locus	-0.8307	0.0253
237475_x_at	SEPP1	Selenoprotein P; plasma; 1	-0.4607	0.0402
237483_at		Transcribed locus	-1.7343	0.0098
237496_at			-1.304	0.003
237502_at	CRLS1	Cardiolipin synthase 1	-0.538	0.0181
237509_at		CDNA FLJ38525 fis; clone HCHON2000851	-1.7405	0.0436
237568_at		Transcribed locus	-0.6004	0.0092
237569_at			-0.1232	0.049
237571_at		Transcribed locus	-0.6851	0.0375
237594_at			-0.8116	0.0345
237618_at			-0.1448	0.0285
237703_at		Transcribed locus	-0.9445	0.0244
237716_at			-0.3955	0.0318
237782_at		Transcribed locus	-0.7652	0.0019
237803_x_at		Transcribed locus	-0.8109	0.0401
237825_x_at		Transcribed locus	-0.3721	0.0336
237831_x_at	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	-0.1152	0.0383
237864_at		CDNA FLJ26101 fis; clone SLV05922	-0.9582	0.0087
237881_at		Transcribed locus	-0.5959	0.0452
237963_x_at			-0.1224	0.032
237968_at	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2	-0.7275	0.0234
238040_at		Transcribed locus	-1.3282	0.0005
238044_at		Transcribed locus	-0.4454	0.0111
238049_at	GRAMD3	GRAM domain containing 3	-0.5343	0.0412
238076_at	GATAD2B	GATA zinc finger domain containing 2B	-0.8704	0.0317
238108_at		Transcribed locus	-0.9493	0.04
238109_at		Homo sapiens; clone IMAGE:4346533; mRNA	-0.671	0.0202
238117_at	PPOX	protoporphyrinogen oxidase	-0.2389	0.0344
238119_at		Transcribed locus	-0.8131	0.0049
238146_at		Transcribed locus	-0.5136	0.0418
238161_at		Transcribed locus	-0.6012	0.0215
238182_at		Transcribed locus	-0.2279	0.0367
238193_at		Transcribed locus	-0.6669	0.0125
238227_at		Transcribed locus	-0.4543	0.0061
238231_at	NFYC	Nuclear transcription factor Y; gamma	-0.2722	0.0191
238252_at		Transcribed locus	-0.2923	0.0073
238277_at			-0.3563	0.047
238281_at		Transcribed locus	-0.2781	0.0074
238311_at		Transcribed locus	-0.967	0.0377
238384_x_at		Transcribed locus	-0.1155	0.0445
238409_x_at	OXR1	oxidation resistance 1	-0.2775	0.0173
238436_s_at	ZNF805	zinc finger protein 805	-0.7238	0.0277
238444_at	ZNF618	zinc finger protein 618	-1.2914	0.0007
238447_at	RBMS3	RNA binding motif; single stranded interacting protein	-1.6445	0.0308
238468_at	TNRC6B	trinucleotide repeat containing 6B	-0.7012	0.0475
238492_at		CDNA FLJ33148 fis; clone UTERU2000238	-0.4097	0.0124
238496_at		Transcribed locus	-0.7548	0.0097
238497_at	TMEM136	transmembrane protein 136	-1.2335	0.0004
238536_at		CDNA FLJ13474 fis; clone PLACE1003593	-1.3186	0.0072
238551_at	FUT11	fucosyltransferase 11 (alpha (1;3) fucosyltransferase)	-0.9093	0.0256
238553_at	BMS1P5	BMS1 pseudogene 5, centaurin; gamma-like family; member 2, centaurin; gamma-like family; member 9 pseudogene, hypothetical protein LOC643564	-0.3549	0.0157
238573_at		Transcribed locus	-0.3546	0.0355
238602_at	DIS3L2	DIS3 mitotic control homolog (S. cerevisiae)-like 2	-0.6851	0.0225
238624_at	NLK	Nemo-like kinase	-1.7314	0.0115
238652_at		Transcribed locus; strongly similar to XP_001111525.1 amine oxidase (flavin containing) domain 2 [Macaca mulatta]	-0.5935	0.0255
238666_at		Transcribed locus	-2.3777	0.002
238672_at		Transcribed locus	-0.5468	0.0221

238700_at		Transcribed locus	-1.4011	0.0013
238714_at		Transcribed locus	-0.7894	0.0412
238736_at	REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	-1.054	0.015
238751_at		CDNA clone IMAGE:4791597	-1.9337	0.0283
238761_at	ELK4	ELK4; ETS-domain protein (SRF accessory protein 1)	-0.6473	0.0158
238768_at	LOC388969	hypothetical LOC388969	-1.1484	0.0048
238769_at		Transcribed locus	-0.1498	0.0188
238774_at			-1.2719	0.0426
238785_at		Transcribed locus	-1.0228	0.0296
238833_at	LOC729088	hypothetical protein LOC729088	-0.7443	0.0478
238875_at		Clone HLS_IMAGE_731119 mRNA sequence	-1.1409	0.0179
238883_at		Transcribed locus	-1.2266	0.0242
238884_at		Transcribed locus	-0.4686	0.0196
238899_at		Transcribed locus	-0.1097	0.0035
238913_at		Transcribed locus	-0.9856	0.0433
238933_at	IRS1	Insulin receptor substrate 1	-1.9666	0.0037
238951_at		Transcribed locus	-0.7089	0.0418
238981_at	MGC3196	hypothetical protein MGC3196	-0.1446	0.0178
239005_at		Transcribed locus	-0.794	0.0239
239014_at	CCAR1	Cell division cycle and apoptosis regulator 1	-1.1007	0.0247
239033_at		MRNA; cDNA DKFZp666M079 (from clone DKFZp666M079)	-1.9394	0.0012
239045_at		Transcribed locus	-0.9148	0.0008
239049_at		CDNA FLJ13202 fis; clone NT2RP3004503	-1.1507	0.0058
239050_s_at		CDNA FLJ13202 fis; clone NT2RP3004503	-0.8339	0.0222
239071_at	RBBP4	Retinoblastoma binding protein 4	-0.6907	0.0092
239076_at	13-Sep	septin 13	-0.1639	0.0223
239121_at		Transcribed locus	-0.4483	0.0236
239131_at		Transcribed locus	-0.8844	0.0341
239151_at	BMS1P5	BMS1 pseudogene 5, hypothetical protein LOC643564	-1.0836	0.0022
239161_at	FDX1	ferredoxin 1	-1.9655	0.0113
239166_at		Transcribed locus	-0.3682	0.0254
239171_at			-0.2961	0.0464
239191_at		Transcribed locus	-0.1106	0.0356
239193_at	LOC158301	hypothetical protein LOC158301	-1.467	0.0032
239210_at		Transcribed locus	-1.1061	0.0305
239224_at	FBXL20	F-box and leucine-rich repeat protein 20	-0.1825	0.037
239227_at			-1.2493	0.003
239232_at	MSI2	Musashi homolog 2 (Drosophila)	-1.1591	0.0002
239238_at		Transcribed locus	-0.9176	0.0338
239243_at	ZNF638	Zinc finger protein 638	-1.5628	0.0159
239246_at	FARP1	FERM; RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-2.1335	0.0156
239251_at		Transcribed locus	-1.1539	0.0082
239285_at	JMJD2C	Jumonji domain containing 2C	-1.3534	0.0091
239300_at		CDNA clone IMAGE:4798675	-1.1835	0.0049
239301_at	LOC644285	hypothetical LOC644285	-0.6729	0.006
239358_at		Transcribed locus	-1.895	0.0167
239363_at		Transcribed locus	-0.8058	0.0337
239387_at		Transcribed locus	-0.2082	0.0294
239390_at	GTDC1	glycosyltransferase-like domain containing 1	-0.6347	0.0315
239418_x_at		Transcribed locus	-0.288	0.0149
239442_at	CEP68	centrosomal protein 68kDa	-0.7892	0.0397
239445_at		Transcribed locus	-0.3875	0.0141
239451_at		CDNA FLJ26407 fis; clone HRT09288	-1.1776	0.0205
239461_at	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	-0.2538	0.0164
239463_at		Transcribed locus	-0.4404	0.0219
239469_at		Transcribed locus	-0.3473	0.0373

239478_x_at		Full-length cDNA clone CS0CAP006YP08 of Thymus of Homo sapiens (human)	-0.2831	0.0074
239519_at		Transcribed locus	-1.0222	0.0438
239536_at		Transcribed locus	-0.6778	0.0154
239540_at			-0.2457	0.041
239545_at		Transcribed locus	-1.6175	0.0067
239548_at	NEGR1	neuronal growth regulator 1	-0.1398	0.0248
239557_at		Transcribed locus	-0.9126	0.0087
239559_at		Partial unknown mRNA from drug-resistant melanoma cells; 3'UTR; clone DMS-9	-1.0977	0.0233
239576_at	MTUS1	Mitochondrial tumor suppressor 1	-1.1193	0.0186
239604_at		Transcribed locus	-0.5129	0.0002
239614_x_at		Transcribed locus	-0.6099	0.0012
239619_at			-1.6728	0.0239
239621_at		Transcribed locus	-0.3163	0.0364
239630_at			-1.0501	0.0227
239635_at	TMEM137	transmembrane protein 137	-0.6092	0.0111
239644_at		CDNA clone IMAGE:5275753	-0.848	0.0407
239682_at		Full-length cDNA clone CS0DC024YB19 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	-0.9959	0.0075
239716_at		Transcribed locus	-0.6034	0.0174
239740_at	ETV6	ets variant gene 6 (TEL oncogene)	-0.8051	0.0362
239742_at	TULP4	Tubby like protein 4	-1.0923	0.0341
239750_x_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A; 33kDa	-0.1696	0.0339
239755_at	ST3GAL5	ST3 beta-galactoside alpha-2;3-sialyltransferase 5	-1.1893	0.0029
239778_x_at		Transcribed locus	-0.7126	0.0433
239784_at		Transcribed locus	-1.4513	0.008
239790_s_at		Transcribed locus	-0.2615	0.0067
239798_at		Transcribed locus	-0.9891	0.0494
239811_at			-0.7084	0.0207
239829_at		Transcribed locus	-0.2593	0.0062
239832_at		Transcribed locus	-0.9947	0.0189
239833_at		Transcribed locus	-0.3914	0.0306
239834_at		Full length insert cDNA clone YR23D07	-0.7024	0.0417
239851_at			-0.2432	0.0389
239861_at		Transcribed locus	-0.3759	0.0073
239867_at		Transcribed locus	-0.3138	0.0117
239924_at	LOC91316	Similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1; pre-B-cell specific)	-0.2447	0.0171
239937_at	ZNF207	Zinc finger protein 207	-0.9897	0.0121
239954_at	ZNF160	zinc finger protein 160	-1.4259	0.0115
239955_at		Transcribed locus	-0.8553	0.0081
239971_at		Transcribed locus	-0.243	0.0362
240016_at		Transcribed locus	-0.2377	0.0383
240018_at		Transcribed locus	-0.1549	0.0162
240088_at	PDE5A	phosphodiesterase 5A; cGMP-specific	-0.3834	0.0081
240090_at		Transcribed locus	-0.2471	0.0003
240120_at		Transcribed locus	-2.0713	0.0068
240135_x_at			-1.0975	0.0464
240148_at	MSH6	MutS homolog 6 (E. coli)	-0.349	0.0324
240168_at	XPO7	exportin 7	-0.6535	0.0173
240188_at			-1.7122	0.0018
240205_x_at			-0.4556	0.0415
240216_at		Transcribed locus	-1.5645	0.0033
240231_at		Transcribed locus	-1.0235	0.0081
240245_at			-1.2871	0.0115
240263_at		Transcribed locus	-1.6483	0.0094
240279_at			-0.8763	0.0225
240307_at		Transcribed locus	-1.0116	0.0042
240326_at		Transcribed locus	-0.9833	0.005

240335_at	SLC35F5	Solute carrier family 35; member F5	-0.195	0.0171
240385_at			-1.4779	0.0163
240446_at		Transcribed locus	-0.429	0.0361
240452_at	GSPT1	G1 to S phase transition 1	-1.0763	0.0317
240498_at			-0.7233	0.0037
240510_at	NBN	Nibrin	-0.219	0.0475
240513_at	PCID1	PCI domain containing 1 (herpesvirus entry mediator)	-0.2242	0.0167
240522_at			-0.2029	0.002
240539_at		Transcribed locus	-1.0098	0.0148
240545_at	LOC286382	hypothetical protein LOC286382	-0.4026	0.0135
240548_at		CDNA clone IMAGE:4791911	-0.1634	0.0471
240557_at		CDNA FLJ41867 fis; clone OCBBF2005546	-0.9011	0.0312
240579_at	NAG	neuroblastoma-amplified protein	-0.3143	0.0166
240594_at		Transcribed locus	-0.919	0.0298
240651_at		Transcribed locus	-1.0821	0.033
240698_s_at		Transcribed locus	-0.2359	0.0278
240725_at		CDNA FLJ42381 fis; clone UTERU2036512	-0.427	0.0169
240726_at		Transcribed locus	-0.1348	0.0332
240738_at		Transcribed locus	-0.2312	0.0475
240757_at	CLASP1	Cytoplasmic linker associated protein 1	-0.2032	0.0335
240758_at			-0.7638	0.0106
240765_at			-0.705	0.0146
240769_at		Transcribed locus	-0.1623	0.0104
240772_at		Transcribed locus	-1.2731	0.0052
240773_at		Transcribed locus	-0.113	0.0334
240788_at		Transcribed locus	-1.2666	0.036
240824_at		Transcribed locus	-1.0743	0.0081
240904_at			-0.1037	0.0261
240922_at		Transcribed locus	-0.1612	0.0356
240934_at			-0.3723	0.0227
240939_x_at		Transcribed locus	-0.5214	0.0068
240964_at		Transcribed locus	-0.2183	0.0291
240968_at		Transcribed locus	-0.1496	0.039
240984_at		Transcribed locus	-0.4266	0.0004
240994_at		Transcribed locus	-0.1865	0.0326
241081_at			-0.1909	0.0359
241102_at		Transcribed locus	-0.4914	0.0463
241147_at		Transcribed locus	-0.1289	0.0418
241152_at		Transcribed locus	-0.1951	0.0267
241154_x_at		Transcribed locus	-0.9182	0.007
241158_at		Transcribed locus	-0.1255	0.0401
241184_x_at		Transcribed locus	-0.1104	0.0353
241191_at			-0.1918	0.0024
241210_at		Transcribed locus	-0.1665	0.0485
241334_at		Transcribed locus	-0.166	0.0075
241387_at		Transcribed locus	-0.8848	0.0116
241425_at	NUPL1	Nucleoporin like 1	-1.2081	0.0115
241438_at		Transcribed locus	-0.7551	0.0166
241457_at		Transcribed locus	-1.8718	0.0231
241479_at			-0.1514	0.0336
241484_x_at			-0.9705	0.0108
241494_at		Transcribed locus	-1.0922	0.0395
241506_at			-2.2859	0.0149
241508_at			-0.4556	0.0109
241509_at			-2.0978	0.0042
241520_x_at		Transcribed locus	-0.2091	0.0226
241560_at		Transcribed locus	-0.2445	0.0357
241577_at			-0.7936	0.0178
241595_at			-0.4842	0.0098
241692_at		Transcribed locus	-1.6641	0.0032
241700_at	ZFHX4	zinc finger homeobox 4	-1.9655	0.0057

241703_at	RPIB9	Rap2-binding protein 9	-1.6488	0.0127
241710_at	hCG_1645220	hCG1645220	-1.1958	0.0254
241716_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-2.7084	0.0001
241724_x_at		Transcribed locus	-0.2287	0.0253
241740_at		Transcribed locus	-0.2447	0.0301
241757_x_at	DYNC2LI1	dynein; cytoplasmic 2; light intermediate chain 1	-0.3317	0.0418
241768_at			-0.4307	0.0282
241770_x_at		Transcribed locus	-0.1231	0.02
241789_at		CDNA FLJ36544 fis; clone TRACH2006378	-0.832	0.0392
241790_at		Transcribed locus	-0.638	0.0162
241792_x_at		CDNA FLJ33355 fis; clone BRACE2005151	-0.3907	0.0258
241794_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-0.1947	0.0005
241838_at		Transcribed locus	-1.4265	0.0152
241848_x_at			-0.2094	0.0041
241851_x_at	LOC730078	Hypothetical protein LOC730078	-0.2994	0.0299
241897_at			-1.8416	0.0021
241903_at		Transcribed locus	-2.0211	0.0007
241905_at	PIK3C2A	Phosphoinositide-3-kinase; class 2; alpha polypeptide	-1.6989	0.0014
241910_x_at	ARL17P1	ADP-ribosylation factor-like 17 pseudogene 1	-0.9765	0.0191
241932_at			-0.3202	0.0397
241938_at	QKI	Quaking homolog; KH domain RNA binding (mouse)	-1.1155	0.0442
241954_at	FDFT1	Farnesyl-diphosphate farnesyltransferase 1	-2.2837	0.0043
241956_at			-2.3698	0.0004
241961_at	SRD5A2L2	steroid 5 alpha-reductase 2-like 2	-0.1032	0.0357
241970_at		Transcribed locus	-1.0925	0.0159
241984_at	FOXN3	forkhead box N3	-0.2144	0.0496
241997_at		Transcribed locus	-0.6438	0.0235
242001_at	IDH1	Isocitrate dehydrogenase 1 (NADP+); soluble	-0.4616	0.0233
242006_at	LCA5	Leber congenital amaurosis 5	-0.5504	0.0034
242022_at		Transcribed locus	-1.6019	0.002
242029_at	FNDC3B	Fibronectin type III domain containing 3B	-0.9473	0.0415
242068_at		Transcribed locus	-1.3137	0.0123
242073_at		Transcribed locus	-0.7641	0.0297
242074_at		Transcribed locus	-0.4844	0.0225
242109_at	SYTL3	Synaptotagmin-like 3	-0.263	0.0138
242110_at		Transcribed locus	-0.9466	0.0158
242111_at	METTL3	methyltransferase like 3	-0.8639	0.0287
242113_at		Transcribed locus	-0.3134	0.0285
242119_at	PROX1	Prospero homeobox 1	-0.4546	0.0307
242125_at		CDNA FLJ36209 fis; clone THYMU2000022	-0.2874	0.0488
242126_at		Transcribed locus	-0.5648	0.0081
242134_at		Transcribed locus	-0.4467	0.0374
242143_at		Transcribed locus	-1.4283	0.008
242172_at	MEIS1	Meis homeobox 1	-1.5877	0.0273
242194_at	CUL4A	Cullin 4A	-0.607	0.0011
242195_x_at	NUMBL	numb homolog (Drosophila)-like	-0.5128	0.0487
242202_at		CDNA clone IMAGE:5302136	-0.1807	0.0324
242210_at	ZNF24	Zinc finger protein 24	-0.4328	0.0145
242235_x_at	NRD1	Nardilysin (N-arginine dibasic convertase)	-0.4985	0.0151
242236_at			-0.2383	0.0126
242239_at		CDNA clone IMAGE:5314281	-1.0803	0.045
242255_at	WDR37	WD repeat domain 37	-1.4411	0.0025
242256_x_at			-0.2172	0.0089
242285_at		Transcribed locus	-0.1369	0.0301
242289_at			-0.8428	0.0107
242290_at	TACC1	transforming; acidic coiled-coil containing protein 1	-0.6707	0.0205
242343_x_at			-1.1742	0.0122
242348_at	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like); member A4	-2.4906	0.0241
242349_at	HECTD1	HECT domain containing 1	-0.9919	0.0061

242361_at	IMMT	Inner membrane protein; mitochondrial (mitofilin)	-0.6019	0.0389
242362_at		Transcribed locus	-0.998	0.0021
242369_x_at		MRNA; cDNA DKFZp313O038 (from clone DKFZp313O038)	-0.4826	0.0356
242371_x_at			-0.1909	0.0381
242376_at		Transcribed locus	-0.2903	0.0249
242385_at	RORB	RAR-related orphan receptor B	-1.7172	0.0247
242389_at		CDNA FLJ33355 fis; clone BRACE2005151	-1.035	0.0033
242391_at			-0.1394	0.0267
242398_x_at		Transcribed locus	-0.2283	0.0311
242407_at			-0.58	0.0233
242416_at			-0.3876	0.0261
242427_at	WAC	WW domain containing adaptor with coiled-coil	-0.6031	0.0143
242438_at			-1.3594	0.0088
242439_s_at			-0.8486	0.0089
242447_at	LOC285382	hypothetical gene supported by AK091454	-2.065	0.0159
242458_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-0.3973	0.0487
242471_at		Clone HLS_IMAGE_238756 mRNA sequence	-1.2328	0.012
242480_at		Transcribed locus	-0.5889	0.0102
242483_at			-0.5626	0.0341
242485_at		Transcribed locus	-0.8098	0.0015
242492_at			-0.6108	0.0055
242493_at	PTPRD	protein tyrosine phosphatase; receptor type; D	-0.1037	0.0411
242494_at		Transcribed locus	-0.5954	0.0141
242498_x_at		Transcribed locus	-0.3994	0.0387
242529_x_at			-0.2115	0.0042
242540_at	C11orf47	chromosome 11 open reading frame 47	-0.2565	0.0046
242546_at	FLJ39632	hypothetical LOC642477	-1.7429	0.0173
242549_at	PRKD3	protein kinase D3	-1.8623	0.0111
242558_at		CDNA FLJ45490 fis; clone BRTHA2005831	-1.9317	0.0002
242576_x_at	PFAAP5	Phosphonoformate immuno-associated protein 5	-0.4721	0.0321
242591_at	DNAH1	Dynein; axonemal; heavy chain 1	-0.1079	0.0495
242608_x_at	C14orf44	Chromosome 14 open reading frame 44	-0.4044	0.0323
242616_at		Transcribed locus	-0.5015	0.0019
242622_x_at	PTEN	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-0.2341	0.0122
242646_at		Transcribed locus	-1.2542	0.0046
242651_at		Transcribed locus	-0.4093	0.0468
242677_at		Transcribed locus	-0.455	0.024
242679_at		CDNA clone IMAGE:5272988	-0.3809	0.0233
242688_at		Transcribed locus	-1.3715	0.0044
242691_at		CDNA FLJ41369 fis; clone BRCAN2006117	-1.4512	0.0181
242700_at	PON2	paraoxonase 2	-0.3332	0.0056
242707_at	MED23	mediator complex subunit 23	-0.4169	0.0458
242721_at			-0.3709	0.0139
242724_x_at			-0.347	0.0274
242726_at		Transcribed locus	-0.4387	0.0001
242732_at		Transcribed locus	-0.4705	0.0461
242738_s_at	ZFHX3	zinc finger homeobox 3	-0.9061	0.0392
242739_at	C6orf201	Chromosome 6 open reading frame 201	-1.7699	0.0096
242748_at	SREBF2	Sterol regulatory element binding transcription factor 2	-0.4333	0.018
242749_at		Transcribed locus	-0.6147	0.0052
242751_at		Transcribed locus	-1.2958	0.0154
242771_at	TTN	Titin	-0.2315	0.002
242776_at	ZCCHC6	zinc finger; CCHC domain containing 6	-0.6782	0.0129
242780_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A; 33kDa	-0.5227	0.0111
242785_at	FLJ42562	similar to echinoderm microtubule associated protein like 5	-1.0915	0.0224
242802_x_at		Transcribed locus	-0.1677	0.0435
242805_at			-0.2982	0.0201

242818_x_at		Transcribed locus	-0.5931	0.0167
242841_at		Full length insert cDNA clone YS02G11	-0.1413	0.0474
242851_at	KIAA1919	KIAA1919	-0.8028	0.0453
242853_at		Transcribed locus	-0.6931	0.0332
242872_at	CIT	citron (rho-interacting; serine/threonine kinase 21)	-0.2823	0.0368
242877_at		Transcribed locus	-1.1341	0.0045
242881_x_at		Clone HLS_IMAGE_626842 mRNA sequence	-2.274	0.0107
242940_x_at	DLX6	distal-less homeobox 6	-1.0696	0.0429
242968_at		Transcribed locus	-1.061	0.0149
242979_at		Transcribed locus	-1.4264	0.0282
243003_at		CDNA FLJ45369 fis; clone BRHIP3017325	-1.2304	0.0473
243009_at	LOC441242	CDNA clone IMAGE:5302136, Hypothetical LOC441242	-0.7553	0.0145
243031_at		Transcribed locus	-1.3208	0.0129
243037_at			-1.1711	0.0049
243041_s_at		Transcribed locus	-0.4534	0.0348
243055_at		Transcribed locus	-0.3299	0.0195
243147_x_at		Transcribed locus	-0.3678	0.0114
243149_at		Transcribed locus	-1.2298	0.022
243163_at		Transcribed locus	-0.1465	0.0343
243184_at			-0.8439	0.0397
243216_x_at		Transcribed locus	-0.3893	0.0219
243218_at		Transcribed locus	-0.291	0.0416
243234_at	TBX3	T-box 3 (ulnar mammary syndrome)	-1.5754	0.0021
243280_at		MRNA; cDNA DKFZp686J19109 (from clone DKFZp686J19109)	-0.4561	0.0168
243286_at		Transcribed locus	-1.0775	0.0094
243318_at	WDR42A	WD repeat domain 42A	-1.1062	0.024
243365_s_at	AUTS2	autism susceptibility candidate 2	-0.4732	0.0047
243388_at		Transcribed locus; strongly similar to XP_519898.1 similar to DKFZP564O0463 protein; HSPC064 protein [Pan troglodytes]	-0.7281	0.0305
243395_at		Transcribed locus	-1.198	0.0248
243400_x_at	LTBR	lymphotoxin beta receptor (TNFR superfamily; member 3)	-0.1602	0.0164
243416_at			-1.0256	0.0434
243428_at	KCNQ1OT1	KCNQ1 overlapping transcript 1	-1.2415	0.0107
243435_at	KCNQ1OT1	KCNQ1 overlapping transcript 1	-1.0485	0.0196
243443_at		Clone IMAGE:120153 mRNA sequence	-0.1386	0.049
243461_at		Transcribed locus	-0.6867	0.0222
243462_s_at		Transcribed locus	-1.5268	0.0029
243480_at			-0.3083	0.044
243498_at		Transcribed locus	-0.3452	0.012
243504_at		Transcribed locus	-0.1006	0.0238
243514_at		Transcribed locus	-1.5675	0.0118
243524_at		Full length insert cDNA YI27F12	-0.725	0.0351
243530_at		Transcribed locus	-0.17	0.0184
243543_at		Transcribed locus	-1.801	0.0272
243546_at		Transcribed locus	-0.6311	0.0016
243554_at		Transcribed locus	-0.2757	0.0098
243559_at		Transcribed locus	-0.4874	0.0076
243561_at		Transcribed locus	-1.1714	0.0438
243578_at		Transcribed locus	-0.4396	0.0022
243581_at	LOC646470	Similar to proteaseome (prosome; macropain) 28 subunit; 3	-0.1381	0.0437
243589_at	KIAA1267	KIAA1267	-1.2436	0.0085
243592_at	REV1	REV1 homolog (S. cerevisiae)	-0.5953	0.0026
243611_at	MICALCL	MICAL C-terminal like	-0.1096	0.0136
243612_at	NSD1	Nuclear receptor binding SET domain protein 1	-0.3818	0.0374
243617_at	LOC152485	Hypothetical protein LOC152485	-0.5013	0.0196
243618_s_at	LOC152485	Hypothetical protein LOC152485	-0.8284	0.0328
243624_at	PIAS2	Protein inhibitor of activated STAT; 2	-0.6963	0.0188

243646_at			-0.9669	0.0087
243648_at			-0.9166	0.0188
243656_at	LOC642852	hypothetical LOC642852	-0.4073	0.011
243689_s_at	C20orf80	Chromosome 20 open reading frame 80	-0.151	0.045
243696_at	KIAA0562	KIAA0562	-0.1997	0.0016
243713_at		Transcribed locus	-0.2774	0.0146
243715_at		CDNA FLJ42410 fis; clone BLADE2000938	-0.4659	0.0124
243736_at		Transcribed locus	-1.2253	0.0054
243739_at		Transcribed locus	-0.3778	0.0464
243759_at	SFRS15	Splicing factor; arginine/serine-rich 15	-0.8712	0.013
243763_x_at		Transcribed locus	-0.2087	0.035
243765_at		Transcribed locus	-0.2363	0.0448
243768_at		Transcribed locus	-1.0171	0.027
243772_at	SDCCAG8	serologically defined colon cancer antigen 8	-0.4196	0.0041
243792_x_at	PTPN13	Protein tyrosine phosphatase; non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	-0.7933	0.0158
243801_x_at		Transcribed locus	-0.4532	0.0147
243808_at		Transcribed locus	-1.3703	0.0136
243827_at		Transcribed locus	-1.0948	0.0186
243851_at	RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	-0.9577	0.0202
243860_at			-0.2463	0.0089
243866_x_at			-0.1923	0.0315
243874_at	LPP	LIM domain containing preferred translocation partner in lipoma	-0.4448	0.034
243876_at		Transcribed locus	-0.1408	0.0449
243895_x_at		Transcribed locus	-0.6634	0.0058
243896_at	C10orf79	chromosome 10 open reading frame 79	-0.1326	0.0341
243908_at			-1.0183	0.0117
243920_x_at		MRNA; cDNA DKFZp686I19109 (from clone DKFZp686I19109)	-0.2059	0.0494
243937_x_at	CTGLF2	centaurin; gamma-like family; member 2	-0.3558	0.0293
243953_at	FADS2	fatty acid desaturase 2	-0.4917	0.0063
243960_x_at		Transcribed locus	-0.1253	0.0392
243963_at	SDCCAG8	Serologically defined colon cancer antigen 8	-0.7918	0.0266
243964_at		Transcribed locus	-0.7361	0.0166
243984_at		Transcribed locus	-0.1121	0.0452
243992_at		Transcribed locus	-1.6328	0.0013
244000_at		CDNA FLJ14364 fis; clone HEMBA1000918	-0.8778	0.024
244007_at			-0.6135	0.0123
244010_at		MRNA; cDNA DKFZp686J08131 (from clone DKFZp686J08131)	-0.9594	0.0348
244057_s_at	C10orf72	chromosome 10 open reading frame 72	-0.7178	0.0203
244058_at	C10orf72	chromosome 10 open reading frame 72	-1.0606	0.0365
244065_at	FLJ37512	similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3)	-1.0363	0.0462
244070_at	SYNE1	spectrin repeat containing; nuclear envelope 1	-0.9576	0.0232
244092_at	ZRANB3	zinc finger; RAN-binding domain containing 3	-0.1834	0.0272
244112_x_at			-1.3247	0.0251
244132_x_at	ZNF518	Zinc finger protein 518	-1.1398	0.0057
244185_at		Transcribed locus	-1.0707	0.0135
244197_x_at			-1.0028	0.0327
244219_at		Transcribed locus	-0.9739	0.0097
244224_x_at	LYNX1	Ly6/neurotoxin 1	-0.8334	0.0154
244247_at		Transcribed locus	-0.2347	0.0339
244265_at			-0.2547	0.0356
244300_at		Transcribed locus	-1.1555	0.0446
244310_at		Full length insert cDNA clone YU07D01	-1.4982	0.0332
244320_at	NHLRC2	NHL repeat containing 2	-0.2585	0.0283
244360_at	FBXL17	F-box and leucine-rich repeat protein 17	-0.4144	0.0283
244401_at	LCA5	Leber congenital amaurosis 5	-0.3367	0.0041
244412_at			-0.1168	0.0091

244433_at			-1.2724	0.0045
244461_at	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	-0.4222	0.0464
244496_at		Transcribed locus	-0.172	0.0075
244503_at		Transcribed locus	-0.8451	0.0408
244518_at		Transcribed locus; moderately similar to XP_530536.1 hypothetical protein XP_530536 [Pan troglodytes]	-0.1283	0.0294
244525_at			-0.1073	0.0323
244536_at		Transcribed locus	-0.2707	0.0413
244586_x_at			-0.1592	0.0353
244605_at			-0.5972	0.0088
244607_at		Transcribed locus	-0.2581	0.0048
244622_at	BRWD1	Bromodomain and WD repeat domain containing 1	-0.1672	0.0431
244633_at		Transcribed locus	-1.7987	0.0052
244646_at		Transcribed locus	-1.2225	0.0005
244655_at	LOC644192	Hypothetical LOC644192	-0.6363	0.0283
244659_at	TRIP12	Thyroid hormone receptor interactor 12	-0.8878	0.0146
244661_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	-0.9655	0.025
244673_at		Transcribed locus	-0.161	0.0028
244689_at	PPARA	peroxisome proliferator-activated receptor alpha	-0.4831	0.0462
244693_at		Transcribed locus	-0.2228	0.0146
244726_at		Transcribed locus	-1.0011	0.0485
244737_at		Transcribed locus	-0.1065	0.0414
244753_at		Transcribed locus	-1.4579	0.0025
244777_at	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	-0.7266	0.0395
244778_x_at			-0.4528	0.0424
244791_at			-0.1658	0.0362
244801_at	PSMB7	Proteasome (prosome; macropain) subunit; beta type; 7	-1.2042	0.0012
244803_at		Transcribed locus	-1.6608	0.0138
244813_at		Transcribed locus	-0.3928	0.0401
244842_x_at		Transcribed locus	-0.4766	0.0424
244868_at		Transcribed locus	-0.1954	0.0472
244873_s_at		Transcribed locus	-0.143	0.0191
31637_s_at	NR1D1	nuclear receptor subfamily 1; group D; member 1, thyroid hormone receptor; alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog; avian)	-1.8543	0.0009
35617_at	MAPK7	mitogen-activated protein kinase 7	-0.5645	0.024
35626_at	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	-0.5921	0.0306
36019_at	STK19	serine/threonine kinase 19	-1.1892	0.0384
36829_at	PER1	period homolog 1 (Drosophila)	-1.0365	0.0285
37433_at	PIAS2	protein inhibitor of activated STAT; 2	-0.904	0.021
38710_at	OTUB1	OTU domain; ubiquitin aldehyde binding 1	-0.6239	0.0388
40093_at	BCAM	basal cell adhesion molecule (Lutheran blood group)	-0.3899	0.0321
40189_at	SET	SET translocation (myeloid leukemia-associated)	-0.4254	0.0151
40284_at	FOXA2	forkhead box A2	-1.1437	0.0492
44702_at	SYDE1	synapse defective 1; Rho GTPase; homolog 1 (C. elegans)	-0.5565	0.0301
49077_at	PPME1	protein phosphatase methylesterase 1	-0.598	0.0324
50376_at	ZNF444	zinc finger protein 444	-0.4037	0.0251
51176_at	MED27	mediator complex subunit 27	-0.7743	0.0388
54051_at	PKNOX1	PBX/knotted 1 homeobox 1	-0.2281	0.0143
64474_g_at	DGCR8	DiGeorge syndrome critical region gene 8	-0.6518	0.0457
65472_at		Transcribed locus	-0.6151	0.018
65884_at	MAN1B1	mannosidase; alpha; class 1B; member 1	-0.8708	0.0443

*For the difference in expression

Supplemental Table 6. Gene set enrichment analysis of ACC patients' cohort for genes related to cell proliferation (dataset GSE10927).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	AIF1	AIF1	allograft inflammatory factor 1	30	0.417639583	0.014017673	Yes
2	SCG2	SCG2	secretogranin II (chromogranin C)	32	0.412185848	0.029264143	Yes
3	FABP6	FABP6	fatty acid binding protein 6, ileal (gastrotropin)	50	0.388875127	0.04285596	Yes
4	CXCL10	CXCL10	chemokine (C-X-C motif) ligand 10	68	0.373264641	0.055868484	Yes
5	PTPRC	PTPRC	protein tyrosine phosphatase, receptor type, C	84	0.357103735	0.06838	Yes
6	LST1	LST1	leukocyte specific transcript 1	97	0.349123091	0.0807434	Yes
7	CSF1R	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	154	0.321420699	0.08990736	Yes
8	RARRES3	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	207	0.301735938	0.09853824	Yes
9	SYK	SYK	spleen tyrosine kinase	297	0.268629342	0.10411458	Yes
10	LYN	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	361	0.254236132	0.11043992	Yes
11	FABP3	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	365	0.252116174	0.11964765	Yes
12	IL15	IL15	interleukin 15	391	0.249108106	0.12765804	Yes
13	GCG	GCG	glucagon	403	0.246872678	0.1362764	Yes
14	LY86	LY86	lymphocyte antigen 86	408	0.246374503	0.14522171	Yes
15	RAPGEF3	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	413	0.245568678	0.15413712	Yes
16	GPC4	GPC4	glypican 4	441	0.241428345	0.16176382	Yes
17	CD74	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	442	0.241261616	0.1707168	Yes
18	CRIP1	CRIP1	cysteine-rich protein 1 (intestinal)	453	0.239757761	0.17912047	Yes
19	CD33	CD33	CD33 molecule	498	0.233311787	0.185607	Yes
20	TIPIN	TIPIN	TIMELESS interacting protein	502	0.232431293	0.19408426	Yes
21	CXCL5	CXCL5	chemokine (C-X-C motif) ligand 5	506	0.231562749	0.20252927	Yes
22	GPNMB	GPNMB	glycoprotein (transmembrane) nmb	538	0.227214798	0.20943111	Yes
23	HCLS1	HCLS1	hematopoietic cell-specific Lyn substrate 1	570	0.221458048	0.21611933	Yes
24	IL15RA	IL15RA	interleukin 15 receptor, alpha	575	0.220710948	0.2241123	Yes
25	WARS	WARS	tryptophanyl-tRNA synthetase	590	0.218839198	0.23154229	Yes
26	CGREF1	CGREF1	cell growth regulator with EF-hand domain 1	594	0.218516111	0.23950316	Yes
27	LAMP3	LAMP3	lysosomal-associated membrane protein 3	626	0.214147061	0.24592008	Yes

28	POU3F2	POU3F2	POU domain, class 3, transcription factor 2	642	0.212912053	0.25308076	Yes
29	CTF1	CTF1	cardiotrophin 1	647	0.212266222	0.26076037	Yes
30	MATK	MATK	megakaryocyte-associated tyrosine kinase	693	0.20639278	0.2661986	Yes
31	REG3A	REG3A	regenerating islet-derived 3 alpha	729	0.202743709	0.27199495	Yes
32	CD86	CD86	CD86 molecule	747	0.201579466	0.2786364	Yes
33	LRP5	LRP5	low density lipoprotein receptor-related protein 5	752	0.200534284	0.28588063	Yes
34	EBI3	EBI3	Epstein-Barr virus induced gene 3	756	0.200241044	0.29316333	Yes
35	IL6	IL6	interleukin 6 (interferon, beta 2)	765	0.199301854	0.30016443	Yes
36	CDK5	CDK5	cyclin-dependent kinase 5	778	0.198399097	0.3069346	Yes
37	TNFRSF11 A	TNFRSF11 A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	834	0.193767995	0.31141084	Yes
38	TCIRG1	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	893	0.18837446	0.31553888	Yes
39	IL7	IL7	interleukin 7	921	0.185417786	0.3210871	Yes
40	FGF18	FGF18	fibroblast growth factor 18	923	0.184986949	0.3279024	Yes
41	PRDM4	PRDM4	PR domain containing 4	1006	0.178534895	0.3304809	Yes
42	CXCL1	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	1014	0.17775473	0.33673173	Yes
43	MCTS1	MCTS1	malignant T cell amplified sequence 1	1191	0.164875627	0.33416432	Yes
44	FIGF	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	1219	0.162916735	0.33887753	Yes
45	TBRG4	TBRG4	transforming growth factor beta regulator 4	1288	0.1590195	0.34142274	Yes
46	CBFA2T3	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1299	0.158238187	0.34680128	Yes
47	IGF1	IGF1	insulin-like growth factor 1 (somatomedin C)	1319	0.157541856	0.35170984	Yes
48	FES	FES	feline sarcoma oncogene	1357	0.155645043	0.3556597	Yes
49	RARRES1	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	1368	0.155280992	0.3609285	Yes
50	EIF5A2	EIF5A2	eukaryotic translation initiation factor 5A2	1514	0.148478404	0.3592825	Yes
51	LRPAP1	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	1538	0.147487625	0.36362055	Yes
52	GAS6	GAS6	growth arrest-specific 6	1625	0.142923504	0.3646801	Yes
53	MXD4	MXD4	MAX dimerization protein 4	1638	0.142366931	0.369371	Yes
54	CREG1	CREG1	cellular repressor of E1A-stimulated genes 1	1764	0.13667804	0.36827412	Yes
55	CDKN3	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	1802	0.134949833	0.371456	Yes
56	JAG2	JAG2	jagged 2	1844	0.133045584	0.3743698	Yes
57	MNAT1	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	2015	0.126640022	0.37067962	Yes
58	SSTR2	SSTR2	somatostatin receptor 2	2037	0.125963882	0.37431765	Yes
59	IL6R	IL6R	interleukin 6 receptor	2085	0.124371856	0.37661347	Yes
60	APC	APC	adenomatosis polyposis coli	2139	0.122778587	0.37855405	Yes

61	IL12RB1	IL12RB1	interleukin 12 receptor, beta 1	2203	0.120651826	0.3799222	Yes
62	PIM2	PIM2	pim-2 oncogene	2215	0.120263301	0.3838422	Yes
63	ZNF259	ZNF259	zinc finger protein 259	2266	0.118319049	0.38576534	Yes
64	IL18	IL18	interleukin 18 (interferon-gamma-inducing factor)	2305	0.117301494	0.38824296	Yes
65	LDOC1	LDOC1	leucine zipper, down-regulated in cancer 1	2323	0.116887227	0.39174157	Yes
66	MT3	MT3	metallothionein 3 (growth inhibitory factor (neurotrophic))	2325	0.116869323	0.3960291	Yes
67	REG1A	REG1A	regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)	2360	0.115648739	0.3986428	Yes
68	RUNX3	RUNX3	runt-related transcription factor 3	2422	0.113624513	0.39984888	Yes
69	VTI1B	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	2437	0.113298215	0.40336236	Yes
70	KRT2	KRT2	keratin 2 (epidermal ichthyosis bullosa of Siemens)	2439	0.113283768	0.40751687	Yes
71	RHOG	RHOG	ras homolog gene family, member G (rho G)	2449	0.11275737	0.41125703	Yes
72	CRTAM	CRTAM	cytotoxic and regulatory T cell molecule	2509	0.111066252	0.41246685	Yes
73	DUSP22	DUSP22	dual specificity phosphatase 22	2527	0.110483758	0.41572785	Yes
74	PTK2B	PTK2B	PTK2B protein tyrosine kinase 2 beta	2566	0.10959819	0.4179196	Yes
75	TUSC2	TUSC2	tumor suppressor candidate 2	2575	0.109338544	0.42158222	Yes
76	CSF1	CSF1	colony stimulating factor 1 (macrophage)	2593	0.108877927	0.42478362	Yes
77	MTCP1	MTCP1	mature T-cell proliferation 1	2597	0.108712189	0.42866978	Yes
78	LRP1	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2691	0.106187202	0.42802063	Yes
79	CD3E	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	2730	0.105320625	0.43005365	Yes
80	TCFL5	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	2737	0.105205007	0.43366158	Yes
81	PIM1	PIM1	pim-1 oncogene	2777	0.104350127	0.43560922	Yes
82	BUB1B	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	2781	0.104309179	0.43933198	Yes
83	FLT3	FLT3	fms-related tyrosine kinase 3	2818	0.103479892	0.4413954	Yes
84	SRA1	SRA1	steroid receptor RNA activator 1	2839	0.102847792	0.44422495	Yes
85	DKC1	DKC1	dyskeratosis congenita 1, dyskerin	2877	0.102077551	0.44618696	Yes
86	S100A11	S100A11	S100 calcium binding protein A11	2892	0.101741247	0.44927156	Yes
87	NDUFS4	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	2944	0.100510009	0.4504845	Yes
88	ISG20	ISG20	interferon stimulated exonuclease gene 20kDa	2946	0.100492157	0.45416433	Yes
89	MIA	MIA	melanoma inhibitory activity	2956	0.100170568	0.4574374	Yes

90	CDK7	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	2957	0.100165501	0.46115443	Yes
91	SERTAD1	SERTAD1	SERTA domain containing 1	3030	0.098670498	0.46126273	Yes
92	TXN	TXN	thioredoxin	3068	0.097696587	0.46306217	Yes
93	SIRPG	SIRPG	signal-regulatory protein gamma	3209	0.094815619	0.45967153	Yes
94	B4GALT7	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	3218	0.094562314	0.46278584	Yes
95	BIN1	BIN1	bridging integrator 1	3315	0.092294231	0.4614731	Yes
96	PYY	PYY	peptide YY	3340	0.091746904	0.46369332	Yes
97	AGGF1	AGGF1	angiogenic factor with G patch and FHA domains 1	3381	0.090796053	0.46508864	Yes
98	TGFA	TGFA	transforming growth factor, alpha	3396	0.090428598	0.46775344	Yes
99	CD24	CD24	CD24 molecule	3520	0.087696806	0.4649376	Yes
100	PDAP1	PDAP1	PDGFA associated protein 1	3552	0.08691138	0.4666329	Yes
101	SCIN	SCIN	scinderin	3570	0.086626694	0.4690086	Yes
102	IL2RA	IL2RA	interleukin 2 receptor, alpha	3606	0.085954085	0.47047096	Yes
103	IFITM1	IFITM1	interferon induced transmembrane protein 1 (9-27)	3634	0.085442178	0.47230917	Yes
104	OSM	OSM	oncostatin M	3822	0.082188398	0.46613047	Yes
105	BMP10	BMP10	bone morphogenetic protein 10	3827	0.082052462	0.46897793	Yes
106	BST2	BST2	bone marrow stromal cell antigen 2	3830	0.081981592	0.4719215	Yes
107	CDC25B	CDC25B	cell division cycle 25B	3882	0.08075539	0.47240135	Yes
108	BTC	BTC	betacellulin	3899	0.080445066	0.47459698	Yes
109	IL1B	IL1B	interleukin 1, beta	3932	0.079624265	0.47597253	Yes
110	LMO1	LMO1	LIM domain only 1 (rhombotin 1)	3949	0.079278514	0.47812486	Yes
111	EEF1E1	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	3958	0.079164051	0.48066774	Yes
112	NDP	NDP	Norrie disease (pseudoglioma)	3968	0.078902021	0.48315156	Yes
113	GAB1	GAB1	GRB2-associated binding protein 1	4019	0.078047626	0.4835803	Yes
114	EREG	EREG	epiregulin	4055	0.077592269	0.4847324	Yes
115	BCAR1	BCAR1	breast cancer anti-estrogen resistance 1	4081	0.077003643	0.48635614	Yes
116	GHRL	GHRL	ghrelin/obestatin preprohormone	4123	0.076217391	0.4871611	Yes
117	PRMT5	PRMT5	protein arginine methyltransferase 5	4242	0.074583776	0.4841054	Yes
118	CGRRF1	CGRRF1	cell growth regulator with ring finger domain 1	4270	0.074184991	0.48552585	Yes
119	ERBB4	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	4334	0.073208384	0.48513344	Yes
120	FOSL1	FOSL1	FOS-like antigen 1	4380	0.072465837	0.48560178	Yes
121	CHRM1	CHRM1	cholinergic receptor, muscarinic 1	4386	0.072375707	0.4880408	Yes
122	ETS1	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	4435	0.071606219	0.4883292	Yes
123	CDCA7	CDCA7	cell division cycle associated 7	4474	0.070858568	0.48908335	Yes
124	PDGFA	PDGFA	platelet-derived growth factor alpha polypeptide	4507	0.07034798	0.49011466	Yes

125	ERF	ERF	Ets2 repressor factor	4533	0.069866955	0.4914736	Yes
126	VIPR1	VIPR1	vasoactive intestinal peptide receptor 1	4612	0.068627417	0.4901709	Yes
127	SFN	SFN	stratifin	4647	0.068043418	0.491018	Yes
128	NANOG	NANOG	Nanog homeobox	4729	0.066931561	0.48950434	Yes
129	PPARD	PPARD	peroxisome proliferative activated receptor, delta	4780	0.0660908	0.48948935	Yes
130	FGF7	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	4827	0.065578558	0.48965275	Yes
131	TNFSF9	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	4914	0.064420536	0.48779914	Yes
132	IFRD2	IFRD2	interferon-related developmental regulator 2	4960	0.063831806	0.4879471	Yes
133	CD160	CD160	CD160 molecule	4963	0.063808598	0.49021626	Yes
134	GNL3	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	4964	0.063803293	0.49258393	Yes
135	EMP2	EMP2	epithelial membrane protein 2	4991	0.063286625	0.49364933	Yes
136	PCNA	PCNA	proliferating cell nuclear antigen	5032	0.062728748	0.4940031	Yes
137	ABI1	ABI1	abl-interactor 1	5041	0.062629864	0.4959324	Yes
138	GFI1B	GFI1B	growth factor independent 1B (potential regulator of CDKN1A, translocated in CML)	5051	0.062513486	0.49780807	Yes
139	DTYMK	DTYMK	deoxythymidylate kinase (thymidylate kinase)	5152	0.061107673	0.4951406	Yes
140	FZD3	FZD3	frizzled homolog 3 (Drosophila)	5167	0.060915731	0.4967102	Yes
141	SLAMF1	SLAMF1	signaling lymphocytic activation molecule family member 1	5175	0.060784291	0.49862042	Yes
142	SLC29A2	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	5195	0.060588785	0.49993113	Yes
143	KRT16	KRT16	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)	5259	0.059659317	0.49903592	No
144	BAP1	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	5360	0.058426004	0.49626896	No
145	GLI1	GLI1	glioma-associated oncogene homolog 1 (zinc finger protein)	5466	0.056865171	0.4931973	No
146	TPX2	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	5528	0.056151588	0.49227062	No
147	KRT4	KRT4	keratin 4	5544	0.055994038	0.49360824	No
148	CDK4	CDK4	cyclin-dependent kinase 4	5599	0.055354338	0.49299744	No
149	FGF4	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene)	5607	0.055250656	0.49470228	No
150	TIMP1	TIMP1	TIMP metallopeptidase inhibitor 1	5672	0.054395471	0.49356237	No
151	CHEK1	CHEK1	CHK1 checkpoint homolog (S. pombe)	5704	0.053977136	0.4940355	No
152	TRIM27	TRIM27	tripartite motif-containing 27	5712	0.053906329	0.4956905	No
153	CKLF	CKLF	chemokine-like factor	5792	0.053021699	0.49375933	No
154	EPHB4	EPHB4	EPH receptor B4	5909	0.051464189	0.4899444	No
155	MFN2	MFN2	mitofusin 2	5964	0.050914217	0.48916882	No
156	CAPNS1	CAPNS1	calpain, small subunit 1	6004	0.050413653	0.48911494	No

157	IL9	IL9	interleukin 9	6198	0.048084922	0.48137456	No
158	TSPO	TSPO	translocator protein (18kDa)	6248	0.04755849	0.4807212	No
159	SSTR1	SSTR1	somatostatin receptor 1	6267	0.047375474	0.48159096	No
160	CDKN1A	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	6336	0.046626952	0.47996536	No
161	TGFBI	TGFBI	transforming growth factor, beta-induced, 68kDa	6449	0.045370299	0.4761217	No
162	FLT3LG	FLT3LG	fms-related tyrosine kinase 3 ligand	6451	0.045344133	0.47775504	No
163	ICOSLG	ICOSLG	inducible T-cell co-stimulator ligand	6510	0.044771466	0.4765541	No
164	EGFR	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	6541	0.044434048	0.47672248	No
165	FOXP3	FOXP3	forkhead box P3	6567	0.044130318	0.47712633	No
166	ELF4	ELF4	E74-like factor 4 (ets domain transcription factor)	6572	0.04408519	0.4785649	No
167	NCK1	NCK1	NCK adaptor protein 1	6594	0.043798596	0.47915384	No
168	ARHGEF2	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	6603	0.043724392	0.4803816	No
169	MYT2	MYT2	myelin transcription factor 2	6619	0.043529756	0.4812567	No
170	POLA1	POLA1	polymerase (DNA directed), alpha 1	6639	0.043274045	0.48192486	No
171	NUDC	NUDC	nuclear distribution gene C homolog (A. nidulans)	6650	0.043169428	0.48303333	No
172	RAF1	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	6658	0.043028835	0.48428464	No
173	ERBB2	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	6666	0.042923324	0.48553202	No
174	TNFRSF8	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	6804	0.041536994	0.48031232	No
175	KITLG	KITLG	KIT ligand	6811	0.041490585	0.4815559	No
176	BNIPL	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	6846	0.041197494	0.48140675	No
177	PLK1	PLK1	polo-like kinase 1 (Drosophila)	6988	0.039680921	0.4759208	No
178	ARTN	ARTN	artemin	6990	0.039660782	0.4773432	No
179	KLK8	KLK8	kallikrein 8 (neuropsin/ovasin)	7001	0.039556656	0.47831762	No
180	CNOT8	CNOT8	CCR4-NOT transcription complex, subunit 8	7100	0.038533125	0.47491112	No
181	KLF4	KLF4	Kruppel-like factor 4 (gut)	7179	0.037712399	0.47246122	No
182	CTBP1	CTBP1	C-terminal binding protein 1	7229	0.037242342	0.47142506	No
183	INSL4	INSL4	insulin-like 4 (placenta)	7337	0.036209162	0.46748817	No
184	FGFBP1	FGFBP1	fibroblast growth factor binding protein 1	7348	0.036088277	0.46833387	No
185	MAS1	MAS1	MAS1 oncogene	7393	0.035602629	0.4674836	No
186	DHPS	DHPS	deoxyhypusine synthase	7486	0.034767173	0.4642335	No
187	FABP7	FABP7	fatty acid binding protein 7, brain	7577	0.033877	0.46104902	No
188	NME1	NME1	non-metastatic cells 1, protein (NM23A) expressed in	7661	0.033150781	0.45818308	No
189	PPM1D	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	7743	0.0322464	0.4553823	No
190	DLEC1	DLEC1	deleted in lung and esophageal cancer 1	7745	0.032233287	0.45652908	No

191	MAGED1	MAGED1	melanoma antigen family D, 1	7800	0.031818885	0.4550449	No
192	DERL2	DERL2	Der1-like domain family, member 2	7882	0.031120319	0.45220232	No
193	EGR4	EGR4	early growth response 4	7913	0.030857066	0.45186687	No
194	CDC27	CDC27	cell division cycle 27	7991	0.030025806	0.44918105	No
195	S100B	S100B	S100 calcium binding protein B	8031	0.029640695	0.4483563	No
196	UMOD	UMOD	uromodulin (uromucoid, Tamm-Horsfall glycoprotein)	8067	0.029349381	0.44771814	No
197	ERG	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	8083	0.02924227	0.44806302	No
198	EHF	EHF	ets homologous factor	8124	0.028781939	0.44715706	No
199	IGFBP4	IGFBP4	insulin-like growth factor binding protein 4	8138	0.028690726	0.4475802	No
200	CD274	CD274	CD274 molecule	8151	0.028555708	0.44804764	No
201	IL11	IL11	interleukin 11	8190	0.028186448	0.44721827	No
202	BNC1	BNC1	basonuclin 1	8275	0.027553087	0.44409525	No
203	DNAJA2	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	8329	0.027096184	0.44248515	No
204	PAWR	PAWR	PRKC, apoptosis, WT1, regulator	8430	0.026108051	0.4385189	No
205	PEMT	PEMT	phosphatidylethanolamine N-methyltransferase	8462	0.025840379	0.43794793	No
206	NPY	NPY	neuropeptide Y	8468	0.025775822	0.4386577	No
207	PDGFRA	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	8683	0.023882287	0.42898282	No
208	CUL1	CUL1	cullin 1	8692	0.023796069	0.42947108	No
209	ALOX15B	ALOX15B	arachidonate 15-lipoxygenase, type B	8734	0.023427062	0.42831704	No
210	COL4A3	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	8785	0.022985715	0.42670247	No
211	IL9R	IL9R	interleukin 9 receptor	8786	0.022981379	0.42755526	No
212	CD79A	CD79A	CD79a molecule, immunoglobulin-associated alpha	8866	0.022165043	0.42447907	No
213	E4F1	E4F1	E4F transcription factor 1	8939	0.021480663	0.42172292	No
214	CDC6	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	8965	0.021250226	0.42127773	No
215	CD28	CD28	CD28 molecule	9049	0.020561455	0.4179446	No
216	MAPRE1	MAPRE1	microtubule-associated protein, RP/EB family, member 1	9067	0.020425664	0.4178636	No
217	TP53I11	TP53I11	tumor protein p53 inducible protein 11	9140	0.019741941	0.41504294	No
218	IL12B	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	9220	0.019072792	0.41185197	No
219	RPS4X	RPS4X	ribosomal protein S4, X-linked	9254	0.018756388	0.41091943	No
220	MAP3K11	MAP3K11	mitogen-activated protein kinase kinase kinase 11	9307	0.018346239	0.40903398	No
221	BAI1	BAI1	brain-specific angiogenesis inhibitor 1	9341	0.018039593	0.40807483	No
222	TNFRSF17	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	9369	0.017709721	0.40739954	No
223	CDK10	CDK10	cyclin-dependent kinase (CDC2-like) 10	9382	0.017634554	0.40746173	No
224	FTH1	FTH1	ferritin, heavy polypeptide 1	9385	0.017602075	0.40801623	No

225	EPS8	EPS8	epidermal growth factor receptor pathway substrate 8	9456	0.017028712	0.40519357	No
226	MNT	MNT	MAX binding protein	9484	0.016858581	0.40448672	No
227	CDC25C	CDC25C	cell division cycle 25C	9644	0.015581897	0.3972181	No
228	EMP3	EMP3	epithelial membrane protein 3	9680	0.015225273	0.39605582	No
229	HTR1A	HTR1A	5-hydroxytryptamine (serotonin) receptor 1A	9772	0.014451792	0.39210117	No
230	GPX1	GPX1	glutathione peroxidase 1	9795	0.014255677	0.39154446	No
231	NPM1	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	9866	0.013464367	0.38858953	No
232	PA2G4	PA2G4	proliferation-associated 2G4, 38kDa	9920	0.012993444	0.3864561	No
233	TNFRSF9	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	10061	0.011918484	0.37998924	No
234	CUL5	CUL5	cullin 5	10134	0.011300193	0.3768553	No
235	REG1B	REG1B	regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	10229	0.010578047	0.37260887	No
236	MS4A2	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	10258	0.010282603	0.37160861	No
237	PRDX1	PRDX1	peroxiredoxin 1	10286	0.01006698	0.3706497	No
238	HGS	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	10421	0.008889277	0.36436653	No
239	NCK2	NCK2	NCK adaptor protein 2	10493	0.008215168	0.36116746	No
240	STAMBP	STAMBP	STAM binding protein	10527	0.007866614	0.35983083	No
241	ATPIF1	ATPIF1	ATPase inhibitory factor 1	10674	0.006650778	0.35287237	No
242	NAB2	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	10737	0.006123609	0.35003984	No
243	GAS8	GAS8	growth arrest-specific 8	10820	0.005366077	0.34619218	No
244	RERG	RERG	RAS-like, estrogen-regulated, growth inhibitor	10864	0.005022839	0.3442565	No
245	RBBP7	RBBP7	retinoblastoma binding protein 7	11279	0.001670888	0.32388717	No
246	VIP	VIP	vasoactive intestinal peptide	11465	2.00E-04	0.31476462	No
247	PRG4	PRG4	proteoglycan 4	11582	-6.61E-04	0.30906442	No
248	SSTR3	SSTR3	somatostatin receptor 3	11689	-0.001711596	0.30389673	No
249	CSE1L	CSE1L	CSE1 chromosome segregation 1-like (yeast)	11770	-0.002352027	0.30003592	No
250	CLEC11A	CLEC11A	C-type lectin domain family 11, member A	11777	-0.002445421	0.29983056	No
251	KHDRBS1	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	11857	-0.003084648	0.29604632	No
252	RASGRP4	RASGRP4	RAS guanyl releasing protein 4	11907	-0.003511682	0.29375842	No
253	RPS27	RPS27	ribosomal protein S27 (metallopanstimulin 1)	12061	-0.004765213	0.28638455	No
254	CHRNA10	CHRNA10	cholinergic receptor, nicotinic, alpha 10	12062	-0.004775717	0.28656176	No
255	EIF2AK2	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	12187	-0.005958047	0.28066334	No
256	IL27	IL27	interleukin 27	12249	-0.006437371	0.2778918	No
257	ING4	ING4	inhibitor of growth family, member 4	12334	-0.007245419	0.2740152	No

258	EDN1	EDN1	endothelin 1	12342	-0.007338135	0.27394205	No
259	POU1F1	POU1F1	POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)	12393	-0.007739552	0.2717617	No
260	CTNNBIP1	CTNNBIP1	catenin, beta interacting protein 1	12456	-0.008377885	0.26901284	No
261	CDKN2D	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	12546	-0.009077905	0.26495746	No
262	ADAMTS8	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	12561	-0.009194675	0.26460776	No
263	CUL3	CUL3	cullin 3	12764	-0.010858037	0.25504178	No
264	CCKBR	CCKBR	cholecystokinin B receptor	12830	-0.011364272	0.25225568	No
265	RBBP4	RBBP4	retinoblastoma binding protein 4	12903	-0.011987611	0.24914725	No
266	ALOX12	ALOX12	arachidonate 12-lipoxygenase	12972	-0.012648899	0.24626076	No
267	FLT4	FLT4	fms-related tyrosine kinase 4	13024	-0.013115887	0.24423058	No
268	SPDYA	SPDYA	speedy homolog A (Drosophila)	13146	-0.014093602	0.23878211	No
269	IL2	IL2	interleukin 2	13243	-0.014918946	0.23459804	No
270	TNFSF15	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	13282	-0.015302985	0.23329057	No
271	TRAIP	TRAIP	TRAF interacting protein	13298	-0.015464076	0.23312417	No
272	THPO	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	13308	-0.015555609	0.23325726	No
273	MST1R	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	13486	-0.017182065	0.22515973	No
274	ATP8A2	ATP8A2	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2	13575	-0.018084973	0.22148795	No
275	CUL2	CUL2	cullin 2	13631	-0.018596528	0.21946375	No
276	NRD1	NRD1	nardilysin (N-arginine dibasic convertase)	13637	-0.018644035	0.21990886	No
277	ZMYND11	ZMYND11	zinc finger, MYND domain containing 11	13667	-0.018909942	0.2191794	No
278	PRTN3	PRTN3	proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen)	13881	-0.02085574	0.20944157	No
279	DEC1	DEC1	deleted in esophageal cancer 1	13961	-0.021702399	0.2063482	No
280	OSMR	OSMR	oncostatin M receptor	14054	-0.022494979	0.20264268	No
281	VHL	VHL	von Hippel-Lindau tumor suppressor	14144	-0.023420185	0.19911954	No
282	ACHE	ACHE	acetylcholinesterase (Yt blood group)	14278	-0.024730179	0.19347356	No
283	IL4	IL4	interleukin 4	14283	-0.024770334	0.19419536	No
284	CAPN1	CAPN1	calpain 1, (mu/I) large subunit	14350	-0.0256449	0.19188985	No
285	BTG4	BTG4	B-cell translocation gene 4	14354	-0.025684085	0.1926949	No
286	OPRM1	OPRM1	opioid receptor, mu 1	14422	-0.026579762	0.19037473	No
287	CDK3	CDK3	cyclin-dependent kinase 3	14448	-0.026796728	0.19013536	No
288	IL3	IL3	interleukin 3 (colony-stimulating factor, multiple)	14598	-0.028505933	0.18383989	No
289	DLG5	DLG5	discs, large homolog 5 (Drosophila)	14629	-0.028868331	0.18343063	No

290	SESN1	SESN1	sestrin 1	14669	-0.029142667	0.1825874	No
291	GML	GML	GPI anchored molecule like protein	14679	-0.029251313	0.18322872	No
292	EVI5	EVI5	ecotropic viral integration site 5	14683	-0.029307252	0.18416823	No
293	CHRM4	CHRM4	cholinergic receptor, muscarinic 4	14707	-0.02950629	0.1841281	No
294	CD40LG	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	14716	-0.029567864	0.18483053	No
295	CDC14A	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	14731	-0.029734731	0.18524306	No
296	CDC16	CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	14811	-0.030523198	0.182477	No
297	IL21	IL21	interleukin 21	14812	-0.030526513	0.18360981	No
298	NAP1L1	NAP1L1	nucleosome assembly protein 1-like 1	14988	-0.032896925	0.17619416	No
299	LGI1	LGI1	leucine-rich, glioma inactivated 1	15020	-0.03330259	0.1759001	No
300	ADRA1D	ADRA1D	adrenergic, alpha-1D-, receptor	15052	-0.033596143	0.17561693	No
301	IGFBP7	IGFBP7	insulin-like growth factor binding protein 7	15164	-0.035080884	0.1714408	No
302	EIF5A	EIF5A	eukaryotic translation initiation factor 5A	15221	-0.035918325	0.17001003	No
303	ADRA1A	ADRA1A	adrenergic, alpha-1A-, receptor	15243	-0.036090989	0.17031296	No
304	IL31RA	IL31RA	interleukin 31 receptor A	15286	-0.0365026	0.1695948	No
305	FGF6	FGF6	fibroblast growth factor 6	15293	-0.03665255	0.17065883	No
306	FGF5	FGF5	fibroblast growth factor 5	15406	-0.038000863	0.16654168	No
307	MPL	MPL	myeloproliferative leukemia virus oncogene	15480	-0.038824845	0.16437982	No
308	CUL4A	CUL4A	cullin 4A	15528	-0.039594535	0.16352963	No
309	SSR1	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	15716	-0.041917346	0.1558565	No
310	SSTR5	SSTR5	somatostatin receptor 5	15720	-0.042039022	0.15726848	No
311	ODZ1	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	15926	-0.044874627	0.14881676	No
312	CD47	CD47	CD47 molecule	15977	-0.045414444	0.1480345	No
313	IL5RA	IL5RA	interleukin 5 receptor, alpha	16002	-0.045741022	0.14854749	No
314	GNRH1	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	16011	-0.045848105	0.14985405	No
315	LIF	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	16138	-0.047530808	0.14539964	No
316	SFTPD	SFTPD	surfactant, pulmonary-associated protein D	16263	-0.049677555	0.14112361	No
317	IL29	IL29	interleukin 29 (interferon, lambda 1)	16385	-0.051480509	0.13706252	No
318	MARK4	MARK4	MAP/microtubule affinity-regulating kinase 4	16506	-0.053092182	0.1331106	No
319	ZFP36L2	ZFP36L2	zinc finger protein 36, C3H type-like 2	16634	-0.055549227	0.1289044	No
320	TGFBR2	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	16656	-0.055906355	0.12994266	No
321	PROK2	PROK2	prokineticin 2	16676	-0.056150336	0.13108867	No
322	CDK9	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	16765	-0.057601675	0.12888332	No
323	CDK2	CDK2	cyclin-dependent kinase 2	16781	-0.057828575	0.13028902	No
324	ADRA1B	ADRA1B	adrenergic, alpha-1B-, receptor	16789	-0.058045365	0.13209757	No

325	ACVRL1	ACVRL1	activin A receptor type II-like 1	16829	-0.058583293	0.13234685	No
326	ENPP7	ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	16884	-0.059567381	0.13189238	No
327	TM4SF4	TM4SF4	transmembrane 4 L six family member 4	16944	-0.060507055	0.13122603	No
328	PRKRIR	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	17022	-0.061765429	0.12971805	No
329	SSTR4	SSTR4	somatostatin receptor 4	17025	-0.061788313	0.13191226	No
330	GLP2R	GLP2R	glucagon-like peptide 2 receptor	17043	-0.062120415	0.13337852	No
331	PLG	PLG	plasminogen	17230	-0.065527178	0.12663087	No
332	CDK5R1	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	17444	-0.069651715	0.11870382	No
333	CDKN2B	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	17591	-0.072521634	0.114189774	No
334	PTHLH	PTHLH	parathyroid hormone-like hormone	17612	-0.073002838	0.11591182	No
335	SPHK1	SPHK1	sphingosine kinase 1	17947	-0.080282651	0.10240778	No
336	TACSTD2	TACSTD2	tumor-associated calcium signal transducer 2	17984	-0.081188291	0.10364397	No
337	EPS15	EPS15	epidermal growth factor receptor pathway substrate 15	18309	-0.089258492	0.09096653	No
338	ADRA2A	ADRA2A	adrenergic, alpha-2A-, receptor	18347	-0.090195641	0.09248762	No
339	TBRG1	TBRG1	transforming growth factor beta regulator 1	18373	-0.091067396	0.09463327	No
340	PRL	PRL	prolactin	18526	-0.095965244	0.09069309	No
341	MDM2	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	18570	-0.097484469	0.092188545	No
342	CSF3	CSF3	colony stimulating factor 3 (granulocyte)	18606	-0.098556504	0.094118595	No
343	IGF1R	IGF1R	insulin-like growth factor 1 receptor	19164	-0.120856248	0.07111493	No

Supplemental Table 7. Gene set enrichment analysis of ACC patients' cohort for genes related to the negative regulation of cell apoptosis (dataset GSE10927).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	SCG2	SCG2	secretogranin II (chromogranin C)	32	0.412185848	0.05129418	Yes
2	GSTP1	GSTP1	glutathione S-transferase pi	89	0.356068641	0.09422191	Yes
3	TNFAIP8	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	321	0.261226714	0.11645308	Yes
4	IL2RB	IL2RB	interleukin 2 receptor, beta	410	0.246092916	0.14371789	Yes
5	CD74	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	442	0.241261616	0.17314312	Yes
6	ANXA1	ANXA1	annexin A1	512	0.230224475	0.19929974	Yes
7	BCL2A1	BCL2A1	BCL2-related protein A1	617	0.21557413	0.22187077	Yes
8	BIRC3	BIRC3	baculoviral IAP repeat-containing 3	680	0.208185136	0.24554268	Yes
9	SNCA	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	718	0.203477532	0.2698302	Yes
10	CCL2	CCL2	chemokine (C-C motif) ligand 2	746	0.201598182	0.29436445	Yes
11	IL6	IL6	interleukin 6 (interferon, beta 2)	765	0.199301854	0.31904316	Yes
12	IL7	IL7	interleukin 7	921	0.185417786	0.3352599	Yes
13	FAIM3	FAIM3	Fas apoptotic inhibitory molecule 3	1164	0.166716486	0.3448355	Yes
14	SEMA4D	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	1178	0.165729195	0.36545303	Yes
15	ASNS	ASNS	asparagine synthetase	1400	0.153782502	0.37439427	Yes
16	NFKB1	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	1487	0.149521858	0.38937324	Yes
17	CLN3	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	1639	0.142353937	0.40026295	Yes
18	BCL3	BCL3	B-cell CLL/lymphoma 3	1853	0.132650033	0.40688455	Yes
19	RASA1	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1909	0.130131677	0.42088902	Yes
20	BCL2L10	BCL2L10	BCL2-like 10 (apoptosis facilitator)	2025	0.126336172	0.43148053	Yes
21	TNFRSF10D	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	2042	0.125862718	0.44683963	Yes
22	BAG1	BAG1	BCL2-associated athanogene	2074	0.12485373	0.4613378	Yes
23	ANXA4	ANXA4	annexin A4	2108	0.123851568	0.47560993	Yes
24	PIM1	PIM1	pim-1 oncogene	2777	0.104350127	0.4564118	Yes
25	SOCS3	SOCS3	suppressor of cytokine signaling 3	2950	0.100399412	0.46089748	Yes
26	FAS	FAS	Fas (TNF receptor superfamily, member 6)	2988	0.099542752	0.47185737	Yes
27	KRT18	KRT18	keratin 18	3059	0.097936563	0.48100188	Yes
28	BNIP1	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	3276	0.093235798	0.48242304	Yes
29	AVEN	AVEN	apoptosis, caspase activation inhibitor	3285	0.092934825	0.49394995	Yes
30	CIAPIN1	CIAPIN1	cytokine induced apoptosis inhibitor 1	3759	0.083455123	0.4815828	Yes
31	DAD1	DAD1	defender against cell death 1	3901	0.080434635	0.48502025	Yes

32	PROC	PROC	protein C (inactivator of coagulation factors Va and VIIIa)	3965	0.079056174	0.4920851	Yes
33	GHRL	GHRL	ghrelin/obestatin preprohormone	4123	0.076217391	0.49420148	Yes
34	HSPB1	HSPB1	heat shock 27kDa protein 1	4289	0.073950745	0.495637	Yes
35	CLCF1	CLCF1	cardiotrophin-like cytokine factor 1	4392	0.072245598	0.49992648	Yes
36	SH3GLB1	SH3GLB1	SH3-domain GRB2-like endophilin B1	4572	0.069263041	0.5000781	Yes
37	TIAF1	TIAF1	TGFB1-induced anti-apoptotic factor 1	4725	0.067000449	0.5012564	Yes
38	PIK3R2	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	4833	0.065514341	0.5044389	Yes
39	BCL2L2	BCL2L2	BCL2-like 2	4845	0.065320849	0.51227856	Yes
40	ACVR1	ACVR1	activin A receptor, type I	5050	0.062554345	0.51035064	Yes
41	BCL2L1	BCL2L1	BCL2-like 1	5232	0.060128078	0.50923336	Yes
42	TXNDC5	TXNDC5	thioredoxin domain containing 5	5399	0.057882886	0.5085597	Yes
43	PAX7	PAX7	paired box gene 7	5463	0.056909494	0.5127847	Yes
44	API5	API5	apoptosis inhibitor 5	5637	0.054723926	0.5113646	No
45	BCL10	BCL10	B-cell CLL/lymphoma 10	5923	0.051277772	0.50404024	No
46	HBXIP	HBXIP	hepatitis B virus x interacting protein	6341	0.046549723	0.48967186	No
47	HSPA1B	HSPA1B	heat shock 70kDa protein 1B	6815	0.041459765	0.4719196	No
48	DFFA	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	6864	0.041000921	0.47483617	No
49	HDAC3	HDAC3	histone deacetylase 3	7835	0.031549904	0.431574	No
50	TNFSF18	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	7862	0.031310402	0.4343209	No
51	TRIAP1	TRIAP1	TP53 regulated inhibitor of apoptosis 1	8333	0.027055824	0.41486794	No
52	CD28	CD28	CD28 molecule	9049	0.020561455	0.3826333	No
53	BCL2	BCL2	B-cell CLL/lymphoma 2	9221	0.019069314	0.37673873	No
54	BRE	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	9399	0.017475726	0.37034717	No
55	BECN1	BECN1	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	9692	0.015112576	0.35804397	No
56	GPX1	GPX1	glutathione peroxidase 1	9795	0.014255677	0.35489732	No
57	NPM1	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	9866	0.013464367	0.3532099	No
58	ARHGDIA	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	10033	0.012189656	0.346677	No
59	BAG4	BAG4	BCL2-associated athanogene 4	10130	0.011358825	0.34345156	No
60	TNF	TNF	tumor necrosis factor (TNF superfamily, member 2)	10388	0.009188766	0.33209568	No
61	HDAC1	HDAC1	histone deacetylase 1	10501	0.008154483	0.327679	No
62	OPA1	OPA1	optic atrophy 1 (autosomal dominant)	10891	0.004681752	0.30930743	No
63	SOD1	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	11050	0.00345061	0.3020441	No
64	TPT1	TPT1	tumor protein, translationally-controlled 1	11101	0.003009678	0.2999915	No
65	IFI6	IFI6	interferon, alpha-inducible protein 6	11512	-1.57E-04	0.28001556	No
66	CFL1	CFL1	cofilin 1 (non-muscle)	11526	-2.45E-04	0.27941296	No
67	BAX	BAX	BCL2-associated X protein	11707	-0.00183459	0.27086943	No
68	AATF	AATF	apoptosis antagonizing transcription factor	11783	-0.002492361	0.26753122	No
69	PRDX2	PRDX2	peroxiredoxin 2	11915	-0.003575593	0.2616007	No
70	ERC1	ERC1	ELKS/RAB6-interacting/CAST family member 1	12205	-0.006080984	0.24828567	No

71	CRYAA	CRYAA	crystallin, alpha A	12294	-0.006901044	0.24487875	No
72	NME5	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	12416	-0.007966447	0.23999901	No
73	CDKN2D	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	12546	-0.009077905	0.23487161	No
74	NUP62	NUP62	nucleoporin 62kDa	12656	-0.010023491	0.23084089	No
75	PPT1	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	12938	-0.012385988	0.21872452	No
76	BRAF	BRAF	v-raf murine sarcoma viral oncogene homolog B1	12968	-0.012630679	0.2189298	No
77	ALOX12	ALOX12	arachidonate 12-lipoxygenase	12972	-0.012648899	0.22040546	No
78	IL2	IL2	interleukin 2	13243	-0.014918946	0.20915036	No
79	RELA	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	13530	-0.017533606	0.1974502	No
80	IL4	IL4	interleukin 4	14283	-0.024770334	0.16395076	No
81	MCL1	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	14324	-0.025252141	0.16523801	No
82	MPO	MPO	myeloperoxidase	14463	-0.026930654	0.16196096	No
83	IL3	IL3	interleukin 3 (colony-stimulating factor, multiple)	14598	-0.028505933	0.15908098	No
84	CD40LG	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	14716	-0.029567864	0.15716629	No
85	RTN4	RTN4	reticulon 4	14724	-0.029670775	0.16062959	No
86	BFAR	BFAR	bifunctional apoptosis regulator	14958	-0.032480717	0.15343097	No
87	ANXA5	ANXA5	annexin A5	15041	-0.033488795	0.15372604	No
88	ALB	ALB	albumin	15067	-0.03378341	0.15683883	No
89	TAX1BP1	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	15186	-0.035461523	0.15563111	No
90	IER3	IER3	immediate early response 3	15440	-0.038352467	0.14821002	No
91	HSP90B1	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	15511	-0.039279148	0.14983284	No
92	PRKCZ	PRKCZ	protein kinase C, zeta	15712	-0.041855119	0.14544575	No
93	SERPINB2	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	15863	-0.044071179	0.14378138	No
94	AKT1S1	AKT1S1	AKT1 substrate 1 (proline-rich)	16023	-0.046010613	0.14192677	No
95	GSK3B	GSK3B	glycogen synthase kinase 3 beta	16466	-0.052606355	0.12711574	No
96	NOL3	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	16631	-0.055510413	0.12623544	No
97	PROK2	PROK2	prokineticin 2	16676	-0.056150336	0.1312897	No
98	DDAH2	DDAH2	dimethylarginine dimethylaminohydrolase 2	16918	-0.060158063	0.12725002	No
99	SPHK1	SPHK1	sphingosine kinase 1	17947	-0.080282651	0.08740814	No
100	CFLAR	CFLAR	CASP8 and FADD-like apoptosis regulator	17979	-0.081036508	0.09628761	No
101	IGF1R	IGF1R	insulin-like growth factor 1 receptor	19164	-0.120856248	0.054040246	No
102	SOCS2	SOCS2	suppressor of cytokine signaling 2	19272	-0.12625657	0.06501171	No

Supplemental Table 8. Gene set enrichment analysis of ACC patients' cohort for genes related to cell proliferation (dataset GSEA49278).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	SCG2	SCG2	secretogranin II (chromogranin C)	88	0.528024495	0.012585526	Yes
2	IGF1	IGF1	insulin-like growth factor 1 (somatomedin C)	165	0.453109026	0.023362676	Yes
3	NANOG	NANOG	Nanog homeobox	197	0.428571761	0.035473235	Yes
4	CXCL10	CXCL10	chemokine (C-X-C motif) ligand 10	239	0.407573014	0.046450302	Yes
5	FZD3	FZD3	frizzled homolog 3 (Drosophila)	259	0.39568767	0.05808276	Yes
6	TGFBI	TGFBI	transforming growth factor, beta-induced, 68kDa	266	0.393182337	0.07024548	Yes
7	ODZ1	ODZ1	odz, odd Oz/ten-m homolog 1(Drosophila)	285	0.386294693	0.08162754	Yes
8	EIF5A2	EIF5A2	eukaryotic translation initiation factor 5A2	341	0.360658169	0.090463325	Yes
9	SCIN	SCIN	scinderin	405	0.345200032	0.09843476	Yes
10	IL7	IL7	interleukin 7	425	0.340098083	0.10830783	Yes
11	RARRES3	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	466	0.32978338	0.11686978	Yes
12	MS4A2	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	467	0.329689175	0.1273043	Yes
13	CD3E	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	639	0.293033749	0.12856069	Yes
14	TM4SF4	TM4SF4	transmembrane 4 L six family member 4	752	0.272762805	0.13194196	Yes
15	KITLG	KITLG	KIT ligand	757	0.271673501	0.14035276	Yes
16	PTPRC	PTPRC	protein tyrosine phosphatase, receptor type, C	779	0.270001113	0.1479135	Yes
17	LDOC1	LDOC1	leucine zipper, down-regulated in cancer 1	784	0.269550681	0.15625711	Yes
18	TNFSF15	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	788	0.269046128	0.16463163	Yes
19	TNFRSF17	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	792	0.268756866	0.17299701	Yes
20	APPL2	null	null	954	0.250093699	0.17336325	Yes
21	EPS8	EPS8	epidermal growth factor receptor pathway substrate 8	986	0.247000024	0.17972715	Yes
22	TCFL5	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	1005	0.244927987	0.18663502	Yes
23	LYN	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	1046	0.240037933	0.19235656	Yes
24	LY86	LY86	lymphocyte antigen 86	1059	0.23850809	0.19934256	Yes
25	CSF1	CSF1	colony stimulating factor 1 (macrophage)	1124	0.232157439	0.20368937	Yes
26	FABP3	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	1133	0.231597304	0.2106442	Yes
27	PAWR	PAWR	PRKC, apoptosis, WT1, regulator	1137	0.2314042	0.21782738	Yes
28	FABP6	FABP6	fatty acid binding protein 6, ileal (gastrotropin)	1222	0.224540159	0.22099532	Yes
29	AIF1	AIF1	allograft inflammatory factor 1	1259	0.221519202	0.2263183	Yes
30	MCTS1	MCTS1	malignant T cell amplified sequence 1	1337	0.215719551	0.2295353	Yes

31	PTHLH	PTHLH	parathyroid hormone-like hormone	1339	0.215710402	0.23631555	Yes
32	NDP	NDP	Norrie disease (pseudoglioma)	1402	0.210322991	0.24006507	Yes
33	IL15	IL15	interleukin 15	1412	0.209720567	0.24628063	Yes
34	BST2	BST2	bone marrow stromal cell antigen 2	1417	0.209491074	0.25272337	Yes
35	EHF	EHF	ets homologous factor	1543	0.201949224	0.25325388	Yes
36	LRPAP1	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	1547	0.201800555	0.25950012	Yes
37	EMP3	EMP3	epithelial membrane protein 3	1562	0.200570658	0.26519164	Yes
38	CD74	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	1578	0.199223205	0.27079365	Yes
39	EDN1	EDN1	endothelin 1	1596	0.198184133	0.27626896	Yes
40	CD274	CD274	CD274 molecule	1625	0.196526065	0.28117603	Yes
41	SYK	SYK	spleen tyrosine kinase	1726	0.190620273	0.2825202	Yes
42	ATP8A2	ATP8A2	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2	1759	0.188890845	0.28699806	Yes
43	SSTR1	SSTR1	somatostatin receptor 1	1764	0.188562289	0.29277843	Yes
44	CSF1R	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	1850	0.184305429	0.29462606	Yes
45	ERBB4	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	1891	0.182185233	0.2985166	Yes
46	TNFSF9	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	1944	0.17837213	0.30172378	Yes
47	NDUFS4	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	1968	0.177008122	0.30624756	Yes
48	RERG	RERG	RAS-like, estrogen-regulated, growth inhibitor	2051	0.172863454	0.30787373	Yes
49	TGFBR2	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	2138	0.169005066	0.3091902	Yes
50	BTC	BTC	betacellulin	2203	0.166291788	0.3114524	Yes
51	PPARD	PPARD	peroxisome proliferative activated receptor, delta	2457	0.155404568	0.30450797	Yes
52	PRDM4	PRDM4	PR domain containing 4	2463	0.155119419	0.309183	Yes
53	IL18	IL18	interleukin 18 (interferon-gamma-inducing factor)	2492	0.154062182	0.3127461	Yes
54	CREG1	CREG1	cellular repressor of E1A-stimulated genes 1	2546	0.151779652	0.31506476	Yes
55	DEC1	DEC1	deleted in esophageal cancer 1	2561	0.151311368	0.31919724	Yes
56	GAB1	GAB1	GRB2-associated binding protein 1	2573	0.15067476	0.32345027	Yes
57	GAS8	GAS8	growth arrest-specific 8	2596	0.149782225	0.32715926	Yes
58	ADRA1B	ADRA1B	adrenergic, alpha-1B-, receptor	2633	0.148645893	0.33017582	Yes
59	IL6R	IL6R	interleukin 6 receptor	2666	0.147008657	0.33332816	Yes
60	HCLS1	HCLS1	hematopoietic cell-specific Lyn substrate 1	2688	0.146225855	0.33697146	Yes
61	CDKN1A	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2811	0.141815111	0.3357394	Yes
62	CTF1	CTF1	cardiotrophin 1	2817	0.141544431	0.33998477	Yes
63	PIM2	PIM2	pim-2 oncogene	2848	0.140406951	0.34302193	Yes
64	VIP	VIP	vasoactive intestinal peptide	2860	0.140080556	0.34693965	Yes
65	ING4	ING4	inhibitor of growth family, member 4	2929	0.137330174	0.34809765	Yes
66	CD86	CD86	CD86 molecule	3056	0.133393303	0.34641147	Yes

67	GAS6	GAS6	growth arrest-specific 6	3162	0.130697861	0.3456247	Yes
68	TIMP1	TIMP1	TIMP metallopeptidase inhibitor 1	3180	0.130131975	0.34894618	Yes
69	POLA1	POLA1	polymerase (DNA directed), alpha 1	3268	0.127477482	0.34890145	Yes
70	REG1A	REG1A	regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)	3337	0.1256928	0.34969112	Yes
71	CDK5	CDK5	cyclin-dependent kinase 5	3490	0.121766418	0.34641787	Yes
72	RPS4X	RPS4X	ribosomal protein S4, X-linked	3515	0.12092831	0.34911987	Yes
73	CAPN1	CAPN1	calpain 1, (mu/I) large subunit	3543	0.120177872	0.35165745	Yes
74	COL4A3	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	3581	0.119040176	0.35369012	Yes
75	IL1B	IL1B	interleukin 1, beta	3655	0.116936028	0.3539682	Yes
76	SSTR3	SSTR3	somatostatin receptor 3	3741	0.114785895	0.35361558	Yes
77	CD79A	CD79A	CD79a molecule, immunoglobulin-associated alpha	3773	0.114015445	0.35577056	Yes
78	CXCL5	CXCL5	chemokine (C-X-C motif) ligand 5	3780	0.11383687	0.35909212	Yes
79	DNAJA2	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	3960	0.109229386	0.35415608	Yes
80	ADRA2A	ADRA2A	adrenergic, alpha-2A-, receptor	4023	0.107724033	0.35465837	Yes
81	TGFA	TGFA	transforming growth factor, alpha	4089	0.105862737	0.3549611	Yes
82	TUSC2	TUSC2	tumor suppressor candidate 2	4114	0.105219945	0.35716593	Yes
83	S100A11	S100A11	S100 calcium binding protein A11	4259	0.101829134	0.35363677	Yes
84	IL2RA	IL2RA	interleukin 2 receptor, alpha	4290	0.100925691	0.35542437	Yes
85	GML	GML	GPI anchored molecule like protein	4384	0.09892308	0.35419458	Yes
86	FOXO4	null	null	4429	0.097892947	0.35522974	Yes
87	CDK7	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	4440	0.09777192	0.3578553	Yes
88	FLT3LG	FLT3LG	fms-related tyrosine kinase 3 ligand	4462	0.097274549	0.35994932	Yes
89	ACHE	ACHE	acetylcholinesterase (Yt blood group)	4560	0.095479816	0.358423	Yes
90	FGF5	FGF5	fibroblast growth factor 5	4652	0.093706019	0.35712186	Yes
91	SERTAD1	SERTAD1	SERTA domain containing 1	4662	0.093544014	0.35966048	Yes
92	IL21	IL21	interleukin 21	4704	0.09272325	0.36067268	Yes
93	IFITM1	IFITM1	interferon induced transmembrane protein 1 (9-27)	4804	0.090650991	0.35889974	Yes
94	MT3	MT3	metallothionein 3 (growth inhibitory factor (neurotrophic))	4888	0.089096226	0.3578278	Yes
95	NUDC	NUDC	nuclear distribution gene C homolog (A. nidulans)	4891	0.089074917	0.36055323	Yes
96	CDC14A	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	4914	0.088645652	0.36232728	Yes
97	APC	APC	adenomatosis polyposis coli	5048	0.086126611	0.35881692	Yes
98	INSL4	INSL4	insulin-like 4 (placenta)	5120	0.084426954	0.35815987	Yes
99	MAGED1	MAGED1	melanoma antigen family D, 1	5153	0.083798811	0.35931164	Yes
100	GFI1B	GFI1B	growth factor independent 1B (potential regulator of CDKN1A, translocated in CML)	5156	0.08374583	0.36186838	Yes
101	AGGF1	AGGF1	angiogenic factor with G patch and FHA domains 1	5204	0.082986191	0.36229107	Yes
102	EBI3	EBI3	Epstein-Barr virus induced gene 3	5398	0.07960777	0.35576105	Yes
103	FES	FES	feline sarcoma oncogene	5466	0.078335702	0.35509878	Yes

104	PTK2B	PTK2B	PTK2B protein tyrosine kinase 2 beta	5490	0.078015648	0.3564895	Yes
105	GNRH1	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	5578	0.076376759	0.35482746	Yes
106	CD33	CD33	CD33 molecule	5583	0.076310657	0.3570551	Yes
107	FABP7	FABP7	fatty acid binding protein 7, brain	5656	0.075128973	0.3560569	Yes
108	BMP10	BMP10	bone morphogenetic protein 10	5666	0.074994437	0.35800844	Yes
109	NCK1	NCK1	NCK adaptor protein 1	5711	0.074164227	0.3582926	Yes
110	CD28	CD28	CD28 molecule	5743	0.073815741	0.3591753	Yes
111	FGFBP1	FGFBP1	fibroblast growth factor binding protein 1	5786	0.073134802	0.35952064	Yes
112	IL12RB1	IL12RB1	interleukin 12 receptor, beta 1	5822	0.072503202	0.3601742	Yes
113	GPX1	GPX1	glutathione peroxidase 1	5849	0.072189413	0.36123988	Yes
114	TNFRSF11A	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	5856	0.07208354	0.36323994	Yes
115	RASGRP4	RASGRP4	RAS guanyl releasing protein 4	5944	0.070813656	0.36140183	No
116	NPM1	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	6055	0.068857245	0.35842335	No
117	MXD4	MXD4	MAX dimerization protein 4	6068	0.068619534	0.36003247	No
118	CCKBR	CCKBR	cholecystokinin B receptor	6138	0.067341849	0.35892847	No
119	PROK2	PROK2	prokineticin 2	6219	0.066174619	0.35727176	No
120	FOXP3	FOXP3	forkhead box P3	6292	0.065065689	0.35595506	No
121	PLG	PLG	plasminogen	6317	0.064623311	0.35687503	No
122	POU1F1	POU1F1	POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)	6344	0.064182088	0.35768723	No
123	IL3	IL3	interleukin 3 (colony-stimulating factor, multiple)	6430	0.062913448	0.35569286	No
124	DUSP22	DUSP22	dual specificity phosphatase 22	6476	0.06238633	0.35555738	No
125	BCAR1	BCAR1	breast cancer anti-estrogen resistance 1	6536	0.061431218	0.3547352	No
126	VHL	VHL	von Hippel-Lindau tumor suppressor	6676	0.059123386	0.35008886	No
127	CDK5R1	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	6684	0.059034295	0.35162905	No
128	MDM2	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	6769	0.057745967	0.34951803	No
129	IL11	IL11	interleukin 11	6775	0.057650555	0.3511082	No
130	SSTR2	SSTR2	somatostatin receptor 2	6826	0.056861244	0.35056338	No
131	UTP20	UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	6838	0.056720529	0.3518428	No
132	LMO1	LMO1	LIM domain only 1 (rhombotin 1)	6943	0.055119812	0.34871086	No
133	FGF7	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	6970	0.054781642	0.34922555	No
134	MYO16	null	null	6986	0.054480046	0.3502465	No
135	PEMT	PEMT	phosphatidylethanolamine N-methyltransferase	7021	0.053992491	0.3503611	No
136	BAI1	BAI1	brain-specific angiogenesis inhibitor 1	7290	0.050045792	0.3393788	No
137	DLG5	DLG5	discs, large homolog 5 (Drosophila)	7414	0.048313707	0.3351406	No
138	CAPNS1	CAPNS1	calpain, small subunit 1	7439	0.04786611	0.3355302	No
139	ZMYND11	ZMYND11	zinc finger, MYND domain containing 11	7455	0.047683381	0.33633602	No
140	ZEB1	null	null	7461	0.047621418	0.33760875	No
141	MAS1	MAS1	MAS1 oncogene	7507	0.046950784	0.33698472	No

142	RBBP7	RBBP7	retinoblastoma binding protein 7	7513	0.046874199	0.33823383	No
143	FGF6	FGF6	fibroblast growth factor 6	7534	0.04657688	0.3387702	No
144	STAMBP	STAMBP	STAM binding protein	7538	0.046561815	0.3401032	No
145	PDAP1	PDAP1	PDGFA associated protein 1	7570	0.046173569	0.34011102	No
146	OPRM1	OPRM1	opioid receptor, mu 1	7732	0.043573722	0.33394098	No
147	ADAMTS8	ADAMTS8	ADAM metallopeptidase with thrombospondin type 1 motif, 8	7790	0.042793784	0.33262274	No
148	ERBB2	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	7967	0.040056281	0.32563803	No
149	ATPIF1	ATPIF1	ATPase inhibitory factor 1	7981	0.039835516	0.32628927	No
150	CUL1	CUL1	cullin 1	8047	0.039010957	0.32447615	No
151	KRT4	KRT4	keratin 4	8083	0.038538091	0.32405478	No
152	ABI1	ABI1	abl-interactor 1	8100	0.038236063	0.3245147	No
153	SLC29A2	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	8137	0.037737481	0.32402107	No
154	CGREF1	CGREF1	cell growth regulator with EF-hand domain 1	8143	0.037700683	0.32497984	No
155	CRTAM	CRTAM	cytotoxic and regulatory T cell molecule	8155	0.037584215	0.32565358	No
156	ADRA1A	ADRA1A	adrenergic, alpha-1A-, receptor	8192	0.03728237	0.32514554	No
157	DLEC1	DLEC1	deleted in lung and esophageal cancer 1	8241	0.036586333	0.32405284	No
158	PCNA	PCNA	proliferating cell nuclear antigen	8285	0.035969004	0.323175	No
159	IL5RA	IL5RA	interleukin 5 receptor, alpha	8468	0.033700049	0.3157078	No
160	NCK2	NCK2	NCK adaptor protein 2	8554	0.032405566	0.31274787	No
161	DKC1	DKC1	dyskeratosis congenita 1, dyskerin	8596	0.031789038	0.31183153	No
162	CTNNBIP1	CTNNBIP1	catenin, beta interacting protein 1	8609	0.03166442	0.31227103	No
163	AIMP1	null	null	8651	0.030933147	0.3113276	No
164	CBFA2T3	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	8777	0.029478479	0.3063995	No
165	CTBP1	CTBP1	C-terminal binding protein 1	8780	0.029432166	0.3072372	No
166	KRT2	KRT2	keratin 2 (epidermal ichthyosis bullosa of Siemens)	8794	0.029229943	0.30755278	No
167	S1PR2	null	null	8815	0.028985383	0.30753237	No
168	JAG2	JAG2	jagged 2	8831	0.028719028	0.30773798	No
169	E4F1	E4F1	E4F transcription factor 1	8865	0.02815721	0.30708182	No
170	CD160	CD160	CD160 molecule	8893	0.027754797	0.30669424	No
171	SRA1	SRA1	steroid receptor RNA activator 1	9071	0.025680745	0.2992077	No
172	GCG	GCG	glucagon	9148	0.024757748	0.2964277	No
173	MATK	MATK	megakaryocyte-associated tyrosine kinase	9166	0.024550863	0.2964076	No
174	NAP1L1	NAP1L1	nucleosome assembly protein 1-like 1	9232	0.023739353	0.2941112	No
175	CD24	CD24	CD24 molecule	9244	0.023602095	0.2943424	No
176	IFRD2	IFRD2	interferon-related developmental regulator 2	9255	0.023445139	0.29461554	No
177	EVI5	EVI5	ecotropic viral integration site 5	9279	0.023190401	0.29427105	No
178	MPL	MPL	myeloproliferative leukemia virus oncogene	9301	0.022921909	0.29401186	No
179	CSF3	CSF3	colony stimulating factor 3 (granulocyte)	9303	0.022906447	0.29468995	No
180	CLEC11A	CLEC11A	C-type lectin domain family	9385	0.02180038	0.29158193	No

			11, member A				
181	MFN2	MFN2	mitofusin 2	9426	0.021287832	0.29038012	No
182	CDK4	CDK4	cyclin-dependent kinase 4	9441	0.021035461	0.29038942	No
183	ENPP7	ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	9465	0.020708427	0.2899664	No
184	EGR4	EGR4	early growth response 4	9498	0.02035578	0.2891102	No
185	ERF	ERF	Ets2 repressor factor	9510	0.020234678	0.28923485	No
186	KHDRBS1	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	9577	0.019383455	0.28675365	No
187	IGFBP7	IGFBP7	insulin-like growth factor binding protein 7	9583	0.019324681	0.28713083	No
188	APPL1	null	null	9584	0.019321905	0.28774235	No
189	SSTR5	SSTR5	somatostatin receptor 5	9590	0.019260006	0.2881175	No
190	IGFBP4	IGFBP4	insulin-like growth factor binding protein 4	9605	0.019042728	0.28806373	No
191	B4GALT7	B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	9642	0.018687377	0.2869672	No
192	RBBP4	RBBP4	retinoblastoma binding protein 4	9771	0.017206419	0.28150997	No
193	IL31RA	IL31RA	interleukin 31 receptor A	9800	0.016836526	0.28072995	No
194	IL9	IL9	interleukin 9	9809	0.016777726	0.28088585	No
195	BTG4	BTG4	B-cell translocation gene 4	9886	0.015942845	0.27782688	No
196	RUNX3	RUNX3	runt-related transcription factor 3	9887	0.015923485	0.27833086	No
197	TNFRSF8	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	9939	0.015352215	0.2764254	No
198	MAPRE1	MAPRE1	microtubule-associated protein, RP/EB family, member 1	9952	0.015192938	0.27634358	No
199	RHOG	RHOG	ras homolog gene family, member G (rho G)	9953	0.015168027	0.27682364	No
200	PYY	PYY	peptide YY	10046	0.01410914	0.27295643	No
201	SFTPD	SFTPD	surfactant, pulmonary-associated protein D	10091	0.013406688	0.27131763	No
202	SESN1	SESN1	sestrin 1	10140	0.012726153	0.26946974	No
203	SSTR4	SSTR4	somatostatin receptor 4	10223	0.011786865	0.2659979	No
204	TNFRSF9	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	10239	0.011632931	0.26566273	No
205	CDC27	CDC27	cell division cycle 27	10325	0.010466292	0.26200843	No
206	ZNF259	ZNF259	zinc finger protein 259	10365	0.009949706	0.26049465	No
207	OSMR	OSMR	oncostatin M receptor	10368	0.009936164	0.26071537	No
208	GHRL	GHRL	ghrelin/obestatin preprohormone	10385	0.009810757	0.26027563	No
209	FGF4	FGF4	fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene)	10438	0.009250442	0.2581302	No
210	PPM1D	PPM1D	protein phosphatase 1D magnesium-dependent, delta isoform	10593	0.007586553	0.25114942	No
211	LRP1	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	10644	0.007028555	0.24902742	No
212	SLAMF1	SLAMF1	signaling lymphocytic activation molecule family member 1	10653	0.006913853	0.24887112	No
213	EIF2AK2	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	10706	0.006356344	0.24663408	No
214	IL12B	IL12B	interleukin 12B (natural killer cell stimulatory factor 2,	10807	0.005214456	0.24211022	No

			cytotoxic lymphocyte maturation factor 2, p40)				
215	IL27	IL27	interleukin 27	10815	0.005176412	0.24194583	No
216	IL2	IL2	interleukin 2	10855	0.004608519	0.24026302	No
217	SIRPG	SIRPG	signal-regulatory protein gamma	10930	0.003745039	0.23691177	No
218	IL9R	IL9R	interleukin 9 receptor	11059	0.002120954	0.23097712	No
219	TACSTD2	TACSTD2	tumor-associated calcium signal transducer 2	11071	0.001951047	0.23052308	No
220	SSR1	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	11074	0.001911267	0.2304898	No
221	CD47	CD47	CD47 molecule	11141	0.001174588	0.22743231	No
222	BNC1	BNC1	basonuclin 1	11197	3.90E-04	0.22486575	No
223	NRD1	NRD1	nardilysin (N-arginine dibasic convertase)	11286	-4.85E-04	0.22075488	No
224	IGF1R	IGF1R	insulin-like growth factor 1 receptor	11357	-0.001375641	0.21751618	No
225	PIM1	PIM1	pim-1 oncogene	11361	-0.001455182	0.21742158	No
226	CXCL1	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	11391	-0.001828295	0.21611966	No
227	FLT4	FLT4	fms-related tyrosine kinase 4	11399	-0.001980319	0.21585412	No
228	IL15RA	IL15RA	interleukin 15 receptor, alpha	11460	-0.002804625	0.21312955	No
229	LGI1	LGI1	leucine-rich, glioma inactivated 1	11482	-0.003088171	0.21224262	No
230	EGFR	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	11514	-0.003537639	0.21090102	No
231	GLI1	GLI1	glioma-associated oncogene homolog 1 (zinc finger protein)	11559	-0.004149484	0.20896925	No
232	ADRA1D	ADRA1D	adrenergic, alpha-1D-, receptor	11576	-0.004366441	0.20835721	No
233	ACVRL1	ACVRL1	activin A receptor type II-like 1	11609	-0.004870047	0.20701091	No
234	CDC25B	CDC25B	cell division cycle 25B	11611	-0.004885202	0.20711863	No
235	UMOD	UMOD	uromodulin (uromucoid, Tamm-Horsfall glycoprotein)	11798	-0.007333958	0.19862941	No
236	EPS15	EPS15	epidermal growth factor receptor pathway substrate 15	11808	-0.007467886	0.19844377	No
237	CNOT8	CNOT8	CCR4-NOT transcription complex, subunit 8	11867	-0.008171789	0.19598284	No
238	TIPIN	TIPIN	TIMELESS interacting protein	11916	-0.008841908	0.19401202	No
239	TXN	TXN	thioredoxin	11921	-0.008901022	0.19410618	No
240	RAF1	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	11945	-0.0090606	0.1933145	No
241	IL29	IL29	interleukin 29 (interferon, lambda 1)	11958	-0.009283854	0.19304566	No
242	NAMPT	null	null	11967	-0.009353611	0.19296658	No
243	REG1B	REG1B	regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	11985	-0.009493417	0.19246994	No
244	ERG	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	12062	-0.01043979	0.18923679	No
245	CSE1L	CSE1L	CSE1 chromosome segregation 1-like (yeast)	12063	-0.010440956	0.18956724	No
246	ALOX12	ALOX12	arachidonate 12-lipoxygenase	12129	-0.011076838	0.18687004	No
247	ZFP36L2	ZFP36L2	zinc finger protein 36, C3H type-like 2	12324	-0.013471508	0.17819996	No
248	SPDYA	SPDYA	speedy homolog A	12352	-0.013731953	0.17736857	No

			(Drosophila)				
249	TBRG4	TBRG4	transforming growth factor beta regulator 4	12432	-0.014684207	0.1741291	No
250	ICOSLG	ICOSLG	inducible T-cell co-stimulator ligand	12453	-0.014981631	0.17366548	No
251	CDC16	CDC16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	12455	-0.01499039	0.17409302	No
252	CDKN2D	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	12563	-0.016349485	0.16959336	No
253	CUL2	CUL2	cullin 2	12700	-0.018184055	0.16379198	No
254	MARK4	MARK4	MAP/microtubule affinity-regulating kinase 4	12704	-0.018218143	0.16422792	No
255	PRKRIR	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	12722	-0.018364217	0.16401203	No
256	OSM	OSM	oncostatin M	12729	-0.018465109	0.1643151	No
257	POU3F2	POU3F2	POU domain, class 3, transcription factor 2	12777	-0.019128788	0.16271675	No
258	PRDX1	PRDX1	peroxiredoxin 1	12807	-0.019464379	0.16197301	No
259	FTH1	FTH1	ferritin, heavy polypeptide 1	12808	-0.019464577	0.16258906	No
260	MST1R	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	12846	-0.019940272	0.16148527	No
261	GPNMB	GPNMB	glycoprotein (transmembrane) nmb	12865	-0.020262079	0.16128255	No
262	TBRG1	TBRG1	transforming growth factor beta regulator 1	12877	-0.020431403	0.16141342	No
263	ARTN	ARTN	artemin	12921	-0.020900715	0.16005869	No
264	DHPS	DHPS	deoxyhypusine synthase	12922	-0.020907035	0.1607204	No
265	TSPO	TSPO	translocator protein (18kDa)	12995	-0.021807577	0.1580346	No
266	CD40LG	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	13002	-0.021888943	0.15844603	No
267	ELF4	ELF4	E74-like factor 4 (ets domain transcription factor)	13100	-0.023208585	0.15463234	No
268	MNT	MNT	MAX binding protein	13125	-0.02354574	0.15425223	No
269	GLP2R	GLP2R	glucagon-like peptide 2 receptor	13146	-0.02383741	0.15406889	No
270	FLT3	FLT3	fms-related tyrosine kinase 3	13151	-0.023950618	0.15463936	No
271	LAMP3	LAMP3	lysosomal-associated membrane protein 3	13284	-0.02554499	0.14925851	No
272	SPHK1	SPHK1	sphingosine kinase 1	13377	-0.026647178	0.1457881	No
273	IL4	IL4	interleukin 4	13385	-0.026708486	0.14630519	No
274	HGS	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	13457	-0.027732605	0.14385381	No
275	PRG4	PRG4	proteoglycan 4	13513	-0.028605865	0.14218028	No
276	MAP3K11	MAP3K11	mitogen-activated protein kinase kinase kinase 11	13549	-0.029045444	0.14145844	No
277	CUL4A	CUL4A	cullin 4A	13612	-0.029651131	0.13948977	No
278	TRAIP	TRAIP	TRAF interacting protein	13630	-0.029986875	0.13964173	No
279	RPS27	RPS27	ribosomal protein S27 (metallopanstimulin 1)	13638	-0.0301228	0.14026688	No
280	PA2G4	PA2G4	proliferation-associated 2G4, 38kDa	13647	-0.030252162	0.14084925	No
281	CHRNA10	CHRNA10	cholinergic receptor, nicotinic, alpha 10	13836	-0.032537669	0.13306393	No
282	S100B	S100B	S100 calcium binding protein B	13859	-0.032822642	0.1330712	No
283	CDK10	CDK10	cyclin-dependent kinase (CDC2-like) 10	13928	-0.033611953	0.13094656	No
284	TCIRG1	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	13965	-0.034129966	0.13033876	No

285	HTR1A	HTR1A	5-hydroxytryptamine (serotonin) receptor 1A	14065	-0.035420097	0.12681778	No
286	EIF5A	EIF5A	eukaryotic translation initiation factor 5A	14073	-0.035506785	0.12761334	No
287	EPHB4	EPHB4	EPH receptor B4	14084	-0.035623845	0.12827192	No
288	THPO	THPO	thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	14092	-0.035756849	0.1290754	No
289	CUL5	CUL5	cullin 5	14222	-0.037620284	0.12421738	No
290	TP53I11	TP53I11	tumor protein p53 inducible protein 11	14296	-0.038501248	0.12201304	No
291	CDK9	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	14306	-0.038669936	0.12281493	No
292	RAPGEF3	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	14356	-0.039359428	0.12176308	No
293	PRTN3	PRTN3	proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen)	14411	-0.040032703	0.1204981	No
294	PRL	PRL	prolactin	14509	-0.041352704	0.11725867	No
295	CDK2	CDK2	cyclin-dependent kinase 2	14536	-0.04187157	0.11736477	No
296	FGF18	FGF18	fibroblast growth factor 18	14676	-0.043856949	0.11223527	No
297	LIF	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	14826	-0.046171289	0.10671012	No
298	CHRM4	CHRM4	cholinergic receptor, muscarinic 4	14871	-0.046956711	0.10613317	No
299	CUL3	CUL3	cullin 3	14895	-0.047236741	0.10654975	No
300	CDKN2B	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	14950	-0.047930207	0.10553472	No
301	GNL3	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	15282	-0.05287857	0.09168807	No
302	RARRES1	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	15330	-0.053544387	0.091178946	No
303	SFN	SFN	stratifin	15462	-0.055465557	0.086791955	No
304	DERL2	DERL2	Der1-like domain family, member 2	15631	-0.05802938	0.080751225	No
305	VIPR1	VIPR1	vasoactive intestinal peptide receptor 1	15638	-0.058087915	0.08230835	No
306	GPC4	GPC4	glypican 4	15707	-0.059067633	0.08098937	No
307	MNAT1	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	15874	-0.061676774	0.07515785	No
308	NPY	NPY	neuropeptide Y	16310	-0.069361366	0.05695643	No
309	IL6	IL6	interleukin 6 (interferon, beta 2)	16656	-0.07504721	0.043154962	No
310	VTI1B	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	16739	-0.07632897	0.04172585	No
311	BAP1	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	16777	-0.07719399	0.04243412	No
312	ALOX15B	ALOX15B	arachidonate 15-lipoxygenase, type B	16778	-0.077236906	0.044878636	No
313	REG3A	REG3A	regenerating islet-derived 3 alpha	16860	-0.07862132	0.04356896	No
314	BNIPL	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	16939	-0.080603831	0.042462703	No
315	LRP5	LRP5	low density lipoprotein receptor-related protein 5	17412	-0.09000086	0.023179622	No
316	CHRM1	CHRM1	cholinergic receptor, muscarinic 1	17431	-0.090610169	0.025203396	No
317	TRIM27	TRIM27	tripartite motif-containing 27	17525	-0.093101576	0.023789352	No

318	BIN1	BIN1	bridging integrator 1	17576	-0.094351873	0.024431102	No
319	KRT16	KRT16	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)	17727	-0.097456351	0.020482216	No
320	ETS1	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	17811	-0.099561855	0.019741526	No
321	CRIP1	CRIP1	cysteine-rich protein 1 (intestinal)	18118	-0.106506787	0.008764412	No
322	NAB2	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	18355	-0.113671437	0.00129628	No
323	ARHGEF2	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	18545	-0.118463278	-0.003816414	No
324	EMP2	EMP2	epithelial membrane protein 2	18708	-0.123332866	-0.007508986	No
325	CGRRF1	CGRRF1	cell growth regulator with ring finger domain 1	18904	-0.130409956	-0.012524906	No
326	WARS	WARS	tryptophanyl-tRNA synthetase	19122	-0.138682723	-0.018310552	No
327	DTYMK	DTYMK	deoxythymidylate kinase (thymidylate kinase)	19242	-0.143337071	-0.019353775	No
328	PDGFA	PDGFA	platelet-derived growth factor alpha polypeptide	19276	-0.14433825	-0.016332865	No
329	KLF4	KLF4	Kruppel-like factor 4 (gut)	19825	-0.168869585	-0.036683343	No
330	PRMT5	PRMT5	protein arginine methyltransferase 5	20307	-0.198735148	-0.05294703	No
331	CDCA7	CDCA7	cell division cycle associated 7	20339	-0.200911999	-0.048041806	No
332	EREG	EREG	epiregulin	20576	-0.219129354	-0.05217224	No
333	ISG20	ISG20	interferon stimulated exonuclease gene 20kDa	20933	-0.262792706	-0.06054742	No
334	CHEK1	CHEK1	CHK1 checkpoint homolog (S. pombe)	21201	-0.319178194	-0.06296491	No
335	FOSL1	FOSL1	FOS-like antigen 1	21384	-0.373894244	-0.059665095	No
336	CDC6	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	21428	-0.394535273	-0.049194444	No
337	TPX2	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	21429	-0.395684868	-0.036671188	No
338	CDC25C	CDC25C	cell division cycle 25C	21458	-0.413165182	-0.024907574	No
339	PLK1	PLK1	polo-like kinase 1 (Drosophila)	21558	-0.52869755	-0.012816524	No
340	CDKN3	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	21582	-0.563470125	0.003938621	No

Supplemental Table 9. Gene set enrichment analysis of ACC patients' cohort for genes related to the negative regulation of cell apoptosis (dataset GSEA49278).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	NME5	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	4	0.860342324	0.098880835	Yes
2	SCG2	SCG2	secretogranin II (chromogranin C)	88	0.528024495	0.15583326	Yes
3	SNCA	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	161	0.456243515	0.20503029	Yes
4	IL7	IL7	interleukin 7	425	0.340098083	0.23199776	Yes
5	FAS	FAS	Fas (TNF receptor superfamily, member 6)	523	0.317924172	0.26410854	Yes
6	ANXA1	ANXA1	annexin A1	690	0.283001095	0.2889988	Yes
7	ALB	ALB	albumin	1207	0.225458503	0.29103547	Yes
8	BCL2L1	BCL2L1	BCL2-like 1	1316	0.217199907	0.3110381	Yes
9	BIRC3	BIRC3	baculoviral IAP repeat-containing 3	1323	0.216733977	0.33571628	Yes
10	CD74	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	1578	0.199223205	0.34687963	Yes
11	RASA1	RASA1	RAS p21 protein activator (GTPase activating protein) 1	1793	0.187307358	0.3585255	Yes
12	HSPB1	HSPB1	heat shock 27kDa protein 1	2237	0.163989902	0.35686886	Yes
13	ANXA4	ANXA4	annexin A4	2559	0.151462734	0.35942626	Yes
14	KRT18	KRT18	keratin 18	3507	0.121187449	0.32947305	Yes
15	NUAK2	NUAK2	NUAK family, SNF1-like kinase, 2	3542	0.120194972	0.3417368	Yes
16	PIK3R2	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	3548	0.120098911	0.35533407	Yes
17	CLN3	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	3686	0.115952492	0.36233371	Yes
18	HBXIP	HBXIP	hepatitis B virus x interacting protein	3844	0.112197995	0.36797372	Yes
19	DFFA	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	3955	0.109345391	0.37546444	Yes
20	IER3	IER3	immediate early response 3	3981	0.108642817	0.38681525	Yes
21	SOCS2	SOCS2	suppressor of cytokine signaling 2	4339	0.099894404	0.38176554	Yes
22	BCL2L10	BCL2L10	BCL2-like 10 (apoptosis facilitator)	4773	0.09131366	0.37220404	Yes
23	IL2RB	IL2RB	interleukin 2 receptor, beta	5038	0.086299635	0.36990088	Yes
24	NAIP	NAIP	-	5248	0.082110353	0.3696654	Yes
25	HDAC3	HDAC3	histone deacetylase 3	5260	0.081986189	0.3785959	Yes
26	BRAF	BRAF	v-raf murine sarcoma viral oncogene homolog B1	5307	0.081282407	0.38582256	Yes
27	TRIAP1	TRIAP1	TP53 regulated inhibitor of apoptosis 1	5498	0.07790155	0.3859834	Yes
28	BCL2	BCL2	B-cell CLL/lymphoma 2	5560	0.076706842	0.39198774	Yes
29	CD28	CD28	CD28 molecule	5743	0.073815741	0.392049	Yes
30	PRKCZ	PRKCZ	protein kinase C, zeta	5796	0.073033877	0.39804772	Yes
31	NFKB1	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	5810	0.072698802	0.40581605	Yes
32	GPX1	GPX1	glutathione peroxidase 1	5849	0.072189413	0.4123666	Yes
33	NOL3	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	6034	0.069300607	0.41181526	Yes
34	NPM1	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	6055	0.068857245	0.4188167	Yes

35	CD27	null	null	6079	0.068466067	0.425634	Yes
36	MCL1	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	6080	0.068434715	0.4335141	Yes
37	BCL3	BCL3	B-cell CLL/lymphoma 3	6103	0.068020105	0.4403264	Yes
38	TNF	TNF	tumor necrosis factor (TNF superfamily, member 2)	6189	0.066427469	0.44403434	Yes
39	PROK2	PROK2	prokineticin 2	6219	0.066174619	0.4503096	Yes
40	PPT1	PPT1	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)	6238	0.065888956	0.45706198	Yes
41	CFLAR	CFLAR	CASP8 and FADD-like apoptosis regulator	6417	0.063088998	0.45607355	Yes
42	IL3	IL3	interleukin 3 (colony-stimulating factor, multiple)	6430	0.062913448	0.4627615	Yes
43	GSTP1	GSTP1	glutathione S-transferase pi	6467	0.062425952	0.46828055	Yes
44	BAX	BAX	BCL2-associated X protein	6888	0.055860892	0.4552395	No
45	ANXA5	ANXA5	annexin A5	6917	0.055520959	0.4603344	No
46	PROC	PROC	protein C (inactivator of coagulation factors Va and VIIIa)	7219	0.05099934	0.45225096	No
47	TNFAIP8	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	7419	0.048167843	0.44857076	No
48	HSPA9	null	null	7553	0.046454042	0.44775328	No
49	BECN1	BECN1	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	7566	0.046241455	0.45252147	No
50	BNIP1	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	7887	0.041333474	0.44244415	No
51	ACVR1	ACVR1	activin A receptor, type I	7936	0.040597793	0.44489336	No
52	MPO	MPO	myeloperoxidase	8020	0.039274715	0.44556743	No
53	HDAC1	HDAC1	histone deacetylase 1	8406	0.034473911	0.43168652	No
54	BAG4	BAG4	BCL2-associated athanogene 4	8719	0.030154433	0.42069283	No
55	FAIM3	FAIM3	Fas apoptotic inhibitory molecule 3	8736	0.029968835	0.42340183	No
56	SH3GLB1	SH3GLB1	SH3-domain GRB2-like endophilin B1	9343	0.022310374	0.39787364	No
57	ERC1	ERC1	ELKS/RAB6-interacting/CAST family member 1	9472	0.020599198	0.39431086	No
58	OPA1	OPA1	optic atrophy 1 (autosomal dominant)	9575	0.019427914	0.39181873	No
59	RTN4	RTN4	reticulon 4	9869	0.01611501	0.38008937	No
60	GHRL	GHRL	ghrelin/obestatin preprohormone	10385	0.009810757	0.3573411	No
61	CCL2	CCL2	chemokine (C-C motif) ligand 2	10441	0.009224033	0.35585314	No
62	IL2	IL2	interleukin 2	10855	0.004608519	0.33723506	No
63	RELA	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	11049	0.002243968	0.328545	No
64	PAX7	PAX7	paired box gene 7	11070	0.00195976	0.32784337	No
65	CRYAA	CRYAA	crystallin, alpha A	11206	2.70E-04	0.3216152	No
66	IGF1R	IGF1R	insulin-like growth factor 1 receptor	11357	-0.001375641	0.31481883	No
67	PIM1	PIM1	pim-1 oncogene	11361	-0.001455182	0.3148473	No
68	IFI6	IFI6	interferon, alpha-inducible protein 6	11376	-0.001573919	0.31437942	No
69	GSK3B	GSK3B	glycogen synthase kinase 3 beta	11412	-0.002145146	0.31300366	No
70	HSP90B1	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	11599	-0.004746776	0.30492637	No
71	CLCF1	CLCF1	cardiotrophin-like cytokine factor 1	11719	-0.006441419	0.30015063	No
72	API5	API5	apoptosis inhibitor 5	11901	-0.008608071	0.29274976	No

73	SEMA4D	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	11910	-0.008731369	0.29338425	No
74	AKT1S1	AKT1S1	AKT1 substrate 1 (proline-rich)	12059	-0.010366861	0.28771594	No
75	XIAP	null	null	12075	-0.010562339	0.2882367	No
76	ALOX12	ALOX12	arachidonate 12-lipoxygenase	12129	-0.011076838	0.28705484	No
77	CIAPIN1	CIAPIN1	cytokine induced apoptosis inhibitor 1	12249	-0.012691939	0.28299883	No
78	CDKN2D	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	12563	-0.016349485	0.2703692	No
79	CFL1	CFL1	cofilin 1 (non-muscle)	12788	-0.019214019	0.2621959	No
80	CD40LG	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	13002	-0.021888943	0.2548406	No
81	BAG1	BAG1	BCL2-associated athanogene	13268	-0.025324056	0.24546988	No
82	SPHK1	SPHK1	sphingosine kinase 1	13377	-0.026647178	0.24353082	No
83	IL4	IL4	interleukin 4	13385	-0.026708486	0.24628168	No
84	BFAR	BFAR	bifunctional apoptosis regulator	13386	-0.026720846	0.24935852	No
85	SOD1	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	13525	-0.028723838	0.24626763	No
86	TAX1BP1	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	13597	-0.029516889	0.24637452	No
87	PRDX2	PRDX2	peroxiredoxin 2	13773	-0.031840499	0.241927	No
88	TNFRSF10D	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	14578	-0.042564835	0.20955078	No
89	TPT1	TPT1	tumor protein, translationally-controlled 1	14978	-0.048434991	0.19662833	No
90	BCL2A1	BCL2A1	BCL2-related protein A1	15504	-0.056140222	0.17875113	No
91	AATF	AATF	apoptosis antagonizing transcription factor	16146	-0.066335693	0.15666956	No
92	BCL10	BCL10	B-cell CLL/lymphoma 10	16205	-0.067594439	0.16176371	No
93	ARHGDIA	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	16304	-0.069322556	0.16520227	No
94	IL6	IL6	interleukin 6 (interferon, beta 2)	16656	-0.07504721	0.15756966	No
95	ASNS	ASNS	asparagine synthetase	17027	-0.082082644	0.14986624	No
96	DAD1	DAD1	defender against cell death 1	17472	-0.091574728	0.13982478	No
97	AVEN	AVEN	apoptosis, caspase activation inhibitor	18711	-0.123373665	0.0966311	No
98	TNFSF18	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	19895	-0.172455892	0.061639197	No
99	SOCS3	SOCS3	suppressor of cytokine signaling 3	20004	-0.177397564	0.07705867	No

Supplemental Table 10. Drug metabolism-related genes with significantly ($P \leq 0.05$, absolute value of log ratio > 0.1) changed expression in tumors from ACC patients (dataset GSE10927) with high *MET* expression relative to those with low *MET* expression.

PROBE	GENE SYMBOL	GENE NAME	FOLD CHANGE (LOG RATIO)	*P*-VALUE*
16657473	OR4F29	olfactory receptor, family 4, subfamily F, member 29	0.2265	0.0088
16657652	MIR200A	microRNA 200a	0.1882	0.0242
16658125			0.1586	0.049
16658184	TPRG1L	tumor protein p63 regulated 1-like	0.3537	0.0397
16658379	LINC00337	long intergenic non-protein coding RNA 337	0.2218	0.0231
16658639			0.2769	0.0071
16658945			0.4781	0.0215
16658991	PTCHD2	patched domain containing 2	0.1928	0.0428
16659021	FBXO44	F-box protein 44	0.2698	0.0014
16659054	AGTRAP	angiotensin II receptor-associated protein	0.4336	0.0114
16659413	PRAMEF15	PRAME family member 15	0.1636	0.027
16659434	PRAMEF15	PRAME family member 15	0.1636	0.027
16659459	PDPN	podoplanin	0.2767	0.0337
16659537	TMEM51	transmembrane protein 51	0.4232	0.0136
16659825	CLCNKB	chloride channel, voltage-sensitive Kb	0.8358	0.019
16659856			0.2083	0.0406
16660103	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF) 10-like	0.2473	0.0169
16660156	IGSF21	immunoglobin superfamily, member 21	0.385	0.0206
16660313	UBXN10	UBX domain protein 10	0.5995	0.018
16660317			0.1481	0.0118
16660356	FAM43B	family with sequence similarity 43, member B	0.3229	0.0179
16660367	PINK1	PTEN induced putative kinase 1	0.5941	0.002
16660481			0.1877	0.0414
16660785	NIPAL3	NIPA-like domain containing 3	0.3284	0.0033
16660810	RCAN3	RCAN family member 3	0.7087	0.006
16660919	TMEM57	transmembrane protein 57	0.4378	0.0023
16661048			0.626	0.0004
16661323	NUDC	nuclear distribution C homolog (A. nidulans)	0.274	0.0194
16661351	WDTC1	WD and tetratricopeptide repeats 1	0.3033	0.0362
16661435			0.7055	0.0014
16661687	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	0.6281	0
16661730	PTPRU	protein tyrosine phosphatase, receptor type, U	0.4675	0.0019
16661832	SERINC2	serine incorporator 2	0.9853	0.0003
16661995	CCDC28B	coiled-coil domain containing 28B	0.2666	0.0306
16662052	LCK	lymphocyte-specific protein tyrosine kinase	0.1549	0.0264
16662209	ADC	arginine decarboxylase	0.1859	0.0369
16662282	LOC402779	uncharacterized LOC402779	0.2725	0.0002
16662537	MAP7D1	MAP7 domain containing 1	0.2756	0.0024
16662662			0.3464	0.0071
16663051	ZNF643	zinc finger protein 643	0.3183	0.0455
16663064	ZNF642	zinc finger protein 642	0.3385	0.029
16663199	FOXO6	forkhead box O6	0.4525	0.0053
16663284	CCDC30	coiled-coil domain containing 30	0.3181	0.0152
16663398	FAM183A	family with sequence similarity 183, member A	0.2093	0.0137
16663413	WDR65	WD repeat domain 65	0.1693	0.0067
16664048	UROD	uroporphyrinogen decarboxylase	0.2879	0.0045
16664388	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1	0.1772	0.0459
16664406	CYP4Z1	cytochrome P450, family 4, subfamily Z, polypeptide 1	0.1672	0.0383
16664516			0.1896	0.0017
16664533	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	0.1513	0.0247
16664849			0.1178	0.0497
16664978	ACOT11	acyl-CoA thioesterase 11	0.8091	0.0016

16665139	MIR4422	microRNA 4422	0.2978	0.0251
16665182	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	0.9582	0.0067
16665302	HOOK1	hook homolog 1 (Drosophila)	1.0627	0.0014
16665343			0.2581	0.0051
16665475	ATG4C	autophagy related 4C, cysteine peptidase	0.2916	0.0329
16665497			0.1681	0.014
16665501			0.1443	0.0446
16665536	EFCAB7	EF-hand calcium binding domain 7	0.3775	0.0029
16665835	TCTEX1D1	Tctex1 domain containing 1	0.1467	0.0325
16666102			0.2701	0.026
16666109			0.1935	0.0071
16666112			0.3704	0.0036
16666143	FPGT-TNNI3K	FPGT-TNNI3K readthrough	0.2618	0.0031
16666196			0.1286	0.0463
16666224	LHX8	LIM homeobox 8	0.1523	0.0237
16666323			0.2155	0.0081
16666485	IFI44L	interferon-induced protein 44-like	0.7086	0.0092
16666610			0.3716	0.014
16666694	WDR63	WD repeat domain 63	0.8667	0.048
16666977			0.5652	0.0162
16666982	LRRC8C	leucine rich repeat containing 8 family, member C	0.2858	0.0447
16667060	BRDT	bromodomain, testis-specific	0.1156	0.0307
16667094	EPHX4	epoxide hydrolase 4	0.6482	0.0248
16667256			0.2454	0.0012
16667258	FNBP1L	formin binding protein 1-like	0.4844	0.0082
16667346	SLC44A3	solute carrier family 44, member 3	0.5234	0.0415
16667496			0.2068	0.0401
16667498	SNX7	sorting nexin 7	0.3984	0.0048
16667512	LOC100129620	uncharacterized LOC100129620	0.17	0.0155
16667530	PALMD	palmdelphin	0.5364	0.0333
16667694	GPR88	G protein-coupled receptor 88	0.2609	0.0013
16667770			0.147	0.0036
16667799			0.1421	0.045
16667801	RNPC3	RNA-binding region (RNP1, RRM) containing 3	0.637	0.0027
16667830	AMY2B	amylase, alpha 2B (pancreatic)	0.4963	0.002
16667850	AMY2A	amylase, alpha 2A (pancreatic)	0.4189	0.0007
16667925	NTNG1	netrin G1	0.1841	0.0426
16667960			0.1644	0.0302
16668047	STXBP3	syntaxin binding protein 3	0.2103	0.0368
16668420	CSF1	colony stimulating factor 1 (macrophage)	0.4268	0.0051
16668513	UBL4B	ubiquitin-like 4B	0.2422	0.0018
16668517	SLC6A17	solute carrier family 6, member 17	1.2918	0.0001
16668548			0.1435	0.0221
16668677	C1orf88	chromosome 1 open reading frame 88	1.1243	0
16668712	RAP1A	RAP1A, member of RAS oncogene family	0.2098	0.0347
16668874			0.2748	0.0055
16668919	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	0.2537	0.0265
16668997	OLFML3	olfactomedin-like 3	0.4136	0.0051
16669161	MIR320B1	microRNA 320b-1	0.3699	0.0003
16669169	CD2	CD2 molecule	0.5162	0.0011
16669278	FAM46C	family with sequence similarity 46, member C	0.6948	0.0084
16669687			0.3087	0.0252
16669796	TXNIP	thioredoxin interacting protein	0.5635	0.0175
16650005			0.7393	0.0104
16650187			0.3949	0.0022
16650227			0.3391	0.0206
16650317			0.2067	0.0181
16650485			0.3291	0.0142
16650495			0.3127	0.0028
16650497			0.6743	0.0242

16650679			0.3747	0.0156
16650755			0.2029	0.0285
16650801			0.2901	0.0313
16650967			0.3271	0.0112
16650969			0.4108	0.0482
16650989			0.4085	0.0058
16651015			0.4197	0.022
16651069			0.1736	0.0393
16651097			0.2769	0.0087
16651141			0.2628	0.0323
16651187			0.5483	0.0035
16651317			0.2513	0.0039
16651401			0.5022	0.0037
16651453			0.4516	0.0374
16651487			0.448	0.0291
16651539			0.3517	0.0418
16651573			0.2182	0.0337
16651711			0.3232	0.0052
16651745			0.3175	0.0059
16651789			0.2551	0.0362
16651887			0.4966	0.021
16651903			0.2959	0.0277
16651915			0.341	0.0443
16651935			0.5834	0.0044
16651985			0.3538	0.0072
16652011			0.8625	0.0011
16652059			0.2206	0.0353
16652069			0.3535	0.0082
16652251			0.2817	0.0474
16652277			0.4681	0.0331
16652339			0.2327	0.0355
16652363			0.2685	0.0406
16652367			0.2035	0.0337
16652411			0.2903	0.0085
16652555			0.2571	0.011
16652579			0.341	0.0443
16652599			0.5834	0.0044
16652649			0.3538	0.0072
16652675			0.8625	0.0011
16652723			0.2206	0.0353
16652733			0.3535	0.0082
16652755			0.4762	0.0354
16652773			0.4156	0.0303
16652949			0.4296	0.0037
16652961			0.4703	0.0008
16653019			0.2791	0.011
16653171			0.2899	0.0053
16653201			0.4275	0.0379
16653269			0.1673	0.048
16653373			0.2252	0.0464
16653379			0.1842	0.0499
16653475			0.2252	0.0464
16653481			0.1842	0.0499
16653573			0.2732	0.0207
16653637			0.3966	0.049
16653641			0.3577	0.0298
16653959			0.2712	0.0442
16653973			0.2844	0.0322
16654001			0.5404	0.018
16654021			0.6917	0.0118
16654027			0.3171	0.024

16654029			0.397	0.0361
16654135			0.4531	0.0114
16654191			0.3186	0.046
16654245			0.321	0.022
16654297			0.4933	0.0029
16654413			0.3069	0.0079
16654425			0.376	0.0109
16654433			0.276	0.0293
16654551			0.1712	0.0472
16654901			0.5115	0.008
16654937			0.35	0.0169
16654955			0.4965	0.0115
16654963			0.4158	0.0016
16654967			0.3628	0.0307
16655013			0.3664	0.0073
16655177			0.3003	0.0033
16655229			0.238	0.0017
16655241			0.3283	0.0403
16655295			0.2544	0.0074
16655395			0.328	0.0388
16655617			0.231	0.037
16655793			0.3496	0.0395
16655899			0.8463	0.0186
16655977			0.5069	0.0164
16656051			0.4687	0.0172
16656079			0.4713	0.0031
16656141			0.3052	0.029
16656145			0.3056	0.0412
16656171			0.1695	0.046
16656173			0.4528	0.0384
16656217			0.4022	0.0234
16656427			0.33	0.0455
16656557			0.7426	0.0022
16656757			0.3403	0.0226
16656773			0.2656	0.0157
16656777			0.4921	0.0095
16656793			0.3491	0.0102
16656809			0.3946	0.0142
16656813			0.4078	0.013
16656815			0.2829	0.0299
16656853			0.3841	0.0378
16656875			0.5041	0.0267
16656969			0.3248	0.0378
16657191			0.3435	0.0349
16657203			0.5116	0.0064
16657255			0.6848	0.0402
16657331			0.2534	0.0181
16657343			0.3775	0.0116
16657369			0.312	0.0115
16657373			0.2221	0.0324
16657395			0.3938	0.0232
16657421			0.4618	0.0096
16670164			0.2558	0.021
16670178			0.6233	0.0243
16670291			0.286	0.0031
16670317	FCGR1C	Fc fragment of IgG, high affinity Ic, receptor (CD64), pseudogene	0.3831	0.0157
16670673			0.389	0.0101
16670681	ANXA9	annexin A9	0.3089	0.0248
16670866	CGN	cingulin	0.2991	0.0096

16670943	RIIAD1	regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1	0.3536	0.0003
16671013			0.2665	0.0294
16671023	CRCT1	cysteine-rich C-terminal 1	0.1573	0.0371
16671100	SPRR4	small proline-rich protein 4	0.2224	0.0142
16671104	SPRR1A	small proline-rich protein 1A	1.6531	0.0451
16671115	SPRR1B	small proline-rich protein 1B	0.6892	0.0169
16671137			0.1245	0.0466
16672298	KIRREL-IT1	KIRREL intronic transcript 1 (non-protein coding)	0.2522	0.014
16672323	CD1C	CD1c molecule	0.2281	0.0276
16672333	CD1E	CD1e molecule	0.259	0.0222
16672373	PYHIN1	pyrin and HIN domain family, member 1	0.2716	0.0108
16672390	IFI16	interferon, gamma-inducible protein 16	0.4303	0.0289
16672494			0.1493	0.0484
16672654	SLAMF7	SLAM family member 7	0.354	0.0064
16672669	LY9	lymphocyte antigen 9	0.1678	0.0335
16672710	KLHDC9	kelch domain containing 9	0.3998	0.0125
16672869			0.3283	0.0049
16672893	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	0.3437	0.0217
16672920	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	0.3583	0.0273
16673032	RN5S61	RNA, 5S ribosomal 61	0.2553	0.0021
16673034	MIR556	microRNA 556	0.1534	0.0054
16673075	DDR2	discoidin domain receptor tyrosine kinase 2	0.6691	0.0092
16673146			0.3799	0.0074
16673182			0.146	0.0159
16673246			0.2975	0.0027
16673345			0.2172	0.0045
16673507	XCL1	chemokine (C motif) ligand 1	0.3266	0.0012
16673598			0.304	0.0337
16673748	FMO4	flavin containing monooxygenase 4	0.7721	0.0005
16673765			0.1153	0.0274
16673883	C1orf105	chromosome 1 open reading frame 105	0.1826	0.0406
16673928	FASLG	Fas ligand (TNF superfamily, member 6)	0.2094	0.0092
16674020	RN5S67	RNA, 5S ribosomal 67	0.3919	0.0036
16674130	KIAA0040	KIAA0040	1.0041	0
16674269	TEX35	testis expressed 35	0.161	0.0362
16674845	LAMC2	laminin, gamma 2	0.2976	0.0238
16674993			0.1734	0.0135
16675197	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	0.5621	0.0014
16675231			0.1486	0.0014
16675278	RGS18	regulator of G-protein signaling 18	0.2619	0.0189
16675301	RGS1	regulator of G-protein signaling 1	0.6734	0.0223
16675428	CFHR3	complement factor H-related 3	0.1368	0.0295
16675578	PTPRC	protein tyrosine phosphatase, receptor type, C	0.4926	0.0068
16675763	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	0.1407	0.0172
16676049			0.1127	0.006
16676052			0.2142	0.0004
16676298			1.438	0.0251
16676308	LOC100506838	uncharacterized LOC100506838	0.2259	0.0029
16676437	TMCC2	transmembrane and coiled-coil domain family 2	0.2187	0.0197
16676641			0.2012	0.0068
16676983	G0S2	G0/G1switch 2	1.0317	0.0002
16677057	SYT14	synaptotagmin XIV	0.7179	0.0211
16677071	SERTAD4	SERTA domain containing 4	0.2023	0.0032
16677610			0.3706	0.0081
16677651			0.2056	0.013
16677808	FAM177B	family with sequence similarity 177, member B	0.3588	0.0046
16678191	ADCK3	aarF domain containing kinase 3	0.4366	0.0171
16678324			0.7847	0.0355

16678499	MIR4666A	microRNA 4666a	0.2449	0.0003
16678828			0.1446	0.0079
16678851	KIAA1804	mixed lineage kinase 4	0.3991	0.0315
16679000			0.2275	0.0024
16679018			0.134	0.0104
16679340			0.1514	0.0399
16679435			0.1051	0.0269
16679565			0.2225	0.0232
16679697	NLRP3	NLR family, pyrin domain containing 3	0.2896	0.0003
16679735			0.1516	0.0346
16679764	OR2L8	olfactory receptor, family 2, subfamily L, member 8	0.288	0.0076
16679783	OR2L3	olfactory receptor, family 2, subfamily L, member 3	0.329	0.0108
16679916			0.3171	0.0214
16679938	OR4F29	olfactory receptor, family 4, subfamily F, member 29	0.2265	0.0088
16680342	TMEM240	transmembrane protein 240	0.2091	0.0201
16680836	MIR551A	microRNA 551a	0.2399	0.0248
16681210	KLHL21	kelch-like 21 (Drosophila)	0.3487	0.0143
16681735	FBXO2	F-box protein 2	0.4419	0.0163
16681827	DHRS3	dehydrogenase/reductase (SDR family) member 3	0.5887	0.0251
16681840			0.2547	0.0095
16681952			0.2395	0.0243
16681957			0.3078	0.001
16681960			0.1245	0.0319
16681971			0.1373	0.0454
16681974	C1orf126	chromosome 1 open reading frame 126	0.2086	0.026
16681981	C1orf195	chromosome 1 open reading frame 195	0.2724	0.0021
16682039			0.2091	0.0199
16682148	RSG1	REM2 and RAB-like small GTPase 1	0.3278	0.0137
16682402	PADI2	peptidyl arginine deiminase, type II	0.4006	0.0131
16682792	PLA2G2C	phospholipase A2, group IIC	0.1736	0.0012
16682801			0.8855	0.0206
16682829	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.8643	0.0001
16683445	FUCA1	fucosidase, alpha-L- 1, tissue	0.5964	0.0086
16683460	CNR2	cannabinoid receptor 2 (macrophage)	0.1435	0.0023
16683574	C1orf201	chromosome 1 open reading frame 201	0.5292	0.0002
16683605	NIPAL3	NIPA-like domain containing 3	0.5312	0.0024
16683612			0.3764	0.0446
16683758	SLC30A2	solute carrier family 30 (zinc transporter), member 2	1.2188	0
16683903	NR0B2	nuclear receptor subfamily 0, group B, member 2	1.1121	0.0421
16683908	C1orf172	chromosome 1 open reading frame 172	0.3715	0.0358
16684212			0.1585	0.0307
16684331	SDC3	syndecan 3	0.3889	0.0436
16684642	LOC100653331	uncharacterized LOC100653331	0.1611	0.0231
16684785	FNDC5	fibronectin type III domain containing 5	0.3653	0.0296
16684902	CSMD2	CUB and Sushi multiple domains 2	0.322	0.0024
16684990			0.2098	0.0404
16685153			0.5972	0.0027
16685198			0.1598	0.0182
16685208	TRAPPC3	trafficking protein particle complex 3	0.2564	0.0163
16685253			0.1335	0.0399
16685851	RIMS3	regulating synaptic membrane exocytosis 3	0.226	0.0058
16686000	CLDN19	claudin 19	0.1698	0.0138
16686040	CCDC23	coiled-coil domain containing 23	0.411	0.0001
16686922	AGBL4-IT1	AGBL4 intronic transcript 1 (non-protein coding)	0.1767	0.0435
16686990	TTC39A	tetratricopeptide repeat domain 39A	0.4962	0.0009
16687067			0.4009	0.0145
16687328	C1orf123	chromosome 1 open reading frame 123	0.3236	0.0007
16687445	YIPF1	Yip1 domain family, member 1	0.338	0.0289
16687487	TMEM59	transmembrane protein 59	0.2552	0.0232
16687583	FAM151A	family with sequence similarity 151, member A	0.3711	0.0015

16687602	TTC22	tetratricopeptide repeat domain 22	0.2675	0.002
16687752	C1orf168	chromosome 1 open reading frame 168	0.1602	0.0073
16687827	DAB1	disabled homolog 1 (Drosophila)	0.3848	0.0062
16688164	JAK1	Janus kinase 1	0.2317	0.049
16688487	ZRANB2	zinc finger, RAN-binding domain containing 2	0.2987	0.0372
16688563	LRRC53	leucine rich repeat containing 53	0.1434	0.0315
16688570			0.2559	0.0222
16688665	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	0.4569	0.0075
16688826			0.18	0.0285
16688937	CTBS	chitobiase, di-N-acetyl-	0.3623	0.0219
16688961	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	0.2226	0.0337
16688992	LPAR3	lysophosphatidic acid receptor 3	0.7138	0.0366
16689223			0.1107	0.0077
16689352	GBP2	guanylate binding protein 2, interferon-inducible	1.5063	0.0002
16689354	GBP2	guanylate binding protein 2, interferon-inducible	1.5052	0.0004
16689400	GBP5	guanylate binding protein 5	0.5075	0.0022
16689441	LRRC8C	leucine rich repeat containing 8 family, member C	0.2152	0.0283
16689456			0.1536	0.0166
16689935			0.2627	0.0346
16689969	DPYD	dihydropyrimidine dehydrogenase	0.7173	0.0056
16690011	MIR137HG	MIR137 host gene (non-protein coding)	0.2207	0.0285
16690060			0.16	0.0133
16690294	AMY1A	amylase, alpha 1A (salivary)	0.426	0.0269
16690316			0.1436	0.0161
16690518			0.3042	0.0079
16690553	MYBPHL	myosin binding protein H-like	0.3459	0.0236
16690566	SORT1	sortilin 1	0.5002	0.0347
16690688			0.2173	0.0149
16690693			0.4716	0.0006
16690925			0.2488	0.0087
16691368			0.1991	0.008
16691396			0.1759	0.0454
16691431			0.1724	0.03
16691434	RN5S55	RNA, 5S ribosomal 55	0.2286	0.0322
16691510	SPAG17	sperm associated antigen 17	0.3621	0.0014
16691574	RN5S56	RNA, 5S ribosomal 56	0.2743	0.0044
16691752			0.419	0.0112
16691972	PDE4DIP	phosphodiesterase 4D interacting protein	0.3966	0.0212
16692073	NUDT4P1	nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	0.3254	0.045
16692269	LOC100509195	uncharacterized LOC100509195	0.4156	0.0144
16692311	FMO5	flavin containing monooxygenase 5	0.354	0.0113
16692368			0.1841	0.0128
16692419	LOC100509195	uncharacterized LOC100509195	0.5288	0.0149
16692589			0.1166	0.0177
16692721			0.2561	0.0028
16692805	GOLPH3L	golgi phosphoprotein 3-like	0.3215	0.045
16692892	CERS2	ceramide synthase 2	0.2691	0.0475
16693187	TDRKH	tudor and KH domain containing	0.4113	0.0189
16693222	RORC	RAR-related orphan receptor C	0.812	0.0001
16693242	C2CD4D	C2 calcium-dependent domain containing 4D	0.1409	0.0237
16693247			0.2976	0.0366
16693291	TCHH	trichohyalin	0.1475	0.0246
16693303	HRNR	hornerin	0.3723	0.0145
16693308	FLG	filaggrin	0.1781	0.0316
16693775			0.2932	0.0101
16694879			0.157	0.031
16694882			0.1833	0.0201
16695013	LOC646268	hCG1654703	0.1818	0.0178
16695023	CD1B	CD1b molecule	0.2114	0.0107
16695042	OR6Y1	olfactory receptor, family 6, subfamily Y, member 1	0.2	0.0204

16695044	OR6P1	olfactory receptor, family 6, subfamily P, member 1	0.3231	0.0006
16695121	AIM2	absent in melanoma 2	0.2594	0.0097
16695142			0.1696	0.0011
16695163			0.3294	0.0003
16695169	VSIG8	V-set and immunoglobulin domain containing 8	0.1828	0.0172
16695392	SLAMF6	SLAM family member 6	0.3381	0.0084
16695437	CD48	CD48 molecule	0.3005	0.0388
16695463	ITLN1	intelectin 1 (galactofuranose binding)	0.2447	0.0269
16695475			0.349	0.0001
16695478	ITLN2	intelectin 2	0.4774	0.0218
16695535	ARHGAP30	Rho GTPase activating protein 30	0.2123	0.0146
16695762	C1orf111	chromosome 1 open reading frame 111	0.181	0.0101
16695923	FAM78B	family with sequence similarity 78, member B	0.241	0.0113
16695931			0.2601	0.0006
16695994	CD247	CD247 molecule	0.2044	0.014
16696100	LOC100505918	uncharacterized LOC100505918	0.1936	0.0074
16696114	XCL2	chemokine (C motif) ligand 2	0.2434	0.0123
16696217	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	0.2998	0.0155
16696295	KIFAP3	kinesin-associated protein 3	0.3347	0.0199
16696346	MIR1295A	microRNA 1295a	0.3772	0.0115
16696348			0.1846	0.0325
16696478	ANKRD45	ankyrin repeat domain 45	0.5851	0.0049
16696488			0.2985	0.0126
16696614	KIAA0040	KIAA0040	0.5283	0.0025
16696624	TNR	tenascin R (restrictin, janusin)	0.5289	0.0175
16697018	RGS16	regulator of G-protein signaling 16	0.4604	0.023
16697062	NMNAT2	nicotinamide nucleotide adenylyltransferase 2	0.8875	0.0031
16697081			0.1995	0.014
16697387			0.2494	0.0452
16697416			0.2703	0.0008
16697647			0.1538	0.0177
16697650			0.2256	0.0434
16697668			0.1713	0.0272
16697927			0.7034	0.0024
16697930	PHLDA3	pleckstrin homology-like domain, family A, member 3	0.3442	0.0177
16698034			0.2093	0.0491
16698304	GOLT1A	golgi transport 1A	0.666	0.025
16698356	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	0.2558	0.0362
16698500	MIR135B	microRNA 135b	0.1745	0.047
16698502	LOC284578	uncharacterized LOC284578	0.1535	0.0446
16698625	C1orf186	chromosome 1 open reading frame 186	0.1757	0.0008
16698718	PIGR	polymeric immunoglobulin receptor	0.1992	0.0462
16698923	IRF6	interferon regulatory factor 6	1.0075	0.0028
16698939	C1orf133	chromosome 1 open reading frame 133	0.1737	0.0265
16698949	KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member 1	0.2269	0.006
16699102			0.1981	0.0047
16699344	LOC728463	uncharacterized LOC728463	0.2323	0.0215
16699357	LOC643723	uncharacterized LOC643723	0.2375	0.0199
16699634	TLR5	toll-like receptor 5	0.6931	0.0002
16699643	SUSD4	sushi domain containing 4	0.7915	0.0204
16700195	C1orf145	chromosome 1 open reading frame 145	0.1384	0.0374
16700274	ACTA1	actin, alpha 1, skeletal muscle	0.2331	0.0252
16700554	PCNXL2	pecanex-like 2 (Drosophila)	0.4646	0.0028
16700806	LYST	lysosomal trafficking regulator	0.4203	0.0134
16700878	MIR1537	microRNA 1537	0.2703	0.0295
16701031			0.34	0.0184
16701110	MAP1LC3C	microtubule-associated protein 1 light chain 3 gamma	0.2566	0.0013
16701117			0.3586	0.009
16701597	OR14A16	olfactory receptor, family 14, subfamily A, member 16	0.198	0.0022

16701599	OR11L1	olfactory receptor, family 11, subfamily L, member 1	0.1554	0.0301
16701914			0.1988	0.0112
16701941			0.2236	0.0006
16701947			0.2004	0.0103
16702007	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	0.6234	0.0223
16702143			0.2191	0.0114
16702345			0.1365	0.0433
16702393			0.2151	0.037
16702431	ECHDC3	enoyl CoA hydratase domain containing 3	0.4531	0.0009
16702501			0.4579	0.0402
16702547	OPTN	optineurin	0.3805	0.0118
16702800	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0.3179	0.0478
16702982	C10orf112	chromosome 10 open reading frame 112	0.2175	0.0403
16703114	COMMD3	COMM domain containing 3	0.2669	0.0249
16703150	SPAG6	sperm associated antigen 6	0.4687	0.0009
16703251	KIAA1217	KIAA1217	0.637	0.0096
16703301	THNSL1	threonine synthase-like 1 (S. cerevisiae)	0.4093	0.0005
16703311	GPR158	G protein-coupled receptor 158	0.3636	0.0154
16703340	MYO3A	myosin IIIA	0.9663	0.001
16703382	GAD2	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	0.4647	0.0316
16703407	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0.706	0.0125
16703429	RN5S307	RNA, 5S ribosomal 307	0.2398	0.0428
16703471			0.2017	0.0219
16703514			0.138	0.0099
16703581			0.1577	0.0322
16703595			0.2392	0.0043
16703598			0.2135	0.0317
16703628			0.1797	0.009
16703934	ANKRD30A	ankyrin repeat domain 30A	0.1722	0.0349
16704006			0.1465	0.04
16704254	ZNF32-AS1	ZNF32 antisense RNA 1 (non-protein coding)	0.331	0.0171
16704257	ZNF32-AS2	ZNF32 antisense RNA 2 (non-protein coding)	0.1978	0.0314
16704320	RASSF4	Ras association (RalGDS/AF-6) domain family member 4	0.2405	0.0317
16704542	FAM21B	family with sequence similarity 21, member B	0.321	0.0011
16704607	FAM25G	family with sequence similarity 25, member G	0.2422	0.0233
16704822	SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3	0.5693	0.0086
16704837	FAM21C	family with sequence similarity 21, member C	0.3441	0.0047
16704920	FAM21A	family with sequence similarity 21, member A	0.3294	0.0003
16705006	MIR605	microRNA 605	0.6655	0.0124
16705039			0.3834	0.0272
16705116	FAM133CP	family with sequence similarity 133, member C, pseudogene	0.2183	0.0026
16705130	PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like	1.0592	0.0403
16705151			1.0082	0.035
16705154			0.3249	0.0031
16705174	LOC100507058	uncharacterized LOC100507058	0.3286	0.0326
16705188	C10orf107	chromosome 10 open reading frame 107	1.3698	0.0003
16705808			0.2478	0.0074
16705839			0.3129	0.001
16705940			0.1579	0.0231
16706459			0.1742	0.0469
16706708			0.1363	0.0476
16706772	LOC170425	uncharacterized LOC170425	0.1706	0.018
16706896	SNCG	synuclein, gamma (breast cancer-specific protein 1)	1.1148	0.009
16707149	FAS	Fas (TNF receptor superfamily, member 6)	0.7528	0.0032
16707169			0.6142	0.0011

16707323			0.1962	0.0245
16707631	PLCE1	phospholipase C, epsilon 1	1.0514	0.0035
16707670			0.188	0.016
16707789			0.1846	0.0386
16707836	CC2D2B	coiled-coil and C2 domain containing 2B	0.2201	0.0328
16707951	LOC100505540	uncharacterized LOC100505540	0.1485	0.0345
16708020	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	0.4771	0.0014
16708146			0.3399	0.0005
16708192	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	1.2788	0.003
16708461			0.1139	0.0435
16708489	DPCD	deleted in primary ciliary dyskinesia homolog (mouse)	0.3019	0.0451
16708794	LOC729020	rcRPE	0.1674	0.0263
16708796	INA	internexin neuronal intermediate filament protein, alpha	0.8734	0.0221
16708862	NEURL	neuralized homolog (Drosophila)	0.1528	0.0356
16708933	GSTO2	glutathione S-transferase omega 2	0.3755	0.0489
16709060			0.1776	0.0108
16709072	ADD3	adducin 3 (gamma)	0.6337	0.001
16709268	ACSL5	acyl-CoA synthetase long-chain family member 5	0.4984	0.0363
16709363			0.101	0.0341
16709367	HABP2	hyaluronan binding protein 2	0.1595	0.038
16709506			0.2138	0.0472
16709610	PNLIPRP3	pancreatic lipase-related protein 3	0.852	0.0398
16709747			0.1446	0.0237
16709760	CASC2	cancer susceptibility candidate 2 (non-protein coding)	0.2789	0.0488
16709865	INPP5F	inositol polyphosphate-5-phosphatase F	0.5149	0.0144
16709936	PPAPDC1A	phosphatidic acid phosphatase type 2 domain containing 1A	0.9623	0.0009
16710608	MGMT	O-6-methylguanine-DNA methyltransferase	0.3283	0.0126
16710740	LRRC27	leucine rich repeat containing 27	0.2269	0.0172
16710852	KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1	0.4783	0.0012
16711360			0.2152	0.0071
16711463			0.5276	0.0175
16711723			0.241	0.0175
16711864			0.1811	0.0179
16712312	LOC100129213	uncharacterized LOC100129213	0.2067	0.0007
16712353			0.2018	0.0266
16712357			0.3811	0.0026
16712482	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.4876	0.0287
16712503			0.1496	0.0183
16712528			0.4035	0.0115
16712531	ARHGAP21	Rho GTPase activating protein 21	0.5174	0.0085
16712598	GPR158-AS1	GPR158 antisense RNA 1 (non-protein coding)	0.1305	0.0043
16712612			0.1714	0.0386
16712786	ARMC4	armadillo repeat containing 4	0.3053	0.0038
16712825	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1.3748	0
16713019	ZNF438	zinc finger protein 438	0.281	0.0302
16713052			0.1399	0.0483
16713330	ZNF248	zinc finger protein 248	0.3321	0.0102
16713498	ZNF32	zinc finger protein 32	0.3695	0.0023
16713652			0.1842	0.0488
16713760	LOC728643	heterogeneous nuclear ribonucleoprotein A1 pseudogene	0.5745	0.0034
16713779	FAM25G	family with sequence similarity 25, member G	0.2245	0.0296
16713860			0.231	0.0039
16713948			0.2292	0.0004
16713955	FAM25G	family with sequence similarity 25, member G	0.2032	0.0313
16714027			0.1839	0.0314
16714030	ARHGAP22	Rho GTPase activating protein 22	0.2208	0.0487

16714170	OGDHL	oxoglutarate dehydrogenase-like	0.9005	0.0002
16714237			0.1842	0.0488
16714368			0.2095	0.0161
16714375			0.7312	0.0166
16714433	PCDH15	protocadherin-related 15	0.4851	0.0494
16714493			0.2737	0.0181
16714501			0.2164	0.0274
16714528			0.4818	0.0001
16714531			0.3764	0
16714534	MIR3924	microRNA 3924	0.5727	0.0072
16714581	SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	0.9064	0.0348
16714720			0.2076	0.0247
16714725	TMEM26	transmembrane protein 26	0.8628	0.0372
16714939			0.3257	0.0009
16715170	PRF1	perforin 1 (pore forming protein)	0.2452	0.0383
16715241	PSAP	prosaposin	0.2458	0.0468
16715434	TTC18	tetratricopeptide repeat domain 18	0.549	0.0156
16715738	DUSP13	dual specificity phosphatase 13	0.1787	0.0265
16716124	LOC642934	uncharacterized LOC642934	0.3714	0.0278
16716213	MMRN2	multimerin 2	0.4726	0.002
16716327	RNLS	renalase, FAD-dependent amine oxidase	0.8347	0.0021
16716339			0.2845	0.0071
16716341	ANKRD22	ankyrin repeat domain 22	0.2655	0.0259
16716367			0.5939	0.0373
16716443	FLJ37201	tigger transposable element derived 2 pseudogene	0.2258	0.0361
16716454			0.3164	0.0001
16716469	HTR7	5-hydroxytryptamine (serotonin) receptor 7, adenylate cyclase-coupled	0.2074	0.014
16716542			0.265	0.0489
16716590	MYOF	myoferlin	1.0106	0.0036
16716657	RN5S323	RNA, 5S ribosomal 323	0.1582	0.0212
16716700			0.2612	0.0096
16716715			0.1471	0.0491
16716718	LOC100128054	uncharacterized LOC100128054	0.4904	0.0012
16717005	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	0.4964	0.0386
16717030	MIR607	microRNA 607	0.1369	0.0063
16717032	SLIT1	slit homolog 1 (Drosophila)	0.1589	0.0172
16717224	MORN4	MORN repeat containing 4	0.39	0.0183
16717314	HPS1	Hermansky-Pudlak syndrome 1	0.293	0.0201
16717412	DNMBP	dynamin binding protein	0.3483	0.0207
16717560			0.2136	0.0148
16717697			0.1485	0.0317
16717869	LDB1	LIM domain binding 1	0.6504	0
16717986	NT5C2	5'-nucleotidase, cytosolic II	0.3297	0.0046
16718473	ZDHHC6	zinc finger, DHHC-type containing 6	0.3211	0.0338
16718553	DCLRE1A	DNA cross-link repair 1A	0.351	0.0229
16718670	GFRA1	GDNF family receptor alpha 1	0.4118	0.0005
16718836	PRLHR	prolactin releasing hormone receptor	0.3882	0.0038
16718938	RGS10	regulator of G-protein signaling 10	0.5479	0.0191
16718977			0.28	0.0029
16719171	CPXM2	carboxypeptidase X (M14 family), member 2	0.4629	0.0468
16719208			0.1763	0.0126
16719233	OAT	ornithine aminotransferase	0.5486	0.0145
16719254	NKX1-2	NK1 homeobox 2	0.1367	0.0188
16719548			0.1711	0.0134
16719598			0.5819	0.0095
16719947	MIR1324	microRNA 1324	0.1213	0.0113
16720044			0.2135	0.0077
16720601	MUC5B	mucin 5B, oligomeric mucus/gel-forming	0.1068	0.0476
16720997	C11orf36	chromosome 11 open reading frame 36	0.1292	0.0458

16721225			0.2545	0.0044
16721280	TRIM22	tripartite motif containing 22	0.4841	0.0039
16721304	OR56B1	olfactory receptor, family 56, subfamily B, member 1	0.2185	0.0085
16721307	OR52N4	olfactory receptor, family 52, subfamily N, member 4	0.227	0.017
16721310	OR52N2	olfactory receptor, family 52, subfamily N, member 2	0.2585	0.0445
16721313	OR52E4	olfactory receptor, family 52, subfamily E, member 4	0.3037	0.0389
16721329			0.1299	0.0243
16721672			0.3912	0.0274
16721680			0.5382	0.0438
16721765			0.1537	0.0206
16722026			0.2555	0.0344
16722360			0.2006	0.0063
16722382			0.1685	0.0281
16722412	NUCB2	nucleobindin 2	0.2373	0.0275
16722544	MRGPRX3	MAS-related GPR, member X3	0.2257	0.0273
16722681			0.1432	0.0056
16722880			0.268	0.0059
16722962			0.2583	0.0221
16723008			0.212	0.0022
16723200			0.2082	0.001
16723318	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	0.4469	0.0203
16723353	DEPDC7	DEP domain containing 7	0.1882	0.0218
16723369	TCP11L1	t-complex 11 (mouse)-like 1	0.3019	0.017
16723422	C11orf41	chromosome 11 open reading frame 41	0.7068	0.0081
16723447			0.7236	0.0038
16723450			0.1857	0.0239
16723614	CD44	CD44 molecule (Indian blood group)	0.5968	0.0177
16724190	CRY2	cryptochrome 2 (photolyase-like)	0.1365	0.0394
16724266			0.2197	0.0068
16724344	MIR4688	microRNA 4688	0.1981	0.0398
16724633	PTPRJ	protein tyrosine phosphatase, receptor type, J	0.3494	0.0214
16724679	OR4A47	olfactory receptor, family 4, subfamily A, member 47	0.192	0.0169
16724706	LOC646813	DEAH (Asp-Glu-Ala-His) box polypeptide 9 pseudogene	0.1906	0.0118
16724715	TRIM48	tripartite motif containing 48	0.2975	0.0422
16724789	OR8J1	olfactory receptor, family 8, subfamily J, member 1	0.1122	0.0445
16725015			0.1839	0.0291
16725112	STX3	syntaxin 3	0.5682	0.0053
16725132	OR10V2P	olfactory receptor, family 10, subfamily V, member 2 pseudogene	0.1744	0.0419
16725172	MS4A2	membrane-spanning 4-domains, subfamily A, member 2	0.2411	0.0089
16725252	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	0.1708	0.0312
16725670	DAGLA	diacylglycerol lipase, alpha	0.7303	0.001
16725783	BEST1	bestrophin 1	0.1603	0.021
16726081	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.6581	0.0046
16726089			0.1541	0.0089
16726520			0.217	0.0202
16727149	CTSW	cathepsin W	0.2681	0.0028
16727388			0.2338	0.0463
16727413	PELI3	pellino E3 ubiquitin protein ligase family member 3	0.223	0.046
16728331	FADD	Fas (TNFRSF6)-associated via death domain	0.1608	0.0496
16728513	KRTAP5-10	keratin associated protein 5-10	0.1928	0.023
16728705			0.1633	0.0416
16728727	STARD10-AS1	STARD10 antisense RNA 1 (non-protein coding)	0.3742	0.0063
16729185			0.168	0.0142
16729527			0.3161	0.0299
16729530			0.2614	0.0414
16729540			0.2573	0.0208
16729835			0.2016	0.025
16730033	CCDC67	coiled-coil domain containing 67	0.363	0.0273
16730250			0.1947	0.0026

16730385	RN5S347	RNA, 5S ribosomal 347	0.1837	0.0435
16730522	BIRC3	baculoviral IAP repeat containing 3	0.3618	0.0438
16730564			0.1708	0.0023
16730754			0.1428	0.0391
16730788	RAB39A	RAB39A, member RAS oncogene family	0.5486	0.0176
16730819	ACAT1	acetyl-CoA acetyltransferase 1	0.4514	0.0025
16730932			0.172	0.0345
16731010	C11orf93	chromosome 11 open reading frame 93	0.5368	0.0129
16731132	DIXDC1	DIX domain containing 1	0.6684	0.0034
16731225	BCO2	beta-carotene oxygenase 2	0.7466	0.0324
16731339	TTC12	tetratricopeptide repeat domain 12	0.3177	0.0026
16731795	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	0.3521	0.0023
16731806	CD3G	CD3g molecule, gamma (CD3-TCR complex)	0.2518	0.0005
16732224	ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	0.1417	0.0114
16732322	LOC100499227	uncharacterized LOC100499227	0.1695	0.0117
16732381	LOC729173	uncharacterized LOC729173	0.1558	0.045
16732584	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	0.8744	0.0219
16732661			0.1159	0.0239
16732797	OR10G4	olfactory receptor, family 10, subfamily G, member 4	0.2398	0.0144
16732807	VWA5A	von Willebrand factor A domain containing 5A	0.639	0.0017
16733325	KIRREL3-AS2	KIRREL3 antisense RNA 2 (non-protein coding)	0.1528	0.0062
16733377	FLI1	Friend leukemia virus integration 1	0.3165	0.0087
16733589			0.1561	0.0015
16733719	GLB1L2	galactosidase, beta 1-like 2	0.5896	0.0021
16734092	CEND1	cell cycle exit and neuronal differentiation 1	0.2037	0.0347
16734291	KRTAP5-4	keratin associated protein 5-4	0.3792	0.0066
16734336			0.2616	0.0096
16734434			0.1396	0.0266
16734644	OR7E12P	olfactory receptor, family 7, subfamily E, member 12 pseudogene	0.2662	0.0463
16734672			0.2165	0.0066
16734742			0.3301	0.0271
16734758	OR52B4	olfactory receptor, family 52, subfamily B, member 4	0.148	0.0102
16734811	OR51G2	olfactory receptor, family 51, subfamily G, member 2	0.2182	0.0391
16734814	OR51G1	olfactory receptor, family 51, subfamily G, member 1	0.1079	0.0417
16734898	OR51B2	olfactory receptor, family 51, subfamily B, member 2	0.159	0.0157
16734956	OR52N1	olfactory receptor, family 52, subfamily N, member 1	0.2846	0.0386
16734961	OR52E8	olfactory receptor, family 52, subfamily E, member 8	0.298	0.0301
16734965	OR56A5	olfactory receptor, family 56, subfamily A, member 5	0.2055	0.0307
16734985	OR52B2	olfactory receptor, family 52, subfamily B, member 2	0.1535	0.0365
16735152	TPP1	tripeptidyl peptidase I	0.3845	0.0295
16735231	ZNF214	zinc finger protein 214	0.5545	0.0008
16735375	STK33	serine/threonine kinase 33	0.7206	0.0044
16735946	LOC100506352	uncharacterized LOC100506352	0.1629	0.0292
16736726	SVIP	small VCP/p97-interacting protein	0.4815	0.0058
16736747			0.1251	0.0145
16736931			0.2569	0.0321
16736966	DCDC5	doublecortin domain containing 5	0.1992	0.0297
16737019	DCDC1	doublecortin domain containing 1	0.289	0.0012
16737099			0.1595	0.0388
16737189	C11orf41	chromosome 11 open reading frame 41	0.3681	0.0488
16737194	C11orf91	chromosome 11 open reading frame 91	0.207	0.0465
16737200	CD59	CD59 molecule, complement regulatory protein	0.5794	0.0089
16737528			0.1873	0.0283
16738345	LOC100507561	ankyrin repeat domain-containing protein 33B-like	0.2516	0.0035
16738395	OR5AP2	olfactory receptor, family 5, subfamily AP, member 2	0.1788	0.0117
16738615	OR5B2	olfactory receptor, family 5, subfamily B, member 2	0.2314	0.003
16738622			0.122	0.0357
16738701			0.1593	0.0437
16738771			0.5232	0.0326

16738803	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	0.5227	0.0004
16738894			0.5869	0.0031
16739235			0.202	0.02
16739239	SCGB1D4	secretoglobin, family 1D, member 4	0.2219	0.0078
16739250			0.145	0.0427
16739796	RCOR2	REST corepressor 2	0.1821	0.0311
16739830			0.6345	0.0057
16740238	BATF2	basic leucine zipper transcription factor, ATF-like 2	0.1673	0.0447
16740549			0.2053	0.0282
16740770	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	0.26	0.038
16740828	CTSF	cathepsin F	0.7019	0.001
16740997	PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	0.4593	0.0003
16741556	ZNF705E	zinc finger protein 705E	0.1858	0.031
16742228	MIR326	microRNA 326	0.1784	0.0329
16742294	MAP6	microtubule-associated protein 6	0.548	0.0263
16742744			0.3604	0.0133
16742747			0.1865	0.0321
16742760			0.1383	0.0074
16742777			0.1687	0.0261
16742879	DLG2	discs, large homolog 2 (Drosophila)	0.5539	0.0092
16743251			0.5141	0
16743449			0.2191	0.0055
16743560			0.1989	0.0156
16743566			0.1561	0.0263
16743793			0.4396	0.0024
16743797			0.4533	0.0009
16743803			0.197	0.0302
16743806			0.2789	0.0156
16743809			0.2565	0.0458
16743854	CASP4	caspase 4, apoptosis-related cysteine peptidase	0.3597	0.0194
16743890	CASP1	caspase 1, apoptosis-related cysteine peptidase	0.3339	0.0168
16743912	CARD16	caspase recruitment domain family, member 16	0.3118	0.0018
16743938			0.453	0.015
16744247	POU2AF1	POU class 2 associating factor 1	0.1445	0.0228
16744949	SCN4B	sodium channel, voltage-gated, type IV, beta subunit	0.2212	0.0035
16744967	AMICA1	adhesion molecule, interacts with CXADR antigen 1	0.3136	0.0327
16745016	CD3D	CD3d molecule, delta (CD3-TCR complex)	0.4425	0.001
16745452	LOC649133	uncharacterized LOC649133	0.1188	0.0408
16745467			0.232	0.0012
16745635	OR10G7	olfactory receptor, family 10, subfamily G, member 7	0.3668	0.0007
16745658	SIAE	sialic acid acetylesterase	0.3942	0.0222
16745752	HEPN1	hepatocellular carcinoma, down-regulated 1	0.1508	0.0038
16745843	PATE2	prostate and testis expressed 2	0.1928	0.0049
16745992			0.2345	0.029
16746095			0.1621	0.0259
16746225	LOC100507431	uncharacterized LOC100507431	0.1074	0.0491
16746269			0.3135	0.0006
16746316			0.1484	0.0308
16746450	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	0.1701	0.005
16746466			0.1604	0.0023
16746492	IQSEC3	IQ motif and Sec7 domain 3	0.2805	0.0272
16746574			0.246	0.0402
16746577			0.2065	0.0405
16746798	CACNA1C-IT1	CACNA1C intronic transcript 1 (non-protein coding)	0.1848	0.0462
16746946	TSPAN9-IT1	TSPAN9 intronic transcript 1 (non-protein coding)	0.1699	0.0292
16746959	PRMT8	protein arginine methyltransferase 8	0.1023	0.0341

16747077	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	0.3336	0.0359
16747211	PLEKHG6	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	0.1761	0.0091
16747270	TAPBPL	TAP binding protein-like	0.4543	0.0012
16747417	CD4	CD4 molecule	0.4437	0.0018
16747566	RPL13P5	ribosomal protein L13 pseudogene 5	0.3544	0.0079
16747658			0.1985	0.0308
16747665	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	0.2505	0.0205
16747852	NANOG	Nanog homeobox	0.3542	0.0109
16747986			0.2469	0.0066
16748010			0.5414	0.0031
16748205	CLEC2D	C-type lectin domain family 2, member D	0.1766	0.0467
16748224			0.1192	0.0449
16748275	CLEC9A	C-type lectin domain family 9, member A	0.4603	0.0029
16748351			0.1357	0.0487
16748498	MIR613	microRNA 613	0.162	0.0162
16748529	GPRC5A	G protein-coupled receptor, family C, group 5, member A	1.1293	0.0006
16748539	LOC100506314	uncharacterized LOC100506314	0.2827	0.0301
16748675	H2AFJ	H2A histone family, member J	0.374	0.0461
16748831	MIR3974	microRNA 3974	0.2411	0.0468
16748835	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	0.5296	0.0461
16749216			0.1261	0.0262
16749398	STK38L	serine/threonine kinase 38 like	0.2391	0.0312
16749423	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.5951	0.0003
16749575	RN5S355	RNA, 5S ribosomal 355	0.3167	0.0451
16749747	C12orf35	chromosome 12 open reading frame 35	0.4489	0.013
16749885			0.1939	0.0362
16750209			0.1722	0.0361
16750317			0.8212	0.0066
16750413			0.3826	0.0038
16750429	MIR4698	microRNA 4698	0.2122	0.0311
16750431			0.6877	0.0426
16750523	PFKM	phosphofructokinase, muscle	0.315	0.0053
16750628			0.1378	0.0344
16751080			0.3288	0.0162
16751180	TMPRSS12	transmembrane (C-terminal) protease, serine 12	0.1082	0.0429
16751202	HIGD1C	HIG1 hypoxia inducible domain family, member 1C	0.2086	0.0358
16751354	LOC728503	uncharacterized LOC728503	0.1904	0.0135
16751518	KRT86	keratin 86	0.2054	0.0313
16751973	LOC400043	uncharacterized LOC400043	0.6353	0.0249
16752021	COPZ1	coatomer protein complex, subunit zeta 1	0.2802	0.0104
16752026			0.5106	0.0305
16752154	OR10A7	olfactory receptor, family 10, subfamily A, member 7	0.1795	0.0191
16752172	OR6C76	olfactory receptor, family 6, subfamily C, member 76	0.1724	0.0109
16752190	RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	0.209	0.0173
16752322	RAB5B	RAB5B, member RAS oncogene family	0.2278	0.0147
16752586	NABP2	nucleic acid binding protein 2	0.2247	0.043
16752624	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)	0.6256	0.015
16753243	LOC100506869	uncharacterized LOC100506869	0.1708	0.0207
16753583			0.3976	0.0041
16753689	HELB	helicase (DNA) B	0.3284	0.0262
16753710			0.2541	0.0212
16753890			0.1429	0.0096
16754177	TMEM19	transmembrane protein 19	0.2766	0.0375
16754316			0.1971	0.0204
16754450			0.1847	0.0113
16754459			0.3751	0.0164
16754463			0.2274	0.0328
16754467			0.1969	0.021

16754779			0.1389	0.0244
16754846	LRRIQ1	leucine-rich repeats and IQ motif containing 1	0.3375	0.0067
16754970			0.1947	0.005
16755101			0.2743	0.0204
16755103	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	0.2903	0.049
16755223	KRT19P2	keratin 19 pseudogene 2	0.3934	0.0352
16755265	MIR331	microRNA 331	0.2449	0.0184
16755462			0.1222	0.0272
16755491			0.2546	0.0178
16755493			0.1483	0.0499
16755540			0.2098	0.0291
16755908	DRAM1	DNA-damage regulated autophagy modulator 1	0.4891	0.0048
16755958	ASCL1	achaete-scute complex homolog 1 (Drosophila)	0.2857	0.0345
16756241	KIAA1033	KIAA1033	0.2484	0.0411
16756286	C12orf75	chromosome 12 open reading frame 75	1.4643	0
16756304			0.4148	0.0328
16756310	TCP11L2	t-complex 11 (mouse)-like 2	0.542	0.0001
16756334	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	0.3218	0.0157
16756503	ASCL4	achaete-scute complex homolog 4 (Drosophila)	0.2048	0.0044
16756507			0.157	0.0277
16756547	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	0.4017	0.0462
16756597	USP30	ubiquitin specific peptidase 30	0.3	0.0193
16756757	UBE3B	ubiquitin protein ligase E3B	0.3122	0.0162
16756829	MIR4497	microRNA 4497	0.4927	0.0004
16756895	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	0.5506	0.0036
16756995	TCTN1	tectonic family member 1	0.5802	0
16757032			0.1349	0.0307
16757160	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	0.5917	0.0261
16757181	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	0.3508	0.0222
16757248			0.2934	0.0141
16757253			0.1847	0.0092
16757255	PTPN11	protein tyrosine phosphatase, non-receptor type 11	0.2577	0.0427
16757427	TPCN1	two pore segment channel 1	0.452	0.0108
16757510			0.3255	0.0002
16757586			0.2669	0.0009
16757603	LINC00173	long intergenic non-protein coding RNA 173	0.4273	0.0204
16757633			0.2605	0.0029
16757684			0.1679	0.01
16757766	HSPB8	heat shock 22kDa protein 8	0.7068	0.0029
16757902	DYNLL1	dynein, light chain, LC8-type 1	0.1948	0.0208
16757969	MLEC	malectin	0.5649	0.0001
16758005			0.1555	0.0337
16758052	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	0.5841	0.0069
16758163	SETD1B	SET domain containing 1B	0.3696	0.0009
16758536	ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4	0.2101	0.007
16758549	ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4	0.3223	0.0008
16758612	TMED2	transmembrane emp24 domain trafficking protein 2	0.2002	0.0258
16758618			0.2601	0.0066
16758619			0.269	0.005
16758671	TCTN2	tectonic family member 2	0.6099	0.0005
16758817	ZNF664	zinc finger protein 664	0.2509	0.0281
16758879	BRI3BP	BRI3 binding protein	0.3094	0.0275
16759081			0.123	0.0444
16759619			0.465	0.0039
16759652	ZNF140	zinc finger protein 140	0.4136	0.0482
16759855	NINJ2	ninjurin 2	0.1301	0.0409
16760139			0.1621	0.0493
16760329	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	0.2819	0.0144
16760380	CD27-AS1	CD27 antisense RNA 1 (non-protein coding)	0.2207	0.0138

16760393	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	0.2228	0.0445
16760406	MRPL51	mitochondrial ribosomal protein L51	0.2016	0.0227
16760516	LPAR5	lysophosphatidic acid receptor 5	0.5075	0.0205
16760523	ACRBP	acrosin binding protein	0.1838	0.0161
16760546	ING4	inhibitor of growth family, member 4	0.3192	0.003
16760896	FAM90A1	family with sequence similarity 90, member A1	0.4841	0.0263
16761130			0.1855	0.005
16761139	LOC100509445	uncharacterized LOC100509445	0.2462	0.027
16761176	KLRB1	killer cell lectin-like receptor subfamily B, member 1	0.4489	0.006
16761193	CLECL1	C-type lectin-like 1	0.2887	0.0021
16761201	CD69	CD69 molecule	0.5	0.0002
16761269	CLEC7A	C-type lectin domain family 7, member A	0.5186	0.0094
16761663	HEBP1	heme binding protein 1	0.5252	0.0028
16761877	EPS8	epidermal growth factor receptor pathway substrate 8	0.5147	0.0208
16762037			0.1363	0.0252
16762234			0.1247	0.0238
16762370	CASC1	cancer susceptibility candidate 1	0.7431	0.0007
16762440			0.2559	0.0108
16762634	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.1577	0.0244
16762686			0.1644	0.0405
16762689			0.1955	0.0065
16762871			0.1934	0.0103
16763060	SYT10	synaptotagmin X	0.1955	0.0438
16763099			0.1185	0.0473
16763280	ZCRB1	zinc finger CCHC-type and RNA binding motif 1	0.4671	0.0007
16763295	PRICKLE1	prickle homolog 1 (Drosophila)	0.2332	0.0391
16763373			0.6251	0.0017
16763375	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	0.5624	0.0042
16763456			0.3309	0.0032
16763458	DBX2	developing brain homeobox 2	0.1467	0.0104
16763882	ASB8	ankyrin repeat and SOCS box containing 8	0.2622	0.0431
16764068	ARF3	ADP-ribosylation factor 3	0.1964	0.0284
16764071			0.2947	0.042
16764080			0.3851	0.0313
16764089			0.2732	0.0352
16764110			0.6994	0.0288
16764111			0.6994	0.0288
16764131	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0.1829	0.0415
16764331			0.1637	0.0254
16764398	FMNL3	formin-like 3	0.3721	0.0262
16764564	LIMA1	LIM domain and actin binding 1	0.4789	0.0156
16764620	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	0.3707	0.0161
16764732	BIN2	bridging integrator 2	0.2123	0.0418
16764791	KRT80	keratin 80	1.1993	0.003
16764805	LOC283403	uncharacterized LOC283403	0.1782	0.0034
16764989	KRT72	keratin 72	0.2266	0.0355
16765404	CALCOCO1	calcium binding and coiled-coil domain 1	0.2391	0.0378
16765476	LOC100240735	uncharacterized LOC100240735	0.937	0.0008
16765491	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	0.1983	0.0442
16765622			0.5317	0.0072
16765900	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	0.2555	0.0328
16765998			0.2967	0.0432
16766334	SDR9C7	short chain dehydrogenase/reductase family 9C, member 7	0.1909	0.0005
16766420	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	0.4128	0.017
16766789			0.2519	0.0027

16766870			0.1698	0.0142
16767081	WIF1	WNT inhibitory factor 1	1.1015	0.0426
16767142	TMBIM4	transmembrane BAX inhibitor motif containing 4	0.272	0.0132
16767170	GRIP1	glutamate receptor interacting protein 1	0.8109	0.0003
16767208			0.6129	0.0095
16767213			0.1371	0.035
16767225			0.1078	0.04
16767306			0.1626	0.0107
16767373	BEST3	bestrophin 3	0.1689	0.0471
16767497			0.1572	0.0097
16767621			0.1308	0.0164
16767642	LOC100507377	uncharacterized LOC100507377	0.2471	0.0492
16767886			0.2247	0.0002
16767896			0.1033	0.032
16767901			0.2377	0.0148
16767911	PAWR	PRKC, apoptosis, WT1, regulator	0.3607	0.0485
16768088			0.1088	0.038
16768094			0.2678	0.0015
16768097			0.1842	0.0125
16768287	LOC728084	uncharacterized LOC728084	0.1748	0.0195
16768526			0.2053	0.0406
16768710			0.208	0.0286
16768890			0.173	0.022
16768896			0.2047	0.0034
16769110	ARL1	ADP-ribosylation factor-like 1	0.2945	0.0229
16769159	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	1.0555	0
16769198			0.3669	0.0022
16769250	IGF1	insulin-like growth factor 1 (somatomedin C)	1.0505	0.0053
16769264	LINC00485	long intergenic non-protein coding RNA 485	0.4398	0.0358
16769270	PAH	phenylalanine hydroxylase	0.8538	0.0398
16769311			0.1456	0.0105
16769347			0.1633	0.0344
16769362	NT5DC3	5'-nucleotidase domain containing 3	0.4607	0.0472
16769514	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0.629	0.0002
16769561			0.2153	0.0238
16769569	NUAK1	NUAK family, SNF1-like kinase, 1	0.5663	0.0212
16769585	CKAP4	cytoskeleton-associated protein 4	0.2106	0.0384
16769646			0.4285	0.0008
16769649	PRDM4	PR domain containing 4	0.426	0.0073
16769770	SELPLG	selectin P ligand	0.4023	0.0384
16769840	SVOP	SV2 related protein homolog (rat)	0.1741	0.0132
16769865	USP30-AS1	USP30 antisense RNA 1 (non-protein coding)	0.4663	0.0004
16770189	FAM109A	family with sequence similarity 109, member A	0.3009	0.0009
16770281	TMEM116	transmembrane protein 116	0.3276	0.0094
16770627	RBM19	RNA binding motif protein 19	0.3745	0.0156
16771004			0.1382	0.0354
16771045			0.5196	0.0042
16771065			0.2319	0.0302
16771242	PXN	paxillin	0.6523	0.007
16771339			0.1815	0.0328
16771356			0.5323	0.0005
16771364			0.1286	0.0469
16771464			0.4084	0.047
16771465			0.3875	0.0237
16771476			0.3561	0.0318
16771502			0.3503	0.0462
16771525			0.4053	0.0476
16771532			1.0525	0.0036
16771652	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	0.3381	0.0258

16771998	RILPL2	Rab interacting lysosomal protein-like 2	0.3026	0.0245
16772039			0.7189	0.0033
16772042	CCDC92	coiled-coil domain containing 92	0.2327	0.0121
16772071			0.3269	0.0005
16772234			0.5574	0.003
16772271			0.1885	0.0142
16772322			0.2079	0.0077
16772552			0.2759	0.0007
16772555			0.1385	0.0435
16772808			0.4223	0.0033
16772864	RNU6-76	RNA, U6 small nuclear 76	0.2524	0.032
16773041			0.1078	0.0409
16773073			0.1945	0.0009
16773157			0.1474	0.0455
16773163			0.1414	0.0299
16773260	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	0.2217	0.0003
16773756			0.2167	0.0395
16773939			0.2214	0.0035
16774384	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	0.1367	0.0297
16774612	RN7SKP5	RNA, 7SK small nuclear pseudogene 5	0.2242	0.015
16774614	RNU6-68	RNA, U6 small nuclear 68	0.236	0.0011
16774616			0.2129	0.01
16774655	HTR2A-AS1	HTR2A antisense RNA 1 (non-protein coding)	0.1436	0.0219
16774679	ITM2B	integral membrane protein 2B	0.3189	0.0453
16774724	CYSLTR2	cysteinyl leukotriene receptor 2	3.0514	0
16775030	TPTE2P3	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 3	0.1851	0.0334
16775096			0.105	0.0427
16775109			0.1407	0.0049
16775201			0.1229	0.0451
16775206			0.1375	0.0343
16775223			0.1911	0.0143
16775260			0.4493	0.0018
16775301	ATXN8OS	ATXN8 opposite strand (non-protein coding)	0.1312	0.0163
16775520	CLN5	ceroid-lipofuscinosis, neuronal 5	0.3709	0.0465
16775665			0.1133	0.0104
16775668			0.1473	0.0282
16775676			0.1176	0.0312
16775871	HS6ST3	heparan sulfate 6-O-sulfotransferase 3	1.3395	0.0125
16775879			0.2375	0.0274
16776080	CLYBL	citrate lyase beta like	0.4049	0.0403
16776583	TEX29	testis expressed 29	0.3083	0.0023
16777112			0.201	0.0185
16777252			0.1627	0.0155
16777756	SLC46A3	solute carrier family 46, member 3	1.1326	0.0048
16777773	MTUS2-AS1	MTUS2 antisense RNA 1 (non-protein coding)	0.2443	0.0084
16777896	HSPH1	heat shock 105kDa/110kDa protein 1	0.3874	0.0468
16778000			0.1619	0.0188
16778053	LINC00457	long intergenic non-protein coding RNA 457	0.1393	0.0153
16778096			0.1599	0.0334
16778235	RN7SKP1	RNA, 7SK small nuclear pseudogene 1	0.1953	0.0003
16778553			0.1262	0.0401
16778559	EPSTI1	epithelial stromal interaction 1 (breast)	0.3668	0.0429
16778644			0.1286	0.0472
16778681			0.1255	0.0339
16778745	SLC25A30	solute carrier family 25, member 30	0.5767	0.0223
16778849	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	0.4198	0.0144
16778879			0.2094	0.0421
16778938	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	0.6097	0.0451

16779104			0.1792	0.0377
16779184	DLEU7	deleted in lymphocytic leukemia, 7	0.2043	0.0039
16779466			0.199	0.023
16779584			0.1515	0.0439
16779587			0.1809	0.0235
16779634			0.2102	0.0391
16779637			0.1648	0.0481
16779839	KCTD12	potassium channel tetramerisation domain containing 12	0.5926	0.0156
16780092	SLITRK1	SLIT and NTRK-like family, member 1	0.1895	0.0091
16780126	RNU6-72	RNA, U6 small nuclear 72	0.225	0.0098
16780229			0.2186	0.0113
16780604			0.205	0.0215
16780699	NALCN	sodium leak channel, non-selective	0.7626	0.0226
16781092	ARHGEF7-AS1	ARHGEF7 antisense RNA 1 (non-protein coding)	0.1798	0.0334
16781268	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	0.1748	0.013
16781285	GAS6	growth arrest-specific 6	0.2549	0.0255
16781315	RASA3	RAS p21 protein activator 3	0.2605	0.0487
16781345			0.1486	0.0295
16781431	OR4N2	olfactory receptor, family 4, subfamily N, member 2	0.1844	0.0205
16781448	OR4K5	olfactory receptor, family 4, subfamily K, member 5	0.1761	0.0299
16781464	OR4K17	olfactory receptor, family 4, subfamily K, member 17	0.1435	0.045
16781591	RNASE6	ribonuclease, RNase A family, k6	0.5437	0.0423
16781834	TRAV4	T cell receptor alpha variable 4	0.2007	0.0163
16781856	TRAV10	T cell receptor alpha variable 10	0.2297	0.0036
16781893	TRAV12-3	T cell receptor alpha variable 12-3	0.3149	0.0175
16781934	TRAV24	T cell receptor alpha variable 24	0.1296	0.0411
16781937	TRAV25	T cell receptor alpha variable 25	0.1601	0.0065
16781954	TRAV29DV5	T cell receptor alpha variable 29/delta variable 5 (gene/pseudogene)	0.2971	0.0009
16782003	TRDC	T cell receptor delta constant	0.5595	0.0044
16782008	TRAJ61	T cell receptor alpha joining 61 (non-functional)	0.188	0.0206
16782018	TRAJ54	T cell receptor alpha joining 54	0.2042	0.038
16782020	TRAJ53	T cell receptor alpha joining 53	0.2153	0.0006
16782022	TRAJ52	T cell receptor alpha joining 52	0.135	0.0487
16782028	TRAJ48	T cell receptor alpha joining 48	0.2608	0.007
16782032	TRAJ46	T cell receptor alpha joining 46	0.3205	0.0423
16782034	TRAJ45	T cell receptor alpha joining 45	0.261	0.0085
16782060	TRAJ32	T cell receptor alpha joining 32	0.3206	0.0051
16782072	TRAJ26	T cell receptor alpha joining 26	0.1565	0.0446
16782078	TRAJ23	T cell receptor alpha joining 23	0.3017	0.0198
16782084	TRAJ20	T cell receptor alpha joining 20	0.2544	0.0176
16782094	TRAJ14	T cell receptor alpha joining 14	0.2618	0.0101
16782096	TRAJ13	T cell receptor alpha joining 13	0.1941	0.0082
16782098	TRAJ12	T cell receptor alpha joining 12	0.1608	0.0124
16782102	TRAJ10	T cell receptor alpha joining 10	0.2379	0.0164
16782106	TRAJ8	T cell receptor alpha joining 8	0.2099	0.0175
16782122	TRAJ17	T cell receptor alpha joining 17	0.9325	0.0025
16782901			0.1248	0.0403
16782939			0.3416	0.0382
16782949			0.41	0.0242
16782980	C14orf23	chromosome 14 open reading frame 23	0.1586	0.0051
16783265	NPAS3	neuronal PAS domain protein 3	0.3009	0.0415
16783467	NKX2-1-AS1	NKX2-1 antisense RNA 1 (non-protein coding)	0.2028	0.0176
16783755			0.2025	0.0167
16784064			0.2671	0.0065
16784201	PTGDR	prostaglandin D2 receptor (DP)	0.5702	0.0002
16784365			0.3853	0.0155
16784556			0.1334	0.0405
16784780			0.2316	0.0056
16785379	HSPA2	heat shock 70kDa protein 2	0.794	0.0037

16786064	RGS6	regulator of G-protein signaling 6	0.1918	0.0096
16787049			0.563	0.0139
16787118	RNU3P3	RNA, U3 small nucleolar pseudogene 3	0.2064	0.0125
16787208	GPR65	G protein-coupled receptor 65	0.4728	0.0218
16787231			0.1656	0.043
16787528	RNU7-30P	RNA, U7 small nuclear 30 pseudogene	0.1815	0.0132
16787597	RIN3	Ras and Rab interactor 3	0.5328	0.006
16788296	EML1	echinoderm microtubule associated protein like 1	0.4481	0.0392
16789174	LOC441698	ras-related protein Rap-2c-like	0.243	0.0383
16789569			0.2099	0.0082
16789573	PLD4	phospholipase D family, member 4	0.2728	0.0306
16790460			0.1405	0.022
16790527			0.2553	0.0257
16791371	RIPK3	receptor-interacting serine-threonine kinase 3	0.1986	0.0032
16791436	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	0.4184	0.0001
16791444	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	0.268	0.0045
16791793	GPR33	G protein-coupled receptor 33 (gene/pseudogene)	0.2139	0.0006
16791800			0.1682	0.0157
16792079			0.1188	0.0377
16792096			0.1959	0.0389
16792144	NKX2-8	NK2 homeobox 8	0.187	0.0206
16792287	FBXO33	F-box protein 33	0.341	0.0084
16792305			0.1228	0.0337
16792888			0.1297	0.0215
16792894	TRIM9	tripartite motif containing 9	0.774	0.0005
16792927			0.1815	0.0084
16793421			0.4647	0.0294
16793822			0.1301	0.0499
16793936			0.1851	0.0411
16794276			0.2688	0.0268
16794401			0.2409	0.022
16794403			0.1404	0.0338
16795268			0.2968	0.0001
16795276			0.1859	0.0157
16795463			0.1173	0.0308
16795908	CATSPERB	catsper channel auxiliary subunit beta	0.1396	0.0321
16796015			0.2265	0.028
16796319			0.1428	0.0487
16796475	LOC100130815	uncharacterized LOC100130815	0.1366	0.0351
16796604			0.2017	0.0281
16796727	BEGAIN	brain-enriched guanylate kinase-associated homolog (rat)	0.2079	0.0441
16797121	MIR3545	microRNA 3545	0.1587	0.0037
16797196	AHNAK2	AHNAK nucleoprotein 2	0.438	0.0034
16797389	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	0.5118	0.0402
16797440	ADAM6	ADAM metallopeptidase domain 6 (pseudogene)	0.4861	0.0102
16797451			0.2713	0.0017
16797483	IGHV3-16	immunoglobulin heavy variable 3-16 (non-functional)	0.1706	0.036
16797545	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	0.2029	0.0163
16797555	IGHM	immunoglobulin heavy constant mu	0.341	0.0114
16797725	OR4N4	olfactory receptor, family 4, subfamily N, member 4	0.1344	0.0074
16797968			0.1927	0.0492
16798343	SNORD115-21	small nucleolar RNA, C/D box 115-21	0.1096	0.048
16798404	SNORD115-30	small nucleolar RNA, C/D box 115-30	0.1329	0.0361
16798426	SNORD115-41	small nucleolar RNA, C/D box 115-41	0.2299	0.0031
16798479	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	0.2048	0.0417
16799109			0.3475	0.0416
16799167			0.1247	0.0314

16799273	C15orf53	chromosome 15 open reading frame 53	0.2072	0.0066
16799289	C15orf54	chromosome 15 open reading frame 54	0.3404	0.0171
16799514			0.158	0.033
16800117	STARD9	StAR-related lipid transfer (START) domain containing 9	0.1786	0.0106
16800229	MAP1A	microtubule-associated protein 1A	0.9052	0.0006
16800242	CKMT1B	creatine kinase, mitochondrial 1B	0.8413	0.0065
16800692			0.3153	0.0028
16800753			0.2633	0.0227
16800962	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	1.8933	0.0008
16800978			0.1876	0.0068
16801108	SCG3	secretogranin III	0.9445	0.0481
16801239			0.1834	0.0027
16801695	C2CD4A	C2 calcium-dependent domain containing 4A	0.2435	0.0318
16801925	FBXL22	F-box and leucine-rich repeat protein 22	0.1763	0.0425
16802247			0.2525	0.0183
16802698			0.1429	0.0305
16802700			0.4687	0.0029
16802900			0.8099	0.0271
16803370	TSPAN3	tetraspanin 3	0.1614	0.041
16803399			0.1612	0.0467
16803417			0.4589	0.014
16803577	LOC646938	TBC1 domain family, member 2B pseudogene	0.2027	0.0096
16803807	IL16	interleukin 16	0.2153	0.0048
16804234			0.1713	0.0337
16804707	MIR3174	microRNA 3174	0.2537	0.0439
16805124	SV2B	synaptic vesicle glycoprotein 2B	1.0337	0.0367
16805151			0.1815	0.041
16805324			0.1495	0.0417
16805486			0.2001	0.0285
16805590			0.2018	0.0057
16805797	OR4F15	olfactory receptor, family 4, subfamily F, member 15	0.1542	0.048
16805804	FAM138E	family with sequence similarity 138, member E	0.2201	0.0041
16805825			0.3741	0.0034
16805870	NBEAP1	neurobeachin pseudogene 1	0.2156	0.0485
16805896			0.5146	0.0105
16805924			0.4255	0.006
16807233			0.2437	0.0222
16807257			0.1843	0.037
16807263			0.1406	0.0206
16807271	FSIP1	fibrous sheath interacting protein 1	0.1492	0.0475
16807420			0.2213	0.0303
16807761	MIR4310	microRNA 4310	0.463	0.0029
16808063			0.1117	0.0402
16808336	PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	0.3743	0.0382
16808550	LOC100652936	uncharacterized LOC100652936	0.554	0.0405
16808665	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	1.0754	0.0013
16808708			0.1646	0.0446
16809027	ATP8B4	ATPase, class I, type 8B, member 4	0.5144	0.0063
16809219	TNFAIP8L3	tumor necrosis factor, alpha-induced protein 8-like 3	0.2731	0.0088
16809319			0.2444	0.0064
16809322			0.1564	0.0277
16810011	MIR2116	microRNA 2116	0.1809	0.0455
16810165			0.2399	0.0486
16810298	MGC15885	uncharacterized protein MGC15885	0.143	0.0346
16810341	CA12	carbonic anhydrase XII	0.2089	0.0098
16811185			0.113	0.0289
16811523	LOXL1-AS1	LOXL1 antisense RNA 1 (non-protein coding)	0.2868	0.0207
16811751			0.1229	0.0091

16812274	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	0.6962	0.0478
16812381	MIR549	microRNA 549	0.1127	0.0125
16813010	DET1	de-etiolated homolog 1 (Arabidopsis)	0.1589	0.0311
16813024	MIR3529	microRNA 3529	0.2167	0.0038
16813038	MFGE8	milk fat globule-EGF factor 8 protein	0.5765	0.0192
16813425			0.1808	0.0213
16813627			0.1382	0.0138
16814170	ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	0.1955	0.0266
16814230	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	0.2065	0.0446
16814310	PIGQ	phosphatidylinositol glycan anchor biosynthesis, class Q	0.2074	0.039
16814619	TPSAB1	tryptase alpha/beta 1	0.3708	0.0461
16814636	UBE2I	ubiquitin-conjugating enzyme E2I	0.3431	0.0007
16814854	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	0.2849	0.0299
16814910	NPW	neuropeptide W	0.2237	0.0101
16815023	MLST8	MTOR associated protein, LST8 homolog (S. cerevisiae)	0.1904	0.0449
16815072	ABCA17P	ATP-binding cassette, sub-family A (ABC1), member 17, pseudogene	0.2585	0.0327
16815128	TBC1D24	TBC1 domain family, member 24	0.3583	0.0036
16815259	FLYWCH1	FLYWCH-type zinc finger 1	0.2176	0.0065
16815461	CLUAP1	clusterin associated protein 1	0.2672	0.0365
16815498	GLIS2	GLIS family zinc finger 2	0.5679	0.0032
16815586	C16orf71	chromosome 16 open reading frame 71	0.1601	0.0064
16815735	ABAT	4-aminobutyrate aminotransferase	2.023	0
16815807	LOC100287628	uncharacterized LOC100287628	0.7736	0.0274
16815828	CIITA	class II, major histocompatibility complex, transactivator	0.5119	0.0194
16815852	LOC100505564	uncharacterized LOC100505564	0.3973	0.0045
16815903			0.225	0.0235
16815918	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	0.2331	0.0198
16816102	NOMO1	NODAL modulator 1	0.3425	0.0445
16816140	PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	0.3328	0.0082
16816171			0.2071	0.0209
16816373	ABCC6P1	ATP-binding cassette, sub-family C, member 6 pseudogene 1	0.4787	0.0034
16816408	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	0.2996	0.0208
16816542	IQCK	IQ motif containing K	0.3254	0.014
16816739	UQCRC2	ubiquinol-cytochrome c reductase core protein II	0.437	0.0016
16817212	RN5S405	RNA, 5S ribosomal 405	0.3223	0.0462
16817254	IL4R	interleukin 4 receptor	0.323	0.0355
16817283	KIAA0556	KIAA0556	0.1891	0.0384
16817314			0.174	0.0126
16817601	LOC606724	coronin, actin binding protein, 1A pseudogene	0.2509	0.0159
16817624	SPN	sialophorin	0.2177	0.0485
16817692	MVP	major vault protein	0.6744	0.001
16817860	MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle	0.1178	0.0416
16817883	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	0.4145	0.0002
16818114	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0.2632	0.018
16818125	STX4	syntaxin 4	0.3192	0.0018
16818165	BCKDK	branched chain ketoacid dehydrogenase kinase	0.49	0.0104
16818305	ITGAD	integrin, alpha D	0.1696	0.0054
16818431	ZNF267	zinc finger protein 267	0.4529	0.0089
16818440			0.2003	0.0272
16818696			0.1917	0.0055
16818820	NOD2	nucleotide-binding oligomerization domain containing 2	0.133	0.0333
16818842	CYLD	cylindromatosis (turban tumor syndrome)	0.4787	0.0121

16818866			0.1564	0.0212
16818880			0.1724	0.0304
16818883			0.1812	0.0056
16818897			0.221	0.0201
16818925			0.1712	0.018
16818980	RBL2	retinoblastoma-like 2 (p130)	0.4586	0.0065
16819010	FTO	fat mass and obesity associated	0.307	0.0081
16819062	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	0.1272	0.0441
16819082	LPCAT2	lysophosphatidylcholine acyltransferase 2	1.436	0.0001
16819099	CAPNS2	calpain, small subunit 2	0.1718	0.0324
16819247	MT1B	metallothionein 1B	0.2058	0.0249
16819262	MT1IP	metallothionein 1I, pseudogene	0.2091	0.0073
16819325	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	0.5559	0.0058
16819336	CETP	cholesteryl ester transfer protein, plasma	0.4342	0.0206
16819355	NLRC5	NLR family, CARD domain containing 5	0.3361	0.014
16819600	KATNB1	katanin p80 (WD repeat containing) subunit B 1	0.2913	0.0169
16819630	TEPP	testis, prostate and placenta expressed	0.1342	0.0193
16819666	CCDC113	coiled-coil domain containing 113	0.5344	0.0213
16819689	NDRG4	NDRG family member 4	1.3194	0.0008
16819714			1.008	0.0066
16819774			0.2577	0
16819813	LOC100505865	uncharacterized LOC100505865	0.6003	0.0055
16819961	C16orf70	chromosome 16 open reading frame 70	0.293	0.0087
16820388	PLA2G15	phospholipase A2, group XV	0.554	0.0058
16820439	ZFP90	zinc finger protein 90 homolog (mouse)	0.4072	0.0249
16820818	SNORD111B	small nucleolar RNA, C/D box 111B	0.2193	0.0167
16820838			0.3636	0.0027
16820849	CALB2	calbindin 2	1.1868	0.0437
16820863	LOC100506105	uncharacterized LOC100506105	0.1375	0.0187
16820868			0.1841	0.0291
16820873	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	0.3937	0.026
16820883	MARVELD3	MARVEL domain containing 3	0.2266	0.0023
16820999	LOC100506172	uncharacterized LOC100506172	0.2096	0.0035
16821008			0.1711	0.0059
16821072	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	0.8622	0.002
16821076	GABARAPL2	GABA(A) receptor-associated protein-like 2	0.4354	0.0058
16821139	MON1B	MON1 homolog B (yeast)	0.2738	0.0354
16821193	WWOX	WW domain containing oxidoreductase	0.236	0.0119
16821266	BCMO1	beta-carotene 15,15'-monooxygenase 1	0.1577	0.0185
16821614	COX4I1	cytochrome c oxidase subunit IV isoform 1	0.2175	0.0122
16821615			0.3963	0.0221
16821618			0.1967	0.013
16821619			0.2375	0.0076
16821620			0.1828	0.0077
16821621	IRF8	interferon regulatory factor 8	0.3023	0.0237
16821687			0.1562	0.0331
16822089	ZNF276	zinc finger protein 276	0.2433	0.0138
16822224	GAS8	growth arrest-specific 8	0.3344	0.0045
16822548	NARFL	nuclear prelamin A recognition factor-like	0.3109	0.0029
16822589	GNG13	guanine nucleotide binding protein (G protein), gamma 13	0.1248	0.0189
16822637	TPSB2	tryptase beta 2 (gene/pseudogene)	0.3946	0.0345
16822762	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	0.2551	0.0107
16823109	ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	0.9408	0.0012
16823200			0.1901	0.0149
16823210			0.2422	0.0473
16823212	PRSS30P	protease, serine, 30 homolog (mouse), pseudogene	0.1639	0.0499

16823215	PRSS22	protease, serine, 22	0.1942	0.0191
16823255	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	0.5279	0.0019
16823393	SLX4	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae)	0.125	0.0284
16823570	C16orf5	chromosome 16 open reading frame 5	0.5306	0.0006
16823666	PPL	periplakin	1.1102	0
16823736			0.1513	0.0153
16823738			0.1674	0.0378
16823744	RNU7-63P	RNA, U7 small nuclear 63 pseudogene	0.2131	0.0062
16824429	NOMO2	NODAL modulator 2	0.2807	0.0456
16824639	ACSM2B	acyl-CoA synthetase medium-chain family member 2B	0.283	0.0102
16824907	IGSF6	immunoglobulin superfamily, member 6	0.3195	0.0416
16824989	CDR2	cerebellar degeneration-related protein 2, 62kDa	0.3291	0.0424
16825035	COG7	component of oligomeric golgi complex 7	0.3254	0.0102
16825193			0.1335	0.0213
16825196	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	0.4903	0.004
16825371	NUPR1	nuclear protein, transcriptional regulator, 1	1.0348	0.0199
16825561	SEZ6L2	seizure related 6 homolog (mouse)-like 2	0.6985	0.0002
16825779	1-Sep	septin 1	0.2424	0.0119
16825800	SEPHS2	selenophosphate synthetase 2	0.3059	0.0246
16825828	ZNF764	zinc finger protein 764	0.2374	0.0261
16825970	PRSS8	protease, serine, 8	0.249	0.0441
16826175	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.4297	0.0006
16826218	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	0.361	0.0034
16826389	ZNF423	zinc finger protein 423	0.7319	0.0034
16826414	BRD7	bromodomain containing 7	0.4584	0.0016
16826435			0.28	0.0254
16826444	SNX20	sorting nexin 20	0.1638	0.0123
16826468			0.1443	0.0417
16826539	AKTIP	AKT interacting protein	0.6338	0.0016
16826743	FAM192A	family with sequence similarity 192, member A	0.2711	0.0165
16826779	DOK4	docking protein 4	0.4255	0.0338
16826892	CSNK2A2	casein kinase 2, alpha prime polypeptide	0.3177	0.0388
16826905			0.1642	0.0297
16827016			0.1507	0.0088
16827086			0.1658	0.0003
16827103	TK2	thymidine kinase 2, mitochondrial	0.4533	0.006
16827227	RRAD	Ras-related associated with diabetes	0.6319	0.009
16827243			0.1459	0.0093
16827483	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	0.3104	0.0185
16827874	HYDIN	HYDIN, axonemal central pair apparatus protein	0.4608	0.0026
16827996	FTSJD1	FtsJ methyltransferase domain containing 1	0.3442	0.0018
16828006	ZNF23	zinc finger protein 23 (KOX 16)	0.238	0.0468
16828450	CFDP1	craniofacial development protein 1	0.3103	0.0052
16828471	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	0.7773	0.0043
16828485	TMEM231	transmembrane protein 231	0.7125	0.0001
16828525			0.3427	0.0224
16828542			0.1039	0.0426
16828630	C16orf46	chromosome 16 open reading frame 46	0.2886	0.0286
16828640	GCSH	glycine cleavage system protein H (aminomethyl carrier)	0.4938	0.0048
16828852	FAM92B	family with sequence similarity 92, member B	0.177	0.0407
16829426	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	0.1471	0.039
16829433	C16orf3	chromosome 16 open reading frame 3	0.2786	0.0075
16829437	LOC100130015	5-hydroxyisourate hydrolase pseudogene	0.3086	0.0022
16829718	OR1A2	olfactory receptor, family 1, subfamily A, member 2	0.1965	0.0324
16830455	TMEM102	transmembrane protein 102	0.3066	0.0495
16830837	SCARNA21	small Cajal body-specific RNA 21	0.2034	0.0154

16830863	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)	0.1388	0.0189
16831247	ARHGAP44	Rho GTPase activating protein 44	0.5284	0.0048
16831523			0.1402	0.0254
16831612			0.1789	0.0068
16832015	LOC100132472	uncharacterized LOC100132472	0.2179	0.0059
16832101			0.1659	0.0139
16832227	CDRT15L2	CMT1A duplicated region transcript 15-like 2	0.2193	0.0473
16832312	FLJ36000	uncharacterized FLJ36000	0.251	0.0262
16833000	RAB11FIP4	RAB11 family interacting protein 4 (class II)	0.6667	0.0028
16833017	MIR193A	microRNA 193a	0.281	0.002
16833024	MIR4725	microRNA 4725	0.2924	0.0312
16833164			0.19	0.0119
16833327	SLFN5	schlafen family member 5	1.0567	0.0007
16833336			0.3216	0.0332
16833409			0.2514	0.0378
16833433	CCL4L2	chemokine (C-C motif) ligand 4-like 2	0.5165	0.0002
16833730	LRRC37A11P	leucine rich repeat containing 37, member A11, pseudogene	0.1771	0.0243
16833876	GRB7	growth factor receptor-bound protein 7	0.2027	0.0202
16833901			0.3706	0.0012
16834108			0.1484	0.0261
16834230	TTC25	tetratricopeptide repeat domain 25	0.3511	0.0005
16834302	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	0.3316	0.0236
16834603	TMEM106A	transmembrane protein 106A	0.4802	0.025
16834621	ARL4D	ADP-ribosylation factor-like 4D	0.4428	0.0182
16834664	C17orf105	chromosome 17 open reading frame 105	0.1237	0.031
16834749	RUNDC3A	RUN domain containing 3A	0.6456	0.0113
16834812	DBF4B	DBF4 homolog B (S. cerevisiae)	0.1596	0.0335
16835174	C17orf57	chromosome 17 open reading frame 57	0.4531	0.0034
16835213	NPEPPS	aminopeptidase puromycin sensitive	0.2757	0.0079
16835672	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	0.5631	0.0305
16835711	PDK2	pyruvate dehydrogenase kinase, isozyme 2	0.5812	0.0031
16836214	TOM1L1	target of myb1 (chicken)-like 1	0.5013	0.0362
16836292	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	0.3454	0.0085
16836311	NOG	noggin	0.2329	0.0043
16836409	OR4D1	olfactory receptor, family 4, subfamily D, member 1	0.2306	0.0153
16836624	MIR21	microRNA 21	0.8041	0.0352
16836677			0.2176	0.0255
16837128	PRKCA	protein kinase C, alpha	0.9637	0.0228
16837292			0.2947	0.0171
16837298	AMZ2	archaelysin family metallopeptidase 2	0.3256	0.0413
16837308	ARSG	arylsulfatase G	0.6136	0.0016
16837324			0.2363	0.0181
16837411			0.163	0.0263
16837418	SOX9	SRY (sex determining region Y)-box 9	0.705	0.0002
16837471	LOC400620	uncharacterized LOC400620	0.1275	0.0412
16837609	RAB37	RAB37, member RAS oncogene family	0.2477	0.0102
16837766			0.1357	0.0275
16837820	LLGL2	lethal giant larvae homolog 2 (Drosophila)	0.3593	0.0359
16838001	TEN1-CDK3	TEN1-CDK3 readthrough	0.1794	0.0188
16838040	RNF157-AS1	RNF157 antisense RNA 1 (non-protein coding)	0.2362	0.0082
16838263			0.1969	0.014
16838300	TMC8	transmembrane channel-like 8	0.23	0.0165
16839425	SLC43A2	solute carrier family 43, member 2	0.4145	0.0106
16839443			0.4157	0.0304
16839853	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	0.31	0.0111
16840015			0.1582	0.0499
16840318	NLRP1	NLR family, pyrin domain containing 1	0.7359	0.0399

16840346			0.2469	0.0021
16840442			0.4174	0.0268
16841106	STX8	syntaxin 8	0.3165	0.0308
16841530	MIR548H3	microRNA 548h-3	0.2739	0.0262
16841788			0.1591	0.0314
16842183	ZNF286B	zinc finger protein 286B	0.146	0.0421
16842219			0.1876	0.0474
16842242	B9D1	B9 protein domain 1	0.3655	0.0018
16842403	LGALS9B	lectin, galactoside-binding, soluble, 9B	0.3198	0.0087
16842510			0.5055	0.0397
16842572	KRT18P55	keratin 18 pseudogene 55	0.2324	0.003
16842626	UNC119	unc-119 homolog (C. elegans)	0.3657	0.0492
16843078	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	0.1817	0.0038
16843115	TMIGD1	transmembrane and immunoglobulin domain containing 1	0.1691	0.0073
16843176			0.2092	0.0184
16843179	C17orf79	chromosome 17 open reading frame 79	0.3617	0.004
16843219	ARGFXP2	arginine-fifty homeobox pseudogene 2	0.2184	0.0356
16843303			0.127	0.0274
16843306			0.1685	0.0095
16843446	SLFN12L	schlafen family member 12-like	0.3456	0.0015
16843469	GAS2L2	growth arrest-specific 2 like 2	0.1313	0.0398
16843511	CCL5	chemokine (C-C motif) ligand 5	0.6809	0.0001
16844207	IKZF3	IKAROS family zinc finger 3 (Aiolos)	0.3487	0.0022
16844533	KRT40	keratin 40	0.159	0.0339
16844585	LOC730755	keratin associated protein 2-4-like	0.1641	0.0147
16844622	KRTAP4-2	keratin associated protein 4-2	0.2464	0.049
16844638	KRTAP16-1	keratin associated protein 16-1	0.1608	0.016
16844752	KRT15	keratin 15	0.1733	0.0027
16844775	KRT19	keratin 19	0.2691	0.0256
16845126	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	0.2686	0.0302
16845290			0.2288	0.0004
16845384	TMEM106A-AS1	TMEM106A antisense RNA 1 (non-protein coding)	0.3885	0.0165
16845427	MEOX1	mesenchyme homeobox 1	0.1001	0.0465
16845526			0.1343	0.0429
16845856	LOC339192	uncharacterized LOC339192	0.2179	0.0003
16846157	PRR15L	proline rich 15-like	0.1742	0.0371
16846543			0.2687	0.0484
16846546	SAMD14	sterile alpha motif domain containing 14	0.132	0.0275
16846685			0.3322	0.0212
16846742			0.2925	0.0023
16846849	COX11	COX11 cytochrome c oxidase assembly homolog (yeast)	0.2319	0.0352
16847251	MIR301A	microRNA 301a	0.2085	0.0061
16847258			0.1155	0.0432
16847296	TBC1D3P1-DHX40P1	TBC1D3P1-DHX40P1 readthrough (non-protein coding)	0.1755	0.0448
16847352	LOC653653	adaptor-related protein complex 1, sigma 2 subunit pseudogene	0.2805	0.0126
16847416			0.1626	0.0496
16847483			0.211	0.0076
16847565	CYB561	cytochrome b-561	0.503	0.0124
16847878	PLEKHM1P	pleckstrin homology domain containing, family M (with RUN domain) member 1 pseudogene	0.1823	0.0134
16848070	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.7661	0.0387
16848361			0.1192	0.0181
16848366			0.2741	0.0105
16848405	FLJ37644	uncharacterized LOC400618	0.1908	0.0162

16848938	WBP2	WW domain binding protein 2	0.3091	0.0409
16848993	FBF1	Fas (TNFRSF6) binding factor 1	0.1825	0.0115
16849339	MIR4316	microRNA 4316	0.366	0.0033
16849355	TMC6	transmembrane channel-like 6	0.1308	0.0245
16849576	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	0.7777	0.0044
16849740	MIR657	microRNA 657	0.2186	0.0217
16850189	CSNK1D	casein kinase 1, delta	0.2574	0.0301
16850402			0.7111	0.022
16850501			0.1675	0.0094
16850841			0.1547	0.0224
16851042	ANKRD62	ankyrin repeat domain 62	0.1324	0.0297
16851060			0.2319	0.0214
16851062	C18orf61	uncharacterized LOC497259	0.1607	0.0168
16851303	MIR3156-2	microRNA 3156-2	0.1626	0.0081
16851727	DSG4	desmoglein 4	0.1738	0.014
16851768	DSG2	desmoglein 2	1.1996	0.0321
16851801	RNF125	ring finger protein 125, E3 ubiquitin protein ligase	0.4921	0.0004
16851866	DTNA	dystrobrevin, alpha	1.3446	0.0003
16852486			0.2081	0.0025
16852489			0.2692	0.0143
16852619			0.2256	0
16852622	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.2604	0.005
16852642			0.242	0.0095
16852666	SEC11C	SEC11 homolog C (S. cerevisiae)	0.6292	0.003
16852683	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.6789	0.0079
16852700			0.453	0.0214
16852718			0.2252	0.002
16852824	SERPINB12	serpin peptidase inhibitor, clade B (ovalbumin), member 12	0.1722	0.0384
16852858	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	0.1188	0.0299
16852886	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	0.105	0.0241
16852938	CDH7	cadherin 7, type 2	0.3099	0.0309
16853068	LOC100505838	uncharacterized LOC100505838	0.1475	0.0066
16853135			0.1922	0.0353
16853214			0.1577	0.0138
16853474	LOC100653102	uncharacterized LOC100653102	0.2227	0.0243
16853799	LOC100192426	uncharacterized LOC100192426	0.167	0.0172
16853812			0.1653	0.0077
16853863			0.2429	0.0346
16853879	PIEZO2	piezo-type mechanosensitive ion channel component 2	1.0848	0.0015
16853982			0.1886	0.0235
16854214			0.2434	0.0224
16854357			0.1644	0.0167
16854411			0.144	0.0428
16854414	AQP4	aquaporin 4	0.2953	0.0271
16854463			0.2382	0.0167
16854533	LOC100652770	uncharacterized LOC100652770	0.258	0.0245
16854805			0.1293	0.0411
16855108			0.1507	0.0409
16855161	MIR4744	microRNA 4744	0.1258	0.0267
16855246	CCDC11	coiled-coil domain containing 11	0.4479	0.0096
16855316			0.1216	0.0018
16855340	SNORA37	small nucleolar RNA, H/ACA box 37	0.3913	0.0089
16855355			0.2135	0.0226
16855421	FLJ45743	uncharacterized LOC642484	0.1834	0.0138
16855541	MIR3591	microRNA 3591	0.1798	0.0159
16855761	CDH19	cadherin 19, type 2	0.1617	0.0485
16855810	CD226	CD226 molecule	0.2736	0.006

16855884	LOC100505776	uncharacterized LOC100505776	0.2012	0.006
16855906	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	0.1232	0.0462
16855950			0.1057	0.0413
16856159	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	0.1461	0.0364
16856239	PALM	paralemmin	0.6069	0.0001
16856249	C19orf21	chromosome 19 open reading frame 21	0.2915	0.0177
16856543	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	0.1949	0.031
16856604	REEP6	receptor accessory protein 6	0.8497	0.0128
16856613	PLK5	polo-like kinase 5	0.1641	0.0116
16856828	ZNF554	zinc finger protein 554	0.4593	0.0097
16856834	ZNF555	zinc finger protein 555	0.4723	0.0003
16857248	MIR7-3HG	MIR7-3 host gene (non-protein coding)	0.6992	0.0303
16857252	MIR7-3	microRNA 7-3	0.1386	0.0378
16857438	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	0.2681	0.0325
16857449	CRB3	crumbs homolog 3 (Drosophila)	0.2184	0.0297
16857459	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	0.291	0.0005
16857465			0.2549	0.0268
16857794	LRRC8E	leucine rich repeat containing 8 family, member E	0.6619	0.008
16857968	OR7E24	olfactory receptor, family 7, subfamily E, member 24	0.2298	0.0423
16858049	C3P1	complement component 3 precursor pseudogene	0.136	0.0447
16858435	CCDC159	coiled-coil domain containing 159	0.3142	0.0067
16858519	ZNF441	zinc finger protein 441	0.4062	0.0293
16858546	ZNF439	zinc finger protein 439	0.8031	0.0162
16858573	ZNF763	zinc finger protein 763	0.4529	0.043
16858581	LOC100507111	uncharacterized LOC100507111	0.2985	0.0245
16858592	ZNF844	zinc finger protein 844	0.9617	0.0059
16858725	LOC100507305	uncharacterized LOC100507305	0.8865	0.0394
16858800	DAND5	DAN domain family, member 5	0.3227	0.0131
16858893	CC2D1A	coiled-coil and C2 domain containing 1A	0.2376	0.0475
16858936	RLN3	relaxin 3	0.1987	0.0054
16859018	TECR	trans-2,3-enoyl-CoA reductase	0.2855	0.0252
16859070			0.3631	0.0495
16859090	CASP14	caspase 14, apoptosis-related cysteine peptidase	0.1689	0.0044
16859115			0.2351	0.003
16859205			0.2029	0.0047
16859213	OR10H4	olfactory receptor, family 10, subfamily H, member 4	0.2405	0.0216
16859437	USE1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	0.2893	0.0313
16859536			0.1209	0.0362
16859711	MAST3	microtubule associated serine/threonine kinase 3	0.3877	0.0228
16859763	IFI30	interferon, gamma-inducible protein 30	0.657	0.0392
16859783			0.3084	0.0028
16859788	PGPEP1	pyroglutamyl-peptidase I	0.8403	0.0063
16859795	GDF15	growth differentiation factor 15	1.4449	0.0003
16859800	MIR3189	microRNA 3189	0.5225	0.0095
16859942	SLC25A42	solute carrier family 25, member 42	0.1201	0.0326
16860047	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	0.2391	0.0249
16860087	ZNF101	zinc finger protein 101	0.2962	0.01
16860508	DPY19L3	dpy-19-like 3 (C. elegans)	0.5098	0.0026
16860531	PDCD5	programmed cell death 5	0.3182	0.0382
16860888	FXYD3	FXYD domain containing ion transport regulator 3	0.1843	0.0123
16860920	FXYD5	FXYD domain containing ion transport regulator 5	0.5089	0.0182
16860959	USF2	upstream transcription factor 2, c-fos interacting	0.318	0.0107
16860971	HAMP	hepcidin antimicrobial peptide	0.564	0.0262
16861118	COX6B1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)	0.2017	0.0265
16861149			0.1802	0.033
16861282	APLP1	amyloid beta (A4) precursor-like protein 1	0.6883	0.0006

16861302	HCST	hematopoietic cell signal transducer	0.4768	0.0165
16861367	TBCB	tubulin folding cofactor B	0.2167	0.0481
16861386			0.2253	0.0386
16861388			0.2233	0.0308
16861389			0.1972	0.0484
16861390			0.2018	0.0335
16861427	ZNF382	zinc finger protein 382	0.468	0.0003
16861465	ZNF345	zinc finger protein 345	0.2925	0.012
16861500	ZNF420	zinc finger protein 420	0.4634	0.0147
16861510	ZNF383	zinc finger protein 383	0.3399	0.0141
16861543	ZNF527	zinc finger protein 527	0.3859	0.0031
16861596			1.0085	0.0045
16861602			0.7875	0.0251
16861604	SIPA1L3	signal-induced proliferation-associated 1 like 3	0.276	0.0079
16861630	SPINT2	serine peptidase inhibitor, Kunitz type, 2	0.8512	0.0054
16862221	SPTBN4	spectrin, beta, non-erythrocytic 4	0.2733	0.0008
16862397	CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	0.1559	0.0365
16862427	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1	0.2816	0.0389
16862529	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	0.2141	0.0005
16862604	CD79A	CD79a molecule, immunoglobulin-associated alpha	0.1998	0.0329
16862904	ZNF223	zinc finger protein 223	0.4471	0.0178
16862936	ZNF234	zinc finger protein 234	0.2874	0.0181
16863036			0.2278	0.0209
16863061			0.1566	0.0269
16863216	PPP1R37	protein phosphatase 1, regulatory subunit 37	0.188	0.0306
16863296	PPM1N	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)	0.2643	0.0301
16863401			0.9718	0.0102
16863884	NUCB1	nucleobindin 1	0.2504	0.0404
16864076	DKKL1	dickkopf-like 1	0.2397	0.0035
16864586	ACPT	acid phosphatase, testicular	0.3106	0.0149
16864600	MGC45922	uncharacterized LOC284365	0.185	0.0048
16864611			0.2864	0.0363
16864829	ZNF610	zinc finger protein 610	0.5319	0.0259
16864839	ZNF880	zinc finger protein 880	0.4692	0.004
16865044	MIR523	microRNA 523	0.3012	0.0128
16865080	MIR518D	microRNA 518d	0.1877	0.0454
16865682			0.741	0.0001
16865714	ZNF524	zinc finger protein 524	0.2907	0.0156
16865900	ZNF583	zinc finger protein 583	0.448	0.0258
16865917	ZNF471	zinc finger protein 471	0.7851	0.0007
16865925	ZFP28	zinc finger protein 28 homolog (mouse)	0.5088	0.0038
16866081	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	0.456	0.0209
16866100	ZNF211	zinc finger protein 211	0.2871	0.0443
16866115	ZSCAN4	zinc finger and SCAN domain containing 4	0.1777	0.018
16866179	LOC100288490	uncharacterized LOC100288490	0.2268	0.0091
16866203	ZNF135	zinc finger protein 135	0.5883	0.0006
16866221	ZNF274	zinc finger protein 274	0.4447	0.0025
16866246			0.4894	0.0359
16866435	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	0.522	0.023
16866974	GNG7	guanine nucleotide binding protein (G protein), gamma 7	1.1844	0.0003
16866981	DIRAS1	DIRAS family, GTP-binding RAS-like 1	0.8134	0.0005
16867278	STAP2	signal transducing adaptor family member 2	1.1472	0.0003
16867784	C3	complement component 3	2.7669	0.0001
16867969	PCP2	Purkinje cell protein 2	0.1705	0.0357
16868158	RAB11B-AS1	RAB11B antisense RNA 1 (non-protein coding)	0.4562	0.0208
16868397	ZNF426	zinc finger protein 426	0.655	0.0121

16868453	ZNF812	zinc finger protein 812	0.3227	0.0422
16868462	ZNF846	zinc finger protein 846	0.4321	0.0085
16868556	ANGPTL6	angiopoietin-like 6	0.2239	0.0044
16868920	TMEM205	transmembrane protein 205	0.3448	0.0405
16868986	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	0.1515	0.0366
16869044	ZNF433	zinc finger protein 433	0.2934	0.0084
16869126	ZNF799	zinc finger protein 799	0.2751	0.0226
16869154	ZNF709	zinc finger protein 709	0.2231	0.0461
16869427	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0.3685	0.0192
16869660	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	0.2122	0.0419
16869713	OR7A5	olfactory receptor, family 7, subfamily A, member 5	0.9567	0.0058
16869891	RASAL3	RAS protein activator like 3	0.2044	0.009
16869977	CIB3	calcium and integrin binding family member 3	0.2032	0.0415
16870200	BST2	bone marrow stromal cell antigen 2	0.715	0.0006
16870274	JAK3	Janus kinase 3	0.8417	0
16870394	LRRC25	leucine rich repeat containing 25	0.7526	0.0067
16870782	ZNF737	zinc finger protein 737	0.7844	0.0094
16870815	LOC100505594	uncharacterized LOC100505594	1.0477	0.0046
16870838	ZNF208	zinc finger protein 208	0.6608	0.0009
16870854	ZNF676	zinc finger protein 676	1.3921	0.0022
16870895			0.1439	0.0365
16871031			0.2469	0.0396
16871256	RPS4XP21	ribosomal protein S4X pseudogene 21	0.1768	0.0023
16871268			0.1557	0.0223
16871272	ZNF599	zinc finger protein 599	0.3069	0.0167
16871467	HSPB6	heat shock protein, alpha-crystallin-related, B6	1.0482	0.0387
16871495	NPHS1	nephrosis 1, congenital, Finnish type (nephrin)	0.1622	0.0143
16871531	NFKBID	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	0.1503	0.0353
16871622	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	0.9932	0.0107
16871642	LOC100506930	uncharacterized LOC100506930	0.2623	0.0429
16871688	ZNF529	zinc finger protein 529	0.4032	0.0154
16871698	ZNF461	zinc finger protein 461	0.2745	0.0493
16871712			0.3565	0.0314
16871740	ZNF829	zinc finger protein 829	0.3048	0.0444
16871751	ZNF585A	zinc finger protein 585A	0.3698	0.0122
16871781			0.2581	0.0333
16871846	ZNF607	zinc finger protein 607	0.5315	0.009
16871857	ZNF573	zinc finger protein 573	0.2222	0.0343
16872163			0.2876	0.0105
16872254	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	0.2985	0.0278
16872447	SERTAD3	SERTA domain containing 3	0.4101	0.0035
16872452	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.6284	0.0057
16872561	B9D2	B9 protein domain 2	0.3832	0.0108
16872978			0.1862	0.0132
16873007	ETHE1	ethylmalonic encephalopathy 1	0.412	0.0173
16873049	CADM4	cell adhesion molecule 4	0.5644	0.0065
16873143			0.2133	0.0036
16873215			0.2169	0.0301
16873507	IGFL4	IGF-like family member 4	1.0086	0.0002
16873513			0.8764	0.0055
16873528	LOC645553	uncharacterized LOC645553	1.2288	0.0145
16873534	CCDC8	coiled-coil domain containing 8	0.5646	0.0305
16873675	BBC3	BCL2 binding component 3	0.2219	0.0128
16873767	ZNF541	zinc finger protein 541	0.2443	0.0161
16873826	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	0.7135	0.015

16874005	DBP	D site of albumin promoter (albumin D-box) binding protein	0.6797	0.0096
16874012	CA11	carbonic anhydrase XI	1.1229	0.0093
16874097	HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	1.1281	0.0058
16874267			0.3855	0.0261
16874467	VRK3	vaccinia related kinase 3	0.2164	0.0423
16874546	NAPSA	napsin A aspartic peptidase	0.2658	0.0284
16874558	FAM71E1	family with sequence similarity 71, member E1	0.4498	0.0154
16874641	SNORD88B	small nucleolar RNA, C/D box 88B	0.509	0.0294
16874645	SNORD88C	small nucleolar RNA, C/D box 88C	0.4472	0.0174
16874647	KLK1	kallikrein 1	1.1713	0.0309
16874656	KLK15	kallikrein-related peptidase 15	0.4841	0.005
16874665	KLKP1	kallikrein pseudogene 1	0.9663	0.0009
16874672	KLK4	kallikrein-related peptidase 4	2.1162	0.0002
16874683	KLK5	kallikrein-related peptidase 5	0.1383	0.0192
16874811	ETFB	electron-transfer-flavoprotein, beta polypeptide	0.37	0.0146
16874828	NKG7	natural killer cell group 7 sequence	0.6796	0.0006
16874890	SIGLEC6	sialic acid binding Ig-like lectin 6	0.1973	0.0162
16874906	FLJ30403	uncharacterized LOC729975	0.2616	0.0148
16874911	SIGLEC5	sialic acid binding Ig-like lectin 5	0.1847	0.0078
16874953	ZNF577	zinc finger protein 577	0.3417	0.0305
16874970	ZNF649	zinc finger protein 649	0.4442	0.0499
16875044	LOC284373	uncharacterized LOC284373	0.2307	0.0376
16875074	ZNF611	zinc finger protein 611	0.3689	0.0101
16875114			0.5931	0.0199
16875126	ZNF816-ZNF321P	ZNF816-ZNF321P readthrough	0.2057	0.0279
16875140	ZNF702P	zinc finger protein 702, pseudogene	0.6119	0.0025
16875412			0.1081	0.043
16875873	ZNF582	zinc finger protein 582	0.4361	0.012
16875879	LOC386758	uncharacterized LOC386758	0.6177	0.0006
16875904	ZNF835	zinc finger protein 835	0.2662	0.0126
16876050	ZNF418	zinc finger protein 418	0.4471	0.0382
16876074	ZNF606	zinc finger protein 606	0.3174	0.0067
16876090	ZSCAN18	zinc finger and SCAN domain containing 18	0.2444	0.0236
16876103	ZNF329	zinc finger protein 329	0.463	0.0033
16876147	ZNF132	zinc finger protein 132	0.5826	0.0099
16876182	CHMP2A	charged multivesicular body protein 2A	0.1682	0.0458
16876200	MZF1	myeloid zinc finger 1	0.2502	0.0162
16876260			0.1622	0.0314
16876337			0.3695	0.0149
16876428			0.6225	0.0355
16876520	SNTG2	syntrophin, gamma 2	0.3372	0.0036
16876739			0.1105	0.0191
16876812			0.4241	0.0169
16877126	C2orf50	chromosome 2 open reading frame 50	0.1856	0.0428
16877427			0.2562	0.0017
16877437			0.1306	0.0385
16877491	MSGN1	mesogenin 1	0.1437	0.0316
16877527			0.1984	0.0353
16877987	MAPRE3	microtubule-associated protein, RP/EB family, member 3	0.4979	0.0029
16878081	KHK	ketohexokinase (fructokinase)	0.4311	0.0449
16878406	MRPL33	mitochondrial ribosomal protein L33	0.4154	0.0377
16878416	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.4045	0.0348
16878659			0.1641	0.0338
16879250	GALM	galactose mutarotase (aldose 1-epimerase)	0.6674	0.0242
16879487			0.1441	0.0356
16879498			0.1848	0.0257

16879601	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	0.2182	0.0055
16879812			0.1874	0.0294
16879863	EPCAM	epithelial cell adhesion molecule	0.8289	0.0414
16879911	LOC644093	hCG2040054	0.1732	0.0381
16880054			0.1359	0.0481
16880291			0.2122	0.0173
16880648			0.2345	0.011
16880663			0.2131	0.008
16880682	AFTPH	aftiphilin	0.2207	0.0421
16880783			0.1381	0.0113
16880911			0.1248	0.0472
16880937			0.1148	0.0364
16880977	PROKR1	prokineticin receptor 1	0.168	0.031
16881458	NOTO	notochord homeobox	0.162	0.0119
16881512			0.156	0.0338
16881676			0.1871	0.0493
16881678	DCTN1-AS1	DCTN1 antisense RNA 1 (non-protein coding)	0.1283	0.0481
16881818	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	0.1637	0.0259
16881902			0.1434	0.0252
16881933			0.1195	0.0214
16881951	REG3G	regenerating islet-derived 3 gamma	0.4599	0.0453
16881977	CTNNA2	catenin (cadherin-associated protein), alpha 2	0.4438	0.039
16882028			0.9798	0.0129
16882055	FUNDC2P2	FUN14 domain containing 2 pseudogene 2	0.1854	0.0267
16882277	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	0.6491	0.0223
16882285	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	0.6897	0.0124
16882555	IGKV3D-7	immunoglobulin kappa variable 3D-7	0.5204	0.0101
16882718	IGKV2D-40	immunoglobulin kappa variable 2D-40	0.5346	0.0026
16882720	IGKV1D-39	immunoglobulin kappa variable 1D-39	0.9715	0.0237
16882723	IGKV1-37	immunoglobulin kappa variable 1-37 (non-functional)	0.7128	0.0025
16882726	IGKV1D-33	immunoglobulin kappa variable 1D-33	0.5339	0.0099
16882736	IGKV2D-29	immunoglobulin kappa variable 2D-29	0.2885	0.0495
16882744	IGKV1D-27	immunoglobulin kappa variable 1D-27 (pseudogene)	0.5944	0.0048
16882750	IGKV2D-24	immunoglobulin kappa variable 2D-24 (non-functional)	0.8365	0.0488
16882759	IGKV2D-24	immunoglobulin kappa variable 2D-24 (non-functional)	0.5635	0.0345
16882770	IGKV1D-16	immunoglobulin kappa variable 1D-16	0.5255	0.0338
16882774	IGKV3D-15	immunoglobulin kappa variable 3D-15 (gene/pseudogene)	0.7617	0.0157
16882786	IGKV3D-11	immunoglobulin kappa variable 3D-11	0.7427	0.0005
16882801	IGKV3D-7	immunoglobulin kappa variable 3D-7	0.4745	0.0039
16882834	MAL	mal, T-cell differentiation protein	0.2223	0.0096
16883809			0.159	0.0164
16883816			0.147	0.048
16883840			0.1628	0.0274
16884030	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	0.3129	0.0092
16884627			0.377	0.0249
16884700			0.4043	0.0016
16884790			0.1998	0.0037
16884913			0.1767	0.0194
16885279			0.1821	0.0359
16885285			0.1995	0.002
16885629	GPR148	G protein-coupled receptor 148	0.1685	0.0274
16885819			0.3789	0.0337
16886041	LOC100507600	uncharacterized LOC100507600	0.1836	0.0312
16886105	HNMT	histamine N-methyltransferase	0.6497	0.0191
16886154	LOC647012	YY1 transcription factor pseudogene	0.192	0.0051
16886160			0.3018	0.003

16886165			0.2734	0.0179
16886168			0.504	0.003
16886174	KYNU	kynureninase	0.3712	0.0436
16886240			0.1803	0.0058
16886329			0.1213	0.0453
16886448	LYPD6	LY6/PLAUR domain containing 6	0.1755	0.0226
16886717	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	0.2976	0.0355
16886734			0.3741	0.0007
16886736	UPP2	uridine phosphorylase 2	0.134	0.0349
16886748	UPP2-IT1	UPP2 intronic transcript 1 (non-protein coding)	0.1071	0.0488
16886751	CCDC148-AS1	CCDC148 antisense RNA 1 (non-protein coding)	0.206	0.0238
16886802			0.1332	0.0406
16887014	GCA	grancalcin, EF-hand calcium binding protein	0.3941	0.0069
16887049			0.334	0.0093
16887062	SCN2A	sodium channel, voltage-gated, type II, alpha subunit	0.2844	0.0248
16887192	MIR4774	microRNA 4774	0.233	0.04
16887332			0.2013	0.037
16887417			0.1534	0.0255
16887482			0.1142	0.032
16887586			0.1556	0.0094
16887675	DLX1	distal-less homeobox 1	0.1701	0.0494
16888080			0.4327	0.0173
16888211			0.3329	0.0315
16888216			0.6111	0.0063
16888222	LOC100506905	uncharacterized LOC100506905	0.3005	0.0114
16888349	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	0.4694	0.0314
16888365	RN5S113	RNA, 5S ribosomal 113	0.2902	0.0039
16888403			0.3664	0.0044
16888433			0.1208	0.0441
16888437	ZNF804A	zinc finger protein 804A	0.2105	0.0099
16888822	MFSD6	major facilitator superfamily domain containing 6	0.7473	0.0006
16888905			0.1525	0.0184
16889011			0.3789	0.0089
16889160	PLCL1	phospholipase C-like 1	1.1946	0.0025
16889819	CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.205	0.0254
16890207	MAP2	microtubule-associated protein 2	0.5454	0.0478
16890347	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	0.6529	0.009
16890417	MIR4776-1	microRNA 4776-1	0.2491	0.0235
16890530			0.1987	0.001
16890540			0.1864	0.0056
16890566	TMEM169	transmembrane protein 169	0.1625	0.01
16891082	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	0.931	0.0055
16891529			0.1083	0.0219
16891546	LOC100507800	uncharacterized LOC100507800	0.3214	0.0146
16891553			0.1105	0.0482
16891555	SGPP2	sphingosine-1-phosphate phosphatase 2	2.0251	0
16891562			0.2615	0.0002
16891833			0.186	0.0014
16892354			0.201	0.0364
16892446	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	0.4794	0.0054
16892601	UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A9	0.3631	0.0077
16892774			0.1715	0.0189
16892777			0.1087	0.0289
16893119			0.1454	0.0403
16893272	AQP12A	aquaporin 12A	0.1662	0.0205
16893941			0.462	0.0024
16894031	LOC100505964	uncharacterized LOC100505964	0.1271	0.0411
16894053			0.2347	0.0146
16894402	ODC1	ornithine decarboxylase 1	0.6545	0.0105
16894422	SNORA80B	small nucleolar RNA, H/ACA box 80B	0.2584	0.0377

16894555	MIR4429	microRNA 4429	0.2029	0.0195
16894693			0.159	0.0027
16894710	FAM49A	family with sequence similarity 49, member A	0.6967	0.0195
16894810	FLJ41481	uncharacterized LOC400945	0.2818	0.0359
16894848	WDR35	WD repeat domain 35	0.3513	0.0235
16894905			0.1159	0.0238
16894908			0.2402	0.038
16895429			0.217	0.0169
16895712	SLC30A3	solute carrier family 30 (zinc transporter), member 3	0.2292	0.0198
16895739	UCN	urocortin	0.2827	0.0026
16895871	IFT172	intraflagellar transport 172 homolog (Chlamydomonas)	0.447	0.0004
16895954	CCDC121	coiled-coil domain containing 121	0.3343	0.0044
16895979			0.3041	0.0139
16895982	RBKS	ribokinase	0.4313	0.0389
16896100			0.1512	0.0149
16896617			0.2865	0.0128
16896647			0.3181	0.0231
16897215			0.2418	0.0033
16897218			0.2251	0.0391
16897338			0.266	0.0264
16897664			0.2275	0.0401
16897872	LOC100129434	uncharacterized LOC100129434	0.1731	0.0343
16897938	MIR4432	microRNA 4432	0.3183	0
16897967	FLJ16341	uncharacterized LOC400957	0.1305	0.0325
16898323			0.1695	0.0048
16898369			0.1239	0.0351
16898375	LOC400958	uncharacterized LOC400958	0.3052	0.0013
16898461			0.1999	0.0475
16898657			0.1767	0.0389
16898788	TGFA	transforming growth factor, alpha	0.1649	0.0217
16898804	ADD2	adducin 2 (beta)	0.294	0.0002
16899378	C2orf65	chromosome 2 open reading frame 65	0.3009	0.009
16899394			0.2189	0.0212
16899474			0.2186	0.0463
16899482			0.1637	0.0192
16899525			0.344	0.0022
16899529			0.8123	0.0224
16899533	LRRTM1	leucine rich repeat transmembrane neuronal 1	0.3311	0.0314
16899543			0.3931	0.001
16899682			0.3849	0.0071
16899943	CD8B	CD8b molecule	0.1856	0.0019
16900044	RNY4P15	RNA, Ro-associated Y4 pseudogene 15	0.2501	0.0095
16900096	IGK@	immunoglobulin kappa locus	1.2809	0.023
16900104	IGKV1-6	immunoglobulin kappa variable 1-6	0.9539	0.0268
16900128	IGKV3-15	immunoglobulin kappa variable 3-15	0.4924	0.0285
16900136	IGKC	immunoglobulin kappa constant	1.1244	0.0103
16900148	IGKV2-24	immunoglobulin kappa variable 2-24	0.7795	0.0158
16900152	IGKV1-27	immunoglobulin kappa variable 1-27	0.6556	0.0246
16900160	IGKV2-29	immunoglobulin kappa variable 2-29 (gene/pseudogene)	0.3014	0.0198
16900166	IGKC	immunoglobulin kappa constant	0.5507	0.0156
16900178	IGKV2-40	immunoglobulin kappa variable 2-40	0.6614	0.0191
16900180	IGKV3D-7	immunoglobulin kappa variable 3D-7	0.8008	0.0192
16900238	LOC100131662	uncharacterized LOC100131662	0.1304	0.0281
16900283			0.2499	0.0405
16900875	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	0.7836	0.0011
16900902			0.2273	0.0113
16901278			0.1447	0.0406
16901327	LOC284998	uncharacterized LOC284998	0.1252	0.0421
16901427	UXS1	UDP-glucuronate decarboxylase 1	0.374	0.0154

16901632	NPHP1	nephronophthisis 1 (juvenile)	0.3575	0.0038
16902128			0.1547	0.047
16902387			0.269	0.0157
16902390			0.2962	0.0113
16902398			0.1835	0.0127
16902670			0.1865	0.0072
16902690	LOC440905	uncharacterized LOC440905	0.3389	0.009
16902975			0.2212	0.0069
16903186	LRP1B	low density lipoprotein receptor-related protein 1B	0.7266	0.0287
16903400			0.1789	0.0246
16903409			0.1256	0.0462
16903966			0.486	0.0145
16903991	CCDC148	coiled-coil domain containing 148	0.5072	0.0002
16904365	IFIH1	interferon induced with helicase C domain 1	0.286	0.017
16904419			0.161	0.0255
16904974			0.1644	0.004
16905106			0.1052	0.041
16905289			0.2088	0.0253
16905425			0.1157	0.0228
16905528	PDE11A	phosphodiesterase 11A	0.5772	0.0279
16905600	TTN	titin	0.5538	0.018
16906031	ZNF385B	zinc finger protein 385B	1.8131	0
16906419	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	0.6159	0.0488
16906571	STAT4	signal transducer and activator of transcription 4	0.3006	0.0069
16906607			0.1286	0.0366
16906651			0.1367	0.0292
16906656	DNAH7	dynein, axonemal, heavy chain 7	0.6577	0.0021
16906733	STK17B	serine/threonine kinase 17b	0.4184	0.0348
16906790			0.1984	0.0097
16906795	LOC100130452	uncharacterized LOC100130452	0.149	0.0227
16907324	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	0.1774	0.0153
16907401			0.3439	0.0225
16907572	GPR1	G protein-coupled receptor 1	0.6077	0.0161
16907739	CRYGA	crystallin, gamma A	0.1526	0.0223
16907812	ACADL	acyl-CoA dehydrogenase, long chain	1.1787	0.0361
16907843	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	0.3119	0.0331
16907863	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	0.207	0.0399
16908220			0.1238	0.016
16908977	SCG2	secretogranin II	1.3888	0.0038
16909401	SLC16A14	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	0.6633	0.0058
16909939	LOC151174	uncharacterized LOC151174	0.1767	0.0344
16910580	DEFB127	defensin, beta 127	0.1764	0.0122
16910618	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	0.2516	0.0186
16910801	TMC2	transmembrane channel-like 2	0.1618	0.0057
16910888	PTPRA	protein tyrosine phosphatase, receptor type, A	0.4967	0
16911077	MAVS	mitochondrial antiviral signaling protein	0.288	0.0276
16911132	PRNP	prion protein	0.3568	0.0481
16911139	PRND	prion protein 2 (dublet)	0.1753	0.0445
16911151	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.4362	0.0016
16911187	C20orf196	chromosome 20 open reading frame 196	0.3391	0.0349
16911201	CHGB	chromogranin B (secretogranin 1)	1.1245	0.0127
16911257			0.3409	0.0423
16911261	BMP2	bone morphogenetic protein 2	0.5131	0.0075
16911271			0.171	0.0188
16911338	PLCB4	phospholipase C, beta 4	0.5473	0.0047
16911391			0.1996	0.0254

16911394	ANKRD5	ankyrin repeat domain 5	0.6243	0.0079
16911411			0.2246	0.0026
16911432	C20orf94	chromosome 20 open reading frame 94	0.2631	0.0179
16911493	SPTLC3	serine palmitoyltransferase, long chain base subunit 3	1.0995	0.0003
16911525	NDUFAF5	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	0.2818	0.0283
16911605	SNRPB2	small nuclear ribonucleoprotein polypeptide B	0.3817	0.0039
16911632	PCSK2	proprotein convertase subtilisin/kexin type 2	0.7864	0.0004
16911651	DSTN	destrin (actin depolymerizing factor)	0.3271	0.008
16911698	CSRP2BP	CSRP2 binding protein	0.5243	0.0106
16911783	DTD1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	0.5201	0.014
16911797	C20orf79	chromosome 20 open reading frame 79	0.1128	0.0202
16911835	RIN2	Ras and Rab interactor 2	0.2974	0.0216
16911853	NAA20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	0.3245	0.0175
16911920			0.222	0.0101
16912016			0.1941	0.0011
16912090			0.2335	0.0023
16912109	FLJ33581	uncharacterized LOC400839	0.1836	0.0211
16912130	CST7	cystatin F (leukocystatin)	0.2502	0.024
16912140	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)	0.3345	0.0152
16912224			0.9993	0.0002
16912264			0.1109	0.0493
16912290	DEFB115	defensin, beta 115	0.1951	0.0456
16912362	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	0.7302	0.0091
16912376			0.359	0.0384
16912445			0.2657	0.0448
16912535	KIF3B	kinesin family member 3B	0.4403	0.0002
16912549			0.2061	0.0212
16912818	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	0.1909	0.0404
16912871	CHMP4B	charged multivesicular body protein 4B	0.4128	0.0013
16912900	ASIP	agouti signaling protein	0.3529	0.0137
16912954	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	0.3837	0.0019
16913063	MIR499A	microRNA 499a	0.1472	0.0443
16913095	CEP250	centrosomal protein 250kDa	0.2448	0.0169
16913206	PHF20	PHD finger protein 20	0.2546	0.0259
16913456	CTNNBL1	catenin, beta like 1	0.2464	0.0413
16913574	RALGAPB	Ral GTPase activating protein, beta subunit (non-catalytic)	0.2468	0.0212
16913627	ARHGAP40	Rho GTPase activating protein 40	0.1797	0.0164
16913737	TOP1	topoisomerase (DNA) I	0.2705	0.0354
16913854			0.1079	0.0094
16914012	GDAP1L1	ganglioside induced differentiation associated protein 1-like 1	0.1825	0.0487
16914070	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	0.4266	0.0228
16914084	WISP2	WNT1 inducible signaling pathway protein 2	1.0478	0.0017
16914103	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	0.2455	0.0075
16914183	SEMG1	semenogelin I	1.3783	0.001
16914213	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing 2	0.2095	0.0316
16914264	WFDC2	WAP four-disulfide core domain 2	0.2302	0.0061
16914297	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	0.287	0.0101
16914345	ZSWIM1	zinc finger, SWIM-type containing 1	0.267	0.0231
16914352	CTSA	cathepsin A	0.6654	0.0004
16914414	SLC12A5	solute carrier family 12 (potassium/chloride transporter), member 5	0.3305	0.0334
16914478	EYA2	eyes absent homolog 2 (Drosophila)	0.5934	0.0014

16914844	PTPN1	protein tyrosine phosphatase, non-receptor type 1	0.3005	0.0296
16914867	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	0.6417	0.0068
16914888	MOCS3	molybdenum cofactor synthesis 3	0.3528	0.0242
16914903			0.1804	0.0348
16914941			0.3188	0.0316
16914972	DOK5	docking protein 5	0.3283	0.0102
16914986			0.2421	0.0003
16914996			1.0631	0.0009
16914999			0.4384	0.0048
16915003			0.7536	0.0002
16915006	MC3R	melanocortin 3 receptor	0.5868	0.0008
16915044	C20orf43	chromosome 20 open reading frame 43	0.2333	0.0344
16915211			0.1783	0.0334
16915260			0.1061	0.0157
16915448	FAM217B	family with sequence similarity 217, member B	0.3346	0.0353
16915671	LOC100506553	uncharacterized LOC100506553	0.2028	0.0066
16915755	OGFR	opioid growth factor receptor	0.2341	0.0463
16915866	MIR124-3	microRNA 124-3	0.1579	0.0232
16915868	BIRC7	baculoviral IAP repeat containing 7	0.8662	0.0422
16915993	PPDPF	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	1.0854	0.0002
16916146	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	0.2065	0.0364
16916289	C20orf96	chromosome 20 open reading frame 96	0.5395	0.0015
16916304	LOC100507459	uncharacterized LOC100507459	0.3495	0.0085
16916328	CSNK2A1P	casein kinase 2, alpha 1 polypeptide pseudogene	0.2788	0.0095
16916352	SRXN1	sulfiredoxin 1	0.445	0.0337
16916544			0.141	0.0048
16916574	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	0.4896	0.0013
16916712	C20orf194	chromosome 20 open reading frame 194	0.3288	0.0239
16916882			0.134	0.0274
16916946	TMEM230	transmembrane protein 230	0.3775	0.0098
16916988	LOC149837	uncharacterized LOC149837	0.3503	0.0421
16916996			0.1557	0.0443
16917004	GPCPD1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	0.5956	0.0118
16917054	LRRN4	leucine rich repeat neuronal 4	0.1983	0.0331
16917061	FERMT1	fermitin family member 1	0.7214	0.0096
16917082			0.1157	0.0447
16917114	TMX4	thioredoxin-related transmembrane protein 4	0.78	0.0002
16917139	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7	0.6548	0.0395
16917173	MKKS	McKusick-Kaufman syndrome	0.443	0.0037
16917247			0.2444	0.0167
16917262			0.1838	0.004
16917281			0.2524	0.0276
16917449	BFSP1	beaded filament structural protein 1, filensin	0.5139	0.0016
16917468	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	0.3341	0.0468
16917652	LOC100287166	uncharacterized LOC100287166	0.1867	0.0046
16917655	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	0.4472	0.0007
16917689	RALGAPA2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0.7848	0.0001
16917874			0.1716	0.0171
16917939	CST3	cystatin C	0.5225	0.0027
16918049	VSX1	visual system homeobox 1	0.2255	0.0357
16918077	ABHD12	abhydrolase domain containing 12	0.498	0.0007
16918244	BCL2L1	BCL2-like 1	0.495	0.012
16918351	COMMD7	COMM domain containing 7	0.2739	0.0116
16918363	SUN5	Sad1 and UNC84 domain containing 5	0.195	0.0109
16918481			0.2647	0.0405
16918522	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	0.3641	0.0276
16918546	NCOA6	nuclear receptor coactivator 6	0.2634	0.0485

16918609	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	0.3263	0.0073
16918656			0.1112	0.0434
16918683	MT1P3	metallothionein 1 pseudogene 3	0.5989	0.0224
16918732			0.2133	0.0119
16918918	LOC647979	uncharacterized LOC647979	0.3153	0.0323
16918953	NDRG3	NDRG family member 3	0.4595	0.0011
16919022	SAMHD1	SAM domain and HD domain 1	0.7563	0.0027
16919225	SNORA71A	small nucleolar RNA, H/ACA box 71A	0.7519	0.0273
16919436			0.1423	0.042
16919448	SERINC3	serine incorporator 3	0.3019	0.0051
16919500	RIMS4	regulating synaptic membrane exocytosis 4	0.2465	0.0007
16919547	SLPI	secretory leukocyte peptidase inhibitor	2.8764	0.0014
16919692	SPATA25	spermatogenesis associated 25	0.3062	0.0015
16919697	NEURL2	neuralized homolog 2 (Drosophila)	0.612	0.0026
16919769	NCOA5	nuclear receptor coactivator 5	0.3285	0.0165
16919828	ELMO2	engulfment and cell motility 2	0.2105	0.0288
16919864	ZNF334	zinc finger protein 334	0.4377	0.0286
16919906	TP53RK	TP53 regulating kinase	0.4042	0.0362
16920018			0.1512	0.0221
16920029			0.2118	0.0038
16920031			0.1529	0.0299
16920091			0.1678	0.0099
16920100	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	0.2966	0.0109
16920121	ZNFX1	zinc finger, NFX1-type containing 1	0.2759	0.0074
16920454	ZNF217	zinc finger protein 217	0.7215	0.0009
16920473	SUMO1P1	SUMO1 pseudogene 1	0.1535	0.031
16920524			0.2483	0.0086
16920531	CBLN4	cerebellin 4 precursor	1.0119	0.0003
16920537			0.5873	0.0014
16920542	RN5S487	RNA, 5S ribosomal 487	0.3583	0.0008
16920544			1.0968	0.0001
16920579			0.2264	0.0085
16920861			0.1626	0.0251
16920931			0.1891	0.0008
16920939	LAMA5	laminin, alpha 5	0.3987	0.0029
16921123	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	0.5071	0.0008
16921368	C20orf181	chromosome 20 open reading frame 181	0.2224	0.0465
16921527	RBM11	RNA binding motif protein 11	0.3295	0.0459
16921714			0.1414	0.0438
16921789			0.1247	0.0311
16921803			0.109	0.0375
16921901			0.2037	0.014
16921914	LINC00113	long intergenic non-protein coding RNA 113	0.3937	0.0212
16921923	LINC00314	long intergenic non-protein coding RNA 314	0.1046	0.0247
16922099			0.1834	0.0026
16922219			0.1379	0.0312
16922424	KCNE2	potassium voltage-gated channel, Isk-related family, member 2	0.2382	0.041
16922779	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.3758	0.0345
16922807			0.1492	0.0214
16922907	DSCAM-AS1	DSCAM antisense RNA 1 (non-protein coding)	0.1074	0.0326
16923666	KRTAP10-11	keratin associated protein 10-11	0.2405	0.0106
16923805	PCBP3	poly(rC) binding protein 3	0.3466	0.0029
16924155	TPTE	transmembrane phosphatase with tensin homology	0.4251	0.0166
16924172	MIR3156-3	microRNA 3156-3	0.1918	0.0017
16924295			0.2546	0.0276
16924320	C21orf91-OT1	C21orf91 overlapping transcript 1 (non-protein coding)	0.1614	0.0294
16924339	CHODL-AS1	CHODL antisense RNA 1 (non-protein coding)	0.1284	0.0492
16924343			0.127	0.0151

16924395			0.1485	0.0167
16924408			0.2196	0.0249
16924845	KRTAP19-7	keratin associated protein 19-7	0.2861	0.007
16924866	KRTAP21-1	keratin associated protein 21-1	0.318	0.0079
16925400			0.2622	0.0171
16925586			0.1518	0.0259
16925591			0.1667	0.0098
16925594			0.179	0.0307
16925893			0.1826	0.0285
16926299			0.3095	0.0001
16926445	PTTG1IP	pituitary tumor-transforming 1 interacting protein	0.2859	0.0278
16926772			0.2304	0.0459
16927824	IGLV3-10	immunoglobulin lambda variable 3-10	0.2508	0.0454
16927836	IGLV4-3	immunoglobulin lambda variable 4-3	0.2567	0.0177
16927840	IGLV3-1	immunoglobulin lambda variable 3-1	0.3423	0.0416
16927973			0.1791	0.0442
16928733			0.1756	0.0195
16929368	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	0.2483	0.024
16929734			0.1747	0.0186
16929741	CYTH4	cytohesin 4	0.3457	0.0045
16930021	MIR4534	microRNA 4534	1.1049	0.0012
16930173	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	0.6237	0.0101
16930532			0.1745	0.0299
16930664	CSDC2	cold shock domain containing C2, RNA binding	0.4434	0.0051
16931068	PARVG	parvin, gamma	0.1636	0.0427
16931499	LOC284930	uncharacterized LOC284930	0.249	0.0356
16931524			0.2947	0.0035
16931884	OR11H1	olfactory receptor, family 11, subfamily H, member 1	0.1825	0.0226
16932686			0.1477	0.0245
16932702	TUBA3FP	tubulin, alpha 3f, pseudogene	0.2457	0.028
16932706	SLC7A4	solute carrier family 7 (orphan transporter), member 4	0.5425	0.0033
16932716	P2RX6P	purinergic receptor P2X, ligand-gated ion channel, 6 pseudogene	0.19	0.0492
16932906	PRAMEL	preferentially expressed antigen in melanoma-like	0.1844	0.0258
16932988	ZDHHC8P1	zinc finger, DHHC-type containing 8 pseudogene 1	0.3954	0.0003
16932995			0.2304	0.0196
16933422			0.1258	0.0074
16933665			0.1148	0.0278
16933960	DUSP18	dual specificity phosphatase 18	0.328	0.0109
16934248	BPIFC	BPI fold containing family C	0.1499	0.0044
16934354			0.1229	0.0042
16934609			0.813	0.0161
16934749	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	0.2683	0.0064
16934780			0.1654	0.041
16935228	PDGFB	platelet-derived growth factor beta polypeptide	0.1619	0.0434
16935274	ENTHD1	ENTH domain containing 1	0.2027	0
16935342	MIR4766	microRNA 4766	0.158	0.0153
16935836	EFCAB6	EF-hand calcium binding domain 6	0.2702	0.0196
16936025			0.2214	0.0152
16936640			0.213	0.0116
16936756			0.1361	0.0206
16937090			0.201	0.0202
16937167	SRGAP3-AS2	SRGAP3 antisense RNA 2 (non-protein coding)	0.6433	0.0009
16937645	SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	0.8013	0.0086
16937671	HRH1	histamine receptor H1	0.2108	0.0212
16937681	ATG7	autophagy related 7	0.2751	0.0304
16937725	SYN2	synapsin II	1.3215	0.0052

16937793			0.4881	0.0252
16937925			0.3588	0.0064
16938112	BTD	biotinidase	0.2385	0.033
16938215			0.1133	0.0161
16938322	UBE2E2	ubiquitin-conjugating enzyme E2E 2	0.47	0.0185
16938394	LOC644990	uncharacterized LOC644990	0.1983	0.0145
16938554			0.1779	0.0319
16938579	RN5S127	RNA, 5S ribosomal 127	0.3602	0.0021
16938581			0.2353	0.0135
16938724	FBXL2	F-box and leucine-rich repeat protein 2	0.4262	0.0112
16938815			0.1722	0.0201
16938875	STAC	SH3 and cysteine rich domain	1.0989	0.006
16938897			0.21	0.008
16938973	C3orf35	chromosome 3 open reading frame 35	0.2135	0.0464
16939023	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.3239	0.0082
16939203	XYLB	xylulokinase homolog (H. influenzae)	0.3153	0.0078
16939369			0.1349	0.0462
16939390	SLC25A38	solute carrier family 25, member 38	0.3884	0.0077
16939590			0.5462	0.0102
16939863	C3orf23	chromosome 3 open reading frame 23	0.276	0.0128
16939942	ZNF502	zinc finger protein 502	0.3604	0.0491
16940154	CXCR6	chemokine (C-X-C motif) receptor 6	0.2649	0.0312
16940182	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)	0.1564	0.0117
16940225	LOC100132146	uncharacterized LOC100132146	0.1503	0.0321
16940988	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	0.2001	0.0267
16941088	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	0.5618	0.0035
16941114	DOCK3	dedicator of cytokinesis 3	0.7882	0.006
16941167	MANF	mesencephalic astrocyte-derived neurotrophic factor	0.2419	0.0196
16941389	GLYCTK	glycerate kinase	0.239	0.0226
16941871	IL17RB	interleukin 17 receptor B	0.22	0.0328
16941885	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3	0.4782	0.0142
16941948			0.1054	0.0405
16941993	ARHGEF3-AS1	ARHGEF3 antisense RNA 1 (non-protein coding)	0.1961	0.0429
16941998	SPATA12	spermatogenesis associated 12	0.1776	0.0339
16942042	PDE12	phosphodiesterase 12	0.2003	0.0409
16942165			0.1742	0.0059
16942266			0.1571	0.0267
16942311	C3orf14	chromosome 3 open reading frame 14	0.6656	0.002
16942511	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.6104	0.0109
16942560	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	0.4309	0.01
16942576	MITF	microphthalmia-associated transcription factor	0.4822	0.0054
16942620			0.1815	0.0207
16942689	PDZRN3-AS1	PDZRN3 antisense RNA 1 (non-protein coding)	0.3008	0.0359
16942717			0.3233	0.0023
16942741	MIR4273	microRNA 4273	0.5267	0.0439
16942806			0.3135	0.0391
16942848			0.2316	0.0462
16942981			0.1838	0.0442
16942987			0.2838	0.0397
16943009	NSUN3	NOP2/Sun domain family, member 3	0.2371	0.0248
16943139			0.2069	0.0129
16943145	OR5H1	olfactory receptor, family 5, subfamily H, member 1	0.2424	0.0018
16943169	OR5K3	olfactory receptor, family 5, subfamily K, member 3	0.1966	0.0079
16943393			0.3159	0.0304
16943575			0.1346	0.0357
16943579			0.3386	0.0206
16943656	HHLA2	HERV-H LTR-associating 2	0.1249	0.0446

16943719	TRAT1	T cell receptor associated transmembrane adaptor 1	0.3259	0.0007
16943729	MORC1-AS1	MORC1 antisense RNA 1 (non-protein coding)	0.1705	0.0248
16943819	PHLDB2	pleckstrin homology-like domain, family B, member 2	0.4155	0.0442
16943868	ABHD10	abhydrolase domain containing 10	0.408	0.0328
16943976	LOC100129297	uncharacterized LOC100129297	0.2259	0.0205
16944055	SIDT1	SID1 transmembrane family, member 1	0.3275	0.0013
16944094	MIR4446	microRNA 4446	0.2299	0.0104
16944120	GRAMD1C	GRAM domain containing 1C	0.8609	0.0003
16944199	TIGIT	T cell immunoreceptor with Ig and ITIM domains	0.1691	0.0366
16944325	UPK1B	uroplakin 1B	0.1588	0.0348
16944399	ADPRH	ADP-ribosylarginine hydrolase	0.2773	0.0209
16944432	C3orf15	chromosome 3 open reading frame 15	0.5242	0.0086
16944588	SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	0.4586	0.0409
16944665	DTX3L	deltex 3-like (Drosophila)	0.3339	0.0088
16944738	PDIA5	protein disulfide isomerase family A, member 5	0.4605	0.0128
16944791	MYLK-AS2	MYLK antisense RNA 2 (non-protein coding)	0.1611	0.0227
16944917			0.2443	0.0341
16945034	CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6	0.2104	0.041
16945124	PODXL2	podocalyxin-like 2	0.4481	0.0012
16945241	RAB7A	RAB7A, member RAS oncogene family	0.263	0.0284
16945300			0.11	0.0438
16945320	COPG1	coatomer protein complex, subunit gamma 1	0.2492	0.0192
16945426	RHO	rhodopsin	0.1694	0.0208
16945434	H1FOO	H1 histone family, member O, oocyte-specific	0.1004	0.0379
16945625	NEK11	NIMA (never in mitosis gene a)- related kinase 11	0.3817	0.0044
16945682	ACPP	acid phosphatase, prostate	0.6987	0.0014
16945841	BFSP2	beaded filament structural protein 2, phakinin	0.2029	0.0099
16945923			0.1939	0.004
16946657	PLSCR5-AS1	PLSCR5 antisense RNA 1 (non-protein coding)	0.1475	0.0062
16946680			0.1733	0.0217
16946744	CPA3	carboxypeptidase A3 (mast cell)	0.7799	0.0058
16946783	HLTF	helicase-like transcription factor	0.1811	0.0077
16946841	RNF13	ring finger protein 13	0.3013	0.0203
16946928	SELT	selenoprotein T	0.2768	0.0107
16946959			0.3598	0.0167
16946964			0.2221	0.0233
16947053	SUCNR1	succinate receptor 1	1.6556	0.0005
16947061	MBNL1	muscleblind-like splicing regulator 1	0.2811	0.0066
16947092			0.17	0.0063
16947377	RSRC1	arginine/serine-rich coiled-coil 1	0.3337	0.0026
16947449	MFSD1	major facilitator superfamily domain containing 1	0.2022	0.0067
16947613	PPM1L	protein phosphatase, Mg2+/Mn2+ dependent, 1L	0.5918	0.0023
16947626	NMD3	NMD3 homolog (S. cerevisiae)	0.2254	0.0266
16947683			0.146	0.0267
16947731			0.1917	0.0173
16947782			0.2774	0.0255
16947787			0.1861	0.015
16947900			0.2066	0.041
16947955			0.2672	0.0241
16947971			0.1418	0.0341
16948249	MFN1	mitofusin 1	0.31	0.0083
16948348			0.2926	0.0243
16948572	KLHL24	kelch-like 24 (Drosophila)	0.3963	0.0399
16949292	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	0.2023	0.0254
16949442	RTP4	receptor (chemosensory) transporter protein 4	0.6924	0.0002
16949619	OSTN	osteocrin	0.1172	0.0336
16949640	PYDC2	pyrin domain containing 2	0.3394	0.006
16949679	HRASLS	HRAS-like suppressor	1.0483	0.0071
16949776			0.2573	0.0257
16950035	SENP5	SUMO1/sentrin specific peptidase 5	0.2801	0.0199

16950328			0.3469	0.0262
16950366	GRM7-AS1	GRM7 antisense RNA 1 (non-protein coding)	0.1939	0.0076
16950375			0.1986	0.001
16950392			0.3154	0.0119
16950399	C3orf32	chromosome 3 open reading frame 32	0.1749	0.0184
16950470	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	0.4195	0.0008
16950752	ATP2B2-IT1	ATP2B2 intronic transcript 1 (non-protein coding)	0.1154	0.0339
16950761	LINC00606	long intergenic non-protein coding RNA 606	0.2237	0.0085
16951007	XPC	xeroderma pigmentosum, complementation group C	0.332	0.0251
16951244			0.6644	0.0002
16951329			0.1948	0.0101
16951452			0.2504	0.0348
16951500	RNY4P22	RNA, Ro-associated Y4 pseudogene 22	0.1845	0.0267
16951508	ZNF385D	zinc finger protein 385D	0.2032	0.0032
16951675	LOC285326	uncharacterized LOC285326	0.1582	0.0011
16951752			0.1789	0.0265
16951756	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.3797	0.0498
16951863	GADL1	glutamate decarboxylase-like 1	0.2156	0.0474
16951997	UBP1	upstream binding protein 1 (LBP-1a)	0.1958	0.0385
16952118	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	0.4878	0.0035
16952379			0.2049	0.0474
16952431	CX3CR1	chemokine (C-X3-C motif) receptor 1	0.9613	0.0002
16952439	FLJ33065	uncharacterized LOC440952	0.3255	0.0023
16952453	RNU5B-2P	RNA, U5B small nuclear 2, pseudogene	0.1849	0.0053
16952469	ULK4	unc-51-like kinase 4 (C. elegans)	0.2716	0.0068
16952523			0.2277	0.016
16952594	HHATL	hedgehog acyltransferase-like	0.5113	0.0444
16952646			0.1442	0.0135
16952656	KRBOX1-AS1	KRBOX1 antisense RNA 1 (non-protein coding)	0.1299	0.0413
16952659	GTDC2	glycosyltransferase-like domain containing 2	0.3788	0.039
16952672	ANO10	anoctamin 10	0.5322	0.001
16952720	ZNF852	zinc finger protein 852	0.4341	0.0021
16952737	KIAA1143	KIAA1143	0.2457	0.0135
16952818	LZTFL1	leucine zipper transcription factor-like 1	0.3519	0.0189
16952841	FYCO1	FYVE and coiled-coil domain containing 1	0.4418	0.0152
16952990	PRSS50	protease, serine, 50	0.1978	0.0017
16953241	MAP4	microtubule-associated protein 4	0.3693	0.0211
16953277			0.2161	0.0375
16953396	SHISA5	shisa homolog 5 (Xenopus laevis)	0.2408	0.0346
16953809	MIR425	microRNA 425	0.1843	0.0369
16954091	NICN1	nicolin 1	0.2295	0.0279
16954217	UBA7	ubiquitin-like modifier activating enzyme 7	0.419	0.0053
16954431	TUSC2	tumor suppressor candidate 2	0.2226	0.0392
16954567	CISH	cytokine inducible SH2-containing protein	0.8137	0
16954730	TWF2	twinfilin, actin-binding protein, homolog 2 (Drosophila)	0.3295	0.0472
16954759	MIRLET7G	microRNA let-7g	0.303	0.0163
16955220			0.1727	0.0239
16955225	ERC2	ELKS/RAB6-interacting/CAST family member 2	0.4081	0.0001
16955255	MIR3938	microRNA 3938	0.1427	0.045
16955595	C3orf67	chromosome 3 open reading frame 67	0.535	0.0058
16956149	FOXP1	forkhead box P1	0.2905	0.0236
16956199	EIF4E3	eukaryotic translation initiation factor 4E family member 3	0.5878	0.0026
16956258	RN5S136	RNA, 5S ribosomal 136	0.241	0.0125
16956260	SHQ1	SHQ1 homolog (S. cerevisiae)	0.26	0.0093
16956316	CNTN3	contactin 3 (plasmacytoma associated)	0.47	0.027
16956356			0.4672	0.0004
16956377			0.1905	0.029
16956512	CADM2-AS2	CADM2 antisense RNA 2 (non-protein coding)	0.1192	0.0193
16956554			0.1289	0.0278

16956569	PROS1	protein S (alpha)	0.973	0
16956607			0.1779	0.0429
16956749	FILIP1L	filamin A interacting protein 1-like	0.3516	0.0387
16956792	ABI3BP	ABI family, member 3 (NESH) binding protein	1.5181	0.0004
16956897	SENP7	SUMO1/sentrin specific peptidase 7	0.2499	0.034
16957033			0.1765	0.0226
16957106	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	0.2907	0.017
16957197			0.167	0.0243
16957312	GCET2	germinal center expressed transcript 2	0.2422	0.0105
16957433	CD200R1	CD200 receptor 1	0.3525	0.0369
16957551	SIDT1-AS1	SIDT1 antisense RNA 1 (non-protein coding)	0.2619	0
16957554	KIAA2018	KIAA2018	0.2207	0.0457
16958044	IQCB1	IQ motif containing B1	0.296	0.0378
16958540	SLC41A3	solute carrier family 41, member 3	0.5291	0.0261
16958618			0.1518	0.0217
16958759	TPRA1	transmembrane protein, adipocyte asscociated 1	0.2078	0.0056
16958807			0.1747	0.0084
16958844	GATA2	GATA binding protein 2	0.2054	0.0137
16958897	KIAA1257	KIAA1257	0.145	0.0362
16959105			0.2287	0.0331
16959148	ASTE1	asteroid homolog 1 (Drosophila)	0.343	0.0041
16959169			1.42	0
16959174			0.2708	0.0368
16959178	LOC339874	uncharacterized LOC339874	0.3465	0.0263
16959208	CPNE4	copine IV	1.5411	0
16959412	RYK	receptor-like tyrosine kinase	0.3336	0.0181
16959701	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	0.4636	0.0028
16959760	COPB2	coatomer protein complex, subunit beta 2 (beta prime)	0.2092	0.0404
16959835			0.2598	0.0148
16959837			0.1658	0.0375
16960054	PCOLCE2	procollagen C-endopeptidase enhancer 2	0.7719	0.0382
16960084	SLC9A9	solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9	0.7211	0.0044
16960254			0.1859	0.0288
16960434	ANKUB1	ankyrin repeat and ubiquitin domain containing 1	0.226	0.0286
16960526	FAM188B2	family with sequence similarity 188, member B2	0.4314	0.0462
16960573	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	0.5789	0.0111
16960601			0.1495	0.0012
16960622			0.1644	0.0227
16960705	PLCH1	phospholipase C, eta 1	0.4092	0.0417
16960801	PA2G4P4	proliferation-associated 2G4 pseudogene 4	0.4267	0.0441
16960803	LOC339894	uncharacterized LOC339894	0.2011	0.0093
16960844	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	1.6066	0.0009
16960881			0.1123	0.0047
16961039	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	0.2945	0.0372
16961056	SPTSSB	serine palmitoyltransferase, small subunit B	0.4034	0.0127
16961157			0.2584	0.0177
16961183			0.1048	0.0446
16961186			0.1022	0.0393
16961188			0.2087	0.014
16961232	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	0.9177	0.0197
16961449	SLC7A14	solute carrier family 7 (orphan transporter), member 14	1.3689	0.0024
16961475	EIF5A2	eukaryotic translation initiation factor 5A2	0.6286	0.0088
16961501	TNIK	TRAF2 and NCK interacting kinase	0.6909	0.0185
16961547	MIR569	microRNA 569	0.3299	0.0018
16961603			0.1795	0.0052
16961629			0.1695	0.008
16961685			0.1316	0.0426
16961695			0.1413	0.0345

16961747			0.3635	0.0002
16961749			0.6038	0.0039
16961773	ZMAT3	zinc finger, matrin-type 3	0.4645	0.0136
16961839			0.3049	0.0393
16961944			0.2693	0.0082
16962181			0.2279	0.0052
16962659			0.1045	0.0376
16963127	MUC4	mucin 4, cell surface associated	0.1395	0.0109
16963292	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	0.1782	0.0491
16963519	BDH1	3-hydroxybutyrate dehydrogenase, type 1	0.3726	0.0114
16963542	LOC220729	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) pseudogene	0.6014	0.0132
16963651	ZNF718	zinc finger protein 718	0.4439	0.0325
16963689	PIGG	phosphatidylinositol glycan anchor biosynthesis, class G	0.3093	0.0322
16963901			0.5961	0.0269
16963906	LOC285463	uncharacterized LOC285463	0.2193	0.0056
16964120	LOC402160	uncharacterized LOC402160	0.2011	0.0375
16964232	ADD1	adducin 1 (alpha)	0.2845	0.0242
16964495	FLJ35424	uncharacterized FLJ35424	0.1784	0.0492
16964667	LOC285484	uncharacterized LOC285484	0.1075	0.0297
16964676	WFS1	Wolfram syndrome 1 (wolframin)	0.4685	0.0224
16964695	MAN2B2	mannosidase, alpha, class 2B, member 2	0.393	0.0289
16964749	KIAA0232	KIAA0232	0.4829	0.0021
16964833	MIR4274	microRNA 4274	0.3621	0.0037
16964950	CPZ	carboxypeptidase Z	0.1678	0.035
16964973	LOC650293	seven transmembrane helix receptor	0.2296	0.0036
16964995	LOC100287144	ubiquitin carboxyl-terminal hydrolase 17-like	0.2313	0.0348
16965048			0.2295	0.0407
16965051			0.2034	0.0403
16965057			0.3135	0.0234
16965081			0.3157	0.0003
16965099			0.3222	0.0115
16965112			0.1815	0.0216
16965126			0.1782	0.0472
16965142	LOC152742	uncharacterized LOC152742	0.7556	0.0458
16965148			0.7265	0.005
16965152			0.4811	0.0106
16965157			0.4579	0.0056
16965160			0.1475	0.0152
16965313	LAP3	leucine aminopeptidase 3	0.4092	0.0049
16965434	PACRGL	PARK2 co-regulated-like	0.3979	0.0102
16965499			0.1248	0.0443
16965505			0.7062	0.0294
16965509			1.1351	0.0105
16965539	ZCCHC4	zinc finger, CCHC domain containing 4	0.3328	0.0142
16965559	ANAPC4	anaphase promoting complex subunit 4	0.3166	0.0186
16965625			0.5678	0.0048
16965628	C4orf52	chromosome 4 open reading frame 52	0.3067	0.0456
16965813			0.1735	0.0322
16965915	C4orf19	chromosome 4 open reading frame 19	0.5279	0.0001
16965983	PTTG2	pituitary tumor-transforming 2	0.2593	0.0251
16966004			0.1174	0.0228
16966074	WDR19	WD repeat domain 19	0.411	0.044
16966137	LIAS	lipoic acid synthetase	0.4604	0.0307
16966276			0.4611	0.0253
16966393	SLC30A9	solute carrier family 30 (zinc transporter), member 9	0.3377	0.0223
16966432	GRXCR1	glutaredoxin, cysteine rich 1	0.1555	0.0447
16966497	GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1	0.148	0.0388
16966548	NIPAL1	NIPA-like domain containing 1	0.1996	0.0137
16966685	SPATA18	spermatogenesis associated 18	1.1672	0.0007

16966704			0.1854	0.013
16966725			0.2386	0.0017
16966727	LOC152578	uncharacterized LOC152578	0.1449	0.0322
16966906			0.1575	0.043
16966940	EXOC1	exocyst complex component 1	0.3147	0.0152
16967171			0.2325	0.0479
16967246			0.2647	0.0361
16967263			0.1897	0.0305
16967286	STAP1	signal transducing adaptor family member 1	0.1785	0.0093
16967465	FDCSP	follicular dendritic cell secreted protein	0.2737	0.0006
16967539	ENAM	enamelin	0.2051	0.0181
16967767			0.1234	0.0215
16967872			0.1747	0.0059
16968077	CCNG2	cyclin G2	0.315	0.0376
16968246	BMP2K	BMP2 inducible kinase	0.6759	0.0052
16968428			0.577	0.0121
16968447	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	0.3533	0.0462
16968497	ARHGAP24	Rho GTPase activating protein 24	0.7647	0.0066
16968521	MIR4451	microRNA 4451	0.5815	0.0187
16968638	DSPP	dentin sialophosphoprotein	0.2062	0.0464
16968675	HSP90AB3P	heat shock protein 90kDa alpha (cytosolic), class B member 3, pseudogene	0.4048	0.0031
16968697	PKD2	polycystic kidney disease 2 (autosomal dominant)	0.4085	0.0454
16968735	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	0.6208	0.0017
16968765	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	0.7825	0.0024
16968797	HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	0.682	0.0043
16968895	FAM190A	family with sequence similarity 190, member A	0.2485	0.0127
16969051	BMPR1B	bone morphogenetic protein receptor, type IB	0.7987	0.0084
16969093	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	0.298	0.0123
16969182	C4orf17	chromosome 4 open reading frame 17	0.152	0.0366
16969197	MTTP	microsomal triglyceride transfer protein	0.3965	0.0289
16969229	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	0.3183	0.0131
16969267	BANK1	B-cell scaffold protein with ankyrin repeats 1	0.8574	0.0008
16969351			0.225	0.0106
16969558	SGMS2	sphingomyelin synthase 2	0.4038	0.0378
16969578	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	0.4719	0.0481
16969638			0.9003	0.0012
16969839	ALPK1	alpha-kinase 1	0.2698	0.0413
16969911	ANK2	ankyrin 2, neuronal	0.9517	0.0026
16969986	MIR1243	microRNA 1243	0.4304	0.0096
16969997			0.1927	0.037
16970027			0.1407	0.0229
16970096	METTL14	methyltransferase like 14	0.3552	0.0065
16970112			0.1812	0.0228
16970115			0.2146	0.0023
16970118	SYNPO2	synaptopodin 2	0.8688	0.0049
16970140	USP53	ubiquitin specific peptidase 53	1.2919	0.0003
16970201			0.2878	0.0186
16970258	KIAA1109	KIAA1109	0.3506	0.0227
16970399	BBS12	Bardet-Biedl syndrome 12	0.5472	0.0047
16970444			0.1602	0.0062
16970713			0.1322	0.0292
16970757			0.141	0.0277
16970923	SCOC	short coiled-coil protein	0.3389	0.0194
16970971	IL15	interleukin 15	0.2677	0.0429
16971265			0.1279	0.0343
16971308	ARHGAP10	Rho GTPase activating protein 10	0.4545	0.0135

16971344			0.3967	0.002
16971350			0.2999	0.009
16971375	RN5S167	RNA, 5S ribosomal 167	0.2728	0.0013
16971382	DCLK2	doublecortin-like kinase 2	0.5677	0.0472
16971435	PRSS48	protease, serine, 48	0.1669	0.0472
16971505	ARFIP1	ADP-ribosylation factor interacting protein 1	0.2533	0.0451
16971631	TLR2	toll-like receptor 2	0.8133	0.0001
16971758	TDO2	tryptophan 2,3-dioxygenase	0.5919	0.0153
16971806	GLRB	glycine receptor, beta	0.7832	0.0011
16971907			0.3626	0.0044
16971995	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.3606	0.0217
16972188			0.1461	0.0157
16972191			0.1342	0.0396
16972198	TLL1	tolloid-like 1	0.6607	0.0092
16972229	ANXA10	annexin A10	0.168	0.0202
16972342			0.2004	0.0198
16972359	LOC100506122	uncharacterized LOC100506122	0.1662	0.0195
16972396	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	0.649	0.0068
16972505	MIR4276	microRNA 4276	0.1277	0.037
16972512			0.2262	0.0045
16972611			0.1707	0.0109
16972614			0.1718	0.0036
16972634			0.3188	0.0162
16972658	RN5S173	RNA, 5S ribosomal 173	0.1077	0.0452
16972912	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	0.5886	0.0036
16972993	TLR3	toll-like receptor 3	0.4941	0.041
16973036			0.6474	0.0017
16973196			0.1386	0.0449
16973375	GAK	cyclin G associated kinase	0.2521	0.0414
16973465	RNF212	ring finger protein 212	0.5364	0.0155
16973493	TMED11P	transmembrane emp24 protein transport domain containing 11, pseudogene	0.3137	0.014
16973723	ZFYVE28	zinc finger, FYVE domain containing 28	0.2772	0.0104
16973832	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	0.419	0.0167
16973857	FAM86EP	family with sequence similarity 86, member E, pseudogene	0.3171	0.0084
16973871	TMEM128	transmembrane protein 128	0.3849	0.0475
16974074	LOC100507376	uncharacterized LOC100507376	0.4602	0.0272
16974458	LINC00504	long intergenic non-protein coding RNA 504	0.2044	0.0078
16974534	PROM1	prominin 1	0.1244	0.0254
16974713	DCAF16	DDB1 and CUL4 associated factor 16	0.3484	0.0293
16974819			0.3549	0.0118
16974830	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	1.2381	0.0001
16974900	CCDC149	coiled-coil domain containing 149	0.3745	0.0019
16974963			0.2152	0.0009
16974968	SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	1.3413	0.0024
16975012	LOC100506024	uncharacterized LOC100506024	0.2043	0.0156
16975023	LOC100506048	uncharacterized LOC100506048	0.2169	0.0108
16975154			0.3536	0.0003
16975157	RELL1	RELT-like 1	0.5741	0.0036
16975170			0.1945	0.0018
16975203	TLR10	toll-like receptor 10	0.2906	0.0013
16975213	TLR1	toll-like receptor 1	0.4651	0.0093
16975226	TLR6	toll-like receptor 6	0.8753	0.0088
16975419	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	0.4779	0.0072
16975458			0.5889	0.0314
16975478			0.1759	0.0364

16975558			0.2624	0.0063
16975560	KCTD8	potassium channel tetramerisation domain containing 8	0.5595	0.0195
16975578	GNPDA2	glucosamine-6-phosphate deaminase 2	0.4512	0.0101
16975707	NFXL1	nuclear transcription factor, X-box binding-like 1	0.3647	0.0316
16975890	OCIAD2	OCIA domain containing 2	0.6651	0.0001
16975954	SCFD2	sec1 family domain containing 2	0.5101	0.0103
16976133	AASDH	aminoadipate-semialdehyde dehydrogenase	0.2886	0.0223
16976177	HOPX	HOP homeobox	0.2318	0.0077
16976239			0.1241	0.0315
16976300	TECRL	trans-2,3-enoyl-CoA reductase-like	1.2969	0.0045
16976558			0.175	0.0119
16976644	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	0.8585	0.0246
16976734	COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.3584	0.0255
16976798	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	0.3207	0.0338
16976926	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	0.9374	0.0004
16977052	CXCL10	chemokine (C-X-C motif) ligand 10	0.7746	0.0173
16977058	CXCL11	chemokine (C-X-C motif) ligand 11	0.3191	0.0131
16977217	PAQR3	progestin and adipoQ receptor family member III	0.4717	0.0003
16977378	TMEM150C	transmembrane protein 150C	0.6941	0.0304
16977758	MIR4452	microRNA 4452	0.3246	0.0086
16977855			0.1382	0.0011
16977868	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	0.8323	0.0086
16977986	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0.7825	0.0037
16978036	HPGDS	hematopoietic prostaglandin D synthase	0.7847	0.0061
16978107			0.1995	0.0166
16978164	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	0.3408	0.0048
16978301	LAMTOR3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	0.3719	0.0255
16978310	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14	0.3126	0.0152
16978346	DDIT4L	DNA-damage-inducible transcript 4-like	0.6977	0.0049
16978444	MANBA	mannosidase, beta A, lysosomal	0.3134	0.0303
16978548	BDH2	3-hydroxybutyrate dehydrogenase, type 2	0.5904	0.0129
16978647			0.1483	0.001
16978661	PPA2	pyrophosphatase (inorganic) 2	0.5392	0.0015
16978710			0.2883	0.0022
16978793	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.405	0.0018
16978813			0.1798	0.0481
16978826			0.3242	0.0023
16978956	SETP20	SET pseudogene 20	0.2141	0.0108
16978976	CFI	complement factor I	1.1999	0.0157
16979110	MIR302D	microRNA 302d	0.4362	0.0155
16979116			0.2445	0.0037
16979125			0.2366	0.0022
16979133	CAMK2D	calcium/calmodulin-dependent protein kinase II delta	0.4246	0.0369
16979182	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	0.8217	0.0159
16979225	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	0.5968	0.0278
16979244			0.1745	0.0418
16979256	SEC24D	SEC24 family, member D (S. cerevisiae)	0.4275	0.0413
16979502	TMEM155	transmembrane protein 155	0.1157	0.0152
16979526	BBS7	Bardet-Biedl syndrome 7	0.4378	0.0356
16979553	TRPC3	transient receptor potential cation channel, subfamily C, member 3	0.5102	0.017
16979787			0.2249	0.0383
16979836			0.144	0.0461
16979946			0.3894	0.0099
16980045	LOC100129858	uncharacterized LOC100129858	0.5488	0.0308
16980051	CLGN	calmegin	1.3752	0.0206

16980361			0.2485	0.0055
16980470	NR3C2	nuclear receptor subfamily 3, group C, member 2	1.0889	0.0004
16980495			0.3065	0.0049
16980497			0.2723	0.0049
16980506	LOC285423	uncharacterized LOC285423	0.1213	0.0197
16980601	SH3D19	SH3 domain containing 19	0.6453	0.0007
16980638	PET112	PET112 homolog (yeast)	0.2743	0.0411
16980716	TMEM154	transmembrane protein 154	0.3133	0.0054
16980730	TIGD4	tigger transposable element derived 4	0.3675	0.0012
16980918	CTSO	cathepsin O	0.753	0.0011
16980972			0.4133	0.0233
16981045			0.5949	0.0185
16981047			0.1373	0.0256
16981119	1-Mar	membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase	0.1944	0.0311
16981177	RN5S170	RNA, 5S ribosomal 170	0.1037	0.0369
16981210			0.1658	0.0215
16981219	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0.695	0
16981426	MFAP3L	microfibrillar-associated protein 3-like	0.3312	0.0157
16981487			0.1345	0.0124
16981502			0.3738	0.0493
16981568			0.1179	0.0432
16981760	AGA	aspartylglucosaminidase	0.5745	0.0168
16981787			0.1276	0.003
16981872			0.1962	0.0261
16981911			0.6046	0.0001
16982092	MIR3945	microRNA 3945	0.2292	0.0079
16982364			0.1354	0.0352
16982413	MIR1324	microRNA 1324	0.1213	0.0113
16982579	EXOC3	exocyst complex component 3	0.3473	0.0032
16982849			0.1047	0.0485
16982868			0.1065	0.0445
16982898	KIAA0947	KIAA0947	0.5545	0.0028
16983013			0.1023	0.0181
16983548			0.1336	0.0056
16983593			0.3143	0.0151
16983597			0.3945	0.0464
16983607			0.294	0.025
16983609			0.2224	0.0479
16983611	LOC643401	uncharacterized LOC643401	1.2018	0.0026
16983672			0.2631	0.0362
16983948			0.3656	0.0076
16983950	SPEF2	sperm flagellar 2	0.5646	0.0041
16984235			0.2174	0.0046
16984238			0.3089	0.0124
16984241			0.1148	0.0414
16984276			0.1303	0.0389
16984336	C5orf51	chromosome 5 open reading frame 51	0.2343	0.0421
16984347	FBXO4	F-box protein 4	0.3293	0.0285
16984394	CCDC152	coiled-coil domain containing 152	0.2576	0.0152
16984408	LOC100129186	uncharacterized LOC100129186	0.4032	0.0408
16984492	NNT	nicotinamide nucleotide transhydrogenase	0.4415	0.0308
16984542	MRPS30	mitochondrial ribosomal protein S30	0.2527	0.0491
16984741	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	0.4271	0.0042
16984783	GZMK	granzyme K (granzyme 3; tryptase II)	0.714	0.0011
16984801	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	1.1423	0.0001
16984940			0.1559	0.0304
16985033	GAPT	GRB2-binding adaptor protein, transmembrane	0.7207	0.0002
16985043	RAB3C	RAB3C, member RAS oncogene family	0.8468	0.0117

16985206			0.409	0.0328
16985217	RNF180	ring finger protein 180	0.8191	0.0019
16985251	CWC27	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	0.4135	0.0017
16985273			0.1513	0.036
16985440	MAST4	microtubule associated serine/threonine kinase family member 4	0.3985	0.0077
16985637	CDK7	cyclin-dependent kinase 7	0.2765	0.0261
16985658	RAD17	RAD17 homolog (S. pombe)	0.2936	0.0225
16985842			0.2438	0.0335
16985939			0.2021	0.0132
16985950	MAP1B	microtubule-associated protein 1B	0.6659	0.0392
16986095			0.2	0.0065
16986138	RGNEF	190 kDa guanine nucleotide exchange factor	0.6344	0.0172
16986198			0.1681	0.0037
16986246			0.2963	0.0446
16986351	IQGAP2	IQ motif containing GTPase activating protein 2	0.6205	0.0154
16986539	SCAMP1	secretory carrier membrane protein 1	0.531	0.0005
16986748	MSH3	mutS homolog 3 (E. coli)	0.3013	0.0312
16986961			0.1843	0.0195
16986983	COX7C	cytochrome c oxidase subunit VIIc	0.2994	0.0192
16987008	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.5236	0.0006
16987076			0.3766	0.0016
16987118			0.1903	0.0015
16987280			0.3274	0.0167
16987287	NR2F1	nuclear receptor subfamily 2, group F, member 1	0.2821	0.0199
16987335			0.1639	0.0076
16987377	GPR150	G protein-coupled receptor 150	0.4594	0.0381
16987459	MIR583	microRNA 583	0.1727	0.0366
16987531	ERAP2	endoplasmic reticulum aminopeptidase 2	1.1423	0.001
16987565	LNPEP	leucyl/cystinyl aminopeptidase	0.2589	0.0475
16987673	PAM	peptidylglycine alpha-amidating monooxygenase	0.5494	0.0109
16987720	PPIP5K2	diphosphoinositol pentakisphosphate kinase 2	0.3636	0.0078
16987795			0.2654	0.0408
16987798	FER	fer (fps/fes related) tyrosine kinase	0.6188	0.0012
16987830			0.6166	0.0136
16987834			0.2019	0.0036
16987883	SLC25A46	solute carrier family 25, member 46	0.4142	0.0038
16988167			0.2034	0.0133
16988232	COMMD10	COMM domain containing 10	0.3371	0.0069
16988251			0.6888	0.0278
16988261			0.3491	0.0152
16988301	DMXL1	Dmx-like 1	0.3124	0.0413
16988441			0.2415	0.0306
16988444			0.1701	0.0277
16988450	SRFBP1	serum response factor binding protein 1	0.3651	0.0055
16988477	SNCAIP	synuclein, alpha interacting protein	0.7856	0.0015
16988510	SNX2	sorting nexin 2	0.3698	0.0027
16988537			0.4936	0.0088
16988562			0.1714	0.0302
16988686	PHAX	phosphorylated adaptor for RNA export	0.4123	0.005
16988725	MEGF10	multiple EGF-like-domains 10	0.3547	0.0134
16988762	PRRC1	proline-rich coiled-coil 1	0.3908	0.0056
16988861	ISOC1	isochorismatase domain containing 1	0.5672	0.0435
16988921	LYRM7	Lyrm7 homolog (mouse)	0.367	0.0435
16988971	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	0.1816	0.009
16989001	SLC22A4	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	0.3073	0.0066
16989018	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5	0.64	0.002
16989038	C5orf56	chromosome 5 open reading frame 56	0.2932	0.0068

16989054	RAD50	RAD50 homolog (S. cerevisiae)	0.4037	0.0267
16989128	RN5S192	RNA, 5S ribosomal 192	0.2098	0.0026
16989171			0.3707	0.0025
16989199			0.174	0.0406
16989265	PHF15	PHD finger protein 15	0.5009	0.0147
16989325	CAMLG	calcium modulating ligand	0.294	0.0422
16989369	C5orf24	chromosome 5 open reading frame 24	0.2305	0.0116
16989408	MIR4461	microRNA 4461	0.1903	0.0115
16989496	TGFBI	transforming growth factor, beta-induced, 68kDa	0.8024	0.0018
16989554	TRPC7-AS2	TRPC7 antisense RNA 2 (non-protein coding)	0.1611	0.0024
16989571	MYOT	myotilin	0.523	0.0205
16989589	PKD2L2	polycystic kidney disease 2-like 2	0.1874	0.0113
16989683	KDM3B	lysine (K)-specific demethylase 3B	0.2234	0.0233
16989750	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	0.3185	0.0151
16989881	UBE2D2	ubiquitin-conjugating enzyme E2D 2	0.1827	0.0363
16989897	CXXC5	CXXC finger protein 5	0.5228	0.0025
16989955	IGIP	IgA-inducing protein homolog (Bos taurus)	0.4007	0.0495
16989977	CYSTM1	cysteine-rich transmembrane module containing 1	0.8455	0
16989986			0.8198	0.0002
16990120			0.3964	0.0313
16990132			0.1947	0.0355
16990135			0.2818	0.0297
16990136			0.3405	0.017
16990190	ZMAT2	zinc finger, matrin-type 2	0.3688	0.0082
16990205	PCDHA11	protocadherin alpha 11	0.372	0.037
16990423	RNF14	ring finger protein 14	0.407	0.0376
16990440	NDFIP1	Nedd4 family interacting protein 1	0.2768	0.0385
16990548	HMHB1	histocompatibility (minor) HB-1	0.1825	0.04
16990553	KCTD16	potassium channel tetramerisation domain containing 16	0.188	0.0041
16990567			0.2914	0.0255
16990678	STK32A	serine/threonine kinase 32A	1.4303	0.0048
16990796	SPINK9	serine peptidase inhibitor, Kazal type 9	0.5213	0.0108
16990946			0.2967	0.0301
16990985	PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	0.2408	0.0365
16991151	SYNPO	synaptopodin	0.4922	0.0012
16991210	GM2A	GM2 ganglioside activator	0.4587	0.007
16991342	MFAP3	microfibrillar-associated protein 3	0.3018	0.0097
16991444			0.219	0.0405
16991447	MRPL22	mitochondrial ribosomal protein L22	0.2794	0.0366
16991624			0.1902	0.0146
16991647			0.6614	0.0138
16991650			0.5164	0.0105
16991663			0.1594	0.0401
16991685	LOC285626	uncharacterized LOC285626	0.1275	0.0231
16991712	TTC1	tetratricopeptide repeat domain 1	0.5887	0.0005
16991816	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	0.195	0.0297
16991839	CCNG1	cyclin G1	0.6633	0.0021
16991886	MAT2B	methionine adenosyltransferase II, beta	0.4035	0.0065
16992122	DOCK2	dedicator of cytokinesis 2	0.4271	0.0095
16992346			0.515	0.0467
16992385			0.107	0.0301
16992456	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	0.3371	0.0172
16992459			0.2799	0.0252
16992460			0.3441	0.0093
16992462			0.5289	0.0047
16992463			0.4215	0.0155
16992464			0.3074	0.0252
16992467	CREBRF	CREB3 regulatory factor	0.3627	0.0183

16992557	CPEB4	cytoplasmic polyadenylation element binding protein 4	0.4755	0.042
16992664	HRH2	histamine receptor H2	0.2266	0.0027
16992705	FAM153B	family with sequence similarity 153, member B	0.4662	0.012
16992789			0.2958	0.0204
16992809	HIGD2A	HIG1 hypoxia inducible domain family, member 2A	0.386	0.0242
16992877			0.531	0.0049
16993088	GRK6	G protein-coupled receptor kinase 6	0.3017	0.0078
16993127	TMED9	transmembrane emp24 protein transport domain containing 9	0.4083	0.017
16993164			0.198	0.0217
16993173	THOC3	THO complex 3	0.5119	0.042
16993183			0.5167	0.0027
16993289	FLJ31183	uncharacterized LOC401225	0.307	0.0007
16993302	ZFP2	zinc finger protein 2 homolog (mouse)	0.4463	0.0315
16993311	ZNF454	zinc finger protein 454	0.5126	0.0051
16993321			0.4722	0.0103
16993324	ZNF879	zinc finger protein 879	0.5451	0
16993335	ZNF354C	zinc finger protein 354C	1.1102	0.0001
16993349	RUFY1	RUN and FYVE domain containing 1	0.3937	0.0009
16993397	CANX	calnexin	0.2506	0.0176
16993403			0.3874	0.0331
16993404			0.7729	0.0219
16993413			0.1517	0.0263
16993415			0.469	0.0067
16993416			0.1748	0.0445
16993423			0.4121	0.0362
16993424			0.4005	0.0329
16993427			0.184	0.0323
16993430			0.5456	0.0006
16993431			0.3125	0.0078
16993432			0.2452	0.0469
16993458	SQSTM1	sequestosome 1	0.2959	0.0497
16993494			0.5737	0.0114
16993596	OR2V2	olfactory receptor, family 2, subfamily V, member 2	0.1758	0.0324
16993681	OR4F29	olfactory receptor, family 4, subfamily F, member 29	0.2265	0.0088
16993851			0.2191	0.0034
16994054	IRX4	iroquois homeobox 4	0.2712	0.0055
16994158			0.232	0.0128
16994230			0.116	0.0457
16994244	FASTKD3	FAST kinase domains 3	0.4758	0.0035
16994309	TAS2R1	taste receptor, type 2, member 1	0.1766	0.038
16994329	FAM173B	family with sequence similarity 173, member B	0.3311	0.0359
16994355	ROPN1L-AS1	ROPN1L antisense RNA 1 (non-protein coding)	0.1441	0.0354
16994373	DAP	death-associated protein	0.4425	0.0017
16994428			0.1995	0.022
16994597	FAM134B	family with sequence similarity 134, member B	0.9466	0.0003
16994616			0.3064	0.0115
16994696			0.2172	0.0058
16994796	LOC340107	uncharacterized LOC340107	0.1794	0.0024
16995039			0.1872	0.0061
16995044			0.2506	0.0061
16995177	PRLR	prolactin receptor	2.4199	0.0003
16995241	UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	0.4055	0.0087
16995254	LMBRD2	LMBR1 domain containing 2	0.4764	0.018
16995301	RANBP3L	RAN binding protein 3-like	0.7071	0.0313
16995326			0.1849	0.0178
16995542			0.3681	0.0214
16995601	FYB	FYN binding protein	0.4365	0.0375
16995678	TTC33	tetratricopeptide repeat domain 33	0.5483	0.0003
16995721	HEATR7B2	HEAT repeat family member 7B2	0.2185	0.0031
16995771	C6	complement component 6	0.8747	0.0035

16995797			0.2027	0.0079
16995802	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	1.3363	0.0035
16995848	SEPP1	selenoprotein P, plasma, 1	0.5739	0.0075
16995866	FLJ32255	uncharacterized LOC643977	0.4507	0.0444
16996089	MOCS2	molybdenum cofactor synthesis 2	0.4711	0.0189
16996152			0.1164	0.0392
16996157	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	0.1255	0.0411
16996252			0.1462	0.0486
16996298	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.3826	0.0126
16996365			0.197	0.017
16996564	ELOVL7	ELOVL fatty acid elongase 7	0.8663	0.0006
16996800			0.359	0.0013
16996872			0.2924	0.0017
16996880			0.6374	0.0222
16996939			0.2438	0.0335
16997065			0.1792	0.0152
16997178			0.1208	0.0214
16997269			0.2169	0.0226
16997389			0.4039	0.0032
16997404	WDR41	WD repeat domain 41	0.3325	0.0222
16997455			0.173	0.0334
16997457	AP3B1	adaptor-related protein complex 3, beta 1 subunit	0.2986	0.0183
16997586			0.1489	0.0245
16997605			0.3346	0.0418
16997646			0.8942	0.0003
16997721	SSBP2	single-stranded DNA binding protein 2	1.0242	0.0002
16997849			0.2009	0.0198
16997851	MIR4280	microRNA 4280	0.1538	0.0032
16997987			0.2532	0.0265
16998007	CETN3	centrin, EF-hand protein, 3	0.4493	0.0013
16998019	MBLAC2	metallo-beta-lactamase domain containing 2	0.3347	0.0181
16998027	LYSMD3	LysM, putative peptidoglycan-binding, domain containing 3	0.352	0.0329
16998097	FLJ42709	uncharacterized LOC441094	0.4111	0.0171
16998132			0.2804	0.0294
16998134	KIAA0825	KIAA0825	0.4544	0.0259
16998211	TTC37	tetratricopeptide repeat domain 37	0.4642	0.004
16998309	ELL2	elongation factor, RNA polymerase II, 2	0.5396	0.0247
16998339			0.3274	0.006
16998621	NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	0.7871	0.0053
16998675			0.1602	0.0261
16998700	FBXL17	F-box and leucine-rich repeat protein 17	0.305	0.0055
16998727	PJA2	praja ring finger 2, E3 ubiquitin protein ligase	0.2346	0.021
16998745	TMEM232	transmembrane protein 232	0.4329	0.0179
16998787			0.2134	0.0337
16998807			0.1391	0.0126
16998850	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	0.6677	0.0302
16998994	CCDC112	coiled-coil domain containing 112	0.3224	0.0351
16999017	TMED7	transmembrane emp24 protein transport domain containing 7	0.2748	0.0048
16999053	ATG12	autophagy related 12	0.242	0.0295
16999076			0.4252	0.0038
16999083	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	0.8914	0.0321
16999203			0.6237	0.0068
16999206			0.2907	0.0306
16999210	MGC32805	uncharacterized LOC153163	0.3595	0.0001
16999219			0.4492	0.0011
16999343			0.3256	0.0478

16999357			0.1783	0.0294
16999379	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	0.3601	0.0281
16999432	C5orf63	chromosome 5 open reading frame 63	0.6598	0.0121
16999440			0.272	0.0036
16999446			0.2872	0.0157
16999456			0.1886	0.0153
16999585			0.4049	0.0195
16999631	FNIP1	folliculin interacting protein 1	0.4252	0.0071
16999754	LOC553103	uncharacterized LOC553103	0.6569	0.0012
16999767	MIR3936	microRNA 3936	0.494	0.001
16999769			0.1698	0.031
16999776	IRF1	interferon regulatory factor 1	0.4604	0.0004
16999974	C5orf15	chromosome 5 open reading frame 15	0.2539	0.026
17000235	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	0.939	0.0313
17000342	NME5	NME/NM23 family member 5	1.3752	0
17000356			0.2935	0.0064
17000358	BRD8	bromodomain containing 8	0.3405	0.0206
17000618	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	0.2437	0.0228
17000680	NRG2	neuregulin 2	0.3033	0.0284
17000713	PFDN1	prefoldin subunit 1	0.3726	0.0051
17000736			0.1254	0.031
17000793	CD14	CD14 molecule	0.6967	0.0219
17000800	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	0.3497	0.0147
17000843			0.3988	0.0052
17000928	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0.3871	0.0229
17001060			0.2199	0.0214
17001134	YIPF5	Yip1 domain family, member 5	0.3216	0.0324
17001152			0.3624	0.026
17001155			0.4081	0.0459
17001249			0.1576	0.0272
17001256	RN5S196	RNA, 5S ribosomal 196	0.9175	0.0011
17001258	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	0.7538	0
17001299	DPYSL3	dihydropyrimidinase-like 3	0.5517	0.002
17001446			0.1635	0.0112
17001448	MIR584	microRNA 584	0.2253	0.005
17001545	CSF1R	colony stimulating factor 1 receptor	0.4889	0.041
17001654	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	0.6205	0.011
17001694			0.1781	0.0205
17001701	RBM22	RNA binding motif protein 22	0.3455	0.0012
17001747	ZNF300	zinc finger protein 300	0.442	0.028
17001763	TNIP1	TNFAIP3 interacting protein 1	0.4793	0.0012
17001800	ANXA6	annexin A6	0.7538	0.0037
17001944			0.1482	0.0369
17001946	ATOX1	ATX1 antioxidant protein 1 homolog (yeast)	0.2333	0.018
17001961	GLRA1	glycine receptor, alpha 1	0.3854	0.0303
17002032			0.3532	0.0034
17002115	TIMD4	T-cell immunoglobulin and mucin domain containing 4	0.2114	0.0476
17002240	CLINT1	clathrin interactor 1	0.4897	0.0002
17002264			0.2031	0.0027
17002278	EBF1	early B-cell factor 1	0.8821	0.0349
17002354	PWWP2A	PWWP domain containing 2A	0.3182	0.0307
17002496			0.1214	0.0286
17002498			0.1992	0.0292
17002503			0.2849	0.0062
17002527			0.2147	0.0146
17002555			0.1962	0.0163
17002584			0.2074	0.006

17002657	MIR218-2	microRNA 218-2	0.2587	0.0017
17002667	FAM196B	family with sequence similarity 196, member B	0.7482	0.0242
17002681	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	0.3582	0.0316
17002720			0.1781	0.0325
17002871			0.3776	0.0097
17002879	NKX2-5	NK2 homeobox 5	0.1752	0.0487
17002972	THOC3	THO complex 3	0.4927	0.0054
17003034	KIAA1191	KIAA1191	0.315	0.042
17003077	RNF44	ring finger protein 44	0.519	0.0015
17003407	FAM153A	family with sequence similarity 153, member A	0.4901	0.0155
17003474			0.1914	0.0145
17003477			0.3594	0.0369
17003479	NHP2	NHP2 ribonucleoprotein homolog (yeast)	0.3407	0.0191
17003530	COL23A1	collagen, type XXIII, alpha 1	0.1582	0.0116
17003610	FLJ31183	uncharacterized LOC401225	0.4257	0.0046
17003725	C5orf60	chromosome 5 open reading frame 60	0.1405	0.0358
17003745	LOC100652779	uncharacterized LOC100652779	0.3132	0.0033
17003781	C5orf45	chromosome 5 open reading frame 45	0.2558	0.0237
17003878	RASGEF1C	RasGEF domain family, member 1C	0.271	0.0048
17003898	MAPK9	mitogen-activated protein kinase 9	0.6566	0.0015
17004084			0.1832	0.015
17004141	FLJ43763	uncharacterized LOC642316	0.2042	0.0233
17004262			0.1907	0.0013
17004374	FAM50B	family with sequence similarity 50, member B	0.2654	0.0073
17004515			0.2641	0.0011
17004518	LY86	lymphocyte antigen 86	0.4653	0.0114
17004526			0.2036	0.0114
17004769	TMEM14B	transmembrane protein 14B	0.3611	0.0351
17005273			0.1402	0.0213
17005326	NRSN1	neurensin 1	0.3241	0.0008
17005488	HIST1H2BA	histone cluster 1, H2ba	0.1003	0.0485
17005542	HFE	hemochromatosis	0.4889	0.0154
17005596	HIST2H4B	histone cluster 2, H4b	0.2117	0.0436
17005655	BTN3A1	butyrophilin, subfamily 3, member A1	0.375	0.0098
17005740	HCG11	HLA complex group 11 (non-protein coding)	0.5373	0.0258
17005888	ZNF165	zinc finger protein 165	0.7819	0.0004
17005894	ZSCAN12P1	zinc finger and SCAN domain containing 12 pseudogene 1	0.4696	0.0011
17005998	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17006060	LOC100507362	uncharacterized LOC100507362	0.1228	0.0495
17006087	HLA-F	major histocompatibility complex, class I, F	0.4912	0.004
17006122	HLA-G	major histocompatibility complex, class I, G	0.5155	0
17006142	HLA-A	major histocompatibility complex, class I, A	0.6047	0.0012
17006222	HLA-L	major histocompatibility complex, class I, L (pseudogene)	0.3453	0.0088
17006261	HLA-E	major histocompatibility complex, class I, E	0.8356	0.0003
17006605	HCP5	HLA complex P5 (non-protein coding)	1.5682	0.0019
17006611			0.259	0.0169
17006614	HCG26	HLA complex group 26 (non-protein coding)	0.765	0.026
17006666	LST1	leukocyte specific transcript 1	0.3373	0.0008
17006683	AIF1	allograft inflammatory factor 1	0.5142	0.017
17006949	CFB	complement factor B	0.6313	0.0027
17007048	C4A	complement component 4A (Rodgers blood group)	1.0789	0.0082
17007118	C4B	complement component 4B (Chido blood group)	1.0981	0.0085
17007257	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.0542	0.0023
17007266	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	0.5462	0.0422
17007292	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.9277	0.0003
17007352	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.763	0.0044
17007368	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	0.6012	0.0043

17007605			0.1785	0.0157
17007654			0.2212	0.0072
17007810	PPARD	peroxisome proliferator-activated receptor delta	0.3528	0.0403
17007847			0.2025	0.0052
17008088	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	0.2198	0.0123
17008179	FLJ45825	uncharacterized LOC100505530	0.1308	0.037
17008216			0.3852	0.0487
17008463	NCR2	natural cytotoxicity triggering receptor 2	0.1396	0.0142
17008542			0.1792	0.0009
17008928	TTBK1	tau tubulin kinase 1	0.1212	0.0131
17009126			0.1917	0.0493
17009193	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	0.7065	0.0068
17009233			0.2072	0.0052
17009316	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	1.2184	0.0062
17009355	TDRD6	tudor domain containing 6	0.2345	0.0277
17009446	GPR115	G protein-coupled receptor 115	0.5484	0.0381
17009521			0.1787	0.0112
17009906			0.193	0.0245
17009993			0.1174	0.0344
17010002			0.1304	0.0392
17010173			0.3352	0.0267
17010273	KCNQ5-IT1	KCNQ5 intronic transcript 1 (non-protein coding)	0.1641	0.0021
17010507			0.1727	0.0043
17010715	CYB5R4	cytochrome b5 reductase 4	0.4195	0.0175
17010737			0.1233	0.0382
17010830	C6orf165	chromosome 6 open reading frame 165	0.3534	0.0266
17010923			0.1705	0.0053
17011279	PRDM1	PR domain containing 1, with ZNF domain	0.4723	0.0081
17011361			0.2741	0
17011365	MIR587	microRNA 587	0.4773	0.0002
17011593	FIG4	FIG4 homolog, SAC1 lipid phosphatase domain containing (S. cerevisiae)	0.322	0.0459
17011708	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	0.9291	0.0075
17011790	RFPL4B	ret finger protein-like 4B	0.3334	0.0072
17011800	LOC100287612	uncharacterized LOC100287612	0.2039	0.0089
17011814			0.118	0.0469
17012045			0.1953	0.0373
17012158			0.485	0.022
17012182	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.2242	0.0072
17012223	CLVS2	clavesin 2	1.6995	0.0003
17012233			0.8339	0.0003
17012245	NKAIN2	Na+/K+ transporting ATPase interacting 2	0.326	0.0037
17012259			0.4128	0.0428
17012340			0.5268	0.0252
17012392	RSPO3	R-spondin 3	0.2502	0.0478
17012442			0.1329	0.0281
17012672			0.1395	0.0116
17012676	LOC100507254	uncharacterized LOC100507254	0.1839	0.0348
17012761	TCF21	transcription factor 21	0.2526	0.0069
17012914			0.1572	0.0092
17012917			0.2229	0.0017
17013126	GPR126	G protein-coupled receptor 126	0.5042	0.002
17013672			0.1683	0.0413
17013856	VIP	vasoactive intestinal peptide	0.1366	0.0448
17013918			0.2395	0.0045
17014012			0.2438	0.0029
17014251			0.1757	0.0037

17014286			0.122	0.0311
17014599			0.2056	0.0132
17014830			0.1534	0.0223
17014959			0.2393	0.0037
17015003			0.1116	0.0412
17015331	F13A1	coagulation factor XIII, A1 polypeptide	0.719	0.0479
17015371			0.3076	0.0249
17015474			0.1258	0.0057
17015493			0.2396	0.0023
17015499	OFCC1	orofacial cleft 1 candidate 1	0.1006	0.0474
17015805			0.1362	0.02
17015817			0.4018	0.0002
17015819	DTNBP1	dystrobrevin binding protein 1	0.2494	0.0254
17015860			0.3405	0.0012
17016017			0.1905	0.0324
17016020			0.1998	0.006
17016060			0.1755	0.0084
17016254			0.2039	0.0079
17016290			0.1832	0.0171
17016522			0.4447	0.0356
17016787	RNF39	ring finger protein 39	0.6051	0.0034
17016799	TRIM31	tripartite motif containing 31	0.2574	0
17017043			0.2663	0.0348
17017126	HLA-C	major histocompatibility complex, class I, C	0.6023	0.0006
17017142			0.158	0.0259
17017403	VWA7	von Willebrand factor A domain containing 7	0.1249	0.0193
17017695	RN5S206	RNA, 5S ribosomal 206	0.2259	0.0331
17017852	C6orf10	chromosome 6 open reading frame 10	0.2525	0.001
17017907	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.6409	0.009
17017926	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.5521	0.0022
17017965	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17018011	HLA-DMA	major histocompatibility complex, class II, DM alpha	0.5523	0.0147
17018025	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7093	0.0054
17018039	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6499	0.0139
17018256	CUTA	cutA divalent cation tolerance homolog (E. coli)	0.3536	0.0004
17018289			0.3715	0.0118
17018476	TULP1	tubby like protein 1	0.1604	0.0097
17018871	KIF6	kinesin family member 6	0.2079	0.0451
17018971			0.5859	0.0108
17019077	TFEB	transcription factor EB	0.2337	0.0048
17019530	LOC285857	uncharacterized LOC285857	0.1358	0.022
17019689	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	1.192	0.0065
17019707	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	0.7462	0.0382
17019724	LOC100131283	uncharacterized LOC100131283	0.293	0.0133
17020059	GSTA2	glutathione S-transferase alpha 2	1.8464	0.0333
17020069	GSTA1	glutathione S-transferase alpha 1	2.077	0.0023
17020079	GSTA5	glutathione S-transferase alpha 5	0.2836	0.0124
17020214	KLHL31	kelch-like 31 (Drosophila)	0.6183	0.0201
17020234			0.2772	0.0208
17020620	LMBRD1	LMBR1 domain containing 1	0.388	0.01
17020691	B3GAT2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	0.2809	0.0082
17020700			0.2773	0.0061
17020703	LOC100507367	uncharacterized LOC100507367	0.3947	0.0163
17020731			0.217	0.0375
17020771	DPPA5	developmental pluripotency associated 5	0.2732	0.0007
17020823	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	0.7649	0.0048
17021281	KIAA1009	KIAA1009	0.2956	0.0474

17021596	RRAGD	Ras-related GTP binding D	0.5594	0.0068
17021789			0.526	0.0063
17021831	GPR63	G protein-coupled receptor 63	0.5072	0.0133
17022211			0.184	0.0182
17022949			0.4717	0.0358
17023118	FAM184A	family with sequence similarity 184, member A	0.457	0.006
17023255	TRDN	triadin	0.7192	0.011
17023296			0.2693	0.0136
17023405	THEMIS	thymocyte selection associated	0.2278	0.0202
17023716	VNN3	vanin 3	0.1592	0.0373
17023868			0.1284	0.0488
17024144	IFNGR1	interferon gamma receptor 1	0.4493	0.0285
17024165			0.1109	0.0255
17024278			0.2913	0.0337
17024301			0.2372	0.0007
17024308	RN5S220	RNA, 5S ribosomal 220	0.1222	0.011
17024329			0.172	0.018
17024728			0.2994	0.0003
17024772			0.4229	0.0004
17025267	SOD2	superoxide dismutase 2, mitochondrial	0.3108	0.026
17025666	RNASET2	ribonuclease T2	0.3099	0.0367
17026109	HLA-A	major histocompatibility complex, class I, A	0.5249	0.0025
17026272	LST1	leukocyte specific transcript 1	0.3489	0.0001
17026444	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.778	0.0034
17026460	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	0.6012	0.0043
17026593	RNF39	ring finger protein 39	0.6051	0.0034
17026762	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17026783	VWA7	von Willebrand factor A domain containing 7	0.1249	0.0193
17027082	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	0.997	0.0007
17027091	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.5578	0.0003
17027130	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17027187	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6512	0.0134
17027217	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17027301			0.4755	0.004
17027330	HLA-G	major histocompatibility complex, class I, G	0.4881	0.0001
17027344	HLA-A	major histocompatibility complex, class I, A	0.5249	0.0025
17027443	HLA-E	major histocompatibility complex, class I, E	0.8278	0.0003
17027581	DDR1	discoidin domain receptor tyrosine kinase 1	0.3945	0.0277
17027701	PSORS1C1	psoriasis susceptibility 1 candidate 1	0.2576	0.0277
17027743	HCP5	HLA complex P5 (non-protein coding)	0.9594	0.0004
17027749	HCG26	HLA complex group 26 (non-protein coding)	1.0293	0.0007
17027801	LST1	leukocyte specific transcript 1	0.362	0.0001
17027817	AIF1	allograft inflammatory factor 1	0.5142	0.017
17028176	C4B	complement component 4B (Chido blood group)	1.1615	0.0062
17028313	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.8758	0.0056
17028326	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	1.5473	0.0001
17028338	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.772	0.0004
17028345	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.9448	0.0002
17028585	OR12D3	olfactory receptor, family 12, subfamily D, member 3	0.1171	0.0484
17028680	RNF39	ring finger protein 39	0.4503	0.0084
17028909	IER3	immediate early response 3	0.3335	0.0464
17029003	HLA-C	major histocompatibility complex, class I, C	0.6427	0.0004
17029082	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17029257	VWA7	von Willebrand factor A domain containing 7	0.142	0.0152
17029712	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	0.8513	0.0006
17029721	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.7864	0.0014
17029735	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.5578	0.0003
17029774	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116

17029807	HLA-DMB	major histocompatibility complex, class II, DM beta	0.5087	0.0356
17029833	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.6919	0.0038
17029847	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6168	0.0151
17030098	OR12D2	olfactory receptor, family 12, subfamily D, member 2	0.1878	0.0192
17030147			0.4893	0.0025
17030176	HLA-G	major histocompatibility complex, class I, G	0.4656	0.0001
17030188	HLA-A	major histocompatibility complex, class I, A	0.421	0.0163
17030288	HLA-E	major histocompatibility complex, class I, E	0.8278	0.0003
17030426	DDR1	discoidin domain receptor tyrosine kinase 1	0.4012	0.0236
17030575	HCG26	HLA complex group 26 (non-protein coding)	1.0293	0.0007
17030627	LST1	leukocyte specific transcript 1	0.3703	0.0001
17030643	AIF1	allograft inflammatory factor 1	0.5327	0.0163
17030967			0.8446	0.0139
17031045	C4B	complement component 4B (Chido blood group)	1.1728	0.0069
17031139	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.9128	0.0049
17031153	LOC100509457	HLA class II histocompatibility antigen, DQ alpha 1 chain-like	0.4167	0.0138
17031178	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.9935	0.0001
17031219	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.763	0.0044
17031373	UBD	ubiquitin D	0.2672	0.0061
17031459	RNF39	ring finger protein 39	0.6051	0.0034
17031469	TRIM31	tripartite motif containing 31	0.2271	0.0001
17031687	IER3	immediate early response 3	0.3335	0.0464
17031781	HLA-C	major histocompatibility complex, class I, C	0.5348	0.0064
17031867	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17032042	VWA7	von Willebrand factor A domain containing 7	0.1249	0.0193
17032389	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	0.4908	0.0051
17032423	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.4811	0.0005
17032462	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17032519	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7248	0.0045
17032533	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6499	0.0139
17032753	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17032811	LOC100507362	uncharacterized LOC100507362	0.1228	0.0495
17032837			0.4893	0.0025
17032870	HLA-G	major histocompatibility complex, class I, G	0.4734	0
17032882	HLA-A	major histocompatibility complex, class I, A	0.3383	0.0083
17032957	HLA-L	major histocompatibility complex, class I, L (pseudogene)	0.7306	0.003
17032993	HLA-E	major histocompatibility complex, class I, E	0.8356	0.0003
17033131	DDR1	discoidin domain receptor tyrosine kinase 1	0.4215	0.0256
17033344	LST1	leukocyte specific transcript 1	0.362	0.0001
17033604	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.8762	0.0051
17033617	LOC100509457	HLA class II histocompatibility antigen, DQ alpha 1 chain-like	0.3061	0.0327
17033646	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	1.0224	0.0003
17033704	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.7763	0.0033
17033915	RNF39	ring finger protein 39	0.581	0.0038
17033925	TRIM31	tripartite motif containing 31	0.2314	0
17034143	IER3	immediate early response 3	0.3335	0.0464
17034254			0.6452	0.0025
17034339	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17034714	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	0.479	0.0052
17034749	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.4483	0.0004
17034777	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17034810	HLA-DMB	major histocompatibility complex, class II, DM beta	0.5011	0.047
17034837	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7248	0.0045
17034851	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6512	0.0134
17034955	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17034996	LOC100507362	uncharacterized LOC100507362	0.1228	0.0495

17035022	HLA-F	major histocompatibility complex, class I, F	0.5213	0.0011
17035037	HLA-G	major histocompatibility complex, class I, G	0.4656	0.0001
17035049	HLA-A	major histocompatibility complex, class I, A	0.6045	0.0025
17035115	HLA-E	major histocompatibility complex, class I, E	0.8356	0.0003
17035371	HCP5	HLA complex P5 (non-protein coding)	1.6983	0.0003
17035373	HCG26	HLA complex group 26 (non-protein coding)	1.0293	0.0007
17035425	LST1	leukocyte specific transcript 1	0.3703	0.0001
17035441	AIF1	allograft inflammatory factor 1	0.5349	0.0177
17035749	C4A	complement component 4A (Rodgers blood group)	1.1674	0.006
17035880	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.8781	0.0051
17035911	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.5762	0.0015
17035918	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.9845	0.0002
17035971	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.778	0.0034
17036198	RNF39	ring finger protein 39	0.6051	0.0034
17036208	TRIM31	tripartite motif containing 31	0.2262	0.0001
17036486	HLA-C	major histocompatibility complex, class I, C	0.3462	0.0348
17036504			0.5829	0.002
17036587	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17036760	VWA7	von Willebrand factor A domain containing 7	0.1249	0.0193
17037192	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	0.5067	0.0265
17037218	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.4811	0.0005
17037257	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4692	0.0141
17037303	HLA-DMA	major histocompatibility complex, class II, DM alpha	0.6229	0.0156
17037317	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7093	0.0054
17037331	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6512	0.0134
17037557	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17037603	LOC100507362	uncharacterized LOC100507362	0.1228	0.0495
17037629			0.4893	0.0025
17037658	HLA-G	major histocompatibility complex, class I, G	0.4881	0.0001
17037670	HLA-A	major histocompatibility complex, class I, A	0.2847	0.0302
17037774	HLA-E	major histocompatibility complex, class I, E	0.8278	0.0003
17037907	DDR1	discoidin domain receptor tyrosine kinase 1	0.4215	0.0256
17038124	LST1	leukocyte specific transcript 1	0.357	0.0003
17038140	AIF1	allograft inflammatory factor 1	0.5142	0.017
17038462			0.8534	0.0133
17038596	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.8781	0.0051
17038609	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	1.4368	0.0001
17038622	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.7723	0.0005
17038629	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.9283	0.0003
17038687	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.7594	0.0032
17038967	TRIM31	tripartite motif containing 31	0.2544	0
17039184	IER3	immediate early response 3	0.2805	0.037
17039199	TIGD1L	tigger transposable element derived 1-like	0.2964	0.0196
17039217	CDSN	corneodesmosin	0.3744	0.0497
17039281	HLA-C	major histocompatibility complex, class I, C	0.517	0.009
17039299			0.6625	0.0011
17039380	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17039907	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	0.9504	0.0013
17039914	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	0.8513	0.0006
17039923	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.7864	0.0014
17039935	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.4483	0.0004
17039963	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17039996	HLA-DMB	major histocompatibility complex, class II, DM beta	0.5011	0.047
17040023	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7021	0.0055
17040037	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6572	0.0117
17040267	C6orf100	chromosome 6 open reading frame 100	0.206	0.0373
17040325	LOC100507362	uncharacterized LOC100507362	0.1228	0.0495
17040375	HLA-G	major histocompatibility complex, class I, G	0.5078	0
17040387	HLA-A	major histocompatibility complex, class I, A	0.5257	0.0221

17040488	HLA-E	major histocompatibility complex, class I, E	0.8278	0.0003
17040665	HCP5	HLA complex P5 (non-protein coding)	0.9578	0.0017
17040719	LST1	leukocyte specific transcript 1	0.3455	0.0005
17040735	AIF1	allograft inflammatory factor 1	0.5142	0.017
17041030	C4B	complement component 4B (Chido blood group)	1.1769	0.006
17041111	C4B	complement component 4B (Chido blood group)	1.1678	0.0065
17041225	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.8781	0.0051
17041240	LOC100509457	HLA class II histocompatibility antigen, DQ alpha 1 chain-like	0.5043	0.0271
17041260	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	0.7885	0.0002
17041318	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.763	0.0044
17041472	OR11A1	olfactory receptor, family 11, subfamily A, member 1	0.1103	0.0297
17041542	RNF39	ring finger protein 39	0.6051	0.0034
17041552	TRIM31	tripartite motif containing 31	0.1882	0.0002
17041752	IER3	immediate early response 3	0.3335	0.0464
17041759	LINC00243	long intergenic non-protein coding RNA 243	0.1808	0.0221
17041782	HLA-C	major histocompatibility complex, class I, C	0.4988	0.0082
17041800			0.6658	0.0021
17041863	LTB	lymphotoxin beta (TNF superfamily, member 3)	0.2808	0.0011
17042035	VWA7	von Willebrand factor A domain containing 7	0.1249	0.0193
17042433	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	0.5608	0.0002
17042473	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.4628	0.0116
17042519	HLA-DMA	major histocompatibility complex, class II, DM alpha	0.5897	0.018
17042534	HLA-DOA	major histocompatibility complex, class II, DO alpha	0.7143	0.0042
17042548	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.6412	0.0147
17042648	DAXX	death-domain associated protein	0.1366	0.0434
17042650	CUTA	cutA divalent cation tolerance homolog (E. coli)	0.3437	0.0005
17042671			0.1859	0.0096
17042726			0.1812	0.0288
17043312	ZNF815P	zinc finger protein 815, pseudogene	0.2379	0.032
17043529	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	0.4521	0.0221
17043550	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila)	0.555	0.0016
17043573	LOC729852	uncharacterized LOC729852	0.2032	0.0482
17043622	NXPH1	neurexophilin 1	1.18	0.0016
17043727	SCIN	scinderin	0.4746	0.0106
17043769			0.2631	0.0083
17043856	AHR	aryl hydrocarbon receptor	0.648	0.0136
17043944			0.2496	0.04
17043950			0.2672	0.0224
17043953			1.2439	0.0001
17043965			0.2207	0.0049
17044315	FAM221A	family with sequence similarity 221, member A	0.3874	0.0435
17044647			0.3229	0.0002
17044758	C7orf41	chromosome 7 open reading frame 41	0.3705	0.0005
17044769			0.3403	0.0065
17044773	ZNRF2	zinc and ring finger 2	0.3613	0.0039
17044795	DKFZP586I1420	uncharacterized protein DKFZp586I1420	0.4451	0.0287
17044877	GHRHR	growth hormone releasing hormone receptor	0.1842	0.0053
17044905	ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	0.4498	0.0197
17045258	GPR141	G protein-coupled receptor 141	0.482	0
17045269	NME8	NME/NM23 family member 8	0.2533	0.014
17045303	STARD3NL	STARD3 N-terminal like	0.2822	0.0279
17045325	POU6F2	POU class 6 homeobox 2	0.1776	0.0308
17045369	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	0.3257	0.0316
17045451			0.1672	0.0289
17045542	STK17A	serine/threonine kinase 17a	0.5063	0.0158
17045555	BLVRA	biliverdin reductase A	0.5991	0.0027

17045802			0.1255	0.0417
17045851			0.1667	0.0171
17046024	VWC2	von Willebrand factor C domain containing 2	0.3164	0.0144
17046041	IKZF1	IKAROS family zinc finger 1 (Ikaros)	0.335	0.0111
17046072			0.1904	0.0028
17046098			0.1648	0.0077
17046407	ZNF727	zinc finger protein 727	0.8788	0.0303
17046453			0.2825	0.0451
17046524			0.3893	0.0418
17046664	KCTD7	potassium channel tetramerisation domain containing 7	0.3713	0.0219
17046834	MIR3914-2	microRNA 3914-2	0.1165	0.0134
17046935	FZD9	frizzled family receptor 9	0.5445	0.0022
17047504	HSPB1	heat shock 27kDa protein 1	0.6022	0.0067
17047593			0.165	0.0325
17047650			0.3554	0.0231
17048033			0.3567	0.0193
17048039			0.2011	0.0246
17048048	ZNF804B	zinc finger protein 804B	0.3115	0.0009
17048068	DPY19L2P4	dpy-19-like 2 pseudogene 4 (C. elegans)	0.4026	0.0484
17048072	STEAP1	six transmembrane epithelial antigen of the prostate 1	0.5432	0.0012
17048083	STEAP2	STEAP family member 2, metalloreductase	0.565	0.0019
17048102	C7orf63	chromosome 7 open reading frame 63	0.549	0.0002
17048167	CLDN12	claudin 12	0.454	0.0122
17048190	CDK14	cyclin-dependent kinase 14	0.8875	0.0005
17048223	CLDN12	claudin 12	1.2025	0.0041
17048244			0.3934	0.0086
17048437	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	0.1346	0.0242
17048639	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1	0.6368	0.0272
17048667			0.27	0.0307
17048706	LMTK2	lemur tyrosine kinase 2	0.495	0.0245
17049330	MEPCE	methylphosphate capping enzyme	0.3335	0.0354
17049366	AGFG2	ArfGAP with FG repeats 2	0.4842	0.0349
17049522	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.199	0.0497
17049814	ORAI2	ORAI calcium release-activated calcium modulator 2	0.4194	0.0064
17050134	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	0.3394	0.0421
17050328	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.4288	0.0353
17050350	LRRN3	leucine rich repeat neuronal 3	1.1722	0.0188
17050358	LOC100506413	uncharacterized LOC100506413	0.3883	0.0103
17050455	FOXP2	forkhead box P2	0.7914	0.0166
17050495	MIR3666	microRNA 3666	0.31	0.0494
17050538	CAV2	caveolin 2	0.2885	0.0386
17050591	MET	met proto-oncogene (hepatocyte growth factor receptor)	2.4135	0
17050622	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	0.3263	0.0096
17050761			0.1248	0.0248
17050765	KCND2	potassium voltage-gated channel, Shal-related subfamily, member 2	1.0873	0.0279
17050887			0.2661	0.041
17050911			0.6933	0.0004
17050988	SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	0.1583	0.041
17051376	TSPAN33	tetraspanin 33	0.8633	0.0049
17051390			0.4002	0.0413
17051409	AHCYL2	adenosylhomocysteinase-like 2	0.4485	0.017
17051504	KLHDC10	kelch domain containing 10	0.2219	0.0372
17051745	EXOC4	exocyst complex component 4	0.2962	0.0098
17051827	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	0.4062	0.0034
17051950			0.2625	0.0119

17052083	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	0.1429	0.0466
17052106			0.2023	0.0398
17052417	TAS2R4	taste receptor, type 2, member 4	0.3286	0.0337
17052542			0.3785	0.0002
17052544			0.2288	0.0134
17052550			0.2422	0.0085
17052552	LOC100124692	maltase-glucoamylase (alpha-glucosidase) pseudogene	0.3964	0.0008
17052584			0.1543	0.0185
17052619	TRBV20-1	T cell receptor beta variable 20-1	0.2668	0.0471
17052648	TRBV29-1	T cell receptor beta variable 29-1	0.2912	0.0017
17052685	TRBC2	T cell receptor beta constant 2	1.0021	0.0001
17052859	LOC100508781	protein FAM115A-like	0.2533	0.0475
17052881	OR2F2	olfactory receptor, family 2, subfamily F, member 2	0.2439	0.0281
17052906	OR2A12	olfactory receptor, family 2, subfamily A, member 12	0.1031	0.036
17052935	OR2A20P	olfactory receptor, family 2, subfamily A, member 20 pseudogene	0.3167	0.0394
17053004	LOC100507538	uncharacterized LOC100507538	0.1496	0.0492
17053290	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	0.2325	0.0216
17053304			0.2821	0.0476
17053316	LRRC61	leucine rich repeat containing 61	0.5007	0.0196
17053325	C7orf29	chromosome 7 open reading frame 29	0.4145	0.0239
17053384	GIMAP4	GTPase, IMAP family member 4	0.3942	0.0393
17053393	GIMAP2	GTPase, IMAP family member 2	0.3435	0.0033
17053421	TMEM176A	transmembrane protein 176A	0.54	0.031
17053455	NOS3	nitric oxide synthase 3 (endothelial cell)	0.2587	0.0342
17053553	SLC4A2	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	0.2522	0.0465
17053850	LOC100132707	uncharacterized LOC100132707	0.3965	0.0078
17054142			0.1694	0.0117
17054145			0.1497	0.018
17054439	TMEM184A	transmembrane protein 184A	0.6595	0.0065
17054527			0.1485	0.0458
17054685			0.2366	0.0016
17055006	FAM220A	family with sequence similarity 220, member A	0.2438	0.0232
17055216	ICA1	islet cell autoantigen 1, 69kDa	0.3206	0.0265
17055295	VWDE	von Willebrand factor D and EGF domains	0.524	0.0036
17055334			0.1675	0.0092
17055603	MIR1302-6	microRNA 1302-6	0.3896	0.0048
17055605			0.1719	0.0255
17055614	TWIST1	twist homolog 1 (Drosophila)	0.7307	0.0008
17055640	TMEM196	transmembrane protein 196	0.5543	0.0004
17055649			0.5507	0.0057
17055684			0.3655	0.0117
17055888			0.1889	0.0489
17055910	DFNA5	deafness, autosomal dominant 5	0.7874	0.0003
17055937	OSBPL3	oxysterol binding protein-like 3	0.7016	0.0005
17056060	KIAA0087	KIAA0087	0.289	0.0053
17056248	CPVL	carboxypeptidase, vitellogenic-like	0.589	0.0413
17056275			0.1339	0.0073
17056558			0.2455	0.0233
17056680	KIAA0895	KIAA0895	0.4413	0.0085
17056701	AOAH	acyloxyacyl hydrolase (neutrophil)	0.5644	0.006
17056734	AOAH-IT1	AOAH intronic transcript 1 (non-protein coding)	0.1724	0.0215
17056813	TARP	TCR gamma alternate reading frame protein	0.3044	0.0067
17056823	TARP	TCR gamma alternate reading frame protein	0.3044	0.0067
17056830	TRGV10	T cell receptor gamma variable 10 (non-functional)	0.3122	0.0185
17056896	VPS41	vacuolar protein sorting 41 homolog (S. cerevisiae)	0.3968	0.0102
17056939	POU6F2-AS2	POU6F2 antisense RNA 2 (non-protein coding)	0.1882	0.001
17056946	POU6F2-AS1	POU6F2 antisense RNA 1 (non-protein coding)	0.1352	0.0099
17056973			0.3904	0.0059

17057496			0.1411	0.0275
17057683	ZPBP	zona pellucida binding protein	0.129	0.0379
17057852			0.2	0.0456
17057859			0.1581	0.0401
17057990	NUPR1L	nuclear protein, transcriptional regulator, 1-like	0.4025	0.019
17058015			0.2171	0.0346
17058065	LOC100509247	uncharacterized LOC100509247	0.2998	0.0224
17058104			0.1681	0.0276
17058118			0.1591	0.0335
17058365	TRIM74	tripartite motif containing 74	0.8035	0.0014
17058445	TRIM50	tripartite motif containing 50	0.7365	0.0075
17058912	SRCRB4D	scavenger receptor cysteine rich domain containing, group B (4 domains)	0.3334	0.0103
17058968	FGL2	fibrinogen-like 2	0.6046	0.0277
17058978	PION	pigeon homolog (Drosophila)	0.4284	0.0311
17059096			0.1712	0.025
17059165	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	0.8462	0.0174
17059292	SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	0.304	0.0472
17059318			0.1574	0.0204
17059321			0.128	0.0274
17059380			0.3626	0.0202
17059383			0.4253	0.0149
17059388	KIAA1324L	KIAA1324-like	1.0399	0.0163
17059427	C7orf23	chromosome 7 open reading frame 23	0.279	0.0422
17059551	SRI	sorcin	0.4606	0.0038
17059594			0.3475	0.0233
17059603			1.2125	0.0023
17059696	ERVW-1	endogenous retrovirus group W, member 1	0.3945	0
17059776	SAMD9L	sterile alpha motif domain containing 9-like	0.4568	0.0293
17059804	CALCR	calcitonin receptor	0.1567	0.0203
17059861			0.3814	0.0027
17060014	LOC100506136	uncharacterized LOC100506136	0.3425	0.0296
17060026	SHFM1	split hand/foot malformation (ectrodactyly) type 1	0.2426	0.0163
17060167	TMEM130	transmembrane protein 130	0.5983	0.0094
17060287	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	1.959	0.0002
17060317	CYP3A7-CYP3AP1	CYP3A7-CYP3AP1 readthrough	1.1021	0.0026
17060337	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	2.1861	0.0002
17060360	TRIM4	tripartite motif containing 4	0.3997	0.0366
17060380	AZGP1	alpha-2-glycoprotein 1, zinc-binding	0.1397	0.0151
17060444	MIR93	microRNA 93	0.2831	0.011
17060554			0.2182	0.0069
17060592	C7orf61	chromosome 7 open reading frame 61	0.1267	0.0303
17060599	TSC22D4	TSC22 domain family, member 4	0.5171	0.002
17060627	LRCH4	leucine-rich repeats and calponin homology (CH) domain containing 4	0.381	0.0125
17060923	RABL5	RAB, member RAS oncogene family-like 5	0.3042	0.0283
17060972			0.2124	0.0038
17061757			0.3102	0.028
17061759	NRCAM	neuronal cell adhesion molecule	1.5724	0.0021
17061843			0.2476	0.0107
17061853			0.349	0.0052
17061859	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.4101	0.0394
17061879			0.8745	0.0249
17061881	DOCK4	dedicator of cytokinesis 4	0.6854	0.0012
17061949	RN5S237	RNA, 5S ribosomal 237	0.3811	0.0433
17061983			0.1538	0.0187
17062013	PPP1R3A	protein phosphatase 1, regulatory subunit 3A	0.1098	0.0459
17062039			0.4053	0.0058
17062049	TFEC	transcription factor EC	0.3605	0.0088

17062112	ST7-AS2	ST7 antisense RNA 2 (non-protein coding)	0.3116	0.0009
17062402	IQUB	IQ motif and ubiquitin domain containing	1.0935	0
17062906	COPG2	coatomer protein complex, subunit gamma 2	0.3942	0.0164
17062915	TSGA13	testis specific, 13	0.3449	0.0007
17062955	FLJ43663	uncharacterized LOC378805	0.4808	0.038
17063073	SLC35B4	solute carrier family 35, member B4	0.2836	0.0455
17063121	C7orf49	chromosome 7 open reading frame 49	0.323	0.0198
17063681	KIAA1147	KIAA1147	0.4019	0.0249
17063708	PRSS37	protease, serine, 37	0.2681	0.0253
17063770	TRBV5-7	T cell receptor beta variable 5-7 (non-functional)	0.188	0.0157
17063776	TRBV6-8	T cell receptor beta variable 6-8	0.1856	0.044
17063948	EPHA1	EPH receptor A1	0.1556	0.0072
17063981	FAM115A	family with sequence similarity 115, member A	0.3828	0.0412
17064002	OR2A20P	olfactory receptor, family 2, subfamily A, member 20 pseudogene	0.3007	0.0424
17064054	TPK1	thiamin pyrophosphokinase 1	0.3843	0.0114
17064226			0.5379	0.0037
17064230			1.0268	0.006
17064235	ACTR3C	ARP3 actin-related protein 3 homolog C (yeast)	0.9659	0.0041
17064249			0.3628	0.0081
17064285	TMEM176B	transmembrane protein 176B	0.712	0.0111
17064299	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0.9705	0.0027
17064325	ATG9B	autophagy related 9B	0.3342	0.0063
17064698			0.3836	0.0001
17064934			0.2072	0.0305
17065284			0.16	0.0444
17065330	MIR4659A	microRNA 4659a	0.4151	0.0364
17065332	LOC100652791	uncharacterized LOC100652791	0.165	0.0169
17065347	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.2216	0.0057
17065352	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.2095	0.0099
17065357	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.2216	0.0057
17065362	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.1964	0.0188
17065367	FAM90A20P	family with sequence similarity 90, member A20, pseudogene	0.1743	0.0398
17065372	DEFB109P1B	defensin, beta 109, pseudogene 1B	0.6236	0.0258
17065398	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.211	0.0054
17065403	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.1889	0.022
17065408	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.1899	0.0137
17065413	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.1889	0.022
17065418	FAM90A10P	family with sequence similarity 90, member A10, pseudogene	0.1825	0.0131
17065423	FAM90A10P	family with sequence similarity 90, member A10, pseudogene	0.2892	0.0029
17065463	LOC100132396	zinc finger protein 705D-like	0.1478	0.0446
17065473	FAM66E	family with sequence similarity 66, member E	0.4643	0.0258
17065513	CLDN23	claudin 23	0.305	0.0474
17065517			0.2121	0.0077
17065521			0.3227	0.0054
17065655			0.2381	0.0041
17065956			0.1691	0.0118
17066183	NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	0.384	0.0029
17066220			0.1187	0.003

17066302	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	0.5323	0.0038
17066346			0.1578	0.0283
17066446	EPB49	erythrocyte membrane protein band 4.9 (dematin)	0.7116	0.001
17066601	SLC39A14	solute carrier family 39 (zinc transporter), member 14	0.4466	0.0006
17066894			0.4182	0.0112
17066921	ADAM28	ADAM metallopeptidase domain 28	0.5568	0.0064
17067011	NEFM	neurofilament, medium polypeptide	1.4093	0.0105
17067326	MIR3622A	microRNA 3622a	0.2652	0.0002
17067410	FZD3	frizzled family receptor 3	0.7794	0.0192
17067424	EXTL3	exostoses (multiple)-like 3	0.2679	0.0227
17067611	RNU5A-3P	RNA, U5A small nuclear 3, pseudogene	0.1702	0.0385
17067996			0.2513	0.0042
17068238	ADAM5P	ADAM metallopeptidase domain 5, pseudogene	0.1552	0.029
17068338			0.3095	0.0078
17068778			0.1602	0.0282
17068900			0.2134	0.0276
17068924			0.1758	0.0451
17069063	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.4943	0.0163
17069087	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	0.244	0.0263
17069325			0.1409	0.0426
17069431			0.176	0.0201
17069444			0.1439	0.026
17069467	BHLHE22	basic helix-loop-helix family, member e22	0.219	0.0005
17069471			0.584	0.0329
17069473			0.1448	0.0455
17069603			0.1722	0.0462
17069782	C8orf34	chromosome 8 open reading frame 34	0.2007	0.0236
17069879			0.1675	0.0282
17069926			0.1252	0.0236
17069971	RN5S271	RNA, 5S ribosomal 271	0.1609	0.004
17070061	LY96	lymphocyte antigen 96	0.7455	0.0057
17070221	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0.2581	0.0427
17070242			0.6342	0.0029
17070317			0.1732	0.0043
17070352			0.4264	0.0388
17070355			0.1538	0.024
17070589	CNBD1	cyclic nucleotide binding domain containing 1	0.1022	0.0297
17070653	OSGIN2	oxidative stress induced growth inhibitor family member 2	0.4394	0.0061
17070798			0.2029	0.0175
17071115			0.2016	0.0474
17071162	CPQ	carboxypeptidase Q	0.4259	0.0018
17071478			0.244	0.0182
17071497	GRHL2	grainyhead-like 2 (Drosophila)	0.1684	0.0021
17071521			0.6883	0.0279
17071620	MIR3151	microRNA 3151	0.3513	0.0015
17072162	COL14A1	collagen, type XIV, alpha 1	1.6042	0.0003
17072269			0.1692	0.0353
17072396			0.1519	0.0347
17072439	FER1L6	fer-1-like 6 (C. elegans)	0.1705	0.0187
17073034			0.3941	0.0041
17073130			0.1873	0.0107
17073163			0.1003	0.0496
17073166	MIR4472-1	microRNA 4472-1	0.2734	0.0236
17073247			0.9152	0.0017
17073754	SCXA	scleraxis homolog A (mouse)	0.5212	0.0346
17074007	OR4F21	olfactory receptor, family 4, subfamily F, member 21	0.1941	0.0371
17074225			0.1734	0.0129

17074342			0.5568	0.0069
17074400	FAM90A7P	family with sequence similarity 90, member A7, pseudogene	0.2164	0.0188
17074427	DEFB109P1B	defensin, beta 109, pseudogene 1B	0.6236	0.0258
17074430	FAM90A12P	family with sequence similarity 90, member A12, pseudogene	0.2707	0.0062
17074462			0.1741	0.0332
17074510			0.1293	0.0236
17074512			0.1896	0.0141
17074539			0.2517	0.0024
17074541			0.1143	0.0411
17074547			0.1773	0.0383
17074773	DEFB109P1	defensin, beta 109, pseudogene 1	0.6783	0.0328
17074776	FAM90A2P	family with sequence similarity 90, member A2, pseudogene	0.3419	0.0058
17074893			0.1526	0.0104
17075082	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	0.5257	0.0048
17075153	LOC100128993	uncharacterized LOC100128993	0.1972	0.0179
17075168	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	0.5468	0.0069
17075198	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	0.1368	0.0316
17075243			0.162	0.0413
17075405	PEBP4	phosphatidylethanolamine-binding protein 4	0.618	0.0072
17075534			0.1067	0.0099
17075569			0.1483	0.0328
17075849			0.2976	0.0004
17075852	FBXO16	F-box protein 16	0.6489	0.0003
17075883	INTS9	integrator complex subunit 9	0.3372	0.0335
17075992	LINC00589	long intergenic non-protein coding RNA 589	0.196	0.0462
17076000			0.2277	0.0032
17076038			0.4745	0.0479
17076215			0.1504	0.0459
17076810	CHRNA6	cholinergic receptor, nicotinic, alpha 6 (neuronal)	0.9502	0.0434
17077188			0.1938	0.0031
17077590			0.113	0.0177
17077723	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	1.0049	0.0011
17077734			0.247	0.0005
17077871	PPP1R42	protein phosphatase 1, regulatory subunit 42	0.1828	0.0184
17077996	LOC286189	uncharacterized LOC286189	0.2209	0.0037
17078290			0.2653	0.0014
17078386			0.3053	0.0236
17078426			0.185	0.036
17078434	IL7	interleukin 7	0.4892	0.0059
17078493	TPD52	tumor protein D52	0.2604	0.0012
17078527			0.2027	0.012
17078856			0.1603	0.0448
17078867			0.1711	0.028
17079132	C8orf87	chromosome 8 open reading frame 87	0.1179	0.0262
17079176			0.1386	0.0439
17079187	CDH17	cadherin 17, LI cadherin (liver-intestine)	0.3125	0.0284
17079405			0.1979	0.0162
17079544	RGS22	regulator of G-protein signaling 22	0.6726	0.012
17080000	DPYS	dihydropyrimidinase	0.4367	0.001
17080042			0.2124	0.0468
17080097			0.2288	0.0032
17080480			0.3252	0.0002
17080788	FBXO32	F-box protein 32	1.0965	0.0002
17081106	GSDMC	gasdermin C	0.1595	0.0129
17081321	HPYR1	Helicobacter pylori responsive 1 (non-protein coding)	0.1761	0.0007
17081323	LRRC6	leucine rich repeat containing 6	0.3926	0.0422
17081822			0.2321	0.0195

17081915			0.2214	0.0127
17081957	LYNX1	Ly6/neurotoxin 1	0.4147	0.0385
17081974	LY6D	lymphocyte antigen 6 complex, locus D	0.9801	0.0019
17082012	LOC100133669	uncharacterized LOC100133669	0.4906	0.0261
17082023	LY6H	lymphocyte antigen 6 complex, locus H	0.1985	0.0167
17082081	RHPN1-AS1	RHPN1 antisense RNA 1 (non-protein coding)	0.2522	0.0352
17082762			0.1315	0.0075
17082969			0.2179	0.0362
17083091			0.5531	0.0207
17083357	CD274	CD274 molecule	0.2467	0.0423
17084228			0.1514	0.0232
17084230	TMEM215	transmembrane protein 215	0.1188	0.0238
17084448	DNAI1	dynein, axonemal, intermediate chain 1	0.1245	0.0394
17085808			0.1995	0.0049
17085811			0.1995	0.0049
17085901	ANXA1	annexin A1	0.6829	0.041
17085942			0.2442	0.0078
17085993			0.166	0.0283
17085996			0.1674	0.0034
17086160			0.2577	0.0011
17086293			0.1782	0.0416
17086330			0.2506	0.0067
17086632			0.3622	0.0001
17086708	SYK	spleen tyrosine kinase	0.3134	0.0282
17086981			0.1593	0.0419
17087025			0.7017	0.002
17087329	TMOD1	tropomodulin 1	0.9189	0.0349
17087785			0.1763	0.0421
17088527	TLR4	toll-like receptor 4	0.6153	0.0328
17088730	MORN5	MORN repeat containing 5	0.1664	0.0468
17088760	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.2914	0.0443
17088809	OR1Q1	olfactory receptor, family 1, subfamily Q, member 1	0.1054	0.0165
17089365			0.4664	0.0023
17089622	TMSB4XP4	thymosin beta 4, X-linked pseudogene 4	0.2644	0.0269
17090032			0.3672	0
17090625	C9orf171	chromosome 9 open reading frame 171	0.1464	0.0494
17090670	GFI1B	growth factor independent 1B transcription repressor	0.1338	0.0253
17090713	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	0.7121	0.0039
17090727	CELP	carboxyl ester lipase pseudogene	0.1949	0.003
17090735			1.1298	0.0009
17091065			0.1538	0.0189
17091069			0.1899	0.021
17091074	C9orf62	chromosome 9 open reading frame 62	0.1931	0.0054
17091110	LCN1	lipocalin 1	0.188	0.0486
17091517	LCNL1	lipocalin-like 1	0.1879	0.011
17091917	FAM138C	family with sequence similarity 138, member C	0.1428	0.0438
17091993			0.2213	0.0306
17092001			0.2614	0.0023
17092177	RLN2	relaxin 2	0.1901	0.0149
17092258			0.2493	0.009
17092671			0.2112	0.0077
17092790			0.1943	0.0281
17092819	IFNA21	interferon, alpha 21	0.1481	0.0078
17093081			0.2899	0.0146
17093424	C9orf24	chromosome 9 open reading frame 24	0.1974	0.0168
17093455	ENHO	energy homeostasis associated	0.1667	0.0329
17094163			0.1714	0.0299
17094368	LOC100132439	protein FAM27E3-like	0.4845	0.0036
17094920			0.2011	0.0106
17094933			0.1215	0.0322

17094936			0.1393	0.0073
17095098	GNA14	guanine nucleotide binding protein (G protein), alpha 14	0.7347	0.0006
17095147			0.1619	0.0484
17095410			0.2111	0.0107
17095522			0.2067	0.0113
17095547			0.1352	0.0357
17095630			0.1603	0.0311
17095638	MIR4290	microRNA 4290	0.2994	0.0006
17095772			0.3552	0.0038
17095959	NINJ1	ninjurin 1	0.4057	0.0146
17096457	CORO2A	coronin, actin binding protein, 2A	0.5286	0.0029
17096819			0.1073	0.0277
17097366			0.1818	0.0195
17097369	ZNF883	zinc finger protein 883	0.7544	0.0002
17098477	ANGPTL2	angiopoietin-like 2	0.7304	0.0078
17099174	FAM78A	family with sequence similarity 78, member A	0.1569	0.0198
17099338	AK8	adenylate kinase 8	0.2015	0.0447
17099400			0.8496	0.011
17099436	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	0.6477	0.0046
17100073	MIR4673	microRNA 4673	0.2576	0.0199
17100287	NPDC1	neural proliferation, differentiation and control, 1	0.2397	0.0318
17100655			0.716	0.0166
17100681	ND5	NADH dehydrogenase, subunit 5 (complex I)	0.1104	0.0037
17100683	CYTB	cytochrome b	0.1031	0.0231
17100697	ND6	NADH dehydrogenase, subunit 6 (complex I)	0.1216	0.0391
17100745			0.1708	0.0092
17100829			0.4959	0.015
17100837			0.5267	0.0439
17100871			0.3531	0.0185
17100965			0.1213	0.0113
17101063	SHOX	short stature homeobox	0.1582	0.0491
17101081	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0.2676	0.0066
17101248	ARSD-AS1	ARSD antisense RNA 1 (non-protein coding)	1.8018	0
17101287	PRKX-AS1	PRKX antisense RNA 1 (non-protein coding)	0.2167	0.0154
17101292	STS	steroid sulfatase (microsomal), isozyme S	0.6926	0.0052
17101319			0.2316	0.0095
17101422	CLCN4	chloride channel, voltage-sensitive 4	0.2653	0.0334
17101447	HCCS	holocytochrome c synthase	0.5564	0.0013
17101465	MSL3	male-specific lethal 3 homolog (Drosophila)	0.3962	0.003
17101515			0.2982	0.0326
17101531	TLR7	toll-like receptor 7	0.841	0.0003
17101537	TLR8	toll-like receptor 8	0.3397	0.0061
17101543	TMSB4X	thymosin beta 4, X-linked	0.3102	0.016
17101616	RAB9A	RAB9A, member RAS oncogene family	0.4649	0.0116
17101622	OFD1	oral-facial-digital syndrome 1	0.3022	0.0112
17101698	BMX	BMX non-receptor tyrosine kinase	0.7387	0.0128
17101775	GRPR	gastrin-releasing peptide receptor	0.8755	0.0436
17101789			0.2922	0.0287
17101792	MIR548AM	microRNA 548am	0.1692	0.0087
17101957	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	0.3868	0.0052
17101981	EIF1AX-AS1	EIF1AX antisense RNA 1 (non-protein coding)	0.2019	0.0257
17101990	CNKSR2	connector enhancer of kinase suppressor of Ras 2	0.6707	0.0348
17102032	YY2	YY2 transcription factor	0.3864	0.0184
17102087	ZNF645	zinc finger protein 645	0.1461	0.0259
17102129	SAT1	spermidine/spermine N1-acetyltransferase 1	0.4851	0.0131
17102290	MAGEB5	melanoma antigen family B, 5	0.1422	0.0427
17102393	TAB3	TGF-beta activated kinase 1/MAP3K7 binding protein 3	0.4151	0.0079
17102396	TAB3-AS2	TAB3 antisense RNA 2 (non-protein coding)	0.5243	0.0022
17102414			0.1419	0.0447

17102483	CXorf30	chromosome X open reading frame 30	0.1208	0.0047
17102512	PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	0.5377	0.0017
17102559			0.5152	0.0111
17102566	SYTL5	synaptotagmin-like 5	0.8523	0.0039
17102626			0.151	0.0277
17102632	MID1IP1	MID1 interacting protein 1	0.9623	0
17102668	ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	0.4748	0.0087
17102748			0.2281	0.0128
17102792	GPR34	G protein-coupled receptor 34	0.6696	0.0111
17102955	RP2	retinitis pigmentosa 2 (X-linked recessive)	0.4113	0.011
17103160	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	0.2338	0.0354
17103185	TIMP1	TIMP metallopeptidase inhibitor 1	0.4486	0.0191
17103243	SSX6	synovial sarcoma, X breakpoint 6 (pseudogene)	0.2202	0.0104
17103282	FTSJ1	FtsJ RNA methyltransferase homolog 1 (E. coli)	0.2471	0.0341
17103396	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	0.2911	0.0271
17103525	CCDC120	coiled-coil domain containing 120	0.1488	0.0455
17103545	MAGIX	MAGI family member, X-linked	0.1961	0.0491
17103560	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	0.4144	0.0167
17103572	CCDC22	coiled-coil domain containing 22	0.2686	0.0313
17103715	USP27X	ubiquitin specific peptidase 27, X-linked	0.4691	0.0136
17103717	CLCN5	chloride channel, voltage-sensitive 5	0.8129	0.0043
17103740	MIR532	microRNA 532	0.1861	0.0177
17103835	SNORA11E	small nucleolar RNA, H/ACA box 11E	0.3555	0.0188
17103869	XAGE2	X antigen family, member 2	0.1629	0.0262
17103974	RIBC1	RIB43A domain with coiled-coils 1	0.2389	0.0248
17103993	TSR2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	0.8403	0.0014
17104001	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	0.244	0.0162
17104021	MAGED2	melanoma antigen family D, 2	1.0054	0.0003
17104049	SNORA11	small nucleolar RNA, H/ACA box 11	1.1175	0.0026
17104082	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	0.6557	0.0001
17104122	MAGEH1	melanoma antigen family H, 1	0.5755	0.0099
17104132	RRAGB	Ras-related GTP binding B	0.5589	0.0081
17104173			0.1331	0.0382
17104176	UBQLN2	ubiquilin 2	0.4225	0.0099
17104196			0.4142	0.0196
17104201	FAAH2	fatty acid amide hydrolase 2	1.4533	0.0012
17104217	ZXDB	zinc finger, X-linked, duplicated B	0.5305	0.0137
17104226			0.2693	0.0272
17104229			0.5891	0.0011
17104234			0.4593	0.0129
17104236			0.4134	0.046
17104240	ZC3H12B	zinc finger CCCH-type containing 12B	0.4022	0.002
17104259	MSN	moesin	0.6912	0.0035
17104332	YIPF6	Yip1 domain family, member 6	0.5228	0.0022
17104382	FAM155B	family with sequence similarity 155, member B	0.5001	0.0095
17104387	EDA	ectodysplasin A	0.7761	0.0005
17104408			1.1499	0.0015
17104416	IGBP1	immunoglobulin (CD79A) binding protein 1	0.4327	0.0033
17104521	GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	0.1517	0.0093
17104540	DLG3	discs, large homolog 3 (Drosophila)	0.7364	0
17104575			0.1467	0.0289
17104662	NONO	non-POU domain containing, octamer-binding	0.2818	0.0036
17104665			0.7257	0.0053
17104675			0.3847	0.0115
17104681			0.3902	0.004
17104683			0.2589	0.0057
17104684			0.2975	0.0094
17104685			0.2622	0.0042
17104686			0.3848	0.0269

17104706	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	0.2181	0.0424
17104817	FLJ46446	uncharacterized LOC441501	0.1889	0.0058
17104821			0.1285	0.0471
17104850	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	0.2254	0.014
17104908	CHIC1	cysteine-rich hydrophobic domain 1	0.743	0
17104960	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	0.4913	0.0012
17104977			0.4314	0.0327
17104995	MAGEE1	melanoma antigen family E, 1	0.4974	0.0004
17105005			0.3598	0.0231
17105010	COX7B	cytochrome c oxidase subunit VIIb	0.6865	0.0002
17105018	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	0.4725	0.0004
17105082	GPR174	G protein-coupled receptor 174	0.3537	0.0006
17105112			0.1403	0.0085
17105114	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	0.3694	0.002
17105138	UBE2DNL	ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene)	0.2581	0.0001
17105143	APOOL	apolipoprotein O-like	0.643	0.0002
17105183	DACH2	dachshund homolog 2 (Drosophila)	0.2495	0.039
17105284	DIAPH2	diaphanous homolog 2 (Drosophila)	0.5875	0.0306
17105319			0.1222	0.0157
17105347	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	0.3702	0.0005
17105393	TMEM35	transmembrane protein 35	0.5988	0.0035
17105463	RPL36A-HNRNPH2	RPL36A-HNRNPH2 readthrough	0.2071	0.0479
17105488	ARMCX4	armadillo repeat containing, X-linked 4	0.581	0.017
17105614	ARMCX5-GPRASP2	ARMCX5-GPRASP2 readthrough	0.2604	0.0256
17105655	BHLHB9	basic helix-loop-helix domain containing, class B, 9	0.3638	0.0405
17105683	RAB40AL	RAB40A, member RAS oncogene family-like	0.1019	0.022
17105733	TCEAL4	transcription elongation factor A (SII)-like 4	0.2744	0.0012
17105757	TCEAL1	transcription elongation factor A (SII)-like 1	0.4958	0.0186
17105778	PLP1	proteolipid protein 1	0.1847	0.0187
17105837	FAM199X	family with sequence similarity 199, X-linked	0.4136	0.0089
17106005	FRMPD3	FERM and PDZ domain containing 3	0.1769	0.0497
17106031	PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.592	0.0022
17106051	MID2	midline 2	0.4433	0.0499
17106080	ATG4A	autophagy related 4A, cysteine peptidase	0.4315	0.0478
17106166			0.1813	0.0216
17106179			0.4781	0.0031
17106202	RGAG1	retrotransposon gag domain containing 1	0.5404	0.0054
17106305			0.215	0.0083
17106341	MIR448	microRNA 448	0.1378	0.0489
17106357	PLS3	plastin 3	0.8122	0.0033
17106398	SLC6A14	solute carrier family 6 (amino acid transporter), member 14	0.1099	0.0162
17106415	WDR44	WD repeat domain 44	0.4654	0.0029
17106438	DOCK11	dedicator of cytokinesis 11	0.8228	0.0027
17106572			0.4768	0.0493
17106574	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	0.3272	0.0445
17106584			0.2738	0.0306
17106587	UBE2A	ubiquitin-conjugating enzyme E2A	0.3807	0.0019
17106604	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	0.4194	0.0003
17106640	ZBTB33	zinc finger and BTB domain containing 33	0.377	0.0157
17106658	MCTS1	malignant T cell amplified sequence 1	0.3526	0.0034
17106688	GRIA3	glutamate receptor, ionotropic, AMPA 3	1.4874	0.0015
17106795	SH2D1A	SH2 domain containing 1A	0.1495	0.0184

17106822	OCRL	oculocerebrorenal syndrome of Lowe	0.3126	0.0444
17106895	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	0.3878	0.0288
17106913	BCORL1	BCL6 corepressor-like 1	0.2031	0.042
17106933	RAB33A	RAB33A, member RAS oncogene family	0.3339	0.023
17106938	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14	0.5427	0.0008
17106959	RBMX2	RNA binding motif protein, X-linked 2	0.4656	0.0006
17107028	PHF6	PHD finger protein 6	0.4679	0.0004
17107093	LOC340581	uncharacterized LOC340581	0.3032	0.0154
17107108			0.3638	0.0466
17107211	SLC9A6	solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6	0.5376	0.0039
17107293	HTATSF1	HIV-1 Tat specific factor 1	0.4774	0.0024
17107339			0.1504	0.0339
17107385			0.2276	0.0254
17107416	SPANXA2-OT1	SPANXA2 overlapping transcript 1 (non-protein coding)	0.2283	0.0101
17107520	FMR1	fragile X mental retardation 1	0.4467	0.0063
17107697	MTM1	myotubularin 1	0.6558	0.0013
17107717	MTMR1	myotubularin related protein 1	0.3362	0.0108
17107904			0.179	0.0023
17108021	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	1.4663	0.0036
17108254	OPN1MW2	opsin 1 (cone pigments), medium-wave-sensitive 2	0.136	0.0297
17108290	EMD	emerin	0.3637	0.0217
17108376	GDI1	GDP dissociation inhibitor 1	0.2352	0.0196
17108546	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	0.4292	0.0187
17108576	TMLHE	trimethyllysine hydroxylase, epsilon	0.6551	0.003
17108605	VAMP7	vesicle-associated membrane protein 7	0.9052	0.0001
17108658	GTPBP6	GTP binding protein 6 (putative)	0.2856	0.041
17108767			0.2156	0.0385
17108779	ARSD	arylsulfatase D	1.3006	0
17108931	HDHD1	haloacid dehalogenase-like hydrolase domain containing 1	0.5015	0.0017
17108943	PNPLA4	patatin-like phospholipase domain containing 4	0.6453	0.0038
17109020	GPR143	G protein-coupled receptor 143	0.4786	0.0063
17109035			0.1928	0.0204
17109042	MID1	midline 1 (Opitz/BBB syndrome)	0.411	0.0427
17109142			0.2201	0.0492
17109150			0.2207	0.0061
17109153	TRAPPC2	trafficking protein particle complex 2	0.2521	0.0297
17109197	GEMIN8	gem (nuclear organelle) associated protein 8	0.4716	0.0092
17109260	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	0.2619	0.0239
17109326	TMEM27	transmembrane protein 27	0.5109	0.0446
17109342	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.5737	0.0001
17109358			0.8084	0.0239
17109432	RAI2	retinoic acid induced 2	0.5998	0.0052
17109644	CXorf23	chromosome X open reading frame 23	0.295	0.0318
17109704	MIR23C	microRNA 23c	0.1686	0.014
17109748			0.1641	0.0227
17109832	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	0.9806	0.0114
17109893	CXorf21	chromosome X open reading frame 21	0.3417	0.0142
17109901	TAB3	TGF-beta activated kinase 1/MAP3K7 binding protein 3	0.3955	0.0109
17109923	FTHL17	ferritin, heavy polypeptide-like 17	0.1915	0.0386
17110026	MIR3915	microRNA 3915	0.1744	0.0054
17110046			0.1519	0.0437
17110050			0.1444	0.0256
17110058	DYNLT3	dynein, light chain, Tctex-type 3	0.7273	0.006
17110122	MID1IP1-AS1	MID1IP1 antisense RNA 1 (non-protein coding)	0.6196	0.0102
17110193	MED14	mediator complex subunit 14	0.2826	0.0127
17110289	MAOB	monoamine oxidase B	1.0737	0.0061
17110322	EFHC2	EF-hand domain (C-terminal) containing 2	0.3714	0.0045

17110367	MIR222	microRNA 222	0.2456	0.0081
17110401	SLC9A7	solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7	0.9024	0.0047
17110404	SLC9A7	solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7	0.6716	0.0013
17110437	ZNF41	zinc finger protein 41	0.251	0.0269
17110447	SYN1	synapsin I	0.9261	0.001
17110495	UXT	ubiquitously-expressed, prefoldin-like chaperone	0.4784	0.0045
17110509	LOC441493	uncharacterized LOC441493	0.1779	0.0363
17110511	ZNF182	zinc finger protein 182	0.2207	0.0297
17110622			0.5838	0.023
17110629			0.193	0.0198
17110639	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	0.299	0.0213
17110654	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	0.3217	0.0154
17110681	OTUD5	OTU domain containing 5	0.3978	0.0104
17110745	TFE3	transcription factor binding to IGHM enhancer 3	0.4582	0.0038
17110771	WDR45	WD repeat domain 45	0.2859	0.0318
17110800	GPKOW	G patch domain and KOW motifs	0.2723	0.0306
17110817	PRICKLE3	prickle homolog 3 (Drosophila)	0.2285	0.0036
17110902	FOXP3	forkhead box P3	0.1169	0.0408
17110934	AKAP4	A kinase (PRKA) anchor protein 4	0.167	0.0054
17111055	SNORA11E	small nucleolar RNA, H/ACA box 11E	0.3555	0.0188
17111067	XAGE2	X antigen family, member 2	0.1629	0.0262
17111193	IQSEC2	IQ motif and Sec7 domain 2	0.3301	0.0136
17111366	PHF8	PHD finger protein 8	0.3653	0.0028
17111435	WNK3	WNK lysine deficient protein kinase 3	1.4055	0.0023
17111501	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	0.2147	0.0451
17111534	FAM104B	family with sequence similarity 104, member B	0.3662	0.0087
17111560			0.2821	0.0105
17111590	ZXDA	zinc finger, X-linked, duplicated A	0.6291	0.0006
17111599	LOC92249	uncharacterized LOC92249	0.3138	0.047
17111674	ZC4H2	zinc finger, C4H2 domain containing	0.7496	0.0002
17111688	LAS1L	LAS1-like (S. cerevisiae)	0.4645	0.009
17111725	EDA2R	ectodysplasin A2 receptor	0.8214	0.0008
17111738	OPHN1	oligophrenin 1	0.8155	0
17111767			0.1732	0.0436
17111808	PDZD11	PDZ domain containing 11	0.5339	0.0017
17111820	DLG3-AS1	DLG3 antisense RNA 1 (non-protein coding)	0.348	0.0009
17111895	IL2RG	interleukin 2 receptor, gamma	0.4027	0.0257
17111978			0.1285	0.0471
17111982	FLJ46446	uncharacterized LOC441501	0.2696	0.0019
17111994	RGAG4	retrotransposon gag domain containing 4	0.7427	0.0033
17112005	RPS4X	ribosomal protein S4, X-linked	0.2728	0.008
17112032	HDAC8	histone deacetylase 8	0.398	0.0156
17112058			0.2687	0.0093
17112060	PHKA1	phosphorylase kinase, alpha 1 (muscle)	0.8152	0.0014
17112137	NAP1L2	nucleosome assembly protein 1-like 2	1.1053	0.0128
17112167			0.4804	0.0148
17112198	RLIM	ring finger protein, LIM domain interacting	0.342	0.0384
17112213	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.4573	0.0011
17112235	ZDHHC15	zinc finger, DHHC-type containing 15	0.5949	0.0054
17112255	MAGEE2	melanoma antigen family E, 2	0.2559	0.0042
17112269	ATRX	alpha thalassemia/mental retardation syndrome X-linked	0.6725	0.0094
17112316	MAGT1	magnesium transporter 1	0.2956	0.044
17112339	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0.4451	0.0191
17112439	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	0.4996	0.0328
17112488	SATL1	spermidine/spermine N1-acetyl transferase-like 1	0.257	0.0287

17112519	CHM	choroideremia (Rab escort protein 1)	0.3148	0.0441
17112550	PABPC5-AS1	PABPC5 antisense RNA 1 (non-protein coding)	0.2381	0.0419
17112656	NOX1	NADPH oxidase 1	0.179	0.0435
17112683			0.6249	0.0011
17112686	TRMT2B	tRNA methyltransferase 2 homolog B (S. cerevisiae)	0.4837	0.0087
17112727			0.119	0.0278
17112735	BTK	Bruton agammaglobulinemia tyrosine kinase	0.2886	0.0082
17112923			0.1562	0.0114
17112956	TCEAL8	transcription elongation factor A (SII)-like 8	0.3855	0.0056
17112969	BEX2	brain expressed X-linked 2	0.5118	0.0347
17113038	LOC100128594	uncharacterized LOC100128594	0.1319	0.0374
17113047	SLC25A53	solute carrier family 25, member 53	0.2659	0.0004
17113053	LOC286437	uncharacterized LOC286437	0.3975	0.0312
17113110	RBM41	RNA binding motif protein 41	0.6034	0.0027
17113129	NUP62CL	nucleoporin 62kDa C-terminal like	1.1006	0.0027
17113184	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.4438	0.0027
17113286	KCNE1L	KCNE1-like	0.1235	0.0239
17113293	ACSL4	acyl-CoA synthetase long-chain family member 4	0.785	0.0101
17113362	CAPN6	calpain 6	0.3077	0.0094
17113492			0.4497	0.0072
17113496			0.3516	0.0337
17113545			0.2495	0.0094
17113577	SLC25A5-AS1	SLC25A5 antisense RNA 1 (non-protein coding)	0.1939	0.025
17113655	LOC100506992	uncharacterized LOC100506992	0.7247	0.0001
17113658	NKAP	NFKB activating protein	0.4897	0.0031
17113690			0.2847	0.0131
17113696	NKAPP1	NFKB activating protein pseudogene 1	0.3556	0.0055
17113725	LAMP2	lysosomal-associated membrane protein 2	0.6178	0.0015
17113744	CUL4B	cullin 4B	0.3729	0.0014
17113774	C1GALT1C1	C1GALT1-specific chaperone 1	0.4588	0.0024
17113817	CT47A7	cancer/testis antigen family 47, member A7	0.2254	0.0424
17113858			0.2199	0.0481
17113928	ODZ1	odz, odd Oz/ten-m homolog 1 (Drosophila)	0.6105	0.0054
17114014			1.5161	0.0015
17114017	ZDHHC9	zinc finger, DHHC-type containing 9	0.4412	0.039
17114051	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	0.539	0.0029
17114114	ENOX2	ecto-NOX disulfide-thiol exchanger 2	0.6129	0.0097
17114134			0.1616	0.036
17114318	MIR450B	microRNA 450b	0.1499	0.0086
17114368	MOSPD1	motile sperm domain containing 1	0.7239	0.0109
17114382	FAM127C	family with sequence similarity 127, member C	0.508	0.0042
17114394	LINC00087	long intergenic non-protein coding RNA 87	1.2476	0.0404
17114489	MAP7D3	MAP7 domain containing 3	0.4219	0.0186
17114546			0.2252	0.0382
17114572			0.2697	0.0022
17114643	ATP11C	ATPase, class VI, type 11C	0.4446	0.008
17114707	LDOC1	leucine zipper, down-regulated in cancer 1	0.6224	0.0188
17114762			0.2104	0.0242
17114766	MIR888	microRNA 888	0.2094	0.0171
17114783	MIR513B	microRNA 513b	0.2517	0.0027
17114785	MIR513A1	microRNA 513a-1	0.4627	0.0355
17114789	MIR506	microRNA 506	1.7115	0.0012
17114803	MIR510	microRNA 510	0.6312	0.0038
17114856	LOC100131434	uncharacterized LOC100131434	0.3929	0.0229
17114934	CD99L2	CD99 molecule-like 2	0.4584	0.0062
17115077	CETN2	centrin, EF-hand protein, 2	0.366	0.0171
17115453	MECP2	methyl CpG binding protein 2 (Rett syndrome)	0.2704	0.0127
17115571	DNASE1L1	deoxyribonuclease I-like 1	0.3105	0.0193
17115608	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0.4706	0.0008

17115617	FAM3A	family with sequence similarity 3, member A	0.3148	0.0123
17115692	MPP1	membrane protein, palmitoylated 1, 55kDa	0.4414	0.0122
17115807	TMLHE	trimethyllysine hydroxylase, epsilon	0.5441	0.006
17115850	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0.4645	0.0031
17116346			0.1045	0.0431
17116684	VAMP7	vesicle-associated membrane protein 7	0.9038	0.0001
17117042			0.1045	0.0431
17117443			0.5404	0.0151
17117476	LOC100128356	protein transactivated by hepatitis B virus E antigen	0.2534	0.0043
17117583	LOC283335	uncharacterized LOC283335	0.1662	0.0458
17117590			0.2172	0.043
17117604			0.3499	0.0419
17117734			0.2491	0.0037
17117786			0.4569	0.0036
17117831			0.2523	0.0247
17118013			0.1673	0.0393
17118140	HP07349	uncharacterized LOC100652853	0.3956	0.0497
17118144	LOC100652886	uncharacterized LOC100652886	1.3436	0.0003
17118228	HLA-E	major histocompatibility complex, class I, E	0.9428	0.0001
17118232	HLA-E	major histocompatibility complex, class I, E	0.9428	0.0001
17118242	HLA-E	major histocompatibility complex, class I, E	0.9428	0.0001
17118246	HLA-E	major histocompatibility complex, class I, E	0.9428	0.0001
17118250	LOC100505829	uncharacterized LOC100505829	0.1058	0.0269
17118279	LOC100130169	uncharacterized LOC100130169	0.2804	0.0035
17118358			0.3429	0.048
17118442			0.1673	0.0393
17118512			0.2376	0.0084
17118518			0.201	0.0111
17118550			0.1258	0.0343
17118566			0.1459	0.0279
17118568			0.1742	0.0446
17118618			0.1116	0.0321
17118626			0.1609	0.0272
17118634			0.2376	0.0084
17118636			0.113	0.0282
17118638			0.1245	0.0499
17118672			0.2068	0.0401
17118748			0.3586	0.009
17118844			0.2001	0.0392
17118868			1.0219	0.0002
17118878			0.2098	0.0291
17118880			0.4328	0.0228
17119114			0.453	0.0214
17119220			0.3212	0.0059
17119240			0.1764	0.0398
17119256			0.2997	0.0185
17119308			0.1484	0.0097
17119386			0.5745	0.0122
17119466			0.1415	0.0234
17119508			0.183	0.026
17119516			0.1201	0.0239
17119572			0.3755	0.023
17119590			0.3842	0.0402
17119602			0.1201	0.0239
17119754			0.2306	0.0296
17119790			0.1879	0.0181
17119820			0.2199	0.0481
17119822			0.1649	0.0234
17119902			0.2635	0.0128
17119904			0.2087	0.034

17119918			0.2743	0.0046
17119942			0.1242	0.0105
17119962			0.4354	0.0106
17120008			0.2193	0.0061
17120034			0.1655	0.0263
17120056			0.5029	0.003
17120058			0.6127	0.0029
17120080			0.2889	0.0097
17120092			0.5003	0.0444
17120110			0.1555	0.0277
17120178			0.463	0
17120300			0.1728	0.0273
17120302			0.2425	0.0439
17120304			0.4669	0.0475
17120320			0.3379	0
17120350			0.46	0.0457
17120352			0.3481	0.0404
17120392			0.1629	0.0057
17120446			0.1901	0.0114
17120450			0.1259	0.0195
17120478			0.276	0.0003
17120524			0.1965	0.0237
17120542			0.1525	0.0439
17120546			0.1773	0.0109
17120592			0.2155	0.0144
17120596			0.1147	0.0341
17120610			0.5772	0.0405
17120618			0.4914	0.0193
17120668			0.1635	0.0287
17120694			0.2191	0.0027
17120736			0.1142	0.0169
17120774			0.1274	0.0138
17120840			0.2734	0.0299
17120890			0.1284	0.006
17120892			0.1644	0.0153
17120900			0.1508	0.009
17120908			0.132	0.039
17120916			0.1367	0.0401
17120924			0.1772	0.0104
17121010			0.1705	0.002
17121020			0.1688	0.0257
17121054			0.157	0.0395
17121056			0.1064	0.0377
17121060			0.1291	0.0026
17121088			0.6068	0.0242
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17121198			0.385	0.0029
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17121252			0.2501	0.0249
17121332			0.2312	0.0042
17121394			0.5267	0.0002
17121426			0.143	0.0439
17121450			0.3163	0.0064
17121452			0.2292	0.0009
17121532			0.4093	0.0002

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17121552			0.1916	0.0153
17121604			0.1928	0.0219
17121614			0.1483	0.0354
17121616			0.2423	0.0021
17121644			0.1516	0.0307
17121744			0.1421	0.0094
17121822			0.2387	0.0098
17121886			0.508	0.0044
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17121922			0.1985	0.0377
17121938			0.1967	0.0423
17121996			0.2425	0.0477
17122018			0.2947	0.0039
17122022			0.3896	0.0035
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17122026			0.8009	0.0012
17122030			0.6108	0.0015
17122032			0.5163	0.0011
17122034			0.6621	0.0012
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17122124			0.2438	0.0023
17122126			0.2469	0.0035
17122132			0.1994	0.0009
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17122370			0.2779	0.0337
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17122412			0.1184	0.0037
17122440			0.1266	0.0202
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17122534			0.5743	0.0142
17122536			0.1931	0.0226
17122540			0.2303	0.0038
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17122566			0.1298	0.0149
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16658159	ARHGEF16	Rho guanine nucleotide exchange factor (GEF) 16	-0.1618	0.0023
16658457	THAP3	THAP domain containing, apoptosis associated protein 3	-0.1789	0.0299
16658571			-0.3492	0.0341
16658800			-0.1415	0.0162
16659102	CLCN6	chloride channel, voltage-sensitive 6	-0.4279	0.0065
16659133	NPPA-AS1	NPPA antisense RNA 1 (non-protein coding)	-0.1806	0.0328
16659343	AADACL4	arylacetamide deacetylase-like 4	-0.1318	0.0246
16659395	PRAMEF22	PRAME family member 22	-0.5443	0.01
16659455			-0.4538	0.0323
16660098			-0.3756	0.0161
16660282	PLA2G5	phospholipase A2, group V	-0.2776	0.0372
16660388	LOC100506824	uncharacterized LOC100506824	-0.3749	0.0009
16660436	ALPL	alkaline phosphatase, liver/bone/kidney	-0.998	0.0124
16660468	CELA3B	chymotrypsin-like elastase family, member 3B	-0.2481	0.0089
16660676			-0.5361	0.0326
16660713	LYPLA2	lysophospholipase II	-0.2036	0.0202
16661206	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	-0.2456	0.0364
16661255	ARID1A	AT rich interactive domain 1A (SWI-like)	-0.1887	0.0483
16661684			-0.1263	0.0438
16661914			-0.2594	0.0167
16662206			-0.426	0.0014
16662338	ZMYM1	zinc finger, MYM-type 1	-0.3224	0.0137
16662648	CDCA8	cell division cycle associated 8	-0.7191	0.0057
16662690			-0.4716	0.016

16662692	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	-0.3654	0.0159
16662755	MACF1	microtubule-actin crosslinking factor 1	-0.2658	0.0222
16662890	BMP8A	bone morphogenetic protein 8a	-0.1821	0.027
16662993	RLF	rearranged L-myc fusion	-0.3516	0.0273
16663514	CDC20	cell division cycle 20 homolog (S. cerevisiae)	-0.8101	0.0029
16663694	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	-0.3123	0.0082
16663812	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	-0.2688	0.0403
16664243	RAD54L	RAD54-like (S. cerevisiae)	-0.4299	0.0031
16664281	NSUN4	NOP2/Sun domain family, member 4	-0.354	0.0054
16665099			-0.1364	0.0396
16665437	MIR3116-1	microRNA 3116-1	-0.3635	0.046
16665960			-0.6808	0.0283
16667000	LRRC8D	leucine rich repeat containing 8 family, member D	-0.4065	0.0359
16667183	MTF2	metal response element binding transcription factor 2	-0.451	0.0264
16667456	PTBP2	polypyrimidine tract binding protein 2	-0.4232	0.0278
16667702	VCAM1	vascular cell adhesion molecule 1	-1.2694	0.0096
16668079	GPSM2	G-protein signaling modulator 2	-0.7583	0.0144
16668503			-0.3969	0.0093
16669288	WDR3	WD repeat domain 3	-0.5228	0.0135
16669361	HAO2-IT1	HAO2 intronic transcript 1 (non-protein coding)	-0.5132	0.0403
16669364	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	-1.5578	0.0057
16669389	PHGDH	phosphoglycerate dehydrogenase	-0.3125	0.0107
16669414			-0.3579	0.0149
16669566			-0.3882	0.0345
16669573	NBPF9	neuroblastoma breakpoint family, member 9	-0.4014	0.0014
16669630			-0.5369	0.0031
16669721	NBPF10	neuroblastoma breakpoint family, member 10	-0.2182	0.0277
16669850	ITGA10	integrin, alpha 10	-0.1961	0.0096
16669997	NBPF12	neuroblastoma breakpoint family, member 12	-0.3348	0.0372
16670197			-0.3882	0.0345
16670250	NBPF16	neuroblastoma breakpoint family, member 16	-0.3448	0.0059
16670359			-0.5239	0.005
16670377	HIST2H4B	histone cluster 2, H4b	-0.5592	0.0175
16670383	HIST2H2AA4	histone cluster 2, H2aa4	-0.6921	0.0008
16670387	HIST2H3D	histone cluster 2, H3d	-0.8126	0.004
16670499	PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	-0.4336	0.0101
16671049	LCE2A	late cornified envelope 2A	-0.3721	0.0015
16671217	INTS3	integrator complex subunit 3	-0.3732	0.002
16671325	RPS27	ribosomal protein S27	-0.3834	0.0133
16671334	UBAP2L	ubiquitin associated protein 2-like	-0.2137	0.0365
16671379			-0.3232	0.0386
16671503	CKS1B	CDC28 protein kinase regulatory subunit 1B	-0.4226	0.0127
16671632	EFNA3	ephrin-A3	-0.4798	0.0369
16671653	SLC50A1	solute carrier family 50 (sugar transporter), member 1	-0.5672	0.0154
16671738	FDPS	farnesyl diphosphate synthase	-0.6975	0.0014
16671784	POU5F1P4	POU class 5 homeobox 1 pseudogene 4	-0.3774	0.0239
16671786	ASH1L-AS1	ASH1L antisense RNA 1 (non-protein coding)	-0.2667	0.0147
16671886			-0.1059	0.0374
16671992	SLC25A44	solute carrier family 25, member 44	-0.3031	0.0236
16672170	PRCC	papillary renal cell carcinoma (translocation-associated)	-0.3456	0.0134
16672975	DUSP12	dual specificity phosphatase 12	-0.2653	0.01
16673056	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	-0.3766	0.0241
16673189	RNU5F-6P	RNA, U5F small nuclear 6, pseudogene	-0.4088	0.0032
16673191	PBX1	pre-B-cell leukemia homeobox 1	-0.753	0.0025
16673229	PBX1	pre-B-cell leukemia homeobox 1	-0.9061	0.0043
16673767	PRRC2C	proline-rich coiled-coil 2C	-0.2878	0.0398
16673877	MIR3120	microRNA 3120	-0.5251	0.0164

16674355	SOAT1	sterol O-acyltransferase 1	-0.5572	0.0065
16674767	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-0.3256	0.0034
16675034			-0.4545	0.0062
16675236			-0.5188	0.0324
16675334	TROVE2	TROVE domain family, member 2	-0.2958	0.0376
16675354	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-0.2929	0.0194
16675794	NAV1	neuron navigator 1	-0.475	0.0112
16675844	IPO9	importin 9	-0.3283	0.01
16675889	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	-0.2661	0.0255
16676228	ZC3H11A	zinc finger CCCH-type containing 11A	-0.4339	0.0021
16676258	ZBED6	zinc finger, BED-type containing 6	-0.9681	0.0002
16676263	ZBED6	zinc finger, BED-type containing 6	-0.96	0
16676461	CDK18	cyclin-dependent kinase 18	-0.2694	0.0068
16676520			-0.264	0.0032
16677104	RCOR3	REST corepressor 3	-0.3312	0.002
16677201	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	-1.0201	0.0049
16677324	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	-0.5402	0.0009
16677407	SMYD2	SET and MYND domain containing 2	-0.6037	0.0216
16677425	CENPF	centromere protein F, 350/400kDa (mitosin)	-1.0798	0.0055
16677646			-0.4524	0.0114
16677913	DEGS1	delta(4)-desaturase, sphingolipid 1	-0.4052	0.0001
16678105	SRP9	signal recognition particle 9kDa	-0.2606	0.0137
16678341			-0.5085	0.0293
16678579	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	-0.4418	0.0107
16678966	TBCE	tubulin folding cofactor E	-0.3896	0.0021
16679411	EXO1	exonuclease 1	-0.5193	0.0334
16679506			-0.1776	0.0173
16679546	DESI2	desumoylating isopeptidase 2	-0.4626	0.0054
16679557	COX20	COX20 Cox2 chaperone homolog (S. cerevisiae)	-0.486	0.0286
16679686			-0.729	0.0057
16679832	ZNF672	zinc finger protein 672	-0.2983	0.0045
16679972	FAM41C	family with sequence similarity 41, member C	-0.1958	0.0403
16679994	NOC2L	nucleolar complex associated 2 homolog (S. cerevisiae)	-0.2263	0.0286
16680258	MXRA8	matrix-remodelling associated 8	-0.3305	0.0268
16680446	NADK	NAD kinase	-0.2575	0.0387
16681192	NOL9	nucleolar protein 9	-0.3144	0.0281
16681370	ENO1	enolase 1, (alpha)	-0.5287	0.0135
16681390	ENO1-IT1	ENO1 intronic transcript 1 (non-protein coding)	-0.5342	0.0069
16681733			-0.1928	0.0217
16681940	LRRC38	leucine rich repeat containing 38	-1.403	0.0042
16681996	CASP9	caspase 9, apoptosis-related cysteine peptidase	-0.2422	0.0061
16682225	NBPF1	neuroblastoma breakpoint family, member 1	-0.8929	0.0014
16682487	IFFO2	intermediate filament family orphan 2	-0.6942	0.0005
16682499	UBR4	ubiquitin protein ligase E3 component n-recognin 4	-0.2411	0.0496
16682702			-0.5638	0.0212
16682733	TMCO4	transmembrane and coiled-coil domains 4	-0.3358	0.0077
16682989	ECE1	endothelin converting enzyme 1	-0.4654	0.0044
16683022	RAP1GAP	RAP1 GTPase activating protein	-0.7816	0.0009
16683237	MIR4253	microRNA 4253	-0.2723	0.0208
16683358	E2F2	E2F transcription factor 2	-0.2016	0.025
16684461	COL16A1	collagen, type XVI, alpha 1	-0.1892	0.0216
16684851			-0.1553	0.0417
16684870	PHC2	polyhomeotic homolog 2 (Drosophila)	-0.2084	0.0309
16685031	LOC653160	uncharacterized LOC653160	-0.1787	0.0096
16685165	CLSPN	claspin	-0.3462	0.0398
16685330	GRIK3	glutamate receptor, ionotropic, kainate 3	-0.2373	0.0367
16685704	HEYL	hairy/enhancer-of-split related with YRPW motif-like	-0.729	0.0077

16685953	GUCA2A	guanylate cyclase activator 2A (guanylin)	-0.2042	0.0087
16686010	LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	-0.3906	0.038
16686176			-0.2236	0.0408
16686297	PTCH2	patched 2	-0.2107	0.0274
16686784	TAL1	T-cell acute lymphocytic leukemia 1	-0.2053	0.0346
16686796	STIL	SCL/TAL1 interrupting locus	-0.5247	0.0326
16686982			-0.2507	0.0324
16687188	ORC1	origin recognition complex, subunit 1	-0.4584	0.0058
16687397			-0.1266	0.0268
16688007	KANK4	KN motif and ankyrin repeat domains 4	-0.1505	0.019
16688115			-0.2863	0.0061
16688149			-0.3414	0.0046
16688386	DEPDC1	DEP domain containing 1	-0.7518	0.0172
16689240			-0.5144	0.0063
16690139	EXTL2	exostoses (multiple)-like 2	-0.5959	0.0082
16690211	COL11A1	collagen, type XI, alpha 1	-1.0448	0.0426
16690930	ST7L	suppression of tumorigenicity 7 like	-0.2102	0.0435
16691023	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-0.4871	0.0032
16691923			-0.6014	0.0025
16691961			-0.6014	0.0025
16692112	GNRHR2	gonadotropin-releasing hormone (type 2) receptor 2	-0.2203	0.046
16692135	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	-0.3509	0.0146
16692168	GPR89A	G protein-coupled receptor 89A	-0.309	0.0267
16692209	NBPF11	neuroblastoma breakpoint family, member 11	-0.4033	0.0033
16692297	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-0.5292	0.0148
16692383	NBPF24	neuroblastoma breakpoint family, member 24	-0.3961	0.0042
16692433			-0.4772	0.0061
16692452	NBPF14	neuroblastoma breakpoint family, member 14	-0.3252	0.0377
16692555			-0.6483	0.0093
16692557			-0.5766	0.0137
16692570	LOC388692	uncharacterized LOC388692	-0.4513	0.0347
16692583	FAM72C	family with sequence similarity 72, member C	-0.4509	0.0122
16692597	LOC388692	uncharacterized LOC388692	-0.4513	0.0347
16692616	HIST2H3D	histone cluster 2, H3d	-0.8126	0.004
16692620	HIST2H2AA4	histone cluster 2, H2aa4	-0.917	0.0007
16692626	HIST2H4B	histone cluster 2, H4b	-0.5592	0.0175
16692632	HIST2H2BE	histone cluster 2, H2be	-0.7009	0.0073
16692667	MTMR11	myotubularin related protein 11	-0.363	0.0334
16692724	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-0.4516	0.0029
16692764	LOC100289061	uncharacterized LOC100289061	-0.1648	0.0093
16692890			-0.2364	0.0104
16692943	CDC42SE1	CDC42 small effector 1	-0.2951	0.0385
16693030	PI4KB	phosphatidylinositol 4-kinase, catalytic, beta	-0.3414	0.0226
16693345			-0.1637	0.0159
16693361	SPRR2B	small proline-rich protein 2B	-1.9682	0.0072
16693515	ILF2	interleukin enhancer binding factor 2, 45kDa	-0.4215	0.0075
16693516			-0.4156	0.0057
16693517			-0.4535	0.0192
16693519			-0.4948	0.0031
16693521			-0.4984	0.0347
16693522			-0.4586	0.006
16693523			-0.5024	0.004
16693524			-0.4646	0.0057
16693525			-0.5107	0.0113
16693528			-0.5092	0.0048
16693530			-0.3924	0.0291
16693531			-0.4044	0.032

16693532			-0.4794	0.0083
16693533			-0.3869	0.0165
16693536			-0.2846	0.0369
16693559	DENND4B	DENN/MADD domain containing 4B	-0.3569	0.0041
16693601	CRTC2	CREB regulated transcription coactivator 2	-0.3257	0.0373
16693762	C1orf43	chromosome 1 open reading frame 43	-0.2854	0.039
16693996	THBS3	thrombospondin 3	-0.4478	0.0018
16694094	FAM189B	family with sequence similarity 189, member B	-0.4385	0.0283
16694117	SCAMP3	secretory carrier membrane protein 3	-0.302	0.0359
16694135	CLK2	CDC-like kinase 2	-0.3013	0.0075
16694176			-1.2981	0.0016
16694178	RUSC1-AS1	RUSC1 antisense RNA 1 (non-protein coding)	-0.3942	0.0172
16694188	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	-0.2393	0.0312
16694322	RIT1	Ras-like without CAAX 1	-0.6026	0.0013
16694529	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	-0.2743	0.036
16694611			-0.6164	0.0377
16694716	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	-0.5288	0.0009
16695189	CCDC19	coiled-coil domain containing 19	-0.1722	0.0141
16695262	KCNJ10	potassium inwardly-rectifying channel, subfamily J, member 10	-0.1716	0.0111
16695319	DCAF8	DDB1 and CUL4 associated factor 8	-0.159	0.0372
16695741	OLFML2B	olfactomedin-like 2B	-0.6962	0.0088
16695823	LOC100505795	uncharacterized LOC100505795	-0.3708	0.0086
16696387	DNM3OS	DNM3 opposite strand/antisense RNA (non-protein coding)	-0.4388	0.0166
16696490	CENPL	centromere protein L	-0.3697	0.0006
16696531	SNORD78	small nucleolar RNA, C/D box 78	-0.7797	0.0074
16696689	ASTN1	astrotactin 1	-0.8115	0.0369
16696870	TOR1AIP2	torsin A interacting protein 2	-0.3494	0.0421
16696903	ACBD6	acyl-CoA binding domain containing 6	-0.3368	0.024
16697245	IVNS1ABP	influenza virus NS1A binding protein	-0.5731	0.0004
16697392			-0.4734	0.0496
16697461			-0.379	0.0239
16697544	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	-1.3611	0.0006
16697580	ZBTB41	zinc finger and BTB domain containing 41	-0.2835	0.0351
16697695	KIF14	kinesin family member 14	-0.7834	0.0057
16697843	TMEM9	transmembrane protein 9	-0.2801	0.0083
16697962	IPO9-AS1	IPO9 antisense RNA 1 (non-protein coding)	-0.3952	0.0187
16697968			-0.217	0.0287
16698023	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-0.6967	0.0049
16698049	KDM5B	lysine (K)-specific demethylase 5B	-0.5435	0.0044
16698556	SLC41A1	solute carrier family 41, member 1	-0.695	0.0019
16698872			-0.1582	0.0056
16698984	NEK2	NIMA (never in mitosis gene a)-related kinase 2	-0.5886	0.0071
16699021	INTS7	integrator complex subunit 7	-0.2822	0.0494
16699174	PTPN14	protein tyrosine phosphatase, non-receptor type 14	-0.3982	0.0223
16699290	ESRRG	estrogen-related receptor gamma	-0.7644	0.0083
16699320	GPATCH2	G patch domain containing 2	-0.2629	0.0199
16699354			-0.1402	0.0239
16699392	EPRS	glutamyl-prolyl-tRNA synthetase	-0.2881	0.0485
16699454	MIR215	microRNA 215	-0.4104	0.022
16699563			-0.1836	0.0154
16699590	TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	-0.3157	0.0222
16699795	NVL	nuclear VCP-like	-0.337	0.0058
16699831	MIR320B2	microRNA 320b-2	-0.2015	0.0339
16699877	LBR	lamin B receptor	-0.2437	0.0127
16699932	TMEM63A	transmembrane protein 63A	-0.5456	0.0057
16700009	SDE2	SDE2 telomere maintenance homolog (S. pombe)	-0.3341	0.0413
16700123			-0.2306	0.036

16700324	ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-0.2837	0.0138
16700363			-0.3408	0.0008
16700367			-0.4394	0.0068
16700456	FAM89A	family with sequence similarity 89, member A	-0.411	0.0389
16700489	EGLN1	egl nine homolog 1 (C. elegans)	-0.3959	0.0063
16700500			-0.3802	0.0289
16700621			-0.213	0.0094
16700678			-0.1602	0.0338
16700715	RBM34	RNA binding motif protein 34	-0.3606	0.0313
16700778	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	-0.4492	0.0106
16700888	NID1	nidogen 1	-0.6925	0.0044
16701037	GREM2	gremlin 2	-1.3108	0.015
16701041			-0.5033	0.0382
16701119	PLD5	phospholipase D family, member 5	-1.7269	0.0017
16701133			-0.7101	0.0224
16701135			-0.4511	0.0167
16701440	AHCTF1	AT hook containing transcription factor 1	-0.4062	0.0094
16701533	RN5S82	RNA, 5S ribosomal 82	-0.3254	0.0476
16701620	OR2T10	olfactory receptor, family 2, subfamily T, member 10	-0.1624	0.0282
16701640	SH3BP5L	SH3-binding domain protein 5-like	-0.247	0.0202
16701657	ZNF692	zinc finger protein 692	-0.2394	0.0208
16701689			-0.4832	0.0316
16701748	GTPBP4	GTP binding protein 4	-0.3822	0.0039
16701775	IDI2-AS1	IDI2 antisense RNA 1 (non-protein coding)	-0.3582	0.0131
16702226			-0.1822	0.0118
16702351	GATA3	GATA binding protein 3	-0.5547	0.0061
16702382			-0.1108	0.0267
16702650	MIR1265	microRNA 1265	-0.1655	0.0335
16702685	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-0.3826	0.0132
16702967	ARL5B	ADP-ribosylation factor-like 5B	-0.4348	0.0322
16703110			-0.2786	0.0317
16703478	MASTL	microtubule associated serine/threonine kinase-like	-0.4933	0.0122
16703752	LOC100653181	uncharacterized LOC100653181	-0.5869	0.0013
16703891	CCNY	cyclin Y	-0.239	0.0213
16704051			-0.5995	0.0014
16704055	HSD17B7P2	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2	-0.8679	0.0096
16704090			-0.1925	0.0079
16704182	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	-0.3368	0.0244
16704770			-0.8439	0.0043
16704844	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	-0.5036	0.0044
16704894	LOC728407	poly (ADP-ribose) glycohydrolase pseudogene	-0.3254	0.0166
16705159	CDK1	cyclin-dependent kinase 1	-0.8436	0.0066
16705450	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	-0.3509	0.0134
16705474	DDX21	DEAD (Asp-Glu-Ala-Asp) box helicase 21	-0.356	0.0078
16705620	TSPAN15	tetraspanin 15	-0.2687	0.0401
16706023	FAM149B1	family with sequence similarity 149, member B1	-0.2919	0.0082
16706117	FUT11	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	-0.4657	0.0233
16706461	MIR548AK	microRNA 548ak	-0.5619	0.004
16706522	SFTPA1	surfactant protein A1	-0.2481	0.0171
16706562	LOC642361	uncharacterized LOC642361	-0.3137	0.0202
16706706			-0.3207	0.0095
16706830			-0.5661	0.0094
16706968	FAM22D	family with sequence similarity 22, member D	-0.192	0.0286
16707221	KIF20B	kinesin family member 20B	-0.5525	0.0474
16707468	KIF11	kinesin family member 11	-0.9661	0.0044
16707551	CEP55	centrosomal protein 55kDa	-0.669	0.0051
16707695	HELLS	helicase, lymphoid-specific	-1.0239	0.0014
16707927	RPL13AP5	ribosomal protein L13a pseudogene 5	-0.1783	0.0212

16707949	C10orf12	chromosome 10 open reading frame 12	-0.4097	0.0177
16708238			-0.3329	0.0314
16708249	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-1.1573	0.0089
16708260	LINC00263	long intergenic non-protein coding RNA 263	-0.4194	0.022
16708370	C10orf2	chromosome 10 open reading frame 2	-0.3152	0.0392
16708419	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	-0.2771	0.0357
16708513			-0.3518	0.0139
16708533	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	-0.3738	0.0036
16708815	PDCD11	programmed cell death 11	-0.2634	0.0412
16709068			-0.3886	0.0039
16709128	DUSP5	dual specificity phosphatase 5	-0.5572	0.0124
16709333	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-0.4493	0.0082
16709673	PNLIPRP2	pancreatic lipase-related protein 2	-0.267	0.038
16709822	GRK5	G protein-coupled receptor kinase 5	-0.6003	0.032
16710017			-0.4257	0.0062
16710271	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.4715	0.0256
16710360	ZRANB1	zinc finger, RAN-binding domain containing 1	-0.4566	0.0179
16710585			-0.3676	0.0149
16711023	TUBB8	tubulin, beta 8 class VIII	-0.3449	0.0006
16711089	LARP4B	La ribonucleoprotein domain family, member 4B	-0.3233	0.0322
16711118	IDI2	isopentenyl-diphosphate delta isomerase 2	-0.3659	0.0165
16711125	IDI1	isopentenyl-diphosphate delta isomerase 1	-0.8815	0.0103
16711138			-0.7352	0.0179
16711450			-0.5205	0.0042
16711520			-0.2164	0.0352
16712605			-0.2567	0.0341
16712703	YME1L1	YME1-like 1 (S. cerevisiae)	-0.3285	0.0143
16712960	MTPAP	mitochondrial poly(A) polymerase	-0.2665	0.0414
16713011			-0.1969	0.0061
16713057	ARHGAP12	Rho GTPase activating protein 12	-0.5849	0.0028
16713230	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	-0.5992	0.0029
16713364	SEPT7L	septin 7-like	-0.2424	0.0195
16713674	PARG	poly (ADP-ribose) glycohydrolase	-0.3598	0.0272
16714081			-0.716	0.0067
16714086	VSTM4	V-set and transmembrane domain containing 4	-1.2516	0.006
16714343			-0.3794	0.0177
16714842			-0.181	0.0036
16715088	AIFM2	apoptosis-inducing factor, mitochondrion-associated, 2	-0.4606	0.024
16715112	SAR1A	SAR1 homolog A (S. cerevisiae)	-0.1846	0.0445
16715216			-0.1828	0.0067
16715389			-0.4309	0.0062
16715409	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	-0.3563	0.0025
16715611	BMS1P4	BMS1 pseudogene 4	-0.5152	0.0253
16715631	LOC100653003	uncharacterized LOC100653003	-0.5906	0.0079
16715791			-0.1333	0.0297
16716117			-0.1465	0.0456
16716374	LIPA	lipase A, lysosomal acid, cholesterol esterase	-0.5983	0.0045
16716795	SORBS1	sorbin and SH3 domain containing 1	-0.4848	0.0138
16717150			-0.169	0.0053
16717235	AVPI1	arginine vasopressin-induced 1	-0.5973	0.0063
16717557			-1.3711	0.0038
16717676			-0.3626	0.0294
16717750			-0.1916	0.0161
16717775	NPM3	nucleophosmin/nucleoplasmin 3	-0.419	0.0255
16718370	SMNDC1	survival motor neuron domain containing 1	-0.2801	0.0373
16718376			-0.6336	0.0162
16718377			-0.4447	0.0436
16718493			-0.4161	0.0053
16718935			-0.3172	0.0105

16719217	CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	-0.4619	0.0019
16719272	METTL10	methyltransferase like 10	-0.3033	0.0029
16719393	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-0.535	0.0246
16719411			-0.4086	0.0115
16719417	ADAM12	ADAM metallopeptidase domain 12	-0.39	0.0339
16719515	MKI67	antigen identified by monoclonal antibody Ki-67	-0.9293	0.0046
16719949			-0.1192	0.0493
16719976	RIC8A	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)	-0.169	0.0379
16720820	MRPL23	mitochondrial ribosomal protein L23	-0.3081	0.0045
16720984			-0.2513	0.0323
16720987	LOC100505870	uncharacterized LOC100505870	-0.3964	0.0235
16721126	RRM1	ribonucleotide reductase M1	-0.5958	0.0007
16721659	EIF3F	eukaryotic translation initiation factor 3, subunit F	-0.3171	0.0206
16721666			-0.5601	0.0164
16721667			-0.4813	0.0087
16721670			-0.4502	0.016
16721673			-0.6271	0.0018
16721674			-0.4459	0.0276
16721676			-0.4346	0.0214
16721681			-0.3528	0.041
16721715	RPL27A	ribosomal protein L27a	-0.2126	0.0198
16721835	WEE1	WEE1 homolog (S. pombe)	-0.5112	0.0213
16721884	SBF2-AS1	SBF2 antisense RNA 1 (non-protein coding)	-0.3354	0.0063
16722075			-0.2866	0.0103
16722212			-0.3664	0.0391
16722217	ARNTL	aryl hydrocarbon receptor nuclear translocator-like	-0.6588	0.0008
16722394			-0.879	0.0038
16722455			-0.8794	0.0138
16722562	SAA1	serum amyloid A1	-1.12	0.0231
16722603	LDHA	lactate dehydrogenase A	-0.5877	0.0057
16722787	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	-0.5331	0.0144
16722799	PRMT3	protein arginine methyltransferase 3	-0.3104	0.013
16723100	MIR610	microRNA 610	-0.2999	0.0275
16723294	EIF3M	eukaryotic translation initiation factor 3, subunit M	-0.502	0.0003
16723507	NAT10	N-acetyltransferase 10 (GCN5-related)	-0.3837	0.0102
16723593	PDHX	pyruvate dehydrogenase complex, component X	-0.3948	0.0083
16723903	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	-0.1911	0.0158
16724162			-0.3252	0.0469
16724194	CRY2	cryptochrome 2 (photolyase-like)	-0.4979	0.0032
16724663	MIR3161	microRNA 3161	-0.3215	0.0411
16724849	SMTNL1	smoothelin-like 1	-0.1916	0.0184
16724901	ZDHHC5	zinc finger, DHHC-type containing 5	-0.2999	0.0105
16725041	FAM111B	family with sequence similarity 111, member B	-0.6596	0.0308
16725556	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	-0.1935	0.0228
16725617			-0.4994	0.0023
16725735	FEN1	flap structure-specific endonuclease 1	-0.554	0.0021
16725742	FADS2	fatty acid desaturase 2	-0.7058	0.0013
16725901	METTL12	methyltransferase like 12	-0.2981	0.0309
16725910	C11orf83	chromosome 11 open reading frame 83	-0.3278	0.0333
16725935	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	-0.3565	0.02
16725969	TMEM179B	transmembrane protein 179B	-0.3045	0.0451
16725980			-0.3507	0.0157
16726372	GPR137	G protein-coupled receptor 137	-0.2245	0.0351
16726572	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta	-0.2921	0.0049
16726707	MRPL49	mitochondrial ribosomal protein L49	-0.3684	0.0113
16726977	PCNXL3	pecanex-like 3 (Drosophila)	-0.4489	0.0125
16727194	SART1	squamous cell carcinoma antigen recognized by T cells	-0.2177	0.0394
16727204			-0.5926	0.0217
16727222			-0.214	0.0397

16727224	BANF1	barrier to autointegration factor 1	-0.2104	0.0147
16727277	PACS1	phosphofurin acidic cluster sorting protein 1	-0.3083	0.0356
16727322			-0.3842	0.0263
16727596	RCE1	RCE1 homolog, prenyl protein protease (S. cerevisiae)	-0.4513	0.0303
16727659	KDM2A	lysine (K)-specific demethylase 2A	-0.3213	0.0181
16727702	ADRBK1	adrenergic, beta, receptor kinase 1	-0.3204	0.0086
16727802	RAD9A	RAD9 homolog A (S. pombe)	-0.2883	0.0018
16728652	INPPL1	inositol polyphosphate phosphatase-like 1	-0.4801	0.0009
16728711			-0.6603	0.0284
16728886			-0.3902	0.0166
16729021			-0.5388	0.0015
16729103	RPS3	ribosomal protein S3	-0.3156	0.0333
16729188	UVRAG	UV radiation resistance associated gene	-0.3725	0.0098
16729444	C11orf67	chromosome 11 open reading frame 67	-0.5787	0.0042
16729548	RPS28	ribosomal protein S28	-0.2439	0.0082
16729611	ANKRD42	ankyrin repeat domain 42	-0.3235	0.0377
16729838			-1.1242	0.0014
16730061	KIAA1731	KIAA1731	-0.3767	0.0163
16730102			-0.4729	0.0277
16730340	CEP57	centrosomal protein 57kDa	-0.4256	0.0183
16730996	FDX1	ferredoxin 1	-0.9575	0.0001
16731169	DLAT	dihydrolipoamide S-acetyltransferase	-0.3513	0.0298
16731253	PTS	6-pyruvoyltetrahydropterin synthase	-0.5009	0.0193
16731490			-0.4696	0.0187
16731526			-0.9302	0.007
16731565			-0.3275	0.0381
16731693	BACE1-AS	BACE1 antisense RNA (non-protein coding)	-0.376	0.0298
16732067	CCDC84	coiled-coil domain containing 84	-0.4621	0.0177
16732088	TRAPPC4	trafficking protein particle complex 4	-0.3288	0.0252
16732419	TMEM136	transmembrane protein 136	-0.5746	0.0151
16732520	TBCEL	tubulin folding cofactor E-like	-0.4394	0.0169
16732569	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	-0.6737	0.012
16732734	LOC341056	SUMO1 activating enzyme subunit 1 pseudogene	-0.1935	0.0274
16733104	CHEK1	checkpoint kinase 1	-0.5324	0.0363
16733260			-0.6873	0.0023
16733262	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	-0.183	0.0473
16733288	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-0.4915	0.0002
16733397	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	-0.5762	0.025
16733407			-0.8013	0.0022
16733759	LOC283177	uncharacterized LOC283177	-0.16	0.0419
16734044	DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila)	-0.2976	0.036
16734154	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	-0.3015	0.0255
16734299	FAM99B	family with sequence similarity 99, member B (non-protein coding)	-0.1491	0.0491
16734467	KCNQ1OT1	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)	-0.4008	0.0325
16734494	NAP1L4	nucleosome assembly protein 1-like 4	-0.3815	0.0018
16734755	RRM1-AS1	RRM1 antisense RNA 1 (non-protein coding)	-1.0067	0.004
16734840	HBB	hemoglobin, beta	-0.3505	0.0272
16735121	RRP8	ribosomal RNA processing 8, methyltransferase, homolog (yeast)	-0.2186	0.0139
16735405	TRIM66	tripartite motif containing 66	-0.2342	0.0301
16735596	DENND5A	DENN/MADD domain containing 5A	-0.3647	0.0238
16735639	TMEM41B	transmembrane protein 41B	-0.5199	0.0099
16735658			-0.195	0.021
16735669	SBF2	SET binding factor 2	-0.2949	0.0388
16735727	RNU7-28P	RNA, U7 small nuclear 28 pseudogene	-0.4474	0.024

16735751	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	-1.4077	0.0002
16735807			-0.9815	0.02
16735873	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	-0.4241	0.0111
16735933			-0.2773	0.0224
16735994	RRAS2	related RAS viral (r-ras) oncogene homolog 2	-0.4595	0.0026
16736049	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-0.2308	0.0448
16736211	RPS13	ribosomal protein S13	-0.3133	0.0026
16736214			-0.3336	0.0026
16736215			-0.3274	0.0065
16736216			-0.5254	0.0293
16736217			-0.3671	0.002
16736219			-0.3265	0.046
16736222			-0.3463	0.0026
16736508	TSG101	tumor susceptibility gene 101	-0.25	0.0146
16736526			-0.1279	0.0495
16736551			-0.42	0.0367
16736638	E2F8	E2F transcription factor 8	-0.3104	0.0434
16736696	RN5S336	RNA, 5S ribosomal 336	-0.252	0.0392
16736821	LGR4	leucine-rich repeat containing G protein-coupled receptor 4	-0.843	0.002
16736847	LIN7C	lin-7 homolog C (C. elegans)	-0.2591	0.04
16736891	KIF18A	kinesin family member 18A	-0.7378	0.0172
16737123	CCDC73	coiled-coil domain containing 73	-0.1385	0.0253
16737614	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-0.6784	0.0241
16737645	PEX16	peroxisomal biogenesis factor 16	-0.2532	0.0149
16737669	PHF21A	PHD finger protein 21A	-0.354	0.0187
16737717	AMBRA1	autophagy/beclin-1 regulator 1	-0.567	0.0011
16737783	CKAP5	cytoskeleton associated protein 5	-0.2283	0.033
16737946	ACP2	acid phosphatase 2, lysosomal	-0.452	0.004
16738023	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	-0.3755	0.0187
16738205	NUP160	nucleoporin 160kDa	-0.5484	0.0053
16738393	OR5M1	olfactory receptor, family 5, subfamily M, member 1	-0.3186	0.0326
16738583	BTBD18	BTB (POZ) domain containing 18	-0.3417	0.0059
16738736	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	-0.3329	0.0342
16739054	CPSF7	cleavage and polyadenylation specific factor 7, 59kDa	-0.444	0.0025
16739132	FADS1	fatty acid desaturase 1	-0.9502	0.0004
16739229			-0.5239	0
16739253			-0.1814	0.0141
16739295	TUT1	terminal uridylyl transferase 1, U6 snRNA-specific	-0.2471	0.012
16739315			-0.2528	0.0292
16739636	SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	-0.3209	0.0341
16740037	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	-0.3628	0.0059
16740074	MEN1	multiple endocrine neoplasia I	-0.3149	0.0444
16740326	FAU	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	-0.2504	0.0015
16740328			-0.3151	0.0092
16740330			-0.5655	0.0415
16740333			-0.3871	0.0002
16740334			-0.4081	0.0077
16740339			-0.5534	0.0043
16740340			-0.7986	0.0004
16740608	FIBP	fibroblast growth factor (acidic) intracellular binding protein	-0.2679	0.0333
16740630	FOSL1	FOS-like antigen 1	-0.5851	0.0023
16740707	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	-0.3613	0.0387
16740994			-0.4097	0.0112
16741023	TMEM134	transmembrane protein 134	-0.335	0.0007

16741040	PITPNM1	phosphatidylinositol transfer protein, membrane-associated 1	-0.2841	0.0057
16741196			-0.2205	0.0487
16741201	CHKA	choline kinase alpha	-0.6092	0.0005
16741287	CPT1A	carnitine palmitoyltransferase 1A (liver)	-0.674	0.0078
16741501	DHCR7	7-dehydrocholesterol reductase	-0.8937	0.0081
16741643	LAMTOR1	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1	-0.2487	0.0441
16741725	PDE2A	phosphodiesterase 2A, cGMP-stimulated	-1.0138	0.0229
16741911			-0.1756	0.0138
16741948	CHCHD8	coiled-coil-helix-coiled-coil-helix domain containing 8	-0.3918	0.002
16742084			-0.5063	0.0277
16742148			-0.1631	0.0387
16742337			-0.1952	0.0212
16742520	RSF1	remodeling and spacing factor 1	-0.4026	0.0105
16742544	RSF1-IT2	RSF1 intronic transcript 2 (non-protein coding)	-0.3726	0.0155
16742550	C11orf67	chromosome 11 open reading frame 67	-0.4553	0.0089
16742553			-0.3265	0.0306
16742556	INTS4	integrator complex subunit 4	-0.4601	0.0011
16742638	KCTD21	potassium channel tetramerisation domain containing 21	-0.3353	0.0063
16742647	GAB2	GRB2-associated binding protein 2	-0.3285	0.0233
16742814	RAB30	RAB30, member RAS oncogene family	-0.518	0.0124
16742849			-0.3564	0.0036
16742945	CREBZF	CREB/ATF bZIP transcription factor	-0.3744	0.0001
16742959	CCDC89	coiled-coil domain containing 89	-0.4779	0.0315
16742963	SYTL2	synaptotagmin-like 2	-1.2834	0.0058
16743293			-0.4741	0.0334
16743296	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	-0.3923	0.0083
16743322	SNORA8	small nucleolar RNA, H/ACA box 8	-0.2941	0.047
16743328	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	-0.4519	0.0026
16743338	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	-0.5184	0.0177
16743340	SNORD6	small nucleolar RNA, C/D box 6	-0.4203	0.0132
16743342	TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	-0.6618	0.0004
16743577	PGR	progesterone receptor	-0.9871	0.0069
16743751	MMP12	matrix metallopeptidase 12 (macrophage elastase)	-0.8486	0.001
16743779	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	-0.4223	0.0439
16744078	NPAT	nuclear protein, ataxia-telangiectasia locus	-0.354	0.0448
16744408	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	-0.3369	0.0452
16744616	CADM1	cell adhesion molecule 1	-0.6882	0.0105
16744774	LOC100652768	uncharacterized LOC100652768	-0.2309	0.02
16744822	BACE1	beta-site APP-cleaving enzyme 1	-0.8023	0.0007
16744844			-0.1344	0.0468
16745144	RPL23AP64	ribosomal protein L23a pseudogene 64	-0.3521	0.0416
16745148	RPS25	ribosomal protein S25	-0.4658	0.0022
16745154			-0.7478	0.0028
16745236	H2AFX	H2A histone family, member X	-0.3368	0.0078
16745956	FLJ39051	uncharacterized LOC399972	-0.2565	0.0251
16746045	TP53AIP1	tumor protein p53 regulated apoptosis inducing protein 1	-0.1934	0.0257
16746057	ARHGAP32	Rho GTPase activating protein 32	-0.6505	0.0042
16746142	PRDM10	PR domain containing 10	-0.1844	0.0342
16746379	NCAPD3	non-SMC condensin II complex, subunit D3	-0.4923	0.0005
16747287	NCAPD2	non-SMC condensin I complex, subunit D2	-0.4345	0.0245
16747439	GPR162	G protein-coupled receptor 162	-0.4931	0.0122
16747865	NANOGP1	Nanog homeobox pseudogene 1	-0.3127	0.0333

16747907	ZNF705A	zinc finger protein 705A	-0.2271	0.0072
16748391			-0.3815	0.042
16748496			-0.7149	0.0153
16748989	PDE3A	phosphodiesterase 3A, cGMP-inhibited	-0.5937	0.0273
16749524	KLHDC5	kelch domain containing 5	-0.236	0.0129
16749653			-0.126	0.0215
16750761	TROAP	trophinin associated protein (tastin)	-0.363	0.0237
16750963	AQP2	aquaporin 2 (collecting duct)	-0.5828	0.0451
16750996	ASIC1	acid-sensing (proton-gated) ion channel 1	-0.1564	0.0077
16751020	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	-0.4099	0.0193
16751116	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	-0.4719	0.0045
16751161			-0.4865	0.0281
16751709	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	-0.5652	0.0007
16751881	LOC100652999	uncharacterized LOC100652999	-0.278	0.0285
16751997			-0.6244	0.0035
16752009			-0.5836	0.0083
16752217	GDF11	growth differentiation factor 11	-0.4115	0.0438
16752242			-0.2831	0.0297
16752244	DGKA	diacylglycerol kinase, alpha 80kDa	-0.3844	0.0116
16752389	RPS26	ribosomal protein S26	-0.579	0.0114
16752652	SPRYD4	SPRY domain containing 4	-0.4923	0.0016
16752834	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	-0.4093	0.015
16753228	XRCC6BP1	XRCC6 binding protein 1	-0.4613	0.0211
16753394			-0.1517	0.0411
16753533	RASSF3	Ras association (RalGDS/AF-6) domain family member 3	-0.5096	0.0178
16753943	FRS2	fibroblast growth factor receptor substrate 2	-0.5713	0.0049
16753964	CCT2	chaperonin containing TCP1, subunit 2 (beta)	-0.3761	0.0404
16754913			-0.674	0.0245
16755312	AMDHD1	amidohydrolase domain containing 1	-0.973	0.0001
16755528			-0.7635	0.023
16756202	EID3	EP300 interacting inhibitor of differentiation 3	-0.3071	0.0313
16756510	WSCD2	WSC domain containing 2	-0.1578	0.0124
16757051			-0.1707	0.005
16757098	SH2B3	SH2B adaptor protein 3	-0.2132	0.0425
16757826			-0.5335	0.0029
16758621			-0.775	0.0091
16758872			-0.5839	0.0157
16758885	AACS	acetoacetyl-CoA synthetase	-0.3931	0.0386
16759202	RAN	RAN, member RAS oncogene family	-0.3702	0.0129
16760048	FOXM1	forkhead box M1	-0.5865	0.0077
16760621	CDCA3	cell division cycle associated 3	-0.7158	0.0015
16760868	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.4522	0.0311
16760911	LOC389634	uncharacterized LOC389634	-0.3176	0.0172
16761148	DDX12P	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12, pseudogene	-0.3168	0.0201
16761231			-0.1877	0.0113
16761541	PRB4	proline-rich protein BstNI subfamily 4	-0.4426	0.0014
16761549	PRB1	proline-rich protein BstNI subfamily 1	-0.3669	0.05
16761776			-0.5985	0.0292
16762337	BCAT1	branched chain amino-acid transaminase 1, cytosolic	-0.8065	0.0279
16762642	LOC100506578	uncharacterized protein C12orf71-like	-0.4696	0.0012
16762692	LOC100506606	uncharacterized LOC100506606	-0.3911	0.02
16763473			-0.3074	0.0038
16763764	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	-0.7992	0.0019
16763970	CCNT1	cyclin T1	-0.2758	0.0332
16764104			-0.3738	0.0235
16764106			-0.789	0.0086
16764328			-0.1692	0.0048

16764334			-0.4115	0.0042
16764343	C1QL4	complement component 1, q subcomponent-like 4	-0.3627	0.0155
16764433	NCKAP5L	NCK-associated protein 5-like	-0.3065	0.0107
16764498			-1.1384	0.0171
16765389	ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C2 (subunit 9)	-0.1843	0.0206
16765446	HOXC-AS5	HOXC cluster antisense RNA 5 (non-protein coding)	-0.1817	0.0499
16765697	ITGA7	integrin, alpha 7	-0.4335	0.0016
16765809	MMP19	matrix metallopeptidase 19	-0.3068	0.0076
16765845			-1.0338	0.0014
16766185	GLS2	glutaminase 2 (liver, mitochondrial)	-0.3076	0.0353
16766279	SNORD59B	small nucleolar RNA, C/D box 59B	-0.8425	0.0115
16766403	TMEM194A	transmembrane protein 194A	-0.5278	0.0142
16766767	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	-0.2726	0.0442
16766912			-0.6832	0.0147
16767420			-0.4924	0.0488
16768738	NTN4	netrin 4	-0.5117	0.0188
16768755			-0.8593	0.0041
16768894			-0.1417	0.0464
16768905			-0.1383	0.0092
16769863			-0.907	0.0077
16770706			-0.1867	0.0205
16770709			-1.1274	0.0137
16771067	CIT	citron (rho-interacting, serine/threonine kinase 21)	-0.7977	0.001
16771499			-0.7437	0.0246
16771570	RHOF	ras homolog family member F (in filopodia)	-0.5886	0.0137
16771571			-1.0321	0.0128
16771572			-1.2641	0.0057
16771574			-0.9058	0.0275
16772144	SCARB1	scavenger receptor class B, member 1	-0.5968	0.0183
16772169			-0.3385	0.021
16772429	LOC100190940	uncharacterized LOC100190940	-0.1645	0.0193
16772452			-0.1039	0.0432
16772510			-0.504	0.0436
16772852			-0.1957	0.0246
16773043	LATS2-AS1	LATS2 antisense RNA 1 (non-protein coding)	-0.4195	0.0198
16773080	ZDHHC20-AS1	ZDHHC20 antisense RNA 1 (non-protein coding)	-0.4808	0.0317
16773348	NUPL1	nucleoporin like 1	-0.329	0.0276
16773650	USPL1	ubiquitin specific peptidase like 1	-0.7355	0.0001
16773932	STARD13-AS2	STARD13 antisense RNA 2 (non-protein coding)	-0.3611	0.0355
16774082	EXOSC8	exosome component 8	-0.4206	0.0209
16774232			-0.2885	0.0429
16774303	RGCC	regulator of cell cycle	-0.4877	0.0284
16774762	RNU6-60	RNA, U6 small nuclear 60	-0.4803	0.0192
16774976	WDFY2	WD repeat and FYVE domain containing 2	-0.5548	0.0018
16775014	CKAP2	cytoskeleton associated protein 2	-0.4814	0.036
16775421	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	-0.4039	0.0477
16775811	GPC6	glypican 6	-0.6902	0.0338
16775968	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-1.1904	0.0001
16776004	MIR3170	microRNA 3170	-0.2404	0.0252
16776006	FARP1-IT1	FARP1 intronic transcript 1 (non-protein coding)	-0.3467	0.0056
16776103	ZIC2	Zic family member 2	-0.3017	0.0299
16776230	LINC00283	long intergenic non-protein coding RNA 283	-0.1374	0.0364
16776335	ABHD13	abhydrolase domain containing 13	-0.2763	0.0373
16776339	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-1.0873	0.0095
16776431	COL4A2	collagen, type IV, alpha 2	-0.8695	0.0005
16776491			-0.5306	0.0041
16776537	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	-0.2016	0.0433

16777020	MIR4502	microRNA 4502	-0.343	0.0294
16777115			-0.4719	0.0117
16777259	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	-0.4525	0.0043
16777272	RNU6-51	RNA, U6 small nuclear 51	-0.4459	0.0362
16777274	RNU4-9P	RNA, U4 small nuclear 9, pseudogene	-0.7401	0.0061
16777278	SKA3	spindle and kinetochore associated complex subunit 3	-0.5919	0.0418
16777309	ZDHHC20	zinc finger, DHHC-type containing 20	-0.4236	0.0211
16777331	ZDHHC20-IT1	ZDHHC20 intronic transcript 1 (non-protein coding)	-0.23	0.0028
16777360			-0.8822	0.0259
16777363	LINC00424	long intergenic non-protein coding RNA 424	-0.2566	0.0095
16777712	PAN3-AS1	PAN3 antisense RNA 1 (non-protein coding)	-0.284	0.0198
16777777	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-1.2079	0.0012
16777998	RNY1P4	RNA, Ro-associated Y1 pseudogene 4	-0.8335	0.0039
16778043	STARD13-IT1	STARD13 intronic transcript 1 (non-protein coding)	-0.3007	0.048
16778351			-0.1162	0.0335
16778370	LINC00548	long intergenic non-protein coding RNA 548	-0.1618	0.0428
16779232	INTS6	integrator complex subunit 6	-0.4269	0.0161
16779278	RNY1P6	RNA, Ro-associated Y1 pseudogene 6	-0.6252	0.0189
16779546	DIAPH3	diaphanous homolog 3 (Drosophila)	-0.8845	0.0054
16779958	EDNRB	endothelin receptor type B	-0.9017	0.0018
16779990	POU4F1	POU class 4 homeobox 1	-0.2619	0.017
16780069	SPRY2	sprouty homolog 2 (Drosophila)	-0.6343	0.0025
16780203	GPC6-AS1	GPC6 antisense RNA 1 (non-protein coding)	-0.2795	0.0158
16780447	RNF113B	ring finger protein 113B	-0.5305	0.0001
16780453	FARP1-AS1	FARP1 antisense RNA 1 (non-protein coding)	-1.0857	0.0001
16780611	RNY3P6	RNA, Ro-associated Y3 pseudogene 6	-0.6334	0.003
16780929	COL4A1	collagen, type IV, alpha 1	-0.9424	0.0016
16780993	COL4A2-AS1	COL4A2 antisense RNA 1 (non-protein coding)	-0.6779	0.0004
16781174	LOC283501	uncharacterized LOC283501	-0.146	0.0415
16781184			-0.1176	0.0308
16781475	OR11H4	olfactory receptor, family 11, subfamily H, member 4	-0.1161	0.0181
16781482	PARP2	poly (ADP-ribose) polymerase 2	-0.692	0.0002
16781516	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-0.5505	0.0002
16781614	METTL17	methyltransferase like 17	-0.4644	0.0065
16781691	RNASE8	ribonuclease, RNase A family, 8	-0.1724	0.0227
16781695	ARHGEF40	Rho guanine nucleotide exchange factor (GEF) 40	-0.6229	0
16781732	C14orf176	chromosome 14 open reading frame 176	-0.4407	0.0022
16781750			-0.4767	0.0002
16781791	TOX4	TOX high mobility group box family member 4	-0.2875	0.0016
16782132	ABHD4	abhydrolase domain containing 4	-0.6718	0.01
16782153	OXA1L	oxidase (cytochrome c) assembly 1-like	-0.2917	0.0366
16782173	MRPL52	mitochondrial ribosomal protein L52	-0.3189	0.0454
16782187	MMP14	matrix metallopeptidase 14 (membrane-inserted)	-0.7746	0.0092
16782255	C14orf164	chromosome 14 open reading frame 164	-0.1535	0.0176
16782280	BCL2L2-PABPN1	BCL2L2-PABPN1 readthrough	-0.2953	0.0022
16782334	NGDN	neuroguidin, EIF4E binding protein	-0.2616	0.0323
16782408			-0.8198	0.0193
16782414			-0.5953	0.0206
16782548	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-0.6462	0.0065
16782576	DCAF11	DDB1 and CUL4 associated factor 11	-0.6685	0.001
16782609	FITM1	fat storage-inducing transmembrane protein 1	-0.931	0.0039
16782637			-0.8346	0.0002
16782640	RNF31	ring finger protein 31	-0.437	0.0008
16782744	TSSK4	testis-specific serine kinase 4	-0.3184	0.0202
16782754	GMPR2	guanosine monophosphate reductase 2	-0.3796	0.0024
16782786	NOP9	NOP9 nucleolar protein homolog (yeast)	-0.4677	0.0005
16782805	LTB4R2	leukotriene B4 receptor 2	-0.3253	0.002
16782811	LTB4R2	leukotriene B4 receptor 2	-0.5216	0.001
16782818	LTB4R	leukotriene B4 receptor	-0.6042	0.0002

16782826	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	-0.7073	0.0056
16782876	KHNYN	KH and NYN domain containing	-0.4328	0.0019
16782889			-0.1852	0.0377
16783047	G2E3	G2/M-phase specific E3 ubiquitin protein ligase	-0.3177	0.0403
16783075	SCFD1	sec1 family domain containing 1	-0.3412	0.0051
16783165			-0.3237	0.003
16783170			-0.33	0.0046
16783215	ARHGAP5	Rho GTPase activating protein 5	-0.5902	0.0011
16783297			-0.341	0.037
16783299			-0.2709	0.0252
16783310	SRP54	signal recognition particle 54kDa	-0.4084	0.0001
16783342	FAM177A1	family with sequence similarity 177, member A1	-0.4719	0.0011
16783368	KIAA0391	KIAA0391	-0.3682	0.0026
16783389	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	-0.3999	0.0001
16783623	GEMIN2	gem (nuclear organelle) associated protein 2	-0.2181	0.0266
16783735			-0.4462	0.0043
16783764	C14orf28	chromosome 14 open reading frame 28	-0.2805	0.0192
16783773	FAM179B	family with sequence similarity 179, member B	-0.3287	0.0378
16783800	PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	-0.3048	0.0496
16783832			-0.5998	0
16783836	FANCM	Fanconi anemia, complementation group M	-0.5159	0.013
16783905	LRR1	leucine rich repeat protein 1	-0.3545	0.0069
16783927	KLHDC1	kelch domain containing 1	-0.3738	0.0087
16783944	KLHDC2	kelch domain containing 2	-0.6541	0
16783974	ARF6	ADP-ribosylation factor 6	-0.2958	0.0005
16784003			-0.3379	0.0496
16784036			-0.2431	0.0222
16784098	FRMD6	FERM domain containing 6	-0.4413	0.0066
16784180	C14orf166	chromosome 14 open reading frame 166	-0.3696	0.0041
16784226			-0.6026	0.0089
16784228	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	-0.4855	0.0004
16784272			-0.2932	0.041
16784275			-0.2831	0.0362
16784299	CDKN3	cyclin-dependent kinase inhibitor 3	-1.0393	0.0028
16784367	SOCS4	suppressor of cytokine signaling 4	-0.4157	0.0006
16784375	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	-0.5913	0.0001
16784398	FBXO34	F-box protein 34	-0.4044	0.0004
16784493			-0.1293	0.0489
16784578			-0.3729	0.0373
16784582	AP5M1	adaptor-related protein complex 5, mu 1 subunit	-0.2843	0.0036
16784605	NAA30	N(alpha)-acetyltransferase 30, NatC catalytic subunit	-0.4216	0.008
16784617	ACTR10	actin-related protein 10 homolog (S. cerevisiae)	-0.3332	0.0063
16784642	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	-0.3246	0.0112
16784664	ARID4A	AT rich interactive domain 4A (RBP1-like)	-0.4213	0.0133
16784707			-0.621	0.0046
16784710	KIAA0586	KIAA0586	-0.4855	0.0029
16784760	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	-0.5413	0.0253
16784829	JKAMP	JNK1/MAPK8-associated membrane protein	-0.2248	0.0034
16784883	C14orf135	chromosome 14 open reading frame 135	-0.5949	0.0005
16785058	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	-0.287	0.0219
16785086	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	-0.3841	0.0302
16785144			-0.5194	0.0026

16785316	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	-0.3445	0.0013
16785367	ZBTB1	zinc finger and BTB domain containing 1	-0.1674	0.0476
16785437	CHURC1-FNTB	CHURC1-FNTB readthrough	-0.4285	0.0005
16785476	LOC100506321	uncharacterized LOC100506321	-0.3304	0.0218
16785631	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	-0.8369	0
16785769	EXD2	exonuclease 3'-5' domain containing 2	-0.2266	0.0093
16785789	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	-0.4438	0.0404
16785821	SLC39A9	solute carrier family 39 (zinc transporter), member 9	-0.4464	0.0002
16785928			-0.3923	0.0094
16785952	PCNX	pecanex homolog (Drosophila)	-0.6695	0
16786007			-0.3277	0.0247
16786010	SIPA1L1	signal-induced proliferation-associated 1 like 1	-0.473	0.0248
16786060	LOC145474	uncharacterized LOC145474	-0.3001	0.0412
16786104	DCAF4	DDB1 and CUL4 associated factor 4	-0.4205	0.0024
16786133	RBM25	RNA binding motif protein 25	-0.3681	0.0123
16786167	PSEN1	presenilin 1	-0.3082	0.0121
16786255	ACOT2	acyl-CoA thioesterase 2	-0.5611	0.0012
16786326	ZNF410	zinc finger protein 410	-0.6466	0.0001
16786367	COQ6	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	-0.3424	0.0212
16786432	LIN52	lin-52 homolog (C. elegans)	-0.2363	0.0229
16786475	FCF1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	-0.3847	0.0048
16786492	YLPM1	YLP motif containing 1	-0.3088	0.0081
16786524	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	-0.3233	0.0049
16786548	EIF2B2	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	-0.5099	0.0055
16786587	FOS	FBJ murine osteosarcoma viral oncogene homolog	-0.6729	0.0152
16786607	JDP2	Jun dimerization protein 2	-0.2172	0.0271
16786652	TTLL5	tubulin tyrosine ligase-like family, member 5	-0.3636	0.0105
16786713	IFT43	intraflagellar transport 43 homolog (Chlamydomonas)	-0.2029	0.0243
16786738	C14orf118	chromosome 14 open reading frame 118	-0.228	0.0115
16786780	C14orf118	chromosome 14 open reading frame 118	-0.4578	0.0001
16786801	VASH1	vasohibin 1	-0.4606	0.0075
16786908	GSTZ1	glutathione S-transferase zeta 1	-0.2303	0.0029
16786941	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	-0.3029	0.0032
16786964			-0.31	0.0088
16786966	SLIRP	SRA stem-loop interacting RNA binding protein	-0.2391	0.0141
16787151			-0.5369	0.0445
16787279	ZC3H14	zinc finger CCCH-type containing 14	-0.4239	0.0002
16787342	LOC100506777	uncharacterized LOC100506777	-0.25	0.019
16787352	LOC400236	uncharacterized LOC400236	-0.271	0.0483
16787364	TDP1	tyrosyl-DNA phosphodiesterase 1	-0.2843	0.0094
16787409	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	-0.3306	0.0021
16787540	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	-0.4836	0
16787669	C14orf109	chromosome 14 open reading frame 109	-0.3388	0.0013
16787679	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	-0.5995	0.0002
16787799	IFI27L1	interferon, alpha-inducible protein 27-like 1	-0.4311	0.0276
16787882	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	-0.4102	0.0378
16787951	GLRX5	glutaredoxin 5	-0.3448	0.0018
16788023	BDKRB2	bradykinin receptor B2	-0.2648	0.0107
16788083	PAPOLA	poly(A) polymerase alpha	-0.4048	0.0034
16788142	VRK1	vaccinia related kinase 1	-0.4774	0.0351
16788223	CCNK	cyclin K	-0.2642	0.007

16788384	YY1	YY1 transcription factor	-0.2237	0.0363
16788390			-0.2218	0.0261
16788393			-0.3785	0.0076
16788488	MEG3	maternally expressed 3 (non-protein coding)	-2.2924	0
16788520	MEG3	maternally expressed 3 (non-protein coding)	-3.2809	0
16788522	MIR770	microRNA 770	-0.9458	0.0001
16788528	MIR665	microRNA 665	-0.4345	0.002
16788530	MIR431	microRNA 431	-0.1508	0.0409
16788534	MIR127	microRNA 127	-0.2128	0.0169
16788540	LOC100288160	esophagus cancer-related gene-2 interaction susceptibility protein	-0.3426	0.0125
16788542	MEG8	maternally expressed 8 (non-protein coding)	-2.0087	0
16788562			-0.3241	0.0012
16788564	MIR370	microRNA 370	-0.575	0.0158
16788566			-1.4039	0.0012
16788568			-1.166	0.001
16788570	SNORD113-1	small nucleolar RNA, C/D box 113-1	-3.0572	0
16788572			-2.7116	0
16788574	SNORD113-2	small nucleolar RNA, C/D box 113-2	-2.0069	0
16788576	SNORD113-3	small nucleolar RNA, C/D box 113-3	-3.8353	0
16788578	SNORD113-4	small nucleolar RNA, C/D box 113-4	-3.2931	0
16788602	SNORD113-5	small nucleolar RNA, C/D box 113-5	-2.0096	0
16788604			-1.1347	0.001
16788606	SNORD113-6	small nucleolar RNA, C/D box 113-6	-0.8624	0.0002
16788608			-2.3912	0
16788610	SNORD113-7	small nucleolar RNA, C/D box 113-7	-1.4934	0
16788612	SNORD113-8	small nucleolar RNA, C/D box 113-8	-3.0544	0
16788614	SNORD113-9	small nucleolar RNA, C/D box 113-9	-2.6627	0
16788616	SNORD114-1	small nucleolar RNA, C/D box 114-1	-3.8007	0
16788618	SNORD114-2	small nucleolar RNA, C/D box 114-2	-3.4684	0
16788620	SNORD114-3	small nucleolar RNA, C/D box 114-3	-3.4192	0
16788622	SNORD114-4	small nucleolar RNA, C/D box 114-4	-2.2937	0
16788624	SNORD114-5	small nucleolar RNA, C/D box 114-5	-0.8958	0.0128
16788626			-2.769	0
16788628	SNORD114-6	small nucleolar RNA, C/D box 114-6	-2.9331	0
16788630			-2.674	0
16788649	SNORD114-7	small nucleolar RNA, C/D box 114-7	-3.3523	0
16788651	SNORD114-8	small nucleolar RNA, C/D box 114-8	-1.7106	0
16788653	SNORD114-9	small nucleolar RNA, C/D box 114-9	-1.5444	0
16788655	SNORD114-10	small nucleolar RNA, C/D box 114-10	-1.8366	0.0001
16788657	SNORD114-11	small nucleolar RNA, C/D box 114-11	-3.0854	0
16788659	SNORD114-12	small nucleolar RNA, C/D box 114-12	-3.3108	0
16788661	SNORD114-13	small nucleolar RNA, C/D box 114-13	-3.0187	0
16788663	SNORD114-14	small nucleolar RNA, C/D box 114-14	-3.0244	0
16788665	SNORD114-15	small nucleolar RNA, C/D box 114-15	-3.0243	0
16788667	SNORD114-16	small nucleolar RNA, C/D box 114-16	-2.0424	0
16788669	SNORD114-17	small nucleolar RNA, C/D box 114-17	-3.0901	0
16788671	SNORD114-18	small nucleolar RNA, C/D box 114-18	-2.0907	0
16788673	SNORD114-19	small nucleolar RNA, C/D box 114-19	-3.9415	0
16788675			-2.3136	0
16788677			-4.3111	0
16788679			-2.0465	0
16788681	SNORD114-20	small nucleolar RNA, C/D box 114-20	-2.0017	0.0001
16788683	SNORD114-21	small nucleolar RNA, C/D box 114-21	-2.8799	0
16788685	SNORD114-22	small nucleolar RNA, C/D box 114-22	-2.0127	0
16788687	SNORD114-23	small nucleolar RNA, C/D box 114-23	-1.6273	0.0001
16788689	SNORD114-24	small nucleolar RNA, C/D box 114-24	-2.3332	0
16788691	SNORD114-25	small nucleolar RNA, C/D box 114-25	-2.308	0
16788693	SNORD114-26	small nucleolar RNA, C/D box 114-26	-2.2381	0
16788695	SNORD114-27	small nucleolar RNA, C/D box 114-27	-2.018	0
16788697	SNORD114-28	small nucleolar RNA, C/D box 114-28	-2.3267	0

16788699	SNORD114-29	small nucleolar RNA, C/D box 114-29	-1.6392	0.0001
16788701	SNORD114-30	small nucleolar RNA, C/D box 114-30	-3.2894	0
16788703	SNORD114-31	small nucleolar RNA, C/D box 114-31	-2.197	0
16788705			-2.1007	0
16788707			-2.2476	0
16788709			-2.4946	0
16788715	MIR299	microRNA 299	-0.5276	0.0099
16788717	MIR380	microRNA 380	-0.91	0.0026
16788719	MIR1197	microRNA 1197	-0.4252	0.0456
16788723	MIR758	microRNA 758	-0.6469	0.0117
16788725	MIR329-1	microRNA 329-1	-0.7988	0.0198
16788727	MIR329-2	microRNA 329-2	-0.5603	0.0295
16788731	MIR1193	microRNA 1193	-0.295	0.0227
16788733	MIR543	microRNA 543	-1.9285	0.0002
16788741	MIR654	microRNA 654	-1.1359	0.0041
16788743	MIR376B	microRNA 376b	-1.0122	0.0352
16788747	MIR300	microRNA 300	-1.1319	0.0035
16788749	MIR1185-1	microRNA 1185-1	-0.7878	0.0381
16788751	MIR1185-2	microRNA 1185-2	-1.7361	0.0002
16788758	MIR487B	microRNA 487b	-1.0011	0.0033
16788760	MIR539	microRNA 539	-0.9024	0.0093
16788762	MIR889	microRNA 889	-0.7785	0.0163
16788764			-1.7521	0.0004
16788772	MIR134	microRNA 134	-0.4257	0.0038
16788774	MIR668	microRNA 668	-1.1054	0.001
16788780	MIR154	microRNA 154	-0.889	0.0422
16788784	MIR377	microRNA 377	-0.6711	0.0371
16788796	MIR656	microRNA 656	-0.4262	0.0424
16788798	MEG9	maternally expressed 9 (non-protein coding)	-0.424	0.0116
16788817			-0.1292	0.035
16788833	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma	-0.5384	0
16788883	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	-0.3476	0.0202
16788973	WDR20	WD repeat domain 20	-0.4365	0.0001
16789019	TECPR2	tectonin beta-propeller repeat containing 2	-0.2104	0.0217
16789059	RCOR1	REST corepressor 1	-0.4407	0.003
16789178	EIF5	eukaryotic translation initiation factor 5	-0.4812	0.0031
16789209	MARK3	MAP/microtubule affinity-regulating kinase 3	-0.4418	0.002
16789258	KLC1	kinesin light chain 1	-0.2664	0.0032
16789289	APOPT1	apoptogenic 1, mitochondrial	-0.3542	0.0009
16789303			-0.4399	0.0006
16789429	C14orf144	chromosome 14 open reading frame 144	-0.2757	0.0401
16789509	SIVA1	SIVA1, apoptosis-inducing factor	-0.3706	0.005
16789536	KIAA0284	KIAA0284	-0.5308	0.0016
16789589	C14orf79	chromosome 14 open reading frame 79	-0.3162	0.0016
16789624	BTBD6	BTB (POZ) domain containing 6	-0.2935	0.0287
16789681	MTA1	metastasis associated 1	-0.3933	0.0017
16789899	TTC5	tetratricopeptide repeat domain 5	-0.412	0.0078
16789926	CCNB1IP1	cyclin B1 interacting protein 1, E3 ubiquitin protein ligase	-0.7131	0.0029
16789953	SNORD126	small nucleolar RNA, C/D box 126	-0.664	0.0067
16789955	RPPH1	ribonuclease P RNA component H1	-0.2944	0.0047
16790059	TMEM55B	transmembrane protein 55B	-0.4543	0.0005
16790110			-0.2351	0.0149
16790202	ZNF219	zinc finger protein 219	-0.2344	0.0444
16790233	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	-0.477	0.0015
16790246			-0.6772	0.0005
16790247			-0.7369	0.0148
16790258			-0.4726	0.0272
16790259			-0.487	0.0006
16790260			-0.659	0.0019
16790261			-0.8201	0.0001

16790262			-0.9054	0.0004
16790264			-0.5084	0.0182
16790267	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-0.5454	0.0006
16790307	CHD8	chromodomain helicase DNA binding protein 8	-0.4967	0.0001
16790364	RAB2B	RAB2B, member RAS oncogene family	-0.3376	0.0081
16790381	METTL3	methyltransferase like 3	-0.2622	0.0482
16790464	DAD1	defender against cell death 1	-0.3332	0.0004
16790467			-1.6187	0
16790468			-0.2678	0.0109
16790469			-0.3261	0.0011
16790470			-0.242	0.0039
16790472			-0.3206	0.0002
16790473			-0.3813	0.001
16790474			-0.5466	0.0035
16790556	PRMT5	protein arginine methyltransferase 5	-0.4088	0.0021
16790659	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5	-0.3566	0.003
16790693	ACIN1	apoptotic chromatin condensation inducer 1	-0.2663	0.0143
16790776	HOMEZ	homeobox and leucine zipper encoding	-0.3139	0.0013
16791023	DHRS4-AS1	DHRS4 antisense RNA 1 (non-protein coding)	-0.292	0.0395
16791044	EMC9	ER membrane protein complex subunit 9	-0.6292	0
16791059	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	-0.3378	0.0058
16791086	IPO4	importin 4	-0.6272	0
16791135	TM9SF1	transmembrane 9 superfamily member 1	-0.3816	0.0014
16791167	MDP1	magnesium-dependent phosphatase 1	-0.2507	0.0042
16791300	CIDEB	cell death-inducing DFFA-like effector b	-0.704	0
16791401	SDR39U1	short chain dehydrogenase/reductase family 39U, member 1	-0.3045	0.0106
16791642	STRN3	striatin, calmodulin binding protein 3	-0.4989	0.0006
16791669	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	-0.3827	0.0099
16791734	HEATR5A	HEAT repeat containing 5A	-0.6963	0
16791781	C14orf126	chromosome 14 open reading frame 126	-0.4592	0
16791810	ARHGAP5-AS1	ARHGAP5 antisense RNA 1 (non-protein coding)	-0.6735	0.0054
16791854	EAPP	E2F-associated phosphoprotein	-0.4336	0.0006
16791873	SNX6	sorting nexin 6	-0.5476	0.0001
16791909	BAZ1A	bromodomain adjacent to zinc finger domain, 1A	-0.306	0.0368
16791962	PPP2R3C	protein phosphatase 2, regulatory subunit B'', gamma	-0.5128	0.0003
16792010	RALGAPA1	Ral GTPase activating protein, alpha subunit 1 (catalytic)	-0.4726	0.0001
16792101	MBIP	MAP3K12 binding inhibitory protein 1	-0.3725	0.0146
16792226	SEC23A	Sec23 homolog A (S. cerevisiae)	-0.4736	0.0001
16792268	TRAPPC6B	trafficking protein particle complex 6B	-0.5027	0.0004
16792281	LOC100288846	uncharacterized LOC100288846	-0.2089	0.0066
16792347	KLHL28	kelch-like 28 (Drosophila)	-0.3941	0.0029
16792369	FKBP3	FK506 binding protein 3, 25kDa	-0.5295	0.0002
16792381	MIS18BP1	MIS18 binding protein 1	-0.5187	0.0097
16792407			-0.179	0.0381
16792486	RPS29	ribosomal protein S29	-0.3663	0.0013
16792501	RPL36AL	ribosomal protein L36a-like	-0.2239	0.0246
16792507			-0.259	0.0078
16792510	DNAAF2	dynein, axonemal, assembly factor 2	-0.293	0.0193
16792550	NEMF	nuclear export mediator factor	-0.3554	0.0063
16792601			-0.3058	0.0039
16792615	C14orf182	chromosome 14 open reading frame 182	-0.1811	0.0337
16792650	METTL21D	methyltransferase like 21D	-0.3542	0.0042
16792659	SOS2	son of sevenless homolog 2 (Drosophila)	-0.3257	0.0226
16792754	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	-0.3929	0.0111
16792798	SAV1	salvador homolog 1 (Drosophila)	-0.4372	0.0004
16792954	NID2	nidogen 2 (osteonidogen)	-0.7666	0.0023
16793024	ERO1L	ERO1-like (S. cerevisiae)	-0.6024	0.0067
16793052	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	-0.2495	0.0343

16793149	CNIH	cornichon homolog (Drosophila)	-0.5399	0
16793159	GMFB	glia maturation factor, beta	-0.4983	0.0001
16793190	WDHD1	WD repeat and HMG-box DNA binding protein 1	-0.6357	0.0083
16793225	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	-1.2553	0.0006
16793252			-0.3767	0.0084
16793259			-0.3505	0.0029
16793263	ATG14	autophagy related 14	-0.4709	0.0011
16793290	KTN1-AS1	KTN1 antisense RNA 1 (non-protein coding)	-0.2142	0.0373
16793353	EXOC5	exocyst complex component 5	-0.5008	0.0001
16793423	C14orf37	chromosome 14 open reading frame 37	-0.7631	0.0387
16793438	FLJ31306	uncharacterized LOC379025	-0.49	0.002
16793455			-0.5265	0.0027
16793460	TIMM9	translocase of inner mitochondrial membrane 9 homolog (yeast)	-0.4439	0.0033
16793475	GPR135	G protein-coupled receptor 135	-0.4793	0.0021
16793488	C14orf149	chromosome 14 open reading frame 149	-0.4007	0.0166
16793553			-0.2679	0.0207
16793632	TRMT5	tRNA methyltransferase 5 homolog (S. cerevisiae)	-0.2949	0.049
16793674			-0.6415	0.004
16793678	HIF1A-AS2	HIF1A antisense RNA 2 (non-protein coding)	-0.3409	0.0084
16793714			-0.2005	0.0089
16793721	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	-0.5083	0.0005
16793741	WDR89	WD repeat domain 89	-0.525	0.0006
16793750	SGPP1	sphingosine-1-phosphate phosphatase 1	-0.232	0.0471
16793805	ZBTB25	zinc finger and BTB domain containing 25	-0.4061	0.0011
16793999	PLEK2	pleckstrin 2	-1.4413	0.0072
16794030	PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	-0.2604	0.0136
16794064	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	-0.7057	0.0014
16794084	ZFYVE26	zinc finger, FYVE domain containing 26	-0.2823	0.0059
16794177	ACTN1	actinin, alpha 1	-0.6315	0.0001
16794220	DCAF5	DDB1 and CUL4 associated factor 5	-0.4234	0.0002
16794241			-0.2401	0.0217
16794256	ERH	enhancer of rudimentary homolog (Drosophila)	-0.4867	0.0002
16794257			-0.4057	0.0007
16794258			-0.4534	0.035
16794260			-0.5558	0.0008
16794261			-0.51	0.0006
16794262			-0.8519	0.0019
16794266	LOC100289511	uncharacterized LOC100289511	-0.2	0.0054
16794326	MED6	mediator complex subunit 6	-0.2677	0.0058
16794368			-0.2365	0.0178
16794373	C14orf56	chromosome 14 open reading frame 56	-0.1063	0.0178
16794441	ZFYVE1	zinc finger, FYVE domain containing 1	-0.4859	0.0004
16794464			-0.2072	0.019
16794476	NUMB	numb homolog (Drosophila)	-0.2479	0.0032
16794514	HEATR4	HEAT repeat containing 4	-0.1303	0.0472
16794555	C14orf43	chromosome 14 open reading frame 43	-0.2989	0.0106
16794586	FAM161B	family with sequence similarity 161, member B	-0.4038	0.0045
16794656	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	-0.2854	0.0219
16794767	KIAA0317	KIAA0317	-0.4469	0.0208
16794861			-0.5673	0.0024
16794888	ACYP1	acylphosphatase 1, erythrocyte (common) type	-0.7019	0.0056
16794898	NEK9	NIMA (never in mitosis gene a)- related kinase 9	-0.4392	0.0003
16794935	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	-0.2361	0.022
16794955			-0.9258	0.0125
16794966	C14orf1	chromosome 14 open reading frame 1	-0.7731	0.004
16794980	TGFB3	transforming growth factor, beta 3	-0.4242	0.0096
16794997			-0.4169	0
16795004			-0.2136	0.03
16795017	LOC100506603	uncharacterized LOC100506603	-0.4561	0

16795021	ANGEL1	angel homolog 1 (Drosophila)	-0.4274	0.0022
16795082	POMT2	protein-O-mannosyltransferase 2	-0.3551	0.0109
16795149	C14orf133	chromosome 14 open reading frame 133	-0.374	0.0028
16795226	SNW1	SNW domain containing 1	-0.3128	0.0008
16795285	DIO2	deiodinase, iodothyronine, type II	-0.2767	0.004
16795351	GTF2A1	general transcription factor IIA, 1, 19/37kDa	-0.4272	0.0018
16795485			-0.3626	0.0472
16795664	FOXN3	forkhead box N3	-0.3135	0.0135
16795878	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	-0.449	0.0012
16796115	MOAP1	modulator of apoptosis 1	-0.4744	0.0001
16796122	C14orf142	chromosome 14 open reading frame 142	-0.3361	0.0047
16796128	BTBD7	BTB (POZ) domain containing 7	-0.3014	0.031
16796207	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-0.2598	0.0059
16796229	IFI27L2	interferon, alpha-inducible protein 27-like 2	-0.3352	0.0043
16796237	SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	-0.2215	0.0169
16796325	DICER1	dicer 1, ribonuclease type III	-0.5467	0.0058
16796373	MIR3173	microRNA 3173	-0.2548	0.0129
16796412	LINC00341	long intergenic non-protein coding RNA 341	-0.4972	0.0179
16796444	SNHG10	small nucleolar RNA host gene 10 (non-protein coding)	-0.429	0.0071
16796469			-0.2222	0.0201
16796479	ATG2B	autophagy related 2B	-0.3492	0.0052
16796531			-0.3865	0.0409
16796662			-0.2579	0.0361
16796694	WARS	tryptophanyl-tRNA synthetase	-0.2924	0.0158
16796749			-3.1752	0
16796752	RTL1	retrotransposon-like 1	-0.4046	0.0054
16796814	LOC100507295	uncharacterized LOC100507295	-0.2768	0.0387
16796823			-0.2184	0.039
16796898	CINP	cyclin-dependent kinase 2 interacting protein	-0.3926	0.0009
16796914	CINP	cyclin-dependent kinase 2 interacting protein	-0.3157	0.0435
16796919	ANKRD9	ankyrin repeat domain 9	-0.2819	0.0069
16796938	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	-0.5591	0.0003
16797014	BAG5	BCL2-associated athanogene 5	-0.282	0.0036
16797025	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	-0.1683	0.0216
16797285	BRF1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	-0.2423	0.0076
16797330			-0.493	0.0034
16797419	IGHJ1	immunoglobulin heavy joining 1	-0.1999	0.0133
16797751	TUBGCP5	tubulin, gamma complex associated protein 5	-0.3618	0.0053
16798528			-0.2514	0.0061
16798765	CHRFAM7A	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion	-1.6232	0.0226
16798801	ARHGAP11B	Rho GTPase activating protein 11B	-0.6873	0.0044
16798810			-0.3471	0.0295
16798812	LOC100288637	OTU domain containing 7A pseudogene	-0.6125	0.0011
16798820			-0.3726	0.0358
16798919	ARHGAP11A	Rho GTPase activating protein 11A	-0.7538	0.0169
16799231	SPRED1	sprouty-related, EVH1 domain containing 1	-0.3857	0.045
16799426	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-0.6517	0.0011
16799492	LOC100505573	uncharacterized LOC100505573	-0.4169	0.022
16799517	C15orf23	chromosome 15 open reading frame 23	-0.3888	0.0064
16799598	CASC5	cancer susceptibility candidate 5	-0.9586	0.0055
16799637	RAD51	RAD51 homolog (S. cerevisiae)	-0.5475	0.0019
16799667	ZFYVE19	zinc finger, FYVE domain containing 19	-0.149	0.0367
16799760	CHP1	calcineurin-like EF hand protein 1	-0.3361	0.0046
16799776	OIP5-AS1	OIP5 antisense RNA 1 (non-protein coding)	-0.4598	0.0042
16799811			-0.1797	0.0091

16799814	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-0.3258	0.0262
16799852	TYRO3	TYRO3 protein tyrosine kinase	-0.5151	0.0001
16800108	HAUS2	HAUS augmin-like complex, subunit 2	-0.5378	0.0015
16800322	SERF2	small EDRK-rich factor 2	-0.2725	0.0083
16800355	WDR76	WD repeat domain 76	-0.7209	0.0059
16800406	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	-0.6915	0
16800431	EIF3J	eukaryotic translation initiation factor 3, subunit J	-0.5388	0.0001
16800506	SORD	sorbitol dehydrogenase	-0.5142	0.0158
16800836			-0.2895	0.0257
16800980	GABPB1-AS1	GABPB1 antisense RNA 1 (non-protein coding)	-0.5308	0.0013
16800991	USP8	ubiquitin specific peptidase 8	-0.2829	0.0316
16801033	SPPL2A	signal peptide peptidase like 2A	-0.4215	0.0035
16801035	AP4E1	adaptor-related protein complex 4, epsilon 1 subunit	-0.4623	0.002
16801063	DCAF13P3	DDB1 and CUL4 associated factor 13 pseudogene 3	-0.4244	0.0137
16801143	TMOD3	tropomodulin 3 (ubiquitous)	-0.4593	0.0006
16801196			-0.3667	0.0482
16801400	CGNL1	cingulin-like 1	-0.7955	0.0336
16801428	GCOM1	GRINL1A complex locus 1	-0.2975	0.0115
16801473	AQP9	aquaporin 9	-0.4366	0.0209
16801529	RNF111	ring finger protein 111	-0.2824	0.0044
16801557	CCNB2	cyclin B2	-1.1262	0.0013
16801624			-0.2362	0.0036
16801656			-0.6726	0.04
16801932			-0.2904	0.0237
16801995	TRIP4	thyroid hormone receptor interactor 4	-0.2203	0.031
16802100	RNU5A-1	RNA, U5A small nuclear 1	-0.3495	0.0413
16802106	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	-0.4731	0.0047
16802152	RAB11A	RAB11A, member RAS oncogene family	-0.2727	0.0499
16802204	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	-0.3733	0.0389
16802519	KIF23	kinesin family member 23	-0.6708	0.0026
16802601			-0.4102	0.0337
16802967	CCDC33	coiled-coil domain containing 33	-0.2189	0.0363
16803018	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	-0.3247	0.0083
16803050	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	-0.1764	0.0469
16803251	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	-0.4835	0.0059
16803501	IREB2	iron-responsive element binding protein 2	-0.3801	0.0019
16803678			-0.6895	0.0072
16803706			-0.7802	0.0063
16803743	FAM108C1	family with sequence similarity 108, member C1	-0.63	0.0083
16804228	SCAND2	SCAN domain containing 2 pseudogene	-0.4195	0.0096
16804294	PDE8A	phosphodiesterase 8A	-0.721	0
16804458	MRPS11	mitochondrial ribosomal protein S11	-0.1832	0.0312
16804490	ISG20	interferon stimulated exonuclease gene 20kDa	-0.4065	0.0005
16804506	ACAN	aggrecan	-0.7932	0.0011
16804559	FANCI	Fanconi anemia, complementation group I	-0.3964	0.0485
16804631	C15orf42	chromosome 15 open reading frame 42	-0.8017	0.0011
16804778	NGRN	neugrin, neurite outgrowth associated	-0.3336	0.0227
16805190			-0.3309	0.0052
16805218	LOC100507217	uncharacterized LOC100507217	-0.4358	0.0066
16805443			-0.1888	0.0423
16805555	LRRC28	leucine rich repeat containing 28	-0.2461	0.0325
16805781			-0.2863	0.0487
16805832	HERC2P3	hect domain and RLD 2 pseudogene 3	-0.3479	0.0134
16805967	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	-0.3047	0.0059
16806122	UBE3A	ubiquitin protein ligase E3A	-0.2873	0.0091
16806145	ATP10A	ATPase, class V, type 10A	-0.7066	0.0254
16806279	HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2	-0.4672	0.0005
16806561			-0.3796	0.034

16806732	WHAMMP1	WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 1	-0.5784	0.0062
16806844	C15orf29	chromosome 15 open reading frame 29	-0.3976	0.022
16807180			-0.1425	0.0178
16807459	FAM82A2	family with sequence similarity 82, member A2	-0.3662	0.0013
16807525	INO80	INO80 homolog (S. cerevisiae)	-0.3331	0
16807600			-0.5467	0.0049
16807605	OIP5	Opa interacting protein 5	-0.5705	0.0036
16807683			-0.2619	0.0252
16807879	TMEM87A	transmembrane protein 87A	-0.395	0.003
16807944	CDAN1	codanin 1	-0.2881	0.0044
16807976	TTBK2	tau tubulin kinase 2	-0.3154	0.0153
16807996	UBR1	ubiquitin protein ligase E3 component n-recognin 1	-0.5223	0.0002
16808363	MIR1282	microRNA 1282	-0.3539	0.0065
16808365	SERINC4	serine incorporator 4	-0.266	0.0119
16808449			-0.1615	0.0091
16808452	LOC645212	uncharacterized LOC645212	-0.1946	0.0162
16808993			-0.5425	0.0022
16809093	GABPB1	GA binding protein transcription factor, beta subunit 1	-0.1751	0.0142
16809113			-0.6966	0.0178
16809116			-0.2721	0.0092
16809138	TRPM7	transient receptor potential cation channel, subfamily M, member 7	-0.4194	0.0107
16809187	SPPL2A	signal peptide peptidase like 2A	-0.4337	0.0043
16809335			-0.2886	0.0007
16809340			-0.5643	0.0054
16809606	RAB27A	RAB27A, member RAS oncogene family	-0.4759	0.0082
16809729	RFX7	regulatory factor X, 7	-0.4204	0.0043
16809746			-0.38	0.0031
16809761	ZNF280D	zinc finger protein 280D	-0.4351	0.0031
16809805			-0.5728	0.0038
16809880	ADAM10	ADAM metallopeptidase domain 10	-0.3624	0.0028
16809915	HSP90AB4P	heat shock protein 90kDa alpha (cytosolic), class B member 4, pseudogene	-0.326	0.0129
16809919			-0.4166	0.0467
16809926			-0.3439	0.0415
16810025	GTF2A2	general transcription factor IIA, 2, 12kDa	-0.2039	0.0432
16810040	BNIP2	BCL2/adenovirus E1B 19kDa interacting protein 2	-0.3054	0.0114
16810104	NARG2	NMDA receptor regulated 2	-0.2993	0.0019
16810376	HERC1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	-0.2668	0.0092
16810514	PPIB	peptidylprolyl isomerase B (cyclophilin B)	-0.2996	0.0185
16810543	KIAA0101	KIAA0101	-0.583	0.0072
16810559	CSNK1G1	casein kinase 1, gamma 1	-0.1661	0.0072
16810572	RBPMS2	RNA binding protein with multiple splicing 2	-0.5953	0.0087
16810585	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	-0.1679	0.0163
16810686	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	-0.2991	0.0156
16810765	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	-0.4417	0.0054
16810847	DENND4A	DENN/MADD domain containing 4A	-0.3755	0.0122
16810954	SNORD18C	small nucleolar RNA, C/D box 18C	-0.231	0.0159
16810958			-0.2534	0.0267
16810959			-0.3137	0.0106
16810960			-0.1593	0.0498
16810962			-0.2105	0.0079
16810963			-0.2218	0.0462
16810965			-0.3646	0.0118
16810966			-0.3598	0.0348
16810967			-0.4559	0.0492
16810970	SNORD18C	small nucleolar RNA, C/D box 18C	-0.9279	0.0003
16810971			-0.9279	0.0003
16810974	SNORD16	small nucleolar RNA, C/D box 16	-0.5166	0.0018

16810975			-0.5166	0.0018
16811073	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	-0.3151	0.0314
16811129	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.4786	0
16811151	ANP32A-IT1	ANP32A intronic transcript 1 (non-protein coding)	-0.1929	0.0223
16811816	PTPN9	protein tyrosine phosphatase, non-receptor type 9	-0.4325	0.0001
16812083	LOC91450	uncharacterized LOC91450	-0.217	0.0085
16812171			-0.1992	0.0343
16812350			-0.3844	0.0233
16812732			-0.1943	0.0178
16812735	LOC100505661	uncharacterized LOC100505661	-0.4373	0.0246
16812800			-0.2389	0.0077
16812831	SEC11A	SEC11 homolog A (S. cerevisiae)	-0.2235	0.0277
16812994			-0.2161	0.04
16813062	RLBP1	retinaldehyde binding protein 1	-0.1701	0.029
16813073	POLG	polymerase (DNA directed), gamma	-0.2104	0.0205
16813148	KIF7	kinesin family member 7	-0.193	0.0115
16813189	PEX11A	peroxisomal biogenesis factor 11 alpha	-0.3931	0.0111
16813265			-0.3875	0.0136
16813342	PRC1	protein regulator of cytokinesis 1	-0.6396	0.009
16813592			-0.1421	0.0286
16813871	CHSY1	chondroitin sulfate synthase 1	-0.6004	0.0021
16813883	VIMP	VCP-interacting membrane protein	-0.4094	0.0005
16813900	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	-0.3206	0.0034
16813922	PCSK6	proprotein convertase subtilisin/kexin type 6	-0.5459	0.044
16814128	HBA1	hemoglobin, alpha 1	-0.6997	0.0452
16814278	SOLH	small optic lobes homolog (Drosophila)	-0.1618	0.0281
16814295	SOLH	small optic lobes homolog (Drosophila)	-0.193	0.0491
16814748	CRAMP1L	Crm, cramped-like (Drosophila)	-0.1629	0.035
16814779	HN1L	hematological and neurological expressed 1-like	-0.5153	0.001
16815394	CASP16	caspase 16, apoptosis-related cysteine peptidase (putative)	-0.3244	0.0228
16815905	RMI2	RMI2, RecQ mediated genome instability 2, homolog (S. cerevisiae)	-0.5304	0.0064
16815910			-0.3068	0.0289
16816948	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-0.3867	0.0137
16817017	PLK1	polo-like kinase 1	-1.0522	0.0017
16817320	SBK1	SH3-binding domain kinase 1	-0.4732	0.0306
16817647	KIF22	kinesin family member 22	-0.304	0.0306
16818068	FBXL19	F-box and leucine-rich repeat protein 19	-0.1633	0.0083
16818359	TGFB1I1	transforming growth factor beta 1 induced transcript 1	-0.7634	0.0025
16818522	RN5-8S2	RNA, 5.8S ribosomal 2	-0.4517	0.0075
16818733	HEATR3	HEAT repeat containing 3	-0.2422	0.036
16819197	MT4	metallothionein 4	-0.1671	0.0291
16819952	CBFB	core-binding factor, beta subunit	-0.4033	0.0022
16820157	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	-0.5066	0.0115
16820296	EDC4	enhancer of mRNA decapping 4	-0.213	0.0337
16820333	NRN1L	neuritin 1-like	-0.4339	0.0094
16820843			-0.2611	0.0113
16821045			-0.3277	0.0457
16821326	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-0.1892	0.0153
16821377	CDH13	cadherin 13, H-cadherin (heart)	-0.548	0.0045
16821414	OSGIN1	oxidative stress induced growth inhibitor 1	-0.5842	0.0052
16821425	NECAB2	N-terminal EF-hand calcium binding protein 2	-0.2603	0.0154
16821788			-0.6844	0.0013
16821790	ZNF469	zinc finger protein 469	-0.4128	0.0322
16821835	MGC23284	uncharacterized LOC197187	-0.595	0.0001
16821869	CDT1	chromatin licensing and DNA replication factor 1	-0.2656	0.0451
16822661	UNKL	unkempt homolog (Drosophila)-like	-0.22	0.0068
16822913	RPS2	ribosomal protein S2	-0.2992	0.0331

16822917	RPS2	ribosomal protein S2	-0.4124	0.0424
16823179	SRRM2-AS1	SRRM2 antisense RNA 1 (non-protein coding)	-0.262	0.0204
16823866	SOCS1	suppressor of cytokine signaling 1	-0.4635	0.0417
16823889	MIR548H2	microRNA 548h-2	-0.4211	0.0097
16824349	LOC100288162	uncharacterized LOC100288162	-0.1839	0.0197
16824352	XYLT1	xylosyltransferase I	-0.7589	0.0018
16826077			-0.2515	0.0289
16826102			-0.2856	0.0133
16826160	SHCBP1	SHC SH2-domain binding protein 1	-0.583	0.0474
16826230	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	-1.2376	0.0008
16826241			-0.742	0.0149
16827502	SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	-0.5101	0.0278
16827687	NOB1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	-0.434	0.0037
16827735	LOC400541	uncharacterized LOC400541	-0.4188	0.0188
16828153	TXNL4B	thioredoxin-like 4B	-0.3334	0.0332
16828762	HSDL1	hydroxysteroid dehydrogenase like 1	-0.4481	0.0494
16828772	TAF1C	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	-0.1887	0.0397
16828921			-0.157	0.0099
16829056	LOC100653213	uncharacterized LOC100653213	-0.2352	0.0119
16829080			-0.2245	0.0211
16829113			-0.1667	0.0066
16829139	MVD	mevalonate (diphospho) decarboxylase	-0.7543	0.0161
16829469			-1.1181	0.0296
16829472	LOC100506388	uncharacterized LOC100506388	-0.9883	0.0046
16829486	FAM57A	family with sequence similarity 57, member A	-0.7084	0.0244
16829505			-0.5504	0.0123
16829638	SGSM2	small G protein signaling modulator 2	-0.2931	0.0246
16829764	GSG2	germ cell associated 2 (haspin)	-0.4071	0.02
16830295	SLC16A13	solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	-0.4496	0.0407
16830575	SNORD10	small nucleolar RNA, C/D box 10	-0.7567	0.0094
16830988	NDEL1	nudE nuclear distribution E homolog (A. nidulans)-like 1	-0.5957	0.0009
16831383	ADORA2B	adenosine A2b receptor	-0.2685	0.0378
16831464	C17orf76-AS1	C17orf76 antisense RNA 1 (non-protein coding)	-0.2378	0.0387
16831598	NT5M	5',3'-nucleotidase, mitochondrial	-0.1934	0.0203
16832133			-0.3416	0.0276
16832138			-0.423	0.0064
16832142			-0.7627	0.0114
16832221			-0.1793	0.0027
16832231			-0.8974	0.0157
16832405	NLK	nemo-like kinase	-0.6902	0.0091
16832421			-0.759	0.0119
16832429	TMEM97	transmembrane protein 97	-1.0947	0.0057
16832438	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-0.3502	0.0266
16832510	SPAG5-AS1	SPAG5 antisense RNA 1 (non-protein coding)	-0.1715	0.0249
16832558	SNORD4A	small nucleolar RNA, C/D box 4A	-0.3045	0.0242
16833032			-0.1688	0.0439
16833139	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-0.2769	0.0247
16833545	TADA2A	transcriptional adaptor 2A	-0.3223	0.0188
16833567	DUSP14	dual specificity phosphatase 14	-0.3151	0.0384
16833616	SOCS7	suppressor of cytokine signaling 7	-0.5782	0.0015
16833802	STARD3	StAR-related lipid transfer (START) domain containing 3	-0.3457	0.0155
16834056	CDC6	cell division cycle 6 homolog (S. cerevisiae)	-0.5982	0.0124
16834196	FKBP10	FK506 binding protein 10, 65 kDa	-0.4955	0.0305
16834252	NKIRAS2	NFKB inhibitor interacting Ras-like 2	-0.2818	0.0298
16834341	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	-0.2164	0.0221
16834516	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	-1.2371	0.0025

16834523	AOC4	amine oxidase, copper containing 3 (vascular adhesion protein 1) pseudogene	-0.247	0.0321
16834540	RPL27	ribosomal protein L27	-0.1556	0.0461
16834541			-0.255	0.0029
16834543			-0.1669	0.0452
16834764			-0.4193	0.0002
16835158	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	-0.3032	0.0161
16835538			-0.2497	0.0498
16835797	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-0.2301	0.0237
16836375	MSI2	musashi homolog 2 (Drosophila)	-0.6811	0.0002
16836476	PPM1E	protein phosphatase, Mg2+/Mn2+ dependent, 1E	-0.6681	0.0045
16836487			-0.1991	0.0482
16836492	PRR11	proline rich 11	-0.9974	0.0009
16837061	SNORD104	small nucleolar RNA, C/D box 104	-0.8165	0.0342
16837270	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	-0.7173	0.0022
16837284	LOC100499466	uncharacterized LOC100499466	-0.2583	0.0226
16837604			-0.1203	0.0391
16837762	LOC100287042	uncharacterized LOC100287042	-0.2705	0.0309
16837768	KIAA0195	KIAA0195	-0.5644	0.0005
16838101	SNORD1B	small nucleolar RNA, C/D box 1B	-0.369	0.0185
16838105			-0.5662	0.0001
16838107	METTL23	methyltransferase like 23	-0.2998	0.0409
16838169	LINC00338	long intergenic non-protein coding RNA 338	-0.3348	0.0215
16838359	BIRC5	baculoviral IAP repeat containing 5	-0.7342	0.0065
16838382			-0.1957	0.0122
16838561	SLC26A11	solute carrier family 26, member 11	-0.3637	0.0369
16838698	RPTOR	regulatory associated protein of MTOR, complex 1	-0.6618	0.0004
16839086	FOXK2	forkhead box K2	-0.4136	0.005
16839104			-0.3479	0.0255
16839220	FAM101B	family with sequence similarity 101, member B	-0.5339	0.0398
16839294	ABR	active BCR-related	-0.6765	0.0266
16839473	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	-0.2645	0.0488
16839474			-0.3068	0.0287
16839481			-0.3623	0.0351
16839485			-0.9315	0.0008
16839486			-0.4725	0.002
16839487			-0.4951	0.0148
16839488			-0.6901	0.0022
16839489			-0.4344	0.0299
16839497			-0.2789	0.036
16839502			-0.3038	0.0431
16839515			-0.4113	0.0221
16839516			-0.3383	0.0227
16839602	SNORD91B	small nucleolar RNA, C/D box 91B	-0.198	0.0186
16839639			-0.2948	0.0143
16839836	C17orf85	chromosome 17 open reading frame 85	-0.2664	0.0419
16839913	ZZEF1	zinc finger, ZZ-type with EF-hand domain 1	-0.2828	0.0322
16840262	NUP88	nucleoporin 88kDa	-0.3426	0.0097
16840846	PER1	period homolog 1 (Drosophila)	-0.3223	0.043
16840902	AURKB	aurora kinase B	-0.4308	0.0112
16841038	CCDC42	coiled-coil domain containing 42	-0.1572	0.0177
16841340	MYH2	myosin, heavy chain 2, skeletal muscle, adult	-0.2482	0.0379
16841577	MIR4731	microRNA 4731	-0.5729	0.0002
16841778	FAM211A	family with sequence similarity 211, member A	-0.3242	0.0274
16841849	MPRIP-AS1	MPRIP antisense RNA 1 (non-protein coding)	-0.3183	0.0097
16841982	TOM1L2	target of myb1-like 2 (chicken)	-0.2928	0.0163
16842206	GRAP	GRB2-related adaptor protein	-0.179	0.0466
16842217			-0.5308	0.045
16842292			-1.5569	0.0011

16842458			-0.366	0.0163
16842659	ALDOC	aldolase C, fructose-bisphosphate	-0.76	0.0098
16842673	SPAG5	sperm associated antigen 5	-0.6075	0.0206
16842701	SGK494	uncharacterized serine/threonine-protein kinase SgK494	-0.253	0.0431
16842722	KIAA0100	KIAA0100	-0.47	0.0062
16842766	SDF2	stromal cell-derived factor 2	-0.3206	0.0397
16842812	TLCD1	TLC domain containing 1	-0.6443	0.0175
16843680	MYO19	myosin XIX	-0.53	0.0001
16843987	PCGF2	polycomb group ring finger 2	-0.375	0.019
16844099	CACNB1	calcium channel, voltage-dependent, beta 1 subunit	-0.2911	0.0026
16844305			-0.4003	0.0355
16844312	TOP2A	topoisomerase (DNA) II alpha 170kDa	-1.3492	0.0044
16844817	KRT16	keratin 16	-0.1567	0.021
16844894	LEPREL4	leprecan-like 4	-0.2795	0.0259
16844936	ACLY	ATP citrate lyase	-0.4476	0.0398
16845169	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	-0.4324	0.0257
16845172	PSMC3IP	PSMC3 interacting protein	-0.2204	0.0372
16845452	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	-0.258	0.0319
16845623	SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	-0.2579	0.0091
16845657	SLC25A39	solute carrier family 25, member 39	-0.4268	0.0005
16845736	GJC1	gap junction protein, gamma 1, 45kDa	-0.5909	0.0201
16845794	KIF18B	kinesin family member 18B	-0.3726	0.0193
16846226	HOXB3	homeobox B3	-0.2872	0.015
16846291	HOXB9	homeobox B9	-0.5638	0.0085
16846359			-0.4182	0.0168
16846587	COL1A1	collagen, type I, alpha 1	-0.5878	0.0275
16846672			-0.2197	0.0262
16847238	SKA2	spindle and kinetochore associated complex subunit 2	-0.2868	0.0357
16847621	FTSJ3	FtsJ homolog 3 (E. coli)	-0.3969	0.0265
16847771	ERN1	endoplasmic reticulum to nucleus signaling 1	-0.6185	0.0195
16848657	FDXR	ferredoxin reductase	-0.2596	0.0317
16849172	QRICH2	glutamine rich 2	-0.2166	0.0183
16849306			-0.7427	0.0346
16849308	JMJD6	jumonji domain containing 6	-0.2587	0.0424
16849379	TK1	thymidine kinase 1, soluble	-0.6213	0.0074
16849646			-0.1256	0.0371
16849667	EIF4A3	eukaryotic translation initiation factor 4A3	-0.6405	0.0006
16849712	FLJ46026	FLJ46026 protein	-0.2841	0.0319
16849773	C17orf56	chromosome 17 open reading frame 56	-0.2129	0.0137
16849913	ARL16	ADP-ribosylation factor-like 16	-0.2902	0.0259
16849939	P4HB	prolyl 4-hydroxylase, beta polypeptide	-0.3232	0.005
16849982	ALYREF	Aly/REF export factor	-0.3044	0.0338
16850090	DUS1L	dihydrouridine synthase 1-like (S. cerevisiae)	-0.2255	0.047
16850107	FASN	fatty acid synthase	-0.7466	0.0026
16850264	WDR45L	WDR45-like	-0.321	0.014
16850286	MIR4525	microRNA 4525	-0.2587	0.0429
16850416			-0.1543	0.0362
16850426			-0.4696	0.0341
16850477	TYMS	thymidylate synthetase	-0.9517	0.0022
16850517	NDC80	NDC80 kinetochore complex component homolog (S. cerevisiae)	-1.1793	0.0023
16850625	TGIF1	TGFB-induced factor homeobox 1	-0.3075	0.0093
16850944	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	-0.2174	0.0487
16851081	TUBB6	tubulin, beta 6 class V	-0.3925	0.0469
16851191	C18orf1	chromosome 18 open reading frame 1	-0.3755	0.0244
16851206	RNMT	RNA (guanine-7-) methyltransferase	-0.3174	0.0425
16851254			-0.5938	0.0224

16851443	RIOK3	RIO kinase 3 (yeast)	-0.4103	0.017
16851688			-0.7488	0.0112
16851786	TTR	transthyretin	-0.1197	0.0037
16852008	MOCOS	molybdenum cofactor sulfurase	-0.6049	0.0003
16852098	PIK3C3	phosphoinositide-3-kinase, class 3	-0.3058	0.0123
16852312	SKA1	spindle and kinetochore associated complex subunit 1	-0.718	0.025
16852568			-0.3868	0.0243
16852692			-0.3983	0.0165
16852773	ZCCHC2	zinc finger, CCHC domain containing 2	-0.3828	0.0001
16852833	SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	-0.122	0.0215
16852993			-0.1282	0.035
16853120	TSHZ1	teashirt zinc finger homeobox 1	-0.2575	0.0271
16853234	ATP9B	ATPase, class II, type 9B	-0.3043	0.0185
16853527	MYOM1	myomesin 1, 185kDa	-0.367	0.0156
16853994			-0.7527	0.0144
16853996	AFG3L2	AFG3 ATPase family gene 3-like 2 (S. cerevisiae)	-0.4599	0.0014
16854044			-0.3943	0.022
16854046	CEP76	centrosomal protein 76kDa	-0.5715	0.0007
16854097	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)	-2.6042	0
16854130			-0.2043	0.0416
16854185	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-0.3039	0.0428
16854227	LOC100128893	uncharacterized LOC100128893	-0.4244	0.0145
16854268	NPC1	Niemann-Pick disease, type C1	-0.5871	0.0163
16854375	SS18	synovial sarcoma translocation, chromosome 18	-0.5023	0.0077
16854437	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	-1.3336	0.0286
16854664			-0.1805	0.0239
16855015	ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	-0.5939	0.0484
16855093	SMAD2	SMAD family member 2	-0.3733	0.027
16855163	RPL17	ribosomal protein L17	-0.2446	0.0193
16855171			-0.3735	0.0166
16855172			-0.2388	0.0068
16855256	MBD1	methyl-CpG binding domain protein 1	-0.2375	0.0457
16855629	RNF152	ring finger protein 152	-0.5276	0.0423
16855723	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	-0.1554	0.0321
16855999	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	-0.3548	0.005
16856015			-0.1733	0.0444
16856021			-0.1919	0.0335
16856101			-0.2064	0.0017
16856130			-0.3949	0.0178
16856567	DAZAP1	DAZ associated protein 1	-0.1896	0.0365
16856634	LOC100288123	uncharacterized LOC100288123	-0.2597	0.0313
16856699	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	-0.4356	0.0176
16856757	OAZ1	ornithine decarboxylase antizyme 1	-0.1943	0.0456
16856910	NCLN	nicalin	-0.4237	0.0231
16857080	PIAS4	protein inhibitor of activated STAT, 4	-0.2993	0.0028
16857143	CCDC94	coiled-coil domain containing 94	-0.2161	0.0113
16857192	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.3495	0.0471
16857254	FEM1A	fem-1 homolog a (C. elegans)	-0.3068	0.0034
16857258	UHRF1	ubiquitin-like with PHD and ring finger domains 1	-0.2171	0.0351
16857282	KDM4B	lysine (K)-specific demethylase 4B	-0.7295	0.0003
16857353	RPL36	ribosomal protein L36	-0.2384	0.0111
16857389	NRTN	neurturin	-0.4161	0.017
16857457			-0.8043	0.0111
16857886	ANGPTL4	angiopoietin-like 4	-0.2954	0.0238
16857931			-0.5916	0.0168
16858235	ILF3	interleukin enhancer binding factor 3, 90kDa	-0.2193	0.0215
16858386	LDLR	low density lipoprotein receptor	-1.0738	0.004

16858496	CNN1	calponin 1, basic, smooth muscle	-0.3439	0.0268
16858820			-0.2592	0.0129
16858970	CD97	CD97 molecule	-0.8737	0.0253
16859314	KLF2	Kruppel-like factor 2 (lung)	-0.3948	0.0261
16859395	MYO9B	myosin IXB	-0.3285	0.0255
16859648	RPL18A	ribosomal protein L18a	-0.2267	0.0464
16859822			-0.1761	0.0114
16859825	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	-0.1353	0.0291
16860041	MIR640	microRNA 640	-0.266	0.0092
16860450	ZNF536	zinc finger protein 536	-0.5903	0.0128
16860610	WDR88	WD repeat domain 88	-0.1184	0.0369
16860667	KCTD15	potassium channel tetramerisation domain containing 15	-0.2402	0.0081
16860766	WTIP	Wilms tumor 1 interacting protein	-0.1894	0.0171
16861395			-0.2973	0.0475
16861887	ECH1	enoyl CoA hydratase 1, peroxisomal	-0.2903	0.0419
16861969	SAMD4B	sterile alpha motif domain containing 4B	-0.1759	0.029
16862101	LGALS13	lectin, galactoside-binding, soluble, 13	-0.2394	0.0451
16862132	LGALS14	lectin, galactoside-binding, soluble, 14	-0.2112	0.0259
16862284	LTBP4	latent transforming growth factor beta binding protein 4	-0.2722	0.0365
16862572	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	-0.1957	0.0184
16862596	RPS19	ribosomal protein S19	-0.1941	0.036
16862666	LOC100132272	uncharacterized LOC100132272	-0.2923	0.0322
16862767			-0.1797	0.0208
16862996	PVR	poliovirus receptor	-0.323	0.0341
16863011	CEACAM19	carcinoembryonic antigen-related cell adhesion molecule 19	-0.3054	0.0223
16863104	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	-0.4472	0.0022
16863148	CLPTM1	cleft lip and palate associated transmembrane protein 1	-0.2575	0.0314
16863287	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-0.5528	0.0225
16863489	LOC400707	uncharacterized LOC400707	-0.5278	0.0204
16863513			-0.2382	0.0337
16863740	ZNF114	zinc finger protein 114	-0.3024	0.0315
16863768	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	-0.2872	0.0226
16864159	RPS11	ribosomal protein S11	-0.104	0.0477
16864161			-0.1247	0.0363
16864162			-0.1046	0.0319
16864164			-0.1514	0.0276
16864565	SNAR-F	small ILF3/NF90-associated RNA F	-0.9324	0.0411
16864778	PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	-0.4473	0.0027
16865028	MIR520F	microRNA 520f	-0.4844	0.0312
16865116	MYADM	myeloid-associated differentiation marker	-0.6432	0.0003
16865214	CNOT3	CCR4-NOT transcription complex, subunit 3	-0.2854	0.0168
16865522	KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	-0.2556	0.0242
16865620	BRSK1	BR serine/threonine kinase 1	-0.3217	0.004
16865647	SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	-0.1343	0.046
16865675	RPL28	ribosomal protein L28	-0.2882	0.0307
16865676			-0.3421	0.007
16865681			-0.7373	0.0001
16865772			-0.4328	0.0093
16865957	MIMT1	MER1 repeat containing imprinted transcript 1 (non-protein coding)	-0.5604	0.012
16866284			-0.292	0.0387
16866285			-0.2272	0.05
16866632	CIRBP-AS1	CIRBP antisense RNA 1 (non-protein coding)	-0.2799	0.0041
16866794	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	-0.2584	0.0243
16866946	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-0.3469	0.0027

16867018	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	-0.2398	0.0329
16867074	MFSD12	major facilitator superfamily domain containing 12	-0.41	0.0108
16867088	TBXA2R	thromboxane A2 receptor	-0.9362	0.0007
16867541	DUS3L	dihydrouridine synthase 3-like (S. cerevisiae)	-0.2564	0.0046
16867579	FUT5	fucosyltransferase 5 (alpha (1,3) fucosyltransferase)	-0.4025	0.0024
16867583	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	-0.3498	0.0011
16867756	TUBB4A	tubulin, beta 4A class IVa	-0.7693	0.0078
16868063	FBN3	fibrillin 3	-0.1905	0.0397
16868472	FBXL12	F-box and leucine-rich repeat protein 12	-0.2398	0.0234
16868811	LOC147727	uncharacterized LOC147727	-0.4639	0.0026
16868838	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.2104	0.049
16869397	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae)	-0.2613	0.0026
16869588	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	-0.6753	0.0033
16869624	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	-0.5266	0.0018
16869942	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	-0.2153	0.0294
16870131	HAUS8	HAUS augmin-like complex, subunit 8	-0.853	0
16870617	SUGP1	SURP and G patch domain containing 1	-0.5295	0.0002
16870690	ATP13A1	ATPase type 13A1	-0.1835	0.0224
16870978	ZNF675	zinc finger protein 675	-0.7465	0.0281
16871082			-0.2266	0.0021
16871359	DMKN	dermokine	-0.5721	0.0211
16872229	RPS16	ribosomal protein S16	-0.1295	0.0317
16872352	AKT2	v-akt murine thymoma viral oncogene homolog 2	-0.2038	0.0131
16872496	C19orf54	chromosome 19 open reading frame 54	-0.379	0.0075
16872990	PHLDB3	pleckstrin homology-like domain, family B, member 3	-0.188	0.0415
16873239	TRAPPC6A	trafficking protein particle complex 6A	-0.4099	0.0444
16873329	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-0.8731	0.0109
16873557	PNMAL2	paraneoplastic Ma antigen family-like 2	-0.6161	0.0207
16873918	CCDC114	coiled-coil domain containing 114	-0.1152	0.0307
16873987	RPL18	ribosomal protein L18	-0.1874	0.0217
16873991			-0.2613	0.0301
16873998			-0.2845	0.0089
16874198	CGB8	chorionic gonadotropin, beta polypeptide 8	-0.2311	0.0209
16875042			-0.234	0.0264
16875237			-0.7522	0.001
16875656	PTPRH	protein tyrosine phosphatase, receptor type, H	-0.7865	0
16875808	NLRP9	NLR family, pyrin domain containing 9	-0.134	0.0201
16875909	PEG3	paternally expressed 3	-0.8231	0.0145
16876139			-0.362	0.0014
16876330			-0.2611	0.0113
16876440	ACP1	acid phosphatase 1, soluble	-0.5469	0.0001
16876458			-0.7572	0.0108
16876819			-0.3156	0.0078
16876950	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	-0.2863	0.0356
16877048	HPCAL1	hippocalcin-like 1	-0.1936	0.018
16877543			-0.2442	0.0353
16877555	RHOB	ras homolog family member B	-0.2717	0.0332
16877559			-0.484	0.0265
16877600			-0.1745	0.0017
16877637	UBXN2A	UBX domain protein 2A	-0.2903	0.0296
16877667	FKBP1B	FK506 binding protein 1B, 12.6 kDa	-0.2543	0.02
16877762	CENPO	centromere protein O	-0.4773	0.0105
16877888	EPT1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	-0.4067	0.024
16878800	BIRC6	baculoviral IAP repeat containing 6	-0.3374	0.0085
16878888	MIR558	microRNA 558	-0.3559	0.0244
16878947	LTBP1	latent transforming growth factor beta binding protein 1	-0.8909	0.0179

16879174	QPCT	glutaminyl-peptide cyclotransferase	-0.954	0.033
16879189			-0.362	0.0464
16879202			-0.1282	0.0261
16879205	FAM82A1	family with sequence similarity 82, member A1	-0.6264	0.0182
16879439			-0.7446	0.0045
16879923	MSH6	mutS homolog 6 (E. coli)	-0.4925	0.0019
16880080	LOC100506338	uncharacterized LOC100506338	-0.3507	0.0236
16880176	EML6	echinoderm microtubule associated protein like 6	-0.9399	0.0175
16880245	PRORSD1P	prolyl-tRNA synthetase associated domain containing 1, pseudogene	-0.3171	0.0431
16880251			-0.4287	0.0046
16880538	EHBP1	EH domain binding protein 1	-0.4113	0.0367
16880669	LGALSL	lectin, galactoside-binding-like	-0.4551	0.0187
16880712	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	-0.7722	0.0011
16881031	ANTXR1	anthrax toxin receptor 1	-0.5359	0.0249
16881059	MIR3126	microRNA 3126	-0.2702	0.0101
16881138	MXD1	MAX dimerization protein 1	-0.4262	0.0065
16881194	VAX2	ventral anterior homeobox 2	-0.2683	0.0464
16882150	KCMF1	potassium channel modulatory factor 1	-0.2593	0.0313
16882366			-0.4802	0.0222
16882507	RGPD2	RANBP2-like and GRIP domain containing 2	-0.2291	0.0311
16882544	ANAPC1	anaphase promoting complex subunit 1	-0.4102	0.0283
16882558			-0.1547	0.0072
16882561	LOC541471	uncharacterized LOC541471	-0.5361	0.0221
16882576	MIR4435-1	microRNA 4435-1	-0.3127	0.0004
16882658	RPIA	ribose 5-phosphate isomerase A	-0.315	0.0157
16882912	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A	-0.2477	0.0372
16882942			-0.5109	0.0479
16882950	LOC285033	uncharacterized LOC285033	-0.2523	0.0068
16882975	NCAPH	non-SMC condensin I complex, subunit H	-0.4469	0.0074
16883498	NPAS2	neuronal PAS domain protein 2	-1.1032	0
16883530			-0.8149	0.0001
16883895	C2orf49	chromosome 2 open reading frame 49	-0.2394	0.0464
16883905	LOC100506494	uncharacterized LOC100506494	-0.4923	0.0143
16883954			-0.1383	0.0342
16883978	RGPD4	RANBP2-like and GRIP domain containing 4	-0.2303	0.0295
16884099	LIMS1	LIM and senescent cell antigen-like domains 1	-0.3921	0.0185
16884204	RGPD6	RANBP2-like and GRIP domain containing 6	-0.2072	0.0385
16884245	LIMS3	LIM and senescent cell antigen-like domains 3	-0.3215	0.021
16884285	LOC440895	two pore channel 3 pseudogene	-0.4662	0.0157
16884357			-0.5335	0.0047
16884360			-0.2885	0.0445
16884461	TTL	tubulin tyrosine ligase	-0.3767	0.0039
16884520			-0.1813	0.0482
16884523	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	-0.3768	0.0192
16884703	CBWD1	COBW domain containing 1	-0.3588	0.0107
16884827	DPP10	dipeptidyl-peptidase 10 (non-functional)	-1.0566	0.003
16884877	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-0.4028	0.0023
16884903			-0.2517	0.0138
16885028	TMEM177	transmembrane protein 177	-0.2337	0.044
16885041	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	-0.3347	0.0161
16885189	RNU4ATAC	RNA, U4atac small nuclear (U12-dependent splicing)	-0.5235	0.0249
16885191	LOC254128	uncharacterized LOC254128	-0.2209	0.0444
16885421	SFT2D3	SFT2 domain containing 3	-0.2489	0.0047
16885526	IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-0.2628	0.0131
16885874	MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-0.5192	0.0001
16885913	CCNT2	cyclin T2	-0.3622	0.0078

16885978	R3HDM1	R3H domain containing 1	-0.36	0.0119
16886020	UBXN4	UBX domain protein 4	-0.2421	0.01
16886246	ZEB2-AS1	ZEB2 antisense RNA 1 (non-protein coding)	-0.3609	0.0131
16886356	EPC2	enhancer of polycomb homolog 2 (Drosophila)	-0.3144	0.0337
16886503	RIF1	RAP1 interacting factor homolog (yeast)	-0.4415	0.0022
16886558			-0.4049	0.0262
16886564	FMNL2	formin-like 2	-0.6411	0.0011
16886602	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	-0.6003	0.0014
16886710			-1.0337	0.0407
16886854	LOC100505957	uncharacterized LOC100505957	-0.4144	0.034
16886864	7-Mar	membrane-associated ring finger (C3HC4) 7, E3 ubiquitin protein ligase	-0.4815	0.0004
16887118	LOC100506134	uncharacterized LOC100506134	-0.2198	0.0301
16887463	SP5	Sp5 transcription factor	-0.2359	0.0357
16887635	HAT1	histone acetyltransferase 1	-0.4159	0.0015
16887736	PDK1	pyruvate dehydrogenase kinase, isozyme 1	-1.1387	0.0001
16887900			-0.4722	0.0422
16887906			-0.1579	0.0351
16887945	HOXD9	homeobox D9	-0.4121	0.027
16887962	HOXD3	homeobox D3	-0.3429	0.0203
16888412	NUP35	nucleoporin 35kDa	-0.2398	0.0263
16889113			-0.3959	0.0392
16889126	HSPE1-MOB4	HSPE1-MOB4 readthrough	-1.1001	0
16889154	MARS2	methionyl-tRNA synthetase 2, mitochondrial	-0.3452	0.0016
16889251	SGOL2	shugoshin-like 2 (S. pombe)	-0.2537	0.0279
16889602	NOP58	NOP58 ribonucleoprotein homolog (yeast)	-0.3388	0.0066
16889631	SNORD11	small nucleolar RNA, C/D box 11	-0.5031	0.0088
16889711			-0.4826	0.0431
16889715			-0.5273	0.0417
16889718			-0.889	0.0107
16889721			-0.8041	0.0271
16889722			-0.5872	0.0358
16889726			-0.8161	0.0074
16889741			-1.1019	0.0007
16889745			-0.8643	0.0407
16889753			-0.5847	0.0435
16889757			-0.882	0.0168
16889758			-0.6542	0.0274
16889759			-1.0399	0.0378
16889779	ABI2	abl-interactor 2	-0.4928	0.0097
16889929			-0.5303	0.0117
16889938	EEF1B2	eukaryotic translation elongation factor 1 beta 2	-0.2184	0.0413
16890118	LOC100507443	uncharacterized LOC100507443	-0.1819	0.022
16890126	PIKFYVE	phosphoinositide kinase, FYVE finger containing	-0.3195	0.0391
16890490	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	-0.3099	0.0137
16890611			-2.5213	0.0001
16890651	RPL37A	ribosomal protein L37a	-0.1562	0.0136
16890716			-0.2992	0.0346
16890915	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-0.4144	0.0003
16891176	ANKZF1	ankyrin repeat and zinc finger domain containing 1	-0.3794	0.0355
16891403	INHA	inhibin, alpha	-1.8912	0
16891409	STK11IP	serine/threonine kinase 11 interacting protein	-0.1897	0.0475
16891453	SLC4A3	solute carrier family 4, anion exchanger, member 3	-0.4529	0.0308
16891523			-0.1165	0.0459
16891603	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	-0.2587	0.0197
16891752	AGFG1	ArfGAP with FG repeats 1	-0.2915	0.0361
16892039	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-0.2234	0.0448

16892153	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	-0.2766	0.0284
16892321	EIF4E2	eukaryotic translation initiation factor 4E family member 2	-0.2787	0.0255
16892356	GIGYF2	GRB10 interacting GYF protein 2	-0.2913	0.0258
16892418			-0.2852	0.0457
16892555	DGKD	diacylglycerol kinase, delta 130kDa	-0.5397	0.0002
16892781	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	-0.3122	0.0376
16893414	ANO7	anoctamin 7	-0.1805	0.0155
16893452			-0.8453	0.0061
16893453			-1.1219	0.0022
16893455			-0.6494	0.0259
16893456			-0.6257	0.0077
16893464			-0.8178	0.0212
16893474			-0.8045	0.0066
16893482	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	-0.3111	0.0278
16893634	GAL3ST2	galactose-3-O-sulfotransferase 2	-0.2522	0.0341
16893663			-0.1517	0.0284
16893709	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	-0.8596	0.0001
16893748	FAM150B	family with sequence similarity 150, member B	-0.6255	0.0063
16893773	TMEM18	transmembrane protein 18	-0.3384	0.0063
16893846	PXDN	peroxidasin homolog (Drosophila)	-0.5776	0.0046
16893986	TSSC1-IT1	TSSC1 intronic transcript 1 (non-protein coding)	-0.5482	0.0031
16893989	TRAPPC12-AS1	TRAPPC12 antisense RNA 1 (non-protein coding)	-0.3519	0.0129
16894155			-0.2305	0.032
16894181	LINC00299	long intergenic non-protein coding RNA 299	-0.356	0.0335
16894335	ADAM17	ADAM metallopeptidase domain 17	-0.3974	0.0068
16894883	MATN3	matrilin 3	-0.9504	0.0357
16894967			-0.4691	0.0025
16894998	C2orf43	chromosome 2 open reading frame 43	-0.4909	0.0144
16895118	ATAD2B	ATPase family, AAA domain containing 2B	-0.3613	0.0049
16895262	LOC100507630	uncharacterized LOC100507630	-0.1957	0.0036
16895530	OTOF	otoferlin	-0.1674	0.0287
16896256	MEMO1	mediator of cell motility 1	-0.2369	0.0392
16896315	RN5S91	RNA, 5S ribosomal 91	-0.2433	0.0407
16896481	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	-0.4303	0.0005
16896502	PRKD3	protein kinase D3	-0.8113	0.0363
16896557			-0.495	0.0361
16896579	ATL2	atlastin GTPase 2	-0.4362	0.0135
16896744	SOS1-IT1	SOS1 intronic transcript 1 (non-protein coding)	-0.2495	0.0328
16896816	THUMPD2	THUMP domain containing 2	-0.2741	0.0286
16896905	KCNG3	potassium voltage-gated channel, subfamily G, member 3	-0.6225	0.0033
16897221			-0.2197	0.0474
16897313	CALM2	calmodulin 2 (phosphorylase kinase, delta)	-0.2117	0.0268
16897560	PSME4	proteasome (prosome, macropain) activator subunit 4	-0.5315	0.0021
16897631			-0.5978	0.0372
16897634			-0.5549	0.0447
16897719	CCDC88A	coiled-coil domain containing 88A	-0.4115	0.0382
16897946	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-0.6981	0.0005
16898002	USP34	ubiquitin specific peptidase 34	-0.5996	0.0027
16898110	XPO1	exportin 1 (CRM1 homolog, yeast)	-0.284	0.0052
16898157			-0.2307	0.0265
16898160	FAM161A	family with sequence similarity 161, member A	-0.3466	0.043
16898403	SPRED2	sprouty-related, EVH1 domain containing 2	-0.3424	0.0428
16898496			-0.3211	0.0183
16898601	NFU1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	-0.2236	0.0476
16898617	AAK1	AP2 associated kinase 1	-0.2392	0.0452
16898665	ASPRV1	aspartic peptidase, retroviral-like 1	-0.2278	0.0219

16898911	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	-0.3806	0.0391
16898954			-0.2427	0.0191
16899288	LBX2	ladybird homeobox 2	-0.3877	0.0197
16899335	AUP1	ancient ubiquitous protein 1	-0.3493	0.026
16899729	C2orf68	chromosome 2 open reading frame 68	-0.2393	0.028
16899764	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	-0.5082	0.0133
16899788			-0.4755	0.0027
16899846	IMMT	inner membrane protein, mitochondrial	-0.3264	0.0103
16899970	LOC285074	anaphase promoting complex subunit 1 pseudogene	-0.2751	0.0248
16899985	RGPD2	RANBP2-like and GRIP domain containing 2	-0.2516	0.0312
16900474	SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	-0.3759	0.0042
16900475			-0.4177	0.0036
16900479			-0.4394	0.0263
16900483			-0.4239	0.0144
16900484			-0.3469	0.0404
16900487			-0.4264	0.0028
16900488			-0.5663	0.0177
16900489			-0.5923	0.0347
16900490			-0.4133	0.0106
16900492			-0.4847	0.0456
16900494			-0.3573	0.0336
16900497			-0.4128	0.0191
16900505			-0.4348	0.0023
16900507			-0.5852	0.0024
16900508			-0.4642	0.0026
16900509			-0.4918	0.0006
16900510			-0.3884	0.0141
16900511			-0.7308	0.0202
16900512			-0.9789	0.0065
16900514			-0.4935	0.0087
16900515			-0.6444	0.0015
16900516			-0.4232	0.0167
16900520			-0.4323	0.002
16900521			-0.4056	0.0227
16900522			-0.4796	0.0008
16900523			-0.3415	0.0146
16900526			-0.3762	0.0322
16900527			-0.366	0.017
16900529			-0.4448	0.0216
16900530			-0.3651	0.0096
16900532			-0.5179	0.0008
16900533			-0.5827	0.0416
16900608	ANKRD39	ankyrin repeat domain 39	-0.1937	0.0187
16900718			-0.303	0.012
16900724			-0.3244	0.0259
16900783	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	-0.3421	0.0476
16900856			-0.3442	0.0388
16901027	REV1	REV1, polymerase (DNA directed)	-0.3976	0.0342
16901158	NPAS2	neuronal PAS domain protein 2	-0.3062	0.0054
16901393	FHL2	four and a half LIM domains 2	-0.5619	0.0405
16901699	LIMS3	LIM and senescent cell antigen-like domains 3	-0.544	0.0087
16901716	RGPD6	RANBP2-like and GRIP domain containing 6	-0.2024	0.04
16901755	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-1.0315	0.001
16901825	MIR4435-1	microRNA 4435-1	-0.3127	0.0004
16901827			-0.5933	0.0147
16901830	ANAPC1	anaphase promoting complex subunit 1	-0.2413	0.0113
16901894	ZC3H8	zinc finger CCCH-type containing 8	-0.2801	0.0301
16901912	RGPD8	RANBP2-like and GRIP domain containing 8	-0.2175	0.0231
16901957	CKAP2L	cytoskeleton associated protein 2-like	-1.0348	0.0015

16902035			-0.4307	0.0084
16902064	SLC35F5	solute carrier family 35, member F5	-0.3884	0.028
16902101			-0.2837	0.026
16902118			-0.5484	0.0053
16902134	LOC389023	uncharacterized LOC389023	-1.0741	0.0026
16902296	CLASP1	cytoplasmic linker associated protein 1	-0.493	0.0037
16902353			-0.4924	0.0379
16902357	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	-0.4217	0.0107
16902567			-0.2236	0.0151
16902603	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	-0.4262	0.0049
16902611	AMMECR1L	AMME chromosomal region gene 1-like	-0.3484	0.0401
16902664	LOC151121	uncharacterized LOC151121	-0.1303	0.0167
16902794	CCDC115	coiled-coil domain containing 115	-0.2258	0.0286
16902865	FAM168B	family with sequence similarity 168, member B	-0.3717	0.0174
16903026			-0.3411	0.0165
16903065			-0.4158	0.0237
16903090	MCM6	minichromosome maintenance complex component 6	-0.5538	0.0143
16903111	DARS	aspartyl-tRNA synthetase	-0.4196	0.0083
16903327	GTDC1	glycosyltransferase-like domain containing 1	-0.3671	0.0055
16903356	ZEB2	zinc finger E-box binding homeobox 2	-0.3712	0.0136
16903403			-0.1302	0.0334
16903427	ORC4	origin recognition complex, subunit 4	-0.3517	0.0262
16903461	MMADHC	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	-0.2637	0.0118
16903529	RBM43	RNA binding motif protein 43	-0.377	0.0093
16903815	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-0.3186	0.0083
16904039	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	-0.3914	0.0256
16904097			-0.4849	0.0441
16904588	TTC21B	tetratricopeptide repeat domain 21B	-0.4477	0.0003
16904780	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.8843	0.0012
16905127			-0.2207	0.0422
16905407	LOC100129455	uncharacterized LOC100129455	-0.3236	0.0091
16906352	COL5A2	collagen, type V, alpha 2	-0.5601	0.0084
16906962	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.5945	0
16907029			-0.1729	0.0021
16907087	TYW5	tRNA-yW synthesizing protein 5	-0.4624	0.0024
16907482			-0.6334	0.0192
16907718			-0.2666	0.0212
16907758	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	-0.5737	0.0016
16907960	BARD1	BRCA1 associated RING domain 1	-0.476	0.0423
16908197	IGFBP5	insulin-like growth factor binding protein 5	-0.9353	0.0182
16908373	USP37	ubiquitin specific peptidase 37	-0.5706	0.0015
16908415	ZNF142	zinc finger protein 142	-0.3435	0.0091
16908433	RNF25	ring finger protein 25	-0.2333	0.0346
16908557	NHEJ1	nonhomologous end-joining factor 1	-0.3441	0.0489
16908618	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	-0.5992	0.0036
16908656	ATG9A	autophagy related 9A	-0.3544	0.0197
16908834	OBSL1	obscurin-like 1	-0.4707	0.0076
16908897	EPHA4	EPH receptor A4	-0.6151	0.0439
16908948	FARSB	phenylalanyl-tRNA synthetase, beta subunit	-0.3934	0.0001
16908972			-0.2644	0.0017
16909021	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	-0.7492	0.0348
16909524	SNORD20	small nucleolar RNA, C/D box 20	-0.6703	0.0138
16909532	NMUR1	neuromedin U receptor 1	-0.2615	0
16909595	KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	-0.2954	0.0383
16909700	HJURP	Holliday junction recognition protein	-0.6644	0.0007

16909828	COL6A3	collagen, type VI, alpha 3	-0.9156	0.0036
16909882			-0.1507	0.0348
16909993			-0.616	0.0028
16910295	LOC200772	uncharacterized LOC200772	-0.1404	0.0437
16910312			-0.3627	0.0332
16910501	DTYMK	deoxythymidylate kinase (thymidylate kinase)	-0.2686	0.0314
16910523			-0.2001	0.0226
16910609	TRIB3	tribbles homolog 3 (Drosophila)	-0.3732	0.0009
16910766	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	-0.1157	0.0217
16911145			-0.6694	0.0194
16911455			-0.201	0.0455
16912379	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-0.8669	0.0281
16913090	GDF5OS	growth differentiation factor 5 opposite strand	-0.1369	0.0304
16913731			-0.6696	0.0172
16913957	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-0.3658	0.033
16914117	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	-0.26	0.0424
16914169			-0.1674	0.0461
16914315	UBE2C	ubiquitin-conjugating enzyme E2C	-0.5911	0.0426
16914757	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	-0.3979	0.0067
16914823	LOC100506115	uncharacterized LOC100506115	-0.2206	0.0452
16915064	FAM209A	family with sequence similarity 209, member A	-0.3131	0.0104
16915091	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	-0.6188	0.0478
16915564			-0.3416	0.0004
16916920	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	-0.4817	0.046
16917183	JAG1	jagged 1	-0.8155	0.0483
16917822	FOXA2	forkhead box A2	-0.5036	0.0263
16917867	LOC200261	uncharacterized LOC200261	-0.1762	0.0211
16917963	CST2	cystatin SA	-1.4966	0.0407
16917969	CST5	cystatin D	-1.4441	0.0335
16918196			-0.3799	0.0217
16918445	E2F1	E2F transcription factor 1	-0.3834	0.0161
16918473	LOC100505490	uncharacterized LOC100505490	-0.3847	0.0037
16918755	FER1L4	fer-1-like 4 (C. elegans) pseudogene	-0.1756	0.0288
16920241			-0.1689	0.0234
16920244	LOC100506153	uncharacterized LOC100506153	-0.2012	0.0388
16920470			-0.126	0.0337
16920548	AURKA	aurora kinase A	-0.4291	0.0318
16921224	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	-0.1356	0.0384
16921525	RN5S488	RNA, 5S ribosomal 488	-0.1281	0.0278
16921565			-0.3479	0.003
16921574			-0.3594	0.0245
16921578			-0.4229	0.0297
16922028			-0.196	0.0138
16922047	GRIK1-AS2	GRIK1 antisense RNA 2 (non-protein coding)	-0.3207	0.0402
16922130	MIS18A-AS1	MIS18A antisense RNA 1 (non-protein coding)	-0.3765	0.0041
16922243	IL10RB	interleukin 10 receptor, beta	-0.4645	0.0137
16922636			-0.2343	0.0191
16922809			-0.1142	0.0451
16922899	PCP4	Purkinje cell protein 4	-1.5306	0.0118
16923417	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	-0.2581	0.0441
16923692	FAM207A	family with sequence similarity 207, member A	-0.1669	0.036
16923745			-0.4958	0.0025
16923766	COL18A1	collagen, type XVIII, alpha 1	-0.3311	0.0364
16924007	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	-0.2481	0.0047
16924061	DIP2A-IT1	DIP2A intronic transcript 1 (non-protein coding)	-0.3602	0.0236

16924101	TEKT4P2	tektin 4 pseudogene 2	-0.4092	0.0071
16924207	HSPA13	heat shock protein 70kDa family, member 13	-0.3248	0.023
16924260			-0.3423	0.0053
16924709	RWDD2B	RWD domain containing 2B	-0.5055	0.0191
16924719	CCT8	chaperonin containing TCP1, subunit 8 (theta)	-0.2672	0.0235
16924828	KRTAP19-2	keratin associated protein 19-2	-0.3299	0.0438
16924920	KRTAP19-8	keratin associated protein 19-8	-0.2415	0.0077
16924928	SCAF4	SR-related CTD-associated factor 4	-0.2707	0.008
16924976			-0.1979	0.0218
16925194	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	-0.4626	0.0003
16925239	DONSON	downstream neighbor of SON	-0.3937	0.0007
16925328	KCNE1	potassium voltage-gated channel, Isk-related family, member 1	-0.1738	0.0273
16925689	BRWD1	bromodomain and WD repeat domain containing 1	-0.2727	0.0211
16925749	BRWD1-IT2	BRWD1 intronic transcript 2 (non-protein coding)	-0.2748	0.0186
16925983	C2CD2	C2 calcium-dependent domain containing 2	-0.8301	0.0009
16926006	C2CD2	C2 calcium-dependent domain containing 2	-0.5759	0.0053
16926011	ZNF295	zinc finger protein 295	-0.2828	0.0187
16926022	C21orf128	chromosome 21 open reading frame 128	-0.1687	0.0291
16926087	WDR4	WD repeat domain 4	-0.2435	0.0311
16926111	CBS	cystathionine-beta-synthase	-0.2992	0.0043
16926148	U2AF1	U2 small nuclear RNA auxiliary factor 1	-0.276	0.0062
16926238			-0.2128	0.0109
16926412	UBE2G2	ubiquitin-conjugating enzyme E2G 2	-0.2718	0.0083
16926527	POFUT2	protein O-fucosyltransferase 2	-0.2166	0.0064
16926547			-0.229	0.0363
16926570	SLC19A1	solute carrier family 19 (folate transporter), member 1	-0.2769	0.0097
16926644	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	-0.6955	0.0223
16926679	MCM3AP	minichromosome maintenance complex component 3 associated protein	-0.2098	0.0344
16926768			-0.2893	0.0046
16926893	BCL2L13	BCL2-like 13 (apoptosis facilitator)	-0.3935	0.0095
16926922	PEX26	peroxisomal biogenesis factor 26	-0.299	0.0361
16927001	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	-0.3336	0.049
16927052	CDC45	cell division cycle 45 homolog (S. cerevisiae)	-0.4582	0.0065
16927082	SEPT5-GP1BB	SEPT5-GP1BB readthrough	-0.2587	0.006
16927198	RANBP1	RAN binding protein 1	-0.4278	0.001
16927283			-0.2061	0.0288
16927292	ZNF74	zinc finger protein 74	-0.2128	0.042
16927401	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-0.298	0.0273
16927486	THAP7-AS1	THAP7 antisense RNA 1 (non-protein coding)	-0.3343	0.0117
16927588	HIC2	hypermethylated in cancer 2	-0.2122	0.0426
16927615	UBE2L3	ubiquitin-conjugating enzyme E2L 3	-0.3181	0.0049
16928098	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-0.3511	0.0141
16928109	DDTL	D-dopachrome tautomerase-like	-0.4162	0.0067
16928115	GSTT2	glutathione S-transferase theta 2	-1.1653	0.0459
16928212	SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1-like	-0.3875	0.0217
16928282	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	-0.373	0.0079
16928337	TOP1P2	topoisomerase (DNA) I pseudogene 2	-0.1538	0.0052
16928372	KIAA1671	KIAA1671	-0.403	0.0176
16928415	CRYBB2P1	crystallin, beta B2 pseudogene 1	-0.322	0.0467
16928550			-0.5276	0.0041
16928553	CRYBA4	crystallin, beta A4	-0.1133	0.0449
16928642	TTC28-AS1	TTC28 antisense RNA 1 (non-protein coding)	-0.2359	0.0243
16928668	HSCB	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	-0.3352	0.037

16928761	EWSR1	Ewing sarcoma breakpoint region 1	-0.3157	0.0052
16928824	NF2	neurofibromin 2 (merlin)	-0.4393	0.0081
16928861	UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	-0.4338	0.0067
16928867	MTMR3	myotubularin related protein 3	-0.4475	0.0064
16928967	MTFP1	mitochondrial fission process 1	-0.5378	0.0124
16929049	MIR3200	microRNA 3200	-0.3031	0.0103
16929056	TUG1	taurine upregulated 1 (non-protein coding)	-0.464	0.0003
16929064	SMTN	smoothelin	-0.2373	0.0002
16929193			-0.1927	0.047
16929203	DRG1	developmentally regulated GTP binding protein 1	-0.4694	0.0083
16929218			-0.3158	0.0096
16929416	FBXO7	F-box protein 7	-0.3524	0.0078
16929442	TIMP3	TIMP metallopeptidase inhibitor 3	-0.8902	0.001
16929459			-0.4143	0.0116
16929509	HMGXB4	HMG box domain containing 4	-0.4603	0.0008
16929562	HMOX1	heme oxygenase (decycling) 1	-0.4664	0.0352
16929573	MCM5	minichromosome maintenance complex component 5	-0.4359	0.0299
16929610	RASD2	RASD family, member 2	-0.586	0.0094
16929719	KCTD17	potassium channel tetramerisation domain containing 17	-0.4273	0.0058
16929782	GGA1	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	-0.2263	0.0382
16929849	PDXP	pyridoxal (pyridoxine, vitamin B6) phosphatase	-0.3887	0.0063
16929882	TRIOBP	TRIO and F-actin binding protein	-0.3793	0.0019
16929920	H1F0	H1 histone family, member 0	-0.6745	0.0327
16929943	EIF3L	eukaryotic translation initiation factor 3, subunit L	-0.3821	0.0328
16930100	GTPBP1	GTP binding protein 1	-0.2417	0.0349
16930144	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	-0.2085	0.0341
16930226	SYNGR1	synaptogyrin 1	-0.2649	0.0076
16930238	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	-0.3189	0.0017
16930271	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	-0.273	0.0337
16930299	ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	-0.5392	0.0004
16930418	ADSL	adenylosuccinate lyase	-0.3322	0.0357
16930518	RBX1	ring-box 1, E3 ubiquitin protein ligase	-0.405	0.0065
16930534	EP300	E1A binding protein p300	-0.3744	0.0199
16930568			-0.3309	0.0324
16930598	ZC3H7B	zinc finger CCCH-type containing 7B	-0.4058	0.039
16930678	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	-0.3013	0.0263
16930758	CCDC134	coiled-coil domain containing 134	-0.6674	0.0002
16930768	SREBF2	sterol regulatory element binding transcription factor 2	-0.8373	0.0003
16930947	BIK	BCL2-interacting killer (apoptosis-inducing)	-0.3762	0.0049
16931169	NUP50	nucleoporin 50kDa	-0.4073	0.0099
16931384	GTSE1	G-2 and S-phase expressed 1	-0.5303	0.0069
16931647	TRABD	TraB domain containing	-0.3088	0.0209
16931677	PPP6R2	protein phosphatase 6, regulatory subunit 2	-0.3713	0.0026
16931729	NCAPH2	non-SMC condensin II complex, subunit H2	-0.1774	0.0135
16931856			-0.1243	0.0325
16931942	CECR5	cat eye syndrome chromosome region, candidate 5	-0.3702	0.0034
16932006			-0.4394	0.0109
16932025	MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	-0.2872	0.0362
16932079			-0.3023	0.008
16932204	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	-0.455	0.0199
16932217	CLTCL1	clathrin, heavy chain-like 1	-0.6109	0.0028
16932261	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	-0.3263	0.0131
16932300	UFD1L	ubiquitin fusion degradation 1 like (yeast)	-0.4103	0.0068

16932341	GNB1L	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-0.2465	0.0145
16932420	TRMT2A	tRNA methyltransferase 2 homolog A (S. cerevisiae)	-0.1977	0.0307
16932526			-0.3434	0.0225
16932732			-0.2586	0.0024
16932831	MAPK1	mitogen-activated protein kinase 1	-0.3999	0.0012
16932914	ZNF280B	zinc finger protein 280B	-0.7651	0.0018
16933044	ZNF70	zinc finger protein 70	-0.3758	0.0099
16933049	VPREB3	pre-B lymphocyte 3	-1.156	0.0229
16933055	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	-0.2455	0.0116
16933088	GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)	-1.1112	0.0438
16933097	DDT	D-dopachrome tautomerase	-0.5885	0.001
16933249			-0.2422	0.0232
16933265	LRP5L	low density lipoprotein receptor-related protein 5-like	-0.1863	0.0327
16933445	PITPNB	phosphatidylinositol transfer protein, beta	-0.364	0.009
16933470	TTC28	tetratricopeptide repeat domain 28	-0.376	0.0129
16933502	CHEK2	checkpoint kinase 2	-0.3862	0.0051
16933564	RHBDD3	rhomboid domain containing 3	-0.247	0.0384
16933630	THOC5	THO complex 5	-0.4365	0.0115
16933774	GATSL3	GATS protein-like 3	-0.2684	0.0498
16933795	TBC1D10A	TBC1 domain family, member 10A	-0.2121	0.0478
16933931	PES1	pescadillo ribosomal biogenesis factor 1	-0.3423	0.0176
16934075	EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1	-0.3681	0.0101
16934109	PISD	phosphatidylserine decarboxylase	-0.327	0.0253
16934140	PRR14L	proline rich 14-like	-0.3714	0.0031
16934227	C22orf28	chromosome 22 open reading frame 28	-0.2723	0.0439
16934229			-0.8171	0.0387
16934230			-0.4913	0.0043
16934232			-0.7169	0.0178
16934234			-0.4137	0.0429
16934239			-0.462	0.0433
16934302			-1.1219	0.0003
16934558	TXN2	thioredoxin 2	-0.5789	0.0151
16934586			-0.4585	0.03
16934590			-0.4117	0.032
16934602			-0.4554	0.0473
16934844			-0.3248	0.0104
16934866	MIR659	microRNA 659	-0.3168	0.0156
16934970	TMEM184B	transmembrane protein 184B	-0.2357	0.029
16934991	CSNK1E	casein kinase 1, epsilon	-0.2464	0.0475
16935130	JOSD1	Josephin domain containing 1	-0.5161	0.0005
16935204			-0.4302	0.0049
16935244	SNORD83B	small nucleolar RNA, C/D box 83B	-0.2082	0.0057
16935320	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	-0.3209	0.0072
16935396	RANGAP1	Ran GTPase activating protein 1	-0.4475	0.008
16935432	PHF5A	PHD finger protein 5A	-0.416	0.0104
16935502			-0.6183	0.0005
16935505	SHISA8	shisa homolog 8 (Xenopus laevis)	-0.2144	0.0181
16935517	CENPM	centromere protein M	-0.3431	0.0259
16935623	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	-0.2569	0.0244
16935648	POLDIP3	polymerase (DNA-directed), delta interacting protein 3	-0.4814	0.0044
16935703	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3	-0.4829	0.0255
16935727	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	-0.3018	0.0228
16935775	TTLL12	tubulin tyrosine ligase-like family, member 12	-0.48	0.048
16935912	LDOC1L	leucine zipper, down-regulated in cancer 1-like	-0.426	0.0158
16935955	LOC100506714	uncharacterized LOC100506714	-0.2272	0.0241
16936230	BRD1	bromodomain containing 1	-0.1938	0.0272
16936253	LOC90834	uncharacterized protein BC001742	-0.2326	0.0132

16936397	MAPK12	mitogen-activated protein kinase 12	-0.2935	0.0055
16936408	MAPK12	mitogen-activated protein kinase 12	-0.1268	0.0227
16936535	SBF1	SET binding factor 1	-0.193	0.005
16936585	LMF2	lipase maturation factor 2	-0.2435	0.0284
16936761	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	-1.1376	0.034
16936816	CNTN6	contactin 6	-0.6558	0.0454
16936898			-0.1823	0.0337
16937201	SETD5	SET domain containing 5	-0.2434	0.0497
16937503	LOC442075	uncharacterized LOC442075	-0.2367	0.036
16938092	LOC100505696	uncharacterized LOC100505696	-0.5247	0.0024
16938098			-1.1967	0.0006
16938133	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	-0.5059	0.0016
16938182	PLCL2	phospholipase C-like 2	-0.5633	0.0064
16938269			-0.4349	0.0172
16938296	SGOL1-AS1	SGOL1 antisense RNA 1 (non-protein coding)	-0.5567	0.0267
16938313			-0.2094	0.0206
16938337			-0.1491	0.0319
16939046	VILL	villin-like	-0.1813	0.016
16939503			-0.5767	0.0237
16939524	ZNF620	zinc finger protein 620	-0.2729	0.0119
16939558	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	-0.3706	0.0408
16939729	HHATL-AS1	HHATL antisense RNA 1 (non-protein coding)	-0.2053	0.0021
16939731	LOC348817	uncharacterized LOC348817	-0.1818	0.0227
16939960	KIF15	kinesin family member 15	-0.5302	0.0137
16940190	CCRL2	chemokine (C-C motif) receptor-like 2	-0.2345	0.0173
16940239	PTH1R	parathyroid hormone 1 receptor	-0.2586	0.0441
16940332	FLJ39534	uncharacterized FLJ39534	-0.2445	0.0155
16940343	KLHL18	kelch-like 18 (Drosophila)	-0.2901	0.005
16940396			-0.6271	0.0141
16941344	ALAS1	aminolevulinate, delta-, synthase 1	-0.8628	0.0025
16942392	ATXN7	ataxin 7	-0.3731	0.0197
16943241	COL8A1	collagen, type VIII, alpha 1	-0.4526	0.0001
16943425			-0.3539	0.0035
16943763	PVRL3	poliovirus receptor-related 3	-0.8056	0.0013
16944894	UMPS	uridine monophosphate synthetase	-0.3055	0.0352
16946077	IL20RB	interleukin 20 receptor beta	-0.1719	0.0241
16946228	MRPS22	mitochondrial ribosomal protein S22	-0.3457	0.0169
16946429			-0.2916	0.0439
16946759			-0.1888	0.0355
16946835	WWTR1-AS1	WWTR1 antisense RNA 1 (non-protein coding)	-0.2548	0.0492
16947556	SMC4	structural maintenance of chromosomes 4	-0.5739	0.0127
16947974	FNDC3B	fibronectin type III domain containing 3B	-0.4517	0.0006
16948021	ECT2	epithelial cell transforming sequence 2 oncogene	-0.4735	0.0402
16948989	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	-0.2616	0.0201
16949011	CHRD	chordin	-0.2001	0.0099
16949286			-0.2017	0.0223
16949759	HES1	hairy and enhancer of split 1, (Drosophila)	-0.4365	0.012
16949814			-0.7984	0.0158
16949977			-0.1675	0.0029
16950895	RPL32	ribosomal protein L32	-0.3755	0.0063
16951150	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-0.5163	0.0002
16951354	PLCL2-AS1	PLCL2 antisense RNA 1 (non-protein coding)	-1.015	0.014
16951485	SGOL1	shugoshin-like 1 (S. pombe)	-0.8289	0.0047
16952198			-0.4894	0.0239
16952797	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	-0.1372	0.0259
16953123	SCAP	SREBF chaperone	-0.7712	0.0002
16953279	CDC25A	cell division cycle 25 homolog A (S. pombe)	-0.474	0.0044
16953597	SLC26A6	solute carrier family 26, member 6	-0.2596	0.037

16953753	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-0.4284	0.0131
16954066	RHOA-IT1	RHOA intronic transcript 1 (non-protein coding)	-0.259	0.0097
16954067			-0.259	0.0097
16954608	RN5S132	RNA, 5S ribosomal 132	-0.2816	0.0469
16954707	POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	-0.2937	0.0418
16954988	MUSTN1	musculoskeletal, embryonic nuclear protein 1	-0.368	0.0065
16955565	FAM107A	family with sequence similarity 107, member A	-0.3735	0.0088
16955935	LOC100508226	HHSL751	-0.3576	0.0407
16956386	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	-0.8173	0.0084
16956532	VGLL3	vestigial like 3 (Drosophila)	-0.363	0.0251
16956980			-0.8412	0.0281
16957396	CCDC80	coiled-coil domain containing 80	-0.6588	0.0429
16957874	LRRC58	leucine rich repeat containing 58	-0.4501	0.0497
16958356	ITGB5	integrin, beta 5	-0.3098	0.0336
16958972	SNORA7B	small nucleolar RNA, H/ACA box 7B	-0.4721	0.0291
16959985	ATR	ataxia telangiectasia and Rad3 related	-0.2939	0.014
16960046			-0.338	0.0419
16960149	PLSCR4	phospholipid scramblase 4	-0.6038	0.0079
16960371	WWTR1	WW domain containing transcription regulator 1	-0.274	0.0489
16961003	TRIM59	tripartite motif containing 59	-0.3242	0.0194
16961374	ACTRT3	actin-related protein T3	-0.3293	0.0034
16961607			-0.36	0.0402
16961637	NCEH1	neutral cholesterol ester hydrolase 1	-0.3338	0.0323
16962083	RN5S151	RNA, 5S ribosomal 151	-0.3246	0.024
16962213	CLCN2	chloride channel, voltage-sensitive 2	-0.5564	0.0004
16962380	ETV5	ets variant 5	-0.6117	0.0189
16962731			-0.1856	0.0264
16962907	CPN2	carboxypeptidase N, polypeptide 2	-1.3139	0.0308
16963113	APOD	apolipoprotein D	-1.1109	0.0065
16963241	TFRC	transferrin receptor (p90, CD71)	-0.6541	0.0081
16963509			-0.4883	0.0006
16963646			-0.4423	0.0362
16963873			-0.5034	0.0119
16964000	TACC3	transforming, acidic coiled-coil containing protein 3	-0.4543	0.0076
16964888	HTRA3	HtrA serine peptidase 3	-0.4041	0.0474
16965346	NCAPG	non-SMC condensin I complex, subunit G	-0.9355	0.0114
16965480			-0.2867	0.0212
16966008	KLF3	Kruppel-like factor 3 (basic)	-0.2678	0.0066
16967684			-0.2463	0.0334
16967771	IL8	interleukin 8	-0.5093	0.0095
16967853	AREG	amphiregulin	-0.3055	0.0309
16967863	AREG	amphiregulin	-0.2642	0.0034
16968051	11-Sep	septin 11	-0.5105	0.0269
16968488	WDFY3-AS2	WDFY3 antisense RNA 2 (non-protein coding)	-0.595	0.0123
16969495	NPNT	nephronectin	-0.6944	0.0363
16969817	C4orf32	chromosome 4 open reading frame 32	-0.4577	0.0163
16969988			-0.2966	0.0282
16970563	PLK4	polo-like kinase 4	-0.4462	0.0272
16971256	POU4F2	POU class 4 homeobox 2	-0.144	0.0495
16972098			-0.4437	0.0068
16972155	MSMO1	methylsterol monooxygenase 1	-0.8708	0.0436
16972607			-0.71	0.0113
16972616	NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0.6474	0.0074
16972842			-0.4602	0.0168
16972981			-0.6995	0.005
16974493			-0.6378	0.0263
16974779	GPR125	G protein-coupled receptor 125	-0.3946	0.01
16975032	FLJ45721	uncharacterized LOC401123	-0.1905	0.0008
16975305			-0.6179	0.0051

16976542			-0.3581	0.0017
16977153			-0.4494	0.0102
16977165			-0.3083	0.0341
16977709			-0.6324	0.007
16977810	HSD17B13	hydroxysteroid (17-beta) dehydrogenase 13	-0.1489	0.0467
16979515	CCNA2	cyclin A2	-1.0663	0.0049
16979917	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	-1.0706	0.0118
16980031	MAML3	mastermind-like 3 (Drosophila)	-0.4761	0.0113
16980364	ZNF827	zinc finger protein 827	-0.3458	0.0271
16980714	MIR3140	microRNA 3140	-0.1176	0.0459
16981077	MIR4454	microRNA 4454	-0.2893	0.0399
16981477			-0.2045	0.0245
16981730	VEGFC	vascular endothelial growth factor C	-0.95	0.004
16981887			-0.6456	0.0085
16981907	LOC389247	uncharacterized LOC389247	-0.2863	0.0405
16981929			-0.2518	0.0063
16981962	LOC728175	uncharacterized LOC728175	-0.3318	0.0032
16982183	SORBS2	sorbin and SH3 domain containing 2	-0.6276	0.0262
16982477			-0.7023	0.0201
16982508	LRRC14B	leucine rich repeat containing 14B	-0.1753	0.0136
16982635	TRIP13	thyroid hormone receptor interactor 13	-0.3129	0.0354
16982845			-0.1835	0.0018
16983148			-0.1587	0.0114
16983800	TARS	threonyl-tRNA synthetase	-0.422	0.0096
16984032	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	-0.6519	0.0035
16984080			-0.4546	0.0364
16984168			-0.183	0.0268
16984417			-0.2591	0.0463
16984629	RN5S182	RNA, 5S ribosomal 182	-0.3557	0.0098
16984646	ITGA1	integrin, alpha 1	-0.4677	0.0454
16986098			-1.9297	0.0009
16986249	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	-0.6169	0.0268
16987970	STARD4-AS1	STARD4 antisense RNA 1 (non-protein coding)	-0.3928	0.043
16989634			-0.1913	0.0253
16989636	KIF20A	kinesin family member 20A	-0.6445	0.0195
16990122			-0.4446	0.0415
16990716			-0.1921	0.0333
16991372	MIR1294	microRNA 1294	-0.2002	0.048
16991741	PTTG1	pituitary tumor-transforming 1	-0.2877	0.0376
16991760	MIR3142	microRNA 3142	-0.1429	0.0454
16992314			-0.2964	0.025
16993433	MAML1	mastermind-like 1 (Drosophila)	-0.2089	0.0238
16993574	BTNL9	butyrophilin-like 9	-0.1935	0.0159
16994211	LOC442132	golgin A6 family-like 1 pseudogene	-0.2475	0.0376
16995047	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	-0.7756	0.0266
16995140	RAD1	RAD1 homolog (S. pombe)	-0.3175	0.0167
16995461	GDNF	glial cell derived neurotrophic factor	-0.1943	0.0256
16995500	LIFR	leukemia inhibitory factor receptor alpha	-0.818	0.0183
16995863			-0.2604	0.0187
16995890	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	-1.0438	0.0202
16996234	PPAP2A	phosphatidic acid phosphatase type 2A	-0.437	0.0109
16996946	GUSBP3	glucuronidase, beta pseudogene 3	-0.3116	0.0257
16996971	GUSBP9	glucuronidase, beta pseudogene 9	-0.3088	0.0111
16997046	GUSBP9	glucuronidase, beta pseudogene 9	-0.3121	0.0369
16997146	FOXD1	forkhead box D1	-0.8037	0.0031
16997919	RN5S187	RNA, 5S ribosomal 187	-0.5585	0.038
16997931	LINC00461	long intergenic non-protein coding RNA 461	-0.4059	0.0111
16998044	LOC100505994	uncharacterized LOC100505994	-0.467	0.0108

16998526			-0.1442	0.0443
16998906	MCC	mutated in colorectal cancers	-0.3919	0.041
16999072			-0.2679	0.0094
16999475	FBN2	fibrillin 2	-0.9373	0.0189
16999575			-0.5165	0.0403
17000104	PITX1	paired-like homeodomain 1	-0.1627	0.0426
17000439	CDC25C	cell division cycle 25 homolog C (S. pombe)	-0.4994	0.0122
17001578	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	-0.7518	0.0148
17001843			-0.6512	0.0202
17002598	PANK3	pantothenate kinase 3	-0.341	0.0305
17003640	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	-0.3399	0.0132
17004198	FOXF2	forkhead box F2	-0.2977	0.0139
17004266	DKFZP686I15217	uncharacterized LOC401232	-0.2612	0.0068
17004335			-0.5619	0.032
17004431	C6orf201	chromosome 6 open reading frame 201	-0.2234	0.0101
17004447			-0.2288	0.0341
17004450	LOC100507506	uncharacterized LOC100507506	-0.3348	0.001
17004491	LOC100129461	uncharacterized LOC100129461	-0.3452	0.0252
17004497	PPP1R3G	protein phosphatase 1, regulatory subunit 3G	-0.647	0.0325
17004866			-0.9509	0.0075
17004879	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	-0.5379	0.001
17004987			-0.8786	0.0023
17005001	CD83	CD83 molecule	-1.5106	0
17005009			-1.1637	0
17005011	LOC100506631	uncharacterized LOC100506631	-0.2398	0.0276
17005023			-0.3937	0.0173
17005042	JARID2	jumonji, AT rich interactive domain 2	-0.4155	0.0242
17005108			-0.1935	0.0387
17005169	KDM1B	lysine (K)-specific demethylase 1B	-0.476	0.0497
17005420	LRRC16A	leucine rich repeat containing 16A	-0.4856	0.0353
17005532	HIST1H3A	histone cluster 1, H3a	-0.431	0.0456
17005589	HIST1H2AE	histone cluster 1, H2ae	-0.617	0.0114
17005593	HIST1H3E	histone cluster 1, H3e	-0.7441	0.0316
17005784			-0.1987	0.0012
17005790	HIST2H4B	histone cluster 2, H4b	-0.2424	0.0294
17005838	LOC100507173	uncharacterized LOC100507173	-0.1666	0.0455
17005844			-0.3489	0.0303
17005858	HIST1H2AI	histone cluster 1, H2ai	-0.9371	0.028
17005871	HIST1H2BN	histone cluster 1, H2bn	-0.9995	0.0016
17005904	ZNF192	zinc finger protein 192	-0.2802	0.0372
17006030			-0.1323	0.047
17006159	HCG9	HLA complex group 9 (non-protein coding)	-0.1878	0.0164
17006276	PRR3	proline rich 3	-0.4183	0.0011
17006291			-0.1498	0.0386
17006309			-0.5496	0.0377
17006374	MDC1-AS1	MDC1 antisense RNA 1 (non-protein coding)	-0.1936	0.0442
17006696	PRRC2A	proline-rich coiled-coil 2A	-0.3079	0.0147
17007029	STK19	serine/threonine kinase 19	-0.3507	0.0146
17007109	CYP21A1P	cytochrome P450, family 21, subfamily A, polypeptide 1 pseudogene	-1.3012	0.001
17007178	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.2775	0.0068
17007426	RPS18	ribosomal protein S18	-0.1607	0.0318
17007617			-0.1733	0.0098
17007824	FANCE	Fanconi anemia, complementation group E	-0.1746	0.0237
17007853	ARMC12	armadillo repeat containing 12	-0.1807	0.0206
17007965	KCTD20	potassium channel tetramerisation domain containing 20	-0.4187	0.0165
17007996	SRSF3	serine/arginine-rich splicing factor 3	-0.2292	0.0307
17008341	DAAM2	dishevelled associated activator of morphogenesis 2	-0.8211	0.0363

17008544	BYSL	bystin-like	-0.3971	0.0005
17008769	RRP36	ribosomal RNA processing 36 homolog (S. cerevisiae)	-0.5887	0.0017
17009008	TJAP1	tight junction associated protein 1 (peripheral)	-0.2721	0.0099
17009032	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	-0.2587	0.0317
17009054	POLH	polymerase (DNA directed), eta	-0.3304	0.0147
17009093	VEGFA	vascular endothelial growth factor A	-0.5568	0.0104
17009282			-0.1486	0.0216
17009558			-0.3584	0.0063
17009885	LOC100653079	uncharacterized LOC100653079	-0.1576	0.0092
17009930	PHF3	PHD finger protein 3	-0.3279	0.0193
17010419	SENP6	SUMO1/sentrin specific peptidase 6	-0.2486	0.0336
17010552	TTK	TTK protein kinase	-0.8765	0.0163
17010789	ZNF292	zinc finger protein 292	-0.4292	0.0015
17010851	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1	-0.3523	0.0128
17010874	C6orf165	chromosome 6 open reading frame 165	-0.3309	0.0132
17010876	ORC3	origin recognition complex, subunit 3	-0.3239	0.0396
17010904	AKIRIN2-AS1	AKIRIN2 antisense RNA 1 (non-protein coding)	-0.8536	0.0003
17010929	PNRC1	proline-rich nuclear receptor coactivator 1	-0.3593	0.0247
17010991	CASP8AP2	caspase 8 associated protein 2	-0.3604	0.0181
17011032	MIR4643	microRNA 4643	-0.5886	0.0397
17011182			-0.2996	0.0456
17011340	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	-0.3507	0.028
17011378	SOBP	sine oculis binding protein homolog (Drosophila)	-0.4686	0.0285
17011391			-0.6679	0.0095
17011496	CEP57L1	centrosomal protein 57kDa-like 1	-0.3472	0.0056
17011635	CDC40	cell division cycle 40 homolog (S. cerevisiae)	-0.2997	0.0455
17011843			-0.1728	0.0367
17011915			-0.2669	0.0227
17012108	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	-0.5354	0.0012
17012127			-0.3186	0.0209
17012130			-0.5621	0.0371
17012165	HSF2	heat shock transcription factor 2	-0.5751	0.0004
17012447	LAMA2	laminin, alpha 2	-1.1594	0.0092
17012559	AKAP7	A kinase (PRKA) anchor protein 7	-0.6664	0.0052
17012598	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-2.0818	0
17012699	RPS12	ribosomal protein S12	-0.5098	0.0112
17012709	SNORD100	small nucleolar RNA, C/D box 100	-0.5043	0.0269
17012859	PDE7B	phosphodiesterase 7B	-0.9182	0.0102
17013468	STXBP5	syntaxin binding protein 5 (tomosyn)	-0.5951	0.0359
17013554	UST	uronyl-2-sulfotransferase	-0.8252	0.0009
17013637	LOC100652739	uncharacterized LOC100652739	-0.284	0.0292
17013670			-0.3259	0.0021
17013837	SYNE1-AS1	SYNE1 antisense RNA 1 (non-protein coding)	-0.3497	0.0061
17013865			-0.5055	0.0005
17013920	SCAF8	SR-related CTD-associated factor 8	-0.3658	0.0044
17014004	CLDN20	claudin 20	-0.3405	0.0417
17014015	MIR1202	microRNA 1202	-0.1489	0.0252
17014031	ARID1B	AT rich interactive domain 1B (SWI1-like)	-0.3934	0.0002
17014091	SNX9	sorting nexin 9	-0.2196	0.0293
17014166			-0.611	0.022
17014186	TMEM181	transmembrane protein 181	-0.3997	0.0095
17014235	C6orf99	chromosome 6 open reading frame 99	-0.263	0.0102
17014309	ACAT2	acetyl-CoA acetyltransferase 2	-1.4076	0.0013
17014442	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	-0.918	0.0042
17014562	QKI	QKI, KH domain containing, RNA binding	-0.2819	0.0219
17014605			-0.2912	0.006
17014608	LINC00602	long intergenic non-protein coding RNA 602	-0.3391	0.007
17014630	FGFR1OP	FGFR1 oncogene partner	-0.3739	0.0063
17014835			-0.2044	0.0476

17014906	FAM120B	family with sequence similarity 120B	-0.1957	0.0343
17015240	ECI2	enoyl-CoA delta isomerase 2	-0.467	0.01
17015277	RPP40	ribonuclease P/MRP 40kDa subunit	-0.5597	0.0063
17015291			-0.5822	0.0025
17015752	RANBP9	RAN binding protein 9	-0.5515	0.0027
17015791			-0.2024	0.0409
17015862	ATXN1	ataxin 1	-0.3912	0.0399
17015975	TPMT	thiopurine S-methyltransferase	-0.6286	0.0141
17015987	DEK	DEK oncogene	-0.3671	0.0034
17016064			-0.4857	0.0369
17016085	LOC729177	uncharacterized LOC729177	-0.3678	0.0294
17016221	FAM65B	family with sequence similarity 65, member B	-0.4936	0.0136
17016363	HIST1H3B	histone cluster 1, H3b	-0.7996	0.0087
17016366	HIST1H2AB	histone cluster 1, H2ab	-0.4562	0.0138
17016400	HIST1H3F	histone cluster 1, H3f	-1.0534	0.0222
17016403	HIST1H3G	histone cluster 1, H3g	-1.2363	0.0179
17016406	HIST2H4B	histone cluster 2, H4b	-0.5746	0.0156
17016444	LOC100270746	uncharacterized LOC100270746	-0.2835	0.0223
17016457	HIST1H2BK	histone cluster 1, H2bk	-0.9443	0.0004
17016568	ZSCAN12	zinc finger and SCAN domain containing 12	-0.3057	0.0191
17016888	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3073	0.0121
17016966	MDC1	mediator of DNA-damage checkpoint 1	-0.2325	0.0288
17017172	ATP6V1G2-DDX39B	ATP6V1G2-DDX39B readthrough (non-protein coding)	-0.2665	0.0199
17017184			-0.8867	0.0288
17017187			-0.2593	0.0354
17017194			-0.5315	0.002
17017196			-0.4787	0.0184
17017198			-0.6109	0.0066
17017201			-0.8352	0.0119
17017219	SNORD117	small nucleolar RNA, C/D box 117	-0.5035	0.0056
17017220			-0.5035	0.0056
17017510	SLC44A4	solute carrier family 44, member 4	-1.2399	0.001
17017622	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17017625	TNXA	tenascin XA (pseudogene)	-1.0146	0.0001
17017638	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17017641	TNXB	tenascin XB	-0.3642	0.0117
17018186	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-0.2764	0.0021
17018240	DAXX	death-domain associated protein	-0.237	0.025
17018395			-0.9015	0.0143
17019134	USP49	ubiquitin specific peptidase 49	-0.2121	0.0319
17019199	GUCA1B	guanylate cyclase activator 1B (retina)	-0.2835	0.018
17019389	LRRC73	leucine rich repeat containing 73	-0.3405	0.034
17019425	XPO5	exportin 5	-0.6131	0
17019484	GTPBP2	GTP binding protein 2	-0.2587	0.0325
17019516	MRPS18A	mitochondrial ribosomal protein S18A	-0.3577	0.0028
17019549	MRPL14	mitochondrial ribosomal protein L14	-0.4225	0.008
17019574	TCTE1	t-complex-associated-testis-expressed 1	-0.1678	0.0463
17020019	MCM3	minichromosome maintenance complex component 3	-0.4491	0.0193
17020103	GSTA4	glutathione S-transferase alpha 4	-0.564	0.0141
17020118	ICK	intestinal cell (MAK-like) kinase	-0.5593	0.0265
17020152	ELOVL5	ELOVL fatty acid elongase 5	-0.5069	0.0043
17020174	GCLC	glutamate-cysteine ligase, catalytic subunit	-0.437	0.0002
17020727	MIR30A	microRNA 30a	-0.3117	0.0164
17021108			-0.4151	0.0242
17021122	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-0.3875	0.0056
17021162			-0.3823	0.0441
17021217	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	-0.5892	0.0106
17021323	TBX18	T-box 18	-0.6679	0.0213
17021385	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	-0.285	0.0088

17021452	RARS2	arginyl-tRNA synthetase 2, mitochondrial	-0.6638	0.0004
17021478	AKIRIN2	akirin 2	-0.7647	0
17021485			-0.3413	0.0327
17021628	MDN1	MDN1, midasin homolog (yeast)	-0.25	0.0216
17021778			-0.4482	0.0158
17021824	UFL1-AS1	UFL1 antisense RNA 1 (non-protein coding)	-0.2325	0.0381
17021978	CCNC	cyclin C	-0.3204	0.0212
17022295	SEC63	SEC63 homolog (S. cerevisiae)	-0.2545	0.0248
17022384			-0.694	0.034
17022623	REV3L	REV3-like, polymerase (DNA directed), zeta, catalytic subunit	-0.508	0.001
17022736	TUBE1	tubulin, epsilon 1	-0.7044	0.0009
17022754	LAMA4	laminin, alpha 4	-0.6707	0.0068
17022834			-0.4248	0.0178
17022854	HDAC2	histone deacetylase 2	-0.2729	0.0299
17022929	COL10A1	collagen, type X, alpha 1	-0.2825	0.045
17022939	TSPYL4	TSPY-like 4	-0.3392	0.0063
17022964	ZUFSP	zinc finger with UFM1-specific peptidase domain	-0.4417	0.0073
17022987	GPRC6A	G protein-coupled receptor, family C, group 6, member A	-0.9472	0.0354
17023066	CEP85L	centrosomal protein 85kDa-like	-0.2723	0.0488
17023484	ARHGAP18	Rho GTPase activating protein 18	-0.4338	0.0171
17023592	MED23	mediator complex subunit 23	-0.2121	0.0425
17023636			-0.3177	0.0053
17023638	OR2A4	olfactory receptor, family 2, subfamily A, member 4	-0.5526	0.0092
17023927	AHI1	Abelson helper integration site 1	-0.323	0.0262
17024002	FAM54A	family with sequence similarity 54, member A	-0.3787	0.0045
17024020	BCLAF1	BCL2-associated transcription factor 1	-0.255	0.0076
17024168			-2.2175	0.0019
17024362	ADAT2	adenosine deaminase, tRNA-specific 2	-0.312	0.0079
17024452	SHPRH	SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase	-0.2767	0.0125
17024549	LOC100128176	uncharacterized LOC100128176	-0.5716	0.0019
17024599	KATNA1	katanin p60 (ATPase containing) subunit A 1	-0.4714	0.0071
17024615	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	-0.4016	0.0002
17024653	LRP11	low density lipoprotein receptor-related protein 11	-0.7417	0.0007
17024667	LOC100507624	uncharacterized LOC100507624	-0.9209	0.003
17024669	RAET1E	retinoic acid early transcript 1E	-0.8056	0.0013
17024685			-0.7944	0.0054
17024746	ZBTB2	zinc finger and BTB domain containing 2	-0.4326	0.0145
17024775	SYNE1	spectrin repeat containing, nuclear envelope 1	-0.635	0.0042
17024980	FBXO5	F-box protein 5	-0.6929	0.0015
17025068			-0.2627	0.0453
17025070	TFB1M	transcription factor B1, mitochondrial	-0.3563	0.0162
17025130	TMEM242	transmembrane protein 242	-0.4231	0.0042
17025144			-0.1982	0.0397
17025152	SERAC1	serine active site containing 1	-0.6336	0.0001
17025294	LOC100129518	uncharacterized LOC100129518	-1.0528	0.003
17025359	LPA	lipoprotein, Lp(a)	-0.4121	0.022
17025417	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	-0.4274	0.0335
17025487	CAHM	colon adenocarcinoma hypermethylated (non-protein coding)	-0.4829	0.0021
17025551			-0.4487	0.0281
17025558			-0.8894	0.0038
17025560	SDIM1	stress responsive DNAJB4 interacting membrane protein 1	-0.8195	0.0058
17025564	LINC00473	long intergenic non-protein coding RNA 473	-1.3586	0.0003
17025844	THBS2	thrombospondin 2	-0.6932	0.0476
17025937	PHF10	PHD finger protein 10	-0.5105	0.0168
17025953			-0.3972	0.0252
17025982			-0.1704	0.0417

17025989	DLL1	delta-like 1 (Drosophila)	-0.3045	0.0397
17026056			-0.1654	0.0355
17026207	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442
17026668	DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	-0.1993	0.031
17026706	MDC1	mediator of DNA-damage checkpoint 1	-0.2278	0.0269
17026760	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17026890	SLC44A4	solute carrier family 44, member 4	-1.2633	0.0009
17027243			-0.1323	0.047
17027360	HCG9	HLA complex group 9 (non-protein coding)	-0.1878	0.0164
17027459	PRR3	proline rich 3	-0.4507	0.0009
17027555	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442
17027830	PRRC2A	proline-rich coiled-coil 2A	-0.3047	0.0152
17028041	C6orf48	chromosome 6 open reading frame 48	-0.4125	0.0386
17028157	STK19	serine/threonine kinase 19	-0.3001	0.0275
17028240	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.3939	0.009
17028475	RPS18	ribosomal protein S18	-0.1607	0.0318
17028781	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3144	0.0132
17028857	MDC1	mediator of DNA-damage checkpoint 1	-0.2002	0.0493
17029036	SNORD84	small nucleolar RNA, C/D box 84	-0.2938	0.0236
17029076	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17029363	SLC44A4	solute carrier family 44, member 4	-1.2399	0.001
17029475	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17029997	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-0.2764	0.0021
17030053	DAXX	death-domain associated protein	-0.2642	0.0114
17030090			-0.1323	0.047
17030203	HCG9	HLA complex group 9 (non-protein coding)	-0.1878	0.0164
17030304	PRR3	proline rich 3	-0.4507	0.0009
17030400	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442
17030577	MICB	MHC class I polypeptide-related sequence B	-0.2926	0.0167
17030589	MCCD1	mitochondrial coiled-coil domain 1	-0.1033	0.0222
17030655	PRRC2A	proline-rich coiled-coil 2A	-0.3124	0.0146
17031103	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.3984	0.009
17031289	RPS18	ribosomal protein S18	-0.1607	0.0318
17031560	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3144	0.0132
17031635	MDC1	mediator of DNA-damage checkpoint 1	-0.2278	0.0269
17031824	DDX39B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	-0.3234	0.0221
17031845	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17031847	SNORD84	small nucleolar RNA, C/D box 84	-0.2378	0.0357
17031857	SNORD84	small nucleolar RNA, C/D box 84	-0.3237	0.0222
17031933	GPANK1	G patch domain and ankyrin repeats 1	-0.1657	0.0168
17032149	SLC44A4	solute carrier family 44, member 4	-1.2399	0.001
17032261	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17032264			-0.6575	0.0001
17032681	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-0.2764	0.0021
17032737	DAXX	death-domain associated protein	-0.2642	0.0114
17032779			-0.1323	0.047
17032900	HCG9	HLA complex group 9 (non-protein coding)	-0.1946	0.01
17033009	PRR3	proline rich 3	-0.4183	0.0011
17033105	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442
17033306	MCCD1	mitochondrial coiled-coil domain 1	-0.1033	0.0222
17033360	PRRC2A	proline-rich coiled-coil 2A	-0.3039	0.015
17033974	HCG18	HLA complex group 18 (non-protein coding)	-0.3296	0.0332
17034014	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3073	0.0121
17034176			-0.213	0.0097
17034296	SNORD84	small nucleolar RNA, C/D box 84	-0.3481	0.0117
17034317	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17034319	SNORD84	small nucleolar RNA, C/D box 84	-0.2378	0.0357
17034329	SNORD84	small nucleolar RNA, C/D box 84	-0.3237	0.0222
17035060	HCG9	HLA complex group 9 (non-protein coding)	-0.1967	0.0231
17035129	PRR3	proline rich 3	-0.4183	0.0011
17035225	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442

17035453	PRRC2A	proline-rich coiled-coil 2A	-0.3077	0.0162
17035730	STK19	serine/threonine kinase 19	-0.3001	0.0275
17035809	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.3992	0.0088
17036038	RPS18	ribosomal protein S18	-0.1606	0.0361
17036281	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3073	0.0121
17036357	MDC1	mediator of DNA-damage checkpoint 1	-0.2002	0.0493
17036426			-0.213	0.0097
17036519	ATP6V1G2-DDX39B	ATP6V1G2-DDX39B readthrough (non-protein coding)	-0.2182	0.0475
17036544	DDX39B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	-0.3234	0.0221
17036565	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17036567	SNORD84	small nucleolar RNA, C/D box 84	-0.2378	0.0357
17036577	SNORD84	small nucleolar RNA, C/D box 84	-0.3237	0.0222
17036856	SLC44A4	solute carrier family 44, member 4	-1.2633	0.0009
17036968	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17037482	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-0.2764	0.0021
17037538	DAXX	death-domain associated protein	-0.272	0.0148
17037693	ZNRD1	zinc ribbon domain containing 1	-0.4241	0.0228
17037788	PRR3	proline rich 3	-0.4507	0.0009
17037884	MDC1	mediator of DNA-damage checkpoint 1	-0.322	0.0217
17038086	MCCD1	mitochondrial coiled-coil domain 1	-0.1033	0.0222
17038153	PRRC2A	proline-rich coiled-coil 2A	-0.3047	0.0152
17038330	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.3795	0.0097
17038759	RPS18	ribosomal protein S18	-0.1607	0.0318
17038792	KIFC1	kinesin family member C1	-0.3305	0.0461
17039057	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3144	0.0132
17039133	MDC1	mediator of DNA-damage checkpoint 1	-0.2659	0.022
17039337	DDX39B	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	-0.3234	0.0221
17039358	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17039360	SNORD84	small nucleolar RNA, C/D box 84	-0.2378	0.0357
17039370	SNORD84	small nucleolar RNA, C/D box 84	-0.3237	0.0222
17039600	SLC44A4	solute carrier family 44, member 4	-1.2559	0.0006
17039711	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17039714	TNXB	tenascin XB	-0.5015	0.0085
17040192	RGL2	ral guanine nucleotide dissociation stimulator-like 2	-0.2923	0.0013
17040248	DAXX	death-domain associated protein	-0.2586	0.0162
17040293			-0.1323	0.047
17040405	HCG9	HLA complex group 9 (non-protein coding)	-0.1946	0.01
17040502	PRR3	proline rich 3	-0.4507	0.0009
17040598	MDC1	mediator of DNA-damage checkpoint 1	-0.1936	0.0442
17040662			-0.3724	0.0211
17040748	PRRC2A	proline-rich coiled-coil 2A	-0.3047	0.0152
17041011	STK19	serine/threonine kinase 19	-0.3001	0.0275
17041090	CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	-1.3927	0.0088
17041345	RPS18	ribosomal protein S18	-0.1843	0.037
17041641	PPP1R10	protein phosphatase 1, regulatory subunit 10	-0.3144	0.0132
17041700	MDC1	mediator of DNA-damage checkpoint 1	-0.215	0.0326
17041815	SNORD84	small nucleolar RNA, C/D box 84	-0.3022	0.0125
17041857	SNORD117	small nucleolar RNA, C/D box 117	-0.5184	0.0071
17042117	SLC44A4	solute carrier family 44, member 4	-1.2633	0.0009
17042216	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17042219	C4A-AS1	C4A antisense RNA 1 (non-protein coding)	-0.6426	0.0143
17042222	TNXB	tenascin XB	-0.6757	0.0007
17042805	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae)	-0.4003	0.0118
17042824	LOC100505531	uncharacterized LOC100505531	-0.3526	0.0382
17042841			-0.2152	0.0388
17042946	EIF3B	eukaryotic translation initiation factor 3, subunit B	-0.33	0.011
17043177	SNORD13P2	small nucleolar RNA, C/D box 13 pseudogene 2	-0.5599	0.0128
17043294	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	-0.9337	0.0038
17043355	AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	-0.3872	0.0001

17043367	ANKRD61	ankyrin repeat domain 61	-0.2453	0.0283
17043380	USP42	ubiquitin specific peptidase 42	-0.2447	0.0126
17044423	CBX3	chromobox homolog 3	-0.4059	0.0148
17044426			-0.4717	0.0189
17044427			-0.7381	0.0133
17044428			-0.5003	0.005
17044431			-1.463	0.0001
17044432			-0.5406	0.003
17044438			-0.4909	0.0046
17044442	SNX10	sorting nexin 10	-0.5646	0.0407
17044491	HOXA-AS2	HOXA cluster antisense RNA 2 (non-protein coding)	-0.2395	0.0414
17044521	HOXA11-AS	HOXA11 antisense RNA (non-protein coding)	-1.0225	0.0018
17044800	GARS	glycyl-tRNA synthetase	-0.2528	0.0447
17044929	CCDC129	coiled-coil domain containing 129	-0.2059	0.0274
17045198	ANLN	anillin, actin binding protein	-0.9489	0.0219
17045528	HECW1-IT1	HECW1 intronic transcript 1 (non-protein coding)	-0.1416	0.0427
17045738	PPIA	peptidylprolyl isomerase A (cyclophilin A)	-0.3915	0.0064
17046254	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	-0.232	0.0237
17046458	LOC641746	glycine cleavage system protein H (aminomethyl carrier) pseudogene	-0.2583	0.0064
17046573	CCT6P1	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1	-0.2916	0.0215
17046595	VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1	-0.2523	0.0464
17046627	CRCP	CGRP receptor component	-0.2453	0.0365
17046673			-0.2431	0.0016
17046683	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	-0.268	0.0129
17046781	AUTS2	autism susceptibility candidate 2	-0.5115	0.0026
17047268			-0.2711	0.021
17047397	RHBDD2	rhomboid domain containing 2	-0.3928	0.034
17047411	POR	P450 (cytochrome) oxidoreductase	-0.4596	0.0041
17047965	DBF4	DBF4 homolog (S. cerevisiae)	-0.5222	0.001
17048473	COL1A2	collagen, type I, alpha 2	-0.6866	0.0253
17048563	PEG10	paternally expressed 10	-2.4602	0.0013
17048613	ASB4	ankyrin repeat and SOCS box containing 4	-1.9237	0.0004
17048625			-0.5916	0.0488
17049003	LOC100289187	transmembrane protein 225-like	-0.3821	0.0063
17049090	ZSCAN21	zinc finger and SCAN domain containing 21	-0.3422	0.0132
17049408	PCOLCE	procollagen C-endopeptidase enhancer	-1.011	0.0443
17049900			-0.1608	0.006
17049904	LRRC17	leucine rich repeat containing 17	-0.6627	0.0344
17049914	NFE4	transcription factor NF-E4	-0.8379	0.042
17050154	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	-1.0288	0.0011
17050443			-0.2212	0.0059
17050915			-0.2587	0.0313
17051626	MEST	mesoderm specific transcript homolog (mouse)	-0.6411	0.0326
17052040			-0.525	0.0319
17052286			-0.1763	0.0308
17052728	C7orf34	chromosome 7 open reading frame 34	-0.1456	0.0145
17052737	PIP	prolactin-induced protein	-0.1474	0.0214
17053892	INSIG1	insulin induced gene 1	-0.9969	0.0147
17054203			-0.6928	0.0381
17054341	MICALL2	MICAL-like 2	-0.2335	0.0339
17054611			-0.6292	0.0037
17054614	GNA12	guanine nucleotide binding protein (G protein) alpha 12	-0.1929	0.028
17054843			-0.9476	0.0033
17054846	LOC100653350	uncharacterized LOC100653350	-1.5164	0.0014
17055095	CCZ1B	CCZ1 vacuolar protein trafficking and biogenesis associated homolog B (S. cerevisiae)	-0.2636	0.0303
17055715	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-0.6135	0.0305
17055863	TRA2A	transformer 2 alpha homolog (Drosophila)	-0.2118	0.041

17056031	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	-0.2312	0.0312
17056160	HOXA10	homeobox A10	-0.2351	0.047
17056181	HOXA11	homeobox A11	-0.9204	0.0073
17056187			-0.6681	0.0019
17056192	HOXA13	homeobox A13	-0.6042	0.0371
17056198			-0.1968	0.0392
17056461	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-0.2232	0.0449
17056493	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	-0.417	0
17056992	GLI3	GLI family zinc finger 3	-0.5616	0.0319
17057130			-0.2589	0.036
17057174	POLD2	polymerase (DNA directed), delta 2, accessory subunit	-0.3824	0.0147
17057329	DDX56	DEAD (Asp-Glu-Ala-Asp) box helicase 56	-0.2429	0.0281
17057378	PURB	purine-rich element binding protein B	-0.5285	0.0001
17057424	NACAD	NAC alpha domain containing	-0.255	0.0302
17057677			-0.3042	0.0003
17057884	SEC61G	Sec61 gamma subunit	-0.1925	0.0245
17058226	LOC493754	RAB guanine nucleotide exchange factor (GEF) 1 pseudogene	-0.5195	0.0002
17058245			-0.2504	0.0454
17058351	SPDYE7P	speedy homolog E7 (Xenopus laevis), pseudogene	-0.2407	0.0294
17058891	STYXL1	serine/threonine/tyrosine interacting-like 1	-0.4286	0.0417
17058960			-0.3086	0.0226
17059451	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-1.1315	0.0048
17059628	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	-0.8194	0.0025
17059756	CDK6	cyclin-dependent kinase 6	-0.8126	0.0036
17059869			-0.8916	0.0127
17059872	SGCE	sarcoglycan, epsilon	-1.3786	0
17059932	PON2	paraoxonase 2	-0.3899	0.0163
17060057			-0.3301	0.0378
17060186	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	-0.5169	0.0077
17060412	MCM7	minichromosome maintenance complex component 7	-0.3895	0.046
17060677	TFR2	transferrin receptor 2	-0.3372	0.04
17060824	VGF	VGF nerve growth factor inducible	-0.6765	0.0322
17060894	CLDN15	claudin 15	-0.2069	0.0196
17061048	UPK3BL	uroplakin 3B-like	-0.2623	0.0223
17061097	RASA4	RAS p21 protein activator 4	-0.5345	0.0434
17061106	RASA4	RAS p21 protein activator 4	-0.3802	0.0375
17061133	RASA4	RAS p21 protein activator 4	-0.1425	0.0149
17061588			-0.5734	0.0378
17062253			-0.6408	0.0291
17062274			-0.1334	0.0493
17062578	MIR592	microRNA 592	-0.1188	0.0209
17062679	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	-0.521	0.0012
17063428	ZC3HAV1	zinc finger CCCH-type, antiviral 1	-0.3507	0.0032
17063573	RN5S248	RNA, 5S ribosomal 248	-0.2094	0.0465
17064105	EZH2	enhancer of zeste homolog 2 (Drosophila)	-0.554	0.0182
17064932	MIR153-2	microRNA 153-2	-0.4624	0.0288
17064984	ESYT2	extended synaptotagmin-like protein 2	-0.4306	0.0047
17065215			-0.2193	0.0144
17065219	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	-0.2853	0.0367
17065811	FDFT1	farnesyl-diphosphate farnesyltransferase 1	-0.8579	0.0058
17065933			-0.7696	0.0033
17065992	EFHA2	EF-hand domain family, member A2	-0.6284	0.0069
17066013			-0.2875	0.0483
17066203	NSAP11	nervous system abundant protein 11	-1.0556	0.0005
17066207			-0.7543	0.0068
17066209			-1.1321	0.0003
17066523	BMP1	bone morphogenetic protein 1	-0.4937	0.0056
17066650	SORBS3	sorbin and SH3 domain containing 3	-0.3385	0.0019

17067102	CDCA2	cell division cycle associated 2	-0.5041	0.0302
17067332	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	-0.2814	0.0346
17067363	ELP3	elongation protein 3 homolog (S. cerevisiae)	-0.329	0.0064
17068061			-0.3817	0.0348
17068136			-0.2315	0.0295
17068365			-0.213	0.0128
17068626			-0.535	0.0173
17068782	MCM4	minichromosome maintenance complex component 4	-0.5527	0.0062
17068814	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	-0.3342	0.0105
17069037			-0.7246	0.0469
17069515			-0.1664	0.0253
17069605	SGK3	serum/glucocorticoid regulated kinase family, member 3	-0.3585	0.0041
17069716	RN5S268	RNA, 5S ribosomal 268	-0.439	0.0122
17070245			-0.4465	0.0151
17070273	ZBTB10	zinc finger and BTB domain containing 10	-0.5431	0.0057
17070456	CA2	carbonic anhydrase II	-1.1606	0
17070478	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.1512	0.0197
17070695	LINC00534	long intergenic non-protein coding RNA 534	-0.2163	0.0489
17071983			-1.2977	0
17071994			-0.2488	0.0236
17072313	WDR67	WD repeat domain 67	-0.3651	0.0261
17072371			-0.6281	0.0192
17072375	WDYHV1	WDYHV motif containing 1	-0.5685	0.0061
17072552	SQLE	squalene epoxidase	-1.4088	0.0028
17072620			-0.3687	0.006
17072669	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-0.7043	0.0023
17072678	PVT1	Pvt1 oncogene (non-protein coding)	-0.3548	0.0136
17072718	PVT1	Pvt1 oncogene (non-protein coding)	-0.2772	0.0376
17072750			-0.6369	0.0007
17072799	PHF20L1	PHD finger protein 20-like 1	-0.3275	0.0429
17072958			-0.2677	0.0312
17073039			-0.3722	0.0035
17073054	CHRAC1	chromatin accessibility complex 1	-0.241	0.0095
17073210			-0.1319	0.0466
17073449	BREA2	breast cancer estrogen-induced apoptosis 2	-0.1818	0.045
17074313	DEFA1B	defensin, alpha 1B	-0.9265	0.0205
17074322	DEFA1B	defensin, alpha 1B	-0.9343	0.0181
17074544			-0.1672	0.0015
17074840	MIR3926-1	microRNA 3926-1	-0.1761	0.0279
17074848	DLC1	deleted in liver cancer 1	-1.0285	0.0001
17075112	PSD3	pleckstrin and Sec7 domain containing 3	-1.223	0
17075151			-0.9917	0.0029
17075776	PBK	PDZ binding kinase	-1.3103	0.0034
17076046	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa	-0.3032	0.0286
17076125			-0.1834	0.0253
17076265			-0.318	0.0102
17076488			-0.6078	0.021
17076510			-0.3182	0.0407
17076606			-0.3566	0.0044
17076621			-0.4027	0.0429
17076857			-0.6391	0.0121
17076976			-0.282	0.0043
17077222	TCEA1	transcription elongation factor A (SII), 1	-0.2323	0.0385
17077540			-0.2192	0.031
17077826	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	-0.7861	0.0073
17077848	VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	-0.3158	0.0234

17078254	SBSPON	somatomedin B and thrombospondin, type 1 domain containing	-0.6953	0.0306
17078296	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	-0.1886	0.0401
17078330	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	-0.2822	0.0117
17078534			-0.4986	0.0322
17078692			-0.7087	0.0456
17078756	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.132	0.0386
17078758	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.1512	0.0197
17078760	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.1512	0.0197
17078762	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.1512	0.0197
17078764	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	-0.1512	0.0197
17078969			-0.3026	0.0143
17079163	FP6628	uncharacterized LOC100132183	-0.3858	0.0485
17079293	CCNE2	cyclin E2	-0.5926	0.0031
17079348	LOC100500773	serine/arginine-rich splicing factor 3 pseudogene	-0.1662	0.0436
17079416	RPL30	ribosomal protein L30	-0.2705	0.0178
17079420			-0.1998	0.0318
17079425			-0.4845	0.0444
17079427			-0.7499	0.0107
17079428			-0.1885	0.0334
17079429			-0.8097	0.0047
17079431			-0.7217	0.0434
17079527			-0.2154	0.0321
17079672	PABPC1	poly(A) binding protein, cytoplasmic 1	-0.293	0.0216
17079830	UBR5	ubiquitin protein ligase E3 component n-recognin 5	-0.3997	0.0049
17080160			-0.1056	0.0466
17080447			-0.1434	0.0272
17080450	EXT1	exostosin 1	-0.4602	0.0103
17080559	TAF2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	-0.3116	0.0339
17080686			-0.6103	0.011
17080749	ATAD2	ATPase family, AAA domain containing 2	-0.7918	0.0073
17081067	TMEM75	transmembrane protein 75	-0.2903	0.004
17081071			-0.4635	0.0029
17081162	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	-0.589	0.0051
17081447	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-0.4604	0.0326
17081706	LOC286109	uncharacterized LOC286109	-0.9767	0.0002
17081708	EIF2C2	eukaryotic translation initiation factor 2C, 2	-0.587	0.001
17082132	NAPRT1	nicotinate phosphoribosyltransferase domain containing 1	-0.2885	0.0468
17082250	FAM83H	family with sequence similarity 83, member H	-0.4565	0.0047
17082263	SCRIB	scribbled homolog (Drosophila)	-0.1626	0.0228
17082453	OPLAH	5-oxoprolinase (ATP-hydrolysing)	-0.1917	0.0111
17082976	PGM5-AS1	PGM5 antisense RNA 1 (non-protein coding)	-0.3626	0.0432
17082982	DOCK8	dedicator of cytokinesis 8	-0.7996	0.0007
17083221	KCNV2	potassium channel, subfamily V, member 2	-0.2743	0.0013
17083229			-0.5267	0.0011
17083282	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-0.3302	0.0316
17083319	JAK2	Janus kinase 2	-0.3326	0.025
17083381	KIAA1432	KIAA1432	-0.3012	0.0213
17083492	KDM4C	lysine (K)-specific demethylase 4C	-0.3042	0.0346
17083647	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	-0.401	0.0122
17083742	CNTLN	centlein, centrosomal protein	-0.5447	0.0108
17083853			-0.1888	0.035
17083988			-0.1719	0.0352

17084069			-1.4268	0.0303
17084280	NFX1	nuclear transcription factor, X-box binding 1	-0.409	0.0095
17084415	SNORD121B	small nucleolar RNA, C/D box 121B	-0.4861	0.0191
17084669	RUSC2	RUN and SH3 domain containing 2	-0.5263	0.0039
17084685	TESK1	testis-specific kinase 1	-0.7665	0
17084707			-0.1653	0.0205
17084710	CCDC107	coiled-coil domain containing 107	-0.4184	0.0099
17084736	CREB3	cAMP responsive element binding protein 3	-0.441	0.0096
17084904	MELK	maternal embryonic leucine zipper kinase	-1.0041	0.0049
17084966	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	-0.3153	0.0117
17084990	POLR1E	polymerase (RNA) I polypeptide E, 53kDa	-0.5299	0.0284
17085040	TRMT10B	tRNA methyltransferase 10 homolog B (S. cerevisiae)	-0.3242	0.0159
17085082	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	-0.5538	0.01
17085139			-0.3913	0.0044
17085142			-0.4516	0.0239
17085236	CBWD5	COBW domain containing 5	-0.5611	0.0002
17085267	FOXD4L2	forkhead box D4-like 2	-0.1722	0.0496
17085271	LOC728034	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	-0.2931	0.0073
17085516	PGM5-AS1	PGM5 antisense RNA 1 (non-protein coding)	-1.1323	0.0237
17085520			-0.4723	0.0276
17085561	CBWD7	COBW domain containing 7	-0.4496	0.0001
17085760	MAMDC2	MAM domain containing 2	-0.9354	0.0172
17085779	SMC5	structural maintenance of chromosomes 5	-0.3941	0.0477
17085817	C9orf85	chromosome 9 open reading frame 85	-0.3498	0.0042
17085951	RORB	RAR-related orphan receptor B	-1.3245	0.0245
17085998	PCSK5	proprotein convertase subtilisin/kexin type 5	-0.7271	0.0089
17086044			-0.6314	0.0268
17086208	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	-0.6214	0.0026
17086350			-0.4759	0.0162
17086353	RMI1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-0.4007	0.0059
17086359			-0.6559	0.0184
17086432	NAA35	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	-0.5663	0.0008
17086634	CKS2	CDC28 protein kinase regulatory subunit 2	-0.9876	0.0002
17086780			-0.2113	0.0467
17086784	CENPP	centromere protein P	-0.6727	0.0007
17086921	FAM120A	family with sequence similarity 120A	-0.2604	0.0027
17086947	FAM120A	family with sequence similarity 120A	-0.3094	0.0205
17086950	PHF2	PHD finger protein 2	-0.3275	0.0004
17087032			-0.6221	0.0153
17087034	HIATL1	hippocampus abundant transcript-like 1	-0.5089	0.0013
17087138	ERCC6L2	excision repair cross-complementing rodent repair deficiency, complementation group 6-like 2	-0.3333	0.0055
17087343	NCBP1	nuclear cap binding protein subunit 1, 80kDa	-0.555	0.0002
17087378			-0.2423	0.0461
17087380	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	-0.266	0.0264
17087426			-0.2112	0.0316
17087430	COL15A1	collagen, type XV, alpha 1	-1.407	0.0021
17087498	SEC61B	Sec61 beta subunit	-0.3505	0.0011
17087517	NR4A3	nuclear receptor subfamily 4, group A, member 3	-1.3127	0.0023
17087535	STX17	syntaxin 17	-0.3795	0.0045
17087555	INVS	inversin	-0.4295	0.0012
17087633	ZNF189	zinc finger protein 189	-0.4584	0.0397
17087861	TMEM38B	transmembrane protein 38B	-0.4188	0.0492
17087900	ZNF462	zinc finger protein 462	-0.6144	0.0017
17087933	RAD23B	RAD23 homolog B (S. cerevisiae)	-0.3737	0.0006
17087954			-0.1845	0.0378
17088084	DNAJC25	DnaJ (Hsp40) homolog, subfamily C , member 25	-0.4126	0.0027

17088098			-0.3669	0.0453
17088100	UGCG	UDP-glucose ceramide glucosyltransferase	-1.1828	0.0033
17088116	MIR4668	microRNA 4668	-0.5358	0.0423
17088124	HSDL2	hydroxysteroid dehydrogenase like 2	-0.5537	0.0033
17088173	SLC31A1	solute carrier family 31 (copper transporters), member 1	-0.8774	0
17088185	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	-0.523	0.0003
17088203			-0.3907	0.0493
17088213	C9orf43	chromosome 9 open reading frame 43	-0.3607	0.004
17088401	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	-0.22	0.0451
17088408	C9orf91	chromosome 9 open reading frame 91	-0.3193	0.0172
17088423			-0.2303	0.0392
17088579	LOC253039	uncharacterized LOC253039	-0.6183	0.0127
17088589	CNTRL	centriolin	-0.2935	0.0478
17088741	MRRF	mitochondrial ribosome recycling factor	-0.7019	0
17088787			-0.3312	0.0135
17088790	OR1J2	olfactory receptor, family 1, subfamily J, member 2	-0.2259	0.0297
17088838	RABGAP1	RAB GTPase activating protein 1	-0.3192	0.0186
17088929	NEK6	NIMA (never in mitosis gene a)-related kinase 6	-0.4385	0.0136
17088991	MIR181A2HG	MIR181A2 host gene (non-protein coding)	-0.433	0.0204
17089056	GAPVD1	GTPase activating protein and VPS9 domains 1	-0.3156	0.0247
17089188	ZBTB43	zinc finger and BTB domain containing 43	-0.3528	0.0008
17089194	ZBTB34	zinc finger and BTB domain containing 34	-0.4425	0.0091
17089460	FPGS	folylpolyglutamate synthase	-0.1917	0.0326
17089542	C9orf16	chromosome 9 open reading frame 16	-0.8094	0.0005
17089638	MIR2964A	microRNA 2964a	-0.1275	0.0403
17089735	SPTAN1	spectrin, alpha, non-erythrocytic 1	-0.3668	0.0289
17089849	TBC1D13	TBC1 domain family, member 13	-0.4147	0.0063
17089898	NUP188	nucleoporin 188kDa	-0.4267	0.0178
17089982	DOLPP1	dolichyl pyrophosphate phosphatase 1	-0.4134	0.0121
17089996			-0.2934	0.0352
17089999	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	-0.2133	0.0459
17090063	LOC100128077	uncharacterized LOC100128077	-0.348	0.0256
17090085	NTMT1	N-terminal Xaa-Pro-Lys N-methyltransferase 1	-0.3478	0.0356
17090100			-0.3013	0.0011
17090357	EXOSC2	exosome component 2	-0.2982	0.009
17090373	ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	-0.41	0.0042
17090394	LAMC3	laminin, gamma 3	-0.9262	0.0045
17090427	AIF1L	allograft inflammatory factor 1-like	-0.4508	0.0172
17090444	NUP214	nucleoporin 214kDa	-0.2817	0.0187
17090526	PRRC2B	proline-rich coiled-coil 2B	-0.3903	0.0008
17090564	SNORD62A	small nucleolar RNA, C/D box 62A	-0.508	0.005
17090566	SNORD62A	small nucleolar RNA, C/D box 62A	-0.508	0.005
17090568	POMT1	protein-O-mannosyltransferase 1	-0.2039	0.0361
17090608			-0.4541	0.0016
17090646	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	-0.4622	0.0043
17090688	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	-0.4028	0.0019
17090893	WDR5	WD repeat domain 5	-0.3538	0.0087
17091087			-0.216	0.0394
17091128	PAEP	progestagen-associated endometrial protein	-0.1851	0.0354
17091203			-0.4879	0.0112
17091239	PMPCA	peptidase (mitochondrial processing) alpha	-0.2654	0.0332
17091392			-0.2302	0.0297
17091397	PHPT1	phosphohistidine phosphatase 1	-0.2196	0.0365
17091527	C9orf142	chromosome 9 open reading frame 142	-0.2156	0.0124
17091571	MAN1B1	mannosidase, alpha, class 1B, member 1	-0.3112	0.0015
17091695	TUBB4B	tubulin, beta 4B class IVb	-0.2746	0.0293
17091710	COBRA1	cofactor of BRCA1	-0.3187	0.0292
17091731			-0.3213	0.005
17091746	MRPL41	mitochondrial ribosomal protein L41	-0.4857	0.0004
17091769	EHMT1	euchromatic histone-lysine N-methyltransferase 1	-0.4075	0.0027

17091815	FLJ40292	uncharacterized LOC643210	-0.4048	0.0004
17091928	FOXD4	forkhead box D4	-0.3314	0.0204
17091932	CBWD1	COBW domain containing 1	-0.3218	0.0323
17091973	C9orf66	chromosome 9 open reading frame 66	-0.6443	0.0001
17091977			-0.318	0.015
17092020	KIAA0020	KIAA0020	-0.6782	0.0006
17092153	AK3	adenylate kinase 3	-0.3346	0.0316
17092205			-0.271	0.0479
17092261			-0.2066	0.0448
17092264	C9orf38	chromosome 9 open reading frame 38	-0.376	0.0091
17092710	SCARNA8	small Cajal body-specific RNA 8	-0.4173	0.0448
17092734			-0.3858	0.0104
17092736			-0.3858	0.0104
17092737	RPS6	ribosomal protein S6	-0.2212	0.0155
17092742			-0.1371	0.0172
17092743			-0.1602	0.035
17092745			-0.5695	0.0183
17092748			-0.7263	0.0062
17092749			-0.5226	0.0139
17092767	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	-0.4998	0.01
17092786	MIR4473	microRNA 4473	-0.156	0.0487
17092788	MIR4474	microRNA 4474	-0.3336	0.0024
17093042	C9orf72	chromosome 9 open reading frame 72	-0.6544	0.0072
17093325	UBAP2	ubiquitin associated protein 2	-0.4277	0.0345
17093595	FANCG	Fanconi anemia, complementation group G	-0.2706	0.015
17093681	FAM166B	family with sequence similarity 166, member B	-1.8576	0
17093990	MIR4540	microRNA 4540	-0.3044	0.0451
17094005	ZBTB5	zinc finger and BTB domain containing 5	-0.5099	0.0004
17094009	FBXO10	F-box protein 10	-0.5768	0.0103
17094028	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)	-0.4923	0.004
17094088	ANKRD18A	ankyrin repeat domain 18A	-0.238	0.0309
17094237			-0.3249	0.043
17094389	CNTNAP3	contactin associated protein-like 3	-0.5894	0.0178
17094459	AQP7P1	aquaporin 7 pseudogene 1	-0.2472	0.0127
17094498			-0.7658	0.0258
17094534	CBWD6	COBW domain containing 6	-0.3786	0.0007
17094582	LOC728034	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	-0.2931	0.0073
17094594	LOC728034	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	-0.2931	0.0073
17094605	LOC728034	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	-0.2931	0.0073
17094609	FOXD4L2	forkhead box D4-like 2	-0.1722	0.0496
17094613	CBWD7	COBW domain containing 7	-0.4874	0.0002
17094662			-0.4307	0.0084
17094667	PGM5-AS1	PGM5 antisense RNA 1 (non-protein coding)	-1.4779	0.0302
17094671	PGM5-AS1	PGM5 antisense RNA 1 (non-protein coding)	-0.9128	0.0337
17094718	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-0.3845	0.0009
17094855	FAM108B1	family with sequence similarity 108, member B1	-0.2891	0.0138
17094876	ZFAND5	zinc finger, AN1-type domain 5	-0.4623	0.0045
17095017			-0.2723	0.0013
17095150	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	-0.9289	0.0003
17095336			-0.7796	0.0312
17095342			-0.1661	0.0483
17095703	NFIL3	nuclear factor, interleukin 3 regulated	-0.8574	0.0038
17095775	IARS	isoleucyl-tRNA synthetase	-0.4988	0.0011
17095828	SNORA84	small nucleolar RNA, H/ACA box 84	-0.5278	0.0136
17095830	NOL8	nucleolar protein 8	-0.284	0.049

17095870	OGN	osteoglycin	-0.5157	0.0323
17095887	ASPN	asporin	-0.5842	0.0241
17095918	IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	-0.3417	0.0176
17095981	FAM120AOS	family with sequence similarity 120A opposite strand	-0.2134	0.0124
17096205	ZNF367	zinc finger protein 367	-0.4741	0.0167
17096242	AAED1	AhpC/TSA antioxidant enzyme domain containing 1	-0.3816	0.0405
17096274			-0.5066	0.0046
17096326			-0.2215	0.0257
17096335	ANKRD18CP	ankyrin repeat domain 18C, pseudogene	-0.1948	0.0484
17096354	TSTD2	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	-0.2629	0.0039
17096379			-0.5328	0.0046
17096394			-0.2119	0.0311
17096433			-0.4754	0.012
17096516	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	-0.177	0.0425
17096555			-0.5986	0.0018
17096561			-0.3216	0.0378
17096580	ERP44	endoplasmic reticulum protein 44	-0.2431	0.0305
17096595	TEX10	testis expressed 10	-0.4046	0.0158
17096631	MRPL50	mitochondrial ribosomal protein L50	-0.3863	0.0048
17096827	KLF4	Kruppel-like factor 4 (gut)	-0.3215	0.0234
17096859	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	-0.3796	0.0047
17096904	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	-0.5177	0.0168
17096929	RN5-8S3	RNA, 5.8S ribosomal 3	-0.6594	0.0345
17096998			-0.2895	0.0205
17097152	KIAA0368	KIAA0368	-0.4202	0.0017
17097240	C9orf84	chromosome 9 open reading frame 84	-1.3799	0.0052
17097277			-0.6587	0.0352
17097308	PTBP3	polypyrimidine tract binding protein 3	-0.3791	0.0462
17097340	INIP	INTS3 and NABP interacting protein	-0.278	0.0153
17097388	FKBP15	FK506 binding protein 15, 133kDa	-0.241	0.024
17097423	CDC26	cell division cycle 26 homolog (S. cerevisiae)	-0.2715	0.0382
17097495	POLE3	polymerase (DNA directed), epsilon 3, accessory subunit	-0.329	0.0007
17097603	DFNB31	deafness, autosomal recessive 31	-0.4853	0.0126
17097811	MIR147A	microRNA 147a	-0.2959	0.0432
17097813	CDK5RAP2	CDK5 regulatory subunit associated protein 2	-0.4191	0.0105
17097880	FBXW2	F-box and WD repeat domain containing 2	-0.3879	0.0025
17097895	PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-0.3759	0.0019
17097914	PHF19	PHD finger protein 19	-0.3823	0.0192
17097941	TRAF1	TNF receptor-associated factor 1	-0.1938	0.0409
17098048	TTLL11	tubulin tyrosine ligase-like family, member 11	-0.3701	0.0055
17098173	ZBTB6	zinc finger and BTB domain containing 6	-0.3578	0.0026
17098222	DENND1A	DENN/MADD domain containing 1A	-0.3035	0.019
17098275	LOC613206	myeloproliferative disease associated tumor antigen 5	-0.3298	0.0254
17098278	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	-0.3589	0.0102
17098293	NR5A1	nuclear receptor subfamily 5, group A, member 1	-1.0362	0
17098322	RPL35	ribosomal protein L35	-0.1506	0.0165
17098324			-0.1987	0.0144
17098328			-0.3427	0.0489
17098329			-0.2468	0.0307
17098331			-0.2575	0.017
17098332	GOLGA1	golgin A1	-0.3898	0.0011
17098395	PPP6C	protein phosphatase 6, catalytic subunit	-0.1999	0.0398
17098745	PTGES2	prostaglandin E synthase 2	-0.2835	0.0045
17098766	CIZ1	CDKN1A interacting zinc finger protein 1	-0.2787	0.0232
17098866	MIR219-2	microRNA 219-2	-0.2135	0.0107
17098932	C9orf114	chromosome 9 open reading frame 114	-0.2262	0.0276

17099001	CRAT	carnitine O-acetyltransferase	-0.3058	0.0196
17099062	ASB6	ankyrin repeat and SOCS box containing 6	-0.6686	0.0002
17099073	LOC100506231	uncharacterized LOC100506231	-0.1723	0.0453
17099083	TOR1A	torsin family 1, member A (torsin A)	-0.3484	0.0028
17099146	LOC100272217	uncharacterized LOC100272217	-0.2118	0.0397
17099165			-0.5036	0.0076
17099167			-0.259	0.0155
17099208	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	-0.693	0.0002
17099309	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	-0.2507	0.0297
17099473	SURF6	surfeit 6	-0.4297	0.0002
17099484	MED22	mediator complex subunit 22	-0.1691	0.0465
17099531	REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	-0.3025	0.0225
17099617	VAV2	vav 2 guanine nucleotide exchange factor	-0.7448	0.0018
17099651	BRD3	bromodomain containing 3	-0.5551	0.0004
17099742			-0.3185	0.0098
17099847	QSOX2	quiescin Q6 sulfhydryl oxidase 2	-0.566	0.0044
17099923	SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	-0.264	0.032
17099947	SDCCAG3	serologically defined colon cancer antigen 3	-0.4183	0.0007
17099980	SEC16A	SEC16 homolog A (S. cerevisiae)	-0.3509	0.015
17100173	EDF1	endothelial differentiation-related factor 1	-0.2901	0.0008
17100183	FBXW5	F-box and WD repeat domain containing 5	-0.4743	0.0129
17100328	DPP7	dipeptidyl-peptidase 7	-0.2922	0.03
17100361	ANAPC2	anaphase promoting complex subunit 2	-0.2288	0.003
17100390	TMEM203	transmembrane protein 203	-0.2308	0.0439
17100585	ZMYND19	zinc finger, MYND-type containing 19	-0.4082	0.0048
17100597	C9orf37	chromosome 9 open reading frame 37	-0.4613	0.0067
17100614			-0.4588	0.0313
17100731			-0.444	0.0034
17100775			-0.4827	0.0045
17100820			-0.2358	0.0034
17100824			-0.2358	0.0034
17100893			-0.4143	0.0306
17100897			-0.4827	0.0045
17100987			-0.4934	0.0405
17101016			-0.2422	0.0232
17101027			-0.4438	0.0072
17102352	GK	glycerol kinase	-0.4208	0.0165
17102658			-0.804	0.005
17102664			-0.9165	0.0292
17103394			-0.5026	0.036
17103837	MAGED4B	melanoma antigen family D, 4B	-0.2137	0.0372
17104363	EFNB1	ephrin-B1	-0.5039	0.0274
17105163	ZNF711	zinc finger protein 711	-1.4408	0.0072
17105269	FAM133A	family with sequence similarity 133, member A	-0.6368	0.0437
17105401	CENPI	centromere protein I	-0.5652	0.006
17105862	NRK	Nik related kinase	-1.6263	0.0315
17107505	CXorf1	chromosome X open reading frame 1	-0.1249	0.038
17107816	FATE1	fetal and adult testis expressed 1	-2.4204	0.0007
17109356	RNU5F-7P	RNA, U5F small nuclear 7, pseudogene	-0.2625	0.0093
17109464	SCML2	sex comb on midleg-like 2 (Drosophila)	-0.5804	0.0062
17110435			-0.3289	0.0096
17111146			-0.2214	0.0343
17113864			-0.7203	0.0382
17113978	RN5S513	RNA, 5S ribosomal 513	-0.4058	0.0229
17114075	ZNF280C	zinc finger protein 280C	-0.4952	0.0172
17114520	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-0.5517	0.0042
17115978			-0.2424	0.0247
17116189			-0.2398	0.0187
17116194	TTTY15	testis-specific transcript, Y-linked 15 (non-protein coding)	-1.1982	0.0426

17116284	TMSB4Y	thymosin beta 4, Y-linked	-0.4072	0.0251
17116745	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	-0.6228	0.0173
17116822	TTTY16	testis-specific transcript, Y-linked 16 (non-protein coding)	-0.264	0.019
17116847	FAM197Y5	family with sequence similarity 197, Y-linked, member 5	-0.1372	0.0032
17116894	FAM197Y5	family with sequence similarity 197, Y-linked, member 5	-0.1382	0.0129
17117173			-0.3285	0.0376
17117460	LOC100505955	putative uncharacterized protein FLJ44672-like	-0.2692	0.0043
17117531	SKCG-1	sporadic kidney cancer gene 1	-0.2029	0.0287
17117537	LOC100131262	uncharacterized LOC100131262	-0.5384	0.0074
17117588	LOC727803	RAN binding protein 1 pseudogene	-0.3249	0.0185
17117626	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma	-0.6125	0.0023
17117629			-0.3789	0.0019
17117631	LOC100128075	uncharacterized LOC100128075	-0.2065	0.0125
17117657	LOC643797	AGVR6190	-0.1865	0.0126
17117697	LOC729313	peptidylprolyl isomerase A (cyclophilin A) pseudogene	-0.2689	0.0393
17117736			-0.8095	0.0444
17117798			-0.3639	0.038
17117817	LOC100652943	putative uncharacterized protein FLJ38264-like	-0.2624	0.0387
17117843			-0.4885	0.0132
17117851	LOC729770	uncharacterized LOC729770	-0.2632	0.0201
17117857	LOC100508950	uncharacterized LOC100508950	-0.5045	0.017
17117869	LOC100506934	uncharacterized LOC100506934	-0.4448	0.0009
17117874	LOC100507307	uncharacterized LOC100507307	-0.5196	0.0343
17117924	LOC100509671	uncharacterized LOC100509671	-0.3112	0.0206
17117934	MGC15705	uncharacterized protein MGC15705	-0.3324	0.0038
17118152	LOC100129033	QIQN5815	-0.675	0.011
17118166	ZNF451	zinc finger protein 451	-0.4095	0.0487
17118173			-0.2296	0.0499
17118187			-0.6138	0.0057
17118281	LOC100506458	putative uncharacterized protein LOC65996-like	-0.272	0.0295
17118303			-1.2224	0.0044
17118401	LOC100132249	uncharacterized LOC100132249	-0.2614	0.0263
17118417	FP2234	uncharacterized LOC100507137	-0.2242	0.0488
17118426	LOC100652907	uncharacterized LOC100652907	-0.4595	0.001
17118430			-1.0417	0.0157
17118478	TEKT4P2	tektin 4 pseudogene 2	-0.4675	0.0231
17118652			-0.5411	0.0476
17118654			-0.6016	0.0177
17118722			-0.7477	0.0081
17118820			-0.4043	0.0346
17118822			-0.252	0.0392
17118830			-0.5371	0.0049
17118854			-0.5534	0.0277
17118856			-0.4421	0.0057
17118930			-2.9779	0
17118988			-0.4452	0.0076
17119010			-0.3068	0.0289
17119058			-0.5268	0.0439
17119068			-0.5677	0.0065
17119096			-0.2794	0.0197
17119286			-0.3825	0.0182
17119332			-0.293	0.0207
17119408			-0.2893	0.0399
17119726			-0.4574	0.0045
17119730			-0.5726	0.0266
17119744			-0.5415	0.0088
17119802			-0.2917	0.0219
17120202			-0.4252	0.0102
17120506			-0.7448	0.0003
17120538			-0.4326	0.0041

17120604			-0.2165	0.0073
17120606			-0.1873	0.0127
17120626			-0.3049	0.0486
17120634			-0.2975	0.011
17120658			-0.1006	0.044
17120686			-0.4014	0.0113
17120722			-0.1944	0.0339
17120806			-0.4687	0.0036
17120936			-1.1078	0.0415
17121084			-0.1537	0.0284
17121132			-0.7785	0.0007
17121144			-0.2191	0.0234
17121146			-0.3038	0.0441
17121150			-0.3808	0.0263
17121166			-0.198	0.0453
17121274			-0.4843	0.0403
17121296			-0.5914	0.0417
17121322			-0.6371	0.0008
17121342			-0.4384	0.0012
17121346			-0.2855	0.0449
17121364			-0.3313	0.0147
17121372			-0.3505	0.0286
17121374			-0.2553	0.0189
17121376			-0.2769	0.0228
17121410			-0.4365	0.0038
17121434			-0.2153	0.0438
17121444			-0.2664	0.0265
17121446			-0.2154	0.0153
17121466			-0.3194	0.0461
17121468			-0.1856	0.0042
17121480			-0.2693	0.0404
17121486			-0.3247	0.01
17121488			-0.5222	0.0019
17121584			-0.5353	0.0097
17121586			-1.0357	0.0067
17121630			-0.3217	0.0432
17121814			-0.2998	0.0423
17121818			-0.3531	0.0197
17121820			-0.3644	0.0233
17121896			-0.479	0.0264
17122038			-0.1994	0.0191
17122052			-0.2076	0.0214
17122162			-0.1615	0.0243
17122246			-0.6669	0.0007
17122252			-0.2364	0.0375
17122268			-0.2815	0.0037
17122286			-0.3322	0.0239
17122446			-0.2616	0.0068
17122462			-0.3206	0.0479
17122468			-0.6842	0.0163
17122470			-0.5713	0.0324
17122472			-0.5295	0.0371
17122474			-0.737	0.006
17122476			-0.3958	0.0079
17122478			-0.4902	0.007
17122482			-0.7685	0.0076
17122484			-0.5731	0.0093
17122486			-0.586	0.0111
17122488			-0.8016	0.0069
17122490			-0.6865	0.0064
17122492			-0.5984	0.0083

17122494			-0.504	0.0175
17122496			-0.7163	0.009
17122498			-0.7227	0.0031
17122500			-0.5356	0.0179
17122504			-0.4491	0.032
17122524			-0.3109	0.0277
17122640			-0.5098	0.0174
17122642			-0.383	0.0252
17122644			-0.3532	0.0208
17122648			-0.4089	0.0298
17122650			-0.7301	0.0043
17122652			-0.567	0.009
17122654			-0.3231	0.0434
17122658			-0.4521	0.0361
17122664			-0.568	0.0136
17122748			-0.1273	0.0424
17122886			-0.5611	0.0263
17122942			-0.5082	0.0359
17122944			-0.6123	0.0161
17122946			-0.2638	0.0217
17122954			-0.2965	0.0312
17122960			-0.2026	0.0229
17123006			-0.1696	0.0202
17123008			-0.1576	0.0236
17123018			-1.1539	0.0461
17123092			-0.2941	0.0273
17123102			-0.3189	0.0029
17123124			-0.2909	0.0057
17123132			-0.2568	0.0365
17123190			-0.3078	0.0447
17123206			-0.6777	0
17123370			-0.1471	0.0452
17123488			-0.2986	0.02
17123540			-0.1904	0.0398
17123628			-0.4163	0.0043
17123638			-0.2431	0.0402
17123640			-0.2341	0.0379
17123642			-0.3	0.0149
17123648			-0.4416	0.0161
17123932			-0.1536	0.0127
17123936			-0.7211	0.0372
17123982			-0.153	0.0241
17124008			-0.5101	0.0141
17124082			-0.243	0.0167
17124118			-0.1067	0.0496
17124126			-0.2264	0.0265
17124158			-0.2611	0.0105
17124262			-0.4918	0.0011
17124264			-0.533	0.0005
17124316			-0.231	0.0162
17124364			-0.6184	0.0109
17124538			-0.5131	0.0013
17124544			-0.4475	0.0048
17124550			-0.3423	0.0096
17124592			-0.2935	0.0004
17124596			-0.5084	0.0002
17124718			-0.1533	0.0307
17124728			-0.2863	0.0167
17124746			-0.2495	0.0195
17124748			-0.4114	0.0012
17124834			-0.1647	0.0248

17124862			-0.137	0.0464
17124970			-0.1225	0.0368
17125092			-0.3233	0.0193
17125094			-0.7444	0.0193
17125106			-0.8639	0.0052
17125158			-0.5834	0.007
17125194			-0.4223	0.0399
17125218			-0.6699	0.0146
17125290			-0.6819	0.0001
17125300			-0.5474	0.0083
17125344			-0.1567	0.0132
17125368			-0.1672	0.0046
17125388			-0.1607	0.0495
17125398			-0.224	0.0091
17125404			-0.1708	0.0465
17125406			-0.206	0.045
17125410			-0.175	0.0154
17125762			-0.4165	0.0485
17125830			-0.3879	0.0196
17125886			-0.4223	0.0066
17125934			-0.4223	0.0066
17126010			-0.2893	0.0399
17126018			-0.3316	0.0014
17126036			-0.6597	0.0208
17126040			-0.5278	0.0219
17126058			-0.5775	0.0026
17126092			-0.1478	0.0464
17126106			-0.6356	0.0012
17126130			-0.1478	0.0464
17126146			-0.6597	0.0208
17126150			-0.5278	0.0219
17126172			-0.69	0.0049
17126186			-0.2307	0.022
17126208			-0.5136	0.0026
17126210			-0.6488	0.0152
17126212			-0.7085	0.0381
17126240			-0.5752	0.0295
17126242			-0.3357	0.0336
17126254			-0.7427	0.048
17126288			-0.1765	0.0389

*For the difference in expression.

Supplemental Table 11. Gene set enrichment analysis detail of ACC patients' cohort for genes associated with resistance and metabolism of cisplatin, etoposide and doxorubicin (dataset GSEA10927).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	GSTP1	GSTP1	glutathione S-transferase pi	89	0.356068641	0.038780537	Yes
2	PSG4	PSG4	pregnancy specific beta-1-glycoprotein 4	197	0.304260194	0.070411734	Yes
3	RAC2	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	209	0.300997138	0.10632141	Yes
4	CYP3A7	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	309	0.264281571	0.1335014	Yes
5	CISH	CISH	cytokine inducible SH2-containing protein	324	0.260883242	0.16440798	Yes
6	FAT4	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	382	0.249488309	0.19184147	Yes
7	MX1	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	426	0.243574277	0.21924044	Yes
8	CYP1B1	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	446	0.240814269	0.24747363	Yes
9	CASP1	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	483	0.23523739	0.27420393	Yes
10	STMN2	STMN2	stathmin-like 2	599	0.217720672	0.29496732	Yes
11	G0S2	G0S2	G0/G1switch 2	615	0.215585738	0.32034054	Yes
12	GDF15	GDF15	growth differentiation factor 15	728	0.202991918	0.3394666	Yes
13	ITM2A	ITM2A	integral membrane protein 2A	760	0.199747086	0.3621431	Yes
14	PLAU	PLAU	plasminogen activator, urokinase	762	0.199639797	0.38626713	Yes
15	NOS3	NOS3	nitric oxide synthase 3 (endothelial cell)	810	0.195634097	0.40766668	Yes
16	CYP3A5	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	886	0.189096108	0.4269115	Yes
17	PTGES	PTGES	prostaglandin E synthase	938	0.183585599	0.44665748	Yes
18	PXN	PXN	paxillin	965	0.181236193	0.46733606	Yes
19	HMMR	HMMR	hyaluronan-mediated motility receptor (RHAMM)	1035	0.1762411	0.4853165	Yes
20	EFEMP1	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	1134	0.16884625	0.5009897	Yes
21	TFPI2	TFPI2	tissue factor pathway inhibitor 2	1362	0.155405194	0.5087553	Yes
22	VAV3	VAV3	vav 3 oncogene	1429	0.152184963	0.52396905	Yes
23	AKR1A1	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	1518	0.148295432	0.53764075	Yes
24	GJA5	GJA5	gap junction protein, alpha 5, 40kDa (connexin 40)	1605	0.143853471	0.550872	Yes
25	FBXL22	FBXL22	F-box and leucine-rich repeat protein 22	1643	0.142207608	0.5662894	Yes
26	GRN	GRN	granulin	1652	0.141414374	0.58302265	Yes
27	P2RY6	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	1703	0.139293849	0.5974544	Yes
28	CDKN3	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	1802	0.134949833	0.6090234	Yes
29	ARHGDIB	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	2174	0.121700726	0.60569763	Yes
30	ITGB4	ITGB4	integrin, beta 4	2180	0.121443547	0.6201588	Yes
31	KIF4A	KIF4A	kinesin family member 4A	2235	0.119613469	0.6320129	Yes
32	NOS1	NOS1	nitric oxide synthase 1 (neuronal)	2357	0.115780853	0.6401412	Yes
33	FOXJ1	FOXJ1	forkhead box J1	2394	0.114480384	0.65225005	Yes
34	TFPI	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	2445	0.11286784	0.66348207	Yes
35	MGST1	MGST1	microsomal glutathione S-	2565	0.109638155	0.67096394	Yes

			transferase 1				
36	CYP3A43	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	2658	0.106932387	0.67943263	Yes
37	BUB1B	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	2781	0.104309179	0.68612325	Yes
38	BMP2	BMP2	bone morphogenetic protein 2	2851	0.102603734	0.6951875	Yes
39	PTGS1	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	3055	0.098132268	0.6971868	Yes
40	NCAPG2	NCAPG2	non-SMC condensin II complex, subunit G2	3459	0.088828593	0.688323	Yes
41	JUP	JUP	junction plakoglobin	3491	0.088271864	0.69750196	Yes
42	IFITM1	IFITM1	interferon induced transmembrane protein 1 (9-27)	3634	0.085442178	0.7009344	Yes
43	PGD	PGD	phosphogluconate dehydrogenase	4004	0.078389779	0.6924619	Yes
44	RFC4	RFC4	replication factor C (activator 1) 4, 37kDa	4049	0.07772103	0.69973046	Yes
45	METTL6	METTL6	methyltransferase like 6	4327	0.073377639	0.6951299	Yes
46	TK1	TK1	thymidine kinase 1, soluble	4353	0.072852165	0.7027339	Yes
47	CENPA	CENPA	centromere protein A	4389	0.072300367	0.7097842	Yes
48	XDH	XDH	xanthine dehydrogenase	4651	0.06801255	0.70531297	No
49	NR1I2	NR1I2	nuclear receptor subfamily 1, group I, member 2	5191	0.060610898	0.6864116	No
50	ABCC1	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	5875	0.051853582	0.65943956	No
51	CDKN1A	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	6336	0.046626952	0.64269096	No
52	ERBB3	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	6358	0.046307657	0.6472756	No
53	EGFR	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	6541	0.044434048	0.64379543	No
54	ZDHHC3	ZDHHC3	zinc finger, DHHC-type containing 3	6634	0.043377973	0.64456886	No
55	CYP3A4	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	6800	0.041557617	0.641568	No
56	ABCC2	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	6802	0.041547775	0.64655	No
57	MDK	MDK	midkine (neurite growth-promoting factor 2)	7059	0.039021924	0.63881195	No
58	PTGS2	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	7111	0.038446415	0.64098424	No
59	SLC22A16	SLC22A16	solute carrier family 22 (organic cation transporter), member 16	7287	0.036752112	0.63691473	No
60	HMGB2	HMGB2	high-mobility group box 2	8961	0.021261426	0.5580422	No
61	SNTB1	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	9053	0.020535868	0.5560986	No
62	RAC1	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	9694	0.015089847	0.5267685	No
63	GPX1	GPX1	glutathione peroxidase 1	9795	0.014255677	0.52362627	No
64	SOD1	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	11050	0.00345061	0.46299544	No
65	RELA	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	13530	-0.01753360	0.34443298	No

Supplemental Table 12. Gene set enrichment analysis detail of ACC patients' cohort for genes associated with resistance and metabolism of cisplatin, etoposide and doxorubicin (dataset GSEA49278).

	PROBE	GENE SYMBOL	GENE NAME	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	CYP3A4	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	12	0.728654146	0.068321966	Yes
2	CYP3A5	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	16	0.705859721	0.13490584	Yes
3	GDF15	GDF15	growth differentiation factor 15	52	0.582792163	0.18837525	Yes
4	CYP3A7	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	94	0.51911968	0.23554817	Yes
5	ABCC2	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	106	0.506755948	0.28294107	Yes
6	G0S2	G0S2	G0/G1switch 2	142	0.472916931	0.3260243	Yes
7	CISH	CISH	cytokine inducible SH2-containing protein	184	0.439882308	0.36570713	Yes
8	BMP2	BMP2	bone morphogenetic protein 2	440	0.336663425	0.385727	Yes
9	PSG4	PSG4	pregnancy specific beta-1-glycoprotein 4	682	0.28498286	0.40150967	Yes
10	PXN	PXN	paxillin	738	0.275306404	0.4249876	Yes
11	EFEMP1	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	745	0.273793638	0.45059076	Yes
12	CASP1	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	1257	0.221594542	0.44788328	Yes
13	GJA5	GJA5	gap junction protein, alpha 5, 40kDa (connexin 40)	1334	0.215924338	0.46477592	Yes
14	PTGS1	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1626	0.196524262	0.4698824	Yes
15	ERBB3	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	1770	0.188211158	0.48105398	Yes
16	MDK	MDK	midkine (neurite growth-promoting factor 2)	2196	0.166640535	0.4771328	Yes
17	MX1	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	2240	0.163561359	0.49060327	Yes
18	CYP1B1	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	2297	0.16127722	0.5032561	Yes
19	FAT4	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	2455	0.15546748	0.51068443	Yes
20	FBXL22	FBXL22	F-box and leucine-rich repeat protein 22	2551	0.151713267	0.5206279	Yes
21	NOS3	NOS3	nitric oxide synthase 3 (endothelial cell)	2622	0.14897491	0.53146976	Yes
22	JUP	JUP	junction plakoglobin	2678	0.146538004	0.5427756	Yes
23	CDKN1A	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2811	0.141815111	0.5500707	Yes
24	XDH	XDH	xanthine dehydrogenase	3472	0.12233384	0.5310832	No
25	RAC2	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	3570	0.119306423	0.53787076	No
26	SNTB1	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	3875	0.111522771	0.53434056	No
27	MGST1	MGST1	microsomal glutathione S-transferase 1	4232	0.102735259	0.5275726	No
28	ITGB4	ITGB4	integrin, beta 4	4595	0.094891481	0.51978546	No
29	IFITM1	IFITM1	interferon induced transmembrane protein 1 (9-27)	4804	0.090650991	0.5187261	No
30	GPX1	GPX1	glutathione peroxidase 1	5849	0.072189413	0.47722337	No
31	NOS1	NOS1	nitric oxide synthase 1 (neuronal)	6083	0.068368115	0.47290045	No
32	GSTP1	GSTP1	glutathione S-transferase pi	6467	0.062425952	0.46107236	No

33	ITM2A	ITM2A	integral membrane protein 2A	7089	0.052972339	0.43733367	No
34	GRN	GRN	granulin	7211	0.051096264	0.43656257	No
35	AKR1A1	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	7539	0.046557929	0.42582676	No
36	TFPI	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	8481	0.033424243	0.38542747	No
37	CYP3A43	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	8787	0.02930673	0.37407935	No
38	METTL6	METTL6	methyltransferase like 6	8799	0.029172504	0.37632775	No
39	VAV3	VAV3	vav 3 oncogene	9036	0.026029108	0.36786377	No
40	P2RY6	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	9128	0.024992732	0.36601388	No
41	PLAU	PLAU	plasminogen activator, urokinase	9588	0.01926429	0.34658784	No
42	NR1I2	NR1I2	nuclear receptor subfamily 1, group I, member 2	9600	0.019127801	0.34788674	No
43	ARHGDIB	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	9795	0.016882371	0.34050235	No
44	RFC4	RFC4	replication factor C (activator 1) 4, 37kDa	10513	0.008421433	0.30810857	No
45	PTGS2	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	10685	0.006564655	0.30081353	No
46	SLC22A16	SLC22A16	solute carrier family 22 (organic cation transporter), member 16	11035	0.002392255	0.2848845	No
47	RELA	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	11049	0.002243968	0.28449485	No
48	EGFR	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	11514	-0.00353764	0.26335075	No
49	ZDHHC3	ZDHHC3	zinc finger, DHHC-type containing 3	11551	-0.00404753	0.26206693	No
50	ABCC1	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	12833	-0.01979615	0.20464087	No
51	RAC1	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	13200	-0.02453878	0.19001836	No
52	SOD1	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	13525	-0.02872384	0.17773561	No
53	HMGB2	HMGB2	high-mobility group box 2	14460	-0.04067291	0.13834555	No
54	PTGES	PTGES	prostaglandin E synthase	14553	-0.04209489	0.138066	No
55	FOXJ1	FOXJ1	forkhead box J1	14609	-0.04297070	0.13958193	No
56	PGD	PGD	phosphogluconate dehydrogenase	17752	-0.09800827	0.003403593	No
57	STMN2	STMN2	stathmin-like 2	18091	-0.10570388	-0.002250518	No
58	TFPI2	TFPI2	tissue factor pathway inhibitor 2	18309	-0.11201523	-0.001706965	No
59	CENPA	CENPA	centromere protein A	18561	-0.11898653	-0.00207829	No
60	NCAPG2	NCAPG2	non-SMC condensin II complex, subunit G2	19660	-0.16081953	-0.037702788	No
61	KIF4A	KIF4A	kinesin family member 4A	19790	-0.16716087	-0.027872976	No
62	HMMR	HMMR	hyaluronan-mediated motility receptor (RHAMM)	21152	-0.30654299	-0.061896916	No
63	TK1	TK1	thymidine kinase 1, soluble	21289	-0.34206420	-0.03585806	No
64	CDKN3	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-assoc. dual specificity phosphatase)	21582	-0.56347013	0.0038884	No