

Table S1: Primers used for RT-PCR. Alpha-tubulin and 18S ribosomal RNA were used as internal controls.

Affymetrix ID	representative public ID	gene title	forward primer	reverse primer
206345_s_at	NM_000446	PON1 (paraoxonase 1)	5' - AGG AGA CCT TTG GGT TGG AT - 3'	5' - CAC TGT GCC AAT CAG CAG TT - 3'
214340_at	AL832768	12-LO (12-lipoxygenase)	5' - GCT GTG CTG AGA CAA TTC CA - 3'	5' - GGG GAC AAT TTG TTC ACC AG - 3'
201693_s_at	NM_001964	EGR1 (early growth response 1)	5' - ATC ACC TAT ACT GGC CGC TTT - 3'	5' - AGT AAA TGG GAC TGC TGT CGT T - 3'
220395_at	NM_018602	DNAJA4 (heat shock protein 40)	5' - GTA ATC TTT CCT GAA AAA CAC TGG - 3'	5' - CGT CTT CGT CCT CCT CGT AG - 3'
201661_s_at	NM_004457	ACSL3 (acyl-CoA synthase, long-chain 3)	5'- CTG GAA AAG TTT GAA ATT CCA GT -3'	5' - TTT TCT TCC ATA CAT TCG CTC A -3'
	BC009238	alpha tubulin	5' - CCT ACA ACT CCA TCC TCA CC -3'	5' - ATC AAA TCT CAG GGA AGC AG - 3'
	NG_002801	18S ribosomal RNA	5' - TGG TTG CAA AGC TGA AAC TTA AAG - 3'	5' - AGT CAA ATT AAG CCG CAG GC - 3'

Table S2: Transcript validation in volunteers V1 to V4 at 1 hour after sevoflurane inhalation.

paraoxonase 1			
	fold change chip	fold change PCR	validation status
V_1	2.13	3.24	+
V_2	1.40	1.76	+
V_3	1.44	2.17	+
V_4	1.62	2.64	+
12-lipoxygenase pseudogene 2			
V_1	1.55	7.45	+
V_2	1.41	1.34	+
V_3	1.24	2.40	+
V_4	1.64	1.91	+
early growth response 1			
V_1	1.19	5.63	+
V_2	1.52	1.64	+
V_3	1.43	3.16	+
V_4	1.39	n.a.	-
heat shock protein 40			
V_1	1.55	7.13	+
V_2	1.29	1.43	+
V_3	1.28	2.09	+
V_4	1.43	1.66	+

Gene ID	Gene Name	Fold Change	q-value(%)	localfdr(%)
1559397_s_ε	proline rich 14	1.6893	2.4969	1.0955
206345_s_at	paraoxonase 1	1.6747	2.4969	0.8040
1553366_s_ε	ankyrin repeat domain 23	1.6043	2.9998	2.4421
1559977_a_ε	solute carrier family 25, member 34	1.5624	2.4969	0.5194
1560035_at	hypothetical protein FLJ33590	1.5458	2.6723	2.1099
207412_x_at	carboxyl ester lipase pseudogene	1.5324	1.7183	1.7288
1561329_s_ε	RNA pseudouridylate synthase domain containing 3	1.5292	2.4969	1.0836
227347_x_at	hairy and enhancer of split 4 (Drosophila)	1.5161	2.4969	1.2415
1555742_at	---	1.5092	2.4969	0.0608
1563405_at	ATPase, H+/K+ exchanging, beta polypeptide	1.5067	2.0702	0.0000
239810_at	vasohibin 1	1.4947	2.0272	0.4478
226451_at	similar to RIKEN cDNA B230118G17 gene	1.4735	2.4969	1.0906
1568598_at	Kazal-type serine peptidase inhibitor domain 1	1.4735	2.6723	1.7731
210924_at	olfactomedin 1	1.4657	2.4969	0.3594
1552558_a_ε	retinoic acid induced 1	1.4590	2.6723	1.9536
232419_at	transmembrane protein 132A	1.4573	2.6723	2.1751
210454_s_at	potassium inwardly-rectifying channel, subfamily J, member 6	1.4566	2.4969	0.5844
224498_x_at	axin 2 (conductin, axil) /// axin 2 (conductin, axil)	1.4524	2.4139	0.0000
235397_at	hypothetical protein LOC285908	1.4503	2.4969	1.4496
219044_at	hypothetical protein FLJ10916	1.4404	2.4139	0.0000
1556507_at	CDNA clone IMAGE:5267328	1.4399	2.0619	0.2425
241486_at	Transmembrane protein 76	1.4345	2.6723	1.6885
1556340_at	Mitogen-activated protein kinase 12	1.4237	2.2769	0.0000
219516_at	transient receptor potential cation channel, subfamily V, member 4	1.4234	2.0702	0.1256
1553900_s_ε	POM121-like protein /// hypothetical protein DKFz434K191 /// hypothetical protein LOC6436	1.4231	2.0702	0.0000
206064_s_at	peptidylprolyl isomerase (cyclophilin)-like 2	1.4152	2.4969	1.3588
240229_at	G protein-coupled receptor kinase interactor 1	1.4112	2.4139	0.0396
227901_at	hypothetical protein LOC648987	1.4102	2.6723	1.8375
201693_s_at	early growth response 1	1.4060	2.0702	0.0974
236445_at	Egl nine homolog 2 (C. elegans)	1.3999	2.6723	2.0245
214340_at	arachidonate 12-lipoxygenase pseudogene 2	1.3992	2.6723	1.6449
237595_at	LIM homeobox transcription factor 1, alpha	1.3974	2.4969	0.1559
211809_x_at	collagen, type XIII, alpha 1	1.3929	2.0702	0.0000
219830_at	retinoic acid induced 1	1.3927	2.6723	1.7712
238230_x_at	Mannosidase, alpha, class 2C, member 1	1.3927	2.4969	1.2216
226454_at	membrane-associated ring finger (C3HC4) 9	1.3879	2.4969	0.2418
221335_x_at	hypothetical protein FLJ12886	1.3854	1.7183	1.7018
210628_x_at	latent transforming growth factor beta binding protein 4	1.3853	2.4139	0.0000
207450_s_at	POU domain, class 6, transcription factor 2	1.3845	2.0702	0.0000
217024_x_at	signal-regulatory protein alpha	1.3844	2.6723	2.0320
207172_s_at	cadherin 11, type 2, OB-cadherin (osteoblast)	1.3841	2.4969	0.2018
220395_at	DnaJ (Hsp40) homolog, subfamily A, member 4	1.3825	2.0702	0.0000
234722_x_at	odorant binding protein 2B /// odorant binding protein 2A	1.3821	1.7183	1.3475
207143_at	cyclin-dependent kinase 6	1.3814	2.0702	0.0000
217088_s_at	natural cytotoxicity triggering receptor 1	1.3810	2.0702	0.0000
228302_x_at	calcium/calmodulin-dependent protein kinase II inhibitor 1	1.3809	2.4969	0.6173
219395_at	RNA binding motif protein 35B	1.3793	2.0702	0.0000
206880_at	purinergic receptor P2X-like 1, orphan receptor	1.3784	2.0702	0.0000
211863_x_at	hemochromatosis	1.3770	2.0702	0.0000
228943_at	microtubule-associated protein 6	1.3767	1.7183	1.2744
232299_at	ASCL830	1.3731	2.0272	0.4641
239470_at	hypothetical protein LOC644809	1.3715	2.4139	0.0000
233250_x_at	hypothetical protein FLJ23322	1.3707	2.4969	0.3916
1563949_at	Solute carrier family 44, member 5	1.3695	2.4969	1.4537
241381_at	chromosome X open reading frame 36	1.3657	2.0702	0.0021
229570_at	Laminin, alpha 5	1.3656	2.0702	0.0180
220563_s_at	SH3 and multiple ankyrin repeat domains 1	1.3643	1.7415	0.6001
1569256_a_ε	family with sequence similarity 43, member B	1.3614	2.9998	2.4742
229330_at	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	1.3611	1.7415	0.7079

240588_at	---	1.3587	2.4969	0.2525
217684_at	thymidylate synthetase	1.3587	2.2769	0.0000
205853_at	zinc finger and BTB domain containing 7B	1.3585	1.7415	0.6855
213394_at	mitogen activated protein kinase binding protein 1	1.3584	2.0702	0.0000
1555871_at	KIAA1648 protein	1.3580	2.0702	0.0000
228896_at	Lupus brain antigen 1	1.3549	2.9998	2.5392
218553_s_at	potassium channel tetramerisation domain containing 15	1.3541	2.4969	0.1959
1555784_s_at	interleukin-1 receptor-associated kinase 1	1.3535	2.4969	0.9038
236676_at	NudC domain containing 3	1.3530	2.0272	0.5349
201474_s_at	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	1.3528	2.4969	0.1811
237654_at	chromosome 14 open reading frame 50	1.3527	2.4969	1.5595
203183_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	1.3524	2.4139	0.0000
202075_s_at	phospholipid transfer protein	1.3512	2.0702	0.0000
222795_s_at	phosphatidylinositol-specific phospholipase C, X domain containing 1	1.3505	2.4969	0.5389
220561_at	insulin-like growth factor 2 antisense	1.3503	1.7415	0.7450
234463_at	---	1.3488	2.4139	0.0227
225531_at	Cdk5 and Abl enzyme substrate 1	1.3486	2.4139	0.0000
1569470_a_at	FERM domain containing 5	1.3464	2.4969	0.5096
1563074_at	hypothetical protein LOC255654	1.3464	2.0619	0.2630
1554938_a_at	acyl-CoA thioesterase 11	1.3457	2.0702	0.0000
205506_at	villin 1	1.3454	2.0619	0.4077
1564431_a_at	FLJ45224 protein	1.3449	2.4969	0.3897
230541_at	hypothetical protein LOC149134	1.3448	2.4969	0.7539
207639_at	frizzled homolog 9 (Drosophila)	1.3446	2.0702	0.0000
206538_at	muscle RAS oncogene homolog	1.3421	2.6723	1.7862
222331_at	---	1.3419	0.0000	1.6570
229484_at	protein phosphatase 1J (PP2C domain containing)	1.3414	2.4969	0.3342
223459_s_at	chromosome 1 open reading frame 56	1.3401	2.4969	1.1449
238223_at	PX domain containing serine/threonine kinase	1.3396	2.2769	0.0000
214478_at	secreted phosphoprotein 2, 24kDa	1.3393	2.6723	2.2272
221157_s_at	F-box protein 24	1.3384	2.4969	0.3106
1555151_s_at	L-threonine dehydrogenase	1.3382	2.9998	2.4163
1563045_at	CDNA clone IMAGE:4827232	1.3371	2.4969	0.1271
232045_at	phosphatase and actin regulator 1	1.3369	2.0702	0.0940
236182_at	hypothetical protein MGC35361 /// hypothetical protein LOC641808 /// hypothetical protein LOC641808	1.3354	0.0000	1.6674
236049_at	Hypothetical protein KIAA1924	1.3337	2.0619	0.2425
205297_s_at	CD79b molecule, immunoglobulin-associated beta	1.3329	2.4969	0.4398
1555236_a_at	progastricsin (pepsinogen C)	1.3324	2.0702	0.0000
240009_at	Chromosome 21 open reading frame 89	1.3301	2.4969	0.2180
234284_at	guanine nucleotide binding protein (G protein), gamma 8	1.3298	2.0702	0.0000
243860_at	Ataxin 1	1.3291	2.0702	0.0000
232025_at	synaptotagmin VII	1.3291	2.4969	1.4993
219656_at	protocadherin 12	1.3273	1.7183	0.8950
217369_at	immunoglobulin heavy constant gamma 1 (G1m marker) /// similar to Ig heavy chain V-III region	1.3265	2.0702	0.0000
206297_at	chymotrypsin C (caldecrin)	1.3246	2.6723	1.9443
1563106_at	CDNA clone IMAGE:4821332	1.3220	2.6723	2.0022
213422_s_at	matrix-remodelling associated 8	1.3206	2.0702	0.0000
206728_at	endothelin converting enzyme 2	1.3200	2.4969	0.4975
210342_s_at	thyroid peroxidase	1.3198	2.4969	0.2412
206966_s_at	Kruppel-like factor 12	1.3193	2.4969	0.5289
205708_s_at	transient receptor potential cation channel, subfamily M, member 2	1.3187	1.7183	0.8818
237947_at	General transcription factor II, i	1.3171	2.6723	2.0909
206313_at	major histocompatibility complex, class II, DO alpha	1.3171	2.4969	0.3444
211205_x_at	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	1.3165	2.4969	0.8464
220677_s_at	ADAM metalloproteinase with thrombospondin type 1 motif, 8	1.3159	2.4139	0.0000
219010_at	chromosome 1 open reading frame 106	1.3151	2.4969	1.1022
1556422_at	Zinc finger protein 28 homolog (mouse)	1.3148	2.2769	0.0000
234334_s_at	laminin, beta 4	1.3147	2.4969	0.2697
239555_at	V-yes-1 Yamaguchi sarcoma viral related oncogene homolog	1.3146	2.4969	1.2900
222615_s_at	PRKR interacting protein 1 (IL11 inducible)	1.3143	2.4139	0.0000

211830_s_at	calcium channel, voltage-dependent, alpha 1I subunit	1.3143	2.4969	1.0976
1566973_at	MRNA; cDNA DKFZp434M1135 (from clone DKFZp434M1135)	1.3141	1.7183	1.1519
213001_at	angiotensin-like 2	1.3121	2.4969	1.2682
204623_at	trefoil factor 3 (intestinal)	1.3111	2.4969	0.3163
223963_s_at	insulin-like growth factor 2 mRNA binding protein 2	1.3106	2.0702	0.0000
204930_s_at	BCL2/adenovirus E1B 19kDa interacting protein 1	1.3106	2.4969	1.0111
216648_s_at	ras responsive element binding protein 1	1.3104	2.4139	0.0000
205142_x_at	ATP-binding cassette, sub-family D (ALD), member 1	1.3092	2.4969	0.0791
211486_s_at	potassium voltage-gated channel, KQT-like subfamily, member 2	1.3078	1.7183	1.1101
1565617_at	CDNA FLJ40309 fis, clone TESTI2029470	1.3058	1.7415	0.8260
226586_at	ankyrin repeat and sterile alpha motif domain containing 6	1.3056	2.4969	1.5136
218975_at	collagen, type V, alpha 3	1.3051	1.7183	1.7306
231177_at	Host cell factor C1 (VP16-accessory protein)	1.3040	2.6723	1.8801
221162_at	HERV-H LTR-associating 1	1.3030	2.4969	1.3747
209351_at	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	1.3022	2.0702	0.0000
1553812_at	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	1.3018	2.0702	0.0000
213676_at	chromosome 6 open reading frame 137	1.3013	2.4969	1.3863
240003_at	---	1.3000	2.4969	0.0546
1553629_a_c	family with sequence similarity 71, member B	1.2985	2.9998	2.4579
239968_at	chromosome 21 open reading frame 84	1.2984	2.4969	0.4880
217070_at	5,10-methylenetetrahydrofolate reductase (NADPH)	1.2979	2.4969	0.5191
244554_at	DKFZP686A01247 hypothetical protein	1.2974	2.4969	0.6215
211314_at	calcium channel, voltage-dependent, alpha 1G subunit	1.2969	2.4969	1.0279
212487_at	KIAA0553	1.2964	2.4969	0.2632
227998_at	S100 calcium binding protein A16	1.2963	2.6723	2.1847
236463_at	testis nuclear RNA-binding protein-like	1.2962	2.6723	2.0362
233889_at	T-box 18	1.2962	2.4969	1.2225
202065_s_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin)	1.2960	1.7183	1.1402
52255_s_at	collagen, type V, alpha 3	1.2956	2.4969	0.8724
220583_at	hypothetical protein FLJ22596	1.2951	2.4969	0.8862
219256_s_at	SH3 domain and tetratricopeptide repeats 1	1.2948	2.4969	0.7490
238603_at	hypothetical protein LOC254559	1.2935	2.6723	1.6738
223534_s_at	ribosomal protein S6 kinase-like 1	1.2929	2.6723	1.9219
205058_at	solute carrier family 26 (sulfate transporter), member 1	1.2928	2.4969	0.4256
205713_s_at	cartilage oligomeric matrix protein	1.2927	2.6723	2.2370
1558954_at	small nucleolar RNA, H/ACA box 78	1.2927	1.7183	1.4537
234395_at	---	1.2927	1.7183	1.7187
1566643_a_c	Guanine nucleotide binding protein (G protein), gamma 7	1.2924	2.0702	0.0000
228034_x_at	alkB, alkylation repair homolog 5 (E. coli)	1.2921	2.0702	0.0000
207457_s_at	lymphocyte antigen 6 complex, locus G6D	1.2914	2.0702	0.0000
223899_at	polybromo 1	1.2911	2.0702	0.0000
203443_at	echinoderm microtubule associated protein like 3	1.2906	2.0272	0.5459
1563247_at	Homo sapiens, clone IMAGE:4992174, mRNA	1.2906	2.4969	0.7661
227217_at	WNK lysine deficient protein kinase 2	1.2898	2.4139	0.0000
233905_at	sperm associated antigen 4-like	1.2896	2.4969	0.8587
204431_at	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	1.2895	2.9998	2.5776
208009_s_at	Rho guanine exchange factor (GEF) 16	1.2894	2.4969	0.5431
1570344_at	CDNA clone IMAGE:4838056	1.2891	1.7415	0.8113
238329_at	Myosin phosphatase-Rho interacting protein	1.2886	2.4969	1.5292
227672_at	chromosome 8 open reading frame 73	1.2881	2.0619	0.2473
214857_at	Chromosome 10 open reading frame 95	1.2877	2.2769	0.0000
223083_s_at	egl nine homolog 2 (C. elegans)	1.2870	2.0702	0.0000
220114_s_at	stabilin 2	1.2866	1.7415	0.6754
230731_x_at	---	1.2863	2.6723	2.2133
208879_x_at	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	1.2862	2.4969	0.1865
206231_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member	1.2861	2.9998	2.6014
233315_at	C-terminal binding protein 2	1.2841	2.4969	1.2197
1561542_at	---	1.2824	2.4969	0.1455
213870_at	collagen, type XI, alpha 2	1.2817	2.0702	0.0000
239145_at	Zinc finger protein 414	1.2815	2.4969	1.1236

208198_x_at	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	1.2814	1.7183	0.9823
242071_x_at	integrin, alpha 8	1.2810	2.4969	0.2243
209400_at	Solute carrier family 12 (potassium/chloride transporters), member 4	1.2806	1.7183	1.4545
234439_at	CDNA FLJ10235 fis. clone HEMBB1000339	1.2803	2.4969	1.2710
206517_at	cadherin 16, KSP-cadherin	1.2798	2.0702	0.0000
242103_at	transmembrane protein 86A	1.2796	2.0272	0.5784
205258_at	inhibin, beta B (activin AB beta polypeptide)	1.2796	2.4969	1.0690
234214_at	Arrestin domain containing 1	1.2789	1.7415	0.7622
207349_s_at	uncoupling protein 3 (mitochondrial, proton carrier)	1.2776	2.4969	0.2783
205397_x_at	SMAD, mothers against DPP homolog 3 (Drosophila)	1.2775	2.0702	0.0000
244772_at	AT rich interactive domain 1B (SWI1-like)	1.2763	2.6723	1.8917
205464_at	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)	1.2762	2.6723	1.6947
212104_s_at	RNA binding motif protein 9	1.2760	2.4139	0.0000
241309_at	Target of myb1-like 2 (chicken)	1.2758	2.0702	0.0000
234102_at	RAS-like, family 11, member B	1.2751	2.4969	0.2187
230924_at	tubulin tyrosine ligase-like family, member 6	1.2749	2.4969	0.7739
1557702_at	CDNA clone IMAGE:5265308	1.2746	1.7183	1.1447
1569153_at	Homo sapiens, clone IMAGE:4551281, mRNA	1.2745	2.4969	0.4310
207896_s_at	deleted in lung and esophageal cancer 1	1.2737	2.0702	0.0000
213556_at	similar to R28379_1	1.2737	2.0702	0.0000
220431_at	transmembrane protease, serine 11E /// similar to transmembrane protease, serine 11E	1.2726	1.7183	1.4191
220373_at	dachous 2 (Drosophila)	1.2726	2.4969	0.2257
218743_at	chromatin modifying protein 6	1.2723	2.4969	1.3763
219920_s_at	GDP-mannose pyrophosphorylase B	1.2721	2.6723	2.1206
208604_s_at	homeobox A3 /// homeobox A3	1.2720	2.6723	1.9023
209324_s_at	regulator of G-protein signalling 16	1.2718	2.4139	0.0000
219997_s_at	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	1.2711	2.4969	1.1784
232498_at	hypothetical protein KIAA1833	1.2710	1.7183	1.5269
202790_at	claudin 7	1.2707	2.6723	1.6801
240372_at	Phosphatidylinositol glycan, class P	1.2707	2.4969	0.3906
223379_s_at	LATS, large tumor suppressor, homolog 2 (Drosophila)	1.2697	2.6723	1.8803
215761_at	Dmx-like 2	1.2697	2.0619	0.2521
229032_at	KIAA0789 gene product	1.2696	2.2769	0.0000
1555650_at	kelch-like 17 (Drosophila)	1.2696	2.2769	0.0000
203808_at	---	1.2684	2.6723	2.0251
211360_s_at	inositol 1,4,5-triphosphate receptor, type 2	1.2684	2.4969	0.8361
240502_at	FERM domain containing 5	1.2667	0.0000	1.5661
1559491_at	MRNA; cDNA DKFZp761L149 (from clone DKFZp761L149)	1.2662	2.4969	1.6158
218690_at	PDZ and LIM domain 4	1.2657	2.0702	0.0000
236452_at	hypothetical protein LOC645401	1.2655	2.6723	2.0242
236066_at	Transcribed locus	1.2648	1.7183	0.9407
1552724_at	paired-like homeobox protein OTEX	1.2637	2.4969	0.2616
242543_at	similar to B-cell linker; B cell linker protein	1.2636	2.0702	0.0699
1554388_at	vacuolar protein sorting 29 (yeast)	1.2632	2.4969	0.9279
222219_s_at	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	1.2629	2.0702	0.0000
1569108_a_z	zinc finger protein 589	1.2617	2.0619	0.2908
243833_at	Unc-5 homolog A (C. elegans)	1.2612	2.6723	2.0492
240501_at	Transcribed locus, weakly similar to NP_689672.2 hypothetical protein MGC45438 [Homo sa	1.2607	2.0702	0.0000
224552_s_at	potassium channel, subfamily K, member 4	1.2603	2.4969	0.4945
1565882_at	Glucocorticoid receptor DNA binding factor 1	1.2602	2.0619	0.2768
216937_s_at	retinoschisis (X-linked, juvenile) 1	1.2600	2.4969	0.2209
213381_at	Chromosome 10 open reading frame 72	1.2598	2.9998	2.5288
215142_at	chromosome X open reading frame 27	1.2598	2.0619	0.4175
224128_at	chromosome 20 open reading frame 43	1.2594	2.0702	0.0000
1558195_at	hypothetical protein LOC283404	1.2593	2.4969	0.5411
242259_at	hypothetical protein FLJ25660	1.2590	2.6723	2.1043
241477_at	nei endonuclease VIII-like 1 (E. coli)	1.2590	2.4969	1.4453
1565905_at	FLJ46026 protein	1.2584	1.7183	0.9221
207065_at	cytokeratin type II	1.2584	2.4969	0.5985
205754_at	coagulation factor II (thrombin)	1.2578	2.9998	2.4326

1566821_at	---	1.2578	2.4969	1.4402
207070_at	retinal G protein coupled receptor	1.2572	1.7415	0.6199
228633_s_at	centrobin, centrosomal BRCA2 interacting protein	1.2570	2.0702	0.0000
217275_at	---	1.2568	2.2769	0.0000
205102_at	transmembrane protease, serine 2	1.2564	2.0702	0.0000
216610_at	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	1.2561	2.0702	0.0000
203074_at	annexin A8 /// annexin A8-like /// annexin A8-like 1	1.2556	2.4969	0.2752
205616_at	CDNA FLJ25134 fis, clone CBR06934	1.2554	1.7183	1.0115
216936_at	---	1.2552	2.6723	2.1032
223905_at	chromosome 16 open reading frame 50	1.2544	2.0702	0.1283
236263_at	Sonic hedgehog homolog (Drosophila)	1.2543	2.4969	1.4515
215527_at	KH domain containing, RNA binding, signal transduction associated 2	1.2536	2.4969	0.5872
232802_at	synaptotagmin VIII	1.2531	2.9998	2.5408
231253_at	intramembrane protease 5	1.2530	2.4969	0.1280
1561534_at	Neuroigin 4, X-linked	1.2526	2.4969	1.0722
222009_at	Amidohydrolase domain containing 2	1.2521	2.4969	1.3301
1560916_a_f	dpy-19-like 1 (C. elegans)	1.2511	2.4969	1.0758
225868_at	tripartite motif-containing 47	1.2499	2.0702	0.0000
219709_x_at	chromosome 16 open reading frame 24	1.2498	2.0702	0.0000
244215_at	Biotinidase	1.2498	2.0702	0.0000
206753_at	retinol dehydrogenase 16 (all-trans)	1.2497	2.0702	0.0000
1568663_a_f	CDNA clone IMAGE:5266772	1.2493	2.4969	0.8747
233325_at	solute carrier family 35, member D2	1.2492	2.2769	0.0000
240209_at	hypothetical protein MGC32905	1.2485	2.4969	1.0027
214371_at	testis-specific serine kinase 2	1.2479	2.4969	0.6013
227592_at	aldehyde dehydrogenase 16 family, member A1	1.2476	2.4969	0.5562
210977_s_at	heat shock transcription factor 4	1.2472	2.0702	0.0000
207144_s_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	1.2471	2.9998	2.3831
1552432_at	hypothetical protein FLJ35773	1.2470	2.6723	1.8731
224092_at	BarH-like 1 (Drosophila)	1.2466	2.4969	0.9708
230976_at	chromosome 9 open reading frame 98	1.2457	2.2769	0.0000
220816_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7	1.2456	2.4969	0.2858
203673_at	thyroglobulin	1.2449	2.6723	2.0047
210099_at	ATP-binding cassette, sub-family A (ABC1), member 2	1.2447	2.0702	0.0000
210063_at	sarcosine dehydrogenase	1.2445	1.7183	1.1360
232924_at	leucine rich repeat containing 17	1.2443	2.4969	0.9252
221340_at	caudal type homeobox transcription factor 4	1.2441	2.4969	1.5058
241488_at	Chaperone, ABC1 activity of bc1 complex like (S. pombe)	1.2441	2.4139	0.0103
1563137_at	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	1.2438	2.4969	0.1116
205652_s_at	tubulin tyrosine ligase-like family, member 1	1.2423	2.0619	0.3571
1553859_at	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	1.2422	2.2769	0.0000
1556149_at	Catechol-O-methyltransferase	1.2418	2.4969	0.4501
232733_s_at	collagen, type XX, alpha 1	1.2417	2.0702	0.0000
235558_at	Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	1.2416	2.4969	0.1458
205093_at	pleckstrin homology domain containing, family A member 6	1.2413	2.9998	2.6017
1570651_at	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotr	1.2413	2.4969	1.4527
220645_at	family with sequence similarity 55, member D	1.2406	2.4969	0.3957
215218_s_at	WD repeat domain 62	1.2402	2.4969	0.2156
222352_at	F-box protein 31	1.2402	2.4969	1.6339
230853_at	Transcribed locus, strongly similar to XP_529987.1 PREDICTED: hypothetical protein XP_52	1.2401	2.9998	2.3736
207788_s_at	sorbin and SH3 domain containing 3	1.2401	2.4969	1.4069
1556796_at	CDNA FLJ32776 fis, clone TESTI2002048	1.2399	2.9998	2.2623
1565751_at	FYVE, RhoGEF and PH domain containing 2	1.2395	2.0272	0.4412
214292_at	integrin, beta 4	1.2392	2.4969	1.1062
242334_at	NACHT, leucine rich repeat and PYD containing 4	1.2390	2.4969	0.1492
205993_s_at	T-box 2	1.2389	2.2769	0.0000
220439_at	Ras and Rab interactor 3	1.2388	1.7415	0.8095
223919_at	similar to p53-regulated apoptosis-inducing protein 1	1.2385	2.0702	0.0000
229446_at	CDNA clone IMAGE:5264834	1.2383	2.4969	1.1092
1558193_at	CDNA clone IMAGE:3931276	1.2382	2.4969	0.2076

243437_at	GRIP and coiled-coil domain containing 1	1.2380	2.4969	0.0884
1554972_at	Development and differentiation enhancing factor-like 1	1.2370	2.9998	2.4537
1556320_at	Stomatin (EPB72)-like 1	1.2365	1.7183	1.0793
240403_at	Chromosome 21 open reading frame 7	1.2364	2.4969	1.5662
233395_at	Regulator of G-protein signalling 3	1.2363	2.4969	1.0198
211876_x_at	protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 10	1.2359	2.4969	0.7096
227248_at	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	1.2358	2.4139	0.0000
231957_s_at	dipeptidyl-peptidase 9	1.2358	2.4969	0.7630
216949_s_at	polycystic kidney disease 1 (autosomal dominant)	1.2358	2.0702	0.0000
1556582_at	CDNA FLJ25946 fis, clone JTH14258	1.2357	1.7415	0.7991
230049_at	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	1.2355	1.7183	1.7303
1559352_a_at	hypothetical protein BC009233	1.2353	2.0272	0.5554
234408_at	interleukin 17F	1.2351	2.9998	2.4356
221099_at	hypothetical protein LOC644951	1.2351	2.4969	0.0902
244807_at	---	1.2349	2.0702	0.0000
208373_s_at	pyrimidinergic receptor P2Y, G-protein coupled, 6	1.2347	2.4969	1.2914
241645_at	Myosin ID	1.2346	2.0619	0.2242
234355_s_at	patched domain containing 2	1.2345	2.4969	0.1403
1568406_at	---	1.2344	2.4139	0.0000
203009_at	basal cell adhesion molecule (Lutheran blood group)	1.2338	2.4969	0.0855
231580_at	---	1.2338	2.4969	0.4038
228072_at	synaptotagmin XII	1.2336	2.4969	0.6035
238582_at	Chromosome 21 open reading frame 2	1.2332	2.4969	0.4698
233962_at	---	1.2331	2.4969	1.2427
230199_at	Hypothetical LOC284184	1.2323	2.4139	0.0000
1553545_at	immunoglobulin-like domain containing receptor 1	1.2317	2.4969	0.8112
227103_s_at	hypothetical protein MGC2408	1.2316	1.7183	1.2157
228278_at	nuclear factor I/X (CCAAT-binding transcription factor)	1.2314	2.4969	0.9269
1562222_at	Homo sapiens, clone IMAGE:5575364, mRNA	1.2305	1.7415	0.6981
235586_at	Guanine nucleotide binding protein (G protein) alpha 12	1.2305	2.0619	0.3527
234421_s_at	Ellis van Creveld syndrome	1.2300	2.4969	0.5535
208108_s_at	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	1.2298	1.7183	1.5958
237604_at	Ciliary neurotrophic factor receptor	1.2291	2.4969	1.2536
217261_at	testis-specific transcript, Y-linked 2	1.2286	2.4969	1.1730
235319_at	CDNA clone IMAGE:5302680	1.2278	2.0702	0.0000
238240_at	---	1.2277	2.4969	0.5420
210298_x_at	four and a half LIM domains 1	1.2275	2.4969	0.1121
1568589_at	Clone FLB3512 mRNA sequence	1.2273	2.4969	0.9611
223573_s_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	1.2272	2.4969	0.8344
237666_at	X-ray radiation resistance associated 1	1.2271	2.0702	0.0023
207207_at	testes-specific heterogenous nuclear ribonucleoprotein G-T	1.2269	2.4969	1.1553
240983_s_at	cysteinyl-tRNA synthetase	1.2268	2.4969	0.2265
237789_at	---	1.2266	2.4969	0.1843
213412_at	tight junction protein 3 (zona occludens 3)	1.2264	2.4969	0.2957
240849_at	Fizzy/cell division cycle 20 related 1 (Drosophila)	1.2263	2.4969	0.1675
214229_at	dynein, axonemal, heavy polypeptide 17	1.2262	1.7415	0.7495
202669_s_at	ephrin-B2	1.2260	2.2769	0.0000
240387_at	Cbl-interacting protein Sts-1	1.2259	2.0702	0.0000
232253_at	RAD50 homolog (S. cerevisiae)	1.2257	2.4969	0.9825
1557421_at	Chromosome 16 open reading frame 34	1.2255	2.4969	1.5691
239686_at	Transcribed locus	1.2253	2.4969	1.0142
240598_at	---	1.2251	2.6723	1.9694
202247_s_at	metastasis associated 1	1.2250	2.4969	1.1668
229316_at	hypothetical protein MGC2749	1.2243	1.7183	1.1547
1557026_at	CDNA clone IMAGE:4825891	1.2241	2.4969	0.3210
32699_s_at	poliovirus receptor	1.2236	2.9998	2.2607
230423_at	Transcribed locus, strongly similar to XP_373845.2 PREDICTED: hypothetical protein XP_373845.2	1.2233	2.4969	0.7820
216880_at	RAD51-like 1 (S. cerevisiae)	1.2231	1.7183	1.3114
216821_at	keratin 8 /// similar to Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) ///	1.2230	2.0702	0.0000
1567591_at	Trapped 3' terminal exon, clone B2G5	1.2227	1.7183	1.3845

230911_at	Sine oculis homeobox homolog 1 (Drosophila)	1.2224	2.0702	0.0000
202134_s_at	WW domain containing transcription regulator 1	1.2222	2.2769	0.0000
230124_at	Transmembrane protein 30B	1.2220	2.0702	0.0000
211918_x_at	pappalysin 2 /// pappalysin 2	1.2215	2.9998	2.2557
1564413_at	hypothetical locus LOC388666	1.2211	2.4969	0.5345
224182_x_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	1.2205	2.2769	0.0000
238715_at	hypothetical protein LOC646014	1.2203	2.4969	0.1177
229452_at	transmembrane protein 88	1.2200	2.4969	0.7465
1559316_at	Hypothetical protein LOC646296	1.2200	2.0702	0.0000
204021_s_at	purine-rich element binding protein A	1.2198	2.0702	0.0000
214609_at	paired-like (aristaless) homeobox 2a	1.2193	2.0702	0.0000
240694_at	Transcribed locus, strongly similar to XP_416473.1 PREDICTED: similar to 45kDa splicing fa	1.2190	2.4969	1.0291
213751_at	hypothetical protein LOC284352	1.2189	2.4969	0.7789
206406_at	sperm mitochondria-associated cysteine-rich protein	1.2188	2.9998	2.5620
233619_at	---	1.2185	2.4969	1.4414
1566934_at	TYRO3P protein tyrosine kinase pseudogene	1.2184	2.4969	0.7812
226129_at	family with sequence similarity 83, member H	1.2182	2.4969	1.3477
207288_at	chromosome X and Y open reading frame 2	1.2179	2.6723	2.0855
201785_at	ribonuclease, RNase A family, 1 (pancreatic)	1.2176	2.4969	1.2141
220446_s_at	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	1.2174	2.4139	0.0000
1557162_at	hypothetical protein FLJ25404	1.2169	2.4969	0.5782
1561101_at	hypothetical protein LOC153469	1.2167	2.4969	1.6020
1554827_a_7	adenylate cyclase 7	1.2166	2.4969	1.0811
1555995_a_7	Diaphanous homolog 3 (Drosophila)	1.2164	2.4969	0.6137
221217_s_at	ataxin 2-binding protein 1	1.2164	2.0702	0.0000
1553157_at	LIM homeobox 4	1.2163	2.9998	2.4467
1556356_at	glutamate-rich 1	1.2156	2.4969	0.4682
220686_s_at	piwi-like 2 (Drosophila)	1.2154	2.0702	0.0000
225150_s_at	rhotekin	1.2152	2.0702	0.0000
229379_at	AT hook, DNA binding motif, containing 1	1.2149	2.0702	0.0000
216047_x_at	seizure related 6 homolog (mouse)-like	1.2139	2.4969	1.0750
229046_s_at	Pleckstrin homology domain containing, family B (evectins) member 1	1.2138	2.6723	2.1284
208321_s_at	calcium binding protein 1 (calbrain)	1.2134	2.0702	0.0515
229837_s_at	Potassium channel tetramerisation domain containing 5	1.2133	2.4969	0.3559
208576_s_at	histone 1, H3b	1.2133	2.0702	0.0000
1568633_a_7	CDNA clone IMAGE:3878708	1.2129	2.4969	0.3090
214546_s_at	purinergic receptor P2Y, G-protein coupled, 11	1.2126	2.6723	2.1884
231180_at	---	1.2124	2.4969	0.6875
213668_s_at	SRY (sex determining region Y)-box 4	1.2123	2.4969	1.2217
242350_s_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	1.2122	2.0702	0.0000
215534_at	MRNA; cDNA DKFZp586C1923 (from clone DKFZp586C1923)	1.2113	2.9998	2.5383
243571_at	Pregnancy-induced growth inhibitor	1.2111	2.0619	0.3049
1560410_at	Homo sapiens, clone IMAGE:5241870, mRNA	1.2111	2.4969	0.3715
231179_at	inositol hexaphosphate kinase 3	1.2110	1.7415	0.7534
39763_at	hemopexin	1.2110	2.4969	0.4434
1555935_s_7	hormonally upregulated Neu-associated kinase	1.2110	2.4969	1.3675
219883_at	similar to potassium channel, subfamily K, member 4	1.2109	2.2769	0.0000
233422_at	Early B-cell factor 3	1.2108	2.4969	1.3420
1556138_a_7	Collagen, type V, alpha 1	1.2108	2.0619	0.4150
219450_at	chromosome 4 open reading frame 19	1.2104	2.6723	1.6777
230584_at	zinc finger protein 75 (D8C6)	1.2098	2.0702	0.0000
207617_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	1.2098	2.2769	0.0000
244877_at	---	1.2093	2.0702	0.0000
240164_at	Mucin 4, cell surface associated	1.2091	2.2769	0.0000
202440_s_at	suppression of tumorigenicity 5	1.2090	2.0702	0.0000
208100_x_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C /// se	1.2087	2.4969	0.2761
1553641_a_7	testis specific, 13	1.2086	2.0702	0.0000
238709_at	CDNA FLJ38461 fis, clone FEBRA2020977	1.2081	2.4969	1.3384
1566932_x_7	transcription factor B2, mitochondrial	1.2081	2.0702	0.0000
239362_at	N-ethylmaleimide-sensitive factor attachment protein, alpha	1.2079	2.6723	1.6489

155788_a_	tribbles homolog 3 (Drosophila)	1.2077	2.4969	0.6564
237581_at	KIAA1671 protein	1.2075	1.7415	0.6836
207187_at	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	1.2071	2.0702	0.0000
231210_at	hypothetical protein LOC283129	1.2070	2.4969	1.2897
233108_at	CDNA FLJ11206 fis. clone PLACE1007846	1.2066	2.2769	0.0000
225682_s_at	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	1.2065	2.4969	0.4190
234798_x_at	chromosome 20 open reading frame 66	1.2063	1.7183	1.6248
206778_at	crystallin, beta B2	1.2062	2.4969	1.1856
217111_at	alpha-methylacyl-CoA racemase	1.2059	2.0702	0.0000
209897_s_at	slit homolog 2 (Drosophila)	1.2057	2.4969	0.8993
231700_at	guanylate cyclase activator 1A (retina)	1.2055	2.2769	0.0000
209237_s_at	solute carrier family 23 (nucleobase transporters), member 2	1.2049	2.0702	0.0490
234476_at	dynein, axonemal, heavy polypeptide 7	1.2048	2.4969	1.4343
208779_x_at	discoidin domain receptor family, member 1	1.2044	2.9998	2.3228
225423_x_at	Mitochondrial ribosomal protein L41	1.2042	2.4969	1.1960
243454_at	Ets variant gene 6 (TEL oncogene)	1.2038	2.9998	2.3203
243304_at	hypothetical protein LOC286109	1.2036	2.0619	0.3251
205985_x_at	chloride channel Kb	1.2036	2.4969	1.1306
219784_at	F-box protein 31	1.2034	2.0702	0.0000
1564729_at	Homo sapiens, clone IMAGE:3891207, mRNA	1.2031	2.4969	1.4057
206040_s_at	mitogen-activated protein kinase 11	1.2028	2.9998	2.3340
209693_at	astrotactin 2	1.2017	2.0702	0.0000
242971_at	---	1.2014	2.4969	0.6593
236604_at	BAH domain and coiled-coil containing 1	1.2011	2.9998	2.2923
1557649_at	UDP-galactose-4-epimerase	1.2011	2.6723	2.1200
210445_at	fatty acid binding protein 6, ileal (gastrotropin)	1.2010	2.6723	1.8568
206168_at	zinc finger CCCH-type containing 7B	1.2010	2.0702	0.0000
208164_s_at	interleukin 9 receptor	1.2009	1.7183	0.9428
240679_at	Serine/threonine kinase 32B	1.2008	2.4969	0.4749
225784_s_at	KIAA1166	1.2008	2.4969	0.1164
235770_at	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	1.2006	2.4969	1.0184
229995_at	syncollin	1.2006	2.4969	0.6569
1560456_at	Leucine-rich alpha-2-glycoprotein 1	1.2002	2.0702	0.1554
230966_at	interleukin 4 induced 1	1.2001	1.7183	1.5688
229799_s_at	neural cell adhesion molecule 1	1.2001	1.7415	0.7858
208531_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 2	1.1997	2.2769	0.0000
210051_at	Rap guanine nucleotide exchange factor (GEF) 3	1.1994	2.2769	0.0000
1554026_a_	Myosin X	1.1994	2.4969	1.1137
244385_at	Jumonji domain containing 2C	1.1993	2.0702	0.0000
207028_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite stra	1.1992	2.0702	0.0000
1552911_at	sialic acid binding Ig-like lectin 11	1.1988	1.7183	1.0201
214105_at	suppressor of cytokine signaling 3	1.1988	2.0702	0.0000
214312_at	Forkhead box A2	1.1988	2.4969	0.3202
214951_at	solute carrier family 26, member 10	1.1988	1.7183	1.6891
201287_s_at	syndecan 1	1.1987	2.4969	0.5040
231231_at	Formin-like 3	1.1987	2.0702	0.0000
235091_at	2'-phosphodiesterase	1.1984	2.2769	0.0000
237014_at	V-myb myeloblastosis viral oncogene homolog (avian)-like 1	1.1983	1.7415	0.6557
228975_at	Sp6 transcription factor	1.1983	2.2769	0.0000
235856_at	Complement component 4A (Rodgers blood group)	1.1980	2.6723	1.9214
238186_at	Transcribed locus	1.1977	2.0702	0.1884
233448_s_at	Hypothetical protein MGC24039	1.1976	2.4139	0.0000
240630_at	Retinoic acid receptor, alpha	1.1976	2.4969	1.3714
239566_at	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	1.1975	2.0702	0.0144
217341_at	dynamin 1	1.1973	1.7415	0.6809
219670_at	chromosome 1 open reading frame 165	1.1973	2.4969	0.7193
214228_x_at	tumor necrosis factor receptor superfamily, member 4	1.1969	2.2769	0.0000
204322_at	golgi phosphoprotein 4	1.1969	2.4969	0.8718
206317_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 8	1.1968	2.4969	1.1408
222008_at	collagen, type IX, alpha 1	1.1967	2.4969	0.4756

231719_at	Interferon responsive gene 15	1.1967	1.7183	1.1225
239777_at	hypothetical protein LOC283551	1.1966	2.0702	0.0000
218665_at	frizzled homolog 4 (Drosophila)	1.1965	2.4969	1.4021
233298_at	spermatogenesis and oogenesis specific basic helix-loop-helix 2	1.1964	2.6723	1.9897
234309_at	testis-specific transcript, Y-linked 7	1.1964	2.0702	0.0000
1552576_at	LOC200420	1.1961	2.9998	2.5531
229805_at	Zinc finger, DHHC-type containing 22	1.1951	2.0702	0.1412
1562425_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	1.1950	2.6723	1.7853
239791_at	Hypothetical LOC404266	1.1943	2.4969	1.0242
236023_at	---	1.1937	2.0702	0.0000
227720_at	ankyrin repeat domain 13B	1.1935	2.6723	2.0617
234708_at	single-strand-selective monofunctional uracil-DNA glycosylase 1	1.1935	2.4969	1.5583
233526_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	1.1932	2.4969	1.5583
205124_at	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)	1.1932	1.7183	1.4981
1553755_at	thioredoxin-like 6	1.1925	2.6723	2.1983
213756_s_at	heat shock transcription factor 1	1.1921	2.4969	0.2633
203516_at	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	1.1919	2.4969	0.4771
208251_at	potassium voltage-gated channel, Shaw-related subfamily, member 4	1.1917	2.4969	0.8648
230294_at	Transcribed locus, weakly similar to XP_517655.1 PREDICTED: similar to KIAA0825 protein	1.1911	2.0702	0.2186
243769_at	---	1.1910	2.0702	0.0000
1557186_s_e	two pore segment channel 1	1.1907	2.6723	1.8964
234919_s_at	syntrophin, gamma 1	1.1906	2.6723	1.7816
242484_at	tetratricopeptide repeat domain 9B	1.1902	2.6723	2.1016
201982_s_at	pregnancy-associated plasma protein A, pappalysin 1	1.1901	2.4969	1.0743
229534_at	acyl-CoA thioesterase 4	1.1897	2.0702	0.0000
216582_at	POM121 membrane glycoprotein-like 2 (rat) /// similar to Nuclear envelope pore membrane p	1.1896	2.4969	1.6173
236681_at	Transcribed locus, strongly similar to NP_000514.1 homeo box D13; homeo box 4I; homeobr	1.1894	2.6723	2.2167
1562447_a_e	CDNA clone IMAGE:5295490 /// CDNA FLJ38930 fis. clone NT2NE2013081	1.1893	2.0702	0.1353
216477_at	---	1.1892	2.4139	0.0140
240534_at	---	1.1889	2.4969	0.0738
237611_at	Transcribed locus	1.1888	2.0702	0.1677
222012_at	Hypothetical protein BC002926	1.1885	1.7415	0.7428
1563821_at	hypothetical protein LOC170425	1.1885	2.6723	2.2030
1555308_at	caspase recruitment domain family, member 14	1.1884	2.0272	0.5391
217642_at	ring finger protein 40	1.1884	2.0702	0.0000
64438_at	hypothetical protein FLJ22222	1.1882	2.6723	2.1540
1558915_a_e	Peroxisomal biogenesis factor 14	1.1878	2.0702	0.0000
208281_x_at	deleted in azoospermia 1 /// deleted in azoospermia 3 /// deleted in azoospermia 2 /// deleted	1.1877	2.0702	0.0000
1559679_a_e	Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	1.1876	2.0702	0.0000
232464_at	tripartite motif-containing pseudogene 1	1.1870	2.4969	0.4101
207502_at	guanylate cyclase activator 2B (uroguanylin)	1.1865	1.7183	1.3442
1552937_s_e	three prime repair exonuclease 1	1.1864	2.9998	2.4789
227381_at	Cerebral endothelial cell adhesion molecule 1	1.1856	1.7183	1.5784
205810_s_at	Wiskott-Aldrich syndrome-like	1.1851	2.4969	0.5231
214300_s_at	topoisomerase (DNA) III alpha	1.1848	2.9998	2.5712
217444_at	MRNA; cDNA DKFZp564J1762 (from clone DKFZp564J1762)	1.1846	1.7183	1.1020
1554927_at	Hypothetical protein LOC646982	1.1844	2.4969	0.7320
237805_at	Hypothetical protein LOC284757	1.1840	2.4969	0.9296
222278_at	Transcribed locus, strongly similar to XP_374169.2 PREDICTED: hypothetical protein XP_37	1.1839	2.6723	2.0708
216906_at	suppression of tumorigenicity 14 (colon carcinoma)	1.1838	2.6723	1.8398
222596_s_at	leucine-rich repeat-containing G protein-coupled receptor 4	1.1833	2.4969	0.8512
239316_at	Chromosome 11 open reading frame 48	1.1833	2.4969	0.6389
237469_at	Topoisomerase (DNA) II alpha 170kDa	1.1829	2.4139	0.0000
228629_s_at	WW domain containing transcription regulator 1	1.1825	2.6723	2.0037
1566722_a_e	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.1822	2.0702	0.2224
36475_at	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	1.1821	2.4969	0.4666
220506_at	guanylate cyclase 1, soluble, beta 2	1.1820	2.4969	0.5143
244550_at	Transcription factor Dp-1	1.1816	2.0619	0.3777
207726_at	estrogen-related receptor beta	1.1814	2.4969	0.5396
228591_at	Trinucleotide repeat containing 6C	1.1812	2.9998	2.2784

1561530_at	Homo sapiens, clone IMAGE:5580856, mRNA	1.1809	2.4969	0.0788
204401_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member	1.1801	2.0702	0.0000
243083_at	hypothetical gene supported by BC040831 /// hypothetical gene supported by BC040831	1.1801	2.0702	0.0000
243621_at	sperm acrosome associated 3	1.1800	2.4969	1.3616
233623_at	Clone FLB3107	1.1796	2.0702	0.1756
203619_s_at	Fas apoptotic inhibitory molecule 2	1.1784	2.9998	2.5480
230989_s_at	testis-specific serine kinase 6	1.1783	2.4969	0.6775
235546_at	Serine peptidase inhibitor, Kunitz type 1	1.1774	2.2769	0.0000
210144_at	TBC1 domain family, member 22A	1.1774	2.0702	0.0000
244886_at	Hypothetical gene supported by AK124295	1.1773	2.4969	0.6300
205605_at	homeobox D9	1.1772	2.2769	0.0000
238269_at	F-box and leucine-rich repeat protein 7	1.1772	2.4969	1.6219
1560628_at	FLJ16124 protein	1.1772	2.0702	0.0000
214270_s_at	microtubule-associated protein, RP/EB family, member 3	1.1764	2.4969	0.4199
1569683_at	xylulokinase homolog (H. influenzae)	1.1762	1.7415	0.8694
232093_at	hypothetical protein LOC147650	1.1761	2.4969	1.0447
1566185_at	CDNA FLJ35138 fis, clone PLACE6009430	1.1756	2.6723	1.7304
1569523_a_7	SLC7A5 pseudogene	1.1754	2.4969	0.1516
217791_s_at	aldehyde dehydrogenase 18 family, member A1	1.1751	2.4969	0.3426
203930_s_at	microtubule-associated protein tau	1.1747	2.0702	0.0000
1555664_at	---	1.1746	2.4969	0.4660
1563945_at	hypothetical protein LOC284100	1.1746	2.0702	0.0000
239864_at	Hypothetical protein LOC92482	1.1736	2.4969	1.2577
221946_at	chromosome 9 open reading frame 116	1.1735	2.0702	0.0000
215709_at	---	1.1734	2.9998	2.3510
215393_s_at	COBL-like 1	1.1732	2.0702	0.2164
207261_at	cyclic nucleotide gated channel alpha 3	1.1730	1.7415	0.7669
53991_at	DENN/MADD domain containing 2A	1.1728	2.0702	0.0000
234458_at	Alanine (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal amin	1.1727	2.6723	1.6531
1557981_at	Ribosomal protein S9	1.1725	2.6723	1.7237
229879_at	Aspartate beta-hydroxylase	1.1724	2.4139	0.0398
212346_s_at	MAX dimerization protein 4	1.1723	2.6723	2.2049
211958_at	insulin-like growth factor binding protein 5	1.1715	2.4969	1.5894
231568_at	hypothetical protein LOC255313 /// similar to hypothetical protein LOC255313 /// similar to hy	1.1715	2.0702	0.0000
220688_s_at	chromosome 1 open reading frame 33	1.1711	2.6723	2.1810
205304_s_at	potassium inwardly-rectifying channel, subfamily J, member 8	1.1710	1.7183	1.5715
238093_at	Hypothetical gene supported by AK097565; BC033939	1.1709	2.4969	0.7602
219422_at	---	1.1709	2.6723	1.7757
234291_s_at	solute carrier family 6 (proline IMINO transporter), member 20	1.1709	2.4969	0.2656
235701_at	R3H domain containing 2	1.1709	2.4139	0.0000
1557335_at	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	1.1705	2.0702	0.0638
206866_at	cadherin 4, type 1, R-cadherin (retinal)	1.1698	2.0272	0.5608
1569872_a_7	Full-length cDNA clone CS0DF015YK23 of Fetal brain of Homo sapiens (human) /// Hypothes	1.1696	2.4139	0.0000
228784_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	1.1689	1.7415	0.6897
243893_at	potassium voltage-gated channel, Shaw-related subfamily, member 3	1.1687	2.4969	1.3111
206506_s_at	suppressor of Ty 3 homolog (S. cerevisiae)	1.1686	2.6723	1.6865
203592_s_at	follistatin-like 3 (secreted glycoprotein)	1.1685	2.4969	1.5453
237755_s_at	Ubiquitin specific peptidase 43	1.1683	1.7183	0.9069
232813_s_at	golgin-like protein /// golgi autoantigen, golgin subfamily a, 6 /// similar to Golgi autoantigen, g	1.1679	2.4969	0.5370
238083_at	poly (ADP-ribose) polymerase family, member 10	1.1679	2.2769	0.0000
239137_x_at	hypothetical protein MGC45491	1.1678	2.6723	2.1362
231662_at	Arginase, liver	1.1672	2.6723	1.9764
1562751_at	CDNA clone IMAGE:4826129	1.1671	2.9998	2.5023
231728_at	calcyphosine	1.1663	2.4139	0.0185
231122_x_at	zinc finger, DHHC-type containing 19	1.1657	2.9998	2.4666
206736_x_at	cholinergic receptor, nicotinic, alpha 4	1.1653	2.6723	1.7386
1558343_at	Full length insert cDNA clone YI54B09	1.1648	2.6723	1.9156
229651_at	seizure related 6 homolog (mouse)	1.1641	2.9998	2.5512
229755_x_at	Delta-like 3 (Drosophila)	1.1637	2.4969	0.1895
240753_at	Transcribed locus	1.1633	2.4139	0.0086

215244_at	DiGeorge syndrome critical region gene 5 (non-coding)	1.1631	2.6723	2.0033
234279_at	---	1.1630	2.0702	0.1706
1563318_s_at	PDZ domain containing, X chromosome	1.1625	2.4969	0.1889
209530_at	calcium channel, voltage-dependent, beta 3 subunit	1.1624	2.4969	0.2473
241872_at	SH3-domain GRB2-like (endophilin) interacting protein 1	1.1623	2.6723	2.1406
240202_x_at	phosphofructokinase, platelet	1.1617	2.6723	2.1128
207490_at	tubulin, alpha 4	1.1612	1.7415	0.6087
1570597_at	Transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	1.1608	2.4969	1.4903
213249_at	F-box and leucine-rich repeat protein 7	1.1605	1.7183	1.1210
1552436_a_at	cadherin-like 23	1.1605	2.4969	1.1068
211679_x_at	gamma-aminobutyric acid (GABA) B receptor, 2 /// gamma-aminobutyric acid (GABA) B receptor	1.1598	2.0702	0.0000
1554033_at	FERM domain containing 4A	1.1596	2.9998	2.5485
1570297_at	Homo sapiens, clone IMAGE:4183849, mRNA	1.1590	2.4969	0.5218
204337_at	regulator of G-protein signalling 4	1.1581	2.0702	0.0000
224329_s_at	cornifelin /// cornifelin	1.1578	2.2769	0.0000
222086_s_at	Wingless-type MMTV integration site family, member 6	1.1572	2.4139	0.0227
1558338_at	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	1.1571	2.6723	2.1456
40560_at	T-box 2	1.1568	2.2769	0.0000
214646_at	Histone 1, H3j	1.1566	2.0702	0.0592
243265_at	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	1.1565	2.4969	0.0597
232430_at	hypothetical protein LOC148696	1.1564	2.4969	1.2164
236787_at	CDNA FLJ35091 fis, clone PLACE6005786	1.1544	2.0702	0.0000
216366_x_at	---	1.1544	2.4969	1.1024
231444_at	---	1.1542	2.4969	0.3569
238080_at	beta-1,4-N-acetyl-galactosaminyl transferase 4	1.1541	2.4969	0.9839
216872_at	Hr44 antigen	1.1537	2.0702	0.0000
232046_at	KIAA1217	1.1536	2.6723	1.8303
240293_at	hypothetical protein LOC283152	1.1533	2.2769	0.0000
234878_at	zinc finger CCCH-type containing 12B	1.1532	2.4139	0.0000
1553843_at	chromosome 10 open reading frame 67	1.1531	2.0702	0.0000
229195_at	mesoderm posterior 1 homolog (mouse)	1.1526	2.6723	2.2400
232995_at	Platelet derived growth factor D	1.1522	2.4969	1.0390
222928_s_at	hypothetical protein FLJ11125	1.1514	2.0702	0.0000
243787_at	WW domain containing E3 ubiquitin protein ligase 2	1.1511	2.6723	2.1258
1553313_s_at	solute carrier family 5 (inositol transporters), member 3	1.1506	2.4969	0.6906
228148_at	zinc finger protein 584	1.1504	2.9998	2.2657
1559017_at	CDNA FLJ38915 fis, clone NT2NE2008867	1.1502	2.0702	0.0000
217075_x_at	---	1.1497	2.6723	2.0840
207150_at	solute carrier family 18 (vesicular acetylcholine), member 3	1.1496	2.4969	1.1321
233517_s_at	hypoxia inducible factor 3, alpha subunit	1.1495	2.9998	2.5625
1558950_at	Homo sapiens, clone IMAGE:4647355, mRNA	1.1493	2.4969	0.1539
1556806_at	Death-associated protein	1.1493	2.0702	0.0561
206825_at	oxytocin receptor	1.1492	2.0702	0.0000
222095_s_at	chromosome 1 open reading frame 76	1.1491	2.4969	0.8541
201718_s_at	erythrocyte membrane protein band 4.1-like 2	1.1490	2.2769	0.0000
224408_at	melanin-concentrating hormone receptor 2 /// melanin-concentrating hormone receptor 2	1.1488	2.4969	1.5685
1559136_s_at	FLJ44451 fis /// hypothetical protein LOC647841 /// hypothetical protein LOC648500	1.1487	2.6723	1.7854
1553131_a_at	GATA binding protein 4	1.1483	2.0619	0.3546
243622_at	hypothetical protein LOC145694	1.1474	2.6723	2.0279
1568804_at	Homo sapiens, clone IMAGE:6062029, mRNA	1.1473	2.4969	1.3319
230062_at	KIAA1666 protein /// similar to Peripheral-type benzodiazepine receptor-associated protein 1	1.1469	2.0702	0.1671
215413_at	exocyst complex component 7	1.1467	2.4969	1.5639
1553845_x_at	chromosome 10 open reading frame 67	1.1461	2.4969	0.6323
222944_s_at	PDZ domain containing, X chromosome	1.1460	2.9998	2.5632
219887_at	coiled-coil domain containing 87	1.1459	2.2769	0.0000
205444_at	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	1.1453	2.4969	1.5072
240699_at	SEC14-like 3 (S. cerevisiae)	1.1451	2.0702	0.0000
204756_at	mitogen-activated protein kinase kinase 5	1.1450	2.4969	0.3622
209991_x_at	gamma-aminobutyric acid (GABA) B receptor, 2	1.1448	2.6723	1.8238
217169_at	immunoglobulin heavy constant alpha 1 /// similar to Ig heavy chain V-III region VH26 precursor	1.1445	2.0702	0.0000

212868_x_at	chromosome 12 open reading frame 47	1.1444	2.4969	1.0399
239169_at	RAD52 motif 1	1.1441	2.0702	0.0000
1570568_at	---	1.1440	2.4969	1.5477
236371_s_at	Nuclear receptor coactivator 6 interacting protein	1.1438	2.4969	0.7912
220880_at	---	1.1435	2.4969	1.5189
231742_at	cone-rod homeobox	1.1432	2.0702	0.0000
233760_at	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	1.1430	2.4969	0.4665
1553424_at	chromosome 12 open reading frame 40	1.1429	2.6723	2.0205
1556621_a_7	Checkpoint with forkhead and ring finger domains	1.1427	2.4969	0.1766
1569436_at	hypothetical gene supported by BC025370	1.1423	2.4969	0.3042
205692_s_at	CD38 molecule	1.1422	2.4969	1.0869
217689_at	Protein tyrosine phosphatase, non-receptor type 1	1.1421	2.4969	0.7603
240945_at	---	1.1419	2.0702	0.0000
234893_s_at	similar to Dynein heavy chain at 16F	1.1417	2.4969	0.1828
237844_at	Hypothetical protein LOC644009	1.1416	2.2769	0.0000
237450_at	hypothetical LOC389332	1.1416	2.6723	2.0190
1559586_at	Methionine sulfoxide reductase A	1.1415	2.4969	0.6158
240917_at	---	1.1410	2.4969	1.1081
1569944_at	CDNA clone IMAGE:5311876	1.1406	2.6723	1.7194
236610_at	Phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	1.1404	2.0619	0.3001
215125_s_at	UDP glucuronosyltransferase 1 family, polypeptide A10 /// UDP glucuronosyltransferase 1 far	1.1403	2.4139	0.0000
234452_at	3-hydroxyisobutyrate dehydrogenase	1.1403	2.4969	1.0627
1562477_at	early B-cell factor 2	1.1403	2.0702	0.0000
1555470_a_7	protein phosphatase 1F (PP2C domain containing)	1.1403	2.4969	1.0911
223524_s_at	transmembrane protein 108	1.1395	2.9998	2.5729
223904_at	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	1.1394	2.4139	0.0000
236845_at	tripartite motif-containing 62 /// similar to tripartite motif-containing 62 /// similar to tripartite mc	1.1391	2.4969	0.3558
237220_at	Hypothetical protein FLJ23834	1.1385	2.9998	2.5584
239370_at	---	1.1383	2.4969	0.3107
49051_g_at	deltex 3 homolog (Drosophila)	1.1380	2.9998	2.3170
217447_at	myelin associated glycoprotein	1.1378	2.9998	2.4913
204416_x_at	apolipoprotein C-I	1.1374	2.4969	0.5187
216928_at	T-cell acute lymphocytic leukemia 1	1.1361	2.4969	1.4363
1569029_at	---	1.1359	2.4969	1.5080
220225_at	iroquois homeobox protein 4	1.1358	2.0702	0.0000
202601_s_at	HIV-1 Tat specific factor 1	1.1351	2.0702	0.0000
233987_at	transcription factor AP-2 delta (activating enhancer binding protein 2 delta)	1.1350	2.4969	1.1101
32029_at	3-phosphoinositide dependent protein kinase-1	1.1346	2.4969	0.3831
229275_at	eEF1A2 binding protein	1.1341	2.6723	1.8352
227892_at	CDNA clone IMAGE:5288757	1.1340	2.4969	0.6351
242935_at	SET binding factor 2	1.1337	2.4969	0.6360
207568_at	cholinergic receptor, nicotinic, alpha 6	1.1326	2.2769	0.0000
210602_s_at	cadherin 6, type 2, K-cadherin (fetal kidney)	1.1318	2.4969	0.6897
243458_at	Tumor necrosis factor, alpha-induced protein 8	1.1313	2.0702	0.0369
1553063_at	G protein-coupled receptor 78	1.1312	2.4969	0.5546
206386_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7	1.1303	2.9998	2.5438
233459_at	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	1.1299	2.4969	0.4475
240560_at	---	1.1298	2.6723	1.8411
1552280_at	T-cell immunoglobulin and mucin domain containing 4	1.1296	2.6723	2.1159
1563681_at	CDNA clone IMAGE:5265658	1.1293	2.4969	0.1727
243874_at	LIM domain containing preferred translocation partner in lipoma	1.1291	2.0702	0.0000
1562278_at	dynein, axonemal, heavy polypeptide 1	1.1289	2.6723	2.1548
1556024_at	Essential meiotic endonuclease 1 homolog 2 (S. pombe)	1.1281	2.4969	0.9462
1561658_at	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	1.1281	2.4969	1.0631
1562436_at	CysteinyI-tRNA synthetase	1.1259	2.4969	0.4084
215934_at	MRNA, Xq terminal portion	1.1254	2.4969	0.1888
1570008_at	Hypothetical LOC253724	1.1251	2.0702	0.0000
1561249_a_7	FKSG88	1.1248	2.4969	0.4210
206878_at	D-amino-acid oxidase	1.1246	2.4969	0.6994
1563398_at	Homo sapiens, clone IMAGE:4248696, mRNA	1.1237	2.4969	0.1782

1552750_at	calcium and integrin binding family member 3	1.1229	2.4139	0.0000
219428_s_at	peroxisomal membrane protein 4, 24kDa	1.1229	2.6723	1.7285
1564786_at	hypothetical protein LOC338667	1.1221	2.4969	0.1280
216426_at	similar to transcription elongation factor B (SIII), polypeptide 1 /// similar to transcription elong	1.1216	2.6723	1.7565
223683_at	zinc finger, MYND-type containing 15	1.1206	2.4969	1.5627
206281_at	adenylate cyclase activating polypeptide 1 (pituitary)	1.1200	2.4969	0.9599
229280_s_at	hypothetical locus LOC401237	1.1200	2.4969	1.4318
235405_at	glutathione S-transferase A4	1.1200	2.0702	0.0000
233096_at	KIAA1109	1.1195	2.4969	0.8732
244036_at	Amiloride binding protein 1 (amine oxidase (copper-containing))	1.1193	2.4969	1.3159
1557312_at	chromosome 12 open reading frame 61	1.1191	2.6723	1.7913
232379_at	SKI-like	1.1189	2.4969	1.3065
209506_s_at	nuclear receptor subfamily 2, group F, member 1	1.1188	2.6723	2.0124
235153_at	ring finger protein 183	1.1186	2.6723	2.1615
210930_s_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived onco	1.1184	2.4969	0.7086
240194_at	hypothetical locus LOC441204	1.1183	2.4969	0.1280
1563108_at	KIAA1904 protein	1.1182	2.4969	0.1976
231801_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1.1178	2.4969	0.0899
206268_at	left-right determination factor 1	1.1177	2.9998	2.5181
201655_s_at	heparan sulfate proteoglycan 2 (perlecan)	1.1173	2.4969	0.1770
210939_s_at	glutamate receptor, metabotropic 1	1.1171	2.2769	0.0000
220182_at	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	1.1168	2.4969	0.5299
239898_x_at	zinc finger protein 286 /// similar to zinc finger protein 286	1.1168	2.9998	2.3231
1560137_at	Muscleblind-like 2 (Drosophila)	1.1167	2.6723	1.9486
231445_at	Transcribed locus, strongly similar to XP_530274.1 PREDICTED: hypothetical protein XP_53	1.1164	2.6723	2.0267
221451_s_at	olfactory receptor, family 2, subfamily W, member 1 /// olfactory receptor, family 2, subfamily 1	1.1151	2.4969	1.5267
1557483_at	hypothetical protein LOC284788	1.1145	2.4969	1.4209
235495_at	coiled-coil domain containing 97	1.1136	2.6723	1.9479
1560954_at	CDNA clone IMAGE:5295357	1.1131	2.6723	1.8474
240208_at	Transcribed locus	1.1127	2.0702	0.1636
244483_at	---	1.1119	2.9998	2.5460
208793_x_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, me	1.1116	2.0702	0.0000
241549_at	Anthrax toxin receptor 1	1.1113	2.4969	0.9794
1556924_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 10	1.1109	2.4969	0.6866
205578_at	receptor tyrosine kinase-like orphan receptor 2	1.1108	2.4969	0.9449
1562892_at	Coiled-coil-helix-coiled-coil-helix domain containing 5	1.1105	2.2769	0.0000
36566_at	cystinosis, nephropathic	1.1102	2.9998	2.5405
1559578_at	Coatomer protein complex, subunit zeta 2	1.1092	2.9998	2.4650
230037_at	CD8b molecule	1.1084	2.0702	0.0000
231334_at	Mitogen-activated protein kinase 8 interacting protein 3	1.1081	2.4969	0.3293
206549_at	insulin-like 4 (placenta)	1.1078	2.6723	1.7144
227628_at	similar to RIKEN cDNA 2310016C16	1.1076	2.4969	1.6189
210533_at	mutS homolog 4 (E. coli)	1.1076	2.4139	0.0000
216868_s_at	---	1.1071	2.2769	0.0000
244223_at	Paired box gene 5 (B-cell lineage specific activator)	1.1070	2.4969	0.3909
243047_at	hypothetical protein FLJ10404	1.1061	2.4969	0.9632
1559270_at	zinc finger homeodomain 4	1.1053	2.4969	1.1785
235492_at	IBR domain containing 1	1.1050	2.4969	0.9102
210599_at	zinc finger protein 614	1.0998	2.0702	0.0000
1559605_a_s	hypothetical protein LOC285043	1.0985	2.4969	1.2124
231195_at	FLJ44186 protein	1.0981	2.4969	1.1946
243821_at	mitochondrial ribosomal protein S31	1.0973	2.9998	2.4385
224535_s_at	mitochondrial ribosomal protein 63 /// mitochondrial ribosomal protein 63	1.0937	2.4969	1.6210
235284_s_at	LOC440570	1.0918	2.4139	0.0000
202035_s_at	secreted frizzled-related protein 1	1.0904	2.6723	2.0168
211181_x_at	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	1.0898	2.4969	1.1648
1564443_at	deleted in lymphocytic leukemia, 2 /// ret finger protein 2 opposite strand	1.0886	2.6723	1.8611
1553413_at	---	1.0879	2.6723	2.2031
226944_at	HtrA serine peptidase 3	1.0837	2.4969	0.5081
239638_at	CDNA FLJ33227 fis. clone ASTRO2001088	1.0833	2.6723	2.1090

Gene ID	Gene Name	Fold Change	q-value(%)	localfdr(%)
225768_at	nuclear receptor subfamily 1, group D, member 2	0.4998	3.2218	3.9635
235385_at	CDNA FLJ34016 fis, clone FCBBF2002541	0.5053	3.2218	5.7045
226444_at	Solute carrier family 39 (zinc transporter), member 10	0.5059	0.0000	5.8212
228652_at	hypothetical protein FLJ38288	0.5107	3.2218	5.4798
227095_at	Leptin receptor	0.5111	3.2218	3.9209
229787_s_at	Transcribed locus	0.5235	0.0000	5.8302
212229_s_at	F-box protein 21	0.5247	3.2218	4.6083
214974_x_at	chemokine (C-X-C motif) ligand 5	0.5274	3.2218	3.9199
208852_s_at	calnexin	0.5307	3.2218	4.7800
200698_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	0.5504	3.2218	3.9991
232681_at	CDNA: FLJ23242 fis, clone COL01514	0.5643	3.2218	4.1618
233080_s_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	0.5656	3.2218	3.9386
228722_at	protein arginine methyltransferase 2	0.5690	3.2218	4.1592
212508_at	modulator of apoptosis 1	0.5788	3.2218	5.7550
222789_at	round spermatid basic protein 1	0.5823	3.2218	5.0612
227527_at	myeloid/lymphoid or mixed-lineage leukemia 2	0.5856	3.2218	4.5406
224820_at	family with sequence similarity 36, member A	0.5989	3.2218	5.5737
202731_at	programmed cell death 4 (neoplastic transformation inhibitor)	0.6004	3.2218	3.9304
235067_at	muskelin 1, intracellular mediator containing kelch motifs	0.6006	0.0000	5.6044
201661_s_at	acyl-CoA synthetase long-chain family member 3	0.6069	3.2218	5.1122
221014_s_at	RAB33B, member RAS oncogene family /// RAB33B, member RAS oncogene family	0.6099	0.0000	5.6227
236155_at	Zinc finger, CCHC domain containing 6	0.6272	3.2218	4.2918
217526_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	0.6350	3.2218	4.1351
213064_at	zinc finger CCCH-type containing 14	0.6370	3.2218	3.9389
219974_x_at	enoyl Coenzyme A hydratase domain containing 1	0.6479	3.2218	4.0000
202550_s_at	VAMP (vesicle-associated membrane protein)-associated protein B and C	0.6493	3.2218	5.4082
227088_at	phosphodiesterase 5A, cGMP-specific	0.6530	3.2218	3.9473
225594_at	HCF-binding transcription factor Zhangfei	0.6592	0.0000	5.7960
225181_at	AT rich interactive domain 1B (SWI1-like)	0.6679	3.2218	3.9487
202193_at	LIM domain kinase 2	0.7048	3.2218	4.3754
202647_s_at	neuroblastoma RAS viral (v-ras) oncogene homolog	0.7086	3.2218	4.4034
222714_s_at	lactamase, beta 2	0.7111	3.2218	4.2264
223441_at	solute carrier family 17 (anion/sugar transporter), member 5	0.7147	3.2218	3.9300
239376_at	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	0.7159	3.2218	5.7355
212209_at	thyroid hormone receptor associated protein 2	0.7204	3.2218	4.4263
223952_x_at	dehydrogenase/reductase (SDR family) member 9	0.7226	3.2218	5.2490
202319_at	SUMO1/sentrin specific peptidase 6	0.7245	3.2218	5.5299
202422_s_at	acyl-CoA synthetase long-chain family member 4	0.7247	3.2218	5.1553
228081_at	Cyclin G2	0.7318	3.2218	4.8529
210425_x_at	golgi autoantigen, golgin subfamily a, 8B	0.7327	3.2218	4.0930
213459_at	ribosomal protein L37a	0.7392	3.2218	5.3721
218166_s_at	remodeling and spacing factor 1	0.7482	3.2218	3.9829
212781_at	retinoblastoma binding protein 6	0.7512	3.2218	4.2806
228996_at	ring finger and CCCH-type zinc finger domains 1	0.7533	3.2218	3.9563
213557_at	Cdc2-related kinase, arginine/serine-rich	0.7566	3.2218	4.6417
226826_at	CDNA FLJ30735 fis, clone FEBRA2000228	0.7618	3.2218	4.3284
1555785_a_a	5'-3' exoribonuclease 1	0.7640	3.2218	5.0260
203225_s_at	riboflavin kinase	0.7659	3.2218	4.1029
222815_at	ring finger protein 12	0.7719	3.2218	4.3846
213292_s_at	sorting nexin 13	0.7719	3.2218	4.9093
221860_at	heterogeneous nuclear ribonucleoprotein L	0.7727	3.2218	4.7879
238064_at	Centrosomal protein 63kDa	0.7739	3.2218	4.4388
229359_at	Transcribed locus	0.7744	3.2218	5.8016
227144_at	chromosome 22 open reading frame 9	0.7880	3.2218	4.0366
238963_at	MRNA full length insert cDNA clone EUROIMAGE 1652049	0.7974	3.2218	4.0259
204627_s_at	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.7994	3.2218	4.0111
225457_s_at	hypothetical LOC25845	0.7995	3.2218	5.4373

225765_at	Transportin 1	0.8062	3.2218	4.5877
232130_at	Sorting nexin 12	0.8212	3.2218	4.6060
227696_at	Exosome component 6	0.8311	0.0000	5.8413
223681_s_at	InaD-like (Drosophila)	0.8453	3.2218	4.0056
238965_at	Chromosome 21 open reading frame 2	0.8690	3.2218	4.1401
230056_at	fetal Alzheimer antigen	0.8784	3.2218	3.9700