Supplementary Information

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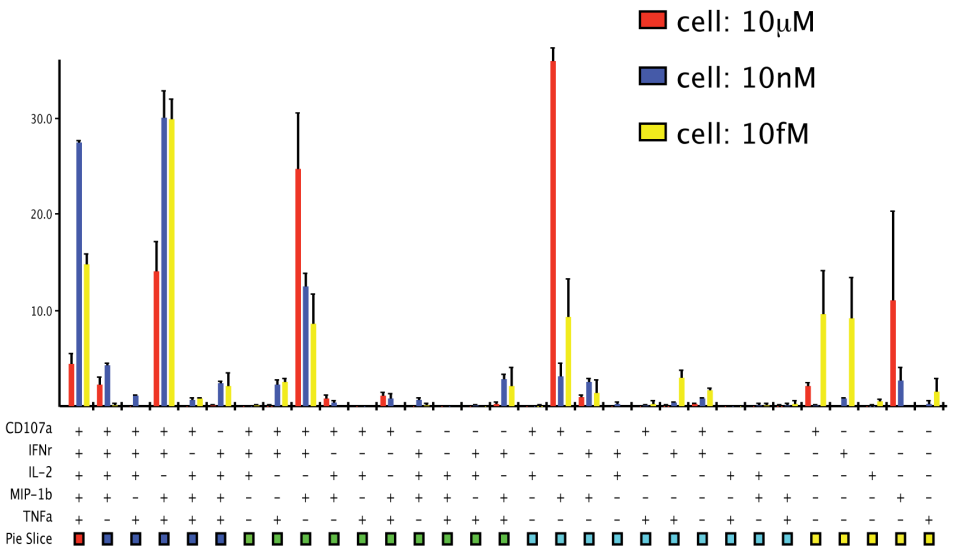
Supplementary Figure 1

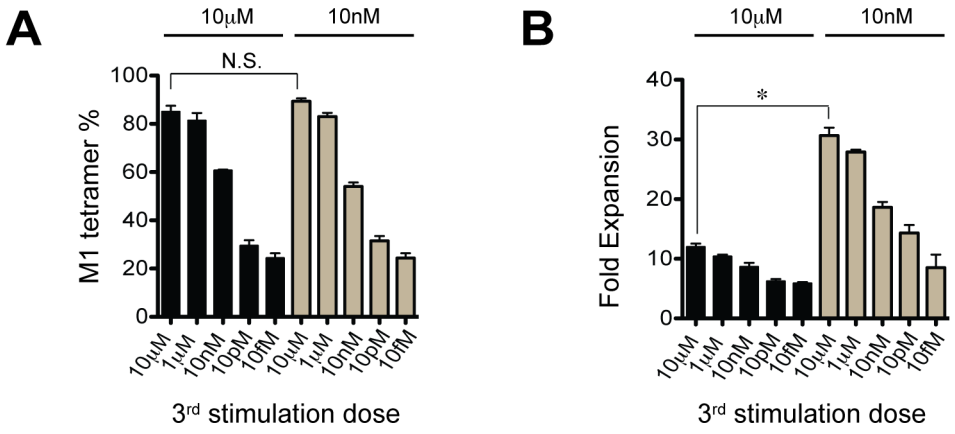
Polyfunctionality profile of T cells induced with different antigen concentrations



Complete polyfunctionality profile of M1-specific T cells on D14. For simplicity, only T cells induced with 10μM moDCs, 10nM moDCs and 10fM moDCs are shown. 10μM moDCs induced T cells with a dominant subpopulation producing MIP-1β and CD107a, but none of the tested cytokines (CD107a+, MIP-1β+, IL-2-, TNFα-, IFNγ-). In contrast, 10nM moDCs induced highest percentage of cells capable of five effector functions simultaneously (CD107a+, MIP-1β+, IL-2+, TNFα+, IFNγ+).

Supplementary Figure 2

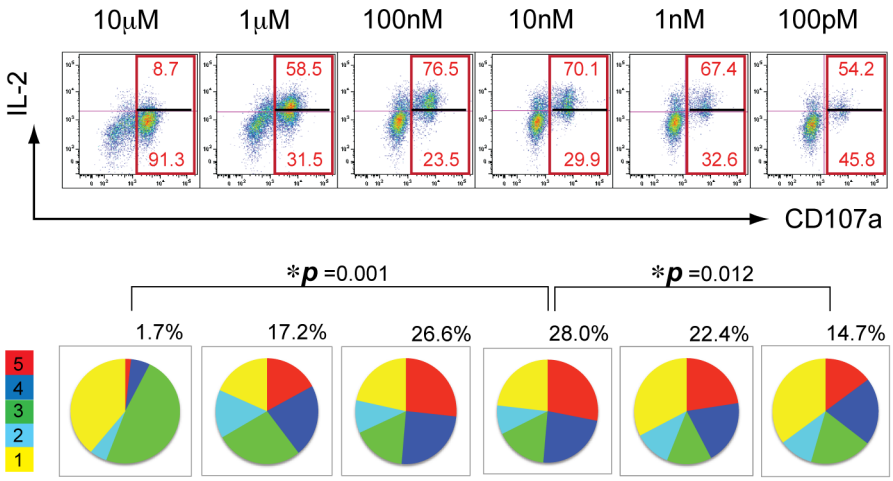
Highly polyfunctional T cells are equipped with superior proliferative capacity



T cells previously stimulated for 2 weeks with either high (10μM) or optimal (10nM) antigen concentration-pulsed moDCs were re-stimulated with different concentrations of antigen pulsed moDCs. After seven days, cells were harvested, counted, analyzed by tetramer staining and assayed for polyfunctionality. (**A**) M1-Tetramer staining, D21. (**B**) Absolute cell expansion after third stimulation. Despite various antigen concentration conditions used for third stimulation, T cells previously stimulated with optimal (10nM) antigen concentration exhibited superior third week cell number expansion (for all restimulation doses, $P < 0.05$).

Supplementary Figure 3

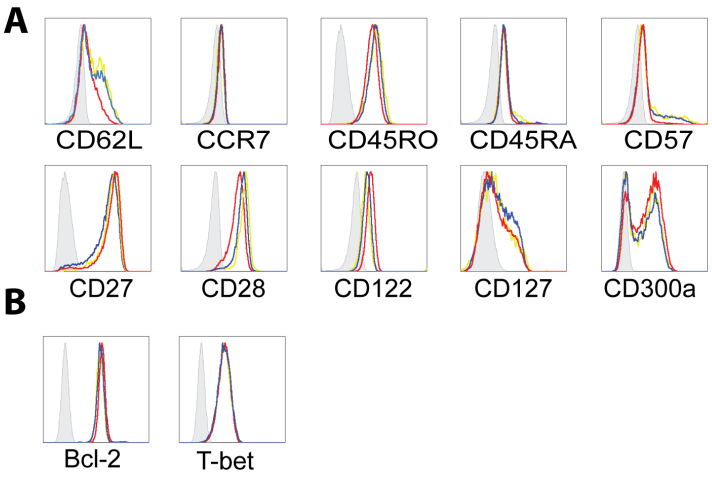
Naïve T cells exhibit impaired polyfunctional response in response to high concentration of anti-CD3/CD28 stimulation



Naïve T cells were isolated using Miltenyi naïve CD8+ T cell isolation kit. Cells were stimulated with plate bound antibodies at the indicated concentrations (equal concentrations of anti-CD3, clone HIT3a and anti-CD28, clone 28.2). Cells were harvested on D7 and restimulated with PMA/ionomycin for 5 hours before staining for intracellular cytokines. Consistent with what was observed with M1-specific T cells, strong stimulation of naïve T cells induced poorly polyfunctional T cells.

Supplementary Figure 4

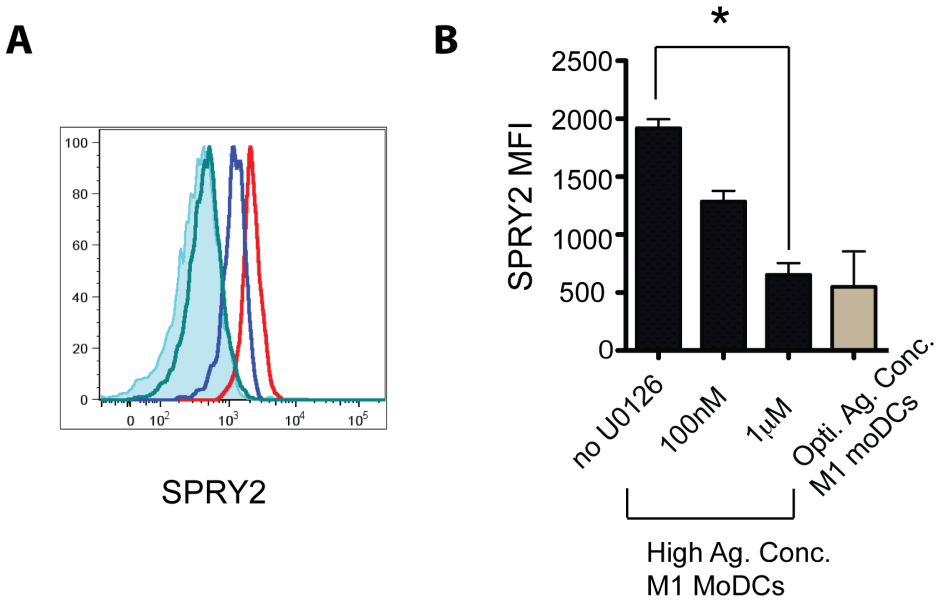
Phenotypic characterization of M1-specific T cells induced by different antigen concentrations



On D14, T cells were harvested and stained with anti-CD8, M1 tetramer and differentiation markers (**a**) or transcription factors (**b**). Representative histograms shown were gated on CD8+, M1 tetramer+ population. Red: 10μM. Blue: 10nM. Yellow: 10fM. All antigen concentrations induced M-1 specific T cells with a CD45RO+, CCR7-, CD28+, CD27+ effector memory phenotype. High (10μM) antigen concentration-induced M1-specific CD8+ T cells expressed significantly lower level of eomesodermin (**Fig.3b**) but maintained high levels of T-bet and bcl-2.

Supplementary Figure 5

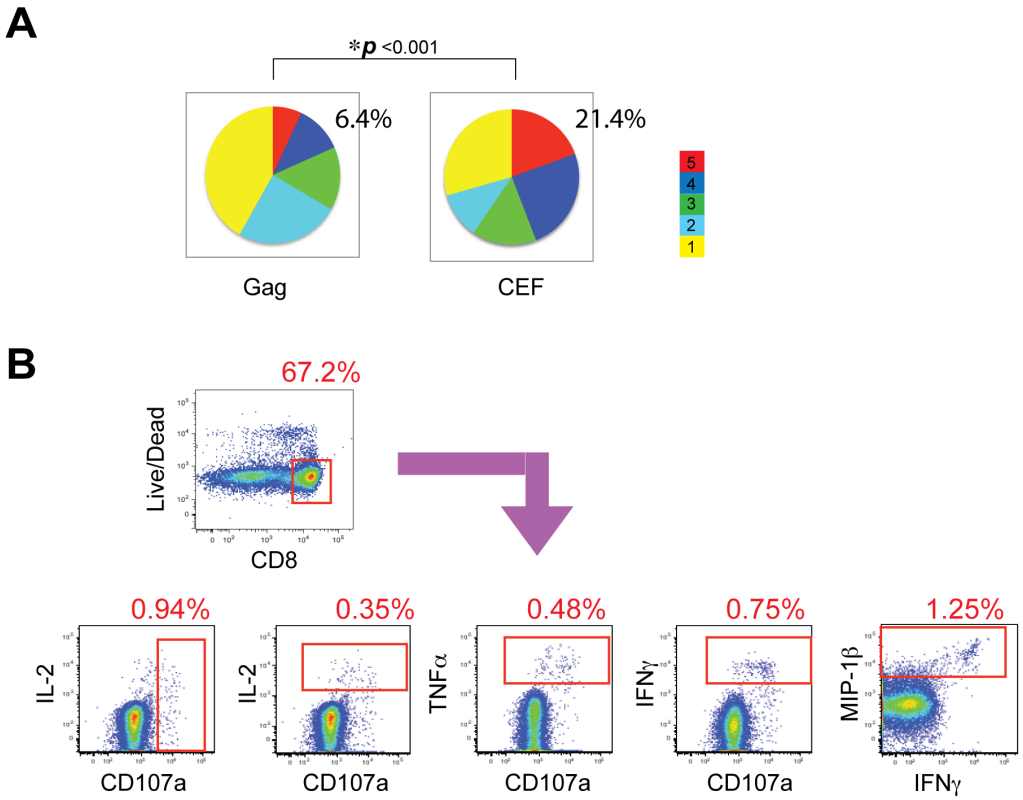
Upregulation of Spry2 in high concentration antigen-induced cells depends on the prior activation of MAPK/ERK pathway



D7 CD8+ T cells were restimulated with either high (10μM) or optimal (10nM) concentration M1 peptide-pulsed moDCs in the presence of different amounts of the ERK inhibitor, U0126. On D14, T cells were harvested and analyzed for SPRY2 levels. (**A**) CD8+ T cells induced with 10μM antigen were analyzed for SPRY2 levels after treatment with varying concentrations of U0126 (1μM, green; 100nM, blue; no U0126, red). SPRY2 levels in T cells induced with optimal concentration of antigen (10nM, shaded teal). (**B**) Inhibition of ERK pathway during prior T cell activation significantly inhibited the subsequent upregulation of SPRY2 (*P value <0.05).

Supplementary Figure 6

Representative HIV-specific T cell polyfunctional response and ex vivo polyfunctionality



PBMCs from HIV-infected patients were thawed, rested overnight and stimulated with peptide pools for six hours prior to cytokine analysis. (**A**) The direct ex vivo Gag and CEF-specific polyfunctional responses. Gag-specific T cells exhibit much less level of polyfunctionality. (**B**) Representative flowcytometry results of Gag-specific polyfunctional response in anti-PD-1 and *SPRY2*-knockdown virus treated cells.

Supplementary Table Legends

Supplementary Table 1

Functional clustering of differentially expressed genes between high (10μM moDCs) and optimal concentration (10nM moDCs)-induced T cells (*P* <0.05, fold change >1.6). Functional clustering was performed by DAVID/BP-FAT platform. For simplicity, only certain functional groups highly related to immune response are shown. Red and blue colored numbers indicate gene expression fold change as compared between different concentration-induced T cells. Refer to Supplementary Table 1 for a full list of differentially expressed genes and Supplementary Table 2 for a full list of functional groups.

Supplementary Table 2

Full list of differentially expressed genes identified by the microarray experiment

Group A: high antigen concentration (10μM) Group B: optimal antigen concentration (10nM)

Supplementary Table 3

A full list of functional groups generated from the full list of differentially expressed genes by GO-BP-FAT (Gene Ontology Biological Process, FAT term) tool on the DAVID platform.

Supplementary Table 1

Differentially expressed genes between high and optimal antigen concentration-induced T cells

Antigen Processing

HLA-DOA	-2.32
HLA-DPB2	-2.20
HLA-DPB1	-2.08
HLA-DPB1	-2.04
HLA-DPB1	-2.04
HLA-DPB1	-2.01
HLA-DRA	-1.97
HLA-DQA1	-1.81
HLA-DRB5	-1.78
HLA-DRB3	-1.77
HLA-DQA1	-1.77
HLA-DQA2	-1.73
HLA-DRB4	-1.66
HLA-DRB1	-1.66
HLA-DPA1	-1.61

Immune Cell Development

SIX1	-2.33
MAL	-2.02
TCF7	-1.98
FOXP1	-1.80
EOMES	-1.69
TBX1	1.63
CSF2	1.86
DYRK3	2.03
KIT	2.23
AIRE	5.22
DLL1	6.77
SALL4	10.43
POU2AF1	43.19

Chemotaxis

CCL17	-21.32
CCL22	-9.66
CXCL9	-4.54
CMTM8	-4.14
CCR7	-4.05
CXCR4	-1.99
CCL18	1.98
CXCR1	1.98
CCL4	2.34
CX3CR1	5.80
CCL3	5.95
CCL3L3	7.15

Inhibitory Receptor

PTGER3	1.66
KLRG1	2.07
PDCD1	2.09
KLRC4	2.12
KLRC3	2.33
KLRC1	2.40
CD244	2.44
KLRD1	2.67

T cell activation

IL13RA1	-6.41
IDO1	-3.46
IL13	-3.35
IL5	-2.42
IL4R	-2.37
IL18R1	-2.12
CD5	-1.86
CD28	-1.85
TNFSF4	1.87
CD40LG	2.48
CD276	5.97

Cytotoxicity

NCR2	1.64
KIR3DX1	1.77
PRF1	1.90
NCR1	1.97
FCGR2A	4.19
KIR2DL2	5.05
FCGR2B	5.77
KIR2DS2	6.27
KIR2DS4	6.45
KIR2DL4	7.59
FCGR3A	8.71
KIR3DL1	9.20
KIR2DL5A	12.58

Cell Death

TNFRSF10D	-2.74
CLU	-2.20
BCL6	-1.82
BCL2L11	-1.77
TNFRSF10A	-1.74
TNFRSF9	2.65
TNFRSF4	2.78
TNFRSF18	3.64
DAPK2	4.44

Intracellular Signaling

MARCKS	-9.02
RCAN2	-6.08
HOMER2	-5.92
SMAD1	-5.44
HOMER3	-4.42
PRKCE	-2.28
SOCS3	-2.17
DKK3	-2.08
NKD2	-1.83
TLR2	-1.80
TLE2	-1.76
TLR6	-1.72
GPR55	-1.70
RASGRP3	-1.69
INSR	-1.69
NOD2	-1.65
MAP4K3	1.62
JUN	1.62
ADAP1	1.63
DOK4	1.63
RGS3	1.65
GRB10	1.65
PDGFRB	1.66
IRAK2	1.66
ADCY9	1.66
RHOC	1.67
DOCK7	1.69
GPR63	1.77
ADCY2	1.78

RHOB	1.78
SOCS2	1.79
TLE1	1.92
LAT2	1.93
PTPRU	1.97
RASGEF1A	2.00
RAB38	2.00
SOX4	2.00
MAPK12	2.10
NDST1	2.21
RASGEF1A	2.25
FZD3	2.29
RAB31	2.38
ROR2	2.43
LRP5	2.44
FZD6	2.77
DOCK5	2.85
SOCS6	2.86
DOK5	3.04
VAV3	3.14
SPRY2	3.30
PDGFA	3.55
RASGRF2	4.98
ZC3H12C	5.74
PLD1	6.72
GEM	7.62
GPR56	7.96
LYN	8.07
WNT11	8.31

Actin Cytoskeleton

FSCN1	-5.07
CGN	-2.22
CORO2A	-1.94
CTNNA1	1.63
CORO1C	1.81
ACTN3	1.87
DST	2.02
MYO1D	4.10
MYOF	8.21

Adhesion

PECAM1	-2.10
SELL	-1.90
SPON2	-1.89
ICAM4	1.66
NRP1	1.69
VCAM1	1.74
ITGA1	1.75
ITGAX	1.78
ITGA2	1.96
NCAM1	19.16
SPOCK1	27.87

Red: up in high antigen concentration-induced T cells
Blue: up in optimal antigen concentration-induced T cells

Supplementary Table 2

A full list of differentially expressed genes from microarray analysis

Group A: high antigen conc. (10mM) Group B: optimal antigen conc. (10nM)

Probeset ID	GeneName	Full Gene Name	FoldChange (A/B)	p-value	t
A_33_P3620881	LOC728218	-	-26.47	0.00455792	-4.87876
A_23_P26325	CCL17	chemokine (C-C motif) ligand 17	-21.32	2.70E-05	-14.6251
A_33_P3224710	TFEC	transcription factor EC	-14.21	0.000128957	-10.604
A_24_P313418	CCL22	chemokine (C-C motif) ligand 22	-9.66	0.00736082	-4.34977
A_23_P421423	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	-9.51	0.000484112	-8.03077
A_23_P214222	MARCKS	myristoylated alanine-rich protein kinase C substrate	-9.02	0.0369292	-2.82412
A_32_P2634	CR604707	-	-8.42	0.000160059	-10.1381
A_23_P81898	UBD	ubiquitin D	-7.76	0.00223105	-5.7503
A_32_P184394	TFEC	transcription factor EC	-7.19	7.80E-05	-11.7664
A_33_P3263217	LRRC4	leucine rich repeat containing 4	-7.16	0.000976111	-6.90511
A_24_P389916	LRRC32	leucine rich repeat containing 32	-7.12	5.91E-05	-12.4596
A_23_P1833	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-6.65	0.000103724	-11.0935
A_24_P280113	IL13RA1	interleukin 13 receptor, alpha 1	-6.41	0.00737058	-4.34836
A_32_P156851	RCAN2	regulator of calcineurin 2	-6.08	0.000139155	-10.4377
A_23_P99906	HOMER2	homer homolog 2 (Drosophila)	-5.92	0.00100357	-6.8635
A_24_P71938	SMAD1	SMAD family member 1	-5.44	3.37E-07	-35.4396
A_33_P3349384	A_33_P3349384	-	-5.20	0.000198629	-9.6915
A_32_P30905	WDFY4	WDFY family member 4	-5.17	0.00290695	-5.41494
A_33_P3411075	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	-5.07	4.36E-05	-13.2603
A_33_P3323535	ENST00000390453	-	-5.06	0.00508355	-4.75464
A_23_P29773	LAMP3	lysosomal-associated membrane protein 3	-4.72	0.0010091	-6.85527
A_33_P3379396	KRT1	keratin 1	-4.68	0.000280822	-9.0125
A_23_P25994	LGMN	legumain	-4.61	9.05E-05	-11.4117
A_23_P18452	CXCL9	chemokine (C-X-C motif) ligand 9	-4.54	0.00455964	-4.87833
A_33_P3372727	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-4.48	0.000379251	-8.45841
A_23_P133691	RRAGD	Ras-related GTP binding D	-4.46	0.00472718	-4.83704
A_33_P3265376	HOMER3	homer homolog 3 (Drosophila)	-4.42	0.00118945	-6.61315
A_23_P386310	HRH4	histamine receptor H4	-4.22	0.000580249	-7.72585
A_23_P74609	G0S2	G0/G1switch 2	-4.22	0.00551167	-4.66411
A_23_P41114	CSTA	cystatin A (stefin A)	-4.19	0.00579323	-4.60892
A_23_P40880	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	-4.14	4.59E-05	-13.1197
A_23_P27795	SPINT2	serine peptidase inhibitor, Kunitz type, 2	-4.06	2.46E-05	-14.9
A_19_P00810351	.:chr14:98359372-9905	-	-4.05	0.000280011	-9.01799
A_23_P343398	CCR7	chemokine (C-C motif) receptor 7	-4.05	0.00185955	-5.9903
A_19_P00321597	.:chr14:98399398-9844	-	-4.02	0.000258135	-9.17358
A_33_P3344504	ENST00000382938	-	-4.02	0.0252425	-3.15479
A_23_P85922	BMP8A	bone morphogenetic protein 8a	-3.88	0.0133129	-3.7486
A_23_P69293	CHDH	choline dehydrogenase	-3.83	0.00267322	-5.5195
A_33_P3293321	OR6C70	olfactory receptor, family 6, subfamily C, member 70	-3.80	0.00458852	-4.87109
A_24_P157370	IL17RB	interleukin 17 receptor B	-3.80	0.00272116	-5.4972
A_33_P3275500	ENST00000412427	-	-3.79	0.0263728	-3.11595
A_23_P420692	PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	-3.74	0.0262327	-3.12066
A_24_P615822	BMS1	BMS1 homolog, ribosome assembly protein (yeast)	-3.73	0.000136063	-10.4865
A_32_P105549	ANXA8L2	annexin A8-like 2	-3.68	1.45E-06	-26.4439
A_19_P00800763	.:chr12:68421607-6842	-	-3.68	1.65E-05	-16.1648
A_32_P208823	PLXDC1	plexin domain containing 1	-3.59	0.00344739	-5.20683
A_23_P119353	RASIP1	Ras interacting protein 1	-3.53	0.00201117	-5.88607
A_33_P3418716	EFHD1	EF-hand domain family, member D1	-3.52	0.0183471	-3.44445
A_23_P112026	IDO1	indoleamine 2,3-dioxygenase 1	-3.46	0.0018927	-5.96667
A_19_P00318940	.:chr14:98411873-9841	-	-3.44	8.48E-05	-11.5639
A_24_P56330	C13orf16	testis expressed 29	-3.42	0.000583006	-7.718
A_33_P3417427	ENST00000377597	-	-3.39	0.00194011	-5.93373
A_23_P251031	IL13	interleukin 13	-3.35	0.00527848	-4.71236
A_23_P208182	SIGLEC10	sialic acid binding Ig-like lectin 10	-3.33	0.0307723	-2.98078

A_33_P3224800	A_33_P3224800	-	-3.32	0.00239588	-5.65844
A_23_P118493	TOM1L1	target of myb1 (chicken)-like 1	-3.29	0.00192533	-5.94389
A_33_P3403942	C20orf123	osteoclast stimulatory transmembrane protein	-3.25	0.0485978	-2.59405
A_33_P3366758	ST8SIA6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	-3.19	0.0020923	-5.83403
A_32_P192376	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-3.13	4.16E-05	-13.3852
A_33_P3395947	ENST00000380922	-	-3.08	0.000614974	-7.63016
A_23_P156880	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-3.06	4.64E-05	-13.0898
A_23_P3911	PLXDC1	plexin domain containing 1	-3.05	0.00287148	-5.43016
A_33_P3375435	AGAP11	ankyrin repeat and GTPase domain Arf GTPase activating protein 11	-3.03	0.000219044	-9.4951
A_33_P3279158	NBPF6	neuroblastoma breakpoint family, member 6	-3.02	0.0445841	-2.66558
A_33_P3257330	DCBLD1	discoidin, CUB and LCCL domain containing 1	-3.02	0.000292824	-8.93342
A_33_P3245126	A_33_P3245126	-	-3.01	0.00152994	-6.25613
A_24_P926960	MEGF6	multiple EGF-like-domains 6	-2.96	0.00647533	-4.48723
A_23_P149545	HIST2H2BE	histone cluster 2, H2be	-2.96	0.0296256	-3.01382
A_33_P3248439	FAM125B	family with sequence similarity 125, member B	-2.95	0.00112322	-6.69669
A_33_P3300253	PTPN20B	protein tyrosine phosphatase, non-receptor type 20B	-2.95	0.000177549	-9.92128
A_33_P3286916	PDZD7	PDZ domain containing 7	-2.94	0.00711523	-4.38589
A_32_P150142	DKFZp434L192	-	-2.93	0.0124275	-3.8157
A_33_P3295623	A_33_P3295623	-	-2.92	0.0077465	-4.29577
A_23_P409462	DCBLD1	discoidin, CUB and LCCL domain containing 1	-2.89	0.00342143	-5.21593
A_23_P433785	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-2.88	0.000369976	-8.50289
A_33_P3374878	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	-2.87	0.00981436	-4.05114
A_33_P3393170	CAPN5	calpain 5	-2.86	0.00104903	-6.79748
A_19_P00316387	:chr2:179914333-1799	-	-2.81	0.0387772	-2.78272
A_23_P37988	CPNE2	copine II	-2.80	9.22E-05	-11.3665
A_23_P354591	FAM125B	family with sequence similarity 125, member B	-2.77	0.00894105	-4.14643
A_24_P51909	CPLX1	complexin 1	-2.76	8.70E-05	-11.5037
A_24_P319684	CCDC121	coiled-coil domain containing 121	-2.76	0.0366513	-2.83054
A_23_P360754	ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	-2.76	4.08E-05	-13.4407
A_33_P3326588	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	-2.74	0.000167972	-10.0367
A_24_P414376	KLF3	Kruppel-like factor 3 (basic)	-2.72	0.00224932	-5.73973
A_33_P3372212	PSG10P	pregnancy specific beta-1-glycoprotein 10, pseudogene	-2.72	0.0130902	-3.76499
A_23_P412562	C1orf162	chromosome 1 open reading frame 162	-2.69	0.00391023	-5.05692
A_33_P3213707	PDCD1LG2	programmed cell death 1 ligand 2	-2.69	0.000372247	-8.49187
A_32_P47643	FAM110C	family with sequence similarity 110, member C	-2.69	0.000196323	-9.71518
A_19_P00330198	:chr2:208360030-2083	-	-2.68	0.0430947	-2.69395
A_24_P48723	PTGIS	prostaglandin I2 (prostacyclin) synthase	-2.66	0.00443635	-4.90985
A_23_P393777	PTGDR	prostaglandin D2 receptor (DP)	-2.65	0.00440492	-4.91805
A_19_P00321651	:chr2:213437296-2137	-	-2.64	0.0371974	-2.81797
A_24_P304071	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	-2.64	0.00620737	-4.53318
A_33_P3252475	C14orf64	chromosome 14 open reading frame 64	-2.64	0.00155963	-6.22953
A_33_P3210099	ALPK3	alpha-kinase 3	-2.62	0.0357038	-2.85286
A_19_P00812190	A:chr1:89874262-8994	-	-2.61	0.0462123	-2.63575
A_23_P75786	SLC15A3	solute carrier family 15, member 3	-2.61	0.0166925	-3.53266
A_32_P142128	BMS1P1	BMS1 pseudogene 1	-2.60	6.95E-06	-19.2672
A_23_P30163	FLJ13197	-	-2.57	0.0171844	-3.50543
A_24_P12136	S100Z	S100 calcium binding protein Z	-2.55	0.00819968	-4.23616
A_23_P154605	SULF2	sulfatase 2	-2.55	0.0151578	-3.62387
A_33_P3642036	LOC100289333	-	-2.54	0.0233357	-3.22499
A_33_P3442605	LOC389641	-	-2.52	0.00364648	-5.13963
A_23_P369899	TMEM158	transmembrane protein 158 (gene/pseudogene)	-2.52	0.0350382	-2.86894
A_24_P165864	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	-2.50	0.0039665	-5.04011
A_33_P3321993	A_33_P3321993	-	-2.50	0.0259545	-3.1301
A_33_P3412658	LOC100289509	-	-2.50	0.0468252	-2.62481
A_33_P3375127	LOC100131581	-	-2.49	0.0325814	-2.93136
A_32_P221958	AGAP7	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7	-2.49	0.00130638	-6.47826
A_33_P3832872	LOC389247	-	-2.48	0.0100543	-4.02667
A_23_P58266	S100P	S100 calcium binding protein P	-2.48	1.91E-06	-25.0042
A_33_P3382137	LOC728671	-	-2.45	0.00164635	-6.15513

A_33_P3363245	NXPH4	neurexophilin 4	-2.43	0.020511	-3.34185
A_33_P3514859	LOC100506342	-	-2.43	0.0067826	-4.43718
A_24_P209047	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	-2.42	0.0234805	-3.21943
A_23_P413760	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-2.42	9.99E-05	-11.1802
A_23_P56659	DQX1	DEAQ box RNA-dependent ATPase 1	-2.42	0.0264004	-3.11502
A_23_P42746	NCF1	neutrophil cytosolic factor 1	-2.41	0.00644417	-4.49246
A_24_P30923	SNN	stannin	-2.40	0.000848948	-7.1177
A_24_P261750	KERA	keratocan	-2.40	0.0402208	-2.75187
A_32_P230196	AGAP7	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7	-2.38	0.00207632	-5.84409
A_33_P3349045	IL4R	interleukin 4 receptor	-2.37	2.98E-06	-22.8607
A_23_P14124	RASL11A	RAS-like, family 11, member A	-2.35	0.00402436	-5.02313
A_19_P00316880	:chr2:235353233-2353(	-	-2.34	0.00565659	-4.63531
A_33_P3337485	CD248	CD248 molecule, endosialin	-2.34	0.00125075	-6.54058
A_23_P76914	SIX1	SIX homeobox 1	-2.33	0.0254388	-3.14791
A_33_P3240972	LOC100134285	-	-2.33	0.0263346	-3.11723
A_33_P3415500	ENST00000541447	-	-2.32	0.000884482	-7.05468
A_32_P356316	HLA-DOA	major histocompatibility complex, class II, DO alpha	-2.32	3.36E-06	-22.3059
A_33_P3780505	MT1DP	metallothionein 1D, pseudogene	-2.30	0.0169411	-3.51878
A_23_P328740	NEURL3	neuralized homolog 3 (Drosophila) pseudogene	-2.30	0.000324182	-8.7438
A_33_P3283824	SLC39A8	solute carrier family 39 (zinc transporter), member 8	-2.30	0.0041862	-4.97708
A_32_P114284	IKZF2	IKAROS family zinc finger 2 (Helios)	-2.29	0.000920354	-6.99403
A_23_P250564	PRKCE	protein kinase C, epsilon	-2.28	0.0025882	-5.56022
A_32_P194312	SDK2	sidekick cell adhesion molecule 2	-2.27	0.0065374	-4.4769
A_33_P3373573	ENST00000444406	-	-2.27	0.00102357	-6.83402
A_33_P3293391	LOC642826	-	-2.27	0.00105666	-6.78673
A_19_P00320622	.:chr22:27068773-2717	-	-2.26	0.00270292	-5.50563
A_33_P3294177	LOC100131043	-	-2.25	0.00155384	-6.23467
A_33_P3422822	GJC2	gap junction protein, gamma 2, 47kDa	-2.25	0.000723783	-7.36741
A_19_P00316881	:chr2:235353233-2353(	-	-2.25	0.0154	-3.60879
A_23_P94319	KBTBD11	kelch repeat and BTB (POZ) domain containing 11	-2.24	0.00303087	-5.36343
A_33_P3395848	VSIG10L	V-set and immunoglobulin domain containing 10 like	-2.23	0.00886723	-4.15497
A_33_P3211666	IL18R1	interleukin 18 receptor 1	-2.23	0.000685168	-7.45496
A_23_P15174	MT1F	metallothionein 1F	-2.23	0.000311714	-8.81647
A_33_P3589543	ENST00000527620	-	-2.22	0.00410586	-4.99967
A_23_P7827	FAM26F	family with sequence similarity 26, member F	-2.22	0.00698435	-4.40573
A_33_P3329974	CGN	cingulin	-2.22	0.0278717	-3.06723
A_19_P00813413	:chr1:229378602-2293(	-	-2.21	0.0310505	-2.97297
A_23_P163087	NID2	nidogen 2 (osteonidogen)	-2.21	0.00911091	-4.12707
A_23_P154338	EFHD1	EF-hand domain family, member D1	-2.21	0.0187619	-3.42375
A_24_P778906	ENST00000435913	-	-2.20	0.00289697	-5.4192
A_23_P215913	CLU	clusterin	-2.20	0.0203185	-3.35046
A_24_P288836	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	-2.20	0.000422622	-8.26631
A_33_P3842551	IKZF2	IKAROS family zinc finger 2 (Helios)	-2.20	0.00469943	-4.84376
A_23_P357185	CHDH	choline dehydrogenase	-2.19	0.000621666	-7.61246
A_19_P00803836	A:chr2:65103471-6518(	-	-2.19	0.0210404	-3.31861
A_23_P331560	SLC26A4	solute carrier family 26, member 4	-2.18	0.046314	-2.63392
A_33_P3245937	LOC100128402	-	-2.18	0.0285334	-3.04664
A_33_P3345836	ENST00000391437	-	-2.17	0.00397565	-5.03741
A_24_P255100	C9orf135	chromosome 9 open reading frame 135	-2.17	0.0132154	-3.75573
A_23_P207058	SOCS3	suppressor of cytokine signaling 3	-2.17	0.00100486	-6.86157
A_33_P3549091	LOC100131347	-	-2.16	0.0421389	-2.71273
A_24_P729905	AGAP7	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7	-2.15	0.00118503	-6.61855
A_19_P00322745	.:chr21:29817053-3004	-	-2.15	0.0116177	-3.88206
A_33_P3364180	FGD5	FYVE, RhoGEF and PH domain containing 5	-2.15	0.0340101	-2.89445
A_33_P3354076	FAM172BP	family with sequence similarity 172, member B, pseudogene	-2.13	0.0205278	-3.3411
A_33_P3251876	IL18R1	interleukin 18 receptor 1	-2.12	0.00134543	-6.43637
A_33_P3268304	LIMS2	LIM and senescent cell antigen-like domains 2	-2.12	2.97E-05	-14.3446
A_23_P425880	TRIO	trio Rho guanine nucleotide exchange factor	-2.10	0.00143545	-6.34502
A_32_P41526	AGAP7	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7	-2.10	0.00271938	-5.49802
A_24_P86993	JAM3	junctional adhesion molecule 3	-2.10	0.00228099	-5.72165
A_23_P321201	DENND5A	DENN/MADD domain containing 5A	-2.10	1.63E-05	-16.2117
A_33_P3398513	LOC728819	-	-2.10	0.0425918	-2.70377
A_33_P3229402	PECAM1	platelet/endothelial cell adhesion molecule 1	-2.10	0.00201053	-5.88649

A_23_P404536	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-2.10	0.000905138	-7.01941
A_23_P18372	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	-2.10	0.0192616	-3.3995
A_23_P359214	LOC643650	-	-2.10	0.00281909	-5.45305
A_23_P408996	MBOAT1	membrane bound O-acyltransferase domain containing 1	-2.09	0.000786323	-7.23675
A_19_P00322461	:chr22:27188218-2719	-	-2.09	0.00976958	-4.05578
A_24_P261417	DKK3	dickkopf 3 homolog (Xenopus laevis)	-2.08	0.0219999	-3.27813
A_33_P3272395	RAB19	RAB19, member RAS oncogene family	-2.08	0.000382872	-8.44139
A_23_P95029	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	-2.08	0.000183666	-9.85138
A_33_P3291379	MSGN1	mesogenin 1	-2.08	0.0403567	-2.74903
A_33_P3248325	EPB41L5	erythrocyte membrane protein band 4.1 like 5	-2.08	0.0130151	-3.77058
A_33_P3865368	LOC254896	-	-2.08	0.00686277	-4.42456
A_33_P3271651	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	-2.08	0.00201344	-5.88458
A_33_P3273885	ENST00000442680	-	-2.07	0.000546965	-7.82416
A_23_P314712	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	-2.07	0.000505275	-7.95781
A_23_P94412	PDCD1LG2	programmed cell death 1 ligand 2	-2.06	0.000453487	-8.14334
A_32_P797019	ENST00000532531	-	-2.06	0.00361083	-5.15134
A_19_P00315508	A:chr7:22611226-2270	-	-2.06	0.0497134	-2.57532
A_24_P204727	ENST00000390624	-	-2.06	0.0460546	-2.63859
A_23_P22444	CFP	complement factor properdin	-2.05	9.79E-06	-17.9756
A_23_P66481	RTN4RL1	reticulon 4 receptor-like 1	-2.04	0.00869679	-4.17501
A_23_P258769	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	-2.04	0.0013236	-6.45961
A_33_P3271635	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	-2.04	0.00345088	-5.20562
A_33_P3241891	ENST00000377823	-	-2.04	0.0386092	-2.78639
A_23_P252471	PECAM1	platelet/endothelial cell adhesion molecule 1	-2.04	0.00224333	-5.74318
A_19_P00319011	:chr2:235358561-2353	-	-2.04	0.00372726	-5.11357
A_19_P00811717	:chr7:105517604-1055	-	-2.04	0.00977192	-4.05554
A_33_P3304983	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	-2.04	0.0408831	-2.73813
A_23_P52986	VWCE	von Willebrand factor C and EGF domains	-2.04	7.30E-05	-11.927
A_33_P3222653	LOC100131366	-	-2.03	0.00807885	-4.25168
A_19_P00812662	A:chr12:5377839-5428	-	-2.03	0.0349756	-2.87047
A_24_P7600	FBXL7	F-box and leucine-rich repeat protein 7	-2.03	0.0019627	-5.91836
A_33_P3368334	ENST00000368186	-	-2.03	0.0260282	-3.12759
A_19_P00322746	:chr21:29817053-3004	-	-2.02	0.0202801	-3.3522
A_24_P659836	C22orf41	synaptonemal complex central element protein 3	-2.02	0.000290105	-8.951
A_19_P00318517	:chr22:27172806-2717	-	-2.02	0.00245734	-5.62608
A_23_P17134	MAL	mal, T-cell differentiation protein	-2.02	2.34E-06	-24.0054
A_19_P00809119	A:chr6:22020628-2211	-	-2.01	0.049071	-2.58605
A_24_P166443	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	-2.01	0.00189178	-5.96733
A_33_P3234138	FAM172BP	family with sequence similarity 172, member B, pseudogene	-2.01	0.035573	-2.85599
A_23_P345220	SH3PXD2A	SH3 and PX domains 2A	-2.01	0.00231863	-5.70053
A_23_P19226	DSE	dermatan sulfate epimerase	-2.00	0.00567249	-4.6322
A_24_P208567	IL18R1	interleukin 18 receptor 1	-2.00	0.000296903	-8.90742
A_33_P3421907	NP105395	-	-2.00	0.00020266	-9.65086
A_33_P3405213	PECAM1	platelet/endothelial cell adhesion molecule 1	-1.99	0.000155094	-10.2048
A_33_P3297020	PSORS1C3	psoriasis susceptibility 1 candidate 3 (non-protein coding)	-1.99	0.0228241	-3.24492
A_24_P357847	LOC100510044	-	-1.99	0.0331538	-2.91636
A_23_P102000	CXCR4	chemokine (C-X-C motif) receptor 4	-1.99	0.00150848	-6.27574
A_33_P3250671	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-1.98	0.00292985	-5.40523
A_33_P3278137	RPL31P11	ribosomal protein L31 pseudogene 11	-1.98	0.0366495	-2.83058
A_23_P399681	TSSK3	testis-specific serine kinase 3	-1.98	0.016439	-3.54704
A_33_P3290089	LOC100505585	-	-1.97	0.0163927	-3.5497
A_23_P101246	VSIG10L	V-set and immunoglobulin domain containing 10 like	-1.97	1.34E-05	-16.8553
A_23_P146849	APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2	-1.97	0.0356565	-2.85399
A_32_P87697	HLA-DRA	major histocompatibility complex, class II, DR alpha	-1.97	0.000687093	-7.45046
A_23_P256624	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	-1.96	0.0046644	-4.85231

A_33_P3350094	PATL2	protein associated with topoisomerase II homolog 2 (yeast)	-1.96	0.000686823	-7.45109
A_23_P212089	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	-1.96	3.19E-05	-14.1387
A_19_P00318710	A:chr6:40308265-4034	-	-1.95	0.0342932	-2.88734
A_19_P00813192	chr11:104771490-1047	-	-1.95	0.00188333	-5.97331
A_24_P193295	RAB15	RAB15, member RAS oncogene family	-1.94	0.000696347	-7.42902
A_33_P3387115	BC021693	-	-1.94	0.0251892	-3.15667
A_32_P60606	ENST00000391437	-	-1.94	0.00709035	-4.38963
A_23_P7582	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-1.94	0.00241063	-5.65059
A_32_P34138	FAM25A	family with sequence similarity 25, member A	-1.94	0.000221514	-9.47282
A_19_P00321345	.:chr21:29818746-3004	-	-1.94	0.00117512	-6.63075
A_23_P421811	C20orf132	chromosome 20 open reading frame 132	-1.94	0.0178667	-3.46909
A_23_P20443	LZTS1	leucine zipper, putative tumor suppressor 1	-1.94	0.00977713	-4.055
A_23_P146444	CORO2A	coronin, actin binding protein, 2A	-1.94	0.000222617	-9.46297
A_33_P3304369	A_33_P3304369	-	-1.93	0.00958702	-4.07497
A_23_P89310	EPN2	epsin 2	-1.93	0.00208837	-5.83649
A_24_P166613	EPDR1	ependymin related protein 1 (zebrafish)	-1.93	0.0245411	-3.1799
A_23_P252106	RIPK2	receptor-interacting serine-threonine kinase 2	-1.92	0.000356546	-8.5697
A_33_P3411372	A_33_P3411372	-	-1.92	0.0109884	-3.93741
A_23_P26024	C15orf48	chromosome 15 open reading frame 48	-1.92	0.0462192	-2.63562
A_19_P00321601	.:chr19:28284384-2828	-	-1.92	0.0489879	-2.58745
A_33_P3383233	NDRG2	NDRG family member 2	-1.92	0.00512941	-4.74452
A_23_P215828	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	-1.92	0.034643	-2.87864
A_24_P925799	ENST00000390369	-	-1.92	0.0423316	-2.7089
A_33_P3226008	GCET2	germinal center expressed transcript 2	-1.92	0.0129999	-3.77172
A_23_P30900	ENST00000383251	-	-1.92	1.61E-05	-16.2481
A_24_P203056	BCL7A	B-cell CLL/lymphoma 7A	-1.92	0.0397935	-2.76087
A_19_P00813375	A:chr5:43011418-4301	-	-1.91	0.00104207	-6.80737
A_19_P00323461	:chr2:158570854-1585	-	-1.91	0.000937472	-6.96607
A_24_P100830	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	-1.91	0.000717508	-7.38126
A_19_P00321346	.:chr21:29818746-3004	-	-1.91	0.00113078	-6.68686
A_19_P00331620	.:chr12:96953169-9699	-	-1.91	0.0379761	-2.80039
A_19_P00319561	A:chrX:73164162-7328	-	-1.91	0.0453489	-2.65142
A_33_P3400273	SELL	selectin L	-1.90	0.000155068	-10.2052
A_23_P21495	FCGBP	Fc fragment of IgG binding protein	-1.90	8.91E-05	-11.4476
A_32_P163858	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-1.90	0.00554676	-4.65706
A_33_P3240722	CNKSR2	connector enhancer of kinase suppressor of Ras 2	-1.90	0.0234201	-3.22175
A_23_P121533	SPON2	spondin 2, extracellular matrix protein	-1.89	0.0172428	-3.50226
A_33_P3245095	LOC100506296	-	-1.89	0.0437562	-2.68122
A_32_P70927	PAGE2	P antigen family, member 2 (prostate associated)	-1.88	0.0159668	-3.57454
A_23_P59976	GML	glycosylphosphatidylinositol anchored molecule like protein	-1.88	0.000331056	-8.70514
A_24_P270460	IFI27	interferon, alpha-inducible protein 27	-1.88	0.000158271	-10.1619
A_23_P129786	SREBF1	sterol regulatory element binding transcription factor 1	-1.88	0.00121443	-6.58305
A_23_P206724	MT1E	metallothionein 1E	-1.88	0.000222555	-9.46352
A_33_P3340852	ENST00000427543	-	-1.87	0.0106494	-3.96875
A_32_P170397	ENST00000309874	-	-1.87	0.00492943	-4.78942
A_33_P3305023	WWOX	WW domain containing oxidoreductase	-1.87	0.0136428	-3.72489
A_33_P3298990	CD5	CD5 molecule	-1.86	0.00022226	-9.46615
A_33_P3413612	AK096239	-	-1.86	0.000868111	-7.08333
A_19_P00807448	:chr1:101518537-1015	-	-1.86	0.0116675	-3.87783
A_23_P41424	SLC39A8	solute carrier family 39 (zinc transporter), member 8	-1.86	2.46E-05	-14.9092
A_33_P3336552	LOC100130701	-	-1.86	0.0435856	-2.68448
A_23_P129556	IL4R	interleukin 4 receptor	-1.85	0.000315962	-8.79133
A_33_P3259253	CD28	CD28 molecule	-1.85	0.00239629	-5.65822
A_33_P3250887	C22orf41	synaptonemal complex central element protein 3	-1.85	0.000162661	-10.1041
A_24_P396753	TRIB2	tribbles homolog 2 (Drosophila)	-1.85	0.006128	-4.54723
A_23_P66241	MT1M	metallothionein 1M	-1.84	0.000460238	-8.11776
A_19_P00811116	A:chr4:23771777-2377	-	-1.84	0.0472306	-2.61767
A_33_P3341269	ENST00000455832	-	-1.84	0.0377452	-2.80556
A_23_P41804	NKD2	naked cuticle homolog 2 (Drosophila)	-1.83	0.00264664	-5.53207
A_33_P3611762	FLJ37798	-	-1.83	0.0133325	-3.74718
A_23_P12733	H2AFY2	H2A histone family, member Y2	-1.82	0.00179698	-6.03627
A_32_P874898	ENST00000390381	-	-1.82	0.0212461	-3.30976

A_23_P57856	BCL6	B-cell CLL/lymphoma 6	-1.82	0.00308741	-5.34074
A_24_P627503	LOC100510678	-	-1.82	0.0394814	-2.76751
A_23_P360804	CPNE5	copine V	-1.82	0.0066401	-4.46006
A_23_P35456	SH3PXD2A	SH3 and PX domains 2A	-1.82	1.14E-05	-17.4149
A_33_P3233070	LOC100505564	-	-1.82	0.04021	-2.7521
A_23_P119943	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	-1.82	0.002619	-5.54529
A_33_P3282354	LOC732443	-	-1.81	0.0174173	-3.49285
A_33_P3273884	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	-1.81	0.00103285	-6.82058
A_23_P140434	MYO5C	myosin VC	-1.81	0.0248297	-3.16947
A_33_P3255914	MYLIP	myosin regulatory light chain interacting protein	-1.81	0.0111019	-3.92716
A_33_P3214310	FOXP1	forkhead box P1	-1.80	1.93E-05	-15.6552
A_19_P00805681	:chr2:138829880-1388	-	-1.80	0.0331765	-2.91577
A_23_P92499	TLR2	toll-like receptor 2	-1.80	0.0135001	-3.73507
A_23_P41217	CD200R1	CD200 receptor 1	-1.79	0.000102109	-11.1296
A_23_P416774	CLIC5	chloride intracellular channel 5	-1.79	0.000809117	-7.19216
A_33_P3315729	ZNF382	zinc finger protein 382	-1.79	0.0165588	-3.54022
A_19_P00315750	IA:chr9:5584489-5588	-	-1.78	0.0483969	-2.59748
A_23_P45099	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	-1.78	0.00057894	-7.72958
A_19_P00322432	IA:chr2:3579402-3584	-	-1.78	0.0107993	-3.95475
A_23_P325155	CD200R1	CD200 receptor 1	-1.77	0.00571533	-4.62388
A_33_P3291619	ENST00000399868	-	-1.77	0.00443966	-4.90899
A_33_P3383912	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	-1.77	0.00421311	-4.96963
A_33_P3398526	BCL2L11	BCL2-like 11 (apoptosis facilitator)	-1.77	0.000218333	-9.50157
A_33_P3293049	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	-1.77	0.00027575	-9.04713
A_23_P93032	ZBED3	zinc finger, BED-type containing 3	-1.77	0.0181534	-3.4543
A_23_P153676	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	-1.76	0.0225524	-3.25572
A_32_P75902	C16orf73	chromosome 16 open reading frame 73	-1.76	0.03165	-2.95641
A_33_P3374087	RBM44	RNA binding motif protein 44	-1.76	0.00536386	-4.69441
A_23_P17811	SEC14L2	SEC14-like 2 (S. cerevisiae)	-1.76	0.00219389	-5.77211
A_19_P00317639	:chr8:126934551-1269	-	-1.76	0.012137	-3.83892
A_19_P00319322	:chr7:105551628-1055	-	-1.76	0.000798595	-7.21256
A_32_P96435	ZNF829	zinc finger protein 829	-1.76	0.0103441	-3.99799
A_33_P3336562	ENST00000442072	-	-1.75	0.0197853	-3.37483
A_33_P3398583	FLJ41649	-	-1.75	0.00358661	-5.15938
A_23_P88095	TBC1D4	TBC1 domain family, member 4	-1.75	0.000143505	-10.3711
A_33_P3255051	LOC100509927	-	-1.75	0.0176923	-3.47823
A_23_P9255	SYK	spleen tyrosine kinase	-1.75	0.0151491	-3.62442
A_19_P00321973	:chr2:111954496-1121	-	-1.75	0.0190328	-3.41051
A_24_P321068	SLC31A1	solute carrier family 31 (copper transporters), member 1	-1.74	0.0151742	-3.62284
A_32_P138032	C1orf61	chromosome 1 open reading frame 61	-1.74	0.00498962	-4.77569
A_33_P3328485	IKZF2	IKAROS family zinc finger 2 (Helios)	-1.74	0.037865	-2.80287
A_33_P3877728	SMCR6	Smith-Magenis syndrome chromosome region, candidate 6	-1.74	0.00813188	-4.24484
A_23_P79221	ACVR1	activin A receptor, type I	-1.74	0.00383676	-5.07929
A_19_P00808319	.:chr12:68383224-6841	-	-1.74	0.0237938	-3.20755
A_23_P103511	C1orf226	chromosome 1 open reading frame 226	-1.74	0.0241118	-3.19566
A_23_P255653	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	-1.74	3.94E-06	-21.6042
A_33_P3309414	LOC643770	-	-1.73	0.0030142	-5.37021
A_32_P453321	C1orf228	chromosome 1 open reading frame 228	-1.73	0.00558304	-4.64982
A_24_P852756	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	-1.73	3.90E-05	-13.5682
A_33_P3607359	LOC399815	-	-1.73	0.0187201	-3.42581
A_33_P3809497	FLJ37505	-	-1.73	0.00544083	-4.67851
A_33_P3371663	LTK	leukocyte receptor tyrosine kinase	-1.73	0.00178128	-6.0481
A_19_P00331485	.:chr10:80112419-8012	-	-1.73	0.00532899	-4.7017
A_24_P865245	BX099599	-	-1.73	0.0325624	-2.93186
A_33_P3245858	LOC100131581	-	-1.73	0.0251683	-3.15741
A_23_P63972	ENST00000495263	-	-1.73	0.00526271	-4.71571
A_23_P24004	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	-1.73	0.00913994	-4.12381
A_32_P176911	NCRNA00239	long intergenic non-protein coding RNA 239	-1.73	0.00510932	-4.74894
A_33_P3350374	C10orf58	family with sequence similarity 213, member A	-1.72	0.000596257	-7.68092

A_23_P40805	KLF15	Kruppel-like factor 15	-1.72	0.0241413	-3.19457
A_33_P3286929	A_33_P3286929	-	-1.72	0.0491374	-2.58493
A_24_P58204	OR51B5	olfactory receptor, family 51, subfamily B, member 5	-1.72	0.0244781	-3.18219
A_33_P3338300	CASZ1	castor zinc finger 1	-1.72	0.00351418	-5.18379
A_23_P256561	TLR6	toll-like receptor 6	-1.72	0.0440589	-2.67547
A_19_P00808547	A:chr4:40157905-4016	-	-1.72	0.0188846	-3.41773
A_32_P120183	ENST00000435531	-	-1.72	0.0217165	-3.28987
A_33_P3348086	A_33_P3348086	-	-1.72	0.0216183	-3.29399
A_33_P3308534	OSBPL1A	oxysterol binding protein-like 1A	-1.71	0.018135	-3.45524
A_24_P303420	LOC221442	-	-1.71	0.00976038	-4.05674
A_19_P00804359	:chr11:69216919-6933	-	-1.71	0.0408674	-2.73845
A_23_P57236	GGT7	gamma-glutamyltransferase 7	-1.71	0.0142757	-3.6812
A_19_P00802475	chr10:124987285-1252	-	-1.71	0.00836433	-4.21544
A_33_P3229477	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-1.71	0.000307981	-8.8389
A_33_P3351440	ENST00000406880	-	-1.71	0.03749	-2.81132
A_33_P3257993	RNF125	ring finger protein 125, E3 ubiquitin protein ligase	-1.71	0.000165314	-10.0701
A_33_P3268181	LIMS2	LIM and senescent cell antigen-like domains 2	-1.71	0.030333	-2.99327
A_19_P00810465	A:chr12:4958789-4970	-	-1.71	0.0433673	-2.68868
A_23_P322625	GPR55	G protein-coupled receptor 55	-1.70	0.000480982	-8.04188
A_23_P37983	MT1B	metallothionein 1B	-1.70	0.000427389	-8.24663
A_24_P657226	NHEDC1	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1	-1.70	0.0421262	-2.71298
A_32_P220770	HCG26	HLA complex group 26 (non-protein coding)	-1.70	0.00134569	-6.4361
A_24_P54390	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	-1.69	1.55E-05	-16.3721
A_24_P97374	EOMES	eomesodermin	-1.69	0.00118213	-6.62211
A_33_P3335725	INSR	insulin receptor	-1.69	0.0424506	-2.70655
A_19_P00809587	A:chr8:96297524-9641	-	-1.69	0.0262618	-3.11968
A_33_P3221432	ZNF284	zinc finger protein 284	-1.69	0.0099934	-4.03281
A_33_P3293573	VPS37D	vacuolar protein sorting 37 homolog D (S. cerevisiae)	-1.69	0.00246404	-5.62261
A_33_P3315314	MT1H	metallothionein 1H	-1.69	0.000250662	-9.23037
A_32_P151782	LOC100507636	-	-1.69	0.0118784	-3.86014
A_23_P427703	MT1L	metallothionein 1L (gene/pseudogene)	-1.69	0.000551018	-7.81181
A_33_P3361422	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	-1.68	0.0359	-2.84819
A_33_P3247072	A_33_P3247072	-	-1.68	0.00232154	-5.69892
A_19_P00317498	:chr7:130793390-1307	-	-1.68	0.0194486	-3.3906
A_19_P00326588	IA:chr4:6664099-6683	-	-1.68	0.0322838	-2.93927
A_19_P00801184	:chr7:105525814-1055	-	-1.68	0.00545288	-4.67605
A_19_P00811922	A:chr8:67304071-6731	-	-1.68	0.00150395	-6.27993
A_19_P00321322	.:chr18:53763304-5376	-	-1.68	0.0357137	-2.85262
A_19_P00806771	.:chr20:61399055-6140	-	-1.67	0.0178103	-3.47204
A_23_P217621	TAF7L	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	-1.67	0.0189138	-3.4163
A_23_P160559	ECM1	extracellular matrix protein 1	-1.67	0.0420025	-2.71544
A_33_P3270668	FAM131B	family with sequence similarity 131, member B	-1.67	0.0100935	-4.02273
A_23_P91095	CD28	CD28 molecule	-1.67	0.000230369	-9.39533
A_19_P00801823	:chr8:126718218-1269	-	-1.67	0.000366098	-8.52188
A_23_P254688	TMEM108	transmembrane protein 108	-1.67	0.0297609	-3.00985
A_19_P00802887	A:chr7:22611311-2261	-	-1.67	0.0187274	-3.42545
A_32_P147622	MCF2L-AS1	MCF2L antisense RNA 1 (non-protein coding)	-1.67	6.66E-05	-12.1553
A_33_P3287223	DPP4	dipeptidyl-peptidase 4	-1.67	4.99E-05	-12.8979
A_33_P3244433	FAM188B	family with sequence similarity 188, member B	-1.67	0.0325831	-2.93131
A_33_P3325978	ENST00000405331	-	-1.66	0.000394421	-8.38837
A_23_P37391	CCDC85C	coiled-coil domain containing 85C	-1.66	0.000689724	-7.44433
A_24_P370472	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	-1.66	0.00193579	-5.93669
A_23_P256542	FAM162A	family with sequence similarity 162, member A	-1.66	0.000176493	-9.93363
A_19_P00803558	A:chr12:4958789-4970	-	-1.66	0.0184233	-3.44061
A_33_P3646051	LOC284408	-	-1.66	0.0293016	-3.02341
A_19_P00322325	:chr6:155265258-1552	-	-1.66	0.0457457	-2.64418
A_24_P343233	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	-1.66	0.00235736	-5.67923
A_33_P3253214	ENST00000369161	-	-1.66	0.0121401	-3.83867
A_24_P142503	SLC47A1	solute carrier family 47, member 1	-1.66	0.0473852	-2.61496
A_23_P420863	NOD2	nucleotide-binding oligomerization domain containing 2	-1.65	0.0112764	-3.91163

A_23_P166297	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	-1.65	0.00865661	-4.1798
A_24_P333733	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	-1.65	0.00125421	-6.53661
A_32_P224522	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	-1.65	0.000249032	-9.24302
A_32_P115438	LOC100128239	-	-1.65	0.0350924	-2.86762
A_23_P135061	CORO2A	coronin, actin binding protein, 2A	-1.65	0.00237593	-5.66916
A_23_P109488	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	-1.65	0.000235885	-9.34883
A_32_P351968	HLA-DMB	major histocompatibility complex, class II, DM beta	-1.65	0.000493141	-7.99919
A_32_P25253	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	-1.65	0.00181089	-6.02589
A_33_P3419785	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	-1.64	0.020235	-3.35423
A_19_P00801649	.:chr20:61399055-6140	-	-1.64	0.0243803	-3.18576
A_23_P142075	ACP5	acid phosphatase 5, tartrate resistant	-1.64	0.00406927	-5.01013
A_23_P385199	EPHA10	EPH receptor A10	-1.64	0.0182417	-3.44979
A_23_P8108	LOC100293977	-	-1.64	0.000690861	-7.44169
A_33_P3311820	FLJ44674	-	-1.64	0.0454221	-2.65008
A_33_P3227880	BTN3A2	butyrophilin, subfamily 3, member A2	-1.64	0.00604099	-4.56288
A_33_P3317925	KRTAP20-4	keratin associated protein 20-4	-1.64	0.0413024	-2.72955
A_33_P3214625	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-1.64	0.000400617	-8.36068
A_33_P3388466	BTN3A1	butyrophilin, subfamily 3, member A1	-1.64	0.00407495	-5.0085
A_33_P3226680	A_33_P3226680	-	-1.64	0.0244845	-3.18195
A_33_P3412188	C1orf86	chromosome 1 open reading frame 86	-1.64	0.0161484	-3.56386
A_33_P3358005	LOC440934	-	-1.63	0.020065	-3.36196
A_33_P3242863	NT5M	5',3'-nucleotidase, mitochondrial	-1.63	0.00716045	-4.37913
A_23_P423457	SERINC5	serine incorporator 5	-1.63	0.0210034	-3.32021
A_33_P3238375	LOC730081	-	-1.63	0.00671528	-4.44792
A_19_P00320253	:chr8:129082378-1291	-	-1.63	0.0404191	-2.74773
A_23_P125078	SLC26A11	solute carrier family 26, member 11	-1.63	1.59E-05	-16.2981
A_33_P3245120	LOC200772	-	-1.63	0.00313269	-5.32291
A_33_P3318449	RNF222	ring finger protein 222	-1.63	0.0174863	-3.48915
A_33_P3233055	BF515046	-	-1.63	0.0110437	-3.9324
A_23_P38427	RAB11FIP4	RAB11 family interacting protein 4 (class II)	-1.63	0.000130275	-10.5816
A_19_P00800116	:chr2:158774431-1587	-	-1.63	0.0075591	-4.32161
A_23_P29096	PDE9A	phosphodiesterase 9A	-1.63	0.0179113	-3.46678
A_24_P17870	HCP5	HLA complex P5 (non-protein coding)	-1.63	0.000348088	-8.61333
A_19_P00800237	.:chr19:53149513-5315	-	-1.63	0.0229433	-3.24023
A_19_P00331128	.:chr13:48450924-4848	-	-1.62	0.0216158	-3.29409
A_33_P3437273	MGC15705	-	-1.62	0.0390104	-2.77765
A_33_P3342156	ENST00000390463	-	-1.62	0.000982228	-6.89572
A_23_P213620	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	-1.62	0.00108036	-6.75392
A_19_P00806502	.:chr16:82167524-8217	-	-1.62	0.0278176	-3.06893
A_24_P50248	FAM110C	family with sequence similarity 110, member C	-1.62	0.0280357	-3.06207
A_24_P320880	SNX16	sorting nexin 16	-1.62	0.0147183	-3.65194
A_19_P00812742	A:chr9:14316575-1432	-	-1.62	0.0447563	-2.66237
A_23_P30913	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	-1.61	0.00557627	-4.65116
A_33_P3360665	ACVR1	activin A receptor, type I	-1.61	0.0100894	-4.02314
A_33_P3350056	MT1X	metallothionein 1X	-1.61	0.000284523	-8.98769
A_33_P3390017	C15orf54	chromosome 15 open reading frame 54	-1.61	0.046651	-2.6279
A_23_P95130	SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-1.61	0.000967319	-6.91872
A_33_P3256031	ENST00000390357	-	-1.61	0.018604	-3.43157
A_33_P3259293	ENST00000493423	-	-1.61	0.00620848	-4.53298
A_24_P122921	BCL2L11	BCL2-like 11 (apoptosis facilitator)	-1.61	0.00152334	-6.26213
A_33_P3232080	CD177	CD177 molecule	-1.61	0.013539	-3.73229
A_33_P3236868	MT1X	metallothionein 1X	-1.60	0.00259508	-5.55687
A_33_P3377190	LOC100131662	-	-1.60	4.02E-05	-13.4803
A_23_P105794	EPSTI1	epithelial stromal interaction 1 (breast)	-1.60	5.84E-05	-12.4862
A_23_P430201	CEP128	centrosomal protein 128kDa	-1.60	0.00179743	-6.03593
A_33_P3404470	UNC93B1	unc-93 homolog B1 (C. elegans)	1.60	3.47E-05	13.8974
A_23_P157766	C9orf68	spermatogenesis associated 6-like	1.60	0.0140871	3.69399
A_23_P367043	CDC14C	CDC14 cell division cycle 14 homolog C (S. cerevisiae)	1.60	0.0260397	3.1272
A_23_P216935	NCRNA00287	MIR600 host gene (non-protein coding)	1.60	0.0046643	4.85233
A_23_P147109	C9orf167	torsin family 4, member A	1.60	0.00516687	4.73634
A_23_P163697	SYT17	synaptotagmin XVII	1.60	0.0110903	3.9282
A_33_P3249936	C3orf67	chromosome 3 open reading frame 67	1.60	0.0296606	3.01279

A_23_P140876	ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	1.60	0.00100255	6.86501
A_33_P3328928	BMP2K	BMP2 inducible kinase	1.60	0.00125992	6.53009
A_19_P00810280	A:chr5:71679069-7168	-	1.60	0.00205279	5.85907
A_24_P152968	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.60	0.000881899	7.05916
A_23_P170378	PMCHL1	pro-melanin-concentrating hormone-like 1, pseudogene	1.60	0.00380724	5.08841
A_33_P3313338	ENST00000390445	-	1.61	0.0135447	3.73187
A_23_P46315	ENST00000369540	-	1.61	0.00907667	4.13094
A_19_P00329363	:chrX:112857842-1128	-	1.61	0.0276072	3.07561
A_33_P3284533	ENST00000390440	-	1.61	0.0487875	2.59084
A_19_P00802346	A:chr5:80172719-8017	-	1.61	0.00123513	6.55867
A_23_P310956	COL6A2	collagen, type VI, alpha 2	1.61	0.0329033	2.92289
A_33_P3357516	SLC10A7	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	1.61	0.0389004	2.78004
A_23_P259166	TCEAL4	transcription elongation factor A (SII)-like 4	1.61	0.00376923	5.10029
A_33_P3631022	LOC100270680	-	1.61	0.00586229	4.59587
A_23_P38567	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	1.61	0.00967823	4.06533
A_19_P00326230	chr14:104345747-1043	-	1.61	0.0190146	3.41139
A_23_P307392	DPF3	D4, zinc and double PHD fingers, family 3	1.61	0.0242461	3.1907
A_33_P3377229	C11orf21	chromosome 11 open reading frame 21	1.61	0.0028862	5.42382
A_33_P3251776	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	1.62	0.00171479	6.09961
A_24_P285522	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	1.62	0.0192096	3.40199
A_19_P00809991	A:chr7:22666693-2266	-	1.62	0.0423814	2.70792
A_32_P209208	CAPS2	calcyphosine 2	1.62	0.0113949	3.90125
A_33_P3251672	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	1.62	0.018241	3.44983
A_23_P57667	PLXNA1	plexin A1	1.62	0.0371811	2.81834
A_23_P113462	KIF21A	kinesin family member 21A	1.62	0.00123513	6.55867
A_33_P3262124	MMP25	matrix metallopeptidase 25	1.62	0.00052075	7.90672
A_23_P398172	FAM135A	family with sequence similarity 135, member A	1.62	0.0352218	2.86447
A_19_P00320517	.:chr17:21438452-2147	-	1.62	0.012344	3.82231
A_23_P54728	FAM173A	family with sequence similarity 173, member A	1.62	0.000435907	8.21211
A_23_P160992	FMO4	flavin containing monooxygenase 4	1.62	0.0071382	4.38245
A_33_P3323298	JUN	jun proto-oncogene	1.62	0.0404006	2.74811
A_24_P96593	EVI5	ecotropic viral integration site 5	1.62	0.0132747	3.75139
A_19_P00806152	.:chr14:88488672-8850	-	1.63	0.0188222	3.42079
A_19_P00318380	.:chr18:48872618-4905	-	1.63	0.0377227	2.80607
A_33_P3365760	STAP1	signal transducing adaptor family member 1	1.63	0.000322443	8.75374
A_23_P211345	TBX1	T-box 1	1.63	0.0491511	2.5847
A_33_P3209506	ENST00000402268	-	1.63	0.0300153	3.00243
A_19_P00800266	.:chr16:17970874-1797	-	1.63	0.00868576	4.17632
A_19_P00331036	:chr2:208360030-2083	-	1.63	0.000302588	8.87189
A_23_P43350	MLANA	melan-A	1.63	0.0211858	3.31234
A_33_P3257503	LOC387647	-	1.63	0.00475517	4.83031
A_33_P3366053	ADPRH	ADP-ribosylarginine hydrolase	1.63	0.0032157	5.29101
A_23_P58647	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	1.63	6.22E-05	12.3269
A_33_P3285565	CLDN3	claudin 3	1.63	0.0035475	5.17249
A_33_P3405434	ENST00000375083	-	1.63	0.0325219	2.93293
A_33_P3422133	ADAP1	ArfGAP with dual PH domains 1	1.63	0.000218519	9.49987
A_19_P00808045	A:chr5:66985594-6699	-	1.63	0.0288951	3.03562
A_23_P254353	NOXA1	NADPH oxidase activator 1	1.63	0.00552149	4.66213
A_23_P68423	JPH2	junctophilin 2	1.63	0.029222	3.02579
A_23_P24135	TACR2	tachykinin receptor 2	1.63	0.01644	3.54699
A_33_P3351609	A_33_P3351609	-	1.63	0.0269231	3.09771
A_19_P00327851	:chr9:132247654-1322	-	1.63	0.010937	3.94208
A_33_P3215948	MPZL2	myelin protein zero-like 2	1.63	0.00445741	4.9044
A_24_P48069	DOK4	docking protein 4	1.63	1.52E-05	16.4417
A_23_P257971	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.63	0.0245692	3.17887
A_23_P26314	ZNF319	zinc finger protein 319	1.63	0.000225797	9.43489
A_19_P00317656	:chr5:102118475-1021	-	1.63	6.15E-05	12.3579

A_23_P76901	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	1.63	0.000260912	9.15298
A_23_P74088	MMP23B	matrix metallopeptidase 23B	1.63	0.00221846	5.75764
A_23_P7503	TIMD4	T-cell immunoglobulin and mucin domain containing 4	1.63	0.000720287	7.37511
A_33_P3345350	DRGX	dorsal root ganglia homeobox	1.64	0.00219127	5.77366
A_23_P36018	VSIG2	V-set and immunoglobulin domain containing 2	1.64	0.0157325	3.58853
A_19_P00805737	:chr13:32533783-3253	-	1.64	0.0321887	2.94182
A_32_P89827	LOC374491	-	1.64	1.72E-05	16.0387
A_23_P413224	NCR2	natural cytotoxicity triggering receptor 2	1.64	0.00767117	4.30607
A_24_P270144	CD63	CD63 molecule	1.64	0.000293711	8.92774
A_33_P3280950	LOC144571	-	1.64	0.000389952	8.40867
A_33_P3293888	AFF2	AF4/FMR2 family, member 2	1.64	0.0185226	3.43563
A_23_P8834	EPHX2	epoxide hydrolase 2, cytoplasmic	1.64	0.0300493	3.00144
A_33_P3420224	ENTPD8	ectonucleoside triphosphate diphosphohydrolase 8	1.64	0.0188767	3.41811
A_33_P3267822	MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	1.65	0.0165467	3.5409
A_32_P812268	CALHM1	calcium homeostasis modulator 1	1.65	0.00017739	9.92313
A_23_P502980	DGKH	diacylglycerol kinase, eta	1.65	0.040781	2.74023
A_24_P377775	RGS3	regulator of G-protein signaling 3	1.65	0.00902285	4.13705
A_33_P3382125	LOC728675	-	1.65	0.000160876	10.1274
A_23_P146922	GAS6	growth arrest-specific 6	1.65	0.018903	3.41683
A_23_P416034	HAUS7	HAUS augmin-like complex, subunit 7	1.65	0.00403766	5.01926
A_19_P00319808	:chr1:205404014-2054(	-	1.65	0.00417806	4.97935
A_19_P00320473	:chr7:104624063-1046:	-	1.65	0.00041316	8.30615
A_24_P235266	GRB10	growth factor receptor-bound protein 10	1.65	0.0157743	3.58602
A_24_P14634	EMID1	EMI domain containing 1	1.65	0.0125188	3.80853
A_19_P00802219	A:chr6:42758417-4275(	-	1.65	0.000273823	9.0605
A_33_P3408177	BCL2L15	BCL2-like 15	1.66	0.0235225	3.21783
A_33_P3363355	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	1.66	0.00704879	4.39591
A_23_P421401	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	1.66	0.00486757	4.80374
A_33_P3237894	ENST00000410098	-	1.66	0.0483146	2.59888
A_19_P00803561	:chr10:29699919-2973	-	1.66	0.00113903	6.67623
A_33_P3236020	TIMD4	T-cell immunoglobulin and mucin domain containing 4	1.66	0.000393512	8.39248
A_23_P55749	COL5A3	collagen, type V, alpha 3	1.66	0.0481871	2.60107
A_24_P160466	GPRIN1	G protein regulated inducer of neurite outgrowth 1	1.66	0.00465852	4.85375
A_33_P3352970	IRAK2	interleukin-1 receptor-associated kinase 2	1.66	0.00131351	6.47051
A_23_P166929	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	1.66	0.0376073	2.80867
A_24_P935103	ADCY9	adenylate cyclase 9	1.66	0.00237161	5.6715
A_23_P137856	MUC1	mucin 1, cell surface associated	1.66	0.000299385	8.89181
A_33_P3588134	PANX2	pannexin 2	1.66	0.00229555	5.71343
A_33_P3265739	PTGER3	prostaglandin E receptor 3 (subtype EP3)	1.66	0.010819	3.95293
A_23_P120056	RTKN	rhotekin	1.66	0.0200552	3.36241
A_33_P3212804	C22orf42	chromosome 22 open reading frame 42	1.67	0.031744	2.95384
A_23_P49849	SEZ6	seizure related 6 homolog (mouse)	1.67	0.0499509	2.57139
A_19_P00327491	:chr16:26384124-2639	-	1.67	0.0479836	2.60457
A_23_P114740	CFH	complement factor H	1.67	0.00254823	5.57992
A_23_P137381	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	1.67	0.000605109	7.65668
A_23_P436353	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	1.67	0.0013135	6.47052
A_23_P406424	RHOC	ras homolog family member C	1.67	6.85E-05	12.0835
A_23_P319557	ENST00000328344	-	1.67	0.0218728	3.28338
A_23_P384551	FLJ32154	-	1.67	0.0125899	3.80299
A_19_P00322941	:chr5:148786525-1487(	-	1.67	0.0302109	2.99678
A_19_P00328630	:chr7:115918514-1159:	-	1.67	0.0456111	2.64663
A_33_P3389558	A_33_P3389558	-	1.67	0.0343829	2.8851
A_23_P101093	COPZ2	coatomer protein complex, subunit zeta 2	1.67	0.000172275	9.98389
A_23_P309396	RP1L1	retinitis pigmentosa 1-like 1	1.67	0.0417394	2.72072
A_24_P179816	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	1.67	0.000342916	8.64063
A_24_P143574	SIRPB1	signal-regulatory protein beta 1	1.67	1.86E-06	25.1304
A_23_P91283	CASS4	Cas scaffolding protein family member 4	1.67	0.000555966	7.79688
A_19_P00801740	A:chr8:29346831-2967(	-	1.67	0.0163188	3.55396
A_33_P3349883	ENST00000366583	-	1.67	0.00581756	4.6043

A_33_P3343007	ENST00000390454	-	1.68	0.000140641	10.4146
A_33_P3262758	UNC93B1	unc-93 homolog B1 (C. elegans)	1.68	0.000382108	8.44497
A_23_P253597	LRRC3	leucine rich repeat containing 3	1.68	0.00413894	4.99031
A_33_P3368014	HVCN1	hydrogen voltage-gated channel 1	1.68	0.000238933	9.32368
A_23_P151820	RIN3	Ras and Rab interactor 3	1.68	0.000157718	10.1693
A_33_P3363710	LOC100506750	-	1.68	0.0300362	3.00182
A_19_P00800875	:chr2:127290980-1273	-	1.68	0.0412311	2.731
A_23_P338372	NR2E1	nuclear receptor subfamily 2, group E, member 1	1.68	0.00486248	4.80493
A_24_P197284	C2orf85	CXXC finger protein 11	1.68	0.0120672	3.84459
A_33_P3310293	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	1.68	0.039648	2.76396
A_23_P26386	TPPP3	tubulin polymerization-promoting protein family member 3	1.68	0.0440946	2.67479
A_24_P135322	NRP1	neuropilin 1	1.69	0.0249549	3.16499
A_23_P203475	PRKCDBP	protein kinase C, delta binding protein	1.69	0.0117365	3.872
A_19_P00318899	A:chr1:61419154-6143	-	1.69	0.0480168	2.604
A_33_P3401711	USH1G	Usher syndrome 1G (autosomal recessive)	1.69	0.0120959	3.84226
A_33_P3340595	A_33_P3340595	-	1.69	0.0111361	3.92409
A_23_P86100	KLHDC9	kelch domain containing 9	1.69	0.00388391	5.06487
A_33_P3303507	HSPA6	heat shock 70kDa protein 6 (HSP70B')	1.69	0.0161105	3.56608
A_23_P75430	C11orf75	chromosome 11 open reading frame 75	1.69	9.53E-05	11.2886
A_33_P3362274	ENST00000390456	-	1.69	0.0313224	2.96541
A_19_P00327659	A:chr1:40004013-4002	-	1.69	0.022101	3.27398
A_23_P170534	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	1.69	0.000954463	6.9389
A_32_P230547	DOCK7	dedicator of cytokinesis 7	1.69	0.0119405	3.85499
A_23_P142205	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	1.69	0.0203667	3.3483
A_23_P132644	NCEH1	neutral cholesterol ester hydrolase 1	1.69	0.000643049	7.55737
A_23_P310022	KIAA1217	KIAA1217	1.69	0.0141662	3.6886
A_23_P151907	PCSK6	proprotein convertase subtilisin/kexin type 6	1.69	0.0185531	3.43411
A_19_P00802517	.:chr15:50648133-5066	-	1.70	0.0393128	2.77113
A_33_P3292241	A_33_P3292241	-	1.70	0.00490954	4.79401
A_23_P159255	PTPRM	protein tyrosine phosphatase, receptor type, M	1.70	0.000567272	7.76336
A_33_P3272580	FUCA2	fucosidase, alpha-L- 2, plasma	1.70	0.000417552	8.28752
A_33_P3318993	A_33_P3318993	-	1.70	0.0497428	2.57483
A_33_P3351180	ENST00000390547	-	1.70	0.00116886	6.63851
A_23_P39561	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	1.70	0.000100472	11.1668
A_23_P217528	KLF8	Kruppel-like factor 8	1.70	0.0345343	2.88133
A_23_P202245	RET	ret proto-oncogene	1.70	0.0228028	3.24576
A_23_P66827	FAM106A	family with sequence similarity 106, member A	1.70	0.0300742	3.00073
A_33_P3227472	SDSL	serine dehydratase-like	1.70	0.002273	5.72618
A_23_P419947	MLF1	myeloid leukemia factor 1	1.70	0.0441542	2.67366
A_33_P3460460	MGC20647	-	1.70	0.00224843	5.74024
A_23_P19182	REEP2	receptor accessory protein 2	1.70	0.0028782	5.42726
A_23_P88691	CHRNA5	cholinergic receptor, nicotinic, alpha 5 (neuronal)	1.70	0.00602793	4.56526
A_33_P3227174	LOC100128304	-	1.70	0.0417832	2.71983
A_19_P00809905	:chr1:198335952-1983	-	1.71	0.0280419	3.06188
A_23_P333705	NEK3	NIMA (never in mitosis gene a)-related kinase 3	1.71	8.04E-05	11.6942
A_24_P587443	A_24_P587443	-	1.71	0.047419	2.61437
A_23_P118	EXTL2	exostoses (multiple)-like 2	1.71	0.00525304	4.71777
A_33_P3343872	SIRPG	signal-regulatory protein gamma	1.71	2.13E-05	15.343
A_19_P00808918	.:chr16:85249449-8558	-	1.71	2.35E-05	15.0423
A_32_P42574	C1orf198	chromosome 1 open reading frame 198	1.71	0.000124404	10.6834
A_23_P30634	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	1.71	0.000504471	7.96052
A_24_P410100	A_24_P410100	-	1.71	0.0467119	2.62682
A_19_P00327396	:chr5:102091626-1021	-	1.71	0.0101088	4.0212
A_23_P122007	C5orf30	chromosome 5 open reading frame 30	1.71	0.00411623	4.99673
A_24_P264943	COMP	cartilage oligomeric matrix protein	1.72	0.0375546	2.80986
A_33_P3287636	ENST00000390449	-	1.72	0.000119428	10.7742
A_33_P3213169	LOC100510454	-	1.72	0.0010099	6.85408
A_33_P3408711	FLNA	filamin A, alpha	1.72	0.0276352	3.07471
A_23_P1452	NPFFR1	neuropeptide FF receptor 1	1.72	0.0430786	2.69426
A_33_P3341442	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1.72	0.00209156	5.83449
A_19_P00319625	:chr6:147172280-1474	-	1.72	0.0221655	3.27135
A_24_P417460	SFMBT2	Scm-like with four mbt domains 2	1.72	0.000743437	7.32495
A_33_P3396224	C12orf69	chromosome 12 open reading frame 69	1.73	0.0388103	2.782
A_19_P00807794	A:chr5:93440069-9345	-	1.73	0.0025384	5.58481

A_23_P48056	CKAP4	cytoskeleton-associated protein 4	1.73	0.00101601	6.84508
A_23_P64898	KLRG1	killer cell lectin-like receptor subfamily G, member 1	1.73	3.12E-05	14.1956
A_23_P71946	BSPRY	B-box and SPRY domain containing	1.73	1.00E-05	17.89
A_24_P70002	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	1.73	0.000921974	6.99136
A_23_P258912	MYOM2	myomesin (M-protein) 2, 165kDa	1.73	0.0226056	3.25359
A_19_P00813495	dA:chr4:6676128-6678	-	1.73	0.000990923	6.88249
A_33_P3217213	PDLIM7	PDZ and LIM domain 7 (enigma)	1.73	0.00736228	4.34956
A_24_P269129	ZDHHC14	zinc finger, DHHC-type containing 14	1.73	0.00133036	6.45237
A_33_P3216458	ADAM23	ADAM metallopeptidase domain 23	1.73	0.0237282	3.21002
A_33_P3342448	ENST00000510382	-	1.73	0.0115665	3.88643
A_23_P50638	LRG1	leucine-rich alpha-2-glycoprotein 1	1.73	0.00723687	4.36782
A_23_P143143	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1.73	5.15E-05	12.8153
A_24_P411561	HAVCR2	hepatitis A virus cellular receptor 2	1.74	0.000213016	9.55075
A_33_P3367692	CFH	complement factor H	1.74	0.00417539	4.98009
A_23_P153372	HSH2D	hematopoietic SH2 domain containing	1.74	0.000688063	7.44819
A_23_P28857	SIRPG	signal-regulatory protein gamma	1.74	4.51E-05	13.1656
A_19_P00808637	A:chrX:47884831-4790	-	1.74	0.0486969	2.59237
A_23_P118203	ZG16B	zymogen granule protein 16 homolog B (rat)	1.74	4.43E-05	13.215
A_23_P34345	VCAM1	vascular cell adhesion molecule 1	1.74	0.0160681	3.56857
A_23_P254507	HOPX	HOP homeobox	1.74	1.77E-05	15.9332
A_33_P3308749	LAMA4	laminin, alpha 4	1.74	0.0229041	3.24178
A_33_P3353791	ITGA1	integrin, alpha 1	1.75	0.00088836	7.04798
A_19_P00323171	.:chr12:13116233-1312	-	1.75	0.0404045	2.74803
A_33_P3296067	CDC14C	CDC14 cell division cycle 14 homolog C (S. cerevisiae)	1.75	0.000186744	9.81725
A_33_P3322589	FANCL	Fanconi anemia, complementation group L	1.75	0.00231302	5.70366
A_33_P3316934	ENST00000494145	-	1.75	0.0304042	2.99123
A_23_P211504	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	1.75	0.0324826	2.93398
A_33_P3316572	A_33_P3316572	-	1.75	0.0227978	3.24596
A_19_P00321625	A:chr2:39743587-3982	-	1.75	0.0148721	3.64201
A_23_P257936	TEX28	testis expressed 28	1.76	0.0208281	3.32785
A_24_P62505	GLT25D2	glycosyltransferase 25 domain containing 2	1.76	0.00184474	6.00102
A_33_P3390357	SPIRE1	spire homolog 1 (Drosophila)	1.76	0.000341394	8.64876
A_33_P3304212	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	1.76	0.00029478	8.9209
A_33_P3251205	ENST00000390316	-	1.76	0.0127024	3.7943
A_24_P784765	CD59	CD59 molecule, complement regulatory protein	1.76	0.000352044	8.59276
A_24_P251661	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	1.76	0.00352732	5.17932
A_33_P3336686	CLIC3	chloride intracellular channel 3	1.76	6.85E-05	12.0848
A_23_P151166	HVCN1	hydrogen voltage-gated channel 1	1.76	0.000749034	7.31311
A_24_P272313	C2orf55	chromosome 2 open reading frame 55	1.76	0.0170772	3.51128
A_33_P3356022	AB305718	-	1.76	0.000782118	7.24514
A_19_P00323720	:chr7:104616164-1046	-	1.77	0.00946104	4.08846
A_33_P3340926	KIR3DX1	killer cell immunoglobulin-like receptor, three domains, X1	1.77	0.00202373	5.87785
A_32_P112910	UBL4B	ubiquitin-like 4B	1.77	0.0307589	2.98116
A_33_P3364959	DQ098707	-	1.77	0.0313329	2.96513
A_19_P00808058	A:chr6:96958729-9696	-	1.77	0.0139541	3.70312
A_33_P3387458	ENST00000379713	-	1.77	0.00225836	5.73454
A_33_P3318172	VN1R103P	vomeronasal 1 receptor 103 pseudogene	1.77	0.00537272	4.69257
A_19_P00319765	A:chr3:72201909-7222	-	1.77	0.00165201	6.15044
A_33_P3302916	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	1.77	0.000174693	9.9549
A_19_P00804421	dA:chr6:3176201-3194	-	1.77	0.0432663	2.69062
A_33_P3306018	AK127893	-	1.77	0.0198467	3.37198
A_24_P944427	SETD5	SET domain containing 5	1.77	0.0395224	2.76664
A_33_P3237775	NR1H3	nuclear receptor subfamily 1, group H, member 3	1.77	0.000730274	7.35324
A_23_P7361	ELOVL6	ELOVL fatty acid elongase 6	1.77	0.00194155	5.93274
A_33_P3373009	A_33_P3373009	-	1.77	0.0167845	3.52749
A_23_P214727	GPR63	G protein-coupled receptor 63	1.77	0.0222166	3.26927
A_23_P399001	CXXC5	CXXC finger protein 5	1.77	0.00113283	6.68421
A_23_P110941	GSTA4	glutathione S-transferase alpha 4	1.77	0.00625733	4.52444
A_33_P3266132	GRHL3	grainyhead-like 3 (Drosophila)	1.77	0.0295366	3.01644
A_33_P3393851	ENST00000342354	-	1.78	0.0430487	2.69484
A_23_P250619	ZDHHC14	zinc finger, DHHC-type containing 14	1.78	3.31E-05	14.0327

A_23_P200138	SLAMF8	SLAM family member 8	1.78	0.0281035	3.05995
A_19_P00804020	A:chrX:64628047-6462	-	1.78	0.00107216	6.76517
A_33_P3328653	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	1.78	0.00350791	5.18593
A_33_P3320217	ADCY2	adenylate cyclase 2 (brain)	1.78	0.0214096	3.30279
A_23_P144896	PDLIM7	PDZ and LIM domain 7 (enigma)	1.78	0.00140058	6.37958
A_23_P312132	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	1.78	7.22E-05	11.9555
A_33_P3212909	ZFHX2	zinc finger homeobox 2	1.78	0.0427776	2.70013
A_33_P3308446	RHOB	ras homolog family member B	1.78	0.00369189	5.1249
A_23_P43504	ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	1.78	0.00256455	5.57183
A_32_P108156	MIR155HG	MIR155 host gene (non-protein coding)	1.79	0.000980189	6.89884
A_19_P00325255	.:chr11:27634574-2765	-	1.79	0.00963737	4.06964
A_23_P257111	FBP1	fructose-1,6-bisphosphatase 1	1.79	0.021459	3.3007
A_23_P135499	CLIC4	chloride intracellular channel 4	1.79	0.0211373	3.31443
A_33_P3305958	TECPR2	tectonin beta-propeller repeat containing 2	1.79	0.0254848	3.1463
A_32_P3572	ENST00000449075	-	1.79	0.00473036	4.83628
A_23_P325690	ANKRD35	ankyrin repeat domain 35	1.79	0.000261999	9.14498
A_24_P65616	PVR	poliovirus receptor	1.79	0.000243767	9.28457
A_23_P128215	SOCS2	suppressor of cytokine signaling 2	1.79	0.013493	3.73558
A_33_P3329176	ENST00000390436	-	1.80	0.00140143	6.37873
A_19_P00321706	:chr5:102144510-1021	-	1.80	0.000594763	7.68505
A_33_P3358104	CD300E	CD300e molecule	1.80	0.012151	3.83779
A_23_P10559	AATK	apoptosis-associated tyrosine kinase	1.80	0.0345701	2.88044
A_33_P3254660	AK124971	-	1.80	0.0132781	3.75114
A_23_P256603	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	1.80	0.0256031	3.14219
A_23_P156632	PGBD1	piggyBac transposable element derived 1	1.80	0.0328369	2.92463
A_32_P69368	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1.80	6.94E-05	12.0541
A_24_P19175	ZNF358	zinc finger protein 358	1.80	0.00343599	5.21082
A_33_P3242753	A_33_P3242753	-	1.80	0.0218057	3.28616
A_23_P211417	RFPL1	ret finger protein-like 1	1.80	0.0101424	4.01785
A_23_P386888	LPA	lipoprotein, Lp(a)	1.80	0.00100534	6.86086
A_19_P00806765	:chr2:200625258-2007	-	1.81	0.000428952	8.24024
A_24_P53051	LACTB	lactamase, beta	1.81	0.00165798	6.14551
A_24_P81947	CORO1C	coronin, actin binding protein, 1C	1.81	0.00117062	6.63633
A_33_P3402868	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	1.81	0.0177106	3.47727
A_33_P3380417	SLC25A30	solute carrier family 25, member 30	1.81	0.00331172	5.25529
A_23_P389897	NGFR	nerve growth factor receptor	1.81	0.0163007	3.555
A_33_P3416563	AIG1	androgen-induced 1	1.81	0.0409567	2.73661
A_23_P125809	ZCCHC12	zinc finger, CCHC domain containing 12	1.81	0.0358871	2.84849
A_23_P114057	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	1.81	0.00203834	5.86837
A_33_P3417944	HDAC11	histone deacetylase 11	1.81	0.0313811	2.96379
A_33_P3278330	FLJ16124	-	1.81	0.0331317	2.91693
A_32_P60065	F2RL2	coagulation factor II (thrombin) receptor-like 2	1.82	0.0313345	2.96508
A_19_P00331762	:chr3:171491881-1715	-	1.82	0.00265567	5.52778
A_23_P145718	AOAH	acyloxyacyl hydrolase (neutrophil)	1.82	0.00136013	6.42097
A_33_P3245952	LOC648570	-	1.82	0.0280912	3.06034
A_24_P350245	DOCK5	dedicator of cytokinesis 5	1.82	0.000347424	8.61681
A_23_P16469	PLAUR	plasminogen activator, urokinase receptor	1.82	0.00323954	5.28203
A_23_P408094	MXD1	MAX dimerization protein 1	1.82	0.00927272	4.10902
A_32_P169735	TTC8	tetratricopeptide repeat domain 8	1.82	9.00E-05	11.4234
A_19_P00805879	A:chr6:33805822-3384	-	1.82	0.0122879	3.82678
A_24_P822704	TMEM198	transmembrane protein 198	1.82	0.000168601	10.0289
A_33_P3290739	D13071	-	1.82	0.0354795	2.85824
A_23_P120899	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1.82	0.00185981	5.99012
A_19_P00320664	:chr6:139013685-1390	-	1.82	0.016173	3.56242
A_33_P3228023	SCPEP1	serine carboxypeptidase 1	1.82	0.000317168	8.78426
A_24_P187351	CNOT4	CCR4-NOT transcription complex, subunit 4	1.82	0.0393847	2.76958
A_19_P00315627	A:chr9:2493073-2521	-	1.82	0.000602308	7.6643
A_33_P3231542	ZFHX3	zinc finger homeobox 3	1.82	0.04999	2.57075
A_33_P3355688	ENST00000379963	-	1.82	0.0369778	2.823
A_19_P00316271	.:chr15:25304317-2530	-	1.82	0.0408161	2.7395

A_23_P8754	AASS	aminoadipate-semialdehyde synthase	1.82	0.0238757	3.20447
A_32_P468341	C1orf127	chromosome 1 open reading frame 127	1.82	0.0470136	2.62148
A_33_P3253832	FV367791	-	1.82	0.000245643	9.26964
A_33_P3373437	LOC100129463	-	1.83	0.00576864	4.61362
A_19_P00319317	:chr15:58549646-5862	-	1.83	0.00179481	6.0379
A_33_P3325723	CHN1	chimerin (chimaerin) 1	1.83	0.0238424	3.20572
A_23_P160849	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	1.83	0.00669636	4.45096
A_19_P00806901	:chr5:148787082-1488	-	1.83	0.000469792	8.08232
A_23_P132956	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	1.83	0.0445349	2.6665
A_33_P3298159	PTGDS	prostaglandin D2 synthase 21kDa (brain)	1.83	0.0115923	3.88423
A_19_P00803113	A:chr6:64467741-6447	-	1.83	0.00787216	4.27884
A_33_P3341105	PDE6G	phosphodiesterase 6G, cGMP-specific, rod, gamma	1.84	0.00197485	5.91018
A_23_P131089	KANK3	KN motif and ankyrin repeat domains 3	1.84	0.000182062	9.86944
A_33_P3410599	FAM46A	family with sequence similarity 46, member A	1.84	0.0421276	2.71295
A_23_P206293	GPR114	G protein-coupled receptor 114	1.84	0.0028238	5.45097
A_24_P397255	ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6	1.84	0.0331002	2.91775
A_33_P3231557	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	1.84	0.044013	2.67633
A_19_P00324182	:chr10:97639610-9766	-	1.84	0.00440553	4.91789
A_33_P3390539	GYLTL1B	glycosyltransferase-like 1B	1.84	0.00302483	5.36588
A_24_P224727	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	1.84	0.0041063	4.99955
A_33_P3257903	GSTA4	glutathione S-transferase alpha 4	1.84	0.0178348	3.47076
A_32_P942508	FAM27L	family with sequence similarity 27-like	1.84	0.046645	2.62801
A_23_P202004	PRTFDC1	phosphoribosyl transferase domain containing 1	1.84	0.0259629	3.12981
A_19_P00324666	A:chr2:20070919-2009	-	1.85	0.00293074	5.40485
A_19_P00327549	:chr3:136790035-1368	-	1.85	0.0270917	3.0922
A_23_P91221	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	1.85	0.0245938	3.17798
A_23_P48109	NINJ2	ninjurin 2	1.85	7.10E-05	11.9965
A_23_P152548	SCPEP1	serine carboxypeptidase 1	1.85	3.20E-05	14.1256
A_33_P3306085	RAD51AP2	RAD51 associated protein 2	1.85	0.0491661	2.58445
A_24_P11575	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	1.85	0.0374034	2.81328
A_33_P3287610	ENST00000390313	-	1.85	0.00706761	4.39306
A_23_P370574	KIR3DL3	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	1.85	0.00185071	5.99668
A_33_P3567961	ENST00000445770	-	1.85	0.0468821	2.6238
A_19_P00800316	:chr13:30510667-3052	-	1.85	0.00989708	4.04262
A_33_P3320408	A_33_P3320408	-	1.85	0.0326951	2.92836
A_33_P3296772	C14orf82	FRMD6 antisense RNA 1 (non-protein coding)	1.86	0.0384056	2.79087
A_33_P3298099	A_33_P3298099	-	1.86	0.0278425	3.06814
A_23_P83200	AK8	adenylate kinase 8	1.86	0.0167941	3.52696
A_33_P3467872	ENST00000454555	-	1.86	0.0400667	2.7551
A_19_P00322327	:chr21:44895804-4489	-	1.86	0.0201709	3.35713
A_23_P64980	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	1.86	0.00693342	4.41357
A_33_P3419696	FGF2	fibroblast growth factor 2 (basic)	1.86	0.00951955	4.08217
A_19_P00320499	:chr6:132224787-1322	-	1.86	0.0450046	2.65776
A_23_P105957	ACTN1	actinin, alpha 1	1.86	0.00589727	4.58932
A_23_P37892	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	1.86	0.0377835	2.8047
A_33_P3409062	TYROBP	TYRO protein tyrosine kinase binding protein	1.86	0.00447464	4.89995
A_23_P309973	C14orf50	protein phosphatase 1, regulatory subunit 36	1.86	0.0489107	2.58875
A_23_P133408	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	1.86	0.0213503	3.30531
A_24_P104512	EVPL	envoplakin	1.86	0.000417109	8.28939
A_24_P245838	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	1.87	0.048681	2.59264
A_24_P11100	ZMAT1	zinc finger, matrin-type 1	1.87	0.0059403	4.58133
A_33_P3335257	TMEM146	catsper channel auxiliary subunit delta	1.87	0.000630235	7.59012
A_23_P138881	ACTN3	actinin, alpha 3	1.87	0.000109558	10.9685
A_23_P126836	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	1.87	0.000405804	8.33789
A_33_P3256655	A_33_P3256655	-	1.87	0.0105318	3.97989
A_23_P45524	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	1.87	4.97E-05	12.9077

A_19_P00316288	:chr15:25360740-2536	-	1.87	0.00647058	4.48803
A_24_P11462	ADC	arginine decarboxylase	1.87	0.00199829	5.89456
A_19_P00803000	:chr8:104254399-1042	-	1.88	0.00667879	4.45379
A_32_P171061	ASCL2	achaete-scute complex homolog 2 (Drosophila)	1.88	0.00090118	7.02609
A_19_P00317684	:chr5:102091017-1021	-	1.88	0.014182	3.68753
A_33_P3419790	ENST00000379413	-	1.88	0.0183107	3.44629
A_23_P166306	CBS	cystathionine-beta-synthase	1.88	0.00539388	4.68818
A_33_P3348924	LOC100128348	-	1.89	0.0251635	3.15758
A_23_P143906	MLF1	myeloid leukemia factor 1	1.89	0.0303823	2.99186
A_33_P3666817	C10orf55	chromosome 10 open reading frame 55	1.89	0.00704945	4.39581
A_23_P110167	MGST2	microsomal glutathione S-transferase 2	1.89	0.00370851	5.11956
A_33_P3302125	LCE2A	late cornified envelope 2A	1.89	0.0355401	2.85678
A_24_P57047	DLL3	delta-like 3 (Drosophila)	1.89	0.0264749	3.11253
A_23_P201376	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	1.89	0.00410251	5.00063
A_33_P3370029	ENST00000390340	-	1.89	0.0210936	3.31631
A_23_P160354	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	1.90	0.000461297	8.11379
A_19_P00804228	:chr5:108527309-1085	-	1.90	0.000790332	7.2288
A_33_P3312676	ENST00000360149	-	1.90	0.0185292	3.4353
A_24_P13083	TSPAN18	tetraspanin 18	1.90	0.00921967	4.1149
A_24_P156388	TTC38	tetratricopeptide repeat domain 38	1.90	3.68E-05	13.7262
A_19_P00316187	:chr3:183165478-1831	-	1.90	0.000547425	7.82275
A_23_P143274	NRSN2	neurensin 2	1.90	0.00363263	5.14416
A_23_P1473	PRF1	perforin 1 (pore forming protein)	1.90	4.11E-06	21.4248
A_32_P202703	ENST00000400890	-	1.91	0.0394845	2.76745
A_33_P3489737	NLN	neurolysin (metallopeptidase M3 family)	1.91	0.0146222	3.65821
A_33_P3298111	ENST00000466831	-	1.91	0.00137775	6.40276
A_33_P3260575	CERCAM	cerebral endothelial cell adhesion molecule	1.91	0.000300025	8.88781
A_33_P3395230	ENST00000458685	-	1.91	0.00615408	4.54259
A_33_P3221403	LOC646743	-	1.91	0.000943403	6.95652
A_33_P3330099	ARSD	arylsulfatase D	1.91	0.00064407	7.5548
A_33_P3315979	OR4Q3	olfactory receptor, family 4, subfamily Q, member 3	1.91	0.0154604	3.60508
A_33_P3261743	SLC37A2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	1.91	0.0165525	3.54057
A_23_P122662	GFOD1	glucose-fructose oxidoreductase domain containing 1	1.91	0.00660052	4.46651
A_23_P138910	DDX25	DEAD (Asp-Glu-Ala-Asp) box helicase 25	1.92	0.0459014	2.64135
A_23_P135239	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	1.92	0.00476078	4.82897
A_23_P400310	REG4	regenerating islet-derived family, member 4	1.92	9.77E-05	11.2307
A_33_P3325384	A_33_P3325384	-	1.92	0.00785999	4.28047
A_33_P3286699	A_33_P3286699	-	1.92	0.0315966	2.95787
A_19_P00813069	:chr3:177832281-1780	-	1.92	0.0141824	3.6875
A_23_P82523	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.92	7.21E-05	11.9587
A_33_P3234472	LOC284751	-	1.92	0.0188819	3.41786
A_23_P47004	DHX32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	1.92	0.000524465	7.89472
A_33_P3364741	MRC2	mannose receptor, C type 2	1.92	9.80E-06	17.9707
A_33_P3284838	ENST00000399806	-	1.93	0.00202108	5.87958
A_23_P259621	LAT2	linker for activation of T cells family, member 2	1.93	0.000951178	6.94411
A_23_P160159	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	1.93	0.00571936	4.6231
A_23_P145408	FUCA2	fucosidase, alpha-L- 2, plasma	1.93	6.60E-06	19.4697
A_19_P00315682	:chr21:39601874-3961	-	1.93	0.0274469	3.08073
A_23_P215735	ST7	suppression of tumorigenicity 7	1.93	6.46E-05	12.233
A_23_P218068	PLEKHA5	pleckstrin homology domain containing, family A member 5	1.93	0.0158987	3.57858
A_24_P295245	ASPH	aspartate beta-hydroxylase	1.94	0.00355439	5.17016
A_33_P3357397	ENST00000422143	-	1.94	0.0202925	3.35163
A_23_P122464	ZNF193	zinc finger protein 193	1.94	1.54E-05	16.3853
A_23_P140648	CYFIP1	cytoplasmic FMR1 interacting protein 1	1.94	0.000660341	7.51439
A_23_P216282	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	1.94	0.045795	2.64328
A_24_P658413	MUC12	mucin 12, cell surface associated	1.94	0.0292229	3.02576
A_33_P3402823	SPIN3	spindlin family, member 3	1.95	0.0313193	2.9655
A_33_P3252588	LOC100130093	-	1.95	0.000782364	7.24465
A_23_P124570	FER	fer (fps/fes related) tyrosine kinase	1.95	0.0220698	3.27526
A_23_P129717	ERI2	ERI1 exoribonuclease family member 2	1.95	0.0126131	3.80119
A_19_P00322717	:chr3:183165459-1831	-	1.95	8.77E-05	11.4852
A_33_P3406661	TMEM63C	transmembrane protein 63C	1.95	0.0302493	2.99567

A_23_P423309	PCDH12	protocadherin 12	1.95	0.0321093	2.94395
A_23_P206661	NQO1	NAD(P)H dehydrogenase, quinone 1	1.95	0.032432	2.93532
A_24_P379750	MXD1	MAX dimerization protein 1	1.95	0.00077669	7.25606
A_24_P79040	CAPN12	calpain 12	1.95	1.01E-05	17.8445
A_23_P215479	CLIP2	CAP-GLY domain containing linker protein 2	1.95	0.000352344	8.59122
A_23_P304304	ARSF	arylsulfatase F	1.95	0.0105827	3.97506
A_24_P194688	EFHA2	EF-hand domain family, member A2	1.95	0.0216977	3.29066
A_19_P00322886	:chr15:25356910-2536	-	1.96	0.0211189	3.31522
A_33_P3336557	CR591103	-	1.96	0.000217967	9.50491
A_19_P00807230	:chr5:108527309-1085	-	1.96	0.0172407	3.50237
A_24_P226755	TOX	thymocyte selection-associated high mobility group box	1.96	4.44E-05	13.2117
A_32_P178800	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.96	0.00607669	4.55643
A_33_P3398331	MMP24	matrix metallopeptidase 24 (membrane-inserted)	1.96	0.0108605	3.9491
A_19_P00319043	A:chr8:52808516-5280	-	1.96	0.0338281	2.89905
A_23_P99253	LIN7A	lin-7 homolog A (C. elegans)	1.96	0.00988059	4.04431
A_33_P3293456	GATA4	GATA binding protein 4	1.96	0.0293681	3.02143
A_33_P3262625	CECR7	cat eye syndrome chromosome region, candidate 7 (non-protein coding)	1.96	0.0219262	3.28117
A_33_P3309491	PTPRU	protein tyrosine phosphatase, receptor type, U	1.97	0.00368418	5.12738
A_33_P3416196	A_33_P3416196	-	1.97	0.000764592	7.28071
A_23_P409623	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	1.97	0.0247382	3.17276
A_33_P3329063	NCR1	natural cytotoxicity triggering receptor 1	1.97	0.0318219	2.95172
A_33_P3289476	LOC100128697	-	1.97	0.0139683	3.70214
A_33_P3263497	ENST00000401884	-	1.97	0.000125152	10.6701
A_33_P3238920	INPP5F	inositol polyphosphate-5-phosphatase F	1.97	5.65E-05	12.5739
A_24_P401870	C9orf139	chromosome 9 open reading frame 139	1.98	0.00427929	4.95153
A_32_P64598	A_32_P64598	-	1.98	0.0012231	6.57278
A_23_P63343	UTS2	urotensin 2	1.98	0.0104997	3.98296
A_24_P159227	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	1.98	0.00733226	4.3539
A_33_P3260669	STK3	serine/threonine kinase 3	1.98	0.00186138	5.98899
A_19_P00801490	A:chr4:76007134-7600	-	1.98	0.023679	3.21188
A_23_P55270	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	1.98	0.00702712	4.3992
A_23_P67932	CXCR1	chemokine (C-X-C motif) receptor 1	1.98	0.000118802	10.786
A_23_P47614	PHLDA2	pleckstrin homology-like domain, family A, member 2	1.98	0.00790346	4.27468
A_33_P3242369	LOC100506975	-	1.98	0.0277346	3.07156
A_23_P254434	RFPL2	ret finger protein-like 2	1.99	0.00393443	5.04966
A_23_P350574	FCRLB	Fc receptor-like B	1.99	8.22E-06	18.6216
A_23_P120794	SLC7A4	solute carrier family 7 (orphan transporter), member 4	1.99	0.00208528	5.83844
A_23_P209564	CYBRD1	cytochrome b reductase 1	1.99	8.60E-05	11.5329
A_33_P3326568	ENST00000467497	-	1.99	0.0270054	3.09501
A_33_P3278362	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	1.99	0.00186039	5.9897
A_33_P3236881	C1orf15-NBL1	-	1.99	2.64E-05	14.6931
A_33_P3519424	LOC386597	-	1.99	0.00461713	4.86397
A_23_P330836	ENST00000357412	-	2.00	0.0364341	2.8356
A_32_P223140	RASGEF1A	RasGEF domain family, member 1A	2.00	0.00118911	6.61356
A_23_P161563	RAB38	RAB38, member RAS oncogene family	2.00	0.00152537	6.26028
A_23_P259901	TKTL1	transketolase-like 1	2.00	9.56E-05	11.2821
A_24_P911676	SOX4	SRY (sex determining region Y)-box 4	2.00	0.0111467	3.92315
A_23_P209954	GNLY	granulysin	2.00	0.000118223	10.7969
A_32_P489662	KRT28	keratin 28	2.00	0.000497572	7.98394
A_19_P00320889	:chr3:171506452-1715	-	2.00	0.0159386	3.57621
A_33_P3254650	A_33_P3254650	-	2.01	0.0456014	2.6468
A_33_P3340129	LOC100128551	-	2.01	0.0466296	2.62828
A_19_P00320155	:chr15:25365058-2536	-	2.02	0.0419599	2.71629
A_24_P66027	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	2.02	0.000312556	8.81145
A_24_P371281	TMEM22	solute carrier family 35, member G2	2.02	0.00675119	4.44218
A_23_P50919	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	2.02	0.00580356	4.60696
A_23_P303718	DST	dystonin	2.02	0.00603951	4.56315
A_19_P00320735	:chr3:160981722-1609	-	2.02	0.0377324	2.80585
A_19_P00803462	:chr6:167455835-1674	-	2.02	0.0322544	2.94006

A_33_P3306272	KIAA0825	KIAA0825	2.02	0.00769375	4.30297
A_23_P163227	CKMT1A	creatine kinase, mitochondrial 1A	2.02	0.0119654	3.85294
A_19_P00323941	A:chrX:71327175-7133	-	2.03	0.00150757	6.27658
A_19_P00316125	A:chr10:3360886-3792	-	2.03	0.0218706	3.28347
A_33_P3241204	CALHM3	calcium homeostasis modulator 3	2.03	0.00711487	4.38594
A_24_P345209	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	2.03	0.00796609	4.2664
A_19_P00808088	A:chr3:8235936-8543	-	2.03	0.0315422	2.95936
A_19_P00323028	:chr15:25246744-2526	-	2.03	0.00346858	5.19947
A_19_P00318384	:chr3:195441633-1954	-	2.04	0.0108091	3.95385
A_23_P98686	ATHL1	ATH1, acid trehalase-like 1 (yeast)	2.04	0.000107634	11.0088
A_24_P943894	SCUBE3	signal peptide, CUB domain, EGF-like 3	2.04	0.00280675	5.45851
A_33_P3316508	RUNX2	runt-related transcription factor 2	2.04	0.00183022	6.01162
A_23_P5018	LOC80054	-	2.04	0.0181734	3.45328
A_33_P3374162	ENST00000390399	-	2.05	0.0104548	3.98727
A_33_P3241771	ENST00000539461	-	2.05	8.52E-05	11.5538
A_23_P209735	ARMC9	armadillo repeat containing 9	2.05	0.0308423	2.97881
A_24_P191312	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.05	4.39E-05	13.2441
A_33_P3227788	PANK1	pantothenate kinase 1	2.05	0.0219814	3.27889
A_23_P376870	C14orf79	chromosome 14 open reading frame 79	2.05	0.000320084	8.76731
A_23_P258088	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	2.06	0.0193182	3.39679
A_23_P138541	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	2.06	0.0134199	3.74084
A_33_P3321657	HSPG2	heparan sulfate proteoglycan 2	2.06	0.00201106	5.88614
A_23_P204246	PHC1	polyhomeotic homolog 1 (Drosophila)	2.06	0.0240171	3.19918
A_33_P3289296	TMEM37	transmembrane protein 37	2.07	0.0201093	3.35994
A_33_P3409477	UBASH3B	ubiquitin associated and SH3 domain containing B	2.07	0.000183925	9.84849
A_33_P3264404	LOC100132593	-	2.07	0.00333286	5.24759
A_33_P3339109	ENST00000512472	-	2.07	0.000175609	9.94405
A_24_P280983	HOXA11-AS1		2.07	0.0242965	3.18884
A_24_P261760	KLRG1	killer cell lectin-like receptor subfamily G, member 1	2.07	0.000219282	9.49294
A_19_P00809534	:chr4:110348751-1103	-	2.07	0.012098	3.84209
A_33_P3376321	ANK1	ankyrin 1, erythrocytic	2.08	0.0430992	2.69386
A_23_P45786	COL9A2	collagen, type IX, alpha 2	2.08	0.000672592	7.48474
A_32_P201979	HECTD2	HECT domain containing E3 ubiquitin protein ligase 2	2.08	0.00271703	5.4991
A_33_P3354604	ENST00000400702	-	2.08	0.012113	3.84087
A_32_P100430	LOC100128737	-	2.08	0.00198709	5.902
A_23_P324523	IQCK	IQ motif containing K	2.08	0.00249276	5.60785
A_23_P350719	PRSS30P	protease, serine, 30 homolog (mouse), pseudogene	2.08	2.09E-05	15.4142
A_32_P201212	CETN4P	centrin EF-hand protein 4, pseudogene	2.08	0.0446019	2.66525
A_33_P3272493	CD209	CD209 molecule	2.08	0.0131517	3.76043
A_24_P289178	C16orf74	chromosome 16 open reading frame 74	2.08	0.00198436	5.90381
A_32_P161762	RUNX2	runt-related transcription factor 2	2.09	0.00251702	5.59555
A_23_P136405	PDCD1	programmed cell death 1	2.09	0.000905529	7.01875
A_23_P387630	STARD8	StAR-related lipid transfer (START) domain containing 8	2.09	0.00858644	4.18823
A_23_P89902	RTN2	reticulon 2	2.09	0.00505223	4.76161
A_33_P3763846	MAPK12	mitogen-activated protein kinase 12	2.10	0.0455899	2.64701
A_33_P3714477	LOC285972	-	2.10	0.00143391	6.34653
A_24_P308229	AIM1L	absent in melanoma 1-like	2.10	0.00659484	4.46744
A_33_P3237096	INPP5F	inositol polyphosphate-5-phosphatase F	2.11	0.000164084	10.0858
A_23_P65532	PELI2	pellino E3 ubiquitin protein ligase family member 2	2.11	0.00421264	4.96976
A_23_P218058	KLRC4	killer cell lectin-like receptor subfamily C, member 4	2.12	0.00404928	5.0159
A_33_P3297150	A_33_P3297150	-	2.12	0.0102558	4.00662
A_33_P3295154	AK023831	-	2.12	0.0190522	3.40957
A_23_P340131	PRSS16	protease, serine, 16 (thymus)	2.12	0.0288576	3.03676
A_23_P23616	PLEKHN1	pleckstrin homology domain containing, family N member 1	2.12	0.000233026	9.37276
A_19_P00807225	:chr21:44919572-4493	-	2.13	0.0125653	3.80491
A_19_P00806946	:chr1:173758702-1737	-	2.13	0.0105921	3.97417
A_33_P3294159	CALY	calcyon neuron-specific vesicular protein	2.13	0.000226597	9.4279
A_33_P3260747	ENST00000373677	-	2.14	0.0132764	3.75127
A_33_P3295458	BK250D10.8	-	2.14	0.0130793	3.7658
A_23_P326319	C16orf45	chromosome 16 open reading frame 45	2.14	7.24E-05	11.9466
A_33_P3319401	ENST00000535396	-	2.14	0.0186257	3.43049
A_19_P00803803	A:chr6:56709666-5671	-	2.15	0.037136	2.81937

A_19_P00812259	A:chrX:64209375-6470	-	2.15	0.000206858	9.60956
A_19_P00805329	.:chr22:22669450-2267	-	2.15	0.000240481	9.31106
A_33_P3363933	FCRL6	Fc receptor-like 6	2.15	0.000110714	10.9447
A_33_P3304707	ENST00000390317	-	2.15	0.0147212	3.65176
A_24_P229151	ENST00000390458	-	2.15	0.00407255	5.00919
A_24_P870620	PTN	pleiotrophin	2.16	0.037554	2.80987
A_24_P147461	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	2.16	0.00567616	4.63148
A_24_P397294	LTC4S	leukotriene C4 synthase	2.16	0.00110517	6.72047
A_33_P3363630	AK058039	-	2.17	0.000253658	9.20737
A_19_P00319244	:chr2:128227291-1282	-	2.17	0.0203489	3.3491
A_32_P117464	MB21D2	Mab-21 domain containing 2	2.17	0.0196853	3.37948
A_33_P3846114	ENST00000448597	-	2.18	0.0226483	3.25189
A_33_P3527317	LOC148638	-	2.18	0.0467593	2.62598
A_33_P3357591	ATHL1	ATH1, acid trehalase-like 1 (yeast)	2.18	0.00171944	6.09592
A_33_P3241661	LOC388780	-	2.18	0.0152823	3.61608
A_23_P215419	ICA1	islet cell autoantigen 1, 69kDa	2.18	0.000898724	7.03026
A_23_P335452	ZCCHC24	zinc finger, CCHC domain containing 24	2.18	0.00162594	6.17223
A_33_P3395314	DB335107	-	2.18	0.0179084	3.46693
A_33_P3382331	HSPA6	heat shock 70kDa protein 6 (HSP70B')	2.19	1.86E-05	15.7736
A_23_P134835	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	2.19	0.000439185	8.19904
A_33_P3414113	ENST00000429784	-	2.20	0.000430523	8.23383
A_19_P00320754	.:chr15:40338196-4034	-	2.20	0.00643258	4.49441
A_33_P3386671	RORC	RAR-related orphan receptor C	2.20	0.00926725	4.10963
A_19_P00810587	.:chr11:36494424-3650	-	2.20	0.00601862	4.56695
A_23_P324813	BCL6B	B-cell CLL/lymphoma 6, member B	2.20	0.0107855	3.95603
A_33_P3282489	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	2.20	7.46E-05	11.8755
A_23_P216108	ANK1	ankyrin 1, erythrocytic	2.21	0.00175666	6.0669
A_33_P3300092	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.21	0.0200304	3.36354
A_23_P67198	CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	2.21	2.92E-06	22.9453
A_24_P175783	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	2.21	0.000413644	8.30409
A_24_P833129	ISPD	isoprenoid synthase domain containing	2.21	0.00959718	4.07389
A_33_P3411945	C19orf38	chromosome 19 open reading frame 38	2.22	0.00288542	5.42415
A_33_P3333224	GLIS2	GLIS family zinc finger 2	2.22	0.0311204	2.97102
A_19_P00321715	chr11:122051045-1222	-	2.23	0.000191133	9.76973
A_23_P110253	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	2.23	0.0475429	2.61221
A_33_P3224495	ENST00000445310	-	2.24	0.00234992	5.68329
A_33_P3422499	A_33_P3422499	-	2.24	1.33E-05	16.8848
A_33_P3879161	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	2.24	0.0201472	3.35821
A_33_P3420020	PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	2.24	0.0336332	2.90401
A_19_P00809632	:chr8:103939574-1040	-	2.24	0.0353172	2.86216
A_19_P00812284	:chr8:103953859-1039	-	2.24	0.00043284	8.22445
A_24_P164505	FAM106CP	family with sequence similarity 106, member C, pseudogene	2.24	0.0231764	3.23114
A_23_P430948	ATP13A4	ATPase type 13A4	2.25	0.0177791	3.47367
A_33_P3287760	RASGEF1A	RasGEF domain family, member 1A	2.25	0.00185079	5.99663
A_33_P3346287	NCRNA00299	long intergenic non-protein coding RNA 299	2.25	0.00529012	4.7099
A_33_P3259712	C12orf33	long intergenic non-protein coding RNA 612	2.26	0.00142681	6.35349
A_23_P13137	LOC100506886	-	2.26	0.0125853	3.80335
A_33_P3270445	BAI2	brain-specific angiogenesis inhibitor 2	2.26	0.0169876	3.51621
A_33_P3410589	FAM43A	family with sequence similarity 43, member A	2.26	0.00143488	6.34558
A_23_P139143	STX3	syntaxin 3	2.27	0.0085974	4.18691
A_24_P910733	CCDC50	coiled-coil domain containing 50	2.27	0.000428414	8.24243
A_23_P58729	SLC34A1	solute carrier family 34 (sodium phosphate), member 1	2.28	0.00136301	6.41797
A_33_P3298810	FFAR3	free fatty acid receptor 3	2.28	0.00400181	5.02971
A_33_P3638471	TRGV7	T cell receptor gamma variable 7 (pseudogene)	2.29	0.0017831	6.04672
A_24_P296508	SLC43A2	solute carrier family 43, member 2	2.29	0.0100321	4.0289
A_32_P787109	DTHD1	death domain containing 1	2.29	0.0265187	3.11107
A_32_P48825	KRT72	keratin 72	2.29	0.000327982	8.72231
A_23_P347468	FZD3	frizzled family receptor 3	2.29	1.68E-06	25.6503
A_33_P3340189	A_33_P3340189	-	2.30	0.011784	3.86801
A_23_P116614	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	2.30	0.00155958	6.22958
A_33_P3422595	ENST00000390343	-	2.30	0.00216751	5.78786
A_33_P3302613	ENST00000402420	-	2.31	0.0193949	3.39315

A_23_P252052	FILIP1L	filamin A interacting protein 1-like	2.31	0.000318082	8.77893
A_19_P00324815	chr11:113591565-1136	-	2.31	0.0207884	3.32959
A_33_P3237899	CHN2	chimerin (chimaerin) 2	2.32	0.000814546	7.18176
A_19_P00809151	A:chr7:39657750-3966	-	2.32	0.00777289	4.29219
A_19_P00322407	:chr6:147163036-1472	-	2.32	0.0472101	2.61803
A_23_P128281	KLRC3	killer cell lectin-like receptor subfamily C, member 3	2.33	4.08E-05	13.4433
A_23_P150857	SUOX	sulfite oxidase	2.33	0.0024364	5.637
A_24_P256512	STH	saitohin	2.33	0.00140313	6.37702
A_33_P3366540	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	2.33	0.0030881	5.34046
A_19_P00327272	:chr10:80112419-8012	-	2.33	0.000384566	8.4335
A_23_P207564	CCL4	chemokine (C-C motif) ligand 4	2.34	0.00181524	6.02267
A_23_P357760	ARSD	arylsulfatase D	2.34	0.0250465	3.16173
A_19_P00317326	:chr3:183170139-1831	-	2.34	0.00921836	4.11504
A_23_P103371	ADC	arginine decarboxylase	2.34	0.00667042	4.45514
A_23_P77493	TUBB3	tubulin, beta 3 class III	2.34	0.00292515	5.40721
A_33_P3354589	ENST00000378350	-	2.34	0.00672256	4.44675
A_23_P134058	C6orf114	glucose-fructose oxidoreductase domain containing 1	2.35	0.0114886	3.89313
A_23_P2181	CYB5R2	cytochrome b5 reductase 2	2.35	0.016788	3.5273
A_33_P3297978	MYO1E	myosin IE	2.35	0.000437834	8.20441
A_24_P110983	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	2.36	7.19E-06	19.1322
A_23_P121215	CAMK1	calcium/calmodulin-dependent protein kinase I	2.36	0.000566678	7.7651
A_33_P3229968	ENST00000455382	-	2.36	0.00305923	5.35198
A_24_P278299	ASB13	ankyrin repeat and SOCS box containing 13	2.36	0.00301723	5.36898
A_23_P151046	KLRC1	killer cell lectin-like receptor subfamily C, member 1	2.36	0.000118142	10.7984
A_19_P00322887	:chr15:25356910-2536	-	2.37	0.0308974	2.97726
A_23_P154566	TOX2	TOX high mobility group box family member 2	2.37	0.000636002	7.57529
A_24_P236799	RAB31	RAB31, member RAS oncogene family	2.38	0.0227243	3.24887
A_24_P45620	UTS2	urotensin 2	2.39	0.00353325	5.17731
A_23_P6422	RFPL3	ret finger protein-like 3	2.39	0.00713767	4.38253
A_23_P100001	FAM174B	family with sequence similarity 174, member B	2.39	0.00067206	7.48601
A_32_P198325	C22orf36	family with sequence similarity 211, member B	2.39	0.000169885	10.013
A_33_P3337272	NRARP	NOTCH-regulated ankyrin repeat protein	2.39	0.0220337	3.27674
A_23_P109171	BFSP1	beaded filament structural protein 1, filensin	2.40	0.000343616	8.63691
A_23_P139654	KLRC1	killer cell lectin-like receptor subfamily C, member 1	2.40	0.000808123	7.19407
A_19_P00318418	:chr7:139487141-1394	-	2.41	0.0018413	6.00352
A_33_P3298775	PRSS57	protease, serine, 57	2.41	0.000404116	8.34527
A_23_P90497	LILRA4	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	2.41	6.38E-05	12.2643
A_23_P140190	KIAA0125	KIAA0125	2.42	0.00249832	5.60502
A_33_P3272291	AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	2.42	0.00583865	4.60032
A_24_P935986	BCAT1	branched chain amino-acid transaminase 1, cytosolic	2.42	0.000728491	7.35712
A_33_P3356210	B7H6	-	2.42	0.00155154	6.23672
A_33_P3284453	C6orf174	SOGA family member 3	2.43	0.00501456	4.77005
A_23_P158318	ROR2	receptor tyrosine kinase-like orphan receptor 2	2.43	0.000930583	6.97725
A_24_P942921	UBXN10	UBX domain protein 10	2.43	0.0376864	2.80688
A_33_P3402646	ENST00000390435	-	2.43	0.000782919	7.24354
A_23_P1505	LRP5	low density lipoprotein receptor-related protein 5	2.44	0.00027977	9.01963
A_23_P85453	CD244	CD244 molecule, natural killer cell receptor 2B4	2.44	1.85E-05	15.7965
A_23_P6771	LMCD1	LIM and cysteine-rich domains 1	2.44	0.000251865	9.22109
A_24_P325520	SORT1	sortilin 1	2.45	0.00179829	6.03529
A_19_P00322400	:chr11:86624442-8662	-	2.45	3.59E-05	13.8017
A_19_P00320136	:chr15:25332807-2533	-	2.45	0.00840805	4.21002
A_23_P49759	CCL1	chemokine (C-C motif) ligand 1	2.46	0.00160706	6.18826
A_24_P353905	MXRA8	matrix-remodelling associated 8	2.47	8.91E-05	11.4486
A_19_P00321578	:chr3:171507069-1715	-	2.47	0.0110861	3.92858
A_33_P3378659	TARP	-	2.48	0.000363853	8.53298
A_33_P3250680	CD40LG	CD40 ligand	2.48	0.0084319	4.20708
A_33_P3234292	CD244	CD244 molecule, natural killer cell receptor 2B4	2.48	0.000418778	8.28237
A_23_P156284	DBN1	drebrin 1	2.50	3.83E-06	21.7297
A_33_P3269539	COL6A2	collagen, type VI, alpha 2	2.50	0.000607527	7.65013
A_33_P3341601	WDR86	WD repeat domain 86	2.50	0.0131617	3.75969
A_23_P146066	SPAG1	sperm associated antigen 1	2.51	0.00517209	4.73521

A_23_P401361	PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	2.51	0.000168442	10.0308
A_33_P3386547	SGPP2	sphingosine-1-phosphate phosphatase 2	2.51	0.000810886	7.18876
A_23_P370588	HOXB8	homeobox B8	2.51	0.0313144	2.96564
A_23_P27424	ZNF418	zinc finger protein 418	2.52	0.00317238	5.30754
A_33_P3236102	IER5L	immediate early response 5-like	2.53	4.19E-07	33.9124
A_23_P99785	FAM164C	zinc finger, C2HC-type containing 1C	2.53	0.00694113	4.41238
A_33_P3354607	CCL4	chemokine (C-C motif) ligand 4	2.54	0.00224249	5.74367
A_19_P00319513	:chr5:146852660-1468	-	2.54	4.25E-05	13.3326
A_23_P169909	DGKI	diacylglycerol kinase, iota	2.54	0.00824782	4.23006
A_23_P215048	KIAA0408	KIAA0408	2.54	0.00125449	6.53629
A_19_P00317616	:chr2:216542666-2165	-	2.54	0.000346684	8.62069
A_23_P30315	TRIM7	tripartite motif containing 7	2.55	0.000198228	9.69559
A_23_P345692	IL17D	interleukin 17D	2.55	0.0111702	3.92105
A_23_P169003	SH2D4A	SH2 domain containing 4A	2.55	0.00660968	4.46502
A_33_P3234197	TRIM45	tripartite motif containing 45	2.55	0.0103424	3.99815
A_33_P3251412	A_33_P3251412	-	2.56	0.0101309	4.01899
A_23_P68669	CHODL	chondrolectin	2.56	0.000212412	9.55642
A_19_P00331670	A:chr6:98418879-9845	-	2.57	2.64E-05	14.6909
A_33_P3225625	TARP	-	2.57	0.000446846	8.16894
A_33_P3358601	IFITM10	interferon induced transmembrane protein 10	2.58	5.92E-05	12.4526
A_23_P114947	RGS2	regulator of G-protein signaling 2, 24kDa	2.59	0.000351751	8.59428
A_32_P4985	CAMTA1	calmodulin binding transcription activator 1	2.60	0.0151914	3.62176
A_23_P116512	PRR5L	proline rich 5 like	2.60	0.000102731	11.1156
A_24_P260443	THBS4	thrombospondin 4	2.61	0.00177871	6.05005
A_33_P3225066	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	2.61	0.0234856	3.21924
A_33_P3285734	FCRL6	Fc receptor-like 6	2.61	0.000655591	7.52606
A_23_P211785	ZNF35	zinc finger protein 35	2.62	0.000210289	9.57654
A_24_P101704	ROR2	receptor tyrosine kinase-like orphan receptor 2	2.62	0.000935068	6.96996
A_23_P259207	THNSL2	threonine synthase-like 2 (S. cerevisiae)	2.62	0.00588696	4.59124
A_33_P3843285	ENST00000460754	-	2.62	0.034107	2.892
A_19_P00811660	:chr8:103953859-1039	-	2.62	4.35E-05	13.2642
A_33_P3301010	SPIRE1	spire homolog 1 (Drosophila)	2.63	9.41E-05	11.3183
A_23_P217946	CDH23	cadherin-related 23	2.64	0.026344	3.11691
A_33_P3278078	LOC100505501	-	2.65	0.0488281	2.59015
A_23_P51936	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	2.65	0.000233902	9.36539
A_23_P163492	BAIAP3	BAI1-associated protein 3	2.66	0.000427566	8.2459
A_33_P3287348	CHN2	chimerin (chimaerin) 2	2.66	5.67E-05	12.5627
A_23_P1912	ZP1	zona pellucida glycoprotein 1 (sperm receptor)	2.67	1.71E-05	16.056
A_23_P31453	STEAP1	six transmembrane epithelial antigen of the prostate 1	2.67	0.000174988	9.9514
A_23_P388900	SLC22A15	solute carrier family 22, member 15	2.67	0.00258689	5.56086
A_23_P205293	EXD2	exonuclease 3'-5' domain containing 2	2.67	0.000168263	10.0331
A_24_P406334	STEAP1	six transmembrane epithelial antigen of the prostate 1	2.67	0.00489678	4.79695
A_33_P3406196	KLRD1	killer cell lectin-like receptor subfamily D, member 1	2.67	1.63E-05	16.1973
A_33_P3210258	ENST00000390345	-	2.68	0.000126136	10.6528
A_23_P31399	PON2	paraoxonase 2	2.68	0.000972628	6.91048
A_23_P53057	ZNF215	zinc finger protein 215	2.69	0.0124582	3.81329
A_23_P17065	CCL20	chemokine (C-C motif) ligand 20	2.70	0.00317301	5.3073
A_23_P214533	ZNF323	zinc finger protein 323	2.71	0.00193515	5.93713
A_33_P3321347	ENST00000444532	-	2.72	0.00286291	5.43387
A_23_P204208	KLRD1	killer cell lectin-like receptor subfamily D, member 1	2.73	7.05E-06	19.21
A_33_P3525062	LOC285626	-	2.73	0.00160929	6.18635
A_23_P211699	A_23_P211699	-	2.73	0.00176999	6.05669
A_23_P209731	ARMC9	armadillo repeat containing 9	2.74	0.000600736	7.6686
A_19_P00329765	:chr11:17378149-1740	-	2.74	0.00465253	4.85522
A_33_P3322363	HMSD	histocompatibility (minor) serpin domain containing	2.75	0.00143248	6.34793
A_33_P3325843	FLJ40039	-	2.77	5.99E-05	12.4234
A_33_P3409392	FZD6	frizzled family receptor 6	2.77	0.00124622	6.54579
A_33_P3286157	TNFRSF4	tumor necrosis factor receptor superfamily, member 4	2.78	0.00393842	5.04846
A_23_P21560	FAM49A	family with sequence similarity 49, member A	2.78	0.000550275	7.81407
A_33_P3218975	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	2.79	0.00532418	4.70271
A_33_P3280157	SNORD116-19	small nucleolar RNA, C/D box 116-19	2.80	0.0106222	3.97132
A_33_P3241269	CES1	carboxylesterase 1	2.80	0.000603103	7.66214
A_23_P211680	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	2.82	1.35E-05	16.836

A_19_P00802873	A:chr10:3521025-3527	-	2.82	0.000588092	7.70365
A_33_P3233580	KIAA1217	KIAA1217	2.83	0.0156552	3.59319
A_32_P205053	UBXN10	UBX domain protein 10	2.84	6.70E-05	12.141
A_23_P119478	EBI3	Epstein-Barr virus induced 3	2.84	0.00031242	8.81226
A_33_P3394380	AKAP5	A kinase (PRKA) anchor protein 5	2.84	0.000151248	10.2583
A_24_P811704	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.84	0.000191476	9.76607
A_33_P3218787	ENST00000373815	-	2.84	0.00111879	6.70248
A_33_P3259775	DOCK5	dedicator of cytokinesis 5	2.85	0.000434844	8.21638
A_23_P397120	C19orf77	chromosome 19 open reading frame 77	2.86	0.000836741	7.14007
A_23_P207981	SOCS6	suppressor of cytokine signaling 6	2.86	0.00446972	4.90122
A_33_P3218980	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	2.87	0.0038666	5.07014
A_19_P00801014	A:chr4:80995226-8100	-	2.87	0.000664747	7.50365
A_23_P70746	AHI1	Abelson helper integration site 1	2.88	7.36E-05	11.9093
A_23_P49499	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	2.88	0.00264807	5.53139
A_23_P368711	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	2.89	7.92E-05	11.729
A_32_P7015	TSPAN15	tetraspanin 15	2.91	0.0157994	3.58451
A_23_P398943	ENST00000482404	-	2.91	0.0440415	2.67579
A_33_P3423185	DPF3	D4, zinc and double PHD fingers, family 3	2.92	0.0294504	3.01899
A_33_P3353921	ENST00000489214	-	2.92	0.000127	10.6377
A_32_P41604	F5	coagulation factor V (proaccelerin, labile factor)	2.92	0.0005235	7.89783
A_23_P5654	IL1F7	interleukin 37	2.93	0.000139977	10.4249
A_33_P3397127	AB306238	-	2.93	3.90E-05	13.5694
A_23_P7412	BTNL8	butyrophilin-like 8	2.93	0.0156387	3.5942
A_23_P113793	ZBED2	zinc finger, BED-type containing 2	2.95	0.00634212	4.50979
A_33_P3327642	AIM1L	absent in melanoma 1-like	2.95	0.00270669	5.50388
A_23_P159956	MID2	midline 2	2.96	0.00141834	6.36185
A_23_P161769	FXYD2	FXYD domain containing ion transport regulator 2	2.96	0.0126953	3.79484
A_23_P302005	STON1	stonin 1	2.97	0.000124242	10.6863
A_24_P203689	KIF7	kinesin family member 7	2.97	0.0030479	5.35654
A_33_P3294917	PRUNE2	prune homolog 2 (Drosophila)	3.01	0.00065245	7.53384
A_23_P13822	STYK1	serine/threonine/tyrosine kinase 1	3.01	1.62E-05	16.2337
A_23_P163216	ATP8B4	ATPase, class I, type 8B, member 4	3.01	3.42E-05	13.9357
A_23_P349406	RIMKLA	ribosomal modification protein rimK-like family member A	3.03	0.00134817	6.43349
A_33_P3228266	CST3	cystatin C	3.03	0.00135897	6.42218
A_23_P40217	DOK5	docking protein 5	3.04	0.000766898	7.27598
A_23_P76364	CD9	CD9 molecule	3.07	7.88E-05	11.7402
A_33_P3394175	ENST00000390363	-	3.07	0.000165117	10.0726
A_24_P67534	LOC644538	-	3.08	0.00890401	4.1507
A_23_P256581	PRDM13	PR domain containing 13	3.09	0.0101242	4.01966
A_23_P29257	H1F0	H1 histone family, member 0	3.09	0.000937642	6.96579
A_33_P3221341	HECTD2	HECT domain containing E3 ubiquitin protein ligase 2	3.09	0.0073673	4.34883
A_32_P25050	RDH10	retinol dehydrogenase 10 (all-trans)	3.10	3.56E-06	22.0478
A_23_P127565	LAYN	layilin	3.10	0.000819336	7.17265
A_24_P38143	AHI1	Abelson helper integration site 1	3.12	1.39E-06	26.6556
A_33_P3256725	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	3.12	0.000251939	9.22052
A_23_P422245	KIAA0825	KIAA0825	3.13	0.0043506	4.93239
A_33_P3391915	BTBD17	BTB (POZ) domain containing 17	3.13	0.0017317	6.08628
A_23_P201551	VAV3	vav 3 guanine nucleotide exchange factor	3.14	2.40E-05	14.9781
A_33_P3317258	ENST00000390344	-	3.14	0.000748275	7.31471
A_33_P3208970	ZNF683	zinc finger protein 683	3.14	0.00552112	4.66221
A_23_P146512	GOLM1	golgi membrane protein 1	3.15	0.0168058	3.5263
A_19_P00321032	:chr3:171506056-1715	-	3.16	4.15E-05	13.3955
A_23_P389102	MYO1D	myosin ID	3.17	3.94E-05	13.5359
A_24_P330303	FRMD6	FERM domain containing 6	3.20	0.00127647	6.51137
A_24_P937405	PRSS23	protease, serine, 23	3.21	5.62E-05	12.5856
A_32_P465742	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	3.21	1.01E-05	17.8742
A_23_P72096	IL1A	interleukin 1, alpha	3.22	0.00808293	4.25115
A_33_P3398156	CYS1	cystin 1	3.23	0.000110975	10.9394
A_33_P3312686	DGAT2L6	diacylglycerol O-acyltransferase 2-like 6	3.23	0.0123317	3.82329
A_23_P83351	DFNB31	deafness, autosomal recessive 31	3.24	2.26E-05	15.1697
A_33_P3348011	LOC222699	-	3.25	0.000500945	7.97244

A_19_P00316395	:chr6:14706597-1470(	-	3.26	0.00160113	6.19333
A_24_P191664	GOLIM4	golgi integral membrane protein 4	3.27	5.71E-05	12.5464
A_33_P3307197	PTGFRN	prostaglandin F2 receptor negative regulator	3.27	0.00481046	4.81715
A_23_P128698	SPRY2	sprouty homolog 2 (Drosophila)	3.30	0.0390355	2.77711
A_23_P216679	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	3.31	0.000321999	8.75628
A_23_P160406	KCTD3	potassium channel tetramerisation domain containing 3	3.32	0.00906114	4.1327
A_32_P70158	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	3.32	0.000161178	10.1234
A_23_P329890	TMEM136	transmembrane protein 136	3.33	0.00322806	5.28635
A_19_P00325490	:chr2:238357611-2383	-	3.33	0.000581128	7.72334
A_33_P3361671	ENST00000488690	-	3.34	0.00622791	4.52958
A_23_P382488	LRRC16B	leucine rich repeat containing 16B	3.36	0.000195532	9.72338
A_23_P202501	RNLS	renalase, FAD-dependent amine oxidase	3.36	0.00241053	5.65064
A_23_P102731	SMOX	spermine oxidase	3.39	0.000686639	7.45151
A_33_P3290343	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	3.40	0.00238188	5.66595
A_23_P27107	TM4SF5	transmembrane 4 L six family member 5	3.40	9.65E-05	11.2605
A_33_P3212432	X04925	-	3.42	0.0338501	2.89849
A_23_P123596	GLDC	glycine dehydrogenase (decarboxylating)	3.44	0.00107395	6.7627
A_23_P204947	GJB2	gap junction protein, beta 2, 26kDa	3.45	0.0409377	2.737
A_33_P3276615	APOL4	apolipoprotein L, 4	3.46	0.0137374	3.71822
A_23_P99642	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	3.48	0.00913502	4.12436
A_23_P106103	AKAP5	A kinase (PRKA) anchor protein 5	3.48	2.67E-05	14.6544
A_23_P209625	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	3.48	0.0147053	3.65279
A_23_P120883	HMOX1	heme oxygenase (decycling) 1	3.49	0.000241907	9.29952
A_33_P3261298	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	3.50	7.70E-05	11.7974
A_33_P3415633	TMEM136	transmembrane protein 136	3.52	0.0047279	4.83687
A_24_P64167	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	3.53	0.00236722	5.67387
A_32_P206839	LOC100288911	-	3.53	1.92E-06	24.9877
A_19_P00802648	:chr3:183160356-1831	-	3.55	0.000778604	7.2522
A_23_P113701	PDGFA	platelet-derived growth factor alpha polypeptide	3.55	0.000556072	7.79656
A_32_P81676	LOC157627	-	3.58	0.000110652	10.946
A_33_P3362178	PROX2	prospero homeobox 2	3.59	0.00134063	6.44144
A_33_P3397599	LILRA6	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	3.60	0.00922105	4.11475
A_23_P147397	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	3.61	0.00087209	7.07631
A_23_P254944	GSTT1	glutathione S-transferase theta 1	3.61	0.000520896	7.90625
A_33_P3259183	FAM78B	family with sequence similarity 78, member B	3.62	0.000334366	8.68687
A_23_P254271	TUBB6	tubulin, beta 6 class V	3.62	0.000156616	10.1841
A_24_P106910	PTCH1	patched 1	3.63	0.00324207	5.28108
A_24_P411121	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	3.64	0.00332309	5.25114
A_33_P3245799	ENST00000349457	-	3.66	0.000496613	7.98723
A_32_P213459	DMRT2	doublesex and mab-3 related transcription factor 2	3.67	0.00212446	5.81405
A_33_P3295655	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1	3.69	0.00010531	11.0587
A_33_P3372044	TPRG1	tumor protein p63 regulated 1	3.71	0.000592569	7.69114
A_33_P3256793	KIAA1324	KIAA1324	3.71	0.000191418	9.76669
A_33_P3258478	LOC100506173	-	3.73	4.29E-05	13.3018
A_23_P69012	CCR8	chemokine (C-C motif) receptor 8	3.73	0.00944141	4.09059
A_23_P250607	PLS3	plastin 3	3.77	0.00561	4.64447
A_33_P3223056	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	3.78	4.19E-06	21.3374
A_33_P3404729	AK075182	-	3.83	1.36E-05	16.8272
A_23_P134419	ZP3	zona pellucida glycoprotein 3 (sperm receptor)	3.84	0.00347723	5.19648
A_33_P3240946	ENST00000366353	-	3.84	0.0115409	3.88863
A_33_P3313899	LOC728228	-	3.85	0.0194985	3.38825
A_23_P130435	LIM2	lens intrinsic membrane protein 2, 19kDa	3.85	0.000199201	9.68567
A_19_P00327046	:chr6:138961057-1390	-	3.86	0.00164466	6.15654
A_23_P216468	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	3.88	0.000112316	10.9122
A_19_P00322962	:chrX:57003000-5701(	-	3.89	0.000202548	9.65198

A_33_P3474319	SLC37A2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	3.91	2.04E-05	15.4813
A_33_P3376806	C10orf67	chromosome 10 open reading frame 67	3.92	0.00152783	6.25804
A_23_P111888	CTHRC1	collagen triple helix repeat containing 1	3.97	0.000286335	8.97569
A_23_P142878	ATOH8	atonal homolog 8 (Drosophila)	3.99	0.00425554	4.95799
A_24_P354715	NT5E	5'-nucleotidase, ecto (CD73)	4.00	0.000103176	11.1056
A_23_P27013	HOXB9	homeobox B9	4.03	0.000223578	9.45444
A_24_P119609	MYO1D	myosin ID	4.10	0.00377128	5.09965
A_33_P3240951	DPF3	D4, zinc and double PHD fingers, family 3	4.11	7.90E-05	11.7359
A_24_P396167	CTSW	cathepsin W	4.15	0.000902561	7.02376
A_33_P3301709	GNG4	guanine nucleotide binding protein (G protein), gamma 4	4.15	0.000148803	10.2932
A_23_P85716	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	4.19	4.67E-06	20.8744
A_33_P3394972	OSBPL5	oxysterol binding protein-like 5	4.24	0.00032035	8.76578
A_24_P226069	FGFBP2	fibroblast growth factor binding protein 2	4.24	5.02E-05	12.8834
A_23_P331928	CD109	CD109 molecule	4.27	2.04E-05	15.49
A_24_P316430	NT5E	5'-nucleotidase, ecto (CD73)	4.31	3.53E-05	13.8427
A_33_P3403576	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	4.33	0.00305588	5.35333
A_23_P311632	NLRP6	NLR family, pyrin domain containing 6	4.35	0.000114865	10.8616
A_23_P114903	HSPA6	heat shock 70kDa protein 6 (HSP70B')	4.41	1.86E-07	39.9079
A_24_P10233	DAPK2	death-associated protein kinase 2	4.44	0.000272569	9.06925
A_23_P10506	HPGDS	hematopoietic prostaglandin D synthase	4.44	5.26E-05	12.7588
A_23_P53081	OSBPL5	oxysterol binding protein-like 5	4.44	0.00023456	9.35988
A_32_P234145	SHC4	SHC (Src homology 2 domain containing) family, member 4	4.61	0.000757354	7.29568
A_33_P3231414	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	4.61	5.09E-05	12.8474
A_23_P406341	AFAP1L2	actin filament associated protein 1-like 2	4.65	0.00012597	10.6557
A_23_P79094	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	4.67	0.000443179	8.18327
A_24_P133905	CCL23	chemokine (C-C motif) ligand 23	4.73	0.00391338	5.05597
A_33_P3724750	BC014063	-	4.78	0.0252646	3.15401
A_33_P3303302	A_33_P3303302	-	4.78	0.000380015	8.4548
A_23_P373724	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	4.82	6.14E-06	19.7542
A_23_P144916	GFPT2	glutamine-fructose-6-phosphate transaminase 2	4.83	0.000682851	7.46039
A_23_P133386	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	4.98	0.000239389	9.31995
A_23_P256107	HPSE	heparanase	5.02	0.000790753	7.22797
A_33_P3313920	KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	5.05	6.41E-05	12.2532
A_24_P251534	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	5.09	1.57E-05	16.3384
A_33_P3222549	ENST00000437648	-	5.09	0.000166938	10.0496
A_33_P3301940	PDE7B	phosphodiesterase 7B	5.11	0.000136607	10.4778
A_33_P3265222	KIAA1324	KIAA1324	5.11	0.000124112	10.6886
A_19_P00321033	chr3:171506056-1715	-	5.14	2.47E-05	14.8922
A_23_P68740	AIRE	autoimmune regulator	5.22	0.00221522	5.75953
A_23_P216966	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	5.27	7.52E-05	11.8554
A_33_P3327617	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene)	5.28	0.000780338	7.24871
A_33_P3321085	ENST00000390424	-	5.30	0.00085271	7.11088
A_33_P3311073	KIR2DS3	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3	5.31	0.000171617	9.99186
A_33_P3389649	PDE4D	phosphodiesterase 4D, cAMP-specific	5.34	0.00215688	5.79427
A_33_P3244312	ENST00000426402	-	5.39	0.000800443	7.20895
A_33_P3338071	A_33_P3338071	-	5.69	9.00E-05	11.4234
A_23_P388993	ZC3H12C	zinc finger CCCH-type containing 12C	5.74	8.06E-05	11.6854
A_23_P34644	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	5.77	0.00103771	6.8136
A_23_P407565	CX3CR1	chemokine (C-X3-C motif) receptor 1	5.80	0.00333806	5.2457
A_33_P3393667	ENST00000542354	-	5.91	1.69E-05	16.0981
A_33_P3316273	CCL3	chemokine (C-C motif) ligand 3	5.95	0.000116574	10.8284
A_33_P3345225	A_33_P3345225	-	5.95	0.000729348	7.35525
A_33_P3222917	CD276	CD276 molecule	5.97	0.00084978	7.11619
A_19_P00319323	chr3:171506370-1715	-	6.00	9.82E-05	11.2208
A_24_P494454	SPIN3	spindlin family, member 3	6.01	0.000672621	7.48467
A_19_P00319324	chr3:171506370-1715	-	6.01	0.000262535	9.14105

A_23_P114084	PHEX	phosphate regulating endopeptidase homolog, X-linked	6.07	2.61E-05	14.73
A_33_P3224882	ENST00000444775	-	6.10	0.000263875	9.13128
A_33_P3251896	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	6.22	0.00111974	6.70124
A_23_P130815	KIR2DS2	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2	6.27	0.000167416	10.0436
A_23_P40847	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	6.32	1.79E-05	15.9035
A_24_P345451	CYBRD1	cytochrome b reductase 1	6.38	0.000263505	9.13397
A_23_P66682	HOXB6	homeobox B6	6.39	0.000625193	7.60322
A_24_P658584	SASH1	SAM and SH3 domain containing 1	6.42	0.000358124	8.5617
A_23_P502590	KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	6.45	0.0003599	8.55273
A_23_P155688	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	6.47	1.16E-06	27.6348
A_23_P398854	DOK7	docking protein 7	6.49	0.000307613	8.84113
A_33_P3236906	NCRNA00271	long intergenic non-protein coding RNA 271	6.49	2.15E-05	15.3203
A_24_P87746	KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	6.59	0.000192891	9.75106
A_33_P3320062	PLD1	phospholipase D1, phosphatidylcholine-specific	6.72	3.06E-05	14.2524
A_23_P406025	PRUNE2	prune homolog 2 (Drosophila)	6.77	8.03E-05	11.6946
A_23_P167920	DLL1	delta-like 1 (Drosophila)	6.77	3.32E-05	14.0243
A_33_P3342528	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	6.86	4.90E-05	12.9486
A_24_P228130	CCL3L3	chemokine (C-C motif) ligand 3-like 3	7.15	0.000138918	10.4414
A_23_P353035	IGFBP7	insulin-like growth factor binding protein 7	7.17	0.0143755	3.67452
A_33_P3296181	CCL3L3	chemokine (C-C motif) ligand 3-like 3	7.29	0.0001058	11.0481
A_24_P288298	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	7.59	3.96E-05	13.5271
A_23_P52676	CATSPER1	cation channel, sperm associated 1	7.60	0.000726772	7.36087
A_23_P257043	GEM	GTP binding protein overexpressed in skeletal muscle	7.62	0.00262222	5.54374
A_33_P3375314	ATP9A	ATPase, class II, type 9A	7.84	2.68E-05	14.6478
A_23_P31064	MOXD1	monooxygenase, DBH-like 1	7.93	0.000185691	9.82886
A_23_P206280	GPR56	G protein-coupled receptor 56	7.96	1.99E-05	15.5651
A_23_P147431	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8.07	2.48E-07	37.6919
A_23_P354387	MYOF	myoferlin	8.21	3.76E-06	21.8164
A_24_P253003	WNT11	wingless-type MMTV integration site family, member 11	8.31	4.29E-06	21.2431
A_24_P224488	MAPT	microtubule-associated protein tau	8.38	0.000218618	9.49897
A_23_P200728	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	8.71	2.00E-06	24.7726
A_23_P50946	RAMP1	receptor (G protein-coupled) activity modifying protein 1	8.79	1.39E-05	16.751
A_33_P3408938	LILRP2	leukocyte immunoglobulin-like receptor pseudogene 2	9.02	0.00043264	8.22525
A_24_P117147	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	9.20	0.000179343	9.90049
A_33_P3233906	RAMP1	receptor (G protein-coupled) activity modifying protein 1	9.65	2.99E-05	14.323
A_23_P109072	SALL4	sal-like 4 (Drosophila)	10.43	3.48E-05	13.8847
A_24_P350622	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	11.53	5.07E-05	12.8556
A_24_P5890	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A	12.58	0.000445649	8.1736
A_33_P3389728	NR5A2	nuclear receptor subfamily 5, group A, member 2	12.77	7.01E-05	12.0288
A_33_P3270346	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A	13.13	0.000537755	7.85262
A_33_P3419314	CHD5	chromodomain helicase DNA binding protein 5	13.97	0.000165308	10.0702
A_33_P3247890	ENST00000390423	-	14.51	0.000305697	8.85279
A_33_P3363799	NCAM1	neural cell adhesion molecule 1	19.16	3.16E-06	22.5827
A_23_P380614	ATP9A	ATPase, class II, type 9A	20.61	6.35E-05	12.2751
A_24_P354689	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	27.87	7.80E-05	11.7664
A_23_P312920	POU2AF1	POU class 2 associating factor 1	43.19	1.07E-05	17.6698

Supplementary Table 3

A full list of functional groups generated from the full list of differentially expressed genes by GO-BP-FAT (Gene Ontology Biological Process, FAT term) tool on the DAVID platform.

	Category Term	Count	PValue
1	GO:0006955~immune response	77	2.03E-13
2	GO:0009611~response to wounding	62	9.50E-12
3	GO:0006952~defense response	66	7.95E-11
4	GO:0006954~inflammatory response	42	1.93E-09
5	GO:0022610~biological adhesion	63	2.04E-07
6	GO:0002684~positive regulation of immune system process	31	3.01E-07
7	GO:0007155~cell adhesion	62	4.40E-07
8	GO:0006935~chemotaxis	24	7.34E-07
9	GO:0042330~taxis	24	7.34E-07
10	GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	11	1.11E-06
11	GO:0006968~cellular defense response	14	2.37E-06
12	GO:0007626~locomotory behavior	31	5.84E-06
13	GO:0050671~positive regulation of lymphocyte proliferation	12	2.68E-05
14	GO:0070665~positive regulation of leukocyte proliferation	12	3.20E-05
15	GO:0032946~positive regulation of mononuclear cell proliferation	12	3.20E-05
16	GO:0002700~regulation of production of molecular mediator of immune response	10	6.70E-05
17	GO:0007610~behavior	41	7.29E-05
18	GO:0050670~regulation of lymphocyte proliferation	14	7.70E-05
19	GO:0070663~regulation of leukocyte proliferation	14	8.74E-05
20	GO:0032944~regulation of mononuclear cell proliferation	14	8.74E-05
21	GO:0051251~positive regulation of lymphocyte activation	15	1.03E-04
22	GO:0002697~regulation of immune effector process	15	1.60E-04
23	GO:0002696~positive regulation of leukocyte activation	15	2.69E-04
24	GO:0051094~positive regulation of developmental process	27	3.30E-04
25	GO:0050867~positive regulation of cell activation	15	4.36E-04
26	GO:0045597~positive regulation of cell differentiation	23	6.49E-04
27	GO:0002637~regulation of immunoglobulin production	7	8.49E-04
28	GO:0050865~regulation of cell activation	19	8.87E-04
29	GO:0043009~chordate embryonic development	29	9.79E-04
30	GO:0051249~regulation of lymphocyte activation	17	9.90E-04
31	GO:0009792~embryonic development ending in birth or egg hatching	29	1.12E-03
32	GO:0019882~antigen processing and presentation	12	1.16E-03
33	GO:0001775~cell activation	26	1.19E-03
34	GO:0002694~regulation of leukocyte activation	18	1.28E-03
35	GO:0045321~leukocyte activation	23	1.34E-03
36	GO:0008284~positive regulation of cell proliferation	33	1.96E-03
37	GO:0050778~positive regulation of immune response	16	2.19E-03
38	GO:0006928~cell motion	36	2.71E-03
39	GO:0048839~inner ear development	11	2.71E-03
40	GO:0002253~activation of immune response	12	3.18E-03
41	GO:0001817~regulation of cytokine production	18	3.22E-03
42	GO:0043583~ear development	12	3.46E-03
43	GO:0043433~negative regulation of transcription factor activity	8	3.63E-03
44	GO:0046649~lymphocyte activation	19	3.71E-03
45	GO:0001932~regulation of protein amino acid phosphorylation	17	4.88E-03
46	GO:0042127~regulation of cell proliferation	52	5.10E-03
47	GO:0042060~wound healing	18	5.56E-03
48	GO:0002221~pattern recognition receptor signaling pathway	5	5.99E-03
49	GO:0051270~regulation of cell motion	18	6.16E-03
50	GO:0050863~regulation of T cell activation	13	6.24E-03
51	GO:0048562~embryonic organ morphogenesis	14	6.76E-03
52	GO:0050870~positive regulation of T cell activation	10	6.78E-03
53	GO:0042102~positive regulation of T cell proliferation	7	7.34E-03
54	GO:0033559~unsaturated fatty acid metabolic process	8	7.36E-03
55	GO:0043392~negative regulation of DNA binding	8	7.36E-03
56	GO:0002757~immune response-activating signal transduction	8	8.18E-03
57	GO:0002218~activation of innate immune response	5	9.08E-03
58	GO:0002758~innate immune response-activating signal transduction	5	9.08E-03
59	GO:0048568~embryonic organ development	16	1.06E-02
60	GO:0030890~positive regulation of B cell proliferation	5	1.10E-02
61	GO:0006805~xenobiotic metabolic process	5	1.10E-02
62	GO:0042325~regulation of phosphorylation	33	1.10E-02
63	GO:0008037~cell recognition	8	1.11E-02
64	GO:0051174~regulation of phosphorus metabolic process	34	1.12E-02
65	GO:0019220~regulation of phosphate metabolic process	34	1.12E-02
66	GO:0032763~regulation of mast cell cytokine production	3	1.14E-02
67	GO:0048598~embryonic morphogenesis	24	1.14E-02
68	GO:0007167~enzyme linked receptor protein signaling pathway	26	1.14E-02
69	GO:0046456~icosanoid biosynthetic process	6	1.15E-02
70	GO:0035239~tube morphogenesis	13	1.17E-02
71	GO:0007166~cell surface receptor linked signal transduction	104	1.18E-02

72	GO:0042472~inner ear morphogenesis	8	1.22E-02
73	GO:0002764~immune response-regulating signal transduction	8	1.22E-02
74	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	19	1.23E-02
75	GO:0007267~cell-cell signaling	40	1.25E-02
76	GO:0002699~positive regulation of immune effector process	7	1.32E-02
77	GO:0050871~positive regulation of B cell activation	6	1.50E-02
78	GO:0030030~cell projection organization	27	1.51E-02
79	GO:0051100~negative regulation of binding	8	1.60E-02
80	GO:0007243~protein kinase cascade	27	1.60E-02
81	GO:0007596~blood coagulation	11	1.61E-02
82	GO:0050817~coagulation	11	1.61E-02
83	GO:0031349~positive regulation of defense response	9	1.62E-02
84	GO:0032870~cellular response to hormone stimulus	13	1.64E-02
85	GO:0006636~unsaturated fatty acid biosynthetic process	6	1.69E-02
86	GO:0051090~regulation of transcription factor activity	11	1.71E-02
87	GO:0007389~pattern specification process	21	1.75E-02
88	GO:0006690~icosanoid metabolic process	7	1.79E-02
89	GO:0009410~response to xenobiotic stimulus	5	1.80E-02
90	GO:0001736~establishment of planar polarity	3	1.84E-02
91	GO:0002703~regulation of leukocyte mediated immunity	8	1.89E-02
92	GO:0042108~positive regulation of cytokine biosynthetic process	7	1.97E-02
93	GO:0051101~regulation of DNA binding	12	2.00E-02
94	GO:0042129~regulation of T cell proliferation	8	2.05E-02
95	GO:0035295~tube development	18	2.07E-02
96	GO:0050873~brown fat cell differentiation	5	2.09E-02
97	GO:0002224~toll-like receptor signaling pathway	4	2.26E-02
98	GO:0007599~hemostasis	11	2.31E-02
99	GO:0045669~positive regulation of osteoblast differentiation	5	2.40E-02
100	GO:0016477~cell migration	21	2.41E-02
101	GO:0006959~humoral immune response	9	2.50E-02
102	GO:0048534~hemopoietic or lymphoid organ development	20	2.54E-02
103	GO:0032735~positive regulation of interleukin-12 production	3	2.67E-02
104	GO:0002639~positive regulation of immunoglobulin production	3	2.67E-02
105	GO:0009405~pathogenesis	3	2.67E-02
106	GO:0032760~positive regulation of tumor necrosis factor production	4	2.73E-02
107	GO:0002702~positive regulation of production of molecular mediator of immune response	4	2.73E-02
108	GO:0042471~ear morphogenesis	8	2.79E-02
109	GO:0060627~regulation of vesicle-mediated transport	10	2.82E-02
110	GO:0048705~skeletal system morphogenesis	11	2.89E-02
111	GO:0001501~skeletal system development	23	3.05E-02
112	GO:0045444~fat cell differentiation	7	3.06E-02
113	GO:0043065~positive regulation of apoptosis	29	3.10E-02
114	GO:0002526~acute inflammatory response	10	3.17E-02
115	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	8	3.22E-02
116	GO:0007242~intracellular signaling cascade	71	3.24E-02
117	GO:0045088~regulation of innate immune response	7	3.32E-02
118	GO:0043068~positive regulation of programmed cell death	29	3.32E-02
119	GO:0007159~leukocyte adhesion	5	3.49E-02
120	GO:0030888~regulation of B cell proliferation	5	3.49E-02
121	GO:0010942~positive regulation of cell death	29	3.54E-02
122	GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors	7	3.59E-02
123	GO:0007185~transmembrane receptor protein tyrosine phosphatase signaling pathway	3	3.63E-02
124	GO:0002532~production of molecular mediator of acute inflammatory response	3	3.63E-02
125	GO:0048870~cell motility	22	3.66E-02
126	GO:0051674~localization of cell	22	3.66E-02
127	GO:0016055~Wnt receptor signaling pathway	12	**3.68E-02**
128	GO:0007229~integrin-mediated signaling pathway	8	3.70E-02
129	GO:0048584~positive regulation of response to stimulus	18	3.74E-02
130	**GO:0000165~MAPKKK cascade**	15	**3.76E-02**
131	GO:0002252~immune effector process	12	3.86E-02
132	GO:0002819~regulation of adaptive immune response	7	3.87E-02
133	GO:0030334~regulation of cell migration	14	4.09E-02
134	GO:0043067~regulation of programmed cell death	48	4.26E-02
135	GO:0016337~cell-cell adhesion	20	4.28E-02
136	GO:0002520~immune system development	20	4.28E-02
137	GO:0002275~myeloid cell activation during immune response	4	4.44E-02
138	GO:0010941~regulation of cell death	48	4.53E-02
139	GO:0035148~tube lumen formation	6	4.60E-02
140	GO:0016053~organic acid biosynthetic process	13	4.63E-02
141	GO:0046394~carboxylic acid biosynthetic process	13	4.63E-02
142	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	3	4.70E-02
143	GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	3	4.70E-02
144	GO:0008653~lipopolysaccharide metabolic process	3	4.70E-02
145	GO:0060122~inner ear receptor stereocilium organization	3	4.70E-02
146	GO:0001819~positive regulation of cytokine production	9	4.87E-02
147	GO:0006693~prostaglandin metabolic process	4	5.10E-02
148	GO:0006692~prostanoid metabolic process	4	5.10E-02
149	GO:0050878~regulation of body fluid levels	12	5.24E-02
150	GO:0043405~regulation of MAP kinase activity	12	5.24E-02

151	GO:0048666~neuron development	23	5.36E-02
152	GO:0018108~peptidyl-tyrosine phosphorylation	6	5.40E-02
153	GO:0045089~positive regulation of innate immune response	6	5.40E-02
154	GO:0030100~regulation of endocytosis	7	5.50E-02
155	GO:0050866~negative regulation of cell activation	7	5.50E-02
156	GO:0042110~T cell activation	11	5.69E-02
157	GO:0048706~embryonic skeletal system development	8	5.70E-02
158	GO:0015698~inorganic anion transport	9	5.71E-02
159	GO:0048638~regulation of developmental growth	6	5.83E-02
160	GO:0044003~modification by symbiont of host morphology or physiology	3	5.87E-02
161	GO:0032874~positive regulation of stress-activated MAPK cascade	3	5.87E-02
162	GO:0060119~inner ear receptor cell development	3	5.87E-02
163	GO:0050853~B cell receptor signaling pathway	3	5.87E-02
164	GO:0051023~regulation of immunoglobulin secretion	3	5.87E-02
165	GO:0007164~establishment of tissue polarity	3	5.87E-02
166	GO:0001738~morphogenesis of a polarized epithelium	3	5.87E-02
167	GO:0046641~positive regulation of alpha-beta T cell proliferation	3	5.87E-02
168	GO:0032526~response to retinoic acid	5	5.87E-02
169	GO:0045765~regulation of angiogenesis	7	6.26E-02
170	GO:0018212~peptidyl-tyrosine modification	6	6.28E-02
171	GO:0006633~fatty acid biosynthetic process	8	6.37E-02
172	GO:0008624~induction of apoptosis by extracellular signals	10	6.44E-02
173	GO:0001569~patterning of blood vessels	4	6.56E-02
174	GO:0070304~positive regulation of stress-activated protein kinase signaling pathway	4	6.56E-02
175	GO:0030097~hemopoiesis	17	6.63E-02
176	GO:0009725~response to hormone stimulus	24	6.70E-02
177	GO:0034101~erythrocyte homeostasis	6	6.75E-02
178	GO:0001525~angiogenesis	12	6.93E-02
179	GO:0031175~neuron projection development	18	6.97E-02
180	GO:0002521~leukocyte differentiation	11	7.02E-02
181	GO:0008202~steroid metabolic process	15	7.09E-02
182	GO:0002828~regulation of T-helper 2 type immune response	3	7.12E-02
183	GO:0032872~regulation of stress-activated MAPK cascade	3	7.12E-02
184	GO:0002886~regulation of myeloid leukocyte mediated immunity	3	7.12E-02
185	GO:0051149~positive regulation of muscle cell differentiation	3	7.12E-02
186	GO:0009968~negative regulation of signal transduction	16	7.28E-02
187	GO:0051272~positive regulation of cell motion	9	7.30E-02
188	GO:0006790~sulfur metabolic process	10	7.35E-02
189	GO:0042981~regulation of apoptosis	46	7.41E-02
190	GO:0033273~response to vitamin	7	7.50E-02
191	GO:0046634~regulation of alpha-beta T cell activation	5	7.62E-02
192	GO:0032675~regulation of interleukin-6 production	5	7.62E-02
193	GO:0002366~leukocyte activation during immune response	5	7.62E-02
194	GO:0002263~cell activation during immune response	5	7.62E-02
195	GO:0035023~regulation of Rho protein signal transduction	9	7.65E-02
196	GO:0050864~regulation of B cell activation	6	7.74E-02
197	GO:0009166~nucleotide catabolic process	6	7.74E-02
198	GO:0044270~nitrogen compound catabolic process	7	7.94E-02
199	GO:0000902~cell morphogenesis	23	8.09E-02
200	GO:0015807~L-amino acid transport	4	8.18E-02
201	GO:0051051~negative regulation of transport	11	8.21E-02
202	GO:0001667~ameboidal cell migration	5	8.25E-02
203	GO:0051098~regulation of binding	12	8.32E-02
204	GO:0046457~prostanoid biosynthetic process	3	8.45E-02
205	GO:0001516~prostaglandin biosynthetic process	3	8.45E-02
206	GO:0048569~post-embryonic organ development	3	8.45E-02
207	GO:0002244~hemopoietic progenitor cell differentiation	3	8.45E-02
208	GO:0002478~antigen processing and presentation of exogenous peptide antigen	3	8.45E-02
209	GO:0048858~cell projection morphogenesis	17	8.63E-02
210	GO:0032493~response to bacterial lipoprotein	2	8.77E-02
211	GO:0032764~negative regulation of mast cell cytokine production	2	8.77E-02
212	GO:0030505~inorganic diphosphate transport	2	8.77E-02
213	GO:0048667~cell morphogenesis involved in neuron differentiation	15	8.79E-02
214	GO:0070302~regulation of stress-activated protein kinase signaling pathway	7	8.87E-02
215	GO:0040008~regulation of growth	22	9.03E-02
216	GO:0060113~inner ear receptor cell differentiation	4	9.05E-02
217	GO:0008610~lipid biosynthetic process	21	9.10E-02
218	GO:0050954~sensory perception of mechanical stimulus	9	9.13E-02
219	GO:0040012~regulation of locomotion	14	9.16E-02
220	GO:0002706~regulation of lymphocyte mediated immunity	6	9.37E-02
221	GO:0032355~response to estradiol stimulus	6	9.37E-02
222	GO:0002429~immune response-activating cell surface receptor signaling pathway	5	9.60E-02
223	GO:0010033~response to organic substance	41	9.63E-02
224	GO:0048812~neuron projection morphogenesis	15	9.87E-02