

Blood / Vascular

Average Change	TIGR/ Affymetrix #	Fold change for each comparison				Annotation
		1	2	3	4	
133.8	TC27670_g_at	122.4	152.2	115.5	145.1	myoglobin
38.4	TC32287_at	40.5	36.6	40	36.5	brain carboxyesterase, hBr3
36.4	TC40225_s_at	42.2	33.2	37.4	32.8	transthyretin
31.575	TC31057_g_at	27.9	34.5	28.4	35.5	brain carboxylesterase, hBr3
21.675	TC35644_s_at	9.5	25.5	8.9	42.8	vascular endothelial growth factor receptor 2
4.25	TC33445_at	5.2	3.8	4.7	3.3	factor-responsive protein, vascular
-6.75	TC24493_at	-4.6	-8.8	-4.7	-8.9	sodium bicarbonate cotransporter, NBC1
-14.525	TC16865_at	-20.5	-5.4	-25	-7.2	angiotensinogen
-34.45	TC30851_at	-33.7	-31.4	-37.6	-35.1	angiotensinogen

Amino Acid Metabolism

Average Change	TIGR/ Affymetrix #	Fold change for each comparison				Annotation
		1	2	3	4	
26.05	TC37650_at	32.3	23.8	27.7	20.4	glutamine aminotransferase
25.275	TC28737_g_at	23.7	26.9	23.5	27	alanine aminotransferase
19.4	TC39031_at	20.2	19.1	18.9	19.4	arginase
14.05	TC28820_g_at	13.5	13.3	14.2	15.2	alanine aminotransferase
4.475	TC19442_at	3.9	4.8	4.1	5.1	cysteine dioxygenase
3.5	TC32932_at	4.6	3.3	3.6	2.5	cholinephosphotransferase
-3.575	TC37346_g_at	-3.7	-3.5	-3.6	-3.5	l-asparaginase
-5.3	TC21815_at	-5.4	-5.1	-5.5	-5.2	similar to glycine decarboxylase
-5.975	TC40291_at	-7.1	-5.6	-6.1	-5.1	tryptophan-2,3-dioxygenase
-6.1	TC39492_at	-7	-6.6	-5.6	-5.2	tryptophan-2,3-dioxygenase
-7.45	TC28329_g_at	-9	-7.5	-7.3	-6	NBAT, amino acid transportor
-13.125	TC31560_s_at	-15.7	-17.3	-9.2	-10.3	D-amino-acid-oxidase
-13.45	TC30372_f_at	-21.4	-3.6	-24.8	-4	glutamate dehydrogenase
-17.925	TC33164_at	-7.4	-25.4	-8.7	-30.2	glycine amidinotransferase
-26.975	TC21186_at	-26.6	-26.5	-27.7	-27.1	glutaminase
-27.8	TC17899_at	-27.8	-29.3	-26.6	-27.5	possible tryptophan decarboxylase
-32.9	TC26764_at	-47.7	-41.1	-25.6	-17.2	possible peptidylglycine monooxygenase

Trafficking/Synapse

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
308.4	TC20337_at	316.4	301.3	318.7	297.2	synapsin
125.475	TC39173_s_at	124.4	104	143.6	129.9	benzodiazepine receptor (MBR)
110.65	TC33406_s_at	103.5	114.3	106.1	118.7	peripheral-type benzodiazepine receptor
53.975	TC36687_at	63	39	71.8	42.1	protein 4.1G
46.2	TC37537_at	49	30.7	62.7	42.4	protein 4.1G
30.675	TC20883_s_at	31.9	26.7	34.9	29.2	Munc18-2
27.1	TC19935_at	44.7	43.5	10.8	9.4	ERGIC-53
20.9	TC31586_at	19.5	16.2	24.9	23	syntaxin 3A
10.375	TC37978_s_at	8.6	8.9	11.8	12.2	protein 4.1G
9.925	TC18190_at	12.2	12	8	7.5	TC10
7.775	TC40937_s_at	6.4	8.3	7.1	9.3	unc 119
-3.8	TC34277_at	-2.8	-4.6	-3	-4.8	sodium dependent neurotransmitter protein
-5.725	TC37996_at	-6.8	-3.9	-7.8	-4.4	DARPP32
-8.5	TC18867_at	-9.1	-7.1	-10	-7.8	alpha-synuclein
-11.225	TC39376_at	-10.4	-8.6	-14.2	-11.7	proSAAS
-11.825	TC36359_at	-13.5	-10.7	-12.4	-10.7	TREK-1 K+ channel subunit
-13.275	TC24926_at	-14.3	-12.1	-14.5	-12.2	meta botropic glutamate receptor
-14	TC38008_at	-7.8	-19.1	-8.4	-20.7	similar to synamon interacter SAPAP
-16.4	TC30073_s_at	-16.1	-12.7	-19.1	-17.7	tyrosine phosphatases
-25.275	TC22188_at	-21.4	-22.3	-28.1	-29.3	calcyon
-32.475	TC28003_at	-46.7	-21.3	-42.6	-19.3	synaptotagmin XI
-38.6	TC19734_at	-44.4	-41.2	-53.3	-15.5	like glutamate receptor epsilon 3
-41.35	TC15940_g_at	-39.9	-47.7	-35.6	-42.2	coat protein gamma-cop

Cell Death

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	

161.225	TC16403_g_at	197.2	126.7	197.1	123.9	cell death activator CIDE-A
152.15	TC37556_at	184.2	126.3	170.1	128	p53
127.525	TC24816_s_at	119.2	133.9	122.5	134.5	cell death-associated protein 1
125.425	TC19787_at	105.7	121.1	130.8	144.1	p53 apoptosis-associated
122.7	TC17513_at	123.6	107.5	138.9	120.8	DAP 1, death associated protein
34.175	TC16227_at	71.1	11	34.1	20.5	similar to cell death receptor 6
9.2	TC19399_at	10.3	8.6	9.6	8.3	ASC, associated to apoptosis

Proteolysis

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
109.225	TC26009_at	91.6	121.1	95.8	128.4	stefin 3, CYT3
27.125	TC22206_at	25	29.3	25.3	28.9	cyt4 stefin homolog
21.4	TC17364_at	21.9	19.1	23.9	20.7	prostasin
17.25	TC31227_i_at	22.5	17.3	16.5	12.7	serine protease like
12.575	TC38179_at	16.1	17.1	8.2	8.9	similar to ACE carboxylpeptidase
11	TC34450_at	12	10.5	11.5	10	possible aminopeptidase
10.525	TC38926_at	7.5	8.1	12.8	13.7	like nephriysin peptidase
9.25	TC21695_at	7.3	6.9	11.7	11.1	serine protease
8.425	TC34175_at	7.6	7.3	9.6	9.2	possible aminopeptidase
5.075	TC41924_s_at	5	4.1	6.2	5	cathepsin L
5.025	TC31101_g_at	6.9	3.4	6.6	3.2	weak similarity to ACE2 peptidase
4.775	TC14570_f_at	4.8	3.9	5.7	4.7	C1 inhibitor
4.5	TC29215_s_at	5.8	5.4	3.5	3.3	Timp-3
4.2	TC16079_at	4.2	4.4	4	4.2	neurotrypsin
4	TC14219_f_at	5.4	3.4	4.4	2.8	cathepsin L
3.325	TC32493_f_at	3.5	3.2	3.5	3.1	cathepsin L
2.775	TC16200_at	3	2.6	2.9	2.6	possible protease
-26.7	TC37008_at	-32.6	-31.2	-22.2	-20.8	MASP2
-50.4	TC26229_at	-85.4	-27	-68.1	-21.1	similar to neprilysin peptide gamma

Structural/Adhesion/Cell Surface

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
84.25	TC14592_at	78	70.9	98.1	90	alpha 2 (IV) collagen
33.45	TC27291_s_at	31	35.9	30.8	36.1	cytokeratin 8
32.35	TC24005_s_at	26.8	36.8	28.3	37.5	57 kd keratin
30.575	TC30949_at	30	33.8	27.3	31.2	claudin-7
30	TC38440_at	37.5	22.5	36.3	23.7	claudin-7
27.625	TC32164_at	30.5	24.4	30.7	24.9	dermatopontin
27.3	TC18507_f_at	20.9	9.9	53.3	25.1	decorin
25.075	TC22866_f_at	12.9	6.2	52.5	28.7	collagen alpha-1
24.7	TC27544_at	18.3	19	30	31.5	collagen like
17.05	TC35765_at	41.1	7.9	10.9	8.3	sciellen
12.375	TC39251_at	12.4	10	14.8	12.3	similar to protocadherin
12.2	TC15396_at	12.9	9.9	14.7	11.3	dermatopontin
12.15	TC21430_at	19	12.2	10.6	6.8	similar to collagen alpha
11	TC38440_g_at	4.1	4.1	18.1	17.7	claudin-7
10.4	TC32399_at	12.7	7.7	13	8.2	Keartin Type II
10.05	TC26960_at	7.4	7.6	12.5	12.7	epidermal keratin subunit II
9.725	TC36729_at	13.6	9.3	9.5	6.5	decorin
7.3	TC22677_at	6.6	6.6	8.6	7.4	collagen alpha 3
6.9	TC19711_s_at	6.6	5.7	8.2	7.1	57 kd keratin

6.375	TC41987_at	7.3	5.5	7	5.7	Desmocollin type 2
5.8	TC32858_f_at	6.5	5.4	6.2	5.1	Lectin L-14
5.625	TC30023_f_at	6.5	3.4	8.4	4.2	Ioricrin
5.2	TC16852_at	6.4	5.1	5.2	4.1	periplakin
3.625	TC16809_at	4	3.2	4	3.3	cell-surface sialomucin, MGC-24
3.625	TC22662_at	4.1	3.5	3.7	3.2	collagen alpha 2
-2.625	TC30560_at	-2.8	-2.6	-2.6	-2.5	cadherin 22
-26.3	TC22483_g_at	-26.7	-26.8	-26.1	-25.6	coronin-1

Signalling / Cell Growth

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
53.2	TC25512_s_at	50.3	62.5	44.7	55.3	Fisp-12
46	TC19633_s_at	30.4	38.4	55.3	59.9	Fisp-12
42.65	TC31161_at	43	41.8	43.2	42.6	IKLF, BTE-binding protein 2
36.725	TC23815_s_at	56.2	20.7	51.2	18.8	SR calcium ATPase
35.875	TC20654_at	28.6	24.2	49.1	41.6	similar to GADD3x inhibitor cell growth
33.95	TC22352_s_at	21.3	26	39	49.5	s100 calcium binding protein
27.4	TC31507_at	18.3	19.4	33.2	38.7	slw type calcium binding protein A14
26.7	TC40393_s_at	25	18.1	38.7	25	pEL98 calcium binding protein
20.4	TC34408_s_at	19.3	30.3	3.3	28.7	CBF-a
16.3	TC24724_s_at	4.7	26.9	3.6	30	JUN-B
10.425	TC17335_at	17.1	15.6	4.7	4.3	phosphodiesterase, PDE8
10.075	TC31533_at	12.1	11	9	8.2	protein kinase type II-beta regulatory subunit
9.875	TC18256_at	5.5	4.7	15.8	13.5	Dyrk2 signaling kinase
6.8	TC34015_at	8.3	5	8.7	5.2	CCAAT/enhancer binding protein
6.125	TC27896_at	6.3	8.4	4.2	5.6	NG27
5.95	TC22758_at	7.4	5.7	5.8	4.9	protein kinase Dyrk2
5.85	TC36530_at	6.2	5.2	6.5	5.5	Mnk2
5.6	TC37488_at	6.3	5.4	5.8	4.9	PTPLB
5.475	TC35223_g_at	6.4	5.6	5.3	4.6	hepatocyte growth factor activator inhibitor type 2
5.3	TC14368_f_at	6.1	5.3	5.2	4.6	p36; calpactin I heavy chain
4.75	TC26799_i_at	4.2	5.3	4.2	5.3	mPRL-3
4.525	TC18449_at	4.5	4.7	4.3	4.6	p57kip2
4.5	TC23200_at	4.7	5.1	3.9	4.3	caveolin-1
4.025	TC29371_at	4.3	4.7	3.5	3.6	FRAG1
3.775	TC34015_g_at	4.2	3.2	4.4	3.3	CCAAT/enhancer binding protein
3.65	TC15924_at	4.6	4.2	3	2.8	protein-tyrosine-phosphatase
3.4	TC33329_at	4.1	3.5	3.2	2.8	caveolin-1 beta isoform
3.4	TC34662_g_at	3.4	3.6	3.2	3.4	FGF binding protein 1
2.9	TC36657_f_at	3	3.1	2.7	2.8	Csa-19
-3.2	TC27773_at	-3.3	-3.7	-2.7	-3.1	SNF1-related kinase
-3.225	TC33206_at	-2.7	-3.8	-2.6	-3.8	SERCA2a; calcium ATPase
-3.75	TC25522_s_at	-3.3	-4	-3.5	-4.2	PCTAIRE-1 protein kinase
-3.925	TC16688_at	-3.2	-4.6	-3.3	-4.6	similar to MAP kinase
-4.125	TC32019_at	-3.3	-4.5	-3.7	-5	type II phosphatidyl inositol phosphate kinase
-4.15	TC33205_at	-3.8	-4.4	-3.9	-4.5	SERCA2a; calcium ATPase

-4.225	TC16332_at	-4.2	-3.8	-4.7	-4.2	protein kinase c
-4.7	TC36544_i_at	-3.7	-4	-5.3	-5.8	phosphodiesterase
-7.2	TC38592_at	-6.4	-7.8	-6.6	-8	cGMP phosphodiesterase A2
-7.95	TC15645_s_at	-6.3	-10	-6	-9.5	type 1 inositol triphosphate phosphatase
-9.425	TC26234_at	-16.3	-8.1	-8.9	-4.4	YSK2 protein kinase
-10.625	TC19737_at	-6.1	-21.9	-5.6	-8.9	regulator of G-protein signaling 3
-11.825	TC18252_at	-14.4	-11.1	-12.2	-9.6	GTP-binding protein sununit alpha
-14.6	TC34425_g_at	-14.5	-14.6	-14.5	-14.8	p59-fyn
-21.575	TC16846_s_at	-9.1	-41.6	-6.4	-29.2	fibroblast growth factor receptor-1
-22.775	TC30389_f_at	-34.3	-11	-34.7	-11.1	p21
-23.45	TC34425_at	-23.6	-24.5	-22.3	-23.4	p59-fyn
-29.45	TC23611_at	-34.1	-32.3	-27	-24.4	PCN1
-30.375	TC16013_g_at	-42.3	-43.3	-19.6	-16.3	G protein gamma 3 subunit

Cytoskeleton Factors

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
172.025	TC15490_s_at	179.3	146.2	200	162.6	troponin T
170.175	TC40790_at	154	138.9	217.3	170.5	myosin light chain 1f
106.575	TC18962_f_at	111.6	91.9	122.1	100.7	beta-tropomyosin
79.675	TC19115_f_at	85.3	73.8	86.3	73.3	troponin I
59.125	TC40898_f_at	75.6	44.3	70.8	45.8	troponin I
33	TC36143_g_at	38.8	22	43.1	28.1	ezrin
29.175	TC41288_at	23.8	23.1	35.5	34.3	myosin heavy chain
24.075	TC19756_at	26.2	20.6	27.7	21.8	actin-related complex 1b
23.8	TC28732_s_at	27.8	21.4	26.1	19.9	myosin heavy chain 2a
23.8	TC38400_at	28.3	21.9	25.6	19.4	like elodin c
21.6	TC40219_at	14.6	12.4	34.1	25.3	integrin alpha 6
21.525	TC35166_at	25.4	18.5	23.5	18.7	homolog to cornia
18.2	TC33465_g_at	22.9	14.8	21.6	13.5	myosin heavy chain
17.075	TC40712_at	21.6	12.4	20.9	13.4	alpha3 connexin
14.725	TC15815_at	18.3	15.7	13.4	11.5	alpha-actin
14.35	TC18963_g_at	5.2	5.8	21.8	24.6	beta-tropomyosin
13.3	TC22502_f_at	16.8	14.3	12.1	10	myosin light chain 2
12.65	TC37498_g_at	18	7.9	16.7	8	titin
12.3	TC40908_at	12.8	9	15.3	12.1	tubulin beta-5 subunit
10.65	TC22827_at	13	10.8	10.3	8.5	alpha tropomyosin
9.45	TC14992_i_at	10.9	9.4	9.4	8.1	LIM protein-1
7.325	TC18964_f_at	12.2	8.9	4.7	3.5	beta-tropomyosin
6.7	TC32100_s_at	7	5.1	8.5	6.2	alpha-actinin
5.725	TC29413_f_at	7.1	5	6.3	4.5	myosin heavy chain 2B
5.475	TC18963_at	9.7	5.2	4	3	beta-tropomyosin
4.45	TC33465_at	5.1	3.8	5.1	3.8	myosin heavy chain
3.8	TC36282_at	5.1	2.9	4.3	2.9	Tcp-1
3.35	TC37498_at	4	2.9	3.8	2.7	titin
3.3	TC39600_f_at	3.4	3.1	3.5	3.2	gelsolin
3.275	TC19756_g_at	3.6	2.8	3.8	2.9	actin-related protein complex 1b
3.25	TC36142_at	3.9	3.3	3.1	2.7	ezrin
3.2	TC40408_s_at	2.6	3	3.3	3.9	myosin regulatory light chain
2.925	TC41813_f_at	3.1	2.9	2.9	2.8	alpha-actin
2.9	TC39868_g_at	3	2.6	3.2	2.8	vimentin
2.85	TC40775_g_at	2.6	3	2.7	3.1	myosin regulatory light subunit

-3.8	TC35418_at	-3.7	-3.5	-4.1	-3.9	alpha-tubulin isotype M-alpha-6
-4.275	TC22801_at	-4.5	-3.7	-4.9	-4	Cdc42/Rac effector PAK-A
-4.425	TC33792_at	-3.4	-4.6	-4.1	-5.6	tubulin beta chain 15
-5.475	TC21995_g_at	-5	-5.5	-5.4	-6	tau microtubule binding protein
-5.525	TC18157_g_at	-6.5	-6	-5	-4.6	microtubule-associated protein 1A
-6.1	TC29662_at	-4.9	-7.8	-4.5	-7.2	actin related protein
-13.675	TC22963_g_at	-8.9	-11.9	-15.5	-18.4	centaurin alpha
-15.4	TC26758_at	-23.3	-14.9	-16.2	-7.2	actin-related protein
-17.675	TC20757_s_at	-27.6	-4.6	-33	-5.5	Ank3
-27.1	TC38163_f_at	-44.8	-5.8	-50.5	-7.3	Tubulin beta 3 chain.
-64.425	TC19832_g_at	-70.9	-70.2	-59.5	-57.1	stathmin-like-protein RB3

Detox/Stress

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
38.675	TC14542_f_at	44.8	32.4	45.3	32.2	plasma glutathione peroxidase
35.35	TC23238_f_at	27.1	40	31.1	43.2	glutathione transferase
29.3	TC34070_f_at	32.7	23.6	33.9	27	Carbonic anhydrase III
22.875	TC36897_s_at	37.1	9.8	34.5	10.1	cytochrome P-450
20.9	TC34069_at	25.7	16	25.7	16.2	Carbonic anhydrase III
19.75	TC15862_at	11.9	7.6	34.3	25.2	cytochrome P450
19.225	TC40306_f_at	24.3	22.3	15.8	14.5	glutathione transferase
17.575	TC41370_s_at	12.9	13.3	21.7	22.4	HSP70
16.275	TC40085_at	18.7	15.7	15.3	15.4	cytochrome P-450
14.15	TC29966_g_at	13.4	15.9	12.4	14.9	ceruloplasmin
10.125	TC24428_s_at	10.7	9.4	10.8	9.6	catalase
10.025	TC23657_at	10.4	10.7	9.3	9.7	HSP70
9.125	TC33871_s_at	7.5	5.2	13.2	10.6	glutathione S-transferase
8	TC16030_s_at	8.9	8	7.9	7.2	glutathione transferase
4.825	TC18707_at	5.4	3.8	5.9	4.2	glutathione S-transferase
4.55	TC23656_g_at	4.2	5	4.1	4.9	HSP70
3.9	TC26484_at	3.9	4.5	3.4	3.8	HSPC194
3.875	TC19090_s_at	4.5	3.8	3.9	3.3	glutathione synthetase type A1
3.85	TC14538_f_at	4.3	3.2	4.5	3.4	plasma glutathione peroxidase
3.8	TC31122_f_at	4.2	4	3.6	3.4	plasma glutathione peroxidase
3	TC41370_i_at	2.7	2.9	3.1	3.3	HSP70

Energy Metabolism

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
163.125	TC18565_i_at	158.5	167.1	161.2	165.7	cytosolic malate dehydrogenase
133.975	TC26633_g_at	148.8	129.1	137.7	120.3	uncoupling protein 2
88.2	TC15537_f_at	108.7	57	119.9	67.2	cytochrome c oxidase VIII-H
54.85	TC34165_at	44.1	33.2	76.3	65.8	UDP-Glucose 6-Dehydrogenase
46.475	TC14736_g_at	51.1	41.1	52.4	41.3	phosphoenolpyruvate carboxykinase
36.825	TC19057_at	41	30.2	43.7	32.4	phosphoglycerate mutase
24.65	TC15436_s_at	19.4	19.4	30	29.8	cytochrome c oxidase VIIa-H
15.575	TC32836_g_at	19.1	15.8	15	12.4	carnitine acetyltransferase
11.65	TC40743_s_at	10.7	12.6	10.7	12.6	transketolase (TKT)
11.45	TC32389_at	15.6	17.7	6.1	6.4	glycogen phosphorylase
10.325	TC32884_f_at	11.6	9.3	11.3	9.1	lactate dehydrogenase A
10.3	TC23942_i_at	11.9	10.9	9.6	8.8	creatine kinase
6.4	TC24979_g_at	6.2	6.2	6.5	6.7	UDP-glucose 6-dehydrogenase
6.3	TC40671_s_at	5.3	3.5	12.1	4.3	Cytochrome B5.

5.8	TC37832_at	5	4.5	7.3	6.4	glycogenin
5.55	TC24979_at	6	5.3	5.8	5.1	UDP-glucose 6-dehydrogenase
5.3	TC40818_at	3.5	4.4	5.9	7.4	possible sucrose phosphate synthase
5.1	TC15342_s_at	6	4.3	5.9	4.2	aldehyde dehydrogenase
4.175	TC40672_g_at	4.7	4.6	3.7	3.7	Cytochrome B5.
3.625	TC14457_f_at	3.5	3.9	3.4	3.7	lactate dehydrogenase-A
3.6	TC37832_g_at	3.7	3.6	3.6	3.5	glycogenin
-3.3	TC39474_f_at	-3.5	-3	-3.7	-3	lactate dehydrogenase-B
-3.65	TC38109_at	-3.6	-3.5	-3.8	-3.7	similar to NADH dehydrogenase subunit 4
-4	TC39475_f_at	-4.7	-3.4	-4.6	-3.3	lactate dehydrogenase-B
-5.275	TC30344_s_at	-5.9	-5	-5.5	-4.7	malate dehydrogenase
-12.9	TC32621_at	-5	-20.2	-5.3	-21.1	UDP-Gal transferase
-17.05	TC23984_g_at	-29.6	-5.4	-28.1	-5.1	Glycogen Phosphorylase

Immune

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
217.7	TC23555_at	233.8	201.9	235.7	199.4	sphingosine kinase
142.75	TC23274_at	123.5	160.7	126.8	160	14-3-3 protein sigma
116.65	TC24755_g_at	106.2	104	130.2	126.2	sphingosine kinase
113.85	TC20347_at	100.4	124.5	104.5	126	prostate stem cell antigen
93.175	TC39719_f_at	98.8	82.6	100.2	91.1	galactin -3
87.85	TC36394_f_at	102.4	69.5	109.4	70.1	galectin-1
49.45	TC15466_f_at	79	77.7	20.7	20.4	lipocortin I/ annexin 1
46.9	TC37183_s_at	50.7	48.3	44.4	44.2	dopachrome tautomerase
44.225	TC34607_s_at	43.4	51.3	39.4	42.8	dbpA murine homologue
41.875	TC39759_at	37.4	40.5	43	46.6	TB2 like 1
40.475	TC14369_f_at	55	42.2	36.6	28.1	lipocortin I/ annexin 1
39.7	TC36715_f_at	49.1	27.2	50.5	32	CRIP
27.9	TC40399_s_at	33.8	22.5	31.9	23.4	hepatitis virus receptor
24.8	TC40929_s_at	9	9.9	38.2	42.1	beta interefon induced protein
24.6	TC32795_at	27.8	26.4	22.9	21.3	similar to human CD9 antigen
17.25	TC24304_g_at	6.8	6.1	28.9	27.2	linear IgA disease antigen homolog
11.975	TC16835_s_at	23	18.1	4.1	2.7	complement protein H
11.425	TC21382_at	12.2	10.5	12.5	10.5	like glucocortical receptor
11.2	TC25579_at	10.9	12.7	9.8	11.4	oncostatin M
9.4	TC28116_g_at	8	7.5	11.4	10.7	tyrosinase-related protein-2; Dopachrome tautomerase
6.95	TC20485_at	7	7.7	6.2	6.9	beta-defensin 1
6.25	TC18855_f_at	6.4	6.8	5.7	6.1	annexin II
5.9	TC37852_at	8.1	8.4	3.3	3.8	junctional adhesion molecule (JAM)
5.6	TC19499_s_at	5.9	5.5	5.7	5.3	Myc basic motif homologue-1
5.275	TC35184_f_at	5.8	5.4	5.1	4.8	Myc basic motif homologue-1
4.05	TC32562_at	5.3	3.8	4.1	3	like host cell factor C1 precursor
3.65	TC32951_s_at	4	3	4.3	3.3	C3F
3.625	TC39824_g_at	3.4	4	4	3.1	BING1
-2.65	TC19616_at	-2.6	-2.7	-2.6	-2.7	similar to Ig-gamma 3
-3.15	TC36543_at	-2.6	-3.5	-2.8	-3.7	paraneoplastic antigen
-3.3	TC37323_at	-3.6	-3	-3.5	-3.1	similar to IgA regulatory protein
-4	TC40427_at	-3.9	-3.9	-4.1	-4.1	T-cell receptor chain
-5.25	TC36118_g_at	-5.6	-5.2	-5	-5.2	IL-16, neuronal IL-16
-11.025	TC16879_s_at	-6.7	-4.6	-17	-15.8	Skinkine
-11.625	TC38700_at	-11.9	-12.1	-10.3	-12.2	MASL1

Lipid Metabolism

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
236.85	TC17654_at	263.1	195.7	281	207.6	saposin
170.575	TC41548_at	198.6	150.9	181.7	151.1	arylacetamide deacetylase
153.675	TC15877_at	27.8	18.3	367.9	200.7	saposin
61.725	TC27653_at	51.3	51	73.4	71.2	3-ketoacyl-CoA thiolase B
44.525	TC38254_g_at	59.1	16.2	58	44.8	peroxisomal D3,D2-enoyl-CoA isomerase

40.85	TC23966_s_at	42.9	34.3	45.2	41	lipoprotein lipase
36.825	TC19057_at	41	30.2	43.7	32.4	phosphoglycerate mutase
29.35	TC36679_s_at	39.1	22.4	34.6	21.3	3 - ketoacyl-coA thiolase
28.9	TC37551_at	37.6	22.7	33	22.3	PON2
28.4	TC37626_at	33.8	23.3	32.1	24.4	acetyl-CoA C-acyltransferase
26.1	TC38959_at	27	27	25.2	25.2	acyl-coA desaturase
22.675	TC15693_s_at	11.6	14.8	28.3	36	amino levulinic acid synthase
20.825	TC35102_at	25.7	14.4	26.4	16.8	stearoyl-CoA desaturase
20.65	TC15810_s_at	18.2	16	26	22.4	3-oxoacyl-CoenzymeA thiolase
19.125	TC39253_s_at	23.1	15.1	22.3	16	peroxisome proliferator activated receptor gamma
16.125	TC19057_g_at	19.2	6.2	31.2	7.9	phosphoglycerate mutase muscle-specific subunit
15.95	TC37903_at	11.2	11.4	20.8	20.4	long chain polyunsaturated fatty acid elongation enzyme
13.525	TC32039_at	15.6	11.1	15.9	11.5	pantothenate kinase beta 1
13.175	TC31025_g_at	18.6	18.8	7.6	7.7	ECH1p
8.575	TC36609_at	9.4	7	10.2	7.7	putative steroid dehydrogenase
8.025	TC42002_at	8	6	4.3	13.8	PEX3
7.9	TC37903_g_at	7	6.5	9.5	8.6	long chain polyunsaturated fatty acid elongation enzyme
7.8	TC40103_at	7.1	7.2	8.4	8.5	peroxisomal biogenesis factor
7.1	TC36608_at	7.1	6.3	7.9	7.1	putative steroid dehydrogenase
7.075	TC31834_g_at	9.8	5.8	8	4.7	dihydroxyacetone phosphate
4.975	TC28402_s_at	4.7	4.3	5.7	5.2	squalene epoxidase
4.975	TC38959_g_at	4.9	5	5	5	acyl-coA desaturase
4.95	TC14864_f_at	6	5	4.8	4	keratinocyte lipid-binding protein (E-FABP)
4.7	TC16399_f_at	4.8	4.2	5.2	4.6	medium-chain acyl-CoA dehydrogenase
4.575	TC35242_s_at	6.1	4.5	4.3	3.4	heme oxygenase
4.175	TC23565_f_at	4.8	4.5	3.8	3.6	apolipoprotein C1
4.125	TC15569_s_at	3.6	2.8	5.7	4.4	squalene epoxidase
4.075	TC33350_at	3.8	4	4.1	4.4	sterol isomerase
4	TC22922_at	3.4	3.5	4.5	4.6	lysosomal thiol reductase
4	TC31690_at	4.2	4.3	3.7	3.8	peroxisomal D3,D2-enoyl-CoA isomerase
3.875	TC19287_g_at	4.2	3.7	4	3.6	3-ketoacyl-coA thiolase
3.875	TC36692_f_at	3.9	3.3	4.5	3.8	PON2
3.65	TC27635_g_at	3.4	3.6	3.7	3.9	3-ketoacyl-CoA thiolase B
3.525	TC37977_at	3	3.8	3.2	4.1	amino levulinate acid synthase
3.525	TC40649_at	4	3	4	3.1	PMP68
3.5	TC30782_at	3.7	3.7	3.3	3.3	long chain polyunsaturated fatty acid elongator factor
3.4	TC37574_at	3.8	3.6	3.2	3	farnesyl pyrophosphate synthase
3.35	TC20385_at	3.7	3.3	3.4	3	acyl-CoA thioesterase
3.025	TC31834_at	3.6	2.6	3.4	2.5	dihydroxyacetone phosphate
2.975	TC33692_at	3.4	3.3	2.6	2.6	enoyl coA/acyl coA hydratase/ dehydrogenase
-3.525	TC27925_i_at	-3.9	-3	-4.1	-3.1	PAF acetylhydrolase
-3.775	TC32923_s_at	-4.1	-3.5	-4.1	-3.4	11-beta-hydroxysteroid dehydrogenase
-3.975	TC38968_at	-4.6	-3.1	-4.9	-3.3	diacylglycerol kinase
-5.45	TC38266_s_at	-3.3	-6	-4.5	-8	glycerophosphate dehydrogenase
-6.05	TC22730_s_at	-8	-5	-6.9	-4.3	brain fatty acid-binding protein
-6.55	TC15835_at	-6.6	-7.4	-5.7	-6.5	oxysterol-binding protein
-7.325	TC38739_at	-8.4	-6.1	-8.5	-6.3	diacylglycerol kinase
-7.325	TC38739_at	-8.4	-6.1	-8.5	-6.3	diacylglycerol kinase,
-13.7	TC23469_at	-19.3	-7.1	-20.4	-8	diacylglycerol kinase
-20.6	TC41804_at	-27.6	-22.3	-17.2	-15.3	ATPase, possible transporter of phospholipids
-72.725	TC36931_at	-76.7	-61.4	-81.5	-71.3	phosphatidic acid phosphatase

Neuronal cell development and function

Average Change	TIGR/ Affymetrix #	Fold change for each comparisons				Annotation
		1	2	3	4	
323.525	TC32454_at	327.3	316.1	328.8	321.9	like maxi K channel subunit
71.625	TC30567_s_at	88.1	54.2	88.6	55.6	syndecan-1
41.05	TC31887_at	43.5	40.3	41.7	38.7	similar to drosophila "prickle"
28.925	TC28006_at	18.1	18.4	39.3	39.9	similar to drosophila neuralized
25.125	TC14674_s_at	21.6	24.1	26.3	28.5	cdr2
23.475	TC23172_at	30.8	38.9	10.7	13.5	proteolipid protein 2
23.225	TC22245_at	22.6	24	22.7	23.6	similar to CC13, human chloride channel protein
20.825	TC34353_at	25	19.3	22.4	16.6	developmental arteries and neural crest EGF-like protein
18.675	TC20429_at	18.9	23.8	14.2	17.8	GSG1
16.625	TC18467_f_at	16.2	13.8	18.8	17.7	cytokeratin 17
16.15	TC39729_at	17.6	8.6	20.8	17.6	synectin
15.85	TC25273_at	16.3	17.4	12.5	17.2	dystonin
15.7	TC29599_at	8.4	7.4	23.8	23.2	TC21
15.025	TC24557_at	16	15.8	14.2	14.1	Dkk-3 protein, dickkopf-3
14.725	TC31277_at	14.7	14.3	14.9	15	retinoid x receptor interacting protein
13.95	TC30575_at	14	15.3	12.6	13.9	Six3b protein like
11.175	TC23777_s_at	9.9	12.6	9.8	12.4	TIS21
11	TC19521_g_at	13	19	5	7	pendulin
10.425	TC33141_s_at	12.5	8	12.8	8.4	ETFR-1
9.85	TC23172_g_at	13.3	15.1	5.3	5.7	proteolipid protein 2
9.325	TC16642_at	12.8	12.3	6.2	6	NF-B, neurofilament B
7.325	TC17543_s_at	4.9	18	2.9	3.5	DRP 3
6.775	TC27164_s_at	5.7	8.8	5.1	7.5	C /EBP delta
6.75	TC22472_g_at	10.1	8.6	4.5	3.8	insulin-like growth factor binding protein
6.05	TC15936_g_at	4.9	6	6	7.3	Cpd1
4.1	TC41791_at	3.1	3	5.8	4.5	PACSIN2
3.925	TC17915_at	3.5	2.9	5.1	4.2	Otx2
3.825	TC41353_at	3.8	4.5	3.2	3.8	glypican-3
3.7	TC24235_at	4	3.6	3.8	3.4	cupidin; homer-2a
3.45	TC33791_at	3.3	3.7	3.2	3.6	Cpd1
3.35	TC26379_g_at	3.1	2.7	4.1	3.5	syndecan-1
3.175	TC42120_at	2.7	2.9	3.4	3.7	liprin beta
3.15	TC36827_at	3.1	3.3	3	3.2	Cpd1
3.075	TC39260_at	3.3	3	3.1	2.9	TBX1 protein
3	TC15936_at	3.1	3.2	2.7	3	Cpd1
2.65	TC22475_at	2.7	2.5	2.7	2.7	SIN3B
-2.55	TC26610_s_at	-2.5	-2.5	-2.6	-2.6	necdin Ca2++
-2.775	TC30862_at	-3	-2.6	-2.9	-2.6	similar to proteolipid protein 2
-3.225	TC39099_at	-2.6	-3.4	-3	-3.9	NF-L, neurofilament L
-3.45	TC22741_at	-3.7	-3.7	-3.3	-3.1	neuronal-specific septin 3
-3.575	TC37536_f_at	-4.1	-3	-4.1	-3.1	NF-66; alpha-internexin
-3.725	TC18246_at	-3.9	-2.7	-4	-4.3	BDM1 protein
-4.2	TC14245_at	-3.6	-3.8	-4.5	-4.9	Ndr1 related protein Ndr2

-4.2	TC26270_s_at	-6	-3.7	-4.4	-2.7	KIF3
-4.4	TC16990_s_at	-5	-4.8	-4	-3.8	visinin-like protein
-4.4	TC17976_at	-4.9	-4.6	-4.2	-3.9	calcium-activated potassium channel rSK2
-5	TC30767_at	-5.6	-4.6	-5.4	-4.4	SCHIP-1
-5.55	TC14245_g_at	-5.5	-4.4	-6.8	-5.5	Ndr1 related protein Ndr2
-5.6	TC41874_g_at	-5.9	-5.2	-6	-5.3	Ndr1 related protein Ndr2
-5.925	TC37308_at	-5	-6	-6.2	-6.5	double cortin like protein
-6.25	TC17814_at	-7.5	-6.4	-6.4	-4.7	similar to corticotropin releasing hormone receptor 2
-6.65	TC31890_g_at	-6.4	-5.9	-7.5	-6.8	secretogranin III
-6.675	TC35356_g_at	-8.7	-4.6	-8.8	-4.6	neuritin
-7.15	TC16362_at	-6.9	-5.8	-8.6	-7.3	NF-M, neurofilament-M
-7.475	TC35356_at	-7.4	-7.4	-7.5	-7.6	neuritin
-10.4	TC14881_at	-6.8	-11.9	-8.4	-14.5	scg10
-10.875	TC34440_g_at	-12.5	-11.2	-9.8	-10	neural plakophilin-related protein
-11.1	TC22283_s_at	-11.8	-8.9	-13.5	-10.2	myelin proteolipid
-12.125	TC22741_g_at	-14.2	-8.9	-15.8	-9.6	neuronal-specific septin 3
-22.2	TC32215_s_at	-27.4	-22.3	-22.2	-16.9	connexin 32
-24.65	TC42007_at	-25.1	-26.2	-22	-25.3	similar to N-WASP human
-25.2	TC28618_s_at	-26.9	-18.4	-31.7	-23.8	nel protein
-27.15	TC40805_at	-29.9	-32.8	-19.8	-26.1	NEDD-4 protien
-27.575	TC24570_at	-11.6	-41.9	-12.4	-44.4	ATN2
-28.575	TC39041_at	-31.6	-25.7	-30.2	-26.8	Nel protien
-29.275	TC33327_i_at	-18.8	-34.1	-22.8	-41.4	Ndr1 related protein Ndr2
-34.375	TC35755_s_at	-44.9	-37.6	-29.1	-25.9	tyro3
-34.875	TC17234_s_at	-26.9	-44.9	-25	-42.7	calbindin
-39.025	TC14635_at	-44	-47.2	-31.5	-33.4	like transcription factor PAX3
-59.825	TC41060_at	-75.7	-59.8	-55.7	-48.1	beta2-cerebellar chimerin
-102.825	TC29998_g_at	-153.8	-52.2	-153.3	-52	myelin basic protein
-145.65	TC29998_at	-259.5	-34.1	-255.4	-33.6	myelin basic protein
-153.9	TC22429_s_at	-242.9	-60.6	-249.8	-62.3	myelin proteolipid