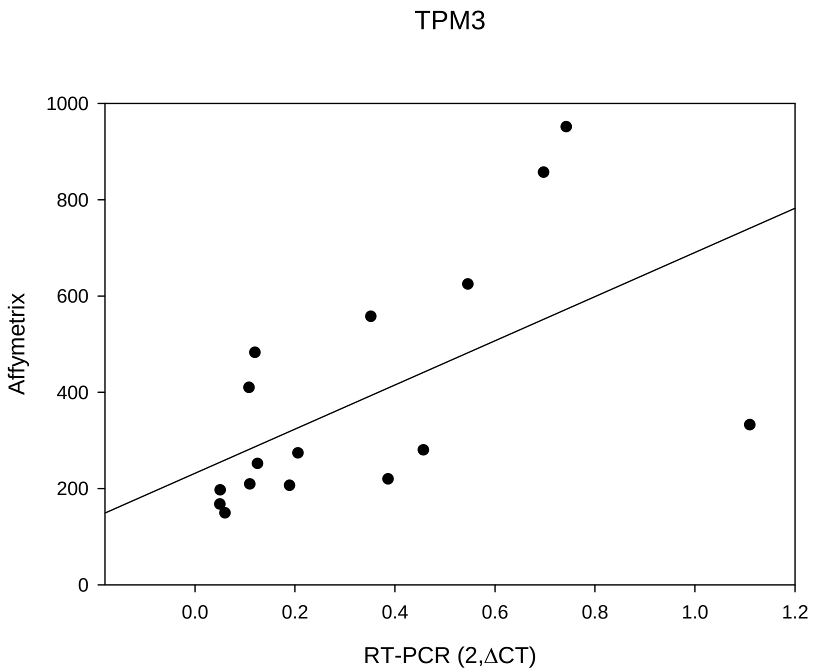
SUPPLEMENTAL MATERIAL

Supplemental Figure 1. Validation of selected genes by quantitative real-time PCR.

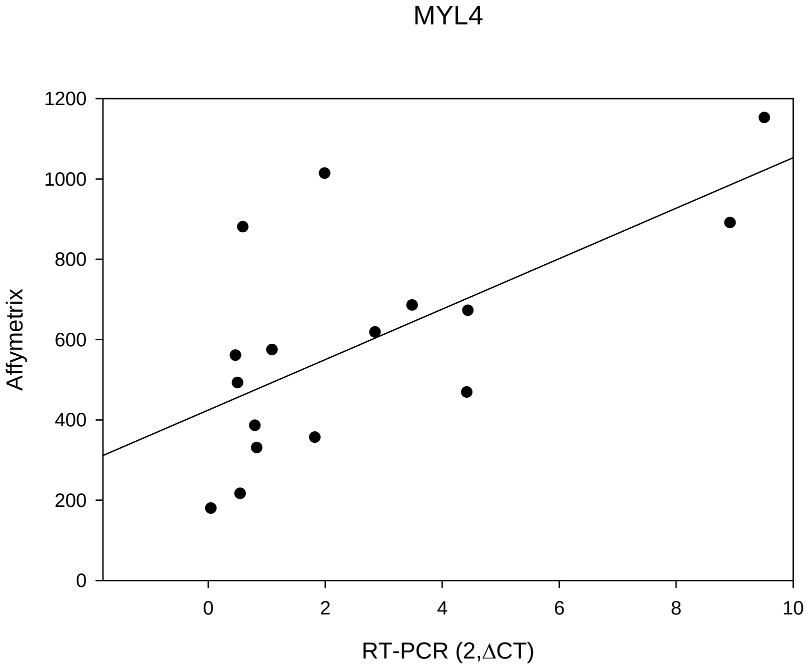
Figure x shows correlation of relative gene expression measured by Affymetrix and RT-PCR for 4 candidate genes in 16 selected samples. Affymetrix values as expressed as units and RT-PCR values were calculated as $\log_2$ of ΔCt_{gene} ($\Delta Ct_{gene}=Ct_{gene}- Ct_{HPRT}$). **xA**: Tropomyosin 3 (TPM3), **xB**: Myosin light chain 4 (MYL4), **xC**: Nitric oxide synthase 1 (NOS1) and **xD**: Phosphorylase kinase beta (PHKB). **r:** Spearman rank correlation coefficient, $P<0.05$.

A



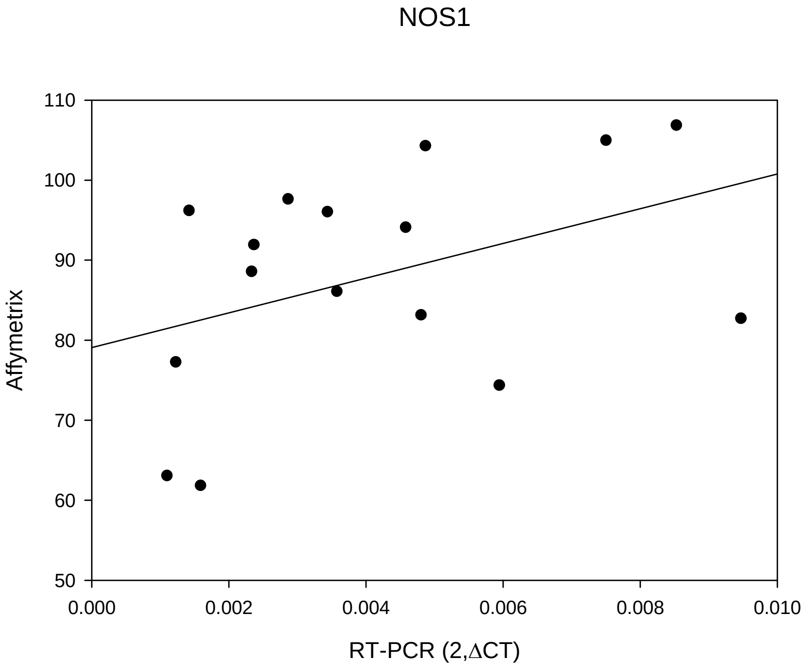
r=0.721, P=0.001

B



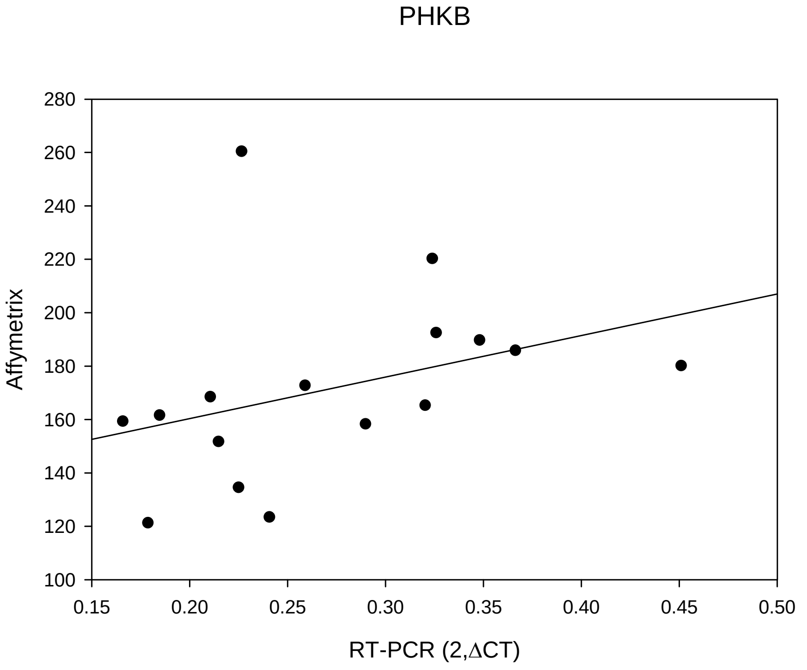
r=0.635, P=0.008

C



r=0.391, P=0.130

D



r=0.597, P=0.014

Supplemental Table 1. Differentially expressed genes for the all male versus female at the FDR adjusted P value significance level set at $P < 0.05$. Expression levels (Av Exp Female, Av Exp Male) are RMA normalized, fold changes (abs FC) are absolute fold changes and P values are FDR adjusted using the Benjamini and Hochberg method.

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
201909_at	RPS4Y1	ribosomal protein S4, Y-linked 1	6192	Hs.282376	88.82	1065.95	144.04	1.36E-71
204409_s_at	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	9086	Hs.461178	12.51	210.22	282.41	2.03E-63
221728_x_at	XIST	X (inactive)-specific transcript	7503	Hs.529901	275.35	37.23	-54.71	6.05E-62
206700_s_at	JARID1D	jumonji, AT rich interactive domain 1D	8284	Hs.80358	68.10	175.69	6.66	6.21E-33
205000_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	8653	Hs.99120	18.34	79.95	19.00	1.09E-32
207063_at	CYorf14	chromosome Y open reading frame 14	55410	Hs.138453	47.30	87.48	3.42	7.56E-27
206624_at	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	8287	Hs.655309	17.05	35.70	4.38	8.89E-17
201029_s_at	CD99	CD99 molecule	4267	Hs.654354	1233.25	1656.04	1.80	6.87E-10
214131_at	CYorf15B	chromosome Y open reading frame 15B	84663	Hs.592254	19.65	23.88	1.48	3.15E-06
207608_x_at	CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	1544	Hs.1361	125.00	100.67	-1.54	1.05E-05
216877_at	DKFZp686O1327	hypothetical gene supported by BC043549; BX648102	401014	Hs.42192	34.92	29.16	-1.43	2.88E-05
219812_at	PVRIG	poliovirus receptor related immunoglobulin domain containing	79037	Hs.521075	107.95	87.57	-1.52	1.13E-04
200933_x_at	RPS4X	ribosomal protein S4, X-linked	6191	Hs.446628	3735.94	3258.38	-1.31	1.38E-04
216342_x_at	LOC390183	similar to 40S ribosomal protein S4, X isoform	390183	Hs.647251	1910.83	1589.74	-1.44	2.20E-04
203461_at	CHD2	chromodomain helicase DNA binding protein 2	1106	Hs.220864	91.80	80.58	-1.30	2.20E-04
208314_at	RRH	retinal pigment epithelium-derived rhodopsin homolog	10692	Hs.658310	49.96	42.15	-1.40	2.61E-04
206281_at	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	116	Hs.592343	47.98	41.60	-1.33	3.54E-04

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
203043_at	ZBED1	zinc finger, BED-type containing 1	9189	Hs.131452	337.70	407.99	1.46	5.23E-04
221137_at			29016		20.83	18.19	-1.31	5.68E-04
210648_x_at	SNX3	sorting nexin 3	8724	Hs.12102	1498.26	1792.50	1.43	5.68E-04
213456_at	SOSTDC1	sclerostin domain containing 1	25928	Hs.648106	28.40	24.53	-1.34	6.06E-04
211224_s_at	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	8647	Hs.658439	33.36	29.86	-1.25	6.30E-04
205879_x_at	RET	ret proto-oncogene	5979	Hs.350321	134.41	112.55	-1.43	9.22E-04
220269_at	FLJ23049	hypothetical protein FLJ23049	79740	Hs.478143	16.79	15.03	-1.25	9.88E-04
203992_s_at	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	7403	Hs.522616	63.28	50.78	-1.55	1.12E-03
207969_x_at	ACRV1	acrosomal vesicle protein 1	56	Hs.169222, Hs.596575	68.46	57.07	-1.44	1.12E-03
220295_x_at	DEPDC1	DEP domain containing 1	55635	Hs.445098	36.78	30.61	-1.44	1.12E-03
216785_at	FKBP1B	FK506 binding protein 1B, 12.6 kDa	2281	Hs.407482	63.21	54.59	-1.34	1.13E-03
220440_at	LGALS13	lectin, galactoside-binding, soluble, 13 (galectin 13)	29124	Hs.23671	32.41	28.27	-1.31	1.13E-03
222053_at			55310		52.67	45.50	-1.34	1.13E-03
204393_s_at	ACPP	acid phosphatase, prostate	55	Hs.433060	20.48	18.28	-1.26	1.13E-03
205671_s_at	HLA-DOB	major histocompatibility complex, class II, DO beta	3112	Hs.1802	42.78	35.20	-1.48	1.14E-03
220040_x_at	KIAA1166	KIAA1166	55906	Hs.28249	120.64	105.47	-1.31	1.15E-03
211364_at	MTAP	methylthioadenosine phosphorylase	4507	Hs.193268	85.14	72.77	-1.37	1.16E-03
220355_s_at	PBRM1	polybromo 1	55193	Hs.189920	141.53	172.71	1.49	1.24E-03
201022_s_at	DSTN	destrin (actin depolymerizing factor)	11034	Hs.304192, Hs.667348	1909.72	2259.38	1.40	1.24E-03
205710_at	LRP2	low density lipoprotein-related protein 2	4036	Hs.470538	47.78	42.57	-1.26	1.24E-03
221258_s_at	KIF18A	kinesin family member 18A	81930	Hs.301052	13.07	12.12	-1.16	1.25E-03
207874_s_at	CFHR4	complement factor H-related 4	10877	Hs.575869	28.39	24.70	-1.32	1.30E-03
216437_at	EPC1	enhancer of polycomb homolog 1 (Drosophila)	80314	Hs.167805, Hs.633485, Hs.654404, Hs.654496	34.33	29.42	-1.36	1.33E-03
217569_x_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	817	Hs.144114	51.13	40.84	-1.57	1.33E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
222121_at	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	26084	Hs.570682	15.13	13.87	-1.19	1.33E-03
220436_at	CNTNAP3	contactin associated protein-like 3	79937	Hs.521495, Hs.604441, Hs.658328	18.21	16.62	-1.20	1.35E-03
221393_at	TAAR3	trace amine associated receptor 3	9288	Hs.679662	35.76	30.74	-1.35	1.46E-03
221685_s_at	CCDC99	coiled-coil domain containing 99	54908	Hs.368710	54.53	48.95	-1.24	1.46E-03
209521_s_at	AMOT	angiomotin	154796	Hs.528051	50.89	45.14	-1.27	1.46E-03
219610_at	RGNEF	Rho-guanine nucleotide exchange factor	64283	Hs.482521	112.41	99.05	-1.29	1.46E-03
220874_at			55441		38.45	32.25	-1.42	1.48E-03
215847_at	LOC283755	hypothetical protein LOC283755	283755	Hs.655732	27.53	23.55	-1.37	1.48E-03
206581_at	BNC1	basonuclin 1	646	Hs.459153	40.21	36.04	-1.25	1.48E-03
220523_at			79880		18.80	16.03	-1.37	1.51E-03
220251_at			80064		87.03	74.19	-1.38	1.52E-03
220025_at	TBR1	T-box, brain, 1	10716	Hs.210862	27.03	23.83	-1.29	1.52E-03
221431_s_at	OR12D3	olfactory receptor, family 12, subfamily D, member 3	81797	Hs.272280	72.12	60.95	-1.40	1.55E-03
203398_s_at	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	2591	Hs.170986	25.29	22.95	-1.21	1.55E-03
220540_at	KCNK15	potassium channel, subfamily K, member 15	60598	Hs.528664	16.19	14.80	-1.20	1.58E-03
220944_at	PGLYRP4	peptidoglycan recognition protein 4	57115	Hs.58356	154.30	131.19	-1.38	1.58E-03
200976_s_at	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	8887	Hs.34576	598.16	770.81	1.66	1.58E-03
207298_at	SLC17A3	solute carrier family 17 (sodium phosphate), member 3	10786	Hs.327179	57.37	49.10	-1.37	1.58E-03
214825_at	LOC728215	similar to transmembrane protein 28	728215	Hs.593580, Hs.653511	47.64	40.63	-1.37	1.58E-03
207902_at	IL5RA	interleukin 5 receptor, alpha	3568	Hs.68876	75.18	66.49	-1.28	1.61E-03
220785_at	UTS2	urotensin 2	10911	Hs.162200	21.46	18.82	-1.30	1.66E-03
215856_at	SIGLEC15	sialic acid binding Ig-like lectin 15	284266	Hs.287692	54.67	46.01	-1.41	1.71E-03
211050_x_at	LOC643313	similar to hypothetical protein LOC284701	643313	Hs.676949	63.12	53.31	-1.40	1.71E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
210409_at	C6orf124	chromosome 6 open reading frame 124	653483	Hs.520556, Hs.667982	41.41	35.46	-1.36	1.81E-03
221467_at	MC4R	melanocortin 4 receptor	4160	Hs.532833	44.73	39.79	-1.26	1.81E-03
215182_x_at	LOC730096	hypothetical protein LOC730096	730096	Hs.572908	189.37	155.32	-1.49	1.91E-03
221932_s_at	GLRX5	glutaredoxin 5	51218	Hs.532683	960.13	1108.02	1.33	1.91E-03
204300_at	PET112L	PET112-like (yeast)	5188	Hs.119316	123.26	154.10	1.56	1.91E-03
220423_at	PLA2G2D	phospholipase A2, group IID	26279	Hs.189507	212.20	177.79	-1.42	1.92E-03
207596_at			55385		13.38	12.30	-1.18	1.93E-03
203974_at	HDHD1A	haloacid dehalogenase-like hydrolase domain containing 1A	8226	Hs.185910	170.43	139.88	-1.48	1.99E-03
219521_at	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	27087	Hs.381050	82.90	71.25	-1.35	1.99E-03
216622_at	LAMB4	laminin, beta 4	22798	Hs.62022	34.49	31.19	-1.22	1.99E-03
220972_s_at	KRTAP9-9	keratin associated protein 9-9	81870	Hs.307010	14.09	12.74	-1.22	1.99E-03
221144_at			55369		18.78	16.75	-1.26	1.99E-03
215019_x_at	ZNF528	zinc finger protein 528	84436	Hs.662043	37.16	33.03	-1.27	1.99E-03
202554_s_at	GSTM3	glutathione S-transferase M3 (brain)	2947	Hs.2006	486.34	662.11	1.85	1.99E-03
209567_at	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	23212	Hs.71827	109.20	127.47	1.36	1.99E-03
206984_s_at	RIT2	Ras-like without CAAX 2	6014	Hs.464985	18.15	16.45	-1.22	1.99E-03
221304_at	UGT1A8	UDP glucuronosyltransferase 1 family, polypeptide A8	54576	Hs.654499	22.33	19.70	-1.29	2.29E-03
204637_at	CGA	glycoprotein hormones, alpha polypeptide	1081	Hs.119689	71.51	59.28	-1.45	2.29E-03
216522_at	OR2B6	olfactory receptor, family 2, subfamily B, member 6	26212	Hs.532145	17.79	16.09	-1.22	2.29E-03
207455_at	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	5028	Hs.654526	18.42	16.76	-1.21	2.32E-03
204082_at	PBX3	pre-B-cell leukemia homeobox 3	5090	Hs.428027	265.76	332.93	1.57	2.49E-03
213828_x_at	H3F3A	H3 histone, family 3A	3020	Hs.533624, Hs.546259	2120.39	2454.04	1.34	2.55E-03
213544_at	ING2	inhibitor of growth family, member 2	3622	Hs.107153	33.19	28.13	-1.39	2.60E-03
208174_x_at	ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	8233	Hs.171909	156.18	135.71	-1.32	2.60E-03
210750_s_at	DLGAP1	discs, large	9229	Hs.654793	72.95	65.04	-1.26	2.60E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(Drosophila) homolog-associated protein 1						
218364_at	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	9209	Hs.475319	185.81	227.55	1.50	2.65E-03
215430_at	GK2	glycerol kinase 2	2712	Hs.98008	30.87	26.51	-1.36	2.77E-03
202678_at	GTF2A2	general transcription factor IIA, 2, 12kDa	2958	Hs.512934	419.86	520.58	1.54	2.77E-03
206513_at	AIM2	absent in melanoma 2	9447	Hs.281898	62.35	52.00	-1.44	2.77E-03
219855_at	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	55190	Hs.200016	131.81	117.54	-1.26	2.77E-03
218123_at	C21orf59	chromosome 21 open reading frame 59	56683	Hs.5811	105.61	126.80	1.44	2.77E-03
201423_s_at	CUL4A	cullin 4A	8451	Hs.339735	264.97	325.10	1.51	2.95E-03
217551_at	LOC441453	similar to olfactory receptor, family 7, subfamily A, member 17	441453	Hs.523504	22.81	19.98	-1.30	2.95E-03
202738_s_at	PHKB	phosphorylase kinase, beta	5257	Hs.78060	143.91	181.02	1.58	2.95E-03
201520_s_at	GRSF1	G-rich RNA sequence binding factor 1	2926	Hs.309763, Hs.634071	368.65	460.56	1.56	2.95E-03
220853_at			29036		70.39	59.35	-1.41	2.95E-03
207951_at	CSN2	casein beta	1447	Hs.2242	39.93	34.95	-1.31	2.95E-03
218773_s_at	MSRB2	methionine sulfoxide reductase B2	22921	Hs.461420	1190.14	1403.61	1.39	2.95E-03
218373_at	AKTIP	AKT interacting protein	64400	Hs.380897	199.24	238.90	1.44	2.98E-03
213909_at	LRRC15	leucine rich repeat containing 15	131578	Hs.288467	88.87	75.66	-1.38	2.98E-03
220717_at	ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif, 20	80070	Hs.287554	13.14	12.12	-1.17	3.03E-03
220049_s_at	PDCD1LG2	programmed cell death 1 ligand 2	80380	Hs.532279	31.59	28.54	-1.23	3.06E-03
207537_at	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	5207	Hs.444304	134.78	113.51	-1.41	3.12E-03
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)	7292	Hs.181097	56.94	50.99	-1.25	3.12E-03
207441_at	SMR3B	submaxillary gland androgen regulated protein 3 homolog B (mouse)	10879	Hs.650650	33.98	29.66	-1.31	3.12E-03
217215_s_at			11134		35.24	30.29	-1.35	3.12E-03
205456_at	CD3E	CD3e molecule, epsilon	916	Hs.3003	169.33	142.39	-1.41	3.12E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(CD3-TCR complex)						
220624_s_at	ELF5	E74-like factor 5 (ets domain transcription factor)	2001	Hs.11713	36.94	32.69	-1.28	3.16E-03
218118_s_at	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	10431	Hs.524308, Hs.661964	128.84	150.47	1.36	3.16E-03
205725_at	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobin)	7356	Hs.523732	36.61	32.45	-1.27	3.17E-03
204624_at	ATP7B	ATPase, Cu++ transporting, beta polypeptide	540	Hs.492280	58.39	52.19	-1.25	3.17E-03
208165_s_at	PRSS16	protease, serine, 16 (thymus)	10279	Hs.274407	27.87	24.34	-1.31	3.19E-03
201632_at	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	1967	Hs.78592	177.74	205.37	1.34	3.20E-03
220232_at	SCD5	stearoyl-CoA desaturase 5	79966	Hs.379191	180.34	126.10	-2.05	3.21E-03
207505_at	PRKG2	protein kinase, cGMP-dependent, type II	5593	Hs.570833	102.30	90.57	-1.28	3.37E-03
215334_at	KIAA0953	KIAA0953	22979	Hs.654648	98.12	86.50	-1.29	3.37E-03
210394_x_at	SSX4	synovial sarcoma, X breakpoint 4	6759	Hs.558402	32.46	28.44	-1.30	3.37E-03
208237_x_at	ADAM22	ADAM metallopeptidase domain 22	53616	Hs.592282	128.78	114.45	-1.27	3.37E-03
220653_at	ZIM2	zinc finger, imprinted 2	23619	Hs.201776	108.54	94.42	-1.32	3.37E-03
210325_at	CD1A	CD1a molecule	909	Hs.1309	116.37	97.70	-1.42	3.37E-03
221173_at			80102		42.03	35.32	-1.42	3.37E-03
210356_x_at	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	931	Hs.438040	40.88	32.28	-1.60	3.45E-03
205636_at	SH3GL3	SH3-domain GRB2-like 3	6457	Hs.270055, Hs.666365	126.28	111.57	-1.28	3.45E-03
211238_at	ADAM7	ADAM metallopeptidase domain 7	8756	Hs.668805	29.53	26.47	-1.24	3.45E-03
203259_s_at	HDDC2	HD domain containing 2	51020	Hs.32826	302.16	383.73	1.61	3.50E-03
207938_at	PI15	peptidase inhibitor 15	51050	Hs.98558	29.15	25.70	-1.29	3.50E-03
220814_at	SLC30A6	solute carrier family 30 (zinc transporter), member 6	55676	Hs.23248	25.36	22.83	-1.23	3.50E-03
206828_at	TXK	TXK tyrosine kinase	7294	Hs.479669	17.42	15.78	-1.22	3.50E-03
219511_s_at	SNCAIP	synuclein, alpha interacting protein (synphilin)	9627	Hs.426463	55.54	49.63	-1.25	3.50E-03
202732_at	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	11142	Hs.651213	614.12	751.40	1.50	3.50E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
217882_at	TMEM111	transmembrane protein 111	55831	Hs.475392	360.98	432.45	1.44	3.50E-03
200761_s_at	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	10550	Hs.518060, Hs.694039	669.09	800.33	1.43	3.68E-03
220428_at	CD207	CD207 molecule, langerin	50489	Hs.199731	38.11	33.57	-1.29	3.71E-03
206525_at	GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1	2569	Hs.437745	20.93	18.65	-1.26	3.71E-03
210595_at	ZNF235	zinc finger protein 235	9310	Hs.298089, Hs.664229	42.97	38.37	-1.25	3.71E-03
216535_at	CADM3	cell adhesion molecule 3	57863	Hs.365689	165.73	139.27	-1.42	3.77E-03
205358_at	GRIA2	glutamate receptor, ionotropic, AMPA 2	2891	Hs.32763	17.41	15.74	-1.22	3.77E-03
222167_at	PVRL3	poliovirus receptor-related 3	25945	Hs.293917	44.00	37.99	-1.34	3.77E-03
221134_at	ANGPT4	angiopoietin 4	51378	Hs.278973	59.61	52.85	-1.27	3.86E-03
206310_at	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	6691	Hs.98243	59.07	50.88	-1.35	3.86E-03
203264_s_at	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	23229	Hs.54697	146.00	179.99	1.52	3.88E-03
220873_at			55428		58.49	48.88	-1.43	3.88E-03
220283_at	KIAA1822L	KIAA1822-like	79802	Hs.665660	53.32	46.47	-1.32	3.95E-03
221859_at	SYT13	synaptotagmin XIII	57586	Hs.436643	76.96	65.83	-1.37	4.04E-03
215970_at	ZP4	zona pellucida glycoprotein 4	57829	Hs.136241	22.02	19.54	-1.27	4.04E-03
206438_x_at	TCTN2	tectonic family member 2	79867	Hs.167165	255.20	216.84	-1.39	4.23E-03
220459_at			55155		17.22	15.49	-1.24	4.26E-03
202432_at	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	5532	Hs.500067	349.41	422.82	1.46	4.26E-03
209771_x_at	CD24	CD24 molecule	934	Hs.644105, Hs.694721	32.40	41.01	1.60	4.33E-03
219551_at	EAF2	ELL associated factor 2	55840	Hs.477325	32.29	28.93	-1.25	4.40E-03
207261_at	CNGA3	cyclic nucleotide gated channel alpha 3	1261	Hs.234785	20.03	17.67	-1.29	4.47E-03
216341_s_at	GNRHR	gonadotropin-releasing hormone receptor	2798	Hs.407587	51.42	43.82	-1.38	4.52E-03
206732_at	SLITRK3	SLIT and NTRK-like family, member 3	22865	Hs.101745	23.24	20.85	-1.24	4.54E-03
208376_at	CCR4	chemokine (C-C motif) receptor 4	1233	Hs.184926	74.93	64.24	-1.36	4.84E-03
207801_s_at	RNF10	ring finger protein 10	9921	Hs.442798	417.67	488.08	1.37	4.87E-03
205480_s_at	UGP2	UDP-glucose	7360	Hs.516217	1159.67	1416.26	1.49	4.89E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		pyrophosphorylase 2						
207068_at	ZFP37	zinc finger protein 37 homolog (mouse)	7539	Hs.150406	29.03	26.58	-1.19	4.91E-03
219859_at	CLEC4E	C-type lectin domain family 4, member E	26253	Hs.236516	35.12	30.67	-1.31	4.91E-03
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	1466	Hs.530904	96.49	121.39	1.58	5.00E-03
204405_x_at	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	27292	Hs.533222	171.66	211.57	1.52	5.08E-03
65517_at	AP1M2	adaptor-related protein complex 1, mu 2 subunit	10053	Hs.18894	156.80	137.91	-1.29	5.08E-03
208172_s_at	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2	9312	Hs.661102	79.33	68.83	-1.33	5.08E-03
203949_at	MPO	myeloperoxidase	4353	Hs.458272	38.19	33.70	-1.28	5.08E-03
206704_at	CLCN5	chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease)	1184	Hs.166486	21.98	19.85	-1.23	5.10E-03
211497_x_at	NKX3-1	NK3 homeobox 1	4824	Hs.55999	119.04	103.62	-1.32	5.15E-03
215057_at	FLJ44451	hypothetical protein FLJ44451	100101122	Hs.496916, Hs.690082	55.03	48.46	-1.29	5.16E-03
221546_at	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	8559	Hs.161181	111.95	97.50	-1.32	5.32E-03
220857_at			29050		30.51	27.36	-1.24	5.32E-03
206319_s_at	SPINLW1	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	57119	Hs.121084	31.59	26.80	-1.39	5.32E-03
213363_at	CA5BL	carbonic anhydrase VB-like	340591	Hs.532326	119.65	106.65	-1.26	5.33E-03
205226_at	PDGFRL	platelet-derived growth factor receptor-like	5157	Hs.458573	47.10	60.86	1.67	5.33E-03
217708_x_at	BRAP	BRCA1 associated protein	8315	Hs.577448	132.84	109.19	-1.48	5.36E-03
206261_at	ZNF239	zinc finger protein 239	8187	Hs.25040	49.33	42.49	-1.35	5.42E-03
210523_at	BMPR1B	bone morphogenetic protein receptor, type IB	658	Hs.661426	65.99	53.56	-1.52	5.44E-03
219652_s_at	CXorf36	chromosome X open reading frame 36	79742	Hs.98321, Hs.648299	131.02	116.19	-1.27	5.64E-03
203261_at	DCTN6	dynactin 6	10671	Hs.158427	435.14	529.57	1.48	5.69E-03
205758_at	CD8A	CD8a molecule	925	Hs.85258	129.14	109.87	-1.38	5.70E-03
205977_s_at	EPHA1	EPH receptor A1	2041	Hs.89839	52.96	47.34	-1.25	5.72E-03
209827_s_at	IL16	interleukin 16 (lymphocyte	3603	Hs.459095	96.91	81.59	-1.41	5.72E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		chemoattractant factor)						
200759_x_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	4779	Hs.514284	1289.27	1507.33	1.37	5.72E-03
210843_s_at	MFAP3L	microfibrillar-associated protein 3-like	9848	Hs.178121, Hs.593942	32.96	29.47	-1.25	5.72E-03
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	23224	Hs.525392	177.81	281.00	2.50	5.72E-03
217287_s_at	TRPC6	transient receptor potential cation channel, subfamily C, member 6	7225	Hs.159003	29.21	26.51	-1.21	5.72E-03
207245_at	UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	7367	Hs.575083	16.10	14.25	-1.28	5.72E-03
207051_at	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	10050	Hs.282931	91.00	79.16	-1.32	5.72E-03
205103_at	C1orf61	chromosome 1 open reading frame 61	10485	Hs.380027	151.75	133.59	-1.29	5.72E-03
220951_s_at	ACF	apobec-1 complementation factor	29974	Hs.499643	79.16	66.29	-1.43	5.74E-03
204967_at	SHROOM2	shroom family member 2	357	Hs.567236	63.98	56.59	-1.28	5.74E-03
220970_s_at	KRTAP2-4	keratin associated protein 2-4	85294	Hs.406714, Hs.560502	31.59	28.65	-1.22	5.84E-03
201935_s_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	8672	Hs.467084	90.62	113.39	1.57	5.84E-03
220568_at	PRO1483	hypothetical protein PRO1483	55448		34.60	31.74	-1.19	5.90E-03
218619_s_at	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	6839	Hs.522639	75.84	67.12	-1.28	5.90E-03
205975_s_at	HOXD1	homeobox D1	3231	Hs.83465	169.78	150.97	-1.26	5.90E-03
208000_at	GML	GPI anchored molecule like protein	2765	Hs.661218	106.39	91.63	-1.35	5.90E-03
201820_at	KRT5	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	3852	Hs.433845, Hs.661062, Hs.674382	53.24	45.36	-1.38	5.90E-03
215210_s_at	DLSTP	dihydrolipoamide S-succinyltransferase pseudogene (E2 component of 2-oxo-glutarate complex)	1744		200.68	269.58	1.80	5.90E-03
208411_x_at	PPEF2	protein phosphatase, EF-hand calcium	5470	Hs.290873	13.04	12.02	-1.18	5.90E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		binding domain 2						
210189_at	HSPA1L	heat shock 70kDa protein 1-like	3305	Hs.690634	86.01	75.05	-1.31	6.18E-03
207161_at	KIAA0087	KIAA0087	9808	Hs.69749	14.15	13.00	-1.19	6.18E-03
207597_at	ADAM18	ADAM metallopeptidase domain 18	8749	Hs.127930	20.11	18.35	-1.20	6.18E-03
204411_at	KIF21B	kinesin family member 21B	23046	Hs.169182	116.46	101.56	-1.31	6.22E-03
211475_s_at	BAG1	BCL2-associated athanogene	573	Hs.377484	331.84	410.56	1.53	6.27E-03
221843_s_at	KIAA1609	KIAA1609	57707	Hs.288274	71.65	62.86	-1.30	6.27E-03
215960_at	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4	6527	Hs.130101	36.34	33.00	-1.21	6.27E-03
47571_at	ZNF236	zinc finger protein 236	7776	Hs.189826	187.31	164.65	-1.29	6.35E-03
213835_x_at	GTPBP3	GTP binding protein 3 (mitochondrial)	84705	Hs.334885	92.23	81.97	-1.27	6.41E-03
221332_at	BMP15	bone morphogenetic protein 15	9210	Hs.532692	49.13	42.78	-1.32	6.41E-03
204711_at	KIAA0753	KIAA0753	9851	Hs.28070	107.54	95.88	-1.26	6.42E-03
221703_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	83990	Hs.532799	16.10	14.75	-1.19	6.47E-03
219614_s_at	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	54716	Hs.413095	32.21	29.19	-1.22	6.51E-03
211144_x_at	TARP	TCR gamma alternate reading frame protein	445347	Hs.534032	79.64	67.30	-1.40	6.51E-03
203860_at	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide	5095	Hs.80741	74.23	87.33	1.38	6.64E-03
203999_at	SYT1	synaptotagmin I	6857	Hs.310545	34.67	30.66	-1.28	6.65E-03
205950_s_at	CA1	carbonic anhydrase I	759	Hs.23118	107.71	95.77	-1.26	6.69E-03
219381_at	FLJ13231	hypothetical protein FLJ13231	65250	Hs.643420	18.27	16.66	-1.20	6.69E-03
205730_s_at	ABLIM3	actin binding LIM protein family, member 3	22885	Hs.49688	312.15	385.62	1.53	6.69E-03
217600_at	SCUBE3	signal peptide, CUB domain, EGF-like 3	222663	Hs.12923	83.73	73.73	-1.29	6.69E-03
217481_x_at	FLJ45455	FLJ45455 protein	388336	Hs.663760	33.85	30.29	-1.25	6.70E-03
213844_at	HOXA5	homeobox A5	3202	Hs.655218	47.27	40.62	-1.35	6.70E-03
208098_at	OR5V1	olfactory receptor, family 5, subfamily V, member 1	81696	Hs.666316	31.23	26.48	-1.39	6.70E-03
218271_s_at	PARL	presenilin associated, rhomboid-like	55486	Hs.478469	320.62	363.82	1.29	6.70E-03
209278_s_at	TFPI2	tissue factor pathway	7980	Hs.438231	28.09	25.31	-1.23	6.70E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		inhibitor 2						
219745_at	TMEM180	transmembrane protein 180	79847	Hs.309069	80.10	71.27	-1.26	6.70E-03
200932_s_at	DCTN2	dynactin 2 (p50)	10540	Hs.289123	517.29	589.11	1.30	6.70E-03
220158_at	LGALS14	lectin, galactoside-binding, soluble, 14	56891	Hs.24236	61.65	55.13	-1.25	6.70E-03
219194_at	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	57715	Hs.591923	113.28	98.66	-1.32	6.80E-03
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	27018	Hs.448588	1994.57	2330.16	1.36	6.81E-03
207733_x_at	PSG9	pregnancy specific beta-1-glycoprotein 9	5678	Hs.502092	102.07	91.05	-1.26	6.81E-03
216042_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	8718	Hs.462529	143.24	129.00	-1.23	6.81E-03
205929_at	GPA33	glycoprotein A33 (transmembrane)	10223	Hs.651244	97.97	86.90	-1.27	6.81E-03
206626_x_at	SSX1	synovial sarcoma, X breakpoint 1	6756	Hs.434142, Hs.694472	89.42	79.69	-1.26	6.82E-03
220421_at	BTNL8	butyrophilin-like 8	79908	Hs.189109	110.31	91.80	-1.44	6.82E-03
206561_s_at	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	57016	Hs.116724	41.40	36.48	-1.29	6.82E-03
207897_at	CRHR2	corticotropin releasing hormone receptor 2	1395	Hs.546246	51.44	44.39	-1.34	6.90E-03
213230_at	CDR2L	cerebellar degeneration-related protein 2-like	30850	Hs.78358	155.94	179.81	1.33	6.90E-03
218250_s_at	CNOT7	CCR4-NOT transcription complex, subunit 7	29883	Hs.598387	226.55	300.00	1.75	6.93E-03
208585_at	BTN2A3	butyrophilin, subfamily 2, member A3	54718	Hs.370522	61.13	54.44	-1.26	6.93E-03
206914_at	CRTAM	cytotoxic and regulatory T cell molecule	56253	Hs.159523	12.23	11.38	-1.16	6.93E-03
220329_s_at	RMND1	required for meiotic nuclear division 1 homolog (S. cerevisiae)	55005	Hs.486835	19.31	21.89	1.29	7.00E-03
202003_s_at	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	10449	Hs.200136	792.49	962.81	1.48	7.04E-03
211831_s_at	THPO	thrombopoietin (myeloproliferative leukemia virus	7066	Hs.1166	39.46	35.60	-1.23	7.04E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		oncogene ligand, megakaryocyte growth and development factor)						
218355_at	KIF4A	kinesin family member 4A	24137	Hs.648326	32.70	28.46	-1.32	7.04E-03
220766_at	BTG4	B-cell translocation gene 4	54766	Hs.128180	34.08	30.19	-1.27	7.04E-03
214842_s_at	ALB	albumin	213	Hs.418167	23.14	20.60	-1.26	7.09E-03
204850_s_at	DCX	doublecortex; lissencephaly, X-linked (doublecortin)	1641	Hs.34780	26.34	23.83	-1.22	7.09E-03
220022_at	ZNF334	zinc finger protein 334	55713	Hs.584933	13.09	12.05	-1.18	7.09E-03
210739_x_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	8671	Hs.5462	148.90	126.50	-1.39	7.09E-03
216476_at	OR7E37P	olfactory receptor, family 7, subfamily E, member 37 pseudogene	26636		97.90	89.21	-1.20	7.09E-03
208154_at	LOC51336	mesenchymal stem cell protein DSCD28	51336	Hs.675523	14.33	13.21	-1.18	7.09E-03
209497_s_at	RBM4B	RNA binding motif protein 4B	83759	Hs.656291	97.02	84.45	-1.32	7.14E-03
220082_at	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	54866	Hs.192927	104.86	93.09	-1.27	7.14E-03
219461_at	PAK6	p21(CDKN1A)-activated kinase 6	56924	Hs.513645	35.98	40.87	1.29	7.14E-03
217240_at	LOC654056	similar to Signal-regulatory protein beta-1 precursor (SIRP-beta-1)	654056		121.56	102.58	-1.40	7.15E-03
208285_at	OR7A5	olfactory receptor, family 7, subfamily A, member 5	26659	Hs.137573	88.39	77.90	-1.29	7.15E-03
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	22974	Hs.244580	52.25	44.19	-1.40	7.16E-03
71933_at	WNT6	wingless-type MMTV integration site family, member 6	7475	Hs.29764	310.87	272.35	-1.30	7.16E-03
219080_s_at	CTPS2	CTP synthase II	56474	Hs.227049	24.01	21.96	-1.20	7.16E-03
219271_at	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	79623	Hs.468058	61.22	52.22	-1.37	7.16E-03
205831_at	CD2	CD2 molecule	914	Hs.523500	137.09	109.57	-1.57	7.25E-03
211469_s_at	CXCR6	chemokine (C-X-C	10663	Hs.34526	69.62	60.40	-1.33	7.27E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		motif) receptor 6						
221397_at	TAS2R10	taste receptor, type 2, member 10	50839	Hs.533756	16.88	15.64	-1.16	7.29E-03
220702_at			55480		19.26	17.51	-1.21	7.37E-03
214567_s_at	XCL2	chemokine (C motif) ligand 2	6846	Hs.458346	36.68	32.59	-1.27	7.37E-03
210447_at	GLUD2	glutamate dehydrogenase 2	2747	Hs.368538	13.08	12.31	-1.13	7.37E-03
220424_at	NPHS2	nephrosis 2, idiopathic, steroid-resistant (podocin)	7827	Hs.412710	107.76	92.77	-1.35	7.37E-03
200642_at	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	6647	Hs.443914	1738.41	1983.88	1.30	7.37E-03
221313_at	GPR52	G protein-coupled receptor 52	9293	Hs.673850	88.92	74.82	-1.41	7.40E-03
201471_s_at	SQSTM1	sequestosome 1	8878	Hs.437277	904.50	1032.27	1.30	7.45E-03
219741_x_at	ZNF552	zinc finger protein 552	79818	Hs.560727	97.56	85.32	-1.31	7.45E-03
203147_s_at	TRIM14	tripartite motif-containing 14	9830	Hs.575631	96.06	84.53	-1.29	7.51E-03
201840_at	NEDD8	neural precursor cell expressed, developmentally down-regulated 8	4738	Hs.531064, Hs.657248	493.99	586.02	1.41	7.55E-03
205318_at	KIF5A	kinesin family member 5A	3798	Hs.151219	108.03	92.28	-1.37	7.56E-03
217908_s_at	IQWD1	IQ motif and WD repeats 1	55827	Hs.435741	283.53	352.35	1.54	7.58E-03
219564_at	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	3773	Hs.463985	15.78	14.53	-1.18	7.63E-03
202364_at	MXI1	MAX interactor 1	4601	Hs.501023, Hs.602078	457.17	563.61	1.52	7.64E-03
218233_s_at			54772		884.79	1014.13	1.31	7.67E-03
220520_s_at	NUP62CL	nucleoporin 62kDa C-terminal like	54830	Hs.163629	17.33	15.90	-1.19	7.72E-03
206928_at	ZNF124	zinc finger protein 124	7678	Hs.421238, Hs.651454, Hs.655205	23.90	21.32	-1.26	7.72E-03
219464_at	CA14	carbonic anhydrase XIV	23632	Hs.528988	125.50	107.86	-1.35	7.78E-03
206235_at	LIG4	ligase IV, DNA, ATP-dependent	3981	Hs.166091	21.13	23.98	1.29	7.78E-03
221445_at	OR1A2	olfactory receptor, family 1, subfamily A, member 2	26189	Hs.532660	35.03	30.34	-1.33	7.78E-03
209249_s_at	GHITM	growth hormone inducible transmembrane protein	27069	Hs.352656	2186.40	2619.87	1.44	7.78E-03
208260_at	AVPR1B	arginine vasopressin	553	Hs.1372	171.01	148.60	-1.32	7.78E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		receptor 1B						
214601_at	TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	7166	Hs.591999	11.02	10.42	-1.12	7.85E-03
219928_s_at	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	26256	Hs.511983	31.12	27.79	-1.25	7.85E-03
205821_at	KLRK1	killer cell lectin-like receptor subfamily K, member 1	22914	Hs.387787	166.23	141.48	-1.38	7.85E-03
215396_at	GPR98	G protein-coupled receptor 98	84059	Hs.591777	20.60	18.40	-1.25	7.85E-03
220833_at			51169		57.83	50.12	-1.33	7.85E-03
208868_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	23710	Hs.524250	242.06	311.89	1.66	7.85E-03
209933_s_at	CD300A	CD300a molecule	11314	Hs.9688	108.18	91.59	-1.39	7.94E-03
218959_at	HOXC10	homeobox C10	3226	Hs.44276	47.88	42.36	-1.28	7.94E-03
209394_at	ASMTL	acetylserotonin O-methyltransferase-like	8623	Hs.533514	174.53	204.01	1.37	7.94E-03
221266_s_at	TM7SF4	transmembrane 7 superfamily member 4	81501	Hs.652230	82.40	72.89	-1.28	8.00E-03
214950_at	IL9R	interleukin 9 receptor	3581	Hs.406228	135.46	121.51	-1.24	8.20E-03
220194_at	NSUN7	NOL1/NOP2/Sun domain family, member 7	79730	Hs.590923	24.37	21.82	-1.25	8.20E-03
207725_at	POU4F2	POU class 4 homeobox 2	5458	Hs.266	17.16	15.29	-1.26	8.24E-03
213240_s_at	KRT4	keratin 4	3851	Hs.654610	66.67	57.86	-1.33	8.24E-03
201175_at	TXNDC14	thioredoxin domain containing 14	51075	Hs.654965	327.24	382.31	1.36	8.25E-03
209861_s_at	METAP2	methionyl aminopeptidase 2	10988	Hs.591005	202.38	258.29	1.63	8.29E-03
215614_at	LOC644974	similar to beta-1,4-mannosyltransferase	644974	Hs.653241	116.38	103.27	-1.27	8.31E-03
221112_at	IL1RAPL2	interleukin 1 receptor accessory protein-like 2	26280	Hs.675519	121.91	107.10	-1.30	8.39E-03
221073_s_at	NOD1	nucleotide-binding oligomerization domain containing 1	10392	Hs.405153	270.91	244.59	-1.23	8.49E-03
205648_at	WNT2	wingless-type MMTV integration site family member 2	7472	Hs.567356	118.21	105.81	-1.25	8.49E-03
220395_at	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	55466	Hs.513053	275.85	245.62	-1.26	8.50E-03
209563_x_at	CALM1	calmodulin 1 (phosphorylase kinase, delta)	801	Hs.282410	1085.97	1228.01	1.28	8.60E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
205825_at	PCSK1	proprotein convertase subtilisin/kexin type 1	5122	Hs.78977	15.28	14.30	-1.14	8.60E-03
219860_at	LY6G5C	lymphocyte antigen 6 complex, locus G5C	80741	Hs.25738	47.50	41.88	-1.29	8.60E-03
209297_at	ITSN1	intersectin 1 (SH3 domain protein)	6453	Hs.160324	243.96	267.81	1.21	8.60E-03
207064_s_at	AOC2	amine oxidase, copper containing 2 (retina-specific)	314	Hs.143102	39.97	35.75	-1.25	8.60E-03
217187_at	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	4586	Hs.534332, Hs.558950, Hs.654574	256.94	212.27	-1.47	8.60E-03
206342_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	3423	Hs.460960	117.80	138.66	1.39	8.60E-03
208248_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	334	Hs.370247	1172.92	1351.34	1.33	8.60E-03
202954_at	UBE2C	ubiquitin-conjugating enzyme E2C	11065	Hs.93002	105.88	91.39	-1.34	8.60E-03
220977_x_at	EPB41L5	erythrocyte membrane protein band 4.1 like 5	57669	Hs.654802	55.31	48.63	-1.29	8.60E-03
212341_at	YIPF6	Yip1 domain family, member 6	286451	Hs.82719, Hs.694797	224.38	266.14	1.41	8.60E-03
221180_at	YSK4	yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)	80122	Hs.659395	255.87	224.53	-1.30	8.60E-03
211201_at	FSHR	follicle stimulating hormone receptor	2492	Hs.1428	30.56	27.13	-1.27	8.62E-03
219968_at	ZNF589	zinc finger protein 589	51385	Hs.172602	129.68	116.11	-1.25	8.62E-03
220223_at	ATAD5	ATPase family, AAA domain containing 5	79915	Hs.528902	51.97	46.37	-1.26	8.62E-03
206904_at	MATN1	matrilin 1, cartilage matrix protein	4146	Hs.150366, Hs.617221	59.70	52.52	-1.29	8.62E-03
201896_s_at	PSRC1	proline/serine-rich coiled-coil 1	84722	Hs.405925	30.55	27.85	-1.20	8.62E-03
206954_at	WIT1	Wilms tumor upstream neighbor 1	51352	Hs.567499	99.27	88.44	-1.26	8.62E-03
203108_at	GPRC5A	G protein-coupled receptor, family C, group 5, member A	9052	Hs.631733	144.59	126.67	-1.30	8.62E-03
206969_at	KRT34	keratin 34	3885	Hs.296942	29.88	26.64	-1.26	8.62E-03
220398_at	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	79158	Hs.46850	78.04	69.46	-1.26	8.62E-03
201652_at	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	10987	Hs.491912	393.18	485.91	1.53	8.62E-03
208273_at	ZNF695	zinc finger protein 695	57116	Hs.669893	25.58	22.90	-1.25	8.62E-03
205900_at	KRT1	keratin 1 (epidermolytic hyperkeratosis)	3848	Hs.80828	62.26	55.40	-1.26	8.62E-03
218089_at	C20orf4	chromosome 20 open	25980	Hs.11314	173.26	158.28	-1.20	8.62E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		reading frame 4						
207429_at	SLC22A2	solute carrier family 22 (organic cation transporter), member 2	6582	Hs.436385	89.83	77.17	-1.36	8.62E-03
205230_at	RPH3A	rabphilin 3A homolog (mouse)	22895	Hs.21239	59.09	54.11	-1.19	8.62E-03
216408_at	OR2B2	olfactory receptor, family 2, subfamily B, member 2	81697	Hs.553551	16.62	15.19	-1.20	8.64E-03
205046_at	CENPE	centromere protein E, 312kDa	1062	Hs.75573	40.56	34.95	-1.35	8.67E-03
207633_s_at	MUSK	muscle, skeletal, receptor tyrosine kinase	4593	Hs.521653	27.49	24.00	-1.31	8.77E-03
219973_at	ARSJ	arylsulfatase family, member J	79642	Hs.22895	18.56	17.46	-1.13	8.77E-03
206299_at	TMEM28	transmembrane protein 28	27112	Hs.87619	158.10	201.57	1.63	8.77E-03
221391_at	TAS2R14	taste receptor, type 2, member 14	50840	Hs.408153, Hs.679406	26.48	24.13	-1.20	8.85E-03
220106_at	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	29881	Hs.567486	80.59	71.02	-1.29	8.86E-03
206282_at	NEUROD1	neurogenic differentiation 1	4760	Hs.440955, Hs.574626	28.76	26.03	-1.22	8.90E-03
221465_at	OR6A2	olfactory receptor, family 6, subfamily A, member 2	8590	Hs.652252	71.46	62.93	-1.29	9.16E-03
207908_at	KRT2	keratin 2 (epidermal ichthyosis bullosa of Siemens)	3849	Hs.707	84.70	73.03	-1.35	9.16E-03
207787_at	KRT33B	keratin 33B	3884	Hs.32950	60.06	53.11	-1.28	9.16E-03
217568_at	FAM12A	family with sequence similarity 12, member A	10876	Hs.304757	30.27	26.17	-1.34	9.19E-03
211036_x_at	ANAPC5	anaphase promoting complex subunit 5	51433	Hs.7101	559.91	618.29	1.22	9.22E-03
215761_at	DMXL2	Dmx-like 2	23312	Hs.511386	87.31	74.47	-1.37	9.22E-03
210130_s_at	TM7SF2	transmembrane 7 superfamily member 2	7108	Hs.31130	260.33	317.94	1.49	9.22E-03
220645_at	FAM55D	family with sequence similarity 55, member D	54827	Hs.179100, Hs.668531	65.00	58.09	-1.25	9.22E-03
206785_s_at	KLRC2	killer cell lectin-like receptor subfamily C, member 2	3822	Hs.591157	12.74	11.86	-1.15	9.22E-03
207759_s_at			80138		28.76	25.69	-1.25	9.22E-03
217374_x_at	TRGV5	T cell receptor gamma variable 5	6978	Hs.534032	62.73	55.55	-1.28	9.36E-03
221302_at	KLF15	Kruppel-like factor 15	28999	Hs.272215	174.80	153.51	-1.30	9.36E-03
217376_at	LOC441938	similar to Signal-regulatory protein	441938	Hs.651103	116.47	101.35	-1.32	9.50E-03

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		gamma precursor (Signal-regulatory protein beta-2) (SIRP-beta-2) (SIRP-b2) (CD172g antigen)						
211231_x_at	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	1579	Hs.1645, Hs.567807	166.11	148.38	-1.25	9.50E-03
200942_s_at	HSBP1	heat shock factor binding protein 1	3281	Hs.250899	676.54	787.10	1.35	9.50E-03
207519_at	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	6532	Hs.591192	85.69	75.99	-1.27	9.50E-03
221297_at	GPRC5D	G protein-coupled receptor, family C, group 5, member D	55507	Hs.644599	92.42	81.67	-1.28	9.50E-03
215315_at	ZNF549	zinc finger protein 549	256051	Hs.564295	17.75	16.18	-1.20	9.50E-03
207944_at	LOC4951	parvalbumin	4951	Hs.510456	31.04	28.13	-1.22	9.50E-03
215881_x_at	SSX3	synovial sarcoma, X breakpoint 3	10214	Hs.558445	103.68	93.67	-1.23	9.53E-03
207774_at			80087		53.17	47.68	-1.24	9.56E-03
216677_at	ZNF154	zinc finger protein 154	7710	Hs.646378	61.93	55.65	-1.24	9.56E-03
200983_x_at	CD59	CD59 molecule, complement regulatory protein	966	Hs.278573, Hs.653685, Hs.693685	1061.48	1313.09	1.53	9.56E-03
219904_at	ZSCAN5	zinc finger and SCAN domain containing 5	79149	Hs.177688	62.72	57.78	-1.18	9.56E-03
38158_at	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	9700	Hs.153479	97.19	86.88	-1.25	9.56E-03
206057_x_at	SPN	sialophorin (leukosialin, CD43)	6693	Hs.632188	162.79	141.91	-1.32	9.68E-03
208106_x_at	PSG6	pregnancy specific beta-1-glycoprotein 6	5675	Hs.654414	111.55	97.04	-1.32	9.81E-03
205753_at	CRP	C-reactive protein, pentraxin-related	1401	Hs.76452, Hs.694799	45.39	40.43	-1.26	9.90E-03
213496_at	LPPR4	plasticity related gene 1	9890	Hs.13245	18.38	16.74	-1.21	9.90E-03
219727_at	DUOX2	dual oxidase 2	50506	Hs.71377	49.37	45.08	-1.20	0.010
214465_at	ORM2	orosomucoid 2	5005	Hs.522356	20.45	18.60	-1.21	0.010
220011_at	C1orf135	chromosome 1 open reading frame 135	79000	Hs.149305	65.55	57.26	-1.31	0.010
207240_s_at	LHCGR	luteinizing hormone/choriogonadotropin receptor	3973	Hs.468490	14.23	13.21	-1.16	0.010
202635_s_at	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	5440	Hs.351475	219.50	279.51	1.62	0.010
211359_s_at	OPRM1	opioid receptor, mu 1	4988	Hs.2353	60.91	53.52	-1.30	0.010
220806_x_at	GNG13	guanine nucleotide	51764	Hs.247888	29.29	26.46	-1.23	0.010

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		binding protein (G protein), gamma 13						
208179_x_at	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	3804	Hs.654605, Hs.654608	78.74	70.39	-1.25	0.010
220783_at	MMP27	matrix metallopeptidase 27	64066	Hs.534479	27.83	25.24	-1.22	0.011
206837_at	ALX1	ALX homeobox 1	8092	Hs.41683	30.96	27.88	-1.23	0.011
201628_s_at	RRAGA	Ras-related GTP binding A	10670	Hs.432330	504.42	580.43	1.32	0.011
207200_at	OTC	ornithine carbamoyltransferase	5009	Hs.117050	34.83	28.30	-1.52	0.011
206713_at	NTNG1	netrin G1	22854	Hs.657434	85.11	73.65	-1.34	0.011
207075_at	NLRP3	NLR family, pyrin domain containing 3	114548	Hs.159483	31.97	28.08	-1.30	0.011
220627_at	CST8	cystatin 8 (cystatin-related epididymal specific)	10047	Hs.121602	50.93	44.71	-1.30	0.011
201077_s_at	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	4809	Hs.182255	787.27	903.27	1.32	0.011
216615_s_at	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	3359	Hs.413899	116.91	103.34	-1.28	0.011
217797_at	UFC1	ubiquitin-fold modifier conjugating enzyme 1	51506	Hs.301412	349.17	404.76	1.34	0.011
217677_at	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	59339	Hs.369123	27.67	25.10	-1.22	0.011
206707_x_at	C6orf32	chromosome 6 open reading frame 32	9750	Hs.559459	59.20	51.48	-1.32	0.011
205625_s_at	CALB1	calbindin 1, 28kDa	793	Hs.65425	24.33	22.32	-1.19	0.011
208283_at	GAGE1	G antigen 1	2543	Hs.632815	18.74	17.00	-1.22	0.011
210853_at	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit	11280	Hs.591657	26.78	24.69	-1.18	0.011
220622_at	LRRC31	leucine rich repeat containing 31	79782	Hs.411295	20.46	18.44	-1.23	0.011
205014_at	FGFBP1	fibroblast growth factor binding protein 1	9982	Hs.1690	81.93	73.95	-1.23	0.011
202416_at	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	7266	Hs.500156	155.03	201.07	1.68	0.011
207911_s_at	TGM5	transglutaminase 5	9333	Hs.129719	174.43	154.10	-1.28	0.011
209586_s_at	PRUNE	prune homolog (Drosophila)	58497	Hs.78524	274.01	321.86	1.38	0.011
218557_at	NIT2	nitrilase family, member 2	56954	Hs.439152	190.84	216.73	1.29	0.011

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
220485_s_at	SIRPG	signal-regulatory protein gamma	55423	Hs.590883	32.46	27.73	-1.37	0.011
202313_at	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	5520	Hs.146339	303.76	350.66	1.33	0.011
219091_s_at	MMRN2	multimerin 2	79812	Hs.524479	125.35	145.07	1.34	0.011
204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	5055	Hs.594481	21.55	19.28	-1.25	0.011
202640_s_at	RANBP3	RAN binding protein 3	8498	Hs.531752	159.21	175.54	1.22	0.011
215040_at	RNASEH2B	ribonuclease H2, subunit B	79621	Hs.306291	180.22	156.46	-1.33	0.011
219642_s_at	PEX5L	peroxisomal biogenesis factor 5-like	51555	Hs.478393	23.19	20.94	-1.23	0.011
216773_at	COMMD1	copper metabolism (Murr1) domain containing 1	150684	Hs.468702	27.52	25.64	-1.15	0.011
220721_at	ZNF614	zinc finger protein 614	80110	Hs.292336	40.12	35.98	-1.24	0.011
218526_s_at	RANGRF	RAN guanine nucleotide release factor	29098	Hs.408233	156.85	179.35	1.31	0.011
211607_x_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	1956	Hs.488293	175.54	155.20	-1.28	0.011
215467_x_at	LOC647070	hypothetical LOC647070	647070	Hs.660884	73.83	64.68	-1.30	0.011
206643_at	HAL	histidine ammonia-lyase	3034	Hs.190783	29.84	26.12	-1.30	0.011
206429_at	F2RL1	coagulation factor II (thrombin) receptor-like 1	2150	Hs.154299	86.05	77.12	-1.25	0.011
206349_at	LGI1	leucine-rich, glioma inactivated 1	9211	Hs.533670	14.78	13.68	-1.17	0.011
213199_at	DKFZP586P0123	hypothetical protein	26005	Hs.557938, Hs.694798	70.35	62.68	-1.26	0.011
203916_at	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	8509	Hs.654758	174.45	157.02	-1.23	0.012
211545_at	GHRHR	growth hormone releasing hormone receptor	2692	Hs.767	68.44	60.33	-1.29	0.012
215756_at	LOC730227	hypothetical protein LOC730227	730227	Hs.293928	88.26	78.11	-1.28	0.012
216738_at	HRH1	histamine receptor H1	3269	Hs.1570, Hs.657237	96.71	83.30	-1.35	0.012
218622_at	NUP37	nucleoporin 37kDa	79023	Hs.444276	80.72	94.71	1.38	0.012
205344_at	CSPG5	chondroitin sulfate proteoglycan 5	10675	Hs.45127	151.29	137.36	-1.21	0.012

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(neuroglycan C)						
221236_s_at	STMN4	stathmin-like 4	81551	Hs.201058	43.36	37.75	-1.32	0.012
215484_at	TRIM3	tripartite motif-containing 3	10612	Hs.591992	102.38	87.11	-1.38	0.012
207126_x_at	UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide A1	54658	Hs.654499	66.09	60.59	-1.19	0.012
203554_x_at	PTTG1	pituitary tumor-transforming 1	9232	Hs.350966	193.42	167.27	-1.34	0.012
220897_at			80029		17.27	16.09	-1.15	0.012
208448_x_at	IFNA16	interferon, alpha 16	3449	Hs.56303	34.93	31.56	-1.22	0.012
221399_at	EDA2R	ectodysplasin A2 receptor	60401	Hs.302017	84.71	75.61	-1.26	0.012
218826_at	SLC35F2	solute carrier family 35, member F2	54733	Hs.524014	56.94	50.35	-1.28	0.012
209629_s_at	NXT2	nuclear transport factor 2-like export factor 2	55916	Hs.25010	31.10	27.61	-1.27	0.012
202705_at	CCNB2	cyclin B2	9133	Hs.194698	73.43	64.07	-1.31	0.012
220615_s_at	MLSTD1	male sterility domain containing 1	55711	Hs.298851	57.33	50.66	-1.28	0.012
205834_s_at	PART1	prostate androgen-regulated transcript 1	25859	Hs.661347	93.38	82.31	-1.29	0.012
219542_at	NEK11	NIMA (never in mitosis gene a)- related kinase 11	79858	Hs.657336	79.81	68.71	-1.35	0.012
203966_s_at	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	5494	Hs.592298	288.13	333.99	1.34	0.012
206137_at	RIMS2	regulating synaptic membrane exocytosis 2	9699	Hs.655271, Hs.675990	64.68	58.09	-1.24	0.012
219165_at	PDLIM2	PDZ and LIM domain 2 (mystique)	64236	Hs.632034	68.13	85.81	1.59	0.012
215523_at	ZNF391	zinc finger protein 391	346157	Hs.651176, Hs.680366	17.35	15.78	-1.21	0.012
220957_at	CTAGE1	cutaneous T-cell lymphoma-associated antigen 1	64693	Hs.406709	18.21	16.39	-1.23	0.012
203702_s_at	TTLL4	tubulin tyrosine ligase-like family, member 4	9654	Hs.471405	57.87	51.87	-1.24	0.012
220958_at	ULK4	unc-51-like kinase 4 (C. elegans)	54986	Hs.656192	42.81	38.25	-1.25	0.012
207443_at	NR2E1	nuclear receptor subfamily 2, group E, member 1	7101	Hs.157688	41.79	37.24	-1.26	0.012
221670_s_at	LHX3	LIM homeobox 3	8022	Hs.148427	188.97	167.76	-1.27	0.012
204868_at	ICT1	immature colon carcinoma transcript 1	3396	Hs.407955	154.27	180.96	1.38	0.012
215515_at	KIRREL	kin of IRRE like	55243	Hs.609291,	80.87	70.52	-1.32	0.012

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(Drosophila)		Hs.657006				
217483_at	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1	2346	Hs.654487	68.22	61.55	-1.23	0.012
212403_at	UBE3B	ubiquitin protein ligase E3B	89910	Hs.374067	191.59	220.60	1.33	0.012
214642_x_at	MAGEA5	melanoma antigen family A, 5	4104	Hs.668021	24.97	23.36	-1.14	0.012
206708_at	FOXN2	forkhead box N2	3344	Hs.468478	31.45	28.14	-1.25	0.012
219939_s_at	CSDE1	cold shock domain containing E1, RNA-binding	7812	Hs.69855	1292.41	1666.59	1.66	0.012
207093_s_at	OMG	oligodendrocyte myelin glycoprotein	4974	Hs.113874	135.61	121.85	-1.24	0.012
206625_at	PRPH2	peripherin 2 (retinal degeneration, slow)	5961	Hs.654489	104.25	94.37	-1.22	0.012
207462_at	GLRA2	glycine receptor, alpha 2	2742	Hs.2700	68.98	60.88	-1.28	0.012
207600_at	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	3748	Hs.467146	63.05	56.98	-1.22	0.013
221451_s_at	OR2W1	olfactory receptor, family 2, subfamily W, member 1	26692	Hs.553526	23.01	21.03	-1.20	0.013
201982_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	5069	Hs.643599, Hs.694735	84.25	75.43	-1.25	0.013
217305_s_at	SAC	testicular soluble adenylyl cyclase	55811	Hs.320892	29.44	27.39	-1.16	0.013
213338_at	TMEM158	transmembrane protein 158	25907	Hs.35861	29.84	26.45	-1.27	0.013
207230_at	CDON	Cdon homolog (mouse)	50937	Hs.38034	85.48	76.26	-1.26	0.013
216907_x_at	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	3812	Hs.645228, Hs.645532	44.69	39.96	-1.25	0.013
210261_at	KCNK2	potassium channel, subfamily K, member 2	3776	Hs.497745	27.10	24.74	-1.20	0.013
209860_s_at	ANXA7	annexin A7	310	Hs.631827	317.73	385.91	1.48	0.013
219715_s_at	TDP1	tyrosyl-DNA phosphodiesterase 1	55775	Hs.209945	57.22	52.12	-1.21	0.013
207143_at	CDK6	cyclin-dependent kinase 6	1021	Hs.119882	55.01	47.90	-1.32	0.013
215704_at	FLG	filaggrin	2312	Hs.654510	13.41	12.72	-1.11	0.013
202645_s_at	MEN1	multiple endocrine neoplasia I	4221	Hs.423348	101.34	91.02	-1.24	0.013
206833_s_at	ACYP2	acylphosphatase 2, muscle type	98	Hs.516173, Hs.642983	245.08	305.30	1.55	0.013

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
48659_at	RP5-1077B9.4	invasion inhibitory protein 45	60672	Hs.8595	210.66	190.61	-1.22	0.013
220133_at	ODAM	odontogenic, ameloblast asssociated	54959	Hs.143811	32.69	29.28	-1.25	0.013
220029_at	ELOVL2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	54898	Hs.656436	49.52	44.16	-1.26	0.013
204770_at	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	6891	Hs.502	73.43	63.32	-1.34	0.013
201256_at	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	9167	Hs.339639	647.18	727.58	1.26	0.013
207400_at	NPY5R	neuropeptide Y receptor Y5	4889	Hs.519058, Hs.598503	50.80	45.45	-1.25	0.013
204454_at	LDOC1	leucine zipper, down-regulated in cancer 1	23641	Hs.45231	142.59	126.31	-1.27	0.013
220743_at	C16orf72	chromosome 16 open reading frame 72	29035	Hs.221497	121.14	106.60	-1.29	0.013
205785_at	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	3684	Hs.172631	64.54	57.60	-1.26	0.013
214639_s_at	HOXA1	homeobox A1	3198	Hs.67397	30.28	26.63	-1.29	0.013
220542_s_at	PLUNC	palate, lung and nasal epithelium carcinoma associated	51297	Hs.211092	131.09	116.08	-1.28	0.013
206849_at	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2	2566	Hs.7195	29.69	25.93	-1.31	0.013
217245_at	EPAG	early lymphoid activation protein	10824	Hs.654372	33.13	28.56	-1.35	0.013
206478_at	KIAA0125	KIAA0125	9834	Hs.632338, Hs.649259	45.18	39.89	-1.28	0.013
206939_at	DCC	deleted in colorectal carcinoma	1630	Hs.694733	45.49	39.56	-1.32	0.013
215582_x_at	MCM3AP	minichromosome maintenance complex component 3 associated protein	8888	Hs.389037	163.15	140.62	-1.35	0.013
219685_at	TMEM35	transmembrane protein 35	59353	Hs.45140	27.82	25.13	-1.23	0.013
208737_at	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	9550	Hs.388654	337.36	429.27	1.62	0.013
216895_at	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	2567	Hs.569475, Hs.592027	21.51	19.46	-1.22	0.013
201522_x_at	SNRPN	small nuclear ribonucleoprotein	6638	Hs.564847, Hs.632166	2231.66	2539.96	1.30	0.013

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		polypeptide N						
205752_s_at	GSTM5	glutathione S-transferase M5	2949	Hs.75652	159.02	140.32	-1.28	0.013
206104_at	ISL1	ISL LIM homeobox 1	3670	Hs.505	19.50	17.64	-1.22	0.013
213601_at	SLIT1	slit homolog 1 (Drosophila)	6585	Hs.632082	83.71	75.08	-1.24	0.013
204529_s_at	TOX	thymocyte selection-associated high mobility group box	9760	Hs.491805, Hs.634856	17.17	15.01	-1.31	0.013
204087_s_at	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	8884	Hs.435735	150.97	136.11	-1.23	0.013
216058_s_at	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	1557	Hs.282409	50.55	45.72	-1.22	0.013
215745_at	NOL14	nucleolar protein 14	8602	Hs.694747	36.62	32.99	-1.23	0.013
210040_at	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5	57468	Hs.21413	49.67	43.11	-1.33	0.013
220148_at	ALDH8A1	aldehyde dehydrogenase 8 family, member A1	64577	Hs.486520	14.39	13.65	-1.11	0.013
215491_at	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	4610	Hs.437922	159.29	143.89	-1.23	0.013
216275_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	699	Hs.469649	98.09	87.92	-1.24	0.013
213036_x_at	ATP2A3	ATPase, Ca++ transporting, ubiquitous	489	Hs.513870	183.97	165.10	-1.24	0.013
220790_s_at	MS4A5	membrane-spanning 4-domains, subfamily A, member 5	64232	Hs.178066	51.00	44.61	-1.31	0.013
221165_s_at	IL22	interleukin 22	50616	Hs.287369	123.81	113.10	-1.20	0.013
221092_at	IKZF3	IKAROS family zinc finger 3 (Aiolos)	22806	Hs.444388	15.82	14.37	-1.21	0.013
216879_at	HR44	Hr44 antigen	27251		62.03	54.93	-1.28	0.013
220567_at	IKZF2	IKAROS family zinc finger 2 (Helios)	22807	Hs.604950	37.98	33.98	-1.25	0.013
204434_at	SPATA2	spermatogenesis associated 2	9825	Hs.48513	98.87	89.37	-1.22	0.013
209995_s_at	TCL1A	T-cell leukemia/lymphoma 1A	8115	Hs.2484	91.54	81.35	-1.27	0.014
206192_at	CDSN	corneodesmosin	1041	Hs.556031	109.17	94.00	-1.35	0.014
205044_at	GABRP	gamma-aminobutyric acid (GABA) A receptor,	2568	Hs.26225	34.60	30.83	-1.26	0.014

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		pi						
207840_at	CD160	CD160 molecule	11126	Hs.488237	22.96	20.91	-1.21	0.014
210131_x_at	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6391	Hs.444472	459.14	543.09	1.40	0.014
202587_s_at	AK1	adenylate kinase 1	203	Hs.175473	990.08	1240.57	1.57	0.014
210143_at	ANXA10	annexin A10	11199	Hs.188401	28.25	24.87	-1.29	0.014
210674_s_at	PCDHA12	protocadherin alpha 12	56137	Hs.199343, Hs.608548	18.47	17.32	-1.14	0.014
209046_s_at	GABARAPL2	GABA(A) receptor-associated protein-like 2	11345	Hs.461379	1464.20	1737.93	1.41	0.014
215105_at	CG030	hypothetical gene CG030	116828	Hs.658751	30.26	27.36	-1.22	0.014
216539_at	ATXN3L	ataxin 3-like	92552	Hs.382641	29.38	26.53	-1.23	0.014
215129_at	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	5288	Hs.22500	22.93	20.75	-1.22	0.014
207628_s_at	WBSCR22	Williams Beuren syndrome chromosome region 22	114049	Hs.647063	237.60	281.52	1.40	0.014
207523_at	C6orf10	chromosome 6 open reading frame 10	10665	Hs.567414	23.50	21.08	-1.24	0.014
221034_s_at	TEX13B	testis expressed 13B	56156	Hs.333130	75.65	67.30	-1.26	0.014
208188_at	KRT9	keratin 9 (epidermolytic palmoplantar keratoderma)	3857	Hs.654569	82.52	74.42	-1.23	0.014
207642_at	HCRT	hypocretin (orexin) neuropeptide precursor	3060	Hs.158348	43.13	38.46	-1.26	0.014
214983_at	TTTY15	testis-specific transcript, Y-linked 15	64595	Hs.433656	22.11	25.08	1.29	0.014
205832_at	CPA4	carboxypeptidase A4	51200	Hs.93764	84.35	74.41	-1.28	0.014
217906_at	KLHDC2	kelch domain containing 2	23588	Hs.509264	472.46	571.16	1.46	0.014
211614_at			51581		150.61	129.27	-1.36	0.014
206761_at	CD96	CD96 molecule	10225	Hs.142023	23.34	21.25	-1.21	0.014
209331_s_at	MAX	MYC associated factor X	4149	Hs.285354	188.05	233.92	1.55	0.014
214482_at	ZBTB25	zinc finger and BTB domain containing 25	7597	Hs.654571	58.65	52.90	-1.23	0.015
206241_at	KPNA5	karyopherin alpha 5 (importin alpha 6)	3841	Hs.182971	12.84	12.02	-1.14	0.015
216242_x_at	POLR2J3	RPB11b2 protein	548644	Hs.654726	175.62	219.40	1.56	0.015
221025_x_at	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	83448	Hs.445814	133.35	120.16	-1.23	0.015
205544_s_at	CR2	complement component (3d/Epstein Barr virus) receptor 2	1380	Hs.445757	21.88	20.05	-1.19	0.015

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
210774_s_at	NCOA4	nuclear receptor coactivator 4	8031	Hs.643658, Hs.656841	1086.06	1278.44	1.39	0.015
207712_at	BAGE	B melanoma antigen	574	Hs.545789, Hs.624542, Hs.624543	14.47	13.53	-1.14	0.015
220787_at			55492		14.66	13.52	-1.18	0.015
202824_s_at	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	6921	Hs.554594	250.12	299.60	1.43	0.015
217852_s_at	ARL8B	ADP-ribosylation factor-like 8B	55207	Hs.250009	378.13	453.92	1.44	0.015
208198_x_at	KIR2DS1	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	3806	Hs.661101	205.02	183.96	-1.24	0.015
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	56997	Hs.118241	379.44	444.08	1.37	0.015
220869_at			55368		29.68	26.39	-1.26	0.015
220613_s_at	SYTL2	synaptotagmin-like 2	54843	Hs.369520	36.21	32.69	-1.23	0.015
208709_s_at	NRD1	nardilysin (N-arginine dibasic convertase)	4898	Hs.584782	461.53	513.01	1.24	0.015
202831_at	GPX2	glutathione peroxidase 2 (gastrointestinal)	2877	Hs.2704	225.09	198.78	-1.28	0.015
218711_s_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	8436	Hs.26530	107.60	147.13	1.87	0.015
221477_s_at	MGC5618	hypothetical protein MGC5618	79099		387.71	490.25	1.60	0.015
209233_at	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	10436	Hs.558447	228.64	259.01	1.28	0.015
207065_at	KRT75	keratin 75	9119	Hs.661062	83.44	72.68	-1.32	0.015
220384_at	TXNDC3	thioredoxin domain containing 3 (spermatozoa)	51314	Hs.134079	24.36	21.86	-1.24	0.015
219964_at	ST7L	suppression of tumorigenicity 7 like	54879	Hs.201921	75.47	68.20	-1.22	0.015
208678_at	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	529	Hs.517338	764.60	864.95	1.28	0.015
221779_at	MICALL1	MICAL-like 1	85377	Hs.517610	122.71	110.95	-1.22	0.015
217993_s_at	MAT2B	methionine adenosyltransferase II, beta	27430	Hs.54642	559.56	672.98	1.45	0.015
213837_at	C20orf194	chromosome 20 open reading frame 194	25943	Hs.516853	110.17	99.19	-1.23	0.015
219071_x_at	C8orf30A	chromosome 8 open reading frame 30A	51236	Hs.300224	247.69	221.14	-1.25	0.015

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
206797_at	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	10	Hs.2	93.63	81.67	-1.31	0.015
210413_x_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	6318	Hs.123035	58.25	51.04	-1.30	0.015
202296_s_at	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	11079	Hs.525527	259.25	304.98	1.38	0.015
206510_at	SIX2	SIX homeobox 2	10736	Hs.101937	43.90	40.10	-1.20	0.015
207599_at	MMP20	matrix metallopeptidase 20 (enamelysin)	9313	Hs.591946	21.93	19.86	-1.22	0.015
210395_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	4635	Hs.463300	388.33	616.54	2.52	0.015
206936_x_at			58479		59.00	51.00	-1.34	0.015
205479_s_at	PLAU	plasminogen activator, urokinase	5328	Hs.77274	141.13	168.04	1.42	0.015
201554_x_at	GYG1	glycogenin 1	2992	Hs.477892	809.58	980.62	1.47	0.015
221675_s_at	CHPT1	choline phosphotransferase 1	56994	Hs.293077	457.91	541.14	1.40	0.015
207915_at	MYCL2	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	4611		47.78	40.26	-1.41	0.015
208680_at	PRDX1	peroxiredoxin 1	5052	Hs.180909	690.71	804.70	1.36	0.015
205342_s_at	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	6819	Hs.436123	39.43	35.44	-1.24	0.015
206486_at	LAG3	lymphocyte-activation gene 3	3902	Hs.409523	29.38	25.75	-1.30	0.015
214859_at	FSTL4	follistatin-like 4	23105	Hs.483390	50.45	46.43	-1.18	0.015
208543_at	OR10H2	olfactory receptor, family 10, subfamily H, member 2	26538	Hs.247694	27.76	25.67	-1.17	0.015
220679_s_at	CDH7	cadherin 7, type 2	1005	Hs.657522	63.05	55.93	-1.27	0.015
207648_at	DRP2	dystrophin related protein 2	1821	Hs.159291	146.44	129.15	-1.29	0.015
208425_s_at	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	26115	Hs.410889	54.21	49.10	-1.22	0.015
206979_at	C8B	complement component 8, beta polypeptide	732	Hs.391835	167.10	148.81	-1.26	0.015
200794_x_at	DAZAP2	DAZ associated protein 2	9802	Hs.369761	945.06	1107.38	1.37	0.015
207267_s_at	DSCR6	Down syndrome critical region gene 6	53820	Hs.254560	25.01	23.15	-1.17	0.015
221602_s_at	FAIM3	Fas apoptotic inhibitory molecule 3	9214	Hs.58831	112.97	97.62	-1.34	0.015

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
215548_s_at	SCFD1	sec1 family domain containing 1	23256	Hs.369168	110.08	129.04	1.37	0.015
220530_at	PRO2266	hypothetical protein PRO2266	55389	Hs.662132	15.16	14.08	-1.16	0.015
219265_at	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)	79817	Hs.690014, Hs.694807	146.87	130.95	-1.26	0.015
206988_at	CCL25	chemokine (C-C motif) ligand 25	6370	Hs.310511	84.03	71.82	-1.37	0.015
206835_at	STATH	statherin	6779	Hs.654495	31.96	28.09	-1.29	0.015
206990_at	TNR	tenascin R (restrictin, janusin)	7143	Hs.659864	61.26	53.96	-1.29	0.015
216149_at	LRRC37B2	leucine rich repeat containing 37, member B2	147172	Hs.568209	33.24	29.95	-1.23	0.015
220646_s_at	KLRF1	killer cell lectin-like receptor subfamily F, member 1	51348	Hs.183125	12.94	12.01	-1.16	0.015
206225_at	ZNF507	zinc finger protein 507	22847	Hs.205392	59.35	51.13	-1.35	0.016
206838_at	TBX19	T-box 19	9095	Hs.645440	66.51	60.23	-1.22	0.016
207509_s_at	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	3904	Hs.43803	69.49	59.36	-1.37	0.016
207706_at	USH2A	Usher syndrome 2A (autosomal recessive, mild)	7399	Hs.655974	17.57	16.36	-1.15	0.016
220737_at	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	27330	Hs.368153	96.06	83.07	-1.34	0.016
209445_x_at	C7orf44	chromosome 7 open reading frame 44	55744	Hs.654779, Hs.655165, Hs.658441	290.18	328.42	1.28	0.016
220100_at	SLC22A11	solute carrier family 22 (organic anion/cation transporter), member 11	55867	Hs.220844	48.20	42.75	-1.27	0.016
207333_at	NMBR	neuromedin B receptor	4829	Hs.654478	23.68	21.14	-1.25	0.016
220880_at			55465		17.16	16.05	-1.14	0.016
204305_at	MIPEP	mitochondrial intermediate peptidase	4285	Hs.507498	137.29	156.26	1.30	0.016
32032_at	DGCR14	DiGeorge syndrome critical region gene 14	8220	Hs.517407, Hs.686112	117.32	108.54	-1.17	0.016
210039_s_at	PRKCQ	protein kinase C, theta	5588	Hs.498570	143.18	128.07	-1.25	0.016
208643_s_at	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)	7520	Hs.388739	370.14	437.17	1.40	0.016

Probe	**Symbol**	**Description**	**Gene**	**UniGene**	**Av Exp Female**	**Av Exp Male**	**Fold Change**	**adj P val**
208597_at	CNTF	ciliary neurotrophic factor	1270	Hs.632114	44.66	40.12	-1.24	0.016
206210_s_at	CETP	cholesteryl ester transfer protein, plasma	1071	Hs.89538	57.49	50.59	-1.29	0.016
218785_s_at	RABL5	RAB, member RAS oncogene family-like 5	64792	Hs.389104	44.05	39.59	-1.24	0.016
207362_at	SLC30A4	solute carrier family 30 (zinc transporter), member 4	7782	Hs.162989	16.94	15.57	-1.18	0.016
204920_at	CPS1	carbamoyl-phosphate synthetase 1, mitochondrial	1373	Hs.149252	71.70	64.57	-1.23	0.016
215011_at	SNHG3	small nucleolar RNA host gene (non-protein coding) 3	8420	Hs.469723	27.21	24.92	-1.19	0.016
202673_at	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	8813	Hs.654951	192.40	237.34	1.52	0.016
215223_s_at	SOD2	superoxide dismutase 2, mitochondrial	6648	Hs.487046	157.11	201.25	1.64	0.016
208375_at	IFNA1	interferon, alpha 1	3439	Hs.37026	19.31	17.93	-1.16	0.016
206998_x_at	PRB3	proline-rich protein BstNI subfamily 3	5544	Hs.73031	54.59	48.82	-1.25	0.016
213118_at	KIAA0701	KIAA0701 protein	23074	Hs.620701	27.57	31.77	1.33	0.016
204272_at	LGALS4	lectin, galactoside-binding, soluble, 4 (galectin 4)	3960	Hs.5302	40.74	36.44	-1.25	0.016
200594_x_at	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	3192	Hs.166463	594.41	737.75	1.54	0.016
217273_at	PRAMEF10	PRAME family member 10	343071	Hs.684629	70.26	61.76	-1.29	0.016
218194_at	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	25996	Hs.7527, Hs.677190	1262.65	1466.38	1.35	0.016
205184_at	GNG4	guanine nucleotide binding protein (G protein), gamma 4	2786	Hs.159711, Hs.591531, Hs.658122	139.28	122.82	-1.29	0.016
215349_at	hCG_1730474	hCG1730474	643376	Hs.652246	47.81	42.62	-1.26	0.016
219657_s_at	KLF3	Kruppel-like factor 3 (basic)	51274	Hs.298658	133.27	118.44	-1.27	0.016
220589_s_at	ITFG2	integrin alpha FG-GAP repeat containing 2	55846	Hs.446098, Hs.448720	34.85	39.63	1.29	0.016
207452_s_at	CNTN5	contactin 5	53942	Hs.656783	15.71	14.67	-1.15	0.016
204124_at	SLC34A2	solute carrier family 34 (sodium phosphate), member 2	10568	Hs.479372	21.93	20.31	-1.17	0.016
219429_at	FA2H	fatty acid 2-hydroxylase	79152	Hs.461329	23.42	21.67	-1.17	0.016

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
206672_at	AQP2	aquaporin 2 (collecting duct)	359	Hs.130730	199.85	183.63	-1.18	0.016
208344_x_at	IFNA13	interferon, alpha 13	3447	Hs.533471	193.33	170.22	-1.29	0.016
202941_at	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	4729	Hs.464572	1185.01	1427.50	1.45	0.016
208521_at	OR5I1	olfactory receptor, family 5, subfamily I, member 1	10798	Hs.533706	61.61	52.52	-1.38	0.017
219454_at	EGFL6	EGF-like-domain, multiple 6	25975	Hs.12844	22.52	20.48	-1.21	0.017
204602_at	DKK1	dickkopf homolog 1 (Xenopus laevis)	22943	Hs.40499	35.46	31.60	-1.26	0.017
206079_at	CHML	choroideremia-like (Rab escort protein 2)	1122	Hs.654545	18.52	16.97	-1.19	0.017
220085_at	HELLS	helicase, lymphoid-specific	3070	Hs.655830	21.18	19.47	-1.18	0.017
208210_at	MAS1	MAS1 oncogene	4142	Hs.99900	89.98	77.81	-1.34	0.017
208263_at			55447		17.99	16.57	-1.18	0.017
208234_x_at	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	2263	Hs.533683	109.32	95.27	-1.32	0.017
210302_s_at	MAB21L2	mab-21-like 2 (C. elegans)	10586	Hs.584852	23.10	21.09	-1.20	0.017
208191_x_at	PSG4	pregnancy specific beta-1-glycoprotein 4	5672	Hs.654468	120.57	107.58	-1.26	0.017
217874_at	SUCLG1	succinate-CoA ligase, GDP-forming, alpha subunit	8802	Hs.270428	1364.35	1551.32	1.29	0.017
216469_at	LOC727867	similar to zinc finger protein 43 (HTF6)	727867		14.57	13.47	-1.17	0.017
212301_at	RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	23168	Hs.511096	113.59	134.25	1.40	0.017
216169_at			84169		17.31	15.74	-1.21	0.017
220413_at	SLC39A2	solute carrier family 39 (zinc transporter), member 2	29986	Hs.175783	152.59	139.35	-1.20	0.017
218341_at	PPCS	phosphopantothenoylcysteine synthetase	79717	Hs.473495	161.84	182.76	1.28	0.017
208134_x_at	PSG2	pregnancy specific beta-1-glycoprotein 2	5670	Hs.654453	33.11	29.55	-1.26	0.017
222244_s_at	TUG1	taurine upregulated	55000	Hs.554829	479.01	572.63	1.43	0.017

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		gene 1						
202926_at	NAG	neuroblastoma-amplified protein	51594	Hs.467759	148.16	166.25	1.26	0.017
222106_at	PRND	prion protein 2 (dublet)	23627	Hs.406696	19.16	17.75	-1.16	0.017
207716_at	KRT38	keratin 38	8687	Hs.248188	58.48	52.74	-1.23	0.017
220115_s_at	CDH10	cadherin 10, type 2 (T2-cadherin)	1008	Hs.92489	35.24	32.54	-1.17	0.017
219502_at	NEIL3	nei endonuclease VIII-like 3 (E. coli)	55247	Hs.405467	25.68	23.63	-1.18	0.017
215532_x_at	ZNF492	zinc finger protein 492	57615	Hs.232108	11.71	11.00	-1.13	0.017
206651_s_at	CPB2	carboxypeptidase B2 (plasma)	1361	Hs.512937	20.41	18.44	-1.22	0.017
215174_at	FMO6P	flavin containing monooxygenase 6 pseudogene	388714	Hs.448988	48.66	44.59	-1.19	0.017
219877_at	ZMAT4	zinc finger, matrin type 4	79698	Hs.591850	92.82	82.69	-1.26	0.017
207183_at	GPR19	G protein-coupled receptor 19	2842	Hs.657862	76.91	66.78	-1.33	0.017
209915_s_at	NRXN1	neurexin 1	9378	Hs.637685	82.98	73.61	-1.27	0.017
201705_at	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	5713	Hs.440604	373.53	426.51	1.30	0.017
200682_s_at	UBE2L3	ubiquitin-conjugating enzyme E2L 3	7332	Hs.108104, Hs.693707	359.55	409.37	1.30	0.017
206639_x_at	HTN1	histatin 1	3346	Hs.250959	20.49	18.91	-1.17	0.017
205798_at	IL7R	interleukin 7 receptor	3575	Hs.591742, Hs.693675	61.75	47.77	-1.67	0.017
207061_at	ERN1	endoplasmic reticulum to nucleus signaling 1	2081	Hs.133982	98.28	90.43	-1.18	0.017
221908_at	TMEM118	transmembrane protein 118	84900	Hs.437195	45.75	41.37	-1.22	0.017
207800_at	AKAP5	A kinase (PRKA) anchor protein 5	9495	Hs.532489	36.45	33.15	-1.21	0.017
202300_at	HBXIP	hepatitis B virus x interacting protein	10542	Hs.439815	691.22	808.20	1.37	0.017
213847_at	PRPH	peripherin	5630	Hs.37044	146.57	128.95	-1.29	0.017
221688_s_at	IMP3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	55272	Hs.513043	119.01	134.74	1.28	0.017
207325_x_at	MAGEA1	melanoma antigen family A, 1 (directs expression of antigen MZ2-E)	4100	Hs.72879	18.34	16.89	-1.18	0.017
217927_at	SPCS1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	28972	Hs.11125, Hs.297304	543.93	645.89	1.41	0.017
221717_at			84098		104.58	94.98	-1.21	0.017
203538_at	CAMLG	calcium modulating	819	Hs.529846	137.66	160.67	1.36	0.017

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		ligand						
200007_at	SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)	6727	Hs.533732	1513.64	1680.58	1.23	0.017
203475_at	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	1588	Hs.654384	37.90	34.00	-1.24	0.017
209627_s_at	OSBPL3	oxysterol binding protein-like 3	26031	Hs.520259	54.38	48.51	-1.26	0.017
217932_at	MRPS7	mitochondrial ribosomal protein S7	51081	Hs.71787	422.39	501.03	1.41	0.017
208158_s_at	OSBPL1A	oxysterol binding protein-like 1A	114876	Hs.370725	227.83	258.43	1.29	0.017
204952_at	LYPD3	LY6/PLAUR domain containing 3	27076	Hs.631594	193.55	172.90	-1.25	0.017
220722_s_at	SLC5A7	solute carrier family 5 (choline transporter), member 7	60482	Hs.287758	52.84	47.61	-1.23	0.017
207878_at	KRT76	keratin 76	51350	Hs.654392	73.42	63.73	-1.33	0.017
206035_at	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	5966	Hs.631886	35.06	31.34	-1.25	0.017
201199_s_at	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	5707	Hs.3887	473.65	528.78	1.25	0.017
200606_at	DSP	desmoplakin	1832	Hs.519873	1112.68	1333.76	1.44	0.017
212119_at	RHOQ	ras homolog gene family, member Q	23433	Hs.693587	1185.89	1485.11	1.57	0.017
208035_at	GRM6	glutamate receptor, metabotropic 6	2916	Hs.248131	56.24	50.04	-1.26	0.017
204197_s_at	RUNX3	runt-related transcription factor 3	864	Hs.170019	56.49	47.90	-1.39	0.017
209571_at	CIR	CBF1 interacting corepressor	9541	Hs.632531	46.87	52.72	1.27	0.017
213587_s_at	ATP6V0E2	ATPase, H+ transporting V0 subunit e2	155066	Hs.556998, Hs.694765	335.66	422.62	1.59	0.017
210393_at	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	8549	Hs.658889	65.72	59.21	-1.23	0.017
219412_at	RAB38	RAB38, member RAS oncogene family	23682	Hs.591975	24.33	22.07	-1.22	0.017
205886_at	REG1B	regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	5968	Hs.4158	48.52	43.31	-1.26	0.017
205012_s_at	HAGH	hydroxyacylglutathione hydrolase	3029	Hs.157394, Hs.513265	272.53	307.54	1.27	0.017

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
201266_at	TXNRD1	thioredoxin reductase 1	7296	Hs.654922	267.64	334.19	1.56	0.017
204398_s_at	EML2	echinoderm microtubule associated protein like 2	24139	Hs.24178	139.27	159.11	1.31	0.017
204033_at	TRIP13	thyroid hormone receptor interactor 13	9319	Hs.436187	72.99	65.42	-1.25	0.017
202777_at	SHOC2	soc-2 suppressor of clear homolog (C. elegans)	8036	Hs.104315	132.32	163.25	1.52	0.017
214838_at	SFT2D2	SFT2 domain containing 2	375035	Hs.645435	122.93	108.38	-1.29	0.017
211703_s_at	TM2D1	TM2 domain containing 1	83941	Hs.656790	108.00	131.86	1.49	0.017
219329_s_at	C2orf28	chromosome 2 open reading frame 28	51374	Hs.9527	667.27	766.51	1.32	0.017
220246_at	CAMK1D	calcium/calmodulin-dependent protein kinase ID	57118	Hs.659517	38.64	34.56	-1.25	0.017
214365_at	TPM3	tropomyosin 3	7170	Hs.535581, Hs.644306, Hs.654421	239.43	373.63	2.44	0.017
201472_at	VBP1	von Hippel-Lindau binding protein 1	7411	Hs.436803	446.42	549.01	1.51	0.017
221453_at	G6PC2	glucose-6-phosphatase, catalytic, 2	57818	Hs.283963	71.69	64.22	-1.25	0.017
202022_at	ALDOC	aldolase C, fructose-bisphosphate	230	Hs.155247	621.75	740.42	1.42	0.017
213925_at	C1orf95	chromosome 1 open reading frame 95	375057	Hs.116827, Hs.592751	94.78	82.11	-1.33	0.017
218386_x_at	USP16	ubiquitin specific peptidase 16	10600	Hs.99819	188.23	233.14	1.53	0.018
208749_x_at	FLOT1	flotillin 1	10211	Hs.179986	994.69	1097.99	1.22	0.018
220059_at	STAP1	signal transducing adaptor family member 1	26228	Hs.435579	23.97	21.82	-1.21	0.018
219916_s_at	RNF39	ring finger protein 39	80352	Hs.121178	134.82	118.61	-1.29	0.018
220603_s_at	MCTP2	multiple C2 domains, transmembrane 2	55784	Hs.592017	37.54	33.85	-1.23	0.018
202488_s_at	FXYD3	FXYD domain containing ion transport regulator 3	5349	Hs.301350	230.03	205.64	-1.25	0.018
208468_at	SOX21	SRY (sex determining region Y)-box 21	11166	Hs.187577	67.45	58.66	-1.32	0.018
220620_at	CRCT1	cysteine-rich C-terminal 1	54544	Hs.110196	21.10	19.04	-1.23	0.018
206520_x_at	SIGLEC6	sialic acid binding Ig-like lectin 6	946	Hs.397255	104.30	94.62	-1.22	0.018
217768_at	C14orf166	chromosome 14 open reading frame 166	51637	Hs.534457	796.50	924.44	1.35	0.018
210864_x_at	HFE	hemochromatosis	3077	Hs.233325	213.44	189.07	-1.27	0.018

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
207209_at	CETN1	centrin, EF-hand protein, 1	1068	Hs.122511	111.26	100.82	-1.22	0.018
203661_s_at	TMOD1	tropomodulin 1	7111	Hs.494595	662.37	770.57	1.35	0.018
202472_at	MPI	mannose phosphate isomerase	4351	Hs.75694	123.59	137.48	1.24	0.018
206617_s_at	RENBP	renin binding protein	5973	Hs.158331	81.51	73.51	-1.23	0.018
218866_s_at	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	51728	Hs.632223	81.61	91.04	1.24	0.018
207060_at	EN2	engrailed homeobox 2	2020	Hs.134989	42.39	38.54	-1.21	0.018
215638_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	2065	Hs.118681	47.98	42.83	-1.26	0.018
211532_x_at	KIR2DS2	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2	3807	Hs.512572, Hs.654605	52.74	46.89	-1.27	0.018
210712_at	LDHAL6B	lactate dehydrogenase A-like 6B	92483	Hs.307052	19.22	17.02	-1.28	0.018
208742_s_at	SAP18	Sin3A-associated protein, 18kDa	10284	Hs.524899	826.35	982.87	1.41	0.018
217147_s_at	TRAT1	T cell receptor associated transmembrane adaptor 1	50852	Hs.138701	16.60	15.32	-1.17	0.018
220496_at	CLEC1B	C-type lectin domain family 1, member B	51266	Hs.409794	34.41	31.67	-1.18	0.018
206985_at	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	3293	Hs.477	100.82	91.43	-1.22	0.018
208578_at	SCN10A	sodium channel, voltage-gated, type X, alpha subunit	6336	Hs.250443	152.95	132.59	-1.33	0.018
203768_s_at	STS	steroid sulfatase (microsomal), isozyme S	412	Hs.522578	106.75	95.42	-1.25	0.018
216881_x_at	PRB4	proline-rich protein BstNI subfamily 4	5545	Hs.528651	114.61	102.54	-1.25	0.018
205884_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	3676	Hs.694732	16.41	14.47	-1.29	0.018
219181_at	LIPG	lipase, endothelial	9388	Hs.465102	31.21	28.63	-1.19	0.018
204691_x_at	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	8398	Hs.170479	191.18	174.67	-1.20	0.018
206872_at	SLC17A1	solute carrier family 17 (sodium phosphate), member 1	6568	Hs.205816	80.05	71.03	-1.27	0.018
204133_at	RRP9	RRP9, small subunit (SSU) processome	9136	Hs.153768	103.77	118.34	1.30	0.018

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		component, homolog (yeast)						
207940_x_at	CNR1	cannabinoid receptor 1 (brain)	1268	Hs.75110, Hs.690472	53.31	47.90	-1.24	0.018
217877_s_at	GPBP1L1	GC-rich promoter binding protein 1-like 1	60313	Hs.238432	274.67	308.14	1.26	0.018
220375_s_at			79808		118.07	107.46	-1.21	0.018
213680_at	KRT6C	keratin 6C	286887	Hs.654613	49.50	44.59	-1.23	0.018
201658_at	ARL1	ADP-ribosylation factor-like 1	400	Hs.372616	163.61	193.01	1.39	0.018
215788_at	LOC339457	hypothetical protein LOC339457	339457	Hs.259619	179.35	160.71	-1.25	0.018
211195_s_at	TP63	tumor protein p63	8626	Hs.137569	101.67	86.89	-1.37	0.018
203390_s_at	KIF3C	kinesin family member 3C	3797	Hs.21611	78.24	70.47	-1.23	0.018
206412_at	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	2241	Hs.221472	58.22	53.99	-1.16	0.018
218285_s_at	BDH2	3-hydroxybutyrate dehydrogenase, type 2	56898	Hs.124696	128.66	152.73	1.41	0.018
209455_at	FBXW11	F-box and WD repeat domain containing 11	23291	Hs.484138	210.96	248.15	1.38	0.018
202858_at	U2AF1	U2 small nuclear RNA auxiliary factor 1	7307	Hs.365116	296.44	341.46	1.33	0.018
206279_at	PRKY	protein kinase, Y-linked	5616	Hs.632287	30.90	34.20	1.22	0.018
220348_at			80137		32.41	29.33	-1.22	0.018
207778_at	REGL	regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat)	5969	Hs.49407, Hs.584797, Hs.654603	75.66	67.16	-1.27	0.018
207403_at	IRS4	insulin receptor substrate 4	8471	Hs.592215	60.28	55.11	-1.20	0.018
220461_at	PCNXL2	pecanex-like 2 (Drosophila)	80003	Hs.370605	56.10	49.38	-1.29	0.018
205064_at	SPRR1B	small proline-rich protein 1B (cornifin)	6699	Hs.1076	43.17	39.54	-1.19	0.018
214606_at	TSPAN2	tetraspanin 2	10100	Hs.310458	11.38	10.78	-1.11	0.018
206991_s_at	CCR5	chemokine (C-C motif) receptor 5	1234	Hs.450802, Hs.536735	157.87	134.51	-1.38	0.018
64486_at	CORO1B	coronin, actin binding protein, 1B	57175	Hs.6191	251.62	229.78	-1.20	0.018
220243_at	ZBTB44	zinc finger and BTB domain containing 44	29068	Hs.178499	111.55	96.43	-1.34	0.018
220867_s_at	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	25769	Hs.283014	91.30	80.06	-1.30	0.018
206110_at	HIST1H3H	histone cluster 1, H3h	8357	Hs.591778	37.67	33.20	-1.29	0.019

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
215419_at	KIAA1086	KIAA1086	23217	Hs.65750	39.56	36.64	-1.17	0.019
221038_at			55474		21.52	20.39	-1.11	0.019
207021_at	ZPBP	zona pellucida binding protein	11055	Hs.388841	29.12	26.84	-1.18	0.019
212021_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	4288	Hs.80976	98.13	87.07	-1.27	0.019
221378_at	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	9350	Hs.248204	77.92	68.01	-1.31	0.019
208761_s_at	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	7341	Hs.81424, Hs.596171	192.99	232.20	1.45	0.019
204822_at	TTK	TTK protein kinase	7272	Hs.169840	17.05	15.68	-1.18	0.019
218651_s_at	LARP6	La ribonucleoprotein domain family, member 6	55323	Hs.416755	234.87	272.10	1.34	0.019
211778_s_at	OVOL2	ovo-like 2 (Drosophila)	58495	Hs.660749, Hs.661013	45.55	41.30	-1.22	0.019
220881_at			55470		57.65	50.04	-1.33	0.019
200903_s_at	AHCY	S-adenosylhomocysteine hydrolase	191	Hs.388004	119.75	139.31	1.35	0.019
201952_at	ALCAM	activated leukocyte cell adhesion molecule	214	Hs.591293	103.87	83.72	-1.54	0.019
220581_at	C6orf97	chromosome 6 open reading frame 97	80129	Hs.660044	36.63	33.02	-1.23	0.019
220359_s_at	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	10777	Hs.475902	20.14	18.42	-1.20	0.019
201287_s_at	SDC1	syndecan 1	6382	Hs.224607	67.77	59.49	-1.30	0.019
218142_s_at	CRBN	cereblon	51185	Hs.18925	257.68	304.00	1.39	0.019
208045_at	SPAR	surfactant protein A binding protein	9981		18.01	16.90	-1.14	0.019
208434_at	MDS1	myelodysplasia syndrome 1	4197	Hs.656395, Hs.659873	45.78	39.79	-1.32	0.019
219792_at	AGMAT	agmatine ureohydrolase (agmatinase)	79814	Hs.567583	47.35	42.84	-1.22	0.019
220347_at			80091		34.64	30.52	-1.29	0.019
201774_s_at	NCAPD2	non-SMC condensin I complex, subunit D2	9918	Hs.5719	42.93	38.89	-1.22	0.019
202025_x_at	ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	30	Hs.693598	323.67	361.14	1.24	0.019
200913_at	PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	5496	Hs.17883	162.28	181.03	1.24	0.019

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
203594_at	RTCD1	RNA terminal phosphate cyclase domain 1	8634	Hs.552835	116.58	149.95	1.65	0.019
221145_at			55371		21.03	19.58	-1.15	0.019
221184_at			80159		43.27	38.50	-1.26	0.019
216832_at	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	862	Hs.368431	125.00	113.25	-1.22	0.019
200915_x_at	KTN1	kinectin 1 (kinesin receptor)	3895	Hs.509414	771.51	915.18	1.41	0.019
219829_at	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	26548	Hs.109999	408.73	481.22	1.39	0.019
219030_at	TPRKB	TP53RK binding protein	51002	Hs.157401	98.60	123.47	1.57	0.020
204510_at	CDC7	cell division cycle 7 homolog (S. cerevisiae)	8317	Hs.533573	26.36	24.21	-1.19	0.020
217911_s_at	BAG3	BCL2-associated athanogene 3	9531	Hs.523309	694.01	825.29	1.41	0.020
204474_at	ZNF142	zinc finger protein 142	7701	Hs.657969	131.69	118.76	-1.23	0.020
220094_s_at	CCDC90A	coiled-coil domain containing 90A	63933	Hs.214043	184.11	223.92	1.48	0.020
208676_s_at	PA2G4	proliferation-associated 2G4, 38kDa	5036	Hs.524498, Hs.573018	260.27	287.85	1.22	0.020
204702_s_at	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	9603	Hs.404741, Hs.651505	16.10	15.04	-1.14	0.020
218083_at	PTGES2	prostaglandin E synthase 2	80142	Hs.495219	333.19	379.49	1.30	0.020
201241_at	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	1653	Hs.440599	765.31	895.51	1.37	0.020
210518_at	CDH8	cadherin 8, type 2	1006	Hs.368322	32.03	29.15	-1.21	0.020
203169_at	KIAA0258	KIAA0258	9827	Hs.493804	84.80	94.02	1.23	0.020
219956_at	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	11226	Hs.505575	38.11	34.33	-1.23	0.020
210442_at	IL1RL1	interleukin 1 receptor-like 1	9173	Hs.66	104.36	92.75	-1.27	0.020
220623_s_at	TSGA10	testis specific, 10	80705	Hs.120267	29.90	27.52	-1.18	0.020
206538_at	MRAS	muscle RAS oncogene homolog	22808	Hs.527021	172.48	199.57	1.34	0.020
206180_x_at	ZNF747	zinc finger protein 747	65988	Hs.592032	276.14	241.78	-1.30	0.020
221388_at	OR1A1	olfactory receptor, family 1, subfamily A, member 1	8383	Hs.532688	53.27	46.46	-1.31	0.020
214354_x_at	SFTPB	surfactant, pulmonary-associated protein B	6439	Hs.512690	167.76	144.32	-1.35	0.020
208517_x_at	BTF3	basic transcription factor 3	689	Hs.591768	1340.37	1525.63	1.30	0.020

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
210762_s_at	DLC1	deleted in liver cancer 1	10395	Hs.134296	283.72	350.31	1.52	0.020
206887_at	CCBP2	chemokine binding protein 2	1238	Hs.656595	70.80	63.19	-1.26	0.020
221412_at	VN1R1	vomeronasal 1 receptor 1	57191	Hs.388810, Hs.677423	22.97	21.18	-1.18	0.020
207185_at	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	6554	Hs.952	110.64	96.76	-1.31	0.020
215211_at	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	730092	Hs.31290, Hs.348979	74.30	67.06	-1.23	0.020
205948_at	PTPRT	protein tyrosine phosphatase, receptor type, T	11122	Hs.526879	114.62	102.46	-1.25	0.020
212231_at	FBXO21	F-box protein 21	23014	Hs.159699	199.25	229.69	1.33	0.020
205599_at	TRAF1	TNF receptor-associated factor 1	7185	Hs.531251	67.35	59.98	-1.26	0.020
221022_s_at	PMFBP1	polyamine modulated factor 1 binding protein 1	83449	Hs.151218	75.69	66.44	-1.30	0.020
207445_s_at	CCR9	chemokine (C-C motif) receptor 9	10803	Hs.225946	23.15	21.23	-1.19	0.020
222327_x_at	OR7E156P	olfactory receptor, family 7, subfamily E, member 156 pseudogene	283491	Hs.363054, Hs.694575	104.86	95.88	-1.20	0.020
221430_s_at	RNF146	ring finger protein 146	81847	Hs.267120	106.39	139.78	1.73	0.020
211388_s_at			51044		66.15	60.42	-1.20	0.020
206799_at	SCGB1D2	secretoglobin, family 1D, member 2	10647	Hs.204096	36.94	32.72	-1.27	0.020
205336_at	PVALB	parvalbumin	5816	Hs.295449	86.88	79.43	-1.20	0.020
44822_s_at	MIER2	mesoderm induction early response 1, family member 2	54531	Hs.101891	176.25	160.63	-1.20	0.020
204744_s_at	IARS	isoleucyl-tRNA synthetase	3376	Hs.445403	371.55	437.34	1.39	0.020
202121_s_at	CHMP2A	chromatin modifying protein 2A	27243	Hs.12107	351.45	410.22	1.36	0.020
207865_s_at	BMP8B	bone morphogenetic protein 8b (osteogenic protein 2)	656	Hs.664022	31.32	28.37	-1.22	0.020
220745_at	IL19	interleukin 19	29949	Hs.661017	129.77	117.00	-1.23	0.020
201906_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	10217	Hs.475963	188.26	215.23	1.31	0.020
212330_at	TFDP1	transcription factor Dp-	7027	Hs.79353	141.55	164.08	1.34	0.020

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		1						
201524_x_at	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	7334	Hs.524630	486.07	546.92	1.27	0.020
207811_at	KRT12	keratin 12 (Meesmann corneal dystrophy)	3859	Hs.66739	40.80	36.82	-1.23	0.020
204603_at	EXO1	exonuclease 1	9156	Hs.498248	57.56	51.22	-1.26	0.020
208941_s_at	SEPHS1	selenophosphate synthetase 1	22929	Hs.124027	141.02	154.42	1.20	0.020
216676_x_at	KIR3DL3	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	115653	Hs.645224	89.02	80.57	-1.22	0.021
202916_s_at	FAM20B	family with sequence similarity 20, member B	9917	Hs.5737, Hs.77961, Hs.449621, Hs.618326	109.56	125.69	1.32	0.021
205747_at	CBLN1	cerebellin 1 precursor	869	Hs.458423	28.64	25.85	-1.23	0.021
209813_x_at	TRGV9	T cell receptor gamma variable 9	6983	Hs.534032	83.75	70.59	-1.41	0.021
206120_at	CD33	CD33 molecule	945	Hs.83731	181.14	158.44	-1.31	0.021
208076_at	HIST1H4D	histone cluster 1, H4d	8360	Hs.248179	35.08	31.41	-1.25	0.021
216134_at	FRMD4B	FERM domain containing 4B	23150	Hs.371681	49.10	45.24	-1.18	0.021
216226_at	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	6875	Hs.369519	49.37	44.48	-1.23	0.021
201823_s_at	RNF14	ring finger protein 14	9604	Hs.483616	101.13	133.70	1.75	0.021
206873_at	CA6	carbonic anhydrase VI	765	Hs.100322	89.81	81.66	-1.21	0.021
216862_s_at	MTCP1	mature T-cell proliferation 1	4515	Hs.6917	456.93	531.95	1.36	0.021
215969_at	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria)	5277	Hs.137154	17.65	16.21	-1.18	0.021
200738_s_at	PGK1	phosphoglycerate kinase 1	5230	Hs.78771	1372.96	1568.19	1.30	0.021
221125_s_at	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	27094	Hs.591285	85.73	78.22	-1.20	0.021
220250_at	ZNF286A	zinc finger protein 286A	57335	Hs.585799, Hs.659318, Hs.660199	70.13	63.81	-1.21	0.021
213266_at	76P	gamma tubulin ring	27229	Hs.654843	116.23	102.54	-1.28	0.021

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		complex protein (76p gene)						
201950_x_at	CAPZB	capping protein (actin filament) muscle Z-line, beta	832	Hs.432760	522.73	620.87	1.41	0.021
209174_s_at	QRICH1	glutamine-rich 1	54870	Hs.297389	218.35	238.97	1.20	0.021
201805_at	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	5571	Hs.530862	526.55	592.23	1.27	0.021
211811_s_at	PCDHA6	protocadherin alpha 6	56142	Hs.199343, Hs.570901, Hs.599714, Hs.621225	22.06	20.17	-1.20	0.021
217102_at	MAG	malignancy-associated protein	27307	Hs.348346	146.99	132.46	-1.23	0.021
207534_at	MAGEB1	melanoma antigen family B, 1	4112	Hs.73021	22.38	20.77	-1.16	0.021
202504_at	TRIM29	tripartite motif-containing 29	23650	Hs.504115	108.63	98.13	-1.23	0.021
204385_at	KYNU	kynureninase (L-kynurenine hydrolase)	8942	Hs.470126	160.22	145.17	-1.22	0.021
202783_at	NNT	nicotinamide nucleotide transhydrogenase	23530	Hs.482043	317.38	410.94	1.68	0.021
205673_s_at	ASB9	ankyrin repeat and SOCS box-containing 9	140462	Hs.19404	47.90	43.64	-1.20	0.021
216714_at	CCL13	chemokine (C-C motif) ligand 13	6357	Hs.414629	98.36	88.65	-1.23	0.021
209063_x_at	LOC645139	similar to poly(A) binding protein interacting protein 1 isoform 1	645139	Hs.567929	284.50	333.31	1.37	0.021
221199_at	GFRA4	GDNF family receptor alpha 4	64096	Hs.302025	132.92	119.18	-1.24	0.021
200681_at	GLO1	glyoxalase I	2739	Hs.268849	665.35	762.86	1.31	0.021
205587_at	FGFR1OP	FGFR1 oncogene partner	11116	Hs.487175	63.87	57.19	-1.25	0.021
206334_at	LIPF	lipase, gastric	8513	Hs.523130	23.45	21.84	-1.15	0.021
218549_s_at	FAM82B	family with sequence similarity 82, member B	51115	Hs.145386	131.77	163.28	1.54	0.021
206119_at	BHMT	betaine-homocysteine methyltransferase	635	Hs.80756	87.82	76.40	-1.32	0.021
221247_s_at	WBSCR16	Williams-Beuren syndrome chromosome region 16	81554	Hs.647031	161.74	178.99	1.22	0.021
219334_s_at	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	64859	Hs.591610	12.01	11.37	-1.12	0.021
203588_s_at	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	7029	Hs.379018	139.16	153.15	1.21	0.021
212627_s_at	EXOSC7	exosome component 7	23016	Hs.115792	179.01	203.51	1.29	0.021

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
219051_x_at	METRN	meteorin, glial cell differentiation regulator	79006	Hs.533772	184.27	224.01	1.48	0.021
206189_at	UNC5C	unc-5 homolog C (C. elegans)	8633	Hs.584831	24.33	22.58	-1.16	0.021
220179_at	DPEP3	dipeptidase 3	64180	Hs.302028	59.19	53.85	-1.21	0.021
207364_at	TEX28	testis expressed 28	1527	Hs.115365	56.23	50.41	-1.24	0.021
208182_x_at	IFNA14	interferon, alpha 14	3448	Hs.93907	64.91	57.14	-1.29	0.021
204890_s_at	LCK	lymphocyte-specific protein tyrosine kinase	3932	Hs.470627	57.64	49.11	-1.38	0.022
205411_at	STK4	serine/threonine kinase 4	6789	Hs.472838	38.91	35.59	-1.20	0.022
208564_at	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2	3737	Hs.248139, Hs.657199	65.46	59.04	-1.23	0.022
219716_at	APOL6	apolipoprotein L, 6	80830	Hs.257352	82.09	70.36	-1.36	0.022
218867_s_at	C12orf49	chromosome 12 open reading frame 49	79794	Hs.592011	87.23	77.70	-1.26	0.022
217918_at	DYNLRB1	dynein, light chain, roadblock-type 1	83658	Hs.593920	719.64	827.96	1.32	0.022
208427_s_at	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	1993	Hs.166109	15.12	13.98	-1.17	0.022
201336_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	9341	Hs.66708	596.71	676.66	1.29	0.022
220882_at			55476		126.39	113.96	-1.23	0.022
217837_s_at	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	51652	Hs.591582	344.56	406.14	1.39	0.022
218666_s_at	STX17	syntaxin 17	55014	Hs.655706	100.54	90.14	-1.24	0.022
210029_at	INDO	indoleamine-pyrrole 2,3 dioxygenase	3620	Hs.840	125.94	103.54	-1.48	0.022
202793_at	MBOAT5	membrane bound O-acyltransferase domain containing 5	10162	Hs.655248	78.99	90.34	1.31	0.022
215124_at	ZNF550	zinc finger protein 550	162972	Hs.180257	53.53	48.30	-1.23	0.022
208350_at	CSN1S1	casein alpha s1	1446	Hs.3155	20.77	19.40	-1.15	0.022
221275_s_at			79826		29.16	26.94	-1.17	0.022
203880_at	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	10063	Hs.534383	505.42	605.15	1.43	0.022
215186_at	KIAA0984	KIAA0984 protein	23329	Hs.192492	78.70	70.99	-1.23	0.022
210950_s_at	FDFT1	farnesyl-diphosphate farnesyltransferase 1	2222	Hs.593928	446.38	503.99	1.27	0.022
212266_s_at	SFRS5	splicing factor, arginine/serine-rich 5	6430	Hs.632326	545.03	682.28	1.57	0.022
216273_at	ZNF460	zinc finger protein 460	10794	Hs.99971	111.16	100.00	-1.24	0.022

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
205829_at	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	3292	Hs.654385, Hs.655222	15.48	14.28	-1.18	0.022
218755_at	KIF20A	kinesin family member 20A	10112	Hs.73625	24.57	22.11	-1.24	0.022
215251_at	SHANK2	SH3 and multiple ankyrin repeat domains 2	22941	Hs.268726	43.63	39.38	-1.23	0.022
220381_at	ARHGAP28	Rho GTPase activating protein 28	79822	Hs.183114	43.24	39.49	-1.20	0.022
206569_at	IL24	interleukin 24	11009	Hs.58831, Hs.658964	34.21	31.38	-1.19	0.022
201527_at	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	9296	Hs.78089	560.60	636.32	1.29	0.022
210092_at	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	4116	Hs.421576	67.95	82.46	1.47	0.022
209076_s_at	WDR45L	WDR45-like	56270	Hs.132161	243.62	274.28	1.27	0.022
221382_at	OR2N1P	olfactory receptor, family 2, subfamily N, member 1 pseudogene	26701		158.33	139.38	-1.29	0.022
219600_s_at	TMEM50B	transmembrane protein 50B	757	Hs.433668	158.88	201.76	1.61	0.022
215809_at	CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	1565	Hs.648256	176.01	158.67	-1.23	0.022
220665_at	LUZP4	leucine zipper protein 4	51213	Hs.242183	91.05	82.94	-1.21	0.022
221600_s_at	C11orf67	chromosome 11 open reading frame 67	28971	Hs.503357	217.43	255.01	1.38	0.022
221238_at	NSBP1	nucleosomal binding protein 1	79366	Hs.282204	26.69	24.49	-1.19	0.022
211753_s_at	RLN1	relaxin 1	6013	Hs.368996	37.52	34.81	-1.16	0.022
209393_s_at	EIF4E2	eukaryotic translation initiation factor 4E family member 2	9470	Hs.292026, Hs.693903	144.94	166.47	1.32	0.022
213133_s_at	GCSH	glycine cleavage system protein H (aminomethyl carrier)	2653	Hs.546256	230.79	272.79	1.40	0.022
201015_s_at	JUP	junction plakoglobin	3728	Hs.514174	345.89	407.84	1.39	0.022
220294_at	KCNV1	potassium channel, subfamily V, member 1	27012	Hs.13285	14.57	13.68	-1.13	0.022
202840_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	8148	Hs.402752	101.80	124.01	1.48	0.022
216800_at			84198		71.51	65.03	-1.21	0.022
217998_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	22822	Hs.602085	222.36	197.63	-1.27	0.022

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218616_at	INTS12	integrator complex subunit 12	57117	Hs.480454	112.18	129.78	1.34	0.022
200978_at	MDH1	malate dehydrogenase 1, NAD (soluble)	4190	Hs.526521	4744.34	5276.81	1.24	0.022
211938_at	EIF4B	eukaryotic translation initiation factor 4B	1975	Hs.648394, Hs.655133	723.37	826.21	1.30	0.022
59433_at	LOC729137	hypothetical protein LOC729137	729137	Hs.636199	66.32	59.78	-1.23	0.022
212833_at	SLC25A46	solute carrier family 25, member 46	91137	Hs.75639	194.47	238.55	1.50	0.022
217980_s_at	MRPL16	mitochondrial ribosomal protein L16	54948	Hs.530734	270.91	311.31	1.32	0.023
206367_at	REN	renin	5972	Hs.3210	77.25	69.24	-1.24	0.023
206571_s_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	9448	Hs.431550	92.31	107.15	1.35	0.023
216673_at	TTTY1	testis-specific transcript, Y-linked 1	50858	Hs.694006	53.90	49.22	-1.20	0.023
201832_s_at	VDP	vesicle docking protein p115	8615	Hs.292689	372.15	435.72	1.37	0.023
203774_at	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	4548	Hs.498187	83.87	100.83	1.45	0.023
213449_at	POP1	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	10940	Hs.252828	41.97	37.71	-1.24	0.023
214645_at			80103		15.06	14.10	-1.14	0.023
205778_at	KLK7	kallikrein-related peptidase 7	5650	Hs.151254	42.97	39.43	-1.19	0.023
214796_at	C8orf79	chromosome 8 open reading frame 79	57604	Hs.121518, Hs.202521, Hs.591846	14.86	13.90	-1.14	0.023
220009_at	LONRF3	LON peptidase N-terminal domain and ring finger 3	79836	Hs.144266	69.30	61.43	-1.27	0.023
212541_at	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	80308	Hs.118666	82.01	89.75	1.20	0.023
221381_s_at	MORF4	mortality factor 4	10934	Hs.534391	228.00	284.03	1.55	0.023
217955_at	BCL2L13	BCL2-like 13 (apoptosis facilitator)	23786	Hs.631672	132.93	161.21	1.47	0.023
205367_at	SH2B2	SH2B adaptor protein 2	10603	Hs.489448	71.08	62.02	-1.31	0.023
210434_x_at	JTB	jumping translocation breakpoint	10899	Hs.6396	855.75	950.85	1.23	0.023
215479_at	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	57556	Hs.156967	211.37	188.08	-1.26	0.023

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
206995_x_at	SCARF1	scavenger receptor class F, member 1	8578	Hs.647430	12.90	12.19	-1.12	0.023
207479_at			55477		18.74	17.59	-1.14	0.023
208384_s_at	MID2	midline 2	11043	Hs.12256	165.69	148.32	-1.25	0.023
216161_at	SBNO1	strawberry notch homolog 1 (Drosophila)	55206	Hs.577403	32.00	29.50	-1.18	0.023
38340_at	HIP1R	huntingtin interacting protein 1 related	9026	Hs.524815, Hs.654842	196.03	176.34	-1.24	0.023
214772_at	C11orf41	chromosome 11 open reading frame 41	25758	Hs.22270, Hs.502266	20.69	19.16	-1.17	0.023
222015_at	CSNK1E	casein kinase 1, epsilon	1454	Hs.474833	184.67	167.96	-1.21	0.023
214614_at	MNX1	motor neuron and pancreas homeobox 1	3110	Hs.37035	100.60	92.11	-1.19	0.023
202078_at	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	8533	Hs.6076	225.89	258.58	1.31	0.024
215284_at	SNX9	sorting nexin 9	51429	Hs.191213	20.63	19.06	-1.17	0.024
206273_at	SLMO1	slowmo homolog 1 (Drosophila)	10650	Hs.514718	56.29	50.44	-1.25	0.024
216517_at	IGKV1D-8	immunoglobulin kappa variable 1D-8	28904	Hs.574701	24.76	22.07	-1.26	0.024
212806_at			23273		18.02	16.67	-1.17	0.024
208847_s_at	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	128	Hs.78989	396.90	458.48	1.33	0.024
205137_x_at	USH1C	Usher syndrome 1C (autosomal recessive, severe)	10083	Hs.502072	100.06	88.28	-1.28	0.024
221172_at	FLJ21075	hypothetical protein FLJ21075	80099	Hs.287647	60.76	54.54	-1.24	0.024
216291_at	ZNF440	zinc finger protein 440	126070	Hs.418192	23.00	21.03	-1.20	0.024
220218_at	C9orf68	chromosome 9 open reading frame 68	55064	Hs.179615	25.77	23.57	-1.19	0.024
219903_s_at	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	1558	Hs.282871	23.92	22.19	-1.16	0.024
214646_at	HIST1H3J	histone cluster 1, H3j	8356	Hs.484990	64.92	57.54	-1.27	0.024
209804_at	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	9937	Hs.1560	68.96	63.72	-1.17	0.024
206846_s_at	HDAC6	histone deacetylase 6	10013	Hs.6764	183.04	167.96	-1.19	0.024
215821_x_at	PSG1	pregnancy specific beta-1-glycoprotein 1	5669	Hs.654413	147.12	129.36	-1.29	0.024
212145_at	MRPS27	mitochondrial ribosomal protein S27	23107	Hs.482491	271.86	307.03	1.28	0.024
209893_s_at	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2526	Hs.390420, Hs.572064, Hs.623098	50.88	46.30	-1.21	0.024

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
204073_s_at	C11orf9	chromosome 11 open reading frame 9	745	Hs.473109	71.00	64.03	-1.23	0.024
221271_at	IL21	interleukin 21	59067	Hs.567559	87.59	79.85	-1.20	0.024
203418_at	CCNA2	cyclin A2	890	Hs.58974	37.52	34.05	-1.21	0.024
215527_at	KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2	202559	Hs.519794	85.31	75.64	-1.27	0.024
211978_x_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	5478	Hs.356331, Hs.598115	2393.54	2653.42	1.23	0.024
207780_at	CYLC2	cylicin, basic protein of sperm head cytoskeleton 2	1539	Hs.3232	26.37	24.41	-1.17	0.024
219584_at	PLA1A	phospholipase A1 member A	51365	Hs.437451	59.86	49.50	-1.46	0.024
201499_s_at	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	7874	Hs.386939	294.59	331.21	1.26	0.024
211381_x_at	SPAG11B	sperm associated antigen 11B	10407	Hs.2717	34.70	30.76	-1.27	0.024
201027_s_at	EIF5B	eukaryotic translation initiation factor 5B	9669	Hs.158688	289.53	343.26	1.41	0.024
214607_at	PAK3	p21 (CDKN1A)-activated kinase 3	5063	Hs.656789	126.52	111.79	-1.28	0.024
203039_s_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	4719	Hs.471207	808.17	948.24	1.38	0.024
212535_at	LYSMD4	LysM, putative peptidoglycan-binding, domain containing 4	145748	Hs.562568	683.97	788.78	1.33	0.024
217615_at	LRRC37A	leucine rich repeat containing 37A	9884	Hs.656994	38.32	35.01	-1.20	0.024
210695_s_at	WWOX	WW domain containing oxidoreductase	51741	Hs.461453	202.40	185.33	-1.19	0.024
205861_at	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	6689	Hs.437905	77.57	69.43	-1.25	0.024
218970_s_at	CUTC	cutC copper transporter homolog (E. coli)	51076	Hs.16606	145.78	169.91	1.36	0.024
213557_at			23106		83.82	77.67	-1.16	0.024
203814_s_at	NQO2	NAD(P)H dehydrogenase, quinone 2	4835	Hs.533050	220.23	286.63	1.69	0.024
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	9837	Hs.658464	20.39	18.60	-1.20	0.024
216493_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	10643	Hs.648088	22.92	21.44	-1.14	0.024

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214476_at	TFF2	trefoil factor 2 (spasmolytic protein 1)	7032	Hs.2979	53.04	47.70	-1.24	0.024
202290_at	PDAP1	PDGFA associated protein 1	11333	Hs.632296	121.02	153.66	1.61	0.024
208622_s_at	VIL2	villin 2 (ezrin)	7430	Hs.693594	281.38	349.49	1.54	0.024
220689_at	NODAL	nodal homolog (mouse)	4838	Hs.370414	107.52	95.12	-1.28	0.024
204565_at	THEM2	thioesterase superfamily member 2	55856	Hs.9676	299.74	356.24	1.41	0.024
211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	26018	Hs.518055	210.27	251.61	1.43	0.024
214493_s_at	INADL	InaD-like (Drosophila)	10207	Hs.478125	29.42	34.18	1.35	0.024
208573_s_at	OR2H2	olfactory receptor, family 2, subfamily H, member 2	7932	Hs.529493, Hs.639423	41.50	37.27	-1.24	0.024
201630_s_at	ACP1	acid phosphatase 1, soluble	52	Hs.558296	279.76	322.16	1.33	0.024
213444_at	LOC643641	hypothetical protein LOC643641	643641	Hs.301277, Hs.694815	198.16	181.79	-1.19	0.024
207781_s_at	ZNF711	zinc finger protein 711	7552	Hs.326801	12.04	11.48	-1.10	0.024
205156_s_at	ACCN2	amiloride-sensitive cation channel 2, neuronal	41	Hs.274361, Hs.647113	202.78	184.84	-1.20	0.024
216973_s_at	HOXB7	homeobox B7	3217	Hs.436181	59.33	55.95	-1.12	0.024
217990_at	GMPR2	guanosine monophosphate reductase 2	51292	Hs.368855	130.75	145.58	1.24	0.025
219704_at	YBX2	Y box binding protein 2	51087	Hs.567494	67.13	61.58	-1.19	0.025
211481_at	SLCO1A2	solute carrier organic anion transporter family, member 1A2	6579	Hs.46440	85.72	78.46	-1.19	0.025
207614_s_at	CUL1	cullin 1	8454	Hs.146806	120.59	141.15	1.37	0.025
220422_at	UBQLN3	ubiquilin 3	50613	Hs.189184	32.94	29.82	-1.22	0.025
210963_s_at	GYG2	glycogenin 2	8908	Hs.567381	87.28	77.91	-1.25	0.025
212530_at	NEK7	NIMA (never in mitosis gene a)-related kinase 7	140609	Hs.24119	764.04	970.27	1.61	0.025
206212_at	CPA2	carboxypeptidase A2 (pancreatic)	1358	Hs.490038	77.14	69.67	-1.23	0.025
205348_s_at	DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1	1780	Hs.440364	181.84	214.58	1.39	0.025
202188_at	NUP93	nucleoporin 93kDa	9688	Hs.276878	158.58	171.64	1.17	0.025
202255_s_at	SIPA1L1	signal-induced proliferation-associated 1 like 1	26037	Hs.654657	119.78	109.86	-1.19	0.025
205896_at	SLC22A4	solute carrier family 22 (organic cation transporter), member 4	6583	Hs.310591, Hs.640104	44.68	40.77	-1.20	0.025
218487_at	ALAD	aminolevulinate, delta-, dehydratase	210	Hs.1227	180.19	214.66	1.42	0.025

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205899_at	CCNA1	cyclin A1	8900	Hs.417050	30.94	28.75	-1.16	0.025
216945_x_at	PASK	PAS domain containing serine/threonine kinase	23178	Hs.694813	64.69	57.97	-1.25	0.025
211460_at	TTTY9A	testis-specific transcript, Y-linked 9A	83864	Hs.567607	48.52	43.43	-1.25	0.025
221690_s_at	NLRP2	NLR family, pyrin domain containing 2	55655	Hs.369279	41.39	38.44	-1.16	0.025
200982_s_at	ANXA6	annexin A6	309	Hs.412117	348.77	428.96	1.51	0.025
219191_s_at	BIN2	bridging integrator 2	51411	Hs.14770	84.07	71.97	-1.36	0.025
208189_s_at	MYO7A	myosin VIIA	4647	Hs.370421	131.37	116.47	-1.27	0.025
202136_at	ZMYND11	zinc finger, MYND domain containing 11	10771	Hs.292265	406.08	486.85	1.44	0.025
217099_s_at	GEMIN4	gem (nuclear organelle) associated protein 4	50628	Hs.499620	140.69	128.37	-1.20	0.025
207243_s_at	CALM2	calmodulin 2 (phosphorylase kinase, delta)	805	Hs.282410, Hs.643483	3220.25	3547.64	1.21	0.025
211011_at	COL19A1	collagen, type XIX, alpha 1	1310	Hs.444842	29.06	27.02	-1.16	0.025
214636_at	CALCB	calcitonin-related polypeptide, beta	797	Hs.534305	20.84	19.48	-1.14	0.025
222099_s_at	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	26065	Hs.407368	198.53	218.99	1.22	0.025
215463_at	OR7E24	olfactory receptor, family 7, subfamily E, member 24	26648	Hs.129832	25.96	23.61	-1.21	0.026
218011_at	UBL5	ubiquitin-like 5	59286	Hs.534477	362.52	430.57	1.41	0.026
200912_s_at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	1974	Hs.599481, Hs.654367	2002.45	2281.28	1.30	0.026
221398_at	TAS2R8	taste receptor, type 2, member 8	50836	Hs.533755	28.58	25.43	-1.26	0.026
219688_at	BBS7	Bardet-Biedl syndrome 7	55212	Hs.591694	11.72	11.17	-1.10	0.026
201272_at	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	231	Hs.521212	988.72	1133.55	1.31	0.026
203413_at	NELL2	NEL-like 2 (chicken)	4753	Hs.505326	57.93	51.91	-1.25	0.026
220752_at	LOC51145	erythrocyte transmembrane protein	51145	Hs.104671	19.90	18.03	-1.22	0.026
215048_at	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	140883	Hs.43834	43.48	40.28	-1.17	0.026
217033_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	4916	Hs.410969, Hs.680479	238.53	213.65	-1.25	0.026
220466_at	CCDC15	coiled-coil domain containing 15	80071	Hs.287555	61.00	55.60	-1.20	0.026
221241_s_at	BCL2L14	BCL2-like 14 (apoptosis facilitator)	79370	Hs.210343	131.52	118.09	-1.24	0.026

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201405_s_at	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	10980	Hs.15591	378.39	421.29	1.24	0.026
215020_at	NRXN3	neurexin 3	9369	Hs.368307	66.07	59.57	-1.23	0.026
209173_at	AGR2	anterior gradient homolog 2 (Xenopus laevis)	10551	Hs.530009	34.14	31.47	-1.18	0.026
215652_at			84346		28.74	26.31	-1.19	0.026
220135_s_at	SLC7A9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	11136	Hs.408567	75.21	67.65	-1.24	0.026
205515_at	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	8492	Hs.654823	23.25	20.86	-1.24	0.026
221198_at	SCT	secretin	6343	Hs.632324	20.63	23.73	1.32	0.026
216288_at	CYSLTR1	cysteinyl leukotriene receptor 1	10800	Hs.201300	12.38	11.81	-1.10	0.026
220338_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	55103	Hs.644008	11.46	10.95	-1.09	0.026
221438_s_at	TEX12	testis expressed 12	56158	Hs.524039	12.79	12.24	-1.09	0.026
202885_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	5519	Hs.584790	77.11	70.74	-1.19	0.026
206777_s_at	CRYBB2	crystallin, beta B2	1415	Hs.373074	88.64	75.15	-1.39	0.026
211297_s_at	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	1022	Hs.184298	41.94	49.32	1.38	0.026
219510_at	POLQ	polymerase (DNA directed), theta	10721	Hs.241517	63.74	57.37	-1.23	0.026
209942_x_at	MAGEA3	melanoma antigen family A, 3	4102	Hs.417816	31.28	28.89	-1.17	0.026
213622_at	COL9A2	collagen, type IX, alpha 2	1298	Hs.418012	65.32	59.66	-1.20	0.026
213407_at	PHLPPL	PH domain and leucine rich repeat protein phosphatase-like	23035	Hs.531564	90.78	82.54	-1.21	0.026
217962_at	NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)	55505	Hs.14317	563.28	642.28	1.30	0.026
204818_at	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	3294	Hs.162795	31.93	29.06	-1.21	0.026
205988_at	CD84	CD84 molecule	8832	Hs.398093	124.09	108.19	-1.32	0.026
211682_x_at	UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	54490	Hs.653154	62.19	55.99	-1.23	0.026

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220435_at	SLC30A10	solute carrier family 30, member 10	55532	Hs.284450, Hs.679909	16.69	15.32	-1.19	0.026
206123_at	LLGL1	lethal giant larvae homolog 1 (Drosophila)	3996	Hs.513983	325.31	291.06	-1.25	0.026
201135_at	ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	1892	Hs.76394	897.76	1026.75	1.31	0.026
205675_at	MTTP	microsomal triglyceride transfer protein	4547	Hs.195799	27.55	25.51	-1.17	0.026
208785_s_at	KRTHB5	keratin, hair, basic, 5	643246	Hs.506947	330.92	386.78	1.37	0.026
217640_x_at	C18orf24	chromosome 18 open reading frame 24	220134	Hs.134726	12.25	11.56	-1.12	0.026
214612_x_at	MAGEA6	melanoma antigen family A, 6	4105	Hs.441113	15.70	14.71	-1.14	0.026
204798_at	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	4602	Hs.654446	23.23	21.27	-1.19	0.026
221084_at	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	9177	Hs.241377	68.56	62.40	-1.21	0.026
200063_s_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	4869	Hs.557550	980.23	1119.79	1.31	0.026
207049_at	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit	6334	Hs.436550	45.39	41.12	-1.22	0.026
206681_x_at	GP2	glycoprotein 2 (zymogen granule membrane)	2813	Hs.53985	153.03	138.48	-1.22	0.026
214938_x_at	HMGB1	high-mobility group box 1	3146	Hs.434102, Hs.593339, Hs.644368	1545.61	1745.90	1.28	0.026
206851_at	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	6037	Hs.73839	82.73	75.72	-1.19	0.026
209715_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	23468	Hs.632724	66.52	74.88	1.27	0.026
220313_at	GPR88	G protein-coupled receptor 88	54112	Hs.170053	14.19	13.38	-1.12	0.026
214569_at	IFNA5	interferon, alpha 5	3442	Hs.37113	18.64	17.08	-1.19	0.026
211870_s_at	PCDHA3	protocadherin alpha 3	56145	Hs.199343	82.69	73.99	-1.25	0.026
219509_at	MYOZ1	myozenin 1	58529	Hs.238756	164.64	145.39	-1.28	0.026
209338_at	TFCP2	transcription factor CP2	7024	Hs.48849	150.46	165.83	1.21	0.026
220621_at	FOXE3	forkhead box E3	2301	Hs.112968	32.86	30.67	-1.15	0.026
220759_at	FAM12B	family with sequence similarity 12, member B (epididymal)	64184	Hs.525202	19.25	17.80	-1.17	0.026
220374_at	KLHL28	kelch-like 28 (Drosophila)	54813	Hs.653206	62.96	58.13	-1.17	0.026

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212416_at	SCAMP1	secretory carrier membrane protein 1	9522	Hs.482587	185.66	211.17	1.29	0.026
203152_at	MRPL40	mitochondrial ribosomal protein L40	64976	Hs.431307	274.66	313.91	1.31	0.026
212862_at	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	8760	Hs.472027	213.10	244.54	1.32	0.026
215932_at	MAGEC2	melanoma antigen family C, 2	51438	Hs.123536	64.96	57.79	-1.26	0.026
219244_s_at	MRPL46	mitochondrial ribosomal protein L46	26589	Hs.534261	302.52	345.80	1.31	0.027
216038_x_at	DAXX	death-associated protein 6	1616	Hs.336916	119.60	108.98	-1.20	0.027
213323_s_at	ZC3H7B	zinc finger CCCH-type containing 7B	23264	Hs.592188	138.92	126.07	-1.21	0.027
200663_at	CD63	CD63 molecule	967	Hs.445570	2196.63	2430.90	1.22	0.027
213744_at	ATRNL1	attractin-like 1	26033	Hs.501127, Hs.648490	37.88	34.53	-1.20	0.027
202849_x_at	GRK6	G protein-coupled receptor kinase 6	2870	Hs.235116	232.17	212.64	-1.19	0.027
206291_at	NTS	neurotensin	4922	Hs.80962	33.64	30.74	-1.20	0.027
210633_x_at	KRT10	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	3858	Hs.99936	304.66	343.47	1.27	0.027
207188_at	CDK3	cyclin-dependent kinase 3	1018	Hs.593566	70.87	64.28	-1.22	0.027
207356_at	DEFB4	defensin, beta 4	1673	Hs.105924	111.82	100.47	-1.24	0.027
221189_s_at	TARS2	threonyl-tRNA synthetase 2, mitochondrial (putative)	80222	Hs.288974	137.93	152.22	1.22	0.027
221052_at	TDRKH	tudor and KH domain containing	11022	Hs.144439	46.52	40.05	-1.35	0.027
208081_s_at	ZNF442	zinc finger protein 442	79973	Hs.253193	16.92	15.55	-1.18	0.027
201425_at	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	217	Hs.632733	865.86	986.18	1.30	0.027
207612_at	WNT8B	wingless-type MMTV integration site family, member 8B	7479	Hs.421281	89.76	80.24	-1.25	0.027
212961_x_at	CXorf40B	chromosome X open reading frame 40B	541578	Hs.545950	186.96	212.51	1.29	0.027
213889_at	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	9487	Hs.499793, Hs.625050	111.63	103.92	-1.15	0.027
221282_x_at	RUNX2	runt-related transcription factor 2	860	Hs.535845	89.06	80.32	-1.23	0.027
208950_s_at	ALDH7A1	aldehyde dehydrogenase 7	501	Hs.483239	116.10	133.77	1.33	0.027

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		family, member A1						
218332_at	BEX1	brain expressed, X-linked 1	55859	Hs.334370	174.73	239.52	1.88	0.027
209536_s_at	EHD4	EH-domain containing 4	30844	Hs.143703	365.87	421.50	1.33	0.027
204105_s_at	NRCAM	neuronal cell adhesion molecule	4897	Hs.21422	37.95	34.96	-1.18	0.027
200896_x_at	HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	3068	Hs.506748	590.16	644.53	1.19	0.027
215837_x_at	PRO1621	PRO1621 protein	29007	Hs.632107	18.43	16.91	-1.19	0.027
204424_s_at	LMO3	LIM domain only 3 (rhombotin-like 2)	55885	Hs.504908	129.20	111.91	-1.33	0.027
217780_at	C19orf56	chromosome 19 open reading frame 56	51398	Hs.108969	533.15	607.36	1.30	0.027
206034_at	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	5271	Hs.368077	61.77	55.11	-1.26	0.027
213780_at	TCHH	trichohyalin	7062	Hs.553300	20.02	18.35	-1.19	0.027
206000_at	MEP1A	meprin A, alpha (PABA peptide hydrolase)	4224	Hs.179704	30.12	27.11	-1.23	0.027
218115_at	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	55723	Hs.26516	131.51	118.80	-1.23	0.027
208842_s_at	GORASP2	golgi reassembly stacking protein 2, 55kDa	26003	Hs.431317	261.80	294.91	1.27	0.027
214530_x_at	EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	2035	Hs.175437, Hs.695416	53.92	48.36	-1.24	0.027
203961_at	NEBL	nebulette	10529	Hs.5025	3077.39	3502.78	1.30	0.027
209004_s_at	FBXL5	F-box and leucine-rich repeat protein 5	26234	Hs.643433	171.27	218.09	1.62	0.027
206876_at	SIM1	single-minded homolog 1 (Drosophila)	6492	Hs.520293	17.01	15.56	-1.20	0.027
220458_at	FLJ10246	FLJ10246	55104	Hs.660687	33.57	31.07	-1.17	0.027
214893_x_at	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	610	Hs.124161	56.29	63.85	1.29	0.027
37831_at	SIPA1L3	signal-induced proliferation-associated 1 like 3	23094	Hs.655502	128.07	117.34	-1.19	0.027
202779_s_at	UBE2S	ubiquitin-conjugating enzyme E2S	27338	Hs.396393, Hs.592114	82.55	96.52	1.37	0.027
202383_at	JARID1C	jumonji, AT rich interactive domain 1C	8242	Hs.631768	251.90	225.50	-1.25	0.027
221370_at	ZNF73	zinc finger protein 73	7624		47.33	42.70	-1.23	0.027
219545_at	KCTD14	potassium channel	65987	Hs.407860	98.71	89.15	-1.23	0.027

Probe	**Symbol**	**Description**	**Gene**	**UniGene**	**Av Exp Female**	**Av Exp Male**	**Fold Change**	**adj P val**
		tetramerisation domain containing 14						
215312_at	LOC644776	similar to DNA repair protein RAD52 homolog	644776	Hs.179697	11.52	11.00	-1.10	0.027
202209_at	LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	27258	Hs.111632	479.85	546.21	1.30	0.027
205175_s_at	KHK	ketohexokinase (fructokinase)	3795	Hs.159525, Hs.567297	76.38	68.12	-1.26	0.028
214234_s_at	CYP3A5P2	cytochrome P450, family 3, subfamily A, polypeptide 5 pseudogene 2	79424	Hs.150276	36.80	32.12	-1.31	0.028
209139_s_at	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	8575	Hs.632540	149.01	180.04	1.46	0.028
203914_x_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	3248	Hs.655491	37.71	33.80	-1.24	0.028
217046_s_at	AGER	advanced glycosylation end product-specific receptor	177	Hs.693583	45.55	52.32	1.32	0.028
214953_s_at	APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	351	Hs.434980	330.60	464.19	1.97	0.028
214648_at	GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	2880	Hs.248129	33.43	30.47	-1.20	0.028
200043_at	ERH	enhancer of rudimentary homolog (Drosophila)	2079	Hs.509791	697.97	779.27	1.25	0.028
214082_at	CA5B	carbonic anhydrase VB, mitochondrial	11238	Hs.653287	76.40	70.01	-1.19	0.028
208349_at	TRPA1	transient receptor potential cation channel, subfamily A, member 1	8989	Hs.667156	60.61	55.98	-1.17	0.028
205939_at	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	1551	Hs.111944	47.23	43.40	-1.18	0.028
220167_s_at	TP53TG3	TP53TG3 protein	24150	Hs.592038	143.58	127.89	-1.26	0.028
206731_at	CNKSR2	connector enhancer of kinase suppressor of Ras 2	22866	Hs.632794	15.00	14.16	-1.12	0.028
216404_at	ATXN8OS	ataxin 8 opposite strand	6315	Hs.676453	119.36	109.30	-1.19	0.028
214529_at	TSHB	thyroid stimulating	7252	Hs.406687	64.63	59.31	-1.19	0.028

Probe	**Symbol**	**Description**	**Gene**	**UniGene**	**Av Exp Female**	**Av Exp Male**	**Fold Change**	**adj P val**
		hormone, beta						
204951_at	RHOH	ras homolog gene family, member H	399	Hs.654594, Hs.694951	107.92	95.15	-1.29	0.028
219575_s_at	PDF	peptide deformylase (mitochondrial)	64146	Hs.693727	57.32	64.35	1.26	0.028
201092_at	RBBP7	retinoblastoma binding protein 7	5931	Hs.495755	459.31	524.11	1.30	0.028
217170_at	TRA@	T cell receptor alpha locus	6955	Hs.74647	180.56	160.96	-1.26	0.028
206231_at	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	3780	Hs.158173	210.95	192.61	-1.20	0.028
220701_at			55451		58.55	51.38	-1.30	0.028
210657_s_at	4-Sep	septin 4	5414	Hs.287518	60.93	69.54	1.30	0.028
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	79094	Hs.155569	120.26	108.76	-1.22	0.028
220048_at	EDAR	ectodysplasin A receptor	10913	Hs.171971	54.01	49.03	-1.21	0.028
219259_at	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	64218	Hs.408846	267.48	242.59	-1.22	0.028
221511_x_at	CCPG1	cell cycle progression 1	9236	Hs.612814	397.08	458.97	1.34	0.028
214905_at	LOC145899	hypothetical protein LOC145899	145899	Hs.459035	42.65	39.03	-1.19	0.028
210004_at	OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	4973	Hs.412484	16.15	15.25	-1.12	0.028
203408_s_at	SATB1	SATB homeobox 1	6304	Hs.517717	256.61	299.77	1.36	0.028
216080_s_at	FADS3	fatty acid desaturase 3	3995	Hs.21765	138.79	169.94	1.50	0.028
201767_s_at	ELAC2	elaC homolog 2 (E. coli)	60528	Hs.434232	95.36	110.19	1.34	0.029
222220_s_at	TSNAXIP1	translin-associated factor X interacting protein 1	55815	Hs.632212	91.33	81.25	-1.26	0.029
200059_s_at	RHOA	ras homolog gene family, member A	387	Hs.247077	961.78	1129.65	1.38	0.029
205776_at	FMO5	flavin containing monooxygenase 5	2330	Hs.642706	34.60	31.52	-1.21	0.029
219915_s_at	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	117247	Hs.591327	58.65	55.25	-1.13	0.029
220056_at	IL22RA1	interleukin 22 receptor, alpha 1	58985	Hs.110915	38.26	34.86	-1.20	0.029
215593_at	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-	2651	Hs.519884	160.84	148.16	-1.18	0.029

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		branching enzyme (I blood group)						
201706_s_at	PEX19	peroxisomal biogenesis factor 19	5824	Hs.517232	239.38	270.50	1.28	0.029
211338_at	IFNA2	interferon, alpha 2	3440	Hs.211575	14.60	13.70	-1.13	0.029
214158_s_at	FABP1	fatty acid binding protein 1, liver	2168	Hs.380135	44.40	40.54	-1.20	0.029
212886_at	CCDC69	coiled-coil domain containing 69	26112	Hs.655336	112.33	136.32	1.47	0.029
202164_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	9337	Hs.26703	76.51	93.01	1.48	0.029
214758_at	WDR21A	WD repeat domain 21A	26094	Hs.331491	44.12	40.63	-1.18	0.029
211767_at	GINS4	GINS complex subunit 4 (Sld5 homolog)	84296	Hs.656996	26.30	24.31	-1.17	0.029
205602_x_at	PSG7	pregnancy specific beta-1-glycoprotein 7	5676	Hs.654467	91.57	82.57	-1.23	0.029
206256_at	CPN1	carboxypeptidase N, polypeptide 1	1369	Hs.2246	62.63	56.52	-1.23	0.029
201519_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	9868	Hs.227253	379.57	438.24	1.33	0.029
206376_at	SLC6A15	solute carrier family 6, member 15	55117	Hs.44424	23.86	22.05	-1.17	0.029
222153_at	MYEF2	myelin expression factor 2	50804	Hs.6638	12.50	11.82	-1.12	0.029
211289_x_at	CDC2L2	cell division cycle 2-like 2 (PITSLRE proteins)	728642	Hs.651228, Hs.654369	117.86	133.66	1.29	0.029
213553_x_at	APOC1	apolipoprotein C-I	341	Hs.110675	220.96	200.38	-1.22	0.029
206058_at	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	6539	Hs.437174	64.38	58.27	-1.22	0.029
207043_s_at	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	6536	Hs.442590	32.50	29.91	-1.18	0.029
211979_at	GPR107	G protein-coupled receptor 107	57720	Hs.512461	195.16	220.11	1.27	0.029
206760_s_at	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	2208	Hs.465778	57.14	50.37	-1.29	0.029
207538_at	IL4	interleukin 4	3565	Hs.73917	16.81	15.67	-1.15	0.029
219275_at	PDCD5	programmed cell death 5	9141	Hs.443831	96.78	114.93	1.41	0.029
221392_at	TAS2R4	taste receptor, type 2, member 4	50832	Hs.669863	32.24	28.76	-1.26	0.029
210925_at	CIITA	class II, major histocompatibility complex, transactivator	4261	Hs.126714	176.11	161.14	-1.19	0.029

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
218176_at	MAGEF1	melanoma antigen family F, 1	64110	Hs.306123	116.74	128.60	1.21	0.029
206377_at	FOXF2	forkhead box F2	2295	Hs.484423	32.89	29.83	-1.22	0.029
220740_s_at	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	9990	Hs.510939	47.58	42.66	-1.24	0.030
221464_at	OR1D2	olfactory receptor, family 1, subfamily D, member 2	4991	Hs.532771	137.29	123.51	-1.24	0.030
202568_s_at	MARK3	MAP/microtubule affinity-regulating kinase 3	4140	Hs.35828	154.97	171.59	1.23	0.030
209177_at	C3orf60	chromosome 3 open reading frame 60	25915	Hs.31387	406.26	472.08	1.35	0.030
205088_at	CXorf6	chromosome X open reading frame 6	10046	Hs.20136	89.42	79.25	-1.27	0.030
210064_s_at	UPK1B	uroplakin 1B	7348	Hs.271580	49.90	45.64	-1.20	0.030
221113_s_at	WNT16	wingless-type MMTV integration site family, member 16	51384	Hs.272375	38.79	35.21	-1.21	0.030
201593_s_at	ZC3H15	zinc finger CCCH-type containing 15	55854	Hs.368598	137.74	192.42	1.95	0.030
204765_at	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	7984	Hs.334, Hs.534621	137.26	125.29	-1.20	0.030
205287_s_at	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	7022	Hs.473152	37.34	33.88	-1.21	0.030
201871_s_at	LOC51035	SAPK substrate protein 1	51035	Hs.351296	188.72	206.12	1.19	0.030
205243_at	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	64849	Hs.655498	118.20	106.83	-1.22	0.030
203371_s_at	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	4709	Hs.109760	1306.44	1485.06	1.29	0.030
206247_at	MICB	MHC class I polypeptide-related sequence B	4277	Hs.211580	26.55	23.06	-1.33	0.030
222199_s_at	BIN3	bridging integrator 3	55909	Hs.654720	107.86	118.52	1.21	0.030
210533_at	MSH4	mutS homolog 4 (E. coli)	4438	Hs.216639	16.75	15.43	-1.18	0.030
206588_at	DAZL	deleted in azoospermia-like	1618	Hs.131179	17.94	16.98	-1.12	0.030
204341_at	TRIM16	tripartite motif-containing 16	10626	Hs.123534	84.69	98.48	1.35	0.030
204444_at	KIF11	kinesin family member 11	3832	Hs.8878	15.06	14.06	-1.15	0.030

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
212380_at	KIAA0082	KIAA0082	23070	Hs.520102	133.95	149.84	1.25	0.030
201244_s_at	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	5894	Hs.159130	372.68	421.94	1.28	0.030
217095_x_at	NCR1	natural cytotoxicity triggering receptor 1	9437	Hs.97084	135.52	122.59	-1.22	0.030
218628_at	CCDC53	coiled-coil domain containing 53	51019	Hs.405692	186.44	219.34	1.38	0.030
214961_at	KIAA0774	KIAA0774	23281	Hs.22287	151.05	201.90	1.79	0.030
221119_at	FLJ20184	hypothetical protein FLJ20184	54848	Hs.675420	129.36	114.39	-1.28	0.030
220503_at	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1	6561	Hs.489849	11.49	10.82	-1.13	0.030
206390_x_at	PF4	platelet factor 4 (chemokine (C-X-C motif) ligand 4)	5196	Hs.81564	121.40	110.98	-1.20	0.030
218810_at	ZC3H12A	zinc finger CCCH-type containing 12A	80149	Hs.656294	87.34	79.81	-1.20	0.030
220373_at	DCHS2	dachsous 2 (Drosophila)	54798	Hs.655664	98.71	90.40	-1.19	0.030
201778_s_at	KIAA0494	KIAA0494	9813	Hs.100874	558.88	627.95	1.26	0.030
209984_at	JMJD2C	jumonji domain containing 2C	23081	Hs.157106	71.28	79.46	1.24	0.030
204469_at	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	5803	Hs.489824	12.86	12.20	-1.11	0.030
220378_at	TCP11	t-complex 11 (mouse)	6954	Hs.435371	63.61	59.34	-1.15	0.030
221299_at	GPR173	G protein-coupled receptor 173	54328	Hs.661815	41.72	37.79	-1.22	0.030
215770_at	OR7E2P	olfactory receptor, family 7, subfamily E, member 2 pseudogene	8587		14.74	13.85	-1.13	0.030
220275_at	CUZD1	CUB and zona pellucida-like domains 1	50624	Hs.647182	58.56	50.67	-1.34	0.031
205240_at	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	29899	Hs.584901	54.84	48.70	-1.27	0.031
215172_at	PTPN20B	protein tyrosine phosphatase, non-receptor type 20B	26095	Hs.440733, Hs.499552	15.28	16.67	1.19	0.031
213167_s_at	MRPS6	mitochondrial ribosomal protein S6	64968	Hs.302742	20.67	19.18	-1.16	0.031
207074_s_at	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	6570	Hs.158322	37.69	34.64	-1.18	0.031
221337_s_at	ADAM29	ADAM metallopeptidase domain 29	11086	Hs.126838	38.44	35.74	-1.16	0.031
200615_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit	163	Hs.514819	287.96	327.49	1.29	0.031

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
210296_s_at	PXMP3	peroxisomal membrane protein 3, 35kDa (Zellweger syndrome)	5828	Hs.437966	122.22	147.69	1.46	0.031
219885_at	SLFN12	schlafen family member 12	55106	Hs.663548	33.06	30.32	-1.19	0.031
207218_at	F9	coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	2158	Hs.522798	23.73	21.97	-1.17	0.031
203512_at	TRAPPC3	trafficking protein particle complex 3	27095	Hs.523131	189.75	205.86	1.18	0.031
205185_at	SPINK5	serine peptidase inhibitor, Kazal type 5	11005	Hs.331555	115.19	100.31	-1.32	0.031
219735_s_at	TFCP2L1	transcription factor CP2-like 1	29842	Hs.156471	143.77	128.57	-1.25	0.031
217155_at	RPL34P2	ribosomal protein L34 pseudogene 2	26513		18.99	17.72	-1.15	0.031
210055_at	TSHR	thyroid stimulating hormone receptor	7253	Hs.160411	21.73	20.07	-1.17	0.031
206435_at	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	2583	Hs.591019	93.98	86.20	-1.19	0.031
220509_at			55469		18.51	17.05	-1.18	0.031
217043_s_at	MFN1	mitofusin 1	55669	Hs.478383	83.49	100.81	1.46	0.031
221171_at	RP4-692D3.1	hypothetical protein LOC728621	728621	Hs.473495	70.61	64.20	-1.21	0.031
215161_at	CAMK1G	calcium/calmodulin-dependent protein kinase IG	57172	Hs.199068	101.73	92.42	-1.21	0.031
204191_at	IFNAR1	interferon (alpha, beta and omega) receptor 1	3454	Hs.529400	60.66	54.67	-1.23	0.032
200723_s_at	CAPRIN1	cell cycle associated protein 1	4076	Hs.471818	210.39	252.92	1.45	0.032
210390_s_at	CCL15	chemokine (C-C motif) ligand 15	6359	Hs.656286	16.13	15.17	-1.13	0.032
210441_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	8556	Hs.127411	102.99	94.25	-1.19	0.032
203430_at	HEBP2	heme binding protein 2	23593	Hs.486589	527.16	614.10	1.36	0.032
218270_at	MRPL24	mitochondrial ribosomal protein L24	79590	Hs.418233	337.65	369.54	1.20	0.032
206745_at	HOXC11	homeobox C11	3227	Hs.127562	177.22	160.79	-1.21	0.032
207477_at	PRO2958	hypothetical protein PRO2958	55414		26.57	24.24	-1.20	0.032
216579_at	GJB4	gap junction protein, beta 4	127534	Hs.351203, Hs.675868	163.33	144.87	-1.27	0.032
214750_at	PLAC4	placenta-specific 4	191585	Hs.472492	123.18	108.27	-1.29	0.032
201078_at	TM9SF2	transmembrane 9 superfamily member 2	9375	Hs.654824	305.88	371.34	1.47	0.032
211245_x_at	KIR2DL4	killer cell	3805	Hs.651287,	68.94	62.34	-1.22	0.032

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4		Hs.661219				
220537_at	MTMR8	myotubularin related protein 8	55613	Hs.442892	25.73	23.14	-1.24	0.032
219132_at	PELI2	pellino homolog 2 (Drosophila)	57161	Hs.657926	66.29	60.85	-1.19	0.032
205654_at	C4BPA	complement component 4 binding protein, alpha	722	Hs.1012	87.03	78.73	-1.22	0.032
216354_at	RPL12L2	ribosomal protein L12-like 2	128467		31.89	29.53	-1.17	0.032
210606_x_at	KLRD1	killer cell lectin-like receptor subfamily D, member 1	3824	Hs.562457	49.22	44.76	-1.21	0.032
215302_at	LOC257152	hypothetical protein LOC257152	257152	Hs.663903	19.38	18.10	-1.15	0.032
202958_at	PTPN9	protein tyrosine phosphatase, non-receptor type 9	5780	Hs.445775	225.27	209.27	-1.16	0.032
205306_x_at	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	8564	Hs.409081	52.84	46.06	-1.32	0.032
208156_x_at	EPPK1	epiplakin 1	83481	Hs.200412	46.11	42.69	-1.17	0.032
205643_s_at	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	5521	Hs.655213	162.98	144.84	-1.27	0.032
214070_s_at	ATP10B	ATPase, Class V, type 10B	23120	Hs.109358	146.50	130.12	-1.27	0.032
201561_s_at	CLSTN1	calsyntenin 1	22883	Hs.29665	320.10	356.25	1.24	0.032
205084_at	BCAP29	B-cell receptor-associated protein 29	55973	Hs.303787	56.50	67.74	1.44	0.032
217541_x_at	ZNF816A	zinc finger protein 816A	125893	Hs.655592	88.08	79.89	-1.22	0.032
221164_x_at	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	23563	Hs.156784	108.43	99.89	-1.18	0.032
208818_s_at	COMT	catechol-O-methyltransferase	1312	Hs.370408	333.43	377.51	1.28	0.032
221458_at	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	3355	Hs.248136	42.01	37.17	-1.28	0.032
203515_s_at	PMVK	phosphomevalonate kinase	10654	Hs.30954	193.21	221.02	1.31	0.032
211755_s_at	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	515	Hs.514870	2085.89	2349.24	1.27	0.032
207315_at	CD226	CD226 molecule	10666	Hs.660130	23.83	21.77	-1.20	0.032
212010_s_at	CDV3	CDV3 homolog (mouse)	55573	Hs.518265	191.87	227.35	1.40	0.032
213265_at	PGA3	pepsinogen 3, group I	643834	Hs.647247	72.47	64.22	-1.27	0.032

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(pepsinogen A)						
222230_s_at	ACTR10	actin-related protein 10 homolog (S. cerevisiae)	55860	Hs.509451	542.96	634.80	1.37	0.032
211848_s_at	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	1087	Hs.74466	76.35	69.57	-1.20	0.032
216063_at	HBBP1	hemoglobin, beta pseudogene 1	3044	Hs.20205	41.49	37.85	-1.20	0.032
219557_s_at	NRIP3	nuclear receptor interacting protein 3	56675	Hs.523467	36.41	33.61	-1.17	0.032
220504_at	KERA	keratocan	11081	Hs.125750	13.00	12.31	-1.12	0.032
220452_x_at			25835		123.87	111.70	-1.23	0.032
221448_s_at	TEX15	testis expressed 15	56154	Hs.458316, Hs.571446	54.39	49.47	-1.21	0.032
220730_at			80220		89.17	81.23	-1.21	0.032
206850_at	RASL10A	RAS-like, family 10, member A	10633	Hs.73088	101.29	91.05	-1.24	0.032
38447_at	ADRBK1	adrenergic, beta, receptor kinase 1	156	Hs.83636	603.45	553.31	-1.19	0.032
211941_s_at	PEBP1	phosphatidylethanolamine binding protein 1	5037	Hs.433863	1319.28	1564.93	1.41	0.032
218071_s_at	MKRN2	makorin, ring finger protein, 2	23609	Hs.591666	114.20	124.73	1.19	0.033
220008_at	SGK269	NKF3 kinase family member	79834	Hs.9587	153.61	139.21	-1.22	0.033
202043_s_at	SMS	spermine synthase	6611	Hs.288487	62.77	73.62	1.38	0.033
222102_at	GSTA3	glutathione S-transferase A3	2940	Hs.102484	36.18	32.45	-1.24	0.033
219768_at	VTCN1	V-set domain containing T cell activation inhibitor 1	79679	Hs.546434	71.31	64.95	-1.21	0.033
219616_at	FLJ21963	FLJ21963 protein	79611	Hs.259559	82.33	74.03	-1.24	0.033
201068_s_at	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	5701	Hs.437366	420.38	487.17	1.34	0.033
206719_at	SYNGR4	synaptogyrin 4	23546	Hs.408333	53.06	48.09	-1.22	0.033
205642_at	CEP110	centrosomal protein 110kDa	11064	Hs.653263	77.54	70.76	-1.20	0.033
221194_s_at	LOC51136	PTD016 protein	51136	Hs.531701	60.46	55.11	-1.20	0.033
202386_s_at	KIAA0430	KIAA0430	9665	Hs.173524	59.22	70.18	1.40	0.033
208872_s_at	REEP5	receptor accessory protein 5	7905	Hs.429608	679.81	795.72	1.37	0.033
211410_x_at	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A	57292	Hs.676464	115.57	103.83	-1.24	0.033
213820_s_at	STARD5	StAR-related lipid transfer (START) domain containing 5	80765	Hs.513075	95.19	86.30	-1.22	0.033

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
221686_s_at	RECQL5	RecQ protein-like 5	9400	Hs.632229	288.12	257.17	-1.26	0.033
207233_s_at	MITF	microphthalmia-associated transcription factor	4286	Hs.166017, Hs.618266	210.23	247.38	1.38	0.033
211153_s_at	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	8600	Hs.333791	53.06	46.82	-1.28	0.033
219819_s_at	MRPS28	mitochondrial ribosomal protein S28	28957	Hs.521124	217.65	262.18	1.45	0.033
207471_at			29026		15.18	14.23	-1.14	0.033
211219_s_at	LHX2	LIM homeobox 2	9355	Hs.445265	34.95	31.85	-1.20	0.033
214763_at	ACOT11	acyl-CoA thioesterase 11	26027	Hs.234786	149.27	170.55	1.31	0.033
218488_at	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	8891	Hs.533549	244.05	269.22	1.22	0.033
200844_s_at	PRDX6	peroxiredoxin 6	9588	Hs.573688	954.33	1104.31	1.34	0.033
220396_at	PRO2268	hypothetical protein PRO2268	55390		183.10	168.23	-1.18	0.033
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	10241	Hs.514920	479.14	546.70	1.30	0.033
220976_s_at	KRTAP1-1	keratin associated protein 1-1	81851	Hs.247934	36.46	33.04	-1.22	0.033
216432_at	SLC28A2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	9153	Hs.367833	91.20	82.40	-1.22	0.033
220741_s_at	PPA2	pyrophosphatase (inorganic) 2	27068	Hs.654957	369.63	426.51	1.33	0.033
210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like	8638	Hs.118633	193.65	178.05	-1.18	0.033
211806_s_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	3772	Hs.411299	124.01	112.37	-1.22	0.033
219732_at	RP11-35N6.1	plasticity related gene 3	54886	Hs.382683	24.59	22.22	-1.22	0.033
220460_at	SLCO1C1	solute carrier organic anion transporter family, member 1C1	53919	Hs.47261	38.09	34.02	-1.25	0.033
220584_at	FLJ22184	hypothetical protein FLJ22184	80164	Hs.288540	147.92	130.58	-1.28	0.033
218554_s_at	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	55870	Hs.491060	115.86	104.05	-1.24	0.033
210924_at	OLFM1	olfactomedin 1	10439	Hs.522484	221.28	199.37	-1.23	0.033
209566_at	INSIG2	insulin induced gene 2	51141	Hs.7089	31.83	36.34	1.30	0.033
202614_at	SLC30A9	solute carrier family 30 (zinc transporter), member 9	10463	Hs.479634	159.98	193.12	1.46	0.033
201071_x_at	SF3B1	splicing factor 3b,	23451	Hs.632554	601.38	696.06	1.34	0.034

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		subunit 1, 155kDa						
212311_at	KIAA0746	KIAA0746 protein	23231	Hs.479384	64.18	56.20	-1.30	0.034
217391_x_at	KIAA0409	KIAA0409	23378	Hs.652255	197.80	175.00	-1.28	0.034
218851_s_at	WDR33	WD repeat domain 33	55339	Hs.620490	17.71	16.48	-1.15	0.034
209075_s_at	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	23479	Hs.615131	1559.60	1746.08	1.25	0.034
208723_at	USP11	ubiquitin specific peptidase 11	8237	Hs.171501	267.56	313.94	1.38	0.034
206280_at	CDH18	cadherin 18, type 2	1016	Hs.317632	78.82	71.40	-1.22	0.034
201953_at	CIB1	calcium and integrin binding 1 (calmyrin)	10519	Hs.135471	270.30	302.34	1.25	0.034
217130_at	C9orf33	chromosome 9 open reading frame 33	90477	Hs.667154	32.65	30.35	-1.16	0.034
212096_s_at	MTUS1	mitochondrial tumor suppressor 1	57509	Hs.7946	682.05	805.42	1.39	0.034
212465_at	SETD3	SET domain containing 3	84193	Hs.510407	299.64	343.43	1.31	0.034
218644_at	PLEK2	pleckstrin 2	26499	Hs.170473	135.49	125.85	-1.16	0.034
206439_at	EPYC	epiphycan	1833	Hs.435680	13.33	12.56	-1.13	0.034
202562_s_at	C14orf1	chromosome 14 open reading frame 1	11161	Hs.15106	96.18	104.97	1.19	0.034
217971_at	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	8649	Hs.647988	127.65	152.13	1.42	0.034
217772_s_at	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	23788	Hs.269944	373.75	422.76	1.28	0.034
208511_at	PTTG3	pituitary tumor-transforming 3	26255	Hs.647156	33.64	30.39	-1.23	0.034
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	1028	Hs.106070	253.16	300.56	1.41	0.034
219344_at	SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	55315	Hs.438419	200.75	183.50	-1.20	0.034
201485_s_at	RCN2	reticulocalbin 2, EF-hand calcium binding domain	5955	Hs.79088	94.09	111.81	1.41	0.034
221107_at	CHRNA9	cholinergic receptor, nicotinic, alpha 9	55584	Hs.272278	28.71	26.63	-1.16	0.034
210861_s_at	WISP3	WNT1 inducible signaling pathway protein 3	8838	Hs.558428	21.41	19.57	-1.20	0.034
201956_s_at	GNPAT	glyceronephosphate O-acyltransferase	8443	Hs.498028	395.87	456.68	1.33	0.034
220725_x_at			80165		154.51	131.81	-1.37	0.034
206408_at	LRRTM2	leucine rich repeat transmembrane neuronal 2	26045	Hs.656653	27.32	25.20	-1.18	0.034
217769_s_at	POMP	proteasome maturation	51371	Hs.268742	854.23	973.66	1.30	0.034

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		protein						
201648_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)	3716	Hs.207538	395.76	460.63	1.35	0.034
209057_x_at	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	988	Hs.485471	286.12	249.75	-1.31	0.034
207205_at	CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4	1089	Hs.12	193.49	179.62	-1.16	0.035
209891_at	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	57405	Hs.421956	16.35	15.39	-1.13	0.035
210690_at	KLRC4	killer cell lectin-like receptor subfamily C, member 4	8302	Hs.387787, Hs.665704	10.82	10.44	-1.08	0.035
201600_at	PHB2	prohibitin 2	11331	Hs.504620	1135.13	1262.83	1.24	0.035
205445_at	PRL	prolactin	5617	Hs.1905	42.07	38.26	-1.21	0.035
220522_at	CRB1	crumbs homolog 1 (Drosophila)	23418	Hs.126135	54.34	49.93	-1.18	0.035
210799_at	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	3351	Hs.123016	72.55	64.37	-1.27	0.035
208382_s_at	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	11144	Hs.339396	31.96	29.24	-1.20	0.035
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	7739	Hs.16622	80.57	72.23	-1.24	0.035
220379_at	FSCN3	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	29999	Hs.430657	216.86	196.16	-1.22	0.035
206121_at	AMPD1	adenosine monophosphate deaminase 1 (isoform M)	270	Hs.89570	40.01	34.76	-1.33	0.035
202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase	5066	Hs.369430	2276.34	2576.14	1.28	0.035
220834_at	MS4A12	membrane-spanning 4-domains, subfamily A, member 12	54860	Hs.272789	33.78	31.12	-1.18	0.035
207503_at	TCP10	t-complex 10 (mouse)	6953	Hs.351, Hs.119929	33.66	30.56	-1.21	0.035
200878_at	EPAS1	endothelial PAS domain protein 1	2034	Hs.468410	1263.80	1430.77	1.28	0.035
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled	1880	Hs.784	19.23	17.06	-1.27	0.035

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		receptor)						
205888_s_at	JAKMIP2	janus kinase and microtubule interacting protein 2	9832	Hs.184323	39.64	36.17	-1.20	0.035
220774_at	DYM	dymeclin	54808	Hs.162996	19.45	18.38	-1.12	0.035
217629_at	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	2793	Hs.181781	93.83	86.81	-1.17	0.035
213990_s_at	PAK7	p21(CDKN1A)-activated kinase 7	57144	Hs.32539	44.01	40.27	-1.19	0.035
207014_at	GABRA2	gamma-aminobutyric acid (GABA) A receptor, alpha 2	2555	Hs.116250	15.67	14.90	-1.11	0.035
202037_s_at	SFRP1	secreted frizzled-related protein 1	6422	Hs.213424	236.22	330.15	1.95	0.035
207385_at	TFDP3	transcription factor Dp family, member 3	51270	Hs.142908	33.84	30.56	-1.23	0.036
49878_at	PEX16	peroxisomal biogenesis factor 16	9409	Hs.100915	365.18	338.36	-1.16	0.036
221375_at	OR1G1	olfactory receptor, family 1, subfamily G, member 1	8390	Hs.248183	63.56	57.96	-1.20	0.036
219767_s_at	CRYZL1	crystallin, zeta (quinone reductase)-like 1	9946	Hs.352671	67.21	78.30	1.36	0.036
44120_at	ADCK2	aarF domain containing kinase 2	90956	Hs.534141	144.37	134.62	-1.15	0.036
221086_s_at	FEZF2	FEZ family zinc finger 2	55079	Hs.241523	15.52	14.34	-1.17	0.036
206989_s_at	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	9169	Hs.210367	120.38	143.90	1.43	0.036
207409_at	LECT2	leukocyte cell-derived chemotaxin 2	3950	Hs.512580	27.51	24.90	-1.22	0.036
209976_s_at	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	1571	Hs.12907	48.36	43.66	-1.23	0.036
203350_at	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	164	Hs.461253	145.17	130.11	-1.24	0.036
207141_s_at	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3	3760	Hs.591606	29.45	26.20	-1.26	0.036
207072_at	IL18RAP	interleukin 18 receptor accessory protein	8807	Hs.158315	27.28	24.61	-1.23	0.036
205242_at	CXCL13	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	10563	Hs.100431	24.79	22.09	-1.26	0.036
208765_s_at	HNRNPR	heterogeneous nuclear ribonucleoprotein R	10236	Hs.373763	222.04	255.14	1.32	0.036
213376_at	ZBTB1	zinc finger and BTB	22890	Hs.655536	69.43	87.74	1.60	0.036

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		domain containing 1						
217060_at	TRBV17	T cell receptor beta variable 17	28570		41.14	37.61	-1.20	0.036
206160_at	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	10930	Hs.555915	484.27	553.08	1.30	0.036
207775_at	MGC4859	hypothetical protein MGC4859 similar to HSPA8	79150	Hs.571301	14.16	13.41	-1.11	0.036
206335_at	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)	2588	Hs.271383	97.56	89.32	-1.19	0.036
206892_at	AMHR2	anti-Mullerian hormone receptor, type II	269	Hs.659889	137.40	124.33	-1.22	0.036
206940_s_at	POU4F1	POU class 4 homeobox 1	5457	Hs.654522	21.16	19.65	-1.16	0.036
211325_x_at	LOC171220	destrin-2 pseudogene	171220	Hs.661103	109.58	118.56	1.17	0.036
203145_at	SPAG5	sperm associated antigen 5	10615	Hs.514033	48.62	44.71	-1.18	0.036
219139_s_at	RBP4	retinol binding protein 4, plasma	5950	Hs.50223	44.90	41.12	-1.19	0.036
215603_x_at	LOC728226	similar to gamma-glutamyltransferase 2	728226	Hs.454906	70.50	63.23	-1.24	0.036
221470_s_at	IL1F7	interleukin 1 family, member 7 (zeta)	27178	Hs.166371	23.31	21.36	-1.19	0.036
205470_s_at	KLK11	kallikrein-related peptidase 11	11012	Hs.57771	87.93	78.37	-1.26	0.036
220150_s_at	C6orf60	chromosome 6 open reading frame 60	79632	Hs.443789	68.34	60.66	-1.27	0.036
207501_s_at	FGF12	fibroblast growth factor 12	2257	Hs.584758	252.37	343.81	1.86	0.036
214342_at	ATXN7L1	ataxin 7-like 1	222255	Hs.489603	38.18	35.15	-1.18	0.036
208524_at	GPR15	G protein-coupled receptor 15	2838	Hs.563128	64.57	58.15	-1.23	0.036
214576_at	KRT36	keratin 36	8689	Hs.248189	28.66	26.46	-1.17	0.036
211835_at	IGHV4-31	immunoglobulin heavy variable 4-31	28396	Hs.510635	85.42	76.26	-1.25	0.036
203195_s_at	NUP98	nucleoporin 98kDa	4928	Hs.524750	106.12	116.38	1.20	0.036
221121_at	CXorf48	chromosome X open reading frame 48	54967	Hs.272804	26.12	24.22	-1.16	0.036
210271_at	NEUROD2	neurogenic differentiation 2	4761	Hs.322431	68.94	61.92	-1.24	0.036
206521_s_at	GTF2A1	general transcription factor IIA, 1, 19/37kDa	2957	Hs.592334, Hs.593630	32.55	30.23	-1.16	0.036
205490_x_at	GJB3	gap junction protein, beta 3, 31kDa	2707	Hs.522561	102.30	93.52	-1.20	0.036

Probe	**Symbol**	**Description**	**Gene**	**UniGene**	**Av Exp Female**	**Av Exp Male**	**Fold Change**	**adj P val**
219974_x_at	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	55862	Hs.486410	170.55	192.20	1.27	0.036
220334_at	RGS17	regulator of G-protein signaling 17	26575	Hs.166313	50.21	46.53	-1.16	0.036
209303_at	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	4724	Hs.528222	551.69	642.56	1.36	0.036
218994_s_at	FLJ13195	stromal antigen 3-like	64940	Hs.632013	21.03	18.88	-1.24	0.036
201034_at	ADD3	adducin 3 (gamma)	120	Hs.501012	578.15	706.28	1.49	0.036
206345_s_at	PON1	paraoxonase 1	5444	Hs.370995	33.71	29.82	-1.28	0.036
210502_s_at	PPIE	peptidylprolyl isomerase E (cyclophilin E)	10450	Hs.524690	108.41	120.97	1.25	0.036
221421_s_at	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	81792	Hs.12680	61.08	55.70	-1.20	0.036
221707_s_at	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	55275	Hs.461819	39.42	36.24	-1.18	0.036
212785_s_at	LARP7	La ribonucleoprotein domain family, member 7	51574	Hs.642978	191.77	228.22	1.42	0.036
204211_x_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	5610	Hs.131431	173.19	159.28	-1.18	0.036
220669_at	OTUD4	OTU domain containing 4	54726	Hs.270851	19.81	18.59	-1.13	0.036
221394_at	TAAR2	trace amine associated receptor 2	9287	Hs.272382	64.58	58.93	-1.20	0.036
221174_at			80107		16.52	15.57	-1.13	0.036
215142_at	CXorf27	chromosome X open reading frame 27	25763	Hs.122959	63.76	57.37	-1.24	0.036
220304_s_at	CNGB3	cyclic nucleotide gated channel beta 3	54714	Hs.154433	35.96	33.07	-1.18	0.036
214539_at	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	5273	Hs.158339	58.75	53.14	-1.22	0.036
206841_at	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	5149	Hs.54471	18.30	17.24	-1.13	0.036
221331_x_at	CTLA4	cytotoxic T-lymphocyte-associated protein 4	1493	Hs.247824	73.34	65.60	-1.25	0.036
210604_at	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	2780	Hs.36973	34.80	31.96	-1.19	0.036

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
200726_at	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	5501	Hs.79081	542.67	634.96	1.37	0.036
221314_at	GDF9	growth differentiation factor 9	2661	Hs.25022	62.57	55.66	-1.26	0.036
221444_at	TAS2R16	taste receptor, type 2, member 16	50833	Hs.272395	29.14	25.78	-1.28	0.037
200617_at	KIAA0152	KIAA0152	9761	Hs.507074	474.79	523.55	1.22	0.037
221102_s_at	TRPM6	transient receptor potential cation channel, subfamily M, member 6	140803	Hs.272225	46.43	42.00	-1.22	0.037
222289_at	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2	3747	Hs.591041	26.75	30.36	1.29	0.037
206326_at	GRP	gastrin-releasing peptide	2922	Hs.153444	51.60	48.14	-1.15	0.037
208259_x_at	IFNA7	interferon, alpha 7	3444	Hs.282274	66.20	60.13	-1.21	0.037
217965_s_at	SAP30BP	SAP30 binding protein	29115	Hs.655088	51.62	57.40	1.24	0.037
48580_at	CXXC1	CXXC finger 1 (PHD domain)	30827	Hs.180933	567.26	529.46	-1.15	0.037
200065_s_at	ARF1	ADP-ribosylation factor 1	375	Hs.286221	1065.96	1189.10	1.24	0.037
207176_s_at	CD80	CD80 molecule	941	Hs.838	68.25	61.64	-1.23	0.037
205260_s_at	ACYP1	acylphosphatase 1, erythrocyte (common) type	97	Hs.18573	31.60	35.64	1.27	0.037
200668_s_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	7323	Hs.518773	628.85	759.10	1.46	0.037
200050_at	ZNF146	zinc finger protein 146	7705	Hs.643436, Hs.651111	81.84	95.36	1.36	0.037
212199_at	MRFAP1L1	Morf4 family associated protein 1-like 1	114932	Hs.593159	204.51	242.52	1.41	0.037
208060_at	PAX7	paired box 7	5081	Hs.113253	57.45	53.75	-1.14	0.037
201651_s_at	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	11252	Hs.162877	510.27	585.92	1.32	0.037
208144_s_at			83400		20.84	19.55	-1.14	0.037
220034_at	IRAK3	interleukin-1 receptor-associated kinase 3	11213	Hs.369265	27.70	25.35	-1.19	0.037
221390_s_at	MTMR7	myotubularin related protein 7	9108	Hs.625674	113.55	102.08	-1.24	0.037
208619_at	DDB1	damage-specific DNA binding protein 1, 127kDa	1642	Hs.290758, Hs.656935	373.48	407.23	1.19	0.037
220181_x_at	SLC30A5	solute carrier family 30 (zinc transporter), member 5	64924	Hs.631975	92.38	83.64	-1.22	0.037

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
207693_at	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	785	Hs.614033	101.62	89.17	-1.30	0.037
214519_s_at	RLN2	relaxin 2	6019	Hs.127032	22.94	21.30	-1.16	0.037
207929_at	GRPR	gastrin-releasing peptide receptor	2925	Hs.567282	252.06	227.62	-1.23	0.037
200987_x_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	10197	Hs.152978	172.48	193.79	1.26	0.037
208378_x_at	FGF5	fibroblast growth factor 5	2250	Hs.37055	58.41	53.72	-1.18	0.038
216750_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	323	Hs.479602	86.97	79.39	-1.20	0.038
211504_x_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	9475	Hs.591600	217.90	198.81	-1.20	0.038
218510_x_at	FAM134B	family with sequence similarity 134, member B	54463	Hs.481704	978.68	1141.11	1.36	0.038
220651_s_at	MCM10	minichromosome maintenance complex component 10	55388	Hs.198363	25.60	23.27	-1.21	0.038
211496_s_at	PDC	phosducin	5132	Hs.654381	16.99	16.01	-1.13	0.038
218034_at	FIS1	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	51024	Hs.423968	540.21	625.12	1.34	0.038
212782_x_at	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	5439	Hs.654952	500.72	602.11	1.45	0.038
213501_at	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	51	Hs.464137	51.18	57.82	1.28	0.038
211123_at	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5	6528	Hs.584804	153.41	140.57	-1.19	0.038
210911_at	ID2B	inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	84099	Hs.591670	17.98	16.75	-1.15	0.038
220577_at			80073		44.52	40.78	-1.19	0.038
218792_s_at	BSPRY	B-box and SPRY domain containing	54836	Hs.632677	63.21	57.07	-1.23	0.038
219444_at	BCORL1	BCL6 co-repressor-like 1	63035	Hs.496748	111.81	103.73	-1.16	0.038
215853_at	SDCCAG8	serologically defined colon cancer antigen 8	10806	Hs.591530	19.30	17.84	-1.17	0.038
211383_s_at	WDR37	WD repeat domain 37	22884	Hs.188495	183.68	208.84	1.29	0.038
213839_at	KIAA0500	KIAA0500 protein	57237	Hs.593760	32.87	30.42	-1.17	0.038
208037_s_at	MADCAM1	mucosal vascular addressin cell adhesion	8174	Hs.102598	55.98	51.65	-1.17	0.038

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		molecule 1						
217781_s_at	ZFP106	zinc finger protein 106 homolog (mouse)	64397	Hs.511143	1702.31	1952.61	1.32	0.038
220694_at	DDEF1IT1	DDEF1 intronic transcript 1	29065	Hs.658387	49.87	44.04	-1.28	0.038
220426_at	C20orf195	chromosome 20 open reading frame 195	79025	Hs.197755	32.74	29.56	-1.23	0.038
221434_s_at	C14orf156	chromosome 14 open reading frame 156	81892	Hs.655105	601.73	714.25	1.41	0.038
210497_x_at	SSX2	synovial sarcoma, X breakpoint 2	6757	Hs.289105, Hs.661107	117.69	107.83	-1.19	0.039
206433_s_at	SPOCK3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	50859	Hs.481133	13.48	12.88	-1.09	0.039
220093_at	ANTXR1	anthrax toxin receptor 1	84168	Hs.165859	75.68	70.43	-1.15	0.039
220575_at	FAM106A	family with sequence similarity 106, member A	80039	Hs.674403	34.64	31.75	-1.19	0.039
211609_x_at	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	5710	Hs.505059	440.04	492.49	1.25	0.039
207148_x_at	MYOZ2	myozenin 2	51778	Hs.381047	3154.00	3543.79	1.26	0.039
208971_at	UROD	uroporphyrinogen decarboxylase	7389	Hs.78601	187.00	207.56	1.23	0.039
221080_s_at	DENND1C	DENN/MADD domain containing 1C	79958	Hs.236449	114.65	103.60	-1.22	0.039
216998_s_at	ADAM5P	ADAM metallopeptidase domain 5 pseudogene	255926	Hs.369765	67.60	61.72	-1.20	0.039
209888_s_at	MYL1	myosin, light chain 1, alkali; skeletal, fast	4632	Hs.187338	66.17	59.02	-1.26	0.039
216817_s_at	OR2H1	olfactory receptor, family 2, subfamily H, member 1	26716	Hs.434715, Hs.686942	80.60	74.47	-1.17	0.039
211312_s_at	WISP1	WNT1 inducible signaling pathway protein 1	8840	Hs.492974	94.93	84.65	-1.26	0.039
214355_x_at	LOC643854	similar to CTAGE family, member 5	643854	Hs.632613	187.25	168.48	-1.24	0.039
206952_at	G6PC	glucose-6-phosphatase, catalytic subunit	2538	Hs.212293	12.91	12.29	-1.10	0.039
206880_at	P2RXL1	purinergic receptor P2X-like 1, orphan receptor	9127	Hs.113275	191.38	174.09	-1.21	0.039
205676_at	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	1594	Hs.524528	59.38	53.73	-1.22	0.039
206608_s_at	RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	57096	Hs.126035	60.40	55.86	-1.17	0.039

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
212406_s_at	MYT1	myelin transcription factor 1	4661	Hs.279562	155.32	197.58	1.62	0.039
212561_at	RAB6IP1	RAB6 interacting protein 1	23258	Hs.501857	423.94	478.48	1.27	0.039
217942_at	MRPS35	mitochondrial ribosomal protein S35	60488	Hs.311072	289.98	327.21	1.27	0.039
206586_at	CNR2	cannabinoid receptor 2 (macrophage)	1269	Hs.73037	132.71	121.65	-1.19	0.039
214876_s_at	TUBGCP5	tubulin, gamma complex associated protein 5	114791	Hs.533898	14.43	15.30	1.12	0.039
207919_at	ART1	ADP-ribosyltransferase 1	417	Hs.382188	126.53	115.47	-1.20	0.039
207111_at	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	2015	Hs.2375	64.41	58.62	-1.21	0.039
203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	51704	Hs.148685	213.99	245.09	1.31	0.039
206947_at	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	10317	Hs.655094	29.21	26.45	-1.22	0.039
208720_s_at	RBM39	RNA binding motif protein 39	9584	Hs.282901	267.79	310.13	1.34	0.040
208909_at	UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	7386	Hs.170107	2698.21	2984.29	1.22	0.040
202736_s_at	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	25804	Hs.515255	140.79	169.52	1.45	0.040
215267_s_at	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2	6543	Hs.172884	73.74	66.72	-1.22	0.040
219403_s_at	HPSE	heparanase	10855	Hs.44227	41.03	36.73	-1.25	0.040
219945_at	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	29118	Hs.420263	19.35	18.09	-1.14	0.040
203577_at	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	2968	Hs.485070	31.31	34.15	1.19	0.040
207392_x_at	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	7366	Hs.150207, Hs.694718	39.57	36.67	-1.16	0.040
200075_s_at	GUK1	guanylate kinase 1	2987	Hs.376933	157.16	193.28	1.51	0.040
211713_x_at	KIAA0101	KIAA0101	9768	Hs.81892	53.55	48.09	-1.24	0.040
201145_at	HAX1	HCLS1 associated protein X-1	10456	Hs.199625	893.72	985.27	1.22	0.040
212453_at	KIAA1279	KIAA1279	26128	Hs.279580	228.14	269.81	1.40	0.040

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
203103_s_at	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	27339	Hs.502705	167.71	183.08	1.19	0.040
213445_at	ZC3H3	zinc finger CCCH-type containing 3	23144	Hs.521915	61.62	56.41	-1.19	0.040
221354_s_at	MCHR1	melanin-concentrating hormone receptor 1	2847	Hs.248122	42.12	38.86	-1.17	0.040
220776_at	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14	3770	Hs.590945, Hs.644912	33.58	30.75	-1.19	0.040
201633_s_at	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	80777	Hs.461131	88.03	97.69	1.23	0.040
209397_at	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	4200	Hs.233119	427.48	497.82	1.36	0.040
200620_at	TMEM59	transmembrane protein 59	9528	Hs.523262	897.66	1012.88	1.27	0.040
219734_at	SIDT1	SID1 transmembrane family, member 1	54847	Hs.591291	14.78	13.73	-1.16	0.040
210454_s_at	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6	3763	Hs.658533	44.65	41.69	-1.15	0.040
45653_at	KCTD13	potassium channel tetramerisation domain containing 13	253980	Hs.534590	80.12	73.39	-1.19	0.040
216678_at	IFT122	intraflagellar transport 122 homolog (Chlamydomonas)	55764	Hs.655284	152.73	138.48	-1.22	0.040
202925_s_at	PLAGL2	pleiomorphic adenoma gene-like 2	5326	Hs.154104	84.44	76.70	-1.21	0.040
206007_at	PRG4	proteoglycan 4	10216	Hs.647723	20.59	19.06	-1.17	0.040
220991_s_at	RNF32	ring finger protein 32	140545	Hs.490715	11.75	11.15	-1.11	0.040
207757_at	ZFP2	zinc finger protein 2 homolog (mouse)	80108	Hs.654533	15.77	14.78	-1.14	0.040
216623_x_at	TOX3	TOX high mobility group box family member 3	27324	Hs.460789	11.71	11.20	-1.09	0.040
207910_at	SCGB1D1	secretoglobin, family 1D, member 1	10648	Hs.202686	18.89	17.72	-1.14	0.040
218898_at	FAM57A	family with sequence similarity 57, member A	79850	Hs.154396	91.34	83.91	-1.18	0.040
221985_at	KLHL24	kelch-like 24 (Drosophila)	54800	Hs.407709	138.19	164.87	1.42	0.040
218263_s_at	ZBED5	zinc finger, BED-type containing 5	58486	Hs.655066	178.21	212.23	1.42	0.040
221202_at			55393		17.16	16.06	-1.14	0.040
205995_x_at	IQCB1	IQ motif containing B1	9657	Hs.604110	165.09	153.20	-1.16	0.041
211956_s_at	EIF1	eukaryotic translation initiation factor 1	10209	Hs.150580	3478.69	3763.18	1.17	0.041

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
220939_s_at	DPP8	dipeptidyl-peptidase 8	54878	Hs.591106	216.94	267.48	1.52	0.041
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	10733	Hs.172052	40.92	38.03	-1.16	0.041
216196_at	LOC440366	hect domain and RLD 2 pseudogene	440366	Hs.633945	42.00	38.53	-1.19	0.041
201114_x_at	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	5688	Hs.233952	654.32	749.54	1.31	0.041
205228_at	RBMS2	RNA binding motif, single stranded interacting protein 2	5939	Hs.645521, Hs.683360	66.80	61.20	-1.19	0.041
212655_at	ZCCHC14	zinc finger, CCHC domain containing 14	23174	Hs.156231	66.55	75.82	1.30	0.041
201672_s_at	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	9097	Hs.464416, Hs.660783	245.85	285.06	1.34	0.041
210411_s_at	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	2904	Hs.654430	49.19	45.46	-1.17	0.041
219205_at	SRR	serine racemase	63826	Hs.461954	159.26	144.39	-1.22	0.041
205432_at	OVGP1	oviductal glycoprotein 1, 120kDa (mucin 9, oviductin)	5016	Hs.1154	261.94	234.81	-1.24	0.041
221072_at	C9orf31	chromosome 9 open reading frame 31	57000	Hs.522373	61.14	55.99	-1.19	0.041
217098_s_at	ZSCAN12	zinc finger and SCAN domain containing 12	9753	Hs.134816	24.00	22.40	-1.15	0.041
214479_at	GFRA3	GDNF family receptor alpha 3	2676	Hs.58042	95.35	87.16	-1.20	0.041
200997_at	RBM4	RNA binding motif protein 4	5936	Hs.533712	207.19	231.16	1.24	0.041
218163_at	MCTS1	malignant T cell amplified sequence 1	28985	Hs.102696	158.79	183.29	1.33	0.041
220942_x_at	C3orf28	chromosome 3 open reading frame 28	26355	Hs.584881	1217.13	1350.69	1.23	0.041
215266_at	DNAH3	dynein, axonemal, heavy chain 3	55567	Hs.526500	151.94	140.40	-1.17	0.041
218403_at	TRIAP1	TP53 regulated inhibitor of apoptosis 1	51499	Hs.69499	236.47	258.74	1.20	0.041
201968_s_at	PGM1	phosphoglucomutase 1	5236	Hs.1869	1254.19	1424.94	1.29	0.041
214077_x_at	MEIS3P1	Meis homeobox 3 pseudogene 1	4213	Hs.356135	122.89	140.68	1.31	0.041
202964_s_at	RFX5	regulatory factor X, 5 (influences HLA class II expression)	5993	Hs.632472	212.30	195.88	-1.17	0.041
206604_at	OVOL1	ovo-like 1(Drosophila)	5017	Hs.134434	58.64	53.54	-1.20	0.041
201348_at	GPX3	glutathione peroxidase 3 (plasma)	2878	Hs.386793	2029.12	2659.30	1.72	0.041
216988_s_at	PTP4A2	protein tyrosine phosphatase type IVA,	8073	Hs.470477	547.60	705.88	1.66	0.041

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		member 2						
209230_s_at	NUPR1	nuclear protein 1	26471	Hs.513463	116.40	136.53	1.38	0.041
207178_s_at	FRK	fyn-related kinase	2444	Hs.89426	13.81	13.18	-1.10	0.041
200965_s_at	ABLIM1	actin binding LIM protein 1	3983	Hs.438236, Hs.538331	1905.74	2137.45	1.26	0.041
216702_x_at	ATP8A2	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2	51761	Hs.444957	61.77	57.38	-1.16	0.041
216732_at	LOC389768	similar to potassium channel tetramerisation domain containing 1	389768	Hs.636875	80.21	73.10	-1.20	0.041
221771_s_at	HSMPP8	M-phase phosphoprotein, mpp8	54737	Hs.269654	106.69	136.36	1.63	0.041
209694_at	PTS	6-pyruvoyltetrahydropterin synthase	5805	Hs.503860	173.78	200.29	1.33	0.041
207497_s_at	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	2206	Hs.386748	30.25	27.99	-1.17	0.041
219418_at	NHEJ1	nonhomologous end-joining factor 1	79840	Hs.225988	114.88	107.37	-1.14	0.041
204119_s_at	ADK	adenosine kinase	132	Hs.656586	204.21	234.37	1.32	0.041
206840_at	AFM	afamin	173	Hs.168718	33.52	30.69	-1.19	0.041
202042_at	HARS	histidyl-tRNA synthetase	3035	Hs.528050	131.90	147.94	1.26	0.041
203540_at	GFAP	glial fibrillary acidic protein	2670	Hs.514227	43.73	40.04	-1.19	0.041
203274_at	F8A1	coagulation factor VIII-associated (intronic transcript) 1	8263	Hs.533543, Hs.593687	303.10	340.19	1.26	0.041
217736_s_at	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	27102	Hs.520205	255.09	289.75	1.29	0.041
215948_x_at	ZMYM5	zinc finger, MYM-type 5	9205	Hs.530988	20.37	19.09	-1.14	0.041
220227_at			79941		52.56	47.96	-1.20	0.041
221160_s_at	CABP5	calcium binding protein 5	56344	Hs.117694	63.36	57.89	-1.20	0.041
219863_at	HERC5	hect domain and RLD 5	51191	Hs.26663	60.48	53.94	-1.26	0.041
208245_at	RAB9P1	RAB9, member RAS oncogene family, pseudogene 1	9366	Hs.158296	11.71	11.23	-1.09	0.042
210453_x_at	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	10632	Hs.486360	2599.40	2828.68	1.18	0.042
218672_at	SCNM1	sodium channel	79005	Hs.432360	347.04	319.57	-1.18	0.042

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		modifier 1						
206772_at	PTHR2	parathyroid hormone receptor 2	5746	Hs.570296	20.04	18.42	-1.18	0.042
219242_at	CEP63	centrosomal protein 63kDa	80254	Hs.443301	74.56	86.10	1.33	0.042
207047_s_at	CLCNKA	chloride channel Ka	1187	Hs.591533	57.65	51.71	-1.24	0.042
206369_s_at	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	5294	Hs.32942	21.60	20.00	-1.17	0.042
210021_s_at	CCNO	cyclin O	10309	Hs.3041	42.57	39.66	-1.15	0.042
202567_at	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	6634	Hs.356549	273.43	304.33	1.24	0.042
221484_at	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	9334	Hs.370487	134.02	155.17	1.34	0.042
216709_at	LOC400655	hypothetical gene supported by BC013370; BC034583	400655	Hs.579378	32.28	29.28	-1.22	0.042
213315_x_at	CXorf40A	chromosome X open reading frame 40A	91966	Hs.654738	208.08	239.14	1.32	0.042
203790_s_at	HRSP12	heat-responsive protein 12	10247	Hs.18426	152.59	176.68	1.34	0.042
208768_x_at	RPL22	ribosomal protein L22	6146	Hs.515329, Hs.554762	2593.46	2799.33	1.17	0.042
206752_s_at	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	1677	Hs.133089	16.64	18.19	1.20	0.042
221414_s_at	DEFB126	defensin, beta 126	81623	Hs.124211	23.64	22.18	-1.14	0.042
220749_at	C10orf68	chromosome 10 open reading frame 68	79741	Hs.585464	110.78	100.46	-1.22	0.042
201703_s_at	PPP1R10	protein phosphatase 1, regulatory (inhibitor) subunit 10	5514	Hs.106019	164.46	151.40	-1.18	0.042
208679_s_at	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa	10109	Hs.529303	417.73	511.73	1.50	0.042
220534_at	TRIM48	tripartite motif-containing 48	79097	Hs.195715	40.17	36.73	-1.20	0.042
202183_s_at	KIF22	kinesin family member 22	3835	Hs.613351	88.65	102.76	1.34	0.042
204137_at	GPR137B	G protein-coupled receptor 137B	7107	Hs.498160	85.42	104.28	1.49	0.042
221612_at	LRTM1	leucine-rich repeats and transmembrane domains 1	57408	Hs.591668	85.35	77.36	-1.22	0.043
208026_at	HIST1H4F	histone cluster 1, H4f	8361	Hs.247816	16.39	15.35	-1.14	0.043
206422_at	GCG	glucagon	2641	Hs.516494	16.11	15.28	-1.11	0.043

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
221958_s_at	GPR177	G protein-coupled receptor 177	79971	Hs.647659	180.77	205.05	1.29	0.043
221215_s_at	RIPK4	receptor-interacting serine-threonine kinase 4	54101	Hs.517310	128.82	118.69	-1.18	0.043
216525_x_at	PMS2L3	postmeiotic segregation increased 2-like 3	5387	Hs.654716, Hs.659871, Hs.661055	98.75	109.05	1.22	0.043
212581_x_at	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	2597	Hs.479728, Hs.544577, Hs.592355	8844.35	9541.34	1.16	0.043
210708_x_at	CASP10	caspase 10, apoptosis-related cysteine peptidase	843	Hs.5353	157.72	143.27	-1.21	0.043
208004_at	PROL1	proline rich, lacrimal 1	58503	Hs.661425	71.46	61.71	-1.34	0.043
215657_at	SLC26A3	solute carrier family 26, member 3	1811	Hs.1650	22.74	21.53	-1.12	0.043
216153_x_at	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	8434	Hs.388918	273.22	226.79	-1.45	0.043
216355_at	PCDHB17	protocadherin beta 17 pseudogene	54661	Hs.284307	48.07	43.63	-1.21	0.043
201384_s_at	NBR1	neighbor of BRCA1 gene 1	4077	Hs.277721, Hs.373818, Hs.546264, Hs.693721	183.57	211.60	1.33	0.043
203477_at	COL15A1	collagen, type XV, alpha 1	1306	Hs.409034	385.28	513.20	1.77	0.043
220884_at			55496		11.67	11.16	-1.09	0.043
208991_at	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	6774	Hs.463059	538.23	665.84	1.53	0.043
205749_at	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	1543	Hs.72912	51.92	48.08	-1.17	0.043
219613_s_at	SIRT6	sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	51548	Hs.423756	148.86	139.37	-1.14	0.043
220852_at	PRO1768	PRO1768 protein	29018	Hs.652968, Hs.673124	54.65	48.83	-1.25	0.043
215887_at	ZNF277P	zinc finger protein 277 pseudogene	11179	Hs.655904	102.91	92.65	-1.23	0.043
214210_at	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	10478	Hs.474938	80.72	74.90	-1.16	0.043
221594_at	DKFZP564O0523	hypothetical protein DKFZp564O0523	84060	Hs.21590	95.02	86.26	-1.21	0.043

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
202675_at	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	6390	Hs.465924	355.54	426.35	1.44	0.043
52169_at	LYK5	protein kinase LYK5	92335	Hs.514402	237.67	223.54	-1.13	0.043
219770_at	GTDC1	glycosyltransferase-like domain containing 1	79712	Hs.44780	121.25	133.88	1.22	0.043
212306_at	CLASP2	cytoplasmic linker associated protein 2	23122	Hs.108614	106.26	129.21	1.48	0.043
211009_s_at	ZNF271	zinc finger protein 271	10778	Hs.314246	49.62	57.69	1.35	0.043
206417_at	CNGA1	cyclic nucleotide gated channel alpha 1	1259	Hs.1323	46.19	41.90	-1.22	0.043
204909_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1656	Hs.654366	21.58	19.78	-1.19	0.043
221007_s_at	FIP1L1	FIP1 like 1 (S. cerevisiae)	81608	Hs.518760	16.63	18.13	1.19	0.043
208311_at	GPR50	G protein-coupled receptor 50	9248	Hs.567390	26.20	24.13	-1.18	0.043
206046_at	ADAM23	ADAM metallopeptidase domain 23	8745	Hs.591643	257.78	292.22	1.28	0.043
206685_at	HCG4	HLA complex group 4	54435	Hs.660431	16.15	15.10	-1.14	0.043
206191_at	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	956	Hs.441145	71.52	64.13	-1.24	0.043
207570_at	SHOX	short stature homeobox	6473	Hs.105932	115.74	106.29	-1.19	0.043
206442_at	SEMG1	semenogelin I	6406	Hs.1968	17.88	16.61	-1.16	0.044
220906_at			80083		23.80	25.60	1.16	0.044
220166_at	CNNM1	cyclin M1	26507	Hs.274579	74.05	69.62	-1.13	0.044
220043_s_at	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	4241	Hs.184727, Hs.694355	45.58	41.33	-1.22	0.044
200918_s_at	SRPR	signal recognition particle receptor ('docking protein')	6734	Hs.591936	502.80	557.90	1.23	0.044
221821_s_at	C12orf41	chromosome 12 open reading frame 41	54934	Hs.505412	116.25	132.13	1.29	0.044
220863_at	MIP	major intrinsic protein of lens fiber	4284	Hs.574026	38.38	35.18	-1.19	0.044
221371_at	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	8995	Hs.248197	65.19	59.41	-1.20	0.044
201172_x_at	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	8992	Hs.484188	925.37	1022.37	1.22	0.044
221452_s_at	TMEM14B	transmembrane protein 14B	81853	Hs.273077	300.70	383.57	1.63	0.044
205928_at	ZNF443	zinc finger protein 443	10224	Hs.631623	91.94	84.00	-1.20	0.044
207256_at	MBL2	mannose-binding lectin	4153	Hs.499674	15.13	14.40	-1.10	0.044

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		(protein C) 2, soluble (opsonic defect)						
217893_s_at	C1orf108	chromosome 1 open reading frame 108	79647	Hs.293563	88.21	100.34	1.29	0.044
216346_at	SEC14L3	SEC14-like 3 (S. cerevisiae)	266629	Hs.505601	25.72	23.24	-1.23	0.044
212849_at	AXIN1	axin 1	8312	Hs.592082	173.79	162.44	-1.14	0.044
214560_at	FPRL2	formyl peptide receptor-like 2	2359	Hs.445466	85.62	76.28	-1.26	0.044
219822_at	MTRF1	mitochondrial translational release factor 1	9617	Hs.382176	29.82	32.36	1.18	0.044
207446_at	TLR6	toll-like receptor 6	10333	Hs.662185	44.40	40.33	-1.21	0.044
214591_at	KLHL4	kelch-like 4 (Drosophila)	56062	Hs.49075	32.12	29.56	-1.18	0.044
206830_at	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10	57282	Hs.333958	12.64	12.04	-1.10	0.044
201455_s_at	NPEPPS	aminopeptidase puromycin sensitive	9520	Hs.443837	187.51	212.96	1.29	0.044
215639_at	SH2D3C	SH2 domain containing 3C	10044	Hs.306412	35.68	33.03	-1.17	0.044
203605_at	SRP54	signal recognition particle 54kDa	6729	Hs.167535	109.14	124.37	1.30	0.044
211945_s_at	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	3688	Hs.643813	1326.68	1499.92	1.28	0.044
221520_s_at	CDCA8	cell division cycle associated 8	55143	Hs.524571	56.30	52.32	-1.16	0.044
206663_at	SP4	Sp4 transcription factor	6671	Hs.88013	51.73	45.64	-1.28	0.044
218180_s_at	EPS8L2	EPS8-like 2	64787	Hs.55016	51.78	47.39	-1.19	0.044
213636_at	KIAA1045	KIAA1045	23349	Hs.7989	42.99	39.80	-1.17	0.044
206733_at	TULP2	tubby like protein 2	7288	Hs.104636	43.90	40.60	-1.17	0.044
208805_at	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	5687	Hs.446260	679.27	773.07	1.30	0.044
206502_s_at	INSM1	insulinoma-associated 1	3642	Hs.89584	16.49	15.33	-1.16	0.044
204733_at	KLK6	kallikrein-related peptidase 6	5653	Hs.79361	57.69	52.37	-1.21	0.044
212123_at	TCTN3	tectonic family member 3	26123	Hs.438991	312.27	288.90	-1.17	0.044
218076_s_at	ARHGAP17	Rho GTPase activating protein 17	55114	Hs.373793	288.67	314.80	1.19	0.044
211023_at	PDHB	pyruvate dehydrogenase (lipoamide) beta	5162	Hs.161357	1124.75	1279.34	1.29	0.044
34858_at	KCTD2	potassium channel	23510	Hs.514468	221.98	243.37	1.20	0.044

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		tetramerisation domain containing 2						
219650_at	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	54821	Hs.47558	21.83	20.77	-1.11	0.044
210031_at	CD247	CD247 molecule	919	Hs.156445	48.96	43.43	-1.27	0.044
212895_s_at	ABR	active BCR-related gene	29	Hs.159306	295.60	332.62	1.27	0.044
220429_at	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	9348	Hs.480596	23.69	21.91	-1.17	0.044
220285_at	FAM108B1	family with sequence similarity 108, member B1	51104	Hs.380389	54.84	49.30	-1.24	0.044
217544_at	LOC729806	similar to Zinc finger protein 492	729806	Hs.635482	20.24	19.01	-1.13	0.044
219809_at	WDR55	WD repeat domain 55	54853	Hs.286261	84.66	78.15	-1.17	0.044
218552_at	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	55268	Hs.476319	265.50	301.86	1.29	0.044
220979_s_at	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	81849	Hs.303609	18.56	17.14	-1.17	0.044
203450_at	CBY1	chibby homolog 1 (Drosophila)	25776	Hs.334911, Hs.596584	248.18	271.93	1.20	0.044
206678_at	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1	2554	Hs.175934	40.85	36.71	-1.24	0.044
206159_at	GDF10	growth differentiation factor 10	2662	Hs.2171	63.19	58.26	-1.18	0.044
220899_at			80038		21.99	20.37	-1.17	0.044
206633_at	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	1134	Hs.434479	73.97	69.39	-1.14	0.044
218814_s_at	C1orf75	chromosome 1 open reading frame 75	55248	Hs.445386	42.27	38.89	-1.18	0.044
211070_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	1622	Hs.78888	1453.22	1617.77	1.24	0.044
207197_at	ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)	7547	Hs.111227	38.74	34.46	-1.26	0.044
200992_at	IPO7	importin 7	10527	Hs.652248	427.93	515.42	1.45	0.044

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204083_s_at	TPM2	tropomyosin 2 (beta)	7169	Hs.300772	339.10	415.99	1.50	0.044
206912_at	FOXE1	forkhead box E1 (thyroid transcription factor 2)	2304	Hs.159234	16.29	15.24	-1.14	0.044
208668_x_at	HMGN2	high-mobility group nucleosomal binding domain 2	3151	Hs.181163	1345.60	1478.21	1.21	0.044
200863_s_at	RAB11A	RAB11A, member RAS oncogene family	8766	Hs.321541	550.93	620.18	1.27	0.044
215500_at	LOC92017	similar to RIKEN cDNA 4933437K13	92017	Hs.585745	47.19	43.56	-1.17	0.044
203074_at	ANXA8L2	annexin A8-like 2	244	Hs.693604	113.25	104.10	-1.18	0.044
209440_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	5631	Hs.56	215.33	237.65	1.22	0.044
220249_at	HYAL4	hyaluronoglucosaminidase 4	23553	Hs.28673	44.29	40.89	-1.17	0.044
208777_s_at	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	5717	Hs.655396	181.16	207.45	1.31	0.045
220559_at	EN1	engrailed homeobox 1	2019	Hs.271977	14.12	13.27	-1.13	0.045
208895_s_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	8886	Hs.363492	210.21	238.35	1.29	0.045
202800_at	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	6507	Hs.481918	271.50	318.93	1.38	0.045
218182_s_at	CLDN1	claudin 1	9076	Hs.439060	22.77	21.59	-1.11	0.045
200066_at	IK	IK cytokine, down-regulator of HLA II	3550	Hs.421245	277.89	312.71	1.27	0.045
208614_s_at	FLNB	filamin B, beta (actin binding protein 278)	2317	Hs.476448, Hs.666396	174.35	191.61	1.21	0.045
207665_at	ADAM21	ADAM metallopeptidase domain 21	8747	Hs.178748	49.82	45.49	-1.20	0.045
221276_s_at	SYNC1	syncoilin, intermediate filament 1	81493	Hs.655938	20.93	24.12	1.33	0.045
207420_at	COLEC10	collectin sub-family member 10 (C-type lectin)	10584	Hs.176615	28.35	26.38	-1.16	0.045
221167_s_at	CCDC70	coiled-coil domain containing 70	83446	Hs.120573	38.42	34.34	-1.25	0.045
200828_s_at	ZNF207	zinc finger protein 207	7756	Hs.500775	308.90	367.62	1.42	0.045
200027_at	NARS	asparaginyl-tRNA synthetase	4677	Hs.465224	660.37	762.93	1.33	0.045
206804_at	CD3G	CD3g molecule, gamma (CD3-TCR complex)	917	Hs.2259	88.30	79.75	-1.23	0.045
203376_at	CDC40	cell division cycle 40 homolog (S. cerevisiae)	51362	Hs.428147	207.30	226.69	1.20	0.045

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214192_at	NUP88	nucleoporin 88kDa	4927	Hs.584784	109.91	99.47	-1.22	0.045
202853_s_at	RYK	RYK receptor-like tyrosine kinase	6259	Hs.654562	191.63	220.38	1.32	0.045
208799_at	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5	5693	Hs.422990	489.10	537.95	1.21	0.045
211733_x_at	SCP2	sterol carrier protein 2	6342	Hs.476365	254.62	323.10	1.61	0.045
202753_at	PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	9861	Hs.152536	598.30	682.18	1.30	0.046
210675_s_at	PTPRR	protein tyrosine phosphatase, receptor type, R	5801	Hs.506076	26.21	24.69	-1.13	0.046
216207_x_at	IGKV1D-13	immunoglobulin kappa variable 1D-13	28902	Hs.390427	224.22	168.59	-1.77	0.046
218170_at	ISOC1	isochorismatase domain containing 1	51015	Hs.483296	203.65	256.57	1.59	0.046
220112_at	ANKRD55	ankyrin repeat domain 55	79722	Hs.436214	26.78	24.16	-1.23	0.046
207766_at	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	8814	Hs.654590	24.82	23.23	-1.14	0.046
211223_at	PROP1	PROP paired-like homeobox 1	5626	Hs.158301	130.55	116.49	-1.26	0.046
209488_s_at	RBPMS	RNA binding protein with multiple splicing	11030	Hs.334587	475.22	569.04	1.43	0.046
201544_x_at	PABPN1	poly(A) binding protein, nuclear 1	8106	Hs.117176	440.54	504.07	1.31	0.046
211107_s_at	AURKC	aurora kinase C	6795	Hs.98338	58.47	52.04	-1.26	0.046
207217_s_at	NOX1	NADPH oxidase 1	27035	Hs.592227	115.83	105.47	-1.21	0.046
209279_s_at	NSDHL	NAD(P) dependent steroid dehydrogenase-like	50814	Hs.57698	73.78	81.47	1.22	0.046
218175_at	CCDC92	coiled-coil domain containing 92	80212	Hs.114111	542.08	608.04	1.26	0.046
213725_x_at	XYLT1	xylosyltransferase I	64131	Hs.22907, Hs.610023	27.96	25.83	-1.17	0.046
219522_at	FJX1	four jointed box 1 (Drosophila)	24147	Hs.39384	53.58	49.56	-1.17	0.046
212885_at	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	10199	Hs.656208	111.40	123.06	1.22	0.046
221449_s_at	ITFG1	integrin alpha FG-GAP repeat containing 1	81533	Hs.42217	509.24	600.19	1.39	0.046
201536_at	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	1845	Hs.181046	1167.14	1293.36	1.23	0.046
212408_at	TOR1AIP1	torsin A interacting protein 1	26092	Hs.496459	290.87	351.66	1.46	0.046

Probe	**Symbol**	**Description**	**Gene**	**UniGene**	**Av Exp Female**	**Av Exp Male**	**Fold Change**	**adj P val**
217409_at	MYO5A	myosin VA (heavy chain 12, myoxin)	4644	Hs.21213	27.93	25.81	-1.17	0.046
219995_s_at	ZNF750	zinc finger protein 750	79755	Hs.464391, Hs.653124	11.02	10.62	-1.08	0.046
204723_at	SCN3B	sodium channel, voltage-gated, type III, beta	55800	Hs.4865	91.22	82.42	-1.23	0.047
202520_s_at	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	4292	Hs.195364	363.54	403.61	1.23	0.047
219498_s_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	53335	Hs.370549	199.97	188.81	-1.12	0.047
216340_s_at	CYP2A7P1	cytochrome P450, family 2, subfamily A, polypeptide 7 pseudogene 1	1550	Hs.250615	67.05	62.01	-1.17	0.047
206171_at	ADORA3	adenosine A3 receptor	140	Hs.281342	122.75	108.80	-1.27	0.047
203584_at	TTC35	tetratricopeptide repeat domain 35	9694	Hs.654351	85.62	103.44	1.46	0.047
202109_at	ARFIP2	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	23647	Hs.75139	222.33	208.40	-1.14	0.047
217004_s_at	MCF2	MCF.2 cell line derived transforming sequence	4168	Hs.387262	23.89	22.61	-1.12	0.047
221622_s_at	TMEM126B	transmembrane protein 126B	55863	Hs.525063	267.24	317.07	1.41	0.047
204290_s_at	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	4329	Hs.293970	280.97	346.20	1.52	0.047
220114_s_at	STAB2	stabilin 2	55576	Hs.408249	109.59	97.69	-1.26	0.047
211534_x_at	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	5799	Hs.490789	185.05	169.18	-1.20	0.047
219218_at			79749		79.34	86.24	1.18	0.047
207295_at	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	6340	Hs.371727	27.76	25.75	-1.16	0.047
200826_at	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	6633	Hs.515472	714.40	797.41	1.25	0.047
214340_at	ALOX12P2	arachidonate 12-lipoxygenase pseudogene 2	245	Hs.378695	121.59	112.26	-1.17	0.047
205052_at	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	549	Hs.175905	201.92	231.74	1.32	0.048
221486_at	ENSA	endosulfine alpha	2029	Hs.632456	537.89	601.04	1.25	0.048
211416_x_at	GGTLA4	gamma-glutamyltransferase-like activity 4	92086	Hs.355394, Hs.450000	80.00	71.40	-1.26	0.048

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
208409_at	SLC14A2	solute carrier family 14 (urea transporter), member 2	8170	Hs.660605	61.86	56.86	-1.18	0.048
207524_at	ST7	suppression of tumorigenicity 7	7982	Hs.368131	161.89	147.79	-1.20	0.048
220288_at	MYO15A	myosin XVA	51168	Hs.462390	33.15	30.88	-1.15	0.048
210530_s_at	NR2C1	nuclear receptor subfamily 2, group C, member 1	7181	Hs.108301	74.53	67.87	-1.21	0.048
212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	10213	Hs.567410	453.59	523.61	1.33	0.048
217765_at	NRBP1	nuclear receptor binding protein 1	29959	Hs.515876	171.81	191.54	1.24	0.048
211955_at	RANBP5	RAN binding protein 5	3843	Hs.643743	150.53	169.54	1.27	0.048
203866_at	NLE1	notchless homolog 1 (Drosophila)	54475	Hs.85570	48.69	44.31	-1.21	0.048
220214_at	ZNF215	zinc finger protein 215	7762	Hs.523457	79.52	73.19	-1.18	0.048
204049_s_at	PHACTR2	phosphatase and actin regulator 2	9749	Hs.654921	157.81	212.64	1.82	0.048
202650_s_at	KIAA0195	KIAA0195	9772	Hs.514474	99.10	91.93	-1.16	0.048
204320_at	COL11A1	collagen, type XI, alpha 1	1301	Hs.523446	26.74	24.73	-1.17	0.048
202593_s_at	MIR16	membrane interacting protein of RGS16	51573	Hs.512607	220.80	293.89	1.77	0.048
204804_at	TRIM21	tripartite motif-containing 21	6737	Hs.532357	105.37	95.47	-1.22	0.048
220872_at	PRO2964	hypothetical protein PRO2964	55415	Hs.621377	17.57	16.57	-1.13	0.048
208780_x_at	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	9218	Hs.165195	1007.95	1154.16	1.31	0.048
204060_s_at	PRKX	protein kinase, X-linked	5613	Hs.390788	29.65	32.80	1.22	0.048
206641_at	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	608	Hs.2556	25.98	23.80	-1.19	0.048
207302_at	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	6445	Hs.37167	780.78	901.21	1.33	0.048
219452_at	DPEP2	dipeptidase 2	64174	Hs.372633	51.61	45.81	-1.27	0.048
219287_at	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	27345	Hs.525529	130.84	116.85	-1.25	0.048
220986_s_at	TIGD6	tigger transposable element derived 6	81789	Hs.169333	12.32	11.77	-1.10	0.048

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
221254_s_at	PITPNM3	PITPNM family member 3	83394	Hs.183983	26.72	24.36	-1.20	0.048
206042_x_at	SNURF	SNRPN upstream reading frame	8926	Hs.564847	749.13	943.26	1.59	0.048
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	3958	Hs.531081	1377.59	1563.13	1.29	0.049
220506_at	GUCY1B2	guanylate cyclase 1, soluble, beta 2	2974	Hs.411573	42.91	39.68	-1.17	0.049
214470_at	KLRB1	killer cell lectin-like receptor subfamily B, member 1	3820	Hs.169824	57.42	49.41	-1.35	0.049
200030_s_at	SLC25A3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	5250	Hs.290404	4317.79	4727.73	1.20	0.049
38707_r_at	E2F4	E2F transcription factor 4, p107/p130-binding	1874	Hs.108371	826.20	758.41	-1.19	0.049
200771_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	3915	Hs.609663	473.61	552.90	1.36	0.049
205216_s_at	APOH	apolipoprotein H (beta-2-glycoprotein I)	350	Hs.445358	63.32	57.86	-1.20	0.049
204041_at	MAOB	monoamine oxidase B	4129	Hs.654473	852.18	956.15	1.26	0.049
207465_at	PRO0628	PRO0628 protein	29053	Hs.655428	12.31	11.70	-1.11	0.049
220643_s_at	FAIM	Fas apoptotic inhibitory molecule	55179	Hs.173438	15.96	17.09	1.15	0.049
206634_at	SIX3	SIX homeobox 3	6496	Hs.658847	32.38	29.11	-1.24	0.049
208671_at	SERINC1	serine incorporator 1	57515	Hs.146668	358.29	439.43	1.50	0.049
205665_at	TSPAN9	tetraspanin 9	10867	Hs.504517	109.31	120.67	1.22	0.049
206154_at	RLBP1	retinaldehyde binding protein 1	6017	Hs.1933	87.96	78.63	-1.25	0.049
215160_x_at			91222		63.21	73.02	1.33	0.049
204923_at	CXorf9	chromosome X open reading frame 9	54440	Hs.61469	128.62	113.20	-1.29	0.049
38964_r_at	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	7454	Hs.2157	418.72	386.41	-1.17	0.049
212728_at			57490		65.75	60.75	-1.17	0.049
203657_s_at	CTSF	cathepsin F	8722	Hs.11590	204.74	234.29	1.31	0.049
210467_x_at	MAGEA12	melanoma antigen family A, 12	4111	Hs.169246	17.41	16.21	-1.15	0.049
221346_at	OR10J1	olfactory receptor, family 10, subfamily J, member 1	26476	Hs.532661	111.38	102.94	-1.17	0.049
207701_at	C22orf24	chromosome 22 open reading frame 24	25775	Hs.226755	137.67	127.07	-1.17	0.049
215840_at	DNAH2	dynein, axonemal, heavy chain 2	146754	Hs.367649	61.94	56.94	-1.18	0.050
216544_at	RBMY2FP	RNA binding motif protein, Y-linked, family 2, member F	159162	Hs.567746, Hs.684794	30.91	28.71	-1.16	0.050

Probe	Symbol	Description	Gene	UniGene	Av Exp Female	Av Exp Male	Fold Change	adj P val
		pseudogene						
220270_at			54513		23.32	21.80	-1.14	0.050
39763_at	HPX	hemopexin	3263	Hs.426485	212.23	196.62	-1.17	0.050
44563_at	WDR79	WD repeat domain 79	55135	Hs.437460	146.75	135.65	-1.17	0.050
220883_at	PRO2012	hypothetical protein PRO2012	55478		19.57	18.21	-1.16	0.050
219159_s_at	SLAMF7	SLAM family member 7	57823	Hs.517265	50.66	46.22	-1.20	0.050
202561_at	TNKS	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	8658	Hs.370267	58.71	68.20	1.35	0.050
220310_at	TUBAL3	tubulin, alpha-like 3	79861	Hs.163079	22.57	21.03	-1.15	0.050
218418_s_at	ANKRD25	ankyrin repeat domain 25	25959	Hs.284208	576.97	660.57	1.31	0.050
220309_at	TTC22	tetratricopeptide repeat domain 22	55001	Hs.16230	56.23	51.15	-1.21	0.050
205265_s_at	SPEG	SPEG complex locus	10290	Hs.21639, Hs.631489	158.53	174.86	1.22	0.050
210321_at	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	2999	Hs.348264	86.97	78.97	-1.21	0.050
201560_at	CLIC4	chloride intracellular channel 4	25932	Hs.440544	556.74	633.53	1.29	0.050
219595_at	ZNF26	zinc finger protein 26	7574	Hs.489608	86.82	78.49	-1.22	0.050
207040_s_at	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	6767	Hs.546303	605.44	687.46	1.29	0.050
221407_at	GJA9	gap junction protein, alpha 9, 36kDa	57369	Hs.283816	137.18	122.26	-1.26	0.050
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	64919	Hs.510396	18.99	17.15	-1.23	0.050
221178_at	BAIAP2L2	BAI1-associated protein 2-like 2	80115	Hs.474822	20.33	18.94	-1.15	0.050
219049_at	ChGn	chondroitin beta1,4 N-acetylgalactosaminyltransferase	55790	Hs.655166	214.54	259.81	1.47	0.050
219046_s_at	PKNOX2	PBX/knotted 1 homeobox 2	63876	Hs.278564	248.56	231.36	-1.15	0.050
208574_at	SOX14	SRY (sex determining region Y)-box 14	8403	Hs.248184	18.23	16.96	-1.16	0.050
207073_at	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	8999	Hs.591698	78.22	69.63	-1.26	0.050
221335_x_at	C19orf61	chromosome 19 open reading frame 61	56006	Hs.466875	89.31	82.92	-1.16	0.050
208088_s_at	CFHR5	complement factor H-related 5	81494	Hs.282594	16.72	15.66	-1.14	0.050

Supplemental Table 2. Overrepresented Gene Ontology Pathways. All, Male versus Female (A-G) and Female, Over versus under 55years (E)

A) GO:0015672, Monovalent inorganic cation transport

EntrezID	ProbeSet ID	Gene symbol	Description
201172_x_at	8992	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
201527_at	9296	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F
202783_at	23530	NNT	nicotinamide nucleotide transhydrogenase
204087_s_at	8884	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
204124_at	10568	SLC34A2	solute carrier family 34 (sodium phosphate), member 2
204723_at	55800	SCN3B	sodium channel, voltage-gated, type III, beta
205156_s_at	41	ACCN2	amiloride-sensitive cation channel 2, neuronal
205243_at	64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
205896_at	6583	SLC22A4	solute carrier family 22 (organic cation transporter), member 4
206231_at	3780	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1
206417_at	1259	CNGA1	cyclic nucleotide gated channel alpha 1
206830_at	57282	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10
206872_at	6568	SLC17A1	solute carrier family 17 (sodium phosphate), member 1
207049_at	6334	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit
207051_at	10050	SLC17A4	solute carrier family 17 (sodium phosphate), member 4
207141_s_at	3760	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3
207185_at	6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
207217_s_at	27035	NOX1	NADPH oxidase 1
207261_at	1261	CNGA3	cyclic nucleotide gated channel alpha 3
207295_at	6340	SCNN1G	sodium channel, nonvoltage-gated 1, gamma
207298_at	10786	SLC17A3	solute carrier family 17 (sodium phosphate), member 3
207600_at	3748	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3
208172_s_at	9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2
208564_at	3737	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2
208578_at	6336	SCN10A	sodium channel, voltage-gated, type X, alpha subunit
208678_at	529	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1
208737_at	9550	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
210040_at	57468	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5
210261_at	3776	KCNK2	potassium channel, subfamily K, member 2
210453_x_at	10632	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G
210454_s_at	3763	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6
210739_x_at	8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
210853_at	11280	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit
211123_at	6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5
211755_s_at	515	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1
211806_s_at	3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15
213036_x_at	489	ATP2A3	ATPase, Ca++ transporting, ubiquitous
213587_s_at	155066	ATP6V0E2	ATPase, H+ transporting V0 subunit e2
214893_x_at	610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2
215267_s_at	6543	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2
215960_at	6527	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4
219287_at	27345	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
219545_at	65987	KCTD14	potassium channel tetramerisation domain containing 14
219564_at	3773	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16
220181_x_at	64924	SLC30A5	solute carrier family 30 (zinc transporter), member 5

220294_at	27012	KCNV1	potassium channel, subfamily V, member 1
220503_at	6561	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1
220540_at	60598	KCNK15	potassium channel, subfamily K, member 15
220559_at	2019	EN1	engrailed homeobox 1
220722_s_at	60482	SLC5A7	solute carrier family 5 (choline transporter), member 7
220740_s_at	9990	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6
220776_at	3770	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14
220867_s_at	25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2
221125_s_at	27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3
222289_at	3747	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2
34858_at	23510	KCTD2	potassium channel tetramerisation domain containing 2
45653_at	253980	KCTD13	potassium channel tetramerisation domain containing 13

B) GO:0007606, Sensory perception of chemical stimulus

EntrezID	ProbeSet ID	Gene symbol	Description
208098_at	81696	OR5V1	olfactory receptor, family 5, subfamily V, member 1
208285_at	26659	OR7A5	olfactory receptor, family 7, subfamily A, member 5
208521_at	10798	OR5I1	olfactory receptor, family 5, subfamily I, member 1
208543_at	26538	OR10H2	olfactory receptor, family 10, subfamily H, member 2
208573_s_at	7932	OR2H2	olfactory receptor, family 2, subfamily H, member 2
215463_at	26648	OR7E24	olfactory receptor, family 7, subfamily E, member 24
216408_at	81697	OR2B2	olfactory receptor, family 2, subfamily B, member 2
216522_at	26212	OR2B6	olfactory receptor, family 2, subfamily B, member 6
216817_s_at	26716	OR2H1	olfactory receptor, family 2, subfamily H, member 1
220806_x_at	51764	GNG13	guanine nucleotide binding protein (G protein), gamma 13
221346_at	26476	OR10J1	olfactory receptor, family 10, subfamily J, member 1
221375_at	8390	OR1G1	olfactory receptor, family 1, subfamily G, member 1
221388_at	8383	OR1A1	olfactory receptor, family 1, subfamily A, member 1
221391_at	50840	TAS2R14	taste receptor, type 2, member 14
221392_at	50832	TAS2R4	taste receptor, type 2, member 4
221397_at	50839	TAS2R10	taste receptor, type 2, member 10
221398_at	50836	TAS2R8	taste receptor, type 2, member 8
221431_s_at	81797	OR12D3	olfactory receptor, family 12, subfamily D, member 3
221444_at	50833	TAS2R16	taste receptor, type 2, member 16
221445_at	26189	OR1A2	olfactory receptor, family 1, subfamily A, member 2
221451_s_at	26692	OR2W1	olfactory receptor, family 2, subfamily W, member 1
221464_at	4991	OR1D2	olfactory receptor, family 1, subfamily D, member 2
221465_at	8590	OR6A2	olfactory receptor, family 6, subfamily A, member 2

C) GO:0006814; Sodium ion transport

Entrez ID	ProbeSet ID	Gene Symbol	Description
210739_x_at	8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
204087_s_at	8884	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
204124_at	10568	SLC34A2	solute carrier family 34 (sodium phosphate), member 2
204723_at	55800	SCN3B	sodium channel, voltage-gated, type III, beta
205156_s_at	41	ACCN2	amiloride-sensitive cation channel 2, neuronal
205243_at	64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
205896_at	6583	SLC22A4	solute carrier family 22 (organic cation transporter), member 4

206830_at	57282	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10
206872_at	6568	SLC17A1	solute carrier family 17 (sodium phosphate), member 1
207049_at	6334	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit
207051_at	10050	SLC17A4	solute carrier family 17 (sodium phosphate), member 4
207185_at	6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
207295_at	6340	SCNN1G	sodium channel, nonvoltage-gated 1, gamma
207298_at	10786	SLC17A3	solute carrier family 17 (sodium phosphate), member 3
214893_x_at	610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2
208578_at	6336	SCN10A	sodium channel, voltage-gated, type X, alpha subunit
210040_at	57468	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5
210853_at	11280	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit
211123_at	6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5
215267_s_at	6543	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2
215960_at	6527	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4
220503_at	6561	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1
220722_s_at	60482	SLC5A7	solute carrier family 5 (choline transporter), member 7
220740_s_at	9990	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6
220867_s_at	25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2

D) GO:0006812; Cation transport

207693_at	785	CACNB4	calcium channel, voltage-dependent, beta 4 subunit
207951_at	1447	CSN2	casein beta
208172_s_at	9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2
208564_at	3737	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2
208578_at	6336	SCN10A	sodium channel, voltage-gated, type X, alpha subunit
208678_at	529	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1
208737_at	9550	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
210040_at	57468	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5
211806_s_at	3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15
210261_at	3776	KCNK2	potassium channel, subfamily K, member 2
210454_s_at	3763	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6
210853_at	11280	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit
211123_at	6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5
211755_s_at	515	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1
34858_at	23510	KCTD2	potassium channel tetramerisation domain containing 2
213587_s_at	155066	ATP6V0E2	ATPase, H+ transporting V0 subunit e2
215267_s_at	6543	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2
215960_at	6527	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4
218792_s_at	54836	BSPRY	B-box and SPRY domain containing
220181_x_at	64924	SLC30A5	solute carrier family 30 (zinc transporter), member 5
219287_at	27345	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
219545_at	65987	KCTD14	potassium channel tetramerisation domain containing 14
219564_at	3773	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16
220043_s_at	4241	MFI2	antigen p97 identified by monoclonal antibodies 133.2 and 96.5
220294_at	27012	KCNV1	potassium channel, subfamily V, member 1
220413_at	29986	SLC39A2	solute carrier family 39 (zinc transporter), member 2
220435_at	55532	SLC30A10	solute carrier family 30, member 10
220503_at	6561	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1
220540_at	60598	KCNK15	potassium channel, subfamily K, member 15
220559_at	2019	EN1	engrailed homeobox 1
220722_s_at	60482	SLC5A7	solute carrier family 5 (choline transporter), member 7
220740_s_at	9990	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6

220776_at	3770	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14
220814_at	55676	SLC30A6	solute carrier family 30 (zinc transporter), member 6
220867_s_at	25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2
221102_s_at	140803	TRPM6	transient receptor potential cation channel, subfamily M, member 6
221107_at	55584	CHRNA9	cholinergic receptor, nicotinic, alpha 9
221125_s_at	27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3
45653_at	253980	KCTD13	potassium channel tetramerisation domain containing 13
222289_at	3747	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2

E) GO:00030001; Metal ion transport

Entrez ID	ProbeSet ID	Gene Symbol	Description
203880_at	10063	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)
204087_s_at	8884	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
204124_at	10568	SLC34A2	solute carrier family 34 (sodium phosphate), member 2
204624_at	540	ATP7B	ATPase, Cu++ transporting, beta polypeptide
204723_at	55800	SCN3B	sodium channel, voltage-gated, type III, beta
205156_s_at	41	ACCN2	amiloride-sensitive cation channel 2, neuronal
205243_at	64849	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
205676_at	1594	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1
205896_at	6583	SLC22A4	solute carrier family 22 (organic cation transporter), member 4
206231_at	3780	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1
206417_at	1259	CNGA1	cyclic nucleotide gated channel alpha 1
206830_at	57282	SLC4A10	solute carrier family 4, sodium bicarbonate transporter-like, member 10
206872_at	6568	SLC17A1	solute carrier family 17 (sodium phosphate), member 1
207049_at	6334	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit
207051_at	10050	SLC17A4	solute carrier family 17 (sodium phosphate), member 4
207141_s_at	3760	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3
207185_at	6554	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
207261_at	1261	CNGA3	cyclic nucleotide gated channel alpha 3
207295_at	6340	SCNN1G	sodium channel, nonvoltage-gated 1, gamma
207298_at	10786	SLC17A3	solute carrier family 17 (sodium phosphate), member 3
207362_at	7782	SLC30A4	solute carrier family 30 (zinc transporter), member 4
207600_at	3748	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3
207693_at	785	CACNB4	calcium channel, voltage-dependent, beta 4 subunit
207951_at	1447	CSN2	casein beta
208172_s_at	9312	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2
208564_at	3737	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2
208578_at	6336	SCN10A	sodium channel, voltage-gated, type X, alpha subunit
210040_at	57468	SLC12A5	solute carrier family 12, (potassium-chloride transporter) member 5
210261_at	3776	KCNK2	potassium channel, subfamily K, member 2
210454_s_at	3763	KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6
210739_x_at	8671	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
210853_at	11280	SCN11A	sodium channel, voltage-gated, type XI, alpha subunit
210864_x_at	3077	HFE	hemochromatosis
211123_at	6528	SLC5A5	solute carrier family 5 (sodium iodide symporter), member 5
211806_s_at	3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15
213036_x_at	489	ATP2A3	ATPase, Ca++ transporting, ubiquitous
214893_x_at	610	HCN2	hyperpolarization activated cyclic nucleotide-gated potassium channel 2
215267_s_at	6543	SLC8A2	solute carrier family 8 (sodium-calcium exchanger), member 2

215960_at	6527	SLC5A4	solute carrier family 5 (low affinity glucose cotransporter), member 4
217287_s_at	7225	TRPC6	transient receptor potential cation channel, subfamily C, member 6
218792_s_at	54836	BSPRY	B-box and SPRY domain containing
219287_at	27345	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
219545_at	65987	KCTD14	potassium channel tetramerisation domain containing 14
219564_at	3773	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16
220043_s_at	4241	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5
220181_x_at	64924	SLC30A5	solute carrier family 30 (zinc transporter), member 5
220294_at	27012	KCNV1	potassium channel, subfamily V, member 1
220413_at	29986	SLC39A2	solute carrier family 39 (zinc transporter), member 2
220503_at	6561	SLC13A1	solute carrier family 13 (sodium/sulfate symporters), member 1
220540_at	60598	KCNK15	potassium channel, subfamily K, member 15
220559_at	2019	EN1	engrailed homeobox 1
220722_s_at	60482	SLC5A7	solute carrier family 5 (choline transporter), member 7
220740_s_at	9990	SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6
220776_at	3770	KCNJ14	potassium inwardly-rectifying channel, subfamily J, member 14
220867_s_at	25769	SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2
221102_s_at	140803	TRPM6	transient receptor potential cation channel, subfamily M, member 6
221107_at	55584	CHRNA9	cholinergic receptor, nicotinic, alpha 9
221125_s_at	27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3
222289_at	3747	KCNC2	potassium voltage-gated channel, Shaw-related subfamily, member 2
34858_at	23510	KCTD2	potassium channel tetramerisation domain containing 2
45653_at	253980	KCTD13	potassium channel tetramerisation domain containing 13

F) GO:0007600; Sensory perception

Entrez ID	ProbeSet ID	Gene Symbol	Description
208098_at	81696	OR5V1	olfactory receptor, family 5, subfamily V, member 1
208285_at	26659	OR7A5	olfactory receptor, family 7, subfamily A, member 5
208521_at	10798	OR5I1	olfactory receptor, family 5, subfamily I, member 1
208543_at	26538	OR10H2	olfactory receptor, family 10, subfamily H, member 2
208573_s_at	7932	OR2H2	olfactory receptor, family 2, subfamily H, member 2
215463_at	26648	OR7E24	olfactory receptor, family 7, subfamily E, member 24
216408_at	81697	OR2B2	olfactory receptor, family 2, subfamily B, member 2
216522_at	26212	OR2B6	olfactory receptor, family 2, subfamily B, member 6
216817_s_at	26716	OR2H1	olfactory receptor, family 2, subfamily H, member 1
220806_x_at	51764	GNG13	guanine nucleotide binding protein (G protein), gamma 13
221346_at	26476	OR10J1	olfactory receptor, family 10, subfamily J, member 1
221375_at	8390	OR1G1	olfactory receptor, family 1, subfamily G, member 1
221388_at	8383	OR1A1	olfactory receptor, family 1, subfamily A, member 1
221391_at	50840	TAS2R14	taste receptor, type 2, member 14
221392_at	50832	TAS2R4	taste receptor, type 2, member 4
221397_at	50839	TAS2R10	taste receptor, type 2, member 10
221398_at	50836	TAS2R8	taste receptor, type 2, member 8
221431_s_at	81797	OR12D3	olfactory receptor, family 12, subfamily D, member 3
221444_at	50833	TAS2R16	taste receptor, type 2, member 16
221445_at	26189	OR1A2	olfactory receptor, family 1, subfamily A, member 2
221451_s_at	26692	OR2W1	olfactory receptor, family 2, subfamily W, member 1
221464_at	4991	OR1D2	olfactory receptor, family 1, subfamily D, member 2
221465_at	8590	OR6A2	olfactory receptor, family 6, subfamily A, member 2

G) GO:0007186; G-protein-coupled receptor signaling pathway

Entrez ID	ProbeSet ID	Gene Symbol	Description
38447_at	156	ADRBK1	adrenergic, beta, receptor kinase 1
211607_x_at	1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
202849_x_at	2870	GRK6	G protein-coupled receptor kinase 6
203108_at	9052	GPRC5A	G protein-coupled receptor, family C, group 5, member A
203632_s_at	51704	GPRC5B	G protein-coupled receptor, family C, group 5, member B
205184_at	2786	GNG4	guanine nucleotide binding protein (G protein), gamma 4
205240_at	29899	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)
205419_at	1880	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
205456_at	916	CD3E	CD3e molecule, epsilon (CD3-TCR complex)
216738_at	3269	HRH1	histamine receptor H1
206171_at	140	ADORA3	adenosine A3 receptor
206281_at	116	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)
206326_at	2922	GRP	gastrin-releasing peptide
206369_s_at	5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide
206422_at	2641	GCG	glucagon
206429_at	2150	F2RL1	coagulation factor II (thrombin) receptor-like 1
206525_at	2569	GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1
206586_at	1269	CNR2	cannabinoid receptor 2 (macrophage)
206678_at	2554	GABRA1	gamma-aminobutyric acid (GABA) A receptor, alpha 1
206772_at	5746	PTHR2	parathyroid hormone receptor 2
206841_at	5149	PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma
206849_at	2566	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2
206887_at	1238	CCBP2	chemokine binding protein 2
211469_s_at	10663	CXCR6	chemokine (C-X-C motif) receptor 6
206988_at	6370	CCL25	chemokine (C-C motif) ligand 25
206991_s_at	1234	CCR5	chemokine (C-C motif) receptor 5
206998_x_at	5544	PRB3	proline-rich protein BstNI subfamily 3
207014_at	2555	GABRA2	gamma-aminobutyric acid (GABA) A receptor, alpha 2
207111_at	2015	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1
207183_at	2842	GPR19	G protein-coupled receptor 19
207240_s_at	3973	LHCGR	luteinizing hormone/choriogonadotropin receptor
207333_at	4829	NMBR	neuromedin B receptor
207356_at	1673	DEFB4	defensin, beta 4
207400_at	4889	NPY5R	neuropeptide Y receptor Y5
207445_s_at	10803	CCR9	chemokine (C-C motif) receptor 9
207455_at	5028	P2RY1	purinergic receptor P2Y, G-protein coupled, 1
207462_at	2742	GLRA2	glycine receptor, alpha 2
207497_s_at	2206	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)
207642_at	3060	HCRT	hypocretin (orexin) neuropeptide precursor
211545_at	2692	GHRHR	growth hormone releasing hormone receptor
207897_at	1395	CRHR2	corticotropin releasing hormone receptor 2
207929_at	2925	GRPR	gastrin-releasing peptide receptor
207940_x_at	1268	CNR1	cannabinoid receptor 1 (brain)
211359_s_at	4988	OPRM1	opioid receptor, mu 1
208035_at	2916	GRM6	glutamate receptor, metabotropic 6
208098_at	81696	OR5V1	olfactory receptor, family 5, subfamily V, member 1
208210_at	4142	MAS1	MAS1 oncogene
208248_x_at	334	APLP2	amyloid beta (A4) precursor-like protein 2

208260_at	553	AVPR1B	arginine vasopressin receptor 1B
208285_at	26659	OR7A5	olfactory receptor, family 7, subfamily A, member 5
208311_at	9248	GPR50	G protein-coupled receptor 50
208314_at	10692	RRH	retinal pigment epithelium-derived rhodopsin homolog
208376_at	1233	CCR4	chemokine (C-C motif) receptor 4
208521_at	10798	OR5I1	olfactory receptor, family 5, subfamily I, member 1
208524_at	2838	GPR15	G protein-coupled receptor 15
208543_at	26538	OR10H2	olfactory receptor, family 10, subfamily H, member 2
208573_s_at	7932	OR2H2	olfactory receptor, family 2, subfamily H, member 2
210055_at	7253	TSHR	thyroid stimulating hormone receptor
210393_at	8549	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5
210604_at	2780	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2
210799_at	3351	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B
211201_at	2492	FSHR	follicle stimulating hormone receptor
211496_s_at	5132	PDC	phosducin
216341_s_at	2798	GNRHR	gonadotropin-releasing hormone receptor
214529_at	7252	TSHB	thyroid stimulating hormone, beta
214560_at	2359	FPRL2	formyl peptide receptor-like 2
215396_at	84059	GPR98	G protein-coupled receptor 98
215463_at	26648	OR7E24	olfactory receptor, family 7, subfamily E, member 24
216288_at	10800	CYSLTR1	cysteinyl leukotriene receptor 1
216408_at	81697	OR2B2	olfactory receptor, family 2, subfamily B, member 2
216522_at	26212	OR2B6	olfactory receptor, family 2, subfamily B, member 6
216817_s_at	26716	OR2H1	olfactory receptor, family 2, subfamily H, member 1
216881_x_at	5545	PRB4	proline-rich protein BstNI subfamily 4
216895_at	2567	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3
217629_at	2793	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2
220313_at	54112	GPR88	G protein-coupled receptor 88
220806_x_at	51764	GNG13	guanine nucleotide binding protein (G protein), gamma 13
221297_at	55507	GPRC5D	G protein-coupled receptor, family C, group 5, member D
221299_at	54328	GPR173	G protein-coupled receptor 173
221313_at	9293	GPR52	G protein-coupled receptor 52
221346_at	26476	OR10J1	olfactory receptor, family 10, subfamily J, member 1
221354_s_at	2847	MCHR1	melanin-concentrating hormone receptor 1
221375_at	8390	OR1G1	olfactory receptor, family 1, subfamily G, member 1
221382_at	26701	OR2N1P	olfactory receptor, family 2, subfamily N, member 1 pseudogene
221388_at	8383	OR1A1	olfactory receptor, family 1, subfamily A, member 1
221391_at	50840	TAS2R14	taste receptor, type 2, member 14
221392_at	50832	TAS2R4	taste receptor, type 2, member 4
221393_at	9288	TAAR3	trace amine associated receptor 3
221394_at	9287	TAAR2	trace amine associated receptor 2
221397_at	50839	TAS2R10	taste receptor, type 2, member 10
221398_at	50836	TAS2R8	taste receptor, type 2, member 8
221412_at	57191	VN1R1	vomeronasal 1 receptor 1
221431_s_at	81797	OR12D3	olfactory receptor, family 12, subfamily D, member 3
221444_at	50833	TAS2R16	taste receptor, type 2, member 16
221445_at	26189	OR1A2	olfactory receptor, family 1, subfamily A, member 2
221451_s_at	26692	OR2W1	olfactory receptor, family 2, subfamily W, member 1
221458_at	3355	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F
221464_at	4991	OR1D2	olfactory receptor, family 1, subfamily D, member 2
221465_at	8590	OR6A2	olfactory receptor, family 6, subfamily A, member 2
221467_at	4160	MC4R	melanocortin 4 receptor

H) GO: 0042770; DNA damage response, signal transduction

Entrez ID	ProbeSet ID	Gene Symbol	Description
202123_s_at	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1
20800_at	2765	GML	GPI anchored molecule like protein
221703_at	83990	BRIP1	BRCA1 interacting protein C-terminal helicase 1

Supplemental Table 3. Transcription factor binding site enrichmen tin male and female biased genes. PWM = positional weight matrix, TF = transcription factor

Binding site enrichment within 1 kb promoters of female biased genes (1.2 fold or greater)

PWM	TF family	TF	Foreground hits	Background hits	Enrichment Score	P	Q-value
M00619	Alx-4	Alx-4	60	162	1.59	0.002	0.036
M00310	APOLYA	APOLYA	77	214	1.54	0.0008	0.023
M01066	BLIMP1	BLIMP1	121	402	1.29	0.007	0.088
M00109	C/EBP	C/EBPbeta	91	287	1.36	0.006	0.081
M00416	Cart-1	Cart-1	50	119	1.80	0.0005	0.019
M00729	CDX	Cdx-2	53	143	1.59	0.003	0.052
M00991	CDX	CDX	44	119	1.58	0.007	0.088
M00269	FOX	XFD-3	63	147	1.83	0.00006	0.005
M00129	FOX	HFH-1	56	155	1.55	0.004	0.058
M00477	FOX	FOXO3	58	166	1.50	0.006	0.078
M00294	FOX	HFH-8	57	165	1.48	0.007	0.089
M00080	GATA	Evi-1	70	159	1.88	0.00001	0.003
M00078	GATA	Evi-1	63	148	1.82	0.00006	0.005
M00082	GATA	Evi-1	70	176	1.70	0.0001	0.008
M00079	GATA	Evi-1	80	221	1.55	0.0005	0.020
M00351	GATA	GATA-3	66	179	1.58	0.001	0.030
M00347	GATA	GATA-1	93	284	1.40	0.003	0.047
M00790	HNF	HNF-1	74	193	1.64	0.0002	0.010
M01011	HNF	HNF1	77	212	1.55	0.0006	0.022
M00206	HNF	HNF-1	69	191	1.55	0.001	0.033
M00132	HNF	HNF-1	79	233	1.45	0.003	0.047
M00639	HNF-6	HNF-6	47	123	1.64	0.003	0.052
M00640	HOXA4	HOXA4	63	165	1.63	0.0007	0.022
M00725	HP1	HP1	62	149	1.78	0.0001	0.008
M00436	IPF1	IPF1	62	169	1.57	0.002	0.036
M00978	LEF1	LEF1TCF1	117	315	1.59	0.00001	0.003
M00671	LEF1	TCF-4	64	192	1.43	0.009	0.096

M00406	MEF2	MEF-2	66	177	1.60	0.0009	0.025
M00405	MEF2	MEF-2	79	237	1.43	0.004	0.058
M00403	MEF2	aMEF-2	61	177	1.48	0.006	0.079
M00241	NKX	Nkx2-5	62	161	1.65	0.0006	0.022
M00240	NKX	Nkx2-5	28	60	2.00	0.002	0.047
M00161	OCT	OCT1	78	192	1.74	0.00003	0.005
M00138	OCT	OCT1	47	103	1.95	0.0002	0.008
M00930	OCT	OCT1	70	196	1.53	0.002	0.036
M00162	OCT	OCT1	42	103	1.75	0.002	0.041
M00210	OCT	OCT-x	72	206	1.50	0.002	0.042
M00795	OCT	Octamer	70	203	1.48	0.003	0.052
M00195	OCT	OCT1	79	240	1.41	0.005	0.073
M00096	PBX	Pbx-1	62	145	1.83	0.00007	0.005
M00802	Pit-1	Pit-1	44	121	1.56	0.008	0.096
M01075	PLZF	PLZF	44	120	1.57	0.008	0.091
M00744	POU	POU1F1	56	146	1.64	0.001	0.033
M00465	POU6F1	POU6F1	59	157	1.61	0.001	0.033
M00042	SRY	Sox-5	90	230	1.68	0.00003	0.005
M00410	SRY	SOX-9	84	225	1.60	0.0002	0.008
M00252	TATA	TATA	128	425	1.29	0.005	0.077
M00311	TATA	ATATA	82	257	1.37	0.008	0.093
M00707	TFIIA	TFIIA	155	529	1.25	0.005	0.077
M00432	TTF1	TTF1	105	287	1.57	0.00005	0.005
M01004	ZNFN1A	Helios_A	68	205	1.42	0.007	0.091

Binding site enrichment within 1 kb promoters of male biased genes (1.2 fold or greater)

PWM	TF family	TF	Foreground hits	Background hits	Enrichment Score	P	Q-value
M00740	E2F	Rb:E2F-1:DP-1	217	1395	1.26	0.0001	0.07
M00425	E2F	E2F	259	1741	1.20	0.0003	0.08

Supplemental Table 4. Genes in the All Male versus Female comparison that exhibit > 2-fold absolute fold change and adjusted *P* value < 0.05.

Probe	Symbol	Description	Chr	LocusLink	UniGene	Gene Ontology	Av exp F	Av exp M	FC	adj.P.Val
204409_s_at	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	Y	9086	Hs.461178	GO:0006413: translational initiation, GO:0003723: RNA binding, GO:0003743: translation initiation factor activity, GO:0005515: protein binding	12.51	210.22	282.40	3.40E-63
201909_at	RPS4Y1	ribosomal protein S4, Y-linked 1	Y	6192	Hs.282376	GO:0006412: translation, GO:0006412: translation, GO:0005622: intracellular, GO:0005840: ribosome, GO:0005843: cytosolic small ribosomal subunit (sensu Eukaryota), GO:0003735: structural constituent of ribosome, GO:0003735: structural constituent of ribosome, GO:0019843: rRNA binding	88.82	1065.96	144.04	2.41E-71
205000_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	Y	8653	Hs.99120	GO:0005634: nucleus, GO:0000166: nucleotide binding, GO:0003677: DNA binding, GO:0003723: RNA binding, GO:0005524: ATP binding, GO:0008026: ATP-dependent helicase activity, GO:0016787: hydrolase activity	18.34	79.94	19.00	1.43E-32
206700_s_at	JARID1D	jumonji, AT rich interactive domain 1D	Y	8284	Hs.80358	GO:0006355: regulation of transcription, DNA-dependent, GO:0007283: spermatogenesis, GO:0005575: cellular_component, GO:0005622: intracellular, GO:0005634: nucleus, GO:0003674: molecular_function, GO:0003677: DNA binding, GO:0005515: protein binding, GO:0008270: zinc ion binding, GO:0046872: metal ion binding	68.10	175.69	6.66	8.09E-33
206624_at	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	Y	8287	Hs.165856	GO:0006511: ubiquitin-dependent protein catabolic process, GO:0006512: ubiquitin cycle, GO:0007283: spermatogenesis, GO:0004221: ubiquitin thiolesterase activity, GO:0005509: calcium ion binding, GO:0005544: calcium-dependent phospholipid binding, GO:0008234: cysteine-type	17.05	35.70	4.38	1.02E-16

						peptidase activity				
207063_at	CYorf14	chromosome Y open reading frame 14	Y	55410			47.30	87.48	3.42	9.28E-27
210395_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	17	4635	Hs.463300	GO:0006941: striated muscle contraction, GO:0007517: muscle development, GO:0005859: muscle myosin complex, GO:0016459: myosin complex, GO:0016459: myosin complex, GO:0003774: motor activity, GO:0005509: calcium ion binding, GO:0008307: structural constituent of muscle	388.3240636	616.5254325	2.520654869	0.015411784
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	14	23224	Hs.525392	GO:0005856: cytoskeleton, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003779: actin binding, GO:0005198: structural molecule activity	177.8113982	280.9962476	2.497363999	0.006245176
214365_at	TPM3	tropomyosin 3	1	7170	Hs.129512, Hs.535581, Hs.644306	GO:0006928: cell motility, GO:0006937: regulation of muscle contraction, GO:0005856: cytoskeleton, GO:0005856: cytoskeleton, GO:0005862: muscle thin filament tropomyosin, GO:0003674: molecular_function, GO:0003779: actin binding	239.4311189	373.6240922	2.435053768	0.017537758
201222_s_at	RAD23B	RAD23 homolog B (S. cerevisiae)	9	5887	Hs.521640	GO:0006289: nucleotide-excision repair, GO:0006464: protein modification, GO:0006512: ubiquitin cycle, GO:0007283: spermatogenesis, GO:0005634: nucleus, GO:0003697: single-stranded DNA binding, GO:0005515: protein binding	127.3214201	191.4833004	2.261824274	0.01095177
209070_s_at	RGS5	regulator of G-protein signalling 5	1	8490	Hs.24950	GO:0008277: regulation of G-protein coupled receptor protein signaling pathway, GO:0009968: negative regulation of signal transduction, GO:0004871: signal transducer activity, GO:0005096: GTPase activator activity	885.5066823	1284.162782	2.103083286	0.021788644
202784_s_at	NNT	nicotinamide nucleotide transhydrogenase	5	23530	Hs.482043	GO:0006099: tricarboxylic acid cycle, GO:0006118: electron transport, GO:0006118: electron transport, GO:0015992: proton transport, GO:0015992: proton transport, GO:0005739:	269.1412	390.0852578	2.100674224	0.029623113

						mitochondrion, GO:0005746: mitochondrial electron transport chain, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0003957: NAD(P)+ transhydrogenase (B-specific) activity, GO:0008750: NAD(P)+ transhydrogenase (AB-specific) activity, GO:0016491: oxidoreductase activity, GO:0050661: NADP binding, GO:0051287: NAD binding				
209896_s_at	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	12	5781	Hs.506852, Hs.646231	GO:0000077: DNA damage checkpoint, GO:0000187: activation of MAPK activity, GO:0006470: protein amino acid dephosphorylation, GO:0007242: intracellular signaling cascade, GO:0007409: axonogenesis, GO:0007605: sensory perception of sound, GO:0046825: regulation of protein export from nucleus, GO:0048011: nerve growth factor receptor signaling pathway, GO:0004726: non-membrane spanning protein tyrosine phosphatase activity, GO:0005515: protein binding, GO:0016787: hydrolase activity	143.3962829	206.8691352	2.081208594	0.034520364
209485_s_at	OSBPL1A	oxysterol binding protein-like 1A	18	114876	Hs.370725	GO:0006869: lipid transport, GO:0008202: steroid metabolic process, GO:0008203: cholesterol metabolic process, GO:0016192: vesicle-mediated transport, GO:0005622: intracellular, GO:0005543: phospholipid binding	96.72617494	138.5502527	2.051760273	0.004236546
201028_s_at	CD99	CD99 molecule	X, Y	4267	Hs.495605	GO:0007155: cell adhesion, GO:0005737: cytoplasm, GO:0005886: plasma membrane, GO:0005887: integral to plasma membrane, GO:0005515: protein binding	321.4002338	457.9935774	2.030609431	0.000638864
220232_at	SCD5	stearoyl-CoA desaturase 5	4	79966	Hs.379191	GO:0006629: lipid metabolic process, GO:0006633: fatty acid biosynthetic process, GO:0005783: endoplasmic reticulum, GO:0016020: membrane, GO:0016021: integral to membrane, GO:0004768: stearoyl-CoA 9-desaturase activity, GO:0005506: iron ion binding, GO:0016491:	180.3372663	126.0962571	-2.045344996	0.003547101

						oxidoreductase activity, GO:0016717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water			
221728_x_at	XIST	X (inactive)-specific transcript	X	7503	Hs.529901		275.3525987	37.22739217	-54.70828873	9.93E-62