

Supplementary table: Up-regulated genes in Huvec-vMIP cells compared to Huvec.

	Parametric p-value	Geometric mean of intensities in class 1 : Control	Geometric mean of intensities in class 2 : vMIP Treated	Fold difference of geometric means	1/Fold difference	Probe set	Description	Gene symbol
1	p < 1e-07	9.4	1830.9	0.005	200.00	213797_at	radical S-adenosyl methionine domain containing 2	RSAD2
2	p < 1e-07	10.8	1887.9	0.006	166.67	203153_at	interferon-induced protein with tetratricopeptide repeats 1 /// interferon-induced protein with tetratricopeptide repeats 1	IFIT1
3	p < 1e-07	11.8	1442.7	0.008	125.00	204994_at	myxovirus (influenza virus) resistance 2 (mouse)	MX2
4	1.00E-07	15.5	1651.3	0.009	111.11	204439_at	interferon-induced protein 44-like	IFI44L
5	p < 1e-07	7.3	706	0.01	100.00	211122_s_at	chemokine (C-X-C motif) ligand 11	CXCL11
6	p < 1e-07	29.4	2761.5	0.011	90.91	202086_at	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) /// myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	MX1
7	p < 1e-07	12.8	884.6	0.014	71.43	204972_at	2'-5'-oligoadenylate synthetase 2, 69/71kDa	OAS2
8	2.10E-05	170.6	529.1	0.322	3.11	212285_s_at	agrin	AGRN
9	p < 1e-07	9.7	660.3	0.015	66.67	204533_at	chemokine (C-X-C motif) ligand 10	CXCL10
10	p < 1e-07	86.9	5022.6	0.017	58.82	214022_s_at	interferon induced transmembrane protein 1 (9-27)	IFITM1
11	1.00E-07	156.9	6871.5	0.023	43.48	204415_at	interferon, alpha-inducible protein (clone IFI-6-16)	G1P3
12	0.0007714	152.9	300.3	0.509	1.96	40148_at	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	APBB2
13	p < 1e-07	18.5	681.8	0.027	37.04	205660_at	2'-5'-oligoadenylate synthetase-like	OASL
14	1.00E-07	30.3	1054.8	0.029	34.48	204747_at	interferon-induced protein with tetratricopeptide repeats 3	IFIT3
15	p < 1e-07	22.9	685.2	0.033	30.30	219209_at	interferon induced with helicase C domain 1	IFIH1
16	p < 1e-07	61.6	1867.8	0.033	30.30	204698_at	interferon stimulated gene 20kDa	ISG20
17	p < 1e-07	34.8	1043.4	0.033	30.30	202869_at	2',5'-oligoadenylate synthetase 1, 40/46kDa	OAS1
18	p < 1e-07	24.9	738.5	0.034	29.41	219352_at	hect domain and RLD 6	HERC6
19	p < 1e-07	9.6	231.6	0.041	24.39	219684_at	28kD interferon responsive protein	IFRG28
20	3.00E-07	12.6	289.1	0.044	22.73	214059_at	Interferon-induced protein 44	IFI44
21	p < 1e-07	10	219.4	0.046	21.74	219863_at	hect domain and RLD 5	HERC5
22	p < 1e-07	17.2	359.6	0.048	20.83	206133_at	XIAP associated factor-1	HSXIAPAF1
23	p < 1e-07	297.2	5883.1	0.051	19.61	205483_s_at	interferon, alpha-inducible protein (clone IFI-15K)	G1P2

24	0.0001018	65.9	236.8	0.278	3.60	210385_s_at	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	ARTS-1
25	p < 1e-07	18.3	355.9	0.051	19.61	200923_at	lectin, galactoside-binding, soluble, 3 binding protein	LGALS3BP
26	p < 1e-07	98.5	1783.8	0.055	18.18	209417_s_at	interferon-induced protein 35	IFI35
27	p < 1e-07	52.7	927.9	0.057	17.54	204279_at	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	PSMB9
28	p < 1e-07	83.2	1445.8	0.058	17.24	218400_at	2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3
29	2.00E-06	40	669.2	0.06	16.67	203595_s_at	interferon-induced protein with tetratricopeptide repeats 5	IFIT5
30	0.0001746	2773.6	5254	0.528	1.89	201891_s_at	beta-2-microglobulin	B2M
31	1.00E-07	15.2	232.7	0.065	15.38	206271_at	toll-like receptor 3	TLR3
32	1.00E-07	69.5	1018.8	0.068	14.71	203236_s_at	lectin, galactoside-binding, soluble, 9 (galectin 9)	LGALS9
33	p < 1e-07	17.6	253.7	0.069	14.49	210118_s_at	interleukin 1, alpha	IL1A
34	8.00E-07	22.7	315.2	0.072	13.89	219691_at	sterile alpha motif domain containing 9	SAMD9
35	p < 1e-07	549.7	7549.3	0.073	13.70	202411_at	interferon, alpha-inducible protein 27	IFI27
36	2.20E-06	107	1385.8	0.077	12.99	218943_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	DDX58
37	p < 1e-07	109.2	1379	0.079	12.66	202307_s_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	TAP1
38	p < 1e-07	32.3	388.3	0.083	12.05	201422_at		
39	p < 1e-07	13	152.4	0.085	11.76	202357_s_at	B-factor, properdin	BF
40	5.80E-06	85.8	1014.9	0.085	11.76	202269_x_at	guanylate binding protein 1, interferon-inducible, 67kDa /// guanylate binding protein 1, interferon-inducible, 67kDa	GBP1
41	4.71E-05	28.8	339.7	0.085	11.76	215071_s_at	histone 1, H2ac	HIST1H2AC
42	p < 1e-07	33.6	396.7	0.085	11.76	219593_at	solute carrier family 15, member 3	SLC15A3
43	0.0005076	84.1	155.4	0.541	1.85	211256_x_at	butyrophilin, subfamily 2, member A1	BTN2A1
44	1.00E-07	37.1	411.1	0.09	11.11	211368_s_at	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	CASP1
45	1.10E-06	44.3	456	0.097	10.31	202902_s_at	cathepsin S	CTSS
46	0.0001223	92.4	198.5	0.465	2.15	212613_at	butyrophilin, subfamily 3, member A2	BTN3A2
47	2.00E-07	730.8	7554.6	0.097	10.31	209140_x_at	major histocompatibility complex, class I, B	HLA-B
48	2.03E-05	34.7	124.5	0.279	3.58	204821_at	butyrophilin, subfamily 3, member A3	BTN3A3
49	p < 1e-07	117.2	1188.9	0.099	10.10	209762_x_at	SP110 nuclear body protein	SP110
50	p < 1e-07	6.4	63.3	0.101	9.90	1405_i_at	chemokine (C-C motif) ligand 5	CCL5
51	2.00E-07	68.9	659.5	0.104	9.62	207069_s_at	SMAD, mothers against DPP homolog 6 (Drosophila)	SMAD6
52	3.00E-07	218.8	2089.6	0.105	9.52	201649_at	ubiquitin-conjugating enzyme E2L 6	UBE2L6

53	5.00E-07	61.6	578.9	0.106	9.43	204502_at	SAM domain and HD domain 1	SAMHD1
54	0.000245	25	93.5	0.267	3.75	207571_x_at	chromosome 1 open reading frame 38	C1orf38
55	0.0008391	574.4	1066	0.539	1.86	221827_at	chromosome 20 open reading frame 18	C20orf18
56	3.00E-07	89.2	812.1	0.11	9.09	202145_at	lymphocyte antigen 6 complex, locus E	LY6E
57	0.0006253	136.6	1236	0.111	9.01	202672_s_at	activating transcription factor 3	ATF3
58	p < 1e-07	47.2	420	0.112	8.93	208436_s_at	interferon regulatory factor 7	IRF7
59	1.00E-06	15.3	133.8	0.114	8.77	218162_at	olfactomedin-like 3	OLFML3
60	1.00E-06	38	330.6	0.115	8.70	204205_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	APOBEC3G
61	8.00E-07	216.7	1808.8	0.12	8.33	214290_s_at	histone 2, H2aa	HIST2H2AA
62	3.66E-05	25.4	199.2	0.128	7.81	202708_s_at	histone 2, H2be	HIST2H2BE
63	2.38E-05	13.4	103.6	0.129	7.75	209909_s_at	transforming growth factor, beta 2	TGFB2
64	4.00E-07	149.5	1130.4	0.132	7.58	209969_s_at	signal transducer and activator of transcription 1, 91kDa	STAT1
65	2.20E-05	372.5	848.7	0.439	2.28	213857_s_at	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	CD47
66	1.10E-05	53.7	396.7	0.135	7.41	209911_x_at	histone 1, H2bd	HIST1H2BD
67	8.00E-07	28.9	213	0.136	7.35	213716_s_at	secreted and transmembrane 1	SECTM1
68	1.50E-06	76.1	542.4	0.14	7.14	205569_at	lysosomal-associated membrane protein 3	LAMP3
69	1.10E-06	15.4	108.2	0.142	7.04	209498_at	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1
70	2.60E-06	200.9	1418.8	0.142	7.04	211799_x_at	Major histocompatibility complex, class I, C	HLA-C
71	7.00E-07	326.6	2254.7	0.145	6.90	201641_at	bone marrow stromal cell antigen 2	BST2
72	2.44E-05	12	82.4	0.146	6.85	221085_at	tumor necrosis factor (ligand) superfamily, member 15	TNFSF15
73	2.00E-07	25.3	171.3	0.148	6.76	219716_at	apolipoprotein L, 6	APOL6
74	1.80E-06	110.3	747.6	0.148	6.76	219211_at	ubiquitin specific protease 18	USP18
75	p < 1e-07	79	528.8	0.149	6.71	53720_at	hypothetical protein FLJ11286	FLJ11286
76	2.00E-07	93.2	627.6	0.149	6.71	203148_s_at	tripartite motif-containing 14	TRIM14
77	0.0004621	236.5	405.8	0.583	1.72	211316_x_at	CASP8 and FADD-like apoptosis regulator	CFLAR
78	7.00E-07	239.5	1542.7	0.155	6.45	221875_x_at	major histocompatibility complex, class I, F	HLA-F
79	2.70E-06	28.7	185.4	0.155	6.45	204070_at	retinoic acid receptor responder (tazarotene induced) 3	RARRES3
80	1.00E-07	50.1	320.5	0.156	6.41	218986_s_at	hypothetical protein FLJ20035	FLJ20035
81	7.00E-07	115.8	737.4	0.157	6.37	202688_at	tumor necrosis factor (ligand) superfamily, member 10 /// tumor necrosis factor (ligand) superfamily, member 10	TNFSF10

82	1.46E-05	15.8	99.5	0.159	6.29	217502_at	interferon-induced protein with tetratricopeptide repeats 2	IFIT2
83	2.00E-07	14.8	91.6	0.162	6.17	204472_at	GTP binding protein overexpressed in skeletal muscle	GEM
84	0.0006402	1621.5	2843.7	0.57	1.75	211980_at	collagen, type IV, alpha 1	COL4A1
85	0.0007524	176.6	1064.1	0.166	6.02	201506_at	transforming growth factor, beta-induced, 68kDa	TGFB1
86	0.0006087	228.3	425.8	0.536	1.87	211966_at	collagen, type IV, alpha 2	COL4A2
87	3.00E-07	140.2	837.4	0.167	5.99	204135_at	downregulated in ovarian cancer 1	DOC1
88	4.20E-06	107.2	636.5	0.168	5.95	209785_s_at	phospholipase A2, group IVC (cytosolic, calcium-independent)	PLA2G4C
89	0.0002521	835.2	1673.5	0.499	2.00	200838_at	cathepsin B	CTSB
90	5.00E-07	31.4	185.8	0.169	5.92	218541_s_at	chromosome 8 open reading frame 4	C8orf4
91	0.0001298	71.9	422.5	0.17	5.88	202644_s_at	tumor necrosis factor, alpha-induced protein 3	TNFAIP3
92	1.00E-07	133	769.4	0.173	5.78	209546_s_at	apolipoprotein L, 1	APOL1
93	4.66E-05	64.5	372.9	0.173	5.78	205547_s_at	transgelin	TAGLN
94	3.80E-06	36.2	201.8	0.179	5.59	221766_s_at	family with sequence similarity 46, member A	FAM46A
95	6.50E-06	26.9	150	0.179	5.59	209631_s_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37
96	9.90E-06	38.1	199.5	0.191	5.24	210689_at	claudin 14	CLDN14
97	5.10E-06	55.9	292	0.191	5.24	219403_s_at	heparanase	HPSE
98	1.00E-07	83.6	430.8	0.194	5.15	204804_at	tripartite motif-containing 21	TRIM21
99	3.04E-05	12.7	64.8	0.196	5.10	214702_at	fibronectin 1	FN1
100	3.38E-05	17.2	87.9	0.196	5.10	205890_s_at	ubiquitin D	UBD
101	0.0002144	27.4	138.8	0.197	5.08	220049_s_at	programmed cell death 1 ligand 2	PDCD1LG2
102	3.90E-06	6.4	32.4	0.198	5.05	209795_at	CD69 antigen (p60, early T-cell activation antigen)	CD69
103	5.00E-07	448.3	2241.4	0.2	5.00	202446_s_at	phospholipid scramblase 1	PLSCR1
104	5.50E-06	1084.9	3018.2	0.359	2.79	214247_s_at	dickkopf homolog 3 (<i>Xenopus laevis</i>)	DKK3
105	1.10E-06	66.5	330.3	0.201	4.98	220104_at	zinc finger CCCH type, antiviral 1	ZC3HAV1
106	0.0001225	115.8	572.4	0.202	4.95	221009_s_at	angiopoietin-like 4	ANGPTL4
107	5.00E-07	17	83	0.205	4.88	207904_s_at	leucyl/cystinyl aminopeptidase	LNPEP
108	1.69E-05	114.4	555.3	0.206	4.85	201010_s_at	thioredoxin interacting protein	TXNIP
109	0.0001002	16.6	33.2	0.5	2.00	221563_at	dual specificity phosphatase 10	DUSP10
110	7.79E-05	27.2	130.9	0.208	4.81	207850_at	chemokine (C-X-C motif) ligand 3	CXCL3
111	4.10E-06	10	47.8	0.209	4.78	208173_at	interferon, beta 1, fibroblast	IFNB1
112	0.0005967	8.5	15.2	0.559	1.79	217497_at	endothelial cell growth factor 1 (platelet-derived)	ECGF1
113	7.00E-07	111	529.1	0.21	4.76	213361_at	tudor domain containing 7	TDRD7
114	3.97E-05	386.4	1789.6	0.216	4.63	211529_x_at	HLA-G histocompatibility antigen, class I, G	HLA-G

115	1.25E-05	119	546.8	0.218	4.59	204224_s_at	GTP cyclohydrolase 1 (dopa-responsive dystonia)	GCH1
116	0.0001647	17.3	35.6	0.486	2.06	201340_s_at	ectodermal-neural cortex (with BTB-like domain)	ENC1
117	1.49E-05	49.5	225.1	0.22	4.55	204780_s_at	Fas (TNF receptor superfamily, member 6)	FAS
118	5.30E-06	110	497.6	0.221	4.52	218999_at	hypothetical protein FLJ11000	FLJ11000
119	1.30E-06	116.4	524.2	0.222	4.50	210511_s_at	inhibin, beta A (activin A, activin AB alpha polypeptide)	INHBA
120	0.000282	59.6	261.6	0.228	4.39	201579_at	FAT tumor suppressor homolog 1 (Drosophila)	FAT
121	3.80E-06	185	803.4	0.23	4.35	209806_at	histone 1, H2bk	HIST1H2BK
122	5.00E-05	9.4	40.5	0.232	4.31	219584_at	phospholipase A1 member A	PLA1A
123	6.70E-06	27.2	115.6	0.235	4.26	203758_at	cathepsin O	CTSO
124	2.80E-06	46.4	191.9	0.242	4.13	213800_at	complement factor H	CFH
125	0.0006669	33.2	136.6	0.243	4.12	209098_s_at	jagged 1 (Alagille syndrome)	JAG1
126	1.10E-06	123.9	508	0.244	4.10	203882_at	interferon-stimulated transcription factor 3, gamma 48kDa	ISGF3G
127	8.40E-06	13.8	56.4	0.245	4.08	204790_at	SMAD, mothers against DPP homolog 7 (Drosophila)	SMAD7
128	6.21E-05	23.9	97.3	0.246	4.07	205992_s_at	interleukin 15	IL15
129	0.0002976	64.3	260.5	0.247	4.05	221841_s_at	Kruppel-like factor 4 (gut)	KLF4
130	3.10E-06	21.3	86.3	0.247	4.05	213261_at	lupus brain antigen 1	LBA1
131	4.70E-06	26.2	102.9	0.255	3.92	210512_s_at	vascular endothelial growth factor	VEGF
132	8.70E-06	22.7	88.8	0.256	3.91	205935_at	forkhead box F1	FOXF1
133	1.37E-05	7.8	30	0.26	3.85	214472_at	histone 1, H3d	HIST1H3D
134	1.30E-05	54.8	210.8	0.26	3.85	204601_at	Nedd4 binding protein 1	N4BP1
135	3.70E-06	64.6	246.5	0.262	3.82	202150_s_at	neural precursor cell expressed, developmentally down-regulated 9	NEDD9
136	2.00E-05	83.5	313.8	0.266	3.76	208579_x_at	H2B histone family, member S	H2BFS
137	1.23E-05	300.4	1122.2	0.268	3.73	221816_s_at	PHD finger protein 11	PHF11
138	9.00E-07	130.9	479.8	0.273	3.66	216250_s_at	leupaxin	LPXN
139	1.80E-06	94.2	343.4	0.274	3.65	203610_s_at	tripartite motif-containing 38	TRIM38
140	2.70E-06	33.6	122.1	0.275	3.64	220987_s_at	chromosome 11 open reading frame 17 /// chromosome 11 open reading frame 17 /// likely ortholog of rat SNF1/AMP-activated protein kinase /// likely ortholog of rat SNF1/AMP-activated protein kinase	C11orf17 /// SNARK
141	7.79E-05	106.6	384.2	0.277	3.61	204715_at	pannexin 1	PANX1
142	0.0001706	85.5	158.5	0.539	1.86	213560_at	Growth arrest and DNA-damage-inducible, beta	GADD45B
143	6.42E-05	30.1	106.7	0.282	3.55	219364_at	likely ortholog of mouse D11lgp2	LGP2
144	0.000666	302.2	519.5	0.582	1.72	1598_g_at	growth arrest-specific 6	GAS6

145	1.40E-06	80.7	285.9	0.282	3.55	203281_s_at	ubiquitin-activating enzyme E1-like	UBE1L
146	0.0001853	253.6	497.4	0.51	1.96	210589_s_at	glucosidase, beta; acid (includes glucosylceramidase) /// glucosidase, beta; acid, pseudogene	GBA /// GBAP
147	2.20E-05	89.1	314.6	0.283	3.53	221087_s_at	apolipoprotein L, 3	APOL3
148	5.92E-05	1971.3	6977.6	0.283	3.53	215313_x_at	major histocompatibility complex, class I, A	HLA-A
149	8.05E-05	135.6	475.2	0.285	3.51	213294_at	Hypothetical protein FLJ38348	FLJ38348
150	8.61E-05	17.4	60.2	0.289	3.46	210538_s_at	baculoviral IAP repeat-containing 3	BIRC3
151	8.20E-06	100	346.5	0.289	3.46	219505_at	cat eye syndrome chromosome region, candidate 1	CECR1
152	8.40E-06	34.6	119.6	0.289	3.46	203438_at	stannocalcin 2	STC2
153	2.25E-05	463.5	1590.5	0.291	3.44	217933_s_at	leucine aminopeptidase 3	LAP3
154	9.80E-06	148	504.2	0.294	3.40	201212_at	legumain	LGMN
155	2.10E-05	150.2	511.5	0.294	3.40	209040_s_at	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	PSMB8
156	8.00E-06	41.8	141.7	0.295	3.39	220178_at	chromosome 19 open reading frame 28	C19orf28
157	2.60E-06	92.6	308.9	0.3	3.33	204211_x_at	eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2
158	6.70E-06	427.1	1406.4	0.304	3.29	205499_at	sushi-repeat-containing protein, X-linked 2	SRPX2
159	2.15E-05	19.7	64.3	0.306	3.27	210387_at	histone 1, H2bg	HIST1H2BG
160	0.0001108	604.9	1321.8	0.458	2.18	200678_x_at	granulin	GRN
161	8.60E-06	82.8	265	0.312	3.21	204937_s_at	zinc finger protein 274	ZNF274
162	4.80E-06	292.3	919.8	0.318	3.14	204820_s_at	butyrophilin, subfamily 3, member A3 /// butyrophilin, subfamily 3, member A2	BTN3A3 /// BTN3A2
163	0.0002192	51.4	160.3	0.321	3.12	203304_at	BMP and activin membrane-bound inhibitor	BAMBI
164	2.39E-05	389.8	1209.1	0.322	3.11	213293_s_at	tripartite motif-containing 22	TRIM22
165	7.05E-05	91.2	281.2	0.324	3.09	218718_at	platelet derived growth factor C	PDGFC
166	0.0001096	53.6	164.8	0.325	3.08	205659_at	histone deacetylase 9	HDAC9
167	4.70E-06	514	1575.6	0.326	3.07	203939_at	5'-nucleotidase, ecto (CD73)	NT5E
168	4.80E-06	63.2	193.9	0.326	3.07	206503_x_at	promyelocytic leukemia	PML
169	0.0004304	270.4	485.4	0.557	1.80	204689_at	hematopoietically expressed homeobox	HHEX
170	1.76E-05	34.2	104.6	0.327	3.06	206382_s_at	brain-derived neurotrophic factor	BDNF
171	4.05E-05	107.5	321.6	0.334	2.99	214791_at	hypothetical protein BC004921	LOC93349
172	2.29E-05	83.2	247.1	0.337	2.97	204512_at	human immunodeficiency virus type I enhancer binding protein 1	HIVEP1
173	3.19E-05	60.5	179.4	0.337	2.97	209447_at	spectrin repeat containing, nuclear envelope 1	SYNE1
174	1.68E-05	85.7	252.8	0.339	2.95	204769_s_at	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	TAP2

175	3.89E-05	38.4	112.9	0.34	2.94	218746_at	TAP binding protein-like	TAPBPL
176	4.99E-05	35	102.5	0.341	2.93	202439_s_at	iduronate 2-sulfatase (Hunter syndrome)	IDS
177	0.0001065	137.5	401.8	0.342	2.92	204334_at	Kruppel-like factor 7 (ubiquitous)	KLF7
178	0.0001015	1140	3327.7	0.343	2.92	200629_at	tryptophanyl-tRNA synthetase	WARS
179	0.000143	14.9	43.2	0.345	2.90	204567_s_at	ATP-binding cassette, sub-family G (WHITE), member 1	ABCG1
180	0.0001272	42.7	123	0.347	2.88	204194_at	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1
181	4.60E-06	411.6	1186.1	0.347	2.88	208912_s_at	2',3'-cyclic nucleotide 3' phosphodiesterase	CNP
182	8.70E-06	408	1171.4	0.348	2.87	216565_x_at	similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U)	LOC391020
183	2.42E-05	14.1	40.5	0.348	2.87	205923_at	reelin	RELN
184	0.0002841	19.2	33.3	0.577	1.73	212641_at	human immunodeficiency virus type I enhancer binding protein 2	HIVEP2
185	2.61E-05	209.7	600	0.349	2.87	212501_at	CCAAT/enhancer binding protein (C/EBP), beta	CEBPB
186	0.0005656	25.3	72.3	0.35	2.86	214995_s_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G /// apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	APOBEC3G /// APOBEC3F
187	9.09E-05	115.6	330.3	0.35	2.86	202748_at	guanylate binding protein 2, interferon-inducible /// guanylate binding protein 2, interferon-inducible	GBP2
188	3.60E-05	315.8	899.7	0.351	2.85	202863_at	nuclear antigen Sp100	SP100
189	6.16E-05	213.2	602.2	0.354	2.82	204187_at	guanosine monophosphate reductase /// guanosine monophosphate reductase	GMPR
190	0.0001593	403.3	828.9	0.487	2.05	200904_at	major histocompatibility complex, class I, E	HLA-E
191	1.91E-05	75.2	211.5	0.356	2.81	209770_at	butyrophilin, subfamily 3, member A1	BTN3A1
192	0.000284	113.2	314	0.361	2.77	204702_s_at	nuclear factor (erythroid-derived 2)-like 3	NFE2L3
193	5.09E-05	120.3	333.1	0.361	2.77	221432_s_at	solute carrier family 25, member 28 /// solute carrier family 25, member 28	SLC25A28
194	2.13E-05	84.7	234	0.362	2.76	212805_at	KIAA0367	KIAA0367
195	0.0009541	100.2	275.9	0.363	2.75	208653_s_at	CD164 antigen, sialomucin	CD164
196	1.30E-05	180.3	494.5	0.365	2.74	221653_x_at	apolipoprotein L, 2	APOL2
197	4.71E-05	13.9	38	0.366	2.73	206082_at	HLA complex P5	HCP5
198	0.0003032	16.6	45.2	0.367	2.72	204284_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	PPP1R3C
199	3.85E-05	71.6	194.4	0.368	2.72	218880_at	FOS-like antigen 2	FOSL2
200	4.08E-05	480.1	1301.4	0.369	2.71	208829_at	TAP binding protein (tapasin)	TAPBP
201	0.0003632	675.1	1401.7	0.482	2.07	208966_x_at	interferon, gamma-inducible protein 16	IFI16
202	4.80E-05	322	861.3	0.374	2.67	221127_s_at	regulated in glioma	RIG

203	4.33E-05	24.8	65.9	0.376	2.66	218651 s at	acheron	FLJ11196
204	0.0001813	15.4	41	0.376	2.66	206675 s at	SKI-like	SKIL
205	5.30E-06	370.5	983.5	0.377	2.65	209124 at	myeloid differentiation primary response gene (88)	MYD88
206	4.41E-05	269.8	713.6	0.378	2.65	204589 at	AMP-activated protein kinase family member 5	ARK5
207	9.19E-05	40	105.9	0.378	2.65	206117 at	tropomyosin 1 (alpha)	TPM1
208	0.0001418	25.5	67.3	0.379	2.64	214099 s at	phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP
209	0.0001516	13.1	34.5	0.38	2.63	208600 s at	G protein-coupled receptor 39	GPR39
210	0.0002685	239.6	628.6	0.381	2.62	213506 at	coagulation factor II (thrombin) receptor-like 1	F2RL1
211	5.26E-05	341.8	896.5	0.381	2.62	209035 at	midkine (neurite growth-promoting factor 2)	MDK
212	8.34E-05	69.4	180.7	0.384	2.60	200974 at	actin, alpha 2, smooth muscle, aorta	ACTA2
213	2.81E-05	772.8	1987.1	0.389	2.57	201786 s at	adenosine deaminase, RNA-specific	ADAR
214	3.87E-05	113.1	290.2	0.39	2.56	217955 at	BCL2-like 13 (apoptosis facilitator)	BCL2L13
215	9.30E-06	151.9	389.3	0.39	2.56	207375 s at	interleukin 15 receptor, alpha	IL15RA
216	1.48E-05	53.6	137	0.391	2.56	208454 s at	plasma glutamate carboxypeptidase	PGCP
217	1.62E-05	109.2	278.6	0.392	2.55	213073 at	zinc finger, FYVE domain containing 26	ZFYVE26
218	0.000154	526.3	1329.2	0.396	2.53	202284 s at	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A
219	4.58E-05	53.6	135.1	0.397	2.52	219737 s at	protocadherin 9	PCDH9
220	9.50E-06	524.5	1313.7	0.399	2.51	202074 s at	optineurin	OPTN
221	2.16E-05	6.7	16.7	0.401	2.49	214455 at	histone 1, H2bc	HIST1H2BC
222	2.91E-05	2527	6305	0.401	2.49	212203 x at	interferon induced transmembrane protein 3 (1-8U)	IFITM3
223	0.0001563	323.9	808.2	0.401	2.49	219892 at	transmembrane 6 superfamily member 1	TM6SF1
224	0.0001831	170.5	425.5	0.401	2.49	200868 s at	zinc finger protein 313	ZNF313
225	0.0004546	808.8	2005	0.403	2.48	221577 x at	growth differentiation factor 15	GDF15
226	3.05E-05	37.7	93.5	0.403	2.48	219826 at	zinc finger protein 419	ZNF419
227	0.00061	179.4	442.9	0.405	2.47	202604 x at	a disintegrin and metalloproteinase domain 10	ADAM10
228	0.000242	169.8	419.1	0.405	2.47	205875 s at	three prime repair exonuclease 1	TREX1
229	7.76E-05	85.7	211	0.406	2.46	202531 at	interferon regulatory factor 1	IRF1
230	0.0001993	58.2	142.5	0.408	2.45	218972 at	tetratricopeptide repeat domain 17	TTC17
231	0.0001995	19.6	47.8	0.41	2.44	219270 at	hypothetical protein MGC4504	MGC4504
232	2.93E-05	519.4	1262.5	0.411	2.43	203041 s at	lysosomal-associated membrane protein 2	LAMP2
233	4.07E-05	45.3	109.1	0.415	2.41	203592 s at	folliculin-like 3 (secreted glycoprotein)	FSTL3
234	5.08E-05	559.4	1347	0.415	2.41	217771 at	golgi phosphoprotein 2	GOLPH2
235	0.0001994	114.3	273.9	0.417	2.40	214703 s at	mannosidase, alpha, class 2B, member 2	MAN2B2
236	0.0002389	40.8	97.5	0.418	2.39	205059 s at	iduronidase, alpha-L-	IDUA
237	0.0001524	153.3	365	0.42	2.38	212950 at	G protein-coupled receptor 116	GPR116

238	9.11E-05	356.7	848.2	0.421	2.38	212662_at	poliovirus receptor	PVR
239	0.000154	131.3	311	0.422	2.37	219400_at	contactin associated protein 1	CNTNAP1
240	0.000276	258.2	608.3	0.424	2.36	209545_s_at	receptor-interacting serine-threonine kinase 2	RIPK2
241	7.33E-05	319.2	748.8	0.426	2.35	201847_at	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	LIPA
242	0.0006602	59.6	139.7	0.427	2.34	219582_at	opioid growth factor receptor-like 1	OGFRL1
243	0.0002621	78.6	182.8	0.43	2.33	208751_at	N-ethylmaleimide-sensitive factor attachment protein, alpha	NAPA
244	6.55E-05	91	211.3	0.431	2.32	209383_at	DNA-damage-inducible transcript 3	DDIT3
245	2.11E-05	14.4	33.4	0.431	2.32	214748_at	CG016	LOC88523
246	0.0003099	16.1	37.3	0.432	2.31	205671_s_at	major histocompatibility complex, class II, DO beta DNA segment, Chr 15, Wayne State University 75, expressed	HLA-DOB
247	7.26E-05	189.5	436.4	0.434	2.30	212527_at	hypothetical protein FLJ23375	D15Wsu75e
248	0.0001158	56.1	129.2	0.434	2.30	218776_s_at	hypothetical protein FLJ23375	FLJ23375
249	0.0003032	41.7	95.3	0.438	2.28	211844_s_at	neuropilin 2	NRP2
250	0.0003528	43.2	98.4	0.439	2.28	208490_x_at	histone 1, H2bf	HIST1H2BF
251	5.47E-05	29.9	68.1	0.439	2.28	208523_x_at	histone 1, H2bi	HIST1H2BI
252	0.0003074	66	150.4	0.439	2.28	204729_s_at	syntaxin 1A (brain)	STX1A
253	0.0008851	6.9	15.6	0.442	2.26	205885_s_at	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	ITGA4
254	8.63E-05	79.2	177.6	0.446	2.24	202597_at	interferon regulatory factor 6	IRF6
255	0.0009039	2036.3	4553	0.447	2.24	210592_s_at	spermidine/spermine N1-acetyltransferase	SAT
256	0.0001257	44.1	98.4	0.448	2.23	213341_at	fem-1 homolog c (C.elegans)	FEM1C
257	0.0002566	61.9	138	0.449	2.23	221667_s_at	heat shock 22kDa protein 8	HSPB8
258	0.0001274	74.9	167	0.449	2.23	204310_s_at	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	NPR2
259	3.69E-05	10.3	22.9	0.45	2.22	219153_s_at	hypothetical protein FLJ13710	FLJ13710
260	0.0009081	10.2	22.6	0.451	2.22	201566_x_at	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	ID2 /// ID2B
261	0.0002159	11.8	26	0.454	2.20	210029_at	indoleamine-pyrrole 2,3 dioxygenase	INDO
262	0.0004507	70	153.8	0.455	2.20	212660_at	PHD finger protein 15	PHF15
263	5.65E-05	201.4	442.2	0.455	2.20	219569_s_at	transmembrane protein 22	TMEM22
264	0.0003276	36.1	74.6	0.484	2.07	208328_s_at	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	MEF2A
265	8.60E-05	15.8	34.7	0.455	2.20	206448_at	zinc finger protein 365	ZNF365
266	0.0003073	10.1	22.1	0.457	2.19	206924_at	interleukin 11	IL11

267	3.17E-05	971.4	2105.2	0.461	2.17	219356_s_at	chromatin modifying protein 5	CHMP5
268	8.34E-05	23.9	51.9	0.461	2.17	207049_at	sodium channel, voltage gated, type VIII, alpha	SCN8A
269	0.0001377	121.3	262.3	0.462	2.16	218901_at	phospholipid scramblase 4	PLSCR4
270	0.0006799	113.4	244.7	0.463	2.16	205047_s_at	asparagine synthetase	ASNS
271	4.70E-05	16.3	35.1	0.464	2.16	201525_at	apolipoprotein D	APOD
272	3.08E-05	116.4	251.1	0.464	2.16	218436_at	endoplasmic reticulum chaperone SIL1, homolog of yeast	SIL1
273	0.0001097	1446.4	3108.2	0.465	2.15	201389_at	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	ITGA5
274	4.62E-05	7.9	16.9	0.467	2.14	207147_at	distal-less homeo box 2	DLX2
275	0.0001231	24.4	52.2	0.467	2.14	219474_at	TPA-induced transmembrane protein	TTMP
276	0.0001023	151.1	322.7	0.468	2.14	203140_at	B-cell CLL/lymphoma 6 (zinc finger protein 51) /// B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6
277	0.0003566	15.4	32.9	0.468	2.14	205668_at	lymphocyte antigen 75	LY75
278	0.0001463	518.4	1106.9	0.468	2.14	212112_s_at	syntaxin 12	STX12
279	5.52E-05	406.6	866.7	0.469	2.13	221449_s_at	T-cell immunomodulatory protein /// T-cell immunomodulatory protein	CDA08
280	0.0002769	372.9	794.7	0.469	2.13	200742_s_at	tripeptidyl peptidase I	TPP1
281	8.44E-05	19.4	41.3	0.47	2.13	219424_at	Epstein-Barr virus induced gene 3	EBI3
282	0.0001223	379.8	806.6	0.471	2.12	219181_at	lipase, endothelial	LIPG
283	0.0002615	40	84.5	0.473	2.11	204069_at	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)	MEIS1
284	5.20E-05	105.3	222.5	0.473	2.11	209453_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	SLC9A1
285	7.98E-05	67.3	141.8	0.475	2.11	205076_s_at	myotubularin related protein 11	MTMR11
286	8.97E-05	143	300.4	0.476	2.10	216061_x_at	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	PDGFB
287	9.63E-05	50.6	105.2	0.481	2.08	219326_s_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3GNT1
288	0.0003381	34.6	72	0.481	2.08	204726_at	cadherin 13, H-cadherin (heart)	CDH13
289	0.000807	98	203.8	0.481	2.08	221218_s_at	thiamin pyrophosphokinase 1	TPK1
290	6.49E-05	92.9	192.8	0.482	2.07	212090_at	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	GRINA
291	0.0002069	83.2	172.5	0.482	2.07	212380_at	KIAA0082	KIAA0082
292	0.0007036	36	74.5	0.483	2.07	205842_s_at	Janus kinase 2 (a protein tyrosine kinase)	JAK2
293	0.0002335	89.6	185.2	0.484	2.07	212558_at	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	SPRY1
294	0.0008871	389.9	805.5	0.484	2.07	218543_s_at	zinc finger CCCH type domain containing 1	ZC3HDC1

295	0.0008703	206.3	424.9	0.486	2.06	220471_s_at	myc target 1	MYCT1
296	8.47E-05	163.7	336.5	0.486	2.06	205846_at	protein tyrosine phosphatase, receptor type, B	PTPRB
297	0.0001157	340	698.6	0.487	2.05	222154_s_at	DNA polymerase-transactivated protein 6	DNAPTP6
298	0.0007501	855.1	1757.3	0.487	2.05	212724_at	Rho family GTPase 3	RND3
299	0.0001012	1089.5	2231.9	0.488	2.05	201762_s_at	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	PSME2
300	0.0003005	49.4	100.6	0.491	2.04	208527_x_at	histone 1, H2be	HIST1H2BE
301	0.0005354	21.4	43.5	0.492	2.03	212374_at	fem-1 homolog b (C. elegans)	FEM1B
302	0.0004133	292	594	0.492	2.03	203934_at	kinase insert domain receptor (a type III receptor tyrosine kinase)	KDR
303	0.0006875	97	197.2	0.492	2.03	205383_s_at	zinc finger and BTB domain containing 20	ZBTB20
304	9.49E-05	2746.6	5576.8	0.493	2.03	201315_x_at	interferon induced transmembrane protein 2 (1-8D)	IFITM2
305	0.0002109	203.1	411.4	0.494	2.02	213112_s_at	sequestosome 1	SQSTM1
306	0.0003667	687.6	1389.2	0.495	2.02	201926_s_at	decay accelerating factor for complement (CD55, Cromer blood group system)	DAF
307	0.0002371	78.8	159.2	0.495	2.02	221050_s_at	GTP binding protein 2	GTPBP2
308	0.0003151	18.4	37.1	0.496	2.02	823_at	chemokine (C-X3-C motif) ligand 1	CX3CL1
309	0.0003226	9.7	19.5	0.497	2.01	210224_at	major histocompatibility complex, class I-related	MR1
310	0.0007763	93.2	187.5	0.497	2.01	205801_s_at	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3
311	0.0006505	256.2	512	0.5	2.00	208934_s_at	lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8
312	0.0002575	853.3	1701.7	0.501	2.00	201243_s_at	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	ATP1B1
313	0.0006733	88.6	176.9	0.501	2.00	219885_at	hypothetical protein FLJ10260	FLJ10260
314	0.0004598	52	103.5	0.502	1.99	215248_at	growth factor receptor-bound protein 10	GRB10
315	0.0001183	1533	3051.7	0.502	1.99	218041_x_at	solute carrier family 38, member 2	SLC38A2
316	0.0001125	73.1	144.5	0.506	1.98	203291_at	CCR4-NOT transcription complex, subunit 4	CNOT4
317	0.0003474	136.4	269.3	0.506	1.98	218686_s_at	rhomboid family 1 (Drosophila)	RHBDF1
318	0.0002721	2822.4	5555.6	0.508	1.97	201162_at	insulin-like growth factor binding protein 7	IGFBP7
319	0.000102	101.6	200	0.508	1.97	213773_x_at	NOL1/NOP2/Sun domain family, member 5	NSUN5
320	0.0001089	67.3	132.4	0.508	1.97	202702_at	tripartite motif-containing 26	TRIM26
321	9.56E-05	28	55.1	0.508	1.97	219360_s_at	transient receptor potential cation channel, subfamily M, member 4	TRPM4
322	0.0002898	205.6	404	0.509	1.96	202659_at	proteasome (prosome, macropain) subunit, beta type, 10	PSMB10
323	0.0001014	22.2	43.5	0.51	1.96	210944_s_at	calpain 3, (p94)	CAPN3
324	0.0003779	14.6	28.5	0.512	1.95	45653_at	potassium channel tetramerisation domain containing 13	KCTD13
325	0.0003123	16.3	31.8	0.513	1.95	214469_at	histone 1, H2ae	HIST1H2AE

326	0.0008977	1740.3	3387.4	0.514	1.95	204602_at	dickkopf homolog 1 (<i>Xenopus laevis</i>)	DKK1
327	0.0002218	291.1	566.1	0.514	1.95	213358_at	KIAA0802	KIAA0802
328	0.0005418	161.1	312.8	0.515	1.94	204203_at	CCAAT/enhancer binding protein (C/EBP), gamma	CEBPG
329	0.0001514	236.9	458.2	0.517	1.93	216264_s_at	laminin, beta 2 (laminin S)	LAMB2
330	0.0004541	68.8	133	0.517	1.93	210015_s_at	microtubule-associated protein 2	MAP2
331	0.0001058	47.8	92.1	0.519	1.93	205142_x_at	ATP-binding cassette, sub-family D (ALD), member 1	ABCD1
332	0.0001654	293.4	562.8	0.521	1.92	203288_at	KIAA0355	KIAA0355
333	0.0002419	32.6	62.5	0.522	1.92	204443_at	arylsulfatase A	ARSA
334	0.0001199	790.3	1510.7	0.523	1.91	202087_s_at	cathepsin L	CTSL
335	0.0001564	440.5	843	0.523	1.91	203725_at	growth arrest and DNA-damage-inducible, alpha	GADD45A
336	0.0001304	259.1	494.1	0.524	1.91	202088_at	solute carrier family 39 (zinc transporter), member 6	SLC39A6
337	0.0001305	244.4	465.7	0.525	1.90	56256_at	SID1 transmembrane family, member 2	SIDT2
338	0.0007174	82.1	155.6	0.528	1.89	206653_at	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)	POLR3G
339	0.0001475	390.1	734.7	0.531	1.88	203857_s_at	protein disulfide isomerase-associated 5	PDIA5
340	0.0001965	556.5	1043.4	0.533	1.88	201412_at	low density lipoprotein receptor-related protein 10	LRP10
341	0.0007098	170.9	320.9	0.533	1.88	203045_at	ninjurin 1	NINJ1
342	0.000908	167	312.3	0.535	1.87	206584_at	lymphocyte antigen 96	LY96
343	0.0003508	200.8	375.6	0.535	1.87	203234_at	uridine phosphorylase 1	UPP1
344	0.0008204	84.6	157.7	0.536	1.87	210794_s_at	maternally expressed 3	MEG3
345	0.0004017	21.7	40.5	0.536	1.87	207303_at	phosphodiesterase 1C, calmodulin-dependent 70kDa	PDE1C
346	0.0001986	86.2	160.9	0.536	1.87	202880_s_at	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	PSCD1
347	0.0008412	420.6	779.1	0.54	1.85	212647_at	related RAS viral (r-ras) oncogene homolog	RRAS
348	0.0008846	62.6	115.3	0.543	1.84	215198_s_at	caldesmon 1	CALD1
349	0.0003062	21.8	40	0.545	1.83	203765_at	grancalcin, EF-hand calcium binding protein /// grancalcin, EF-hand calcium binding protein	GCA
350	0.0003247	10.9	20	0.545	1.83	222150_s_at	hypothetical protein LOC54103	LOC54103
351	0.0002981	430.5	788.4	0.546	1.83	217867_x_at	beta-site APP-cleaving enzyme 2	BACE2
352	0.0006518	47.2	86.5	0.546	1.83	204166_at	KIAA0963	KIAA0963
353	0.0005218	918.2	1682.4	0.546	1.83	209278_s_at	tissue factor pathway inhibitor 2	TFPI2
354	0.0001577	323.1	591.2	0.547	1.83	218627_at	hypothetical protein FLJ11259	FLJ11259
355	0.0009175	11.3	20.6	0.549	1.82	220315_at	poly (ADP-ribose) polymerase family, member 11	PARP11
356	0.0003405	86.5	157.1	0.551	1.81	209716_at	colony stimulating factor 1 (macrophage)	CSF1

357	0.0002357	136.7	247.9	0.551	1.81	203370_s_at	PDZ and LIM domain 7 (enigma)	PDLIM7
358	0.0007551	130.1	236	0.551	1.81	204158_s_at	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	TCIRG1
359	0.0009867	556.6	1004.9	0.554	1.81	203964_at	N-myc (and STAT) interactor	NMI
360	0.0002316	14.4	25.9	0.556	1.80	209906_at	complement component 3a receptor 1	C3AR1
361	0.0009279	112.1	200.8	0.558	1.79	219202_at	rhomboid, veinlet-like 6 (Drosophila)	RHBDL6
362	0.0006352	40.8	73	0.559	1.79	219523_s_at	odz, odd Oz/ten-m homolog 3 (Drosophila)	ODZ3
363	0.0006991	100.2	178.9	0.56	1.79	213150_at	homeo box A10	HOXA10
364	0.00043	66.6	118.7	0.561	1.78	207765_s_at	KIAA1539	KIAA1539
365	0.000755	46.5	82.9	0.561	1.78	203578_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	SLC7A6
366	0.0002921	154.8	275.4	0.562	1.78	217984_at	ribonuclease T2	RNASET2
367	0.0004736	409.2	727.1	0.563	1.78	200815_s_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	PAFAH1B1
368	0.0004169	120.4	213.3	0.564	1.77	205289_at	bone morphogenetic protein 2	BMP2
369	0.0005787	66.8	118.4	0.564	1.77	207513_s_at	zinc finger protein 189	ZNF189
370	0.0006835	519	916.2	0.566	1.77	207760_s_at	nuclear receptor co-repressor 2	NCOR2
371	0.0006508	210.1	371.3	0.566	1.77	205618_at	proline rich Gla (G-carboxyglutamic acid) 1	PRRG1
372	0.0008606	329.5	581.3	0.567	1.76	217730_at	PP1201 protein	PP1201
373	0.0006149	205.3	360.9	0.569	1.76	203233_at	interleukin 4 receptor	IL4R
374	0.0003282	282.9	496	0.57	1.75	204518_s_at	peptidylprolyl isomerase C (cyclophilin C)	PPIC
375	0.0006987	26.6	46.5	0.572	1.75	209525_at	Hepatoma-derived growth factor, related protein 3 /// Hepatoma-derived growth factor, related protein 3	HDGFRP3
376	0.0002756	1046.3	1828.3	0.572	1.75	201061_s_at	stomatin	STOM
377	0.0006247	134	234	0.573	1.75	202841_x_at	opioid growth factor receptor	OGFR
378	0.0004013	574.6	995	0.577	1.73	203440_at	cadherin 2, type 1, N-cadherin (neuronal)	CDH2
379	0.0003947	90.8	157.3	0.577	1.73	201474_s_at	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	ITGA3
380	0.0004997	312.1	540.3	0.578	1.73	200827_at	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	PLOD1
381	0.0003119	266.5	459.9	0.579	1.73	204257_at	fatty acid desaturase 3	FADS3
382	0.0003209	186.9	322.7	0.579	1.73	219397_at	hypothetical protein FLJ13448	FLJ13448
383	0.0005205	77.3	133.6	0.579	1.73	203739_at	zinc finger protein 217	ZNF217
384	0.000946	371.7	636.9	0.584	1.71	202239_at	poly (ADP-ribose) polymerase family, member 4	PARP4
385	0.0004921	25.1	42.8	0.586	1.71	214482_at	zinc finger protein 46 (KUP)	ZNF46
386	0.000703	81.5	138.9	0.587	1.70	203490_at	E74-like factor 4 (ets domain transcription factor)	ELF4

387	0.0008674	163	277	0.588	1.70	214244 s at	ATPase, H ⁺ transporting, lysosomal 9kDa, V0 subunit e	ATP6V0E
388	0.0005375	30.7	52.2	0.588	1.70	219078 at	G patch domain containing 2	GPATC2
389	0.000976	18.1	30.8	0.588	1.70	213916 at	zinc finger protein 20 (KOX 13)	ZNF20
390	0.0008313	10.4	17.5	0.594	1.68	205239 at	amphiregulin (schwannoma-derived growth factor)	AREG
391	0.0007314	122.4	206.2	0.594	1.68	220036 s at	lipocalin-interacting membrane receptor	LIMR
392	0.0006667	23.6	39.7	0.594	1.68	219810 at	valosin containing protein (p97)/p47 complex interacting protein 1	VCIPI1
393	0.0004086	259.8	436.9	0.595	1.68	218360 at	RAB22A, member RAS oncogene family	RAB22A
394	0.0009422	174.6	293	0.596	1.68	218004 at	hypothetical protein FLJ10276	FLJ10276
395	0.0009808	369.6	619.9	0.596	1.68	217795 s at	transmembrane protein 43	TMEM43
396	0.0008338	780.4	1304.5	0.598	1.67	204214 s at	RAB32, member RAS oncogene family	RAB32
397	0.0005659	112	187	0.599	1.67	204872 at	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4
398	0.0004759	108.8	181.4	0.6	1.67	222125 s at	hypoxia-inducible factor prolyl 4-hydroxylase	PH-4
399	0.0006735	1208.4	2011.5	0.601	1.66	218995 s at	endothelin 1	EDN1
400	0.0006061	82.8	137.8	0.601	1.66	35254 at	FLN29 gene product	FLN29
401	0.0005997	299	496.9	0.602	1.66	220419 s at	ubiquitin specific protease 25	USP25
402	0.0008467	313	519.2	0.603	1.66	210817 s at	nuclear domain 10 protein	NDP52
403	0.000969	514.1	849.9	0.605	1.65	202185 at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	PLOD3
404	0.0008163	143	235.9	0.606	1.65	203385 at	diacylglycerol kinase, alpha 80kDa	DGKA
405	0.0006942	266.1	437	0.609	1.64	209310 s at	caspase 4, apoptosis-related cysteine protease	CASP4
406	0.0006244	109.7	180.2	0.609	1.64	218584 at	hypothetical protein FLJ21127	FLJ21127
407	0.0006356	1798.8	2924.8	0.615	1.63	211071 s at	ALL1-fused gene from chromosome 1q /// ALL1-fused gene from chromosome 1q	AF1Q
408	0.000945	453.2	735.4	0.616	1.62	219099 at	chromosome 12 open reading frame 5	C12orf5
409	0.0006852	2068.2	3346.1	0.618	1.62	200871 s at	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	PSAP
410	0.0009463	1600.5	2578.9	0.621	1.61	201944 at	hexosaminidase B (beta polypeptide)	HEXB
411	0.0009942	80.8	129.9	0.622	1.61	210113 s at	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1	NALP1
412	0.0007469	617.4	991.3	0.623	1.61	201301 s at	annexin A4	ANXA4
413	0.0008176	675.6	1080.6	0.625	1.60	208959 s at	thioredoxin domain containing 4 (endoplasmic reticulum)	TXNDC4