

[HELP](#)**Description of the problem:**

Number of classes: 2  
 Number of genes used for random variance estimation: 31099  
 Number of genes that passed filtering criteria: 10067  
 Type of univariate test used: Two-sample T-test (with random variance model)  
 Column of the Experiment Descriptors sheet that defines class variable : ctrlvsdiff

Nominal significance level of each univariate test: 0.001

**Summary of Results:**

Number of genes significant at 0.001 level of the univariate test: 379

**Genes which discriminate among classes:**

Table 1 - Sorted by p-value of the univariate test.  
 The first 379 genes are significant at the nominal 0.001 level of the univariate test

	Parametric p-value	FDR	Geom mean of intensities in class 1 : 0	Geom mean of intensities in class 2 : 1	Fold difference of geom means	Probe set	Description	Annotations	Gene symbol
1	< 1e-07	< 1e-07	508.2	15.3	33.216	<a href="#">1386965_at</a>	lipoprotein lipase	<a href="#">Info</a>	<a href="#">Lpl</a>
2	< 1e-07	< 1e-07	10	495.9	0.02	<a href="#">1385722_at</a>	Transcribed locus, weakly similar to NP_035507.1 single-minded homolog 2 [Mus musculus]	<a href="#">Info</a>	
3	1e-07	0.0003356	276.7	9.2	30.076	<a href="#">1389253_at</a>	vanin 1 (predicted)	<a href="#">Info</a>	<a href="#">Vnn1_predicted</a>
4	2e-07	0.0004027	10.4	123.9	0.084	<a href="#">1379411_at</a>	similar to ENSANGP00000020885	<a href="#">Info</a>	<a href="#">LOC306366</a>
5	2e-07	0.0004027	299	20	14.95	<a href="#">1372989_at</a>	Transcribed locus	<a href="#">Info</a>	
6	7e-07	0.0011745	134	11	12.182	<a href="#">1382453_at</a>	Similar to Zinc finger protein ZIC 3 (Zinc finger protein of the cerebellum 3)	<a href="#">Info</a>	
7	9e-07	0.0012943	111.8	23.8	4.697	<a href="#">1388255_x_at</a>	RT1 class I, CE5	<a href="#">Info</a>	<a href="#">RT1-CE5</a>
8	1.9e-06	0.0023909	23.6	361.3	0.065	<a href="#">1387715_at</a>	extracellular peptidase inhibitor	<a href="#">Info</a>	<a href="#">Expi</a>
9	2.2e-06	0.0024608	15.3	156.1	0.098	<a href="#">1380804_at</a>	Transcribed locus	<a href="#">Info</a>	
10	2.9e-06	0.0028523	4054.2	758.2	5.347	<a href="#">1373401_at</a>	Transcribed locus	<a href="#">Info</a>	
11	3.4e-06	0.0028523	66.8	226.5	0.295	<a href="#">1389164_at</a>	hect domain and RLD 3 (predicted)	<a href="#">Info</a>	<a href="#">Herc3_predicted</a>
12	3.4e-06	0.0028523	196	12.1	16.198	<a href="#">1371209_at</a>	RT1 class I, CE5	<a href="#">Info</a>	<a href="#">RT1-CE5</a>
13	3.9e-06	0.0030201	238.7	18.1	13.188	<a href="#">1377899_at</a>	similar to RIKEN cDNA 2810025M15 (predicted)	<a href="#">Info</a>	<a href="#">RGD1304982_prec</a>
14	5.4e-06	0.0037583	233.2	32.1	7.265	<a href="#">1370885_at</a>	cathepsin Z	<a href="#">Info</a>	<a href="#">Ctsz</a>
15	5.6e-06	0.0037583	113.9	21.5	5.298	<a href="#">1368097_a_at</a>	reticulon 1	<a href="#">Info</a>	<a href="#">Rtn1</a>
16	8e-06	0.0046396	109.9	722.1	0.152	<a href="#">1377792_at</a>	Megf10 protein	<a href="#">Info</a>	<a href="#">Megf10</a>
17	9e-06	0.0046396	142	54	2.63	<a href="#">1372084_at</a>	protein tyrosine phosphatase 4a3 (predicted)	<a href="#">Info</a>	<a href="#">Ptp4a3_predicted</a>
18	9.2e-06	0.0046396	1838.4	286.5	6.417	<a href="#">1369926_at</a>	glutathione peroxidase 3	<a href="#">Info</a>	<a href="#">Gpx3</a>
19	9.7e-06	0.0046396	280.9	36.1	7.781	<a href="#">1368685_at</a>	chondroitin sulfate proteoglycan 4	<a href="#">Info</a>	<a href="#">Cspg4</a>
20	9.9e-06	0.0046396	1113.9	3984.3	0.28	<a href="#">1379452_at</a>	similar to growth arrest-specific protein 2 - mouse	<a href="#">Info</a>	<a href="#">LOC499156</a>
21	1.01e-05	0.0046396	236.3	541.9	0.436	<a href="#">1392249_at</a>	Similar to protein 4.1G	<a href="#">Info</a>	

22	1.04e-05	0.0046396	61.2	16.6	3.687	<a href="#">1383518_at</a>	Transcribed locus	<a href="#">Info</a>	
23	1.06e-05	0.0046396	143.2	21.7	6.599	<a href="#">1368470_at</a>	gamma-glutamyl hydrolase	<a href="#">Info</a>	<a href="#">Ggh</a>
24	1.15e-05	0.0047919	9.8	23	0.426	<a href="#">1397440_at</a>	Megf10 protein	<a href="#">Info</a>	<a href="#">Megf10</a>
25	1.19e-05	0.0047919	196.8	37	5.319	<a href="#">1368593_at</a>	CD1d1 antigen	<a href="#">Info</a>	<a href="#">Cd1d1</a>
26	1.29e-05	0.0049948	286.2	123.6	2.316	<a href="#">1383605_at</a>	similar to alpha-fetoprotein	<a href="#">Info</a>	<a href="#">LOC360919</a>
27	1.39e-05	0.0051826	123.3	28.6	4.311	<a href="#">1370414_at</a>	Rab38, member of RAS oncogene family	<a href="#">Info</a>	<a href="#">Rab38</a>
28	1.5e-05	0.0052765	36.5	12.6	2.897	<a href="#">1372162_at</a>	acetyl-Coenzyme A synthetase 2 (AMP forming)-like (predicted)	<a href="#">Info</a>	<a href="#">Acas2l_predicted</a>
29	1.52e-05	0.0052765	41	298.7	0.137	<a href="#">1393645_at</a>	hypothetical protein LOC317274	<a href="#">Info</a>	<a href="#">LOC317274</a>
30	1.96e-05	0.0065771	86.4	9.5	9.095	<a href="#">1387968_at</a>	solute carrier family 6 (neurotransmitter transporter), member 15	<a href="#">Info</a>	<a href="#">Slc6a15</a>
31	2.28e-05	0.0074041	52	24.4	2.131	<a href="#">1370197_a_at</a>	protein kinase C, zeta	<a href="#">Info</a>	<a href="#">Prkcz</a>
32	2.46e-05	0.0076687	136	24.8	5.484	<a href="#">1388920_at</a>	bone morphogenetic protein 6	<a href="#">Info</a>	<a href="#">Bmp6</a>
33	2.53e-05	0.0076687	536.5	169.6	3.163	<a href="#">1367800_at</a>	plasminogen activator, tissue	<a href="#">Info</a>	<a href="#">Plat</a>
34	2.59e-05	0.0076687	104.9	22.9	4.581	<a href="#">1388398_at</a>		<a href="#">Info</a>	
35	3.08e-05	0.0084924	405.2	117.6	3.446	<a href="#">1379292_at</a>	Similar to 5730420B22Rik protein (predicted)	<a href="#">Info</a>	
36	3.1e-05	0.0084924	4456.1	686.1	6.495	<a href="#">1368187_at</a>	glycoprotein (transmembrane) nmb	<a href="#">Info</a>	<a href="#">Gpnmb</a>
37	3.16e-05	0.0084924	300.6	25.7	11.696	<a href="#">1383610_at</a>		<a href="#">Info</a>	
38	3.24e-05	0.0084924	55.9	114.4	0.489	<a href="#">1382587_at</a>	Family with sequence similarity 33, member A (predicted)	<a href="#">Info</a>	<a href="#">MGC109093</a>
39	3.29e-05	0.0084924	336	103	3.262	<a href="#">1387010_s_at</a>	sodium channel, voltage-gated, type I, beta polypeptide	<a href="#">Info</a>	<a href="#">Scn1b</a>
40	3.42e-05	0.0085201	589.4	299.2	1.97	<a href="#">1379389_at</a>	Neural cell adhesion molecule 1	<a href="#">Info</a>	<a href="#">Ncam1</a>
41	3.47e-05	0.0085201	28.1	7.9	3.557	<a href="#">1384061_at</a>	Similar to Zinc finger protein ZIC 3 (Zinc finger protein of the cerebellum 3)	<a href="#">Info</a>	
42	3.85e-05	0.0091722	49	738.5	0.066	<a href="#">1387137_at</a>	cartilage oligomeric matrix protein	<a href="#">Info</a>	<a href="#">Comp</a>
43	3.95e-05	0.0091722	194.8	603.5	0.323	<a href="#">1379824_at</a>	Transcribed locus	<a href="#">Info</a>	
44	4.1e-05	0.0091722	80.5	26.8	3.004	<a href="#">1384771_at</a>	similar to hypothetical protein	<a href="#">Info</a>	<a href="#">LOC287564</a>
45	4.1e-05	0.0091722	2985.1	58.4	51.115	<a href="#">1373674_at</a>	microfibrillar associated protein 5 (predicted)	<a href="#">Info</a>	<a href="#">Mfap5_predicted</a>
46	4.56e-05	0.0099795	111.1	31.6	3.516	<a href="#">1368008_at</a>	prominin 1	<a href="#">Info</a>	<a href="#">Prom1</a>
47	4.84e-05	0.0102348	1209.1	182.2	6.636	<a href="#">1387659_at</a>	guanine deaminase	<a href="#">Info</a>	<a href="#">Gda</a>
48	4.88e-05	0.0102348	93	235.3	0.395	<a href="#">1393467_at</a>	proprotein convertase subtilisin/kexin type 5	<a href="#">Info</a>	<a href="#">Pcsk5</a>
49	5.04e-05	0.0103546	192.2	27.3	7.04	<a href="#">1373596_at</a>	similar to hypothetical protein FLJ31737 (predicted)	<a href="#">Info</a>	<a href="#">RGD1310423_prec</a>
50	5.62e-05	0.0109175	636.4	61.8	10.298	<a href="#">1388545_at</a>	Transcribed locus	<a href="#">Info</a>	
51	5.77e-05	0.0109175	75.4	22.6	3.336	<a href="#">1395471_at</a>	Transcribed locus	<a href="#">Info</a>	
52	5.79e-05	0.0109175	64	19.9	3.216	<a href="#">1367918_at</a>	fasciculation and elongation protein zeta 1 (zygin I)	<a href="#">Info</a>	<a href="#">Fez1</a>
53	5.9e-05	0.0109175	220.1	105.1	2.094	<a href="#">1389782_at</a>	similar to RIKEN cDNA 2010107G23 (predicted)	<a href="#">Info</a>	<a href="#">RGD1305587_prec</a>
54	6.03e-05	0.0109175	46.2	197.9	0.233	<a href="#">1376972_at</a>	Solute carrier family 39 (iron-regulated transporter), member 1	<a href="#">Info</a>	<a href="#">Slc40a1</a>
55	6.21e-05	0.0109175	505.9	70.4	7.186	<a href="#">1388347_at</a>	similar to lymphocyte antigen 6 complex, locus E	<a href="#">Info</a>	<a href="#">LOC362934</a>

56	6.26e-05	0.0109175	139.2	13.1	10.626	<a href="#">1394946_at</a>	similar to intracellular protein transport like (XM453) (predicted)	<a href="#">Info</a>	<a href="#">RGD1307525_prec</a>
57	6.29e-05	0.0109175	110.3	16	6.894	<a href="#">1388395_at</a>	G0/G1 switch gene 2 (predicted)	<a href="#">Info</a>	<a href="#">G0s2_predicted</a>
58	6.29e-05	0.0109175	98.7	14	7.05	<a href="#">1376868_at</a>		<a href="#">Info</a>	
59	6.45e-05	0.0110054	17.7	64.7	0.274	<a href="#">1380763_at</a>		<a href="#">Info</a>	
60	6.95e-05	0.0116609	73.9	32.5	2.274	<a href="#">1397615_at</a>	Transcribed locus	<a href="#">Info</a>	
61	7.12e-05	0.0117503	181	47.2	3.835	<a href="#">1372584_at</a>	similar to DKFZP566K1924 protein (predicted)	<a href="#">Info</a>	<a href="#">RGD1308373_prec</a>
62	7.27e-05	0.0118044	88.1	16.8	5.244	<a href="#">1377390_at</a>	beta-site APP-cleaving enzyme 2	<a href="#">Info</a>	<a href="#">RGD:1303241</a>
63	7.6e-05	0.0118516	63.2	24.6	2.569	<a href="#">1373912_at</a>	Transcribed locus, weakly similar to XP_488820.1 PREDICTED: hypothetical protein XP_488820 [Mus musculus]	<a href="#">Info</a>	
64	7.69e-05	0.0118516	407.8	188.9	2.159	<a href="#">1368320_at</a>	neural cell adhesion molecule 1	<a href="#">Info</a>	<a href="#">Ncam1</a>
65	7.7e-05	0.0118516	143.8	793.8	0.181	<a href="#">1390412_at</a>	Solute carrier family 39 (iron-regulated transporter), member 1	<a href="#">Info</a>	<a href="#">Slc40a1</a>
66	7.77e-05	0.0118516	533.8	292	1.828	<a href="#">1385573_at</a>	Homer homolog 3 (Drosophila)	<a href="#">Info</a>	<a href="#">Homer3</a>
67	8.12e-05	0.0122006	162.9	55.5	2.935	<a href="#">1387984_at</a>	chemokine-like factor 1	<a href="#">Info</a>	<a href="#">Cklf1</a>
68	8.28e-05	0.0122581	137.1	359.6	0.381	<a href="#">1391173_at</a>	Transcribed locus	<a href="#">Info</a>	
69	8.43e-05	0.0122992	538.8	223.7	2.409	<a href="#">1368104_at</a>	tetraspan 2	<a href="#">Info</a>	<a href="#">Tspan2</a>
70	8.57e-05	0.0123249	106.2	20.7	5.13	<a href="#">1384406_at</a>	Similar to 5730439E10Rik protein (predicted)	<a href="#">Info</a>	
71	9.1e-05	0.012671	978.2	27.9	35.061	<a href="#">1384063_at</a>	collagen triple helix repeat containing 1	<a href="#">Info</a>	<a href="#">Cthrc1</a>
72	9.25e-05	0.012671	54.2	23.7	2.287	<a href="#">1393109_at</a>	CDNA clone IMAGE:7302574	<a href="#">Info</a>	
73	9.3e-05	0.012671	76.7	13.4	5.724	<a href="#">1370464_at</a>	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	<a href="#">Info</a>	<a href="#">Abcb1a</a>
74	9.39e-05	0.012671	22.4	39.4	0.569	<a href="#">1393523_at</a>	Coilin	<a href="#">Info</a>	<a href="#">Coil</a>
75	9.44e-05	0.012671	65	35.5	1.831	<a href="#">1370388_at</a>	solute carrier family 9 (sodium/hydrogen exchanger), isoform 5	<a href="#">Info</a>	<a href="#">Slc9a5</a>
76	9.81e-05	0.0129944	500.4	195.1	2.565	<a href="#">1368105_at</a>	tetraspan 2	<a href="#">Info</a>	<a href="#">Tspan2</a>
77	0.0001022	0.0133617	748.8	1854.4	0.404	<a href="#">1374060_at</a>	Transcribed locus	<a href="#">Info</a>	
78	0.000106	0.0135586	483.9	182.4	2.653	<a href="#">1387004_at</a>	neuroblastoma, suppression of tumorigenicity 1	<a href="#">Info</a>	<a href="#">Nbl1</a>
79	0.0001064	0.0135586	306	184.9	1.655	<a href="#">1377768_at</a>	vitamin A-deficient testicular protein 5	<a href="#">Info</a>	<a href="#">Vad5</a>
80	0.0001116	0.013938	179.9	660.4	0.272	<a href="#">1372226_at</a>	Transcribed locus, strongly similar to NP_055665.1 SLIT-ROBO Rho GTPase-activating protein 2; SLIT-ROBO Rho GTPase-activating protein 3; WAVE-associated Rac GTPase activating protein [Homo sapiens]	<a href="#">Info</a>	
81	0.0001126	0.013938	36.2	18.4	1.967	<a href="#">1377453_at</a>	similar to hypothetical protein FLJ23554 (predicted)	<a href="#">Info</a>	<a href="#">RGD1309108_prec</a>
82	0.0001138	0.013938	32.5	84.5	0.385	<a href="#">1396939_at</a>	Transcribed locus	<a href="#">Info</a>	
83	0.000116	0.013938	71.6	36.5	1.962	<a href="#">1385670_at</a>	serine dehydratase-like (predicted)	<a href="#">Info</a>	<a href="#">Sdsl_predicted</a>
84	0.0001163	0.013938	131.6	40.5	3.249	<a href="#">1367835_at</a>	proprotein convertase subtilisin/kexin type 1 inhibitor	<a href="#">Info</a>	<a href="#">Pcsk1n</a>
85	0.0001187	0.0140583	24.6	83.6	0.294	<a href="#">1368411_a_at</a>	microtubule-associated protein 2	<a href="#">Info</a>	<a href="#">Mtap2</a>

86	0.0001201	0.0140587	178.9	419.2	0.427	<a href="#">1368002_at</a>	mutS homolog 2 (E. coli)	<a href="#">Info</a>	<a href="#">Msh2</a>
87	0.0001232	0.0141504	235.7	136.3	1.729	<a href="#">1372955_at</a>	Similar to KIAA0965 protein	<a href="#">Info</a>	
88	0.0001248	0.0141504	268.8	23.3	11.536	<a href="#">1392852_at</a>		<a href="#">Info</a>	
89	0.0001251	0.0141504	244.8	25.6	9.562	<a href="#">1374778_at</a>	cathepsin C	<a href="#">Info</a>	<a href="#">Ctsc</a>
90	0.0001268	0.0141587	82.6	25.7	3.214	<a href="#">1376350_at</a>	Transcribed locus	<a href="#">Info</a>	
91	0.0001297	0.0141587	51.9	95.8	0.542	<a href="#">1392554_a_at</a>		<a href="#">Info</a>	
92	0.0001298	0.0141587	607.2	1240.4	0.49	<a href="#">1376587_at</a>	F-box only protein 11	<a href="#">Info</a>	<a href="#">RGD:727935</a>
93	0.0001308	0.0141587	39.2	17	2.306	<a href="#">1376060_at</a>	Protein phosphatase 1H (PP2C domain containing) (predicted)	<a href="#">Info</a>	
94	0.000136	0.0144739	160.8	346.1	0.465	<a href="#">1392773_at</a>	proprotein convertase subtilisin/kexin type 5	<a href="#">Info</a>	<a href="#">Pcsk5</a>
95	0.0001377	0.0144739	951.4	113.9	8.353	<a href="#">1372011_at</a>	Guanine deaminase	<a href="#">Info</a>	<a href="#">Gda</a>
96	0.0001385	0.0144739	130.8	75.1	1.742	<a href="#">1372691_at</a>	uridine phosphorylase 1 (predicted)	<a href="#">Info</a>	<a href="#">Upp1_predicted</a>
97	0.0001405	0.0144739	323.9	789.7	0.41	<a href="#">1383112_at</a>	Transcribed locus	<a href="#">Info</a>	
98	0.0001409	0.0144739	307	176.8	1.736	<a href="#">1373310_at</a>	Transcribed locus	<a href="#">Info</a>	
99	0.0001434	0.0145061	1477.9	83.3	17.742	<a href="#">1372256_at</a>		<a href="#">Info</a>	
100	0.0001461	0.0145061	656.1	1062	0.618	<a href="#">1388488_at</a>	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)	<a href="#">Info</a>	<a href="#">Lsm3_predicted</a>
101	0.0001472	0.0145061	48.5	14	3.464	<a href="#">1390873_at</a>	Transcribed locus, strongly similar to XP_125798.5 PREDICTED: BTB (POZ) domain containing 11 [Mus musculus]	<a href="#">Info</a>	
102	0.0001475	0.0145061	2079.7	42.8	48.591	<a href="#">1370154_at</a>	lysozyme	<a href="#">Info</a>	<a href="#">Lyz</a>
103	0.0001506	0.0145061	45.4	11.1	4.09	<a href="#">1383783_at</a>	protocadherin 9 (predicted)	<a href="#">Info</a>	<a href="#">Pcdh9_predicted</a>
104	0.0001507	0.0145061	1246.7	677	1.842	<a href="#">1370245_at</a>	cathepsin L	<a href="#">Info</a>	<a href="#">Ctsl</a>
105	0.0001513	0.0145061	95.5	21.8	4.381	<a href="#">1384655_at</a>	kin of IRRE like 3 (Drosophila) (predicted)	<a href="#">Info</a>	<a href="#">Kirrel3_predicted</a>
106	0.0001556	0.0145264	104.9	21.5	4.879	<a href="#">1368975_at</a>	CD38 antigen	<a href="#">Info</a>	<a href="#">Cd38</a>
107	0.0001572	0.0145264	161	70.7	2.277	<a href="#">1397317_at</a>	Transcribed locus	<a href="#">Info</a>	
108	0.0001612	0.0145264	107.8	53.5	2.015	<a href="#">1377761_at</a>	glutamine-fructose-6-phosphate transaminase 2	<a href="#">Info</a>	<a href="#">RGD:1303097</a>
109	0.0001612	0.0145264	31.1	116.4	0.267	<a href="#">1369128_at</a>	glutamate receptor, ionotropic, kainate 5	<a href="#">Info</a>	<a href="#">Grik5</a>
110	0.0001655	0.0145264	296.4	44	6.736	<a href="#">1397655_at</a>		<a href="#">Info</a>	
111	0.0001657	0.0145264	54.6	8.6	6.349	<a href="#">1384302_at</a>	solute carrier family 6 (neurotransmitter transporter), member 17	<a href="#">Info</a>	<a href="#">Slc6a17</a>
112	0.000166	0.0145264	124.3	32.3	3.848	<a href="#">1376709_at</a>	solute carrier family 39 (metal ion transporter), member 8 (predicted)	<a href="#">Info</a>	<a href="#">Slc39a8_predicted</a>
113	0.0001675	0.0145264	535.7	299.3	1.79	<a href="#">1380665_at</a>	CGI-58-like protein	<a href="#">Info</a>	<a href="#">LOC316122</a>
114	0.0001686	0.0145264	252	788.9	0.319	<a href="#">1373897_at</a>		<a href="#">Info</a>	
115	0.0001692	0.0145264	1992.2	865.2	2.303	<a href="#">1383284_at</a>	Transcribed locus	<a href="#">Info</a>	
116	0.0001709	0.0145264	290.3	162.7	1.784	<a href="#">1376804_at</a>	similar to Myosin VI	<a href="#">Info</a>	<a href="#">LOC315840</a>
117	0.0001711	0.0145264	106.4	201.6	0.528	<a href="#">1368453_at</a>	fatty acid desaturase 2	<a href="#">Info</a>	<a href="#">Fads2</a>
118	0.0001719	0.0145264	32.6	10.8	3.019	<a href="#">1393075_at</a>	Transcribed locus	<a href="#">Info</a>	
119	0.0001734	0.0145264	1746.9	867.6	2.013	<a href="#">1383404_at</a>	Transcribed locus	<a href="#">Info</a>	
120	0.0001742	0.0145264	334.6	165.6	2.021	<a href="#">1373998_at</a>	Transcribed locus	<a href="#">Info</a>	
121	0.0001746	0.0145264	14.6	76.6	0.191	<a href="#">1385202_at</a>	Transcribed locus	<a href="#">Info</a>	

122	0.0001796	0.0146995	172.6	64.8	2.664	<a href="#">1368372_at</a>	steroid sulfatase	<a href="#">Info</a>	<a href="#">Sts</a>
123	0.0001796	0.0146995	75	124.4	0.603	<a href="#">1375054_at</a>	Transcribed locus	<a href="#">Info</a>	
124	0.0001877	0.0152385	187.1	54.6	3.427	<a href="#">1373431_at</a>	leucine-rich repeat-containing 5 (predicted)	<a href="#">Info</a>	<a href="#">Lrrc5_predicted</a>
125	0.0001899	0.0152938	197.3	362	0.545	<a href="#">1382053_at</a>	similar to MEGF12 (predicted)	<a href="#">Info</a>	<a href="#">RGD1305653_prec</a>
126	0.0001941	0.015508	73.2	16.4	4.463	<a href="#">1393659_at</a>	translocation associated membrane protein 1-like 1 (predicted)	<a href="#">Info</a>	<a href="#">Tram111_predicted</a>
127	0.0001959	0.0155285	85.7	165.6	0.518	<a href="#">1392467_at</a>	inositol (myo)-1(or 4)-monophosphatase 2	<a href="#">Info</a>	<a href="#">Impa2</a>
128	0.0002038	0.0159511	365	885.9	0.412	<a href="#">1385227_at</a>	trichorhinophalangeal syndrome I (predicted)	<a href="#">Info</a>	<a href="#">Trps1_predicted</a>
129	0.0002044	0.0159511	266.6	155.2	1.718	<a href="#">1381063_at</a>	adenylate cyclase 9 (predicted)	<a href="#">Info</a>	<a href="#">Adcy9_predicted</a>
130	0.0002198	0.0168134	241.1	55.1	4.376	<a href="#">1371840_at</a>	endothelial differentiation sphingolipid G-protein-coupled receptor 1	<a href="#">Info</a>	<a href="#">Edg1</a>
131	0.0002205	0.0168134	267.9	425.6	0.629	<a href="#">1393009_at</a>	similar to RIKEN cDNA 2410002F23 (predicted)	<a href="#">Info</a>	<a href="#">RGD1309326_prec</a>
132	0.0002214	0.0168134	48.5	13.7	3.54	<a href="#">1370465_at</a>	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	<a href="#">Info</a>	<a href="#">Abcb1a</a>
133	0.0002226	0.0168134	1092.3	250.8	4.355	<a href="#">1390107_at</a>	synaptotagmin-like 2 (predicted)	<a href="#">Info</a>	<a href="#">Syt12_predicted</a>
134	0.0002238	0.0168134	102.4	39.9	2.566	<a href="#">1388201_at</a>	bone morphogenetic protein 6	<a href="#">Info</a>	<a href="#">Bmp6</a>
135	0.0002264	0.0168827	4743.7	2830.1	1.676	<a href="#">1370328_at</a>	Dickkopf homolog 3 (Xenopus laevis)	<a href="#">Info</a>	<a href="#">Dkk3</a>
136	0.0002283	0.0168992	78.7	16.9	4.657	<a href="#">1383606_at</a>	membrane targeting (tandem) C2 domain containing 1	<a href="#">Info</a>	<a href="#">Mtac2d1</a>
137	0.000236	0.0173417	40.5	19.8	2.045	<a href="#">1385653_at</a>		<a href="#">Info</a>	
138	0.0002412	0.0174566	44.4	165.8	0.268	<a href="#">1395109_at</a>	Transcribed locus	<a href="#">Info</a>	
139	0.0002425	0.0174566	23.1	10.9	2.119	<a href="#">1381269_at</a>	Transcribed locus	<a href="#">Info</a>	
140	0.0002432	0.0174566	2197.7	4126.8	0.533	<a href="#">1368883_at</a>	nephroblastoma overexpressed gene	<a href="#">Info</a>	<a href="#">Nov</a>
141	0.0002445	0.0174566	391.2	886.8	0.441	<a href="#">1388167_at</a>	nuclear factor I/B	<a href="#">Info</a>	<a href="#">Nfib</a>
142	0.0002491	0.0176137	58.9	99.5	0.592	<a href="#">1391536_at</a>	similar to cDNA sequence BC020002 (predicted)	<a href="#">Info</a>	<a href="#">RGD1308432_prec</a>
143	0.0002502	0.0176137	78.3	201.5	0.389	<a href="#">1394031_at</a>	similar to Protein C20orf129 homolog	<a href="#">Info</a>	<a href="#">LOC311598</a>
144	0.0002583	0.0179551	190.2	405.8	0.469	<a href="#">1377299_at</a>	nuclear autoantigenic sperm protein	<a href="#">Info</a>	<a href="#">RGD:1359609</a>
145	0.0002603	0.0179551	91.7	37.4	2.452	<a href="#">1373759_at</a>	Transcribed locus	<a href="#">Info</a>	
146	0.0002604	0.0179551	236.5	538.5	0.439	<a href="#">1393629_at</a>	H2.0-like homeo box 1 (Drosophila) (predicted)	<a href="#">Info</a>	<a href="#">Hlx1_predicted</a>
147	0.0002638	0.0180146	56.6	115.2	0.491	<a href="#">1391477_at</a>	Transcribed locus	<a href="#">Info</a>	
148	0.0002682	0.0180146	157.5	351.2	0.448	<a href="#">1378038_at</a>	Polypyrimidine tract binding protein 2	<a href="#">Info</a>	<a href="#">Ptbp2</a>
149	0.0002683	0.0180146	124.7	35.9	3.474	<a href="#">1370106_at</a>	fibroblast growth factor 18	<a href="#">Info</a>	<a href="#">Fgf18</a>
150	0.0002707	0.0180146	1052.5	211	4.988	<a href="#">1378927_at</a>		<a href="#">Info</a>	
151	0.0002718	0.0180146	78.8	139.4	0.565	<a href="#">1375897_at</a>	Transcribed locus	<a href="#">Info</a>	
152	0.000272	0.0180146	76.8	132.4	0.58	<a href="#">1380118_at</a>	similar to hypothetical gene supported by AK085276	<a href="#">Info</a>	<a href="#">LOC315646</a>
153	0.000275	0.0180943	18.8	8.9	2.112	<a href="#">1391011_at</a>	Transcribed locus	<a href="#">Info</a>	
154	0.0002832	0.0185128	86.7	182	0.476	<a href="#">1385068_at</a>	Transcribed locus	<a href="#">Info</a>	
155	0.0002881	0.018561	372.7	924.4	0.403	<a href="#">1384948_at</a>	Transcribed locus	<a href="#">Info</a>	

156	0.0002912	0.018561	91.7	26.7	3.434	<a href="#">1398661_at</a>		<a href="#">Info</a>	
157	0.0002929	0.018561	331.3	812.7	0.408	<a href="#">1373644_at</a>	CDNA clone IMAGE:7308494	<a href="#">Info</a>	
158	0.0002933	0.018561	170.9	51.2	3.338	<a href="#">1367682_at</a>	midkine	<a href="#">Info</a>	<a href="#">Mdk</a>
159	0.000295	0.018561	1255.3	8609.9	0.146	<a href="#">1367700_at</a>	fibromodulin	<a href="#">Info</a>	<a href="#">Fmod</a>
160	0.000295	0.018561	575.1	339.7	1.693	<a href="#">1384286_at</a>	Transcribed locus	<a href="#">Info</a>	
161	0.0003002	0.0187444	41.1	72.8	0.565	<a href="#">1384042_at</a>	Transcribed locus	<a href="#">Info</a>	
162	0.000302	0.0187444	1419.2	3133.6	0.453	<a href="#">1371131_a_at</a>	upregulated by 1,25-dihydroxyvitamin D-3	<a href="#">Info</a>	<a href="#">Txnip</a>
163	0.0003035	0.0187444	369.5	715.3	0.517	<a href="#">1369971_a_at</a>	heterogeneous nuclear ribonucleoprotein D	<a href="#">Info</a>	<a href="#">Hnrpd</a>
164	0.0003071	0.0188511	103	22.2	4.64	<a href="#">1383304_at</a>	Transcribed locus	<a href="#">Info</a>	
165	0.0003199	0.0194729	303.1	140.4	2.159	<a href="#">1378477_a_at</a>	similar to Formin homology 2 domain containing 1	<a href="#">Info</a>	<a href="#">LOC291964</a>
166	0.0003224	0.0194729	99.3	176.9	0.561	<a href="#">1384925_at</a>	Similar to IL-17D	<a href="#">Info</a>	
167	0.0003292	0.0194729	103.4	11.5	8.991	<a href="#">1372455_at</a>	transmembrane 4 superfamily member 12 (predicted)	<a href="#">Info</a>	<a href="#">Tm4sf12_predicted</a>
168	0.000338	0.0194729	964.6	286	3.373	<a href="#">1391435_at</a>	phospholipid transfer protein (predicted)	<a href="#">Info</a>	<a href="#">Pltp_predicted</a>
169	0.0003436	0.0194729	93.1	23.9	3.895	<a href="#">1398511_at</a>	sushi domain containing 2 (predicted)	<a href="#">Info</a>	<a href="#">Susd2_predicted</a>
170	0.0003438	0.0194729	670.8	1026.9	0.653	<a href="#">1383162_at</a>		<a href="#">Info</a>	
171	0.000344	0.0194729	503.6	799	0.63	<a href="#">1373387_at</a>		<a href="#">Info</a>	
172	0.0003449	0.0194729	1531.8	937.9	1.633	<a href="#">1372610_at</a>	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	<a href="#">Info</a>	<a href="#">P4ha2_predicted</a>
173	0.0003457	0.0194729	40.3	170.4	0.237	<a href="#">1374794_at</a>	kinesin-like 7	<a href="#">Info</a>	<a href="#">Kns17</a>
174	0.0003475	0.0194729	73.2	155.9	0.47	<a href="#">1397297_at</a>	Transcribed locus	<a href="#">Info</a>	
175	0.0003491	0.0194729	66.6	16.5	4.036	<a href="#">1396405_at</a>	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]	<a href="#">Info</a>	
176	0.0003513	0.0194729	37.6	117.5	0.32	<a href="#">1393615_at</a>	Transcribed locus	<a href="#">Info</a>	
177	0.0003528	0.0194729	68.3	148.4	0.46	<a href="#">1377967_at</a>	Retroviral integration site 2 (predicted)	<a href="#">Info</a>	
178	0.0003528	0.0194729	65.2	172.2	0.379	<a href="#">1381472_at</a>	Similar to Mitochondrial folate transporter/carrier	<a href="#">Info</a>	
179	0.0003555	0.0194729	284.5	19.9	14.296	<a href="#">1379416_at</a>	Autism susceptibility candidate 2 (predicted)	<a href="#">Info</a>	
180	0.0003563	0.0194729	51	177.5	0.287	<a href="#">1380775_at</a>	M-phase phosphoprotein 1 (predicted)	<a href="#">Info</a>	<a href="#">Mphosph1_predict</a>
181	0.0003579	0.0194729	304.3	182	1.672	<a href="#">1370848_at</a>	solute carrier family 2 (facilitated glucose transporter), member 1	<a href="#">Info</a>	<a href="#">Slc2a1</a>
182	0.0003603	0.0194729	76	139.1	0.546	<a href="#">1390181_at</a>		<a href="#">Info</a>	
183	0.0003604	0.0194729	350.5	181.5	1.931	<a href="#">1368254_a_at</a>	sphingosine kinase 1	<a href="#">Info</a>	<a href="#">Sphk1</a>
184	0.0003613	0.0194729	193.5	38.7	5	<a href="#">1389186_at</a>	Transcribed locus	<a href="#">Info</a>	
185	0.0003644	0.0194729	27.4	56.2	0.488	<a href="#">1369771_at</a>	insulin receptor substrate 1	<a href="#">Info</a>	<a href="#">Irs1</a>
186	0.0003644	0.0194729	113.4	16.4	6.915	<a href="#">1393433_at</a>	similar to Agrin (predicted)	<a href="#">Info</a>	<a href="#">RGD1306592_prec</a>
187	0.0003644	0.0194729	1924.6	656	2.934	<a href="#">1369947_at</a>	cathepsin K	<a href="#">Info</a>	<a href="#">Ctsk</a>
188	0.0003658	0.0194729	104.2	51.4	2.027	<a href="#">1372515_at</a>	Transcribed locus	<a href="#">Info</a>	

189	0.0003676	0.0194729	645.1	300.3	2.148	<a href="#">1368379_at</a>	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	<a href="#">Info</a>	<a href="#">Scarb2</a>
190	0.0003712	0.0194729	154.8	29.3	5.283	<a href="#">1373545_at</a>	Transcribed locus	<a href="#">Info</a>	
191	0.0003744	0.0194729	147.6	31.7	4.656	<a href="#">1386666_at</a>	eyes absent 2 homolog (Drosophila)	<a href="#">Info</a>	<a href="#">Eya2</a>
192	0.0003747	0.0194729	126.3	79.8	1.583	<a href="#">1380404_at</a>		<a href="#">Info</a>	
193	0.0003752	0.0194729	441.8	28.4	15.556	<a href="#">1397808_at</a>	Cathepsin C	<a href="#">Info</a>	<a href="#">Ctsc</a>
194	0.0003802	0.0194729	254.3	83.8	3.035	<a href="#">1367905_at</a>	ectonucleotide pyrophosphatase/phosphodiesterase 3	<a href="#">Info</a>	<a href="#">Enpp3</a>
195	0.0003815	0.0194729	153.2	404.2	0.379	<a href="#">1367780_at</a>	pituitary tumor-transforming 1	<a href="#">Info</a>	<a href="#">Pttg1</a>
196	0.0003821	0.0194729	125	201.1	0.622	<a href="#">1373338_at</a>	Transcribed locus	<a href="#">Info</a>	
197	0.0003852	0.0194729	552.6	259.6	2.129	<a href="#">1390385_at</a>	Similar to D-glucuronyl C5-epimerase	<a href="#">Info</a>	
198	0.0003862	0.0194729	80	214.6	0.373	<a href="#">1379801_at</a>	LOC499790	<a href="#">Info</a>	
199	0.0003871	0.0194729	39.9	9.1	4.385	<a href="#">1378665_at</a>	Protocadherin 9 (predicted)	<a href="#">Info</a>	
200	0.0003877	0.0194729	180.9	38.6	4.687	<a href="#">1373617_at</a>	epithelial membrane protein 2	<a href="#">Info</a>	<a href="#">RGD:1359629</a>
201	0.0003888	0.0194729	150.1	42.6	3.523	<a href="#">1374544_at</a>	CDNA clone MGC:112715 IMAGE:7377326	<a href="#">Info</a>	
202	0.0003917	0.019509	28.9	49.4	0.585	<a href="#">1393655_at</a>	RAD54 like (S. cerevisiae) (predicted)	<a href="#">Info</a>	<a href="#">Rad54l_predicted</a>
203	0.000398	0.019509	118.2	261.2	0.453	<a href="#">1384591_at</a>	Similar to hypothetical protein FLJ32884 (predicted)	<a href="#">Info</a>	
204	0.0003999	0.019509	171	57.2	2.99	<a href="#">1371702_at</a>	transmembrane 4 superfamily member 2	<a href="#">Info</a>	<a href="#">Tm4sf2</a>
205	0.0004004	0.019509	46.5	16.1	2.888	<a href="#">1371210_s_at</a>	RT1 class Ib, locus Aw2 /// RT1 class I, CE5	<a href="#">Info</a>	<a href="#">RT1-Aw2 /// RT1-</a>
206	0.0004021	0.019509	24.8	65.8	0.377	<a href="#">1369218_at</a>	met proto-oncogene	<a href="#">Info</a>	<a href="#">Met</a>
207	0.0004035	0.019509	239.2	1468.5	0.163	<a href="#">1368422_at</a>	mesenchyme homeo box 2	<a href="#">Info</a>	<a href="#">Meox2</a>
208	0.0004057	0.019509	212.8	78.8	2.701	<a href="#">1368754_at</a>	pyrimidinergic receptor P2Y, G-protein coupled, 6	<a href="#">Info</a>	<a href="#">P2ry6</a>
209	0.0004059	0.019509	1830.9	1011.8	1.81	<a href="#">1367765_at</a>	transcobalamin 2	<a href="#">Info</a>	<a href="#">Tcn2</a>
210	0.0004081	0.019509	47.3	25.6	1.848	<a href="#">1382663_at</a>	basic leucine zipper transcription factor, ATF-like (predicted)	<a href="#">Info</a>	<a href="#">Batf_predicted</a>
211	0.0004089	0.019509	154.3	261.6	0.59	<a href="#">1373935_at</a>	polymerase (DNA directed), delta 2, regulatory subunit (predicted)	<a href="#">Info</a>	<a href="#">Pold2_predicted</a>
212	0.0004179	0.0197953	377.8	640	0.59	<a href="#">1382612_at</a>	Transcribed locus	<a href="#">Info</a>	
213	0.0004194	0.0197953	21	34	0.618	<a href="#">1389506_x_at</a>		<a href="#">Info</a>	
214	0.0004251	0.0197953	870.1	504.7	1.724	<a href="#">1383842_at</a>	Galactosidase, beta 1-like (predicted)	<a href="#">Info</a>	
215	0.0004255	0.0197953	171.6	273.8	0.627	<a href="#">1372343_at</a>	exosome component 8 (predicted)	<a href="#">Info</a>	<a href="#">Exosc8_predicted</a>
216	0.000426	0.0197953	60.1	112.5	0.534	<a href="#">1374961_at</a>		<a href="#">Info</a>	
217	0.0004267	0.0197953	47.6	153	0.311	<a href="#">1383926_at</a>	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	<a href="#">Info</a>	<a href="#">Bub1b</a>
218	0.0004337	0.0199409	5394.1	8693.8	0.62	<a href="#">1376749_at</a>	osteolectin (predicted)	<a href="#">Info</a>	<a href="#">Ogn_predicted</a>
219	0.0004338	0.0199409	60.6	166.7	0.364	<a href="#">1376039_at</a>	serine/threonine kinase 6	<a href="#">Info</a>	<a href="#">Stk6</a>
220	0.0004376	0.0199595	182.8	352.6	0.518	<a href="#">1381933_at</a>	Transcribed locus	<a href="#">Info</a>	
221	0.0004382	0.0199595	40.9	88.5	0.462	<a href="#">1370178_at</a>	calcium channel, voltage-dependent, beta 2 subunit	<a href="#">Info</a>	<a href="#">Cacnb2</a>

222	0.0004418	0.0199595	649.9	421.6	1.542	<a href="#">1382048_at</a>	ATPase, H+ transporting, V1 subunit A, isoform 1 (predicted)	<a href="#">Info</a>	<a href="#">Atp6v1a1_predicted</a>
223	0.0004442	0.0199595	151.4	256.5	0.59	<a href="#">1382978_at</a>	Transcribed locus	<a href="#">Info</a>	
224	0.0004444	0.0199595	84.4	34.1	2.475	<a href="#">1379660_at</a>	Transcribed locus	<a href="#">Info</a>	
225	0.0004461	0.0199595	304	671.8	0.453	<a href="#">1389601_at</a>	CDNA clone IMAGE:7308494	<a href="#">Info</a>	
226	0.0004482	0.0199647	228.1	366.4	0.623	<a href="#">1374840_at</a>		<a href="#">Info</a>	
227	0.0004539	0.0201296	59.6	94	0.634	<a href="#">1385164_at</a>	Similar to solute carrier family 16 (monocarboxylic acid transporters), member 4	<a href="#">Info</a>	
228	0.0004583	0.0202351	62.9	115.2	0.546	<a href="#">1397307_at</a>	Similar to Tescalcin	<a href="#">Info</a>	
229	0.0004603	0.0202351	41.6	23.7	1.755	<a href="#">1378490_at</a>	Autism susceptibility candidate 2 (predicted)	<a href="#">Info</a>	
230	0.0004653	0.020317	65.3	177	0.369	<a href="#">1395376_at</a>	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i> ) (predicted)	<a href="#">Info</a>	<a href="#">Ddx11_predicted</a>
231	0.0004662	0.020317	1387.8	916	1.515	<a href="#">1399019_at</a>	abhydrolase domain containing 4 (predicted)	<a href="#">Info</a>	<a href="#">Abhd4_predicted</a>
232	0.0004703	0.0204074	21.6	44.6	0.484	<a href="#">1381321_at</a>	Similar to RIKEN cDNA D030060M11 (predicted)	<a href="#">Info</a>	
233	0.000473	0.0204364	773.4	144	5.371	<a href="#">1380318_at</a>	LOC499196	<a href="#">Info</a>	
234	0.0004757	0.0204653	48.2	85.2	0.566	<a href="#">1368811_at</a>	lamin B1	<a href="#">Info</a>	<a href="#">Lmnb1</a>
235	0.0004785	0.0204981	36.9	24.6	1.5	<a href="#">1379970_at</a>	similar to Eph receptor A4	<a href="#">Info</a>	<a href="#">LOC316539</a>
236	0.0004824	0.0205776	24	12	2	<a href="#">1368751_at</a>	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	<a href="#">Info</a>	<a href="#">Kcns3</a>
237	0.0004859	0.0206395	968.3	1557.4	0.622	<a href="#">1373983_at</a>	LOC360807	<a href="#">Info</a>	<a href="#">LOC360807</a>
238	0.0004958	0.0209715	91.1	22.9	3.978	<a href="#">1372682_at</a>	similar to RIKEN cDNA 2810432L12 (predicted)	<a href="#">Info</a>	<a href="#">RGD1307218_prec</a>
239	0.0004991	0.0210228	98.4	54.4	1.809	<a href="#">1375093_at</a>	ribokinase (predicted)	<a href="#">Info</a>	<a href="#">Rbks_predicted</a>
240	0.0005027	0.0210446	444.2	236.8	1.876	<a href="#">1374265_at</a>	Similar to arylacetamide deacetylase (esterase) (predicted)	<a href="#">Info</a>	
241	0.0005038	0.0210446	57.5	25	2.3	<a href="#">1387058_at</a>	phosphatidylcholine transfer protein	<a href="#">Info</a>	<a href="#">Pctp</a>
242	0.000506	0.0210492	714.9	96.1	7.439	<a href="#">1383392_at</a>	complement component 2	<a href="#">Info</a>	<a href="#">C2</a>
243	0.0005108	0.0211614	27.2	171.5	0.159	<a href="#">1376106_at</a>	similar to hypothetical protein MGC33926	<a href="#">Info</a>	<a href="#">RGD:1303057</a>
244	0.0005155	0.0212686	19.4	13.4	1.448	<a href="#">1381388_at</a>	similar to Nasopharyngeal epithelium specific protein 1	<a href="#">Info</a>	<a href="#">MGC116217</a>
245	0.0005177	0.0212722	35.2	19.4	1.814	<a href="#">1373480_at</a>	Transcribed locus	<a href="#">Info</a>	
246	0.0005258	0.0215172	173.9	51.1	3.403	<a href="#">1393638_at</a>	Prostaglandin E receptor 4 (subtype EP4)	<a href="#">Info</a>	<a href="#">Ptger4</a>
247	0.0005389	0.0218326	309.7	464.5	0.667	<a href="#">1378360_at</a>	Transcribed locus	<a href="#">Info</a>	
248	0.0005422	0.0218326	97.2	170.2	0.571	<a href="#">1382370_at</a>	cyclin F	<a href="#">Info</a>	<a href="#">Ccnf</a>
249	0.000543	0.0218326	92.4	177.6	0.52	<a href="#">1394651_at</a>	similar to hypothetical protein FLJ32884 (predicted)	<a href="#">Info</a>	<a href="#">RGD1309453_prec</a>
250	0.0005463	0.0218326	23	9.5	2.421	<a href="#">1392633_at</a>	Transcribed locus	<a href="#">Info</a>	
251	0.0005471	0.0218326	12.8	7.9	1.62	<a href="#">1390557_at</a>	Transcribed locus	<a href="#">Info</a>	
252	0.0005475	0.0218326	247.3	167.3	1.478	<a href="#">1373869_at</a>	sterol O-acyltransferase 1	<a href="#">Info</a>	<a href="#">Soat1</a>
253	0.0005489	0.0218326	105.7	36	2.936	<a href="#">1374959_at</a>	NAD(P)H dehydrogenase, quinone 2	<a href="#">Info</a>	<a href="#">RGD:1303320</a>



254	0.0005523	0.0218326	180.4	100.3	1.799	<a href="#">1390863_at</a>	solute carrier family 19 (thiamine transporter), member 2 (predicted)	<a href="#">Info</a>	<a href="#">Slc19a2_predicted</a>
255	0.0005555	0.0218326	66.4	25.3	2.625	<a href="#">1391089_at</a>	similar to RGD1309360_predicted protein	<a href="#">Info</a>	<a href="#">LOC499521</a>
256	0.0005575	0.0218326	2620.2	1577.7	1.661	<a href="#">1390021_at</a>	histone 1, H2bh (predicted)	<a href="#">Info</a>	<a href="#">Hist1h2bh_predict</a>
257	0.0005583	0.0218326	33.9	142.3	0.238	<a href="#">1384512_at</a>		<a href="#">Info</a>	
258	0.000561	0.0218326	70	28.4	2.465	<a href="#">1378684_at</a>	rad and gem related GTP binding protein 1 (predicted)	<a href="#">Info</a>	<a href="#">Rem1_predicted</a>
259	0.0005617	0.0218326	217	332.8	0.652	<a href="#">1388436_at</a>	small nuclear ribonucleoprotein polypeptide A (predicted)	<a href="#">Info</a>	<a href="#">Snrpa_predicted</a>
260	0.0005706	0.0220932	77.8	161.3	0.482	<a href="#">1376055_at</a>	Transcribed locus	<a href="#">Info</a>	
261	0.0005771	0.0222593	389.6	22.3	17.471	<a href="#">1368885_at</a>	ectonucleoside triphosphate diphosphohydrolase 1	<a href="#">Info</a>	<a href="#">Entpd1</a>
262	0.0005813	0.0223357	42.3	84.6	0.5	<a href="#">1377175_at</a>	Similar to hypothetical protein A730008H23 (predicted)	<a href="#">Info</a>	
263	0.0005849	0.0223885	75.6	44.4	1.703	<a href="#">1382027_at</a>	LOC498010	<a href="#">Info</a>	<a href="#">Itgb3</a>
264	0.0005981	0.0225541	604.8	1099.4	0.55	<a href="#">1373369_at</a>	Transcribed locus	<a href="#">Info</a>	
265	0.000601	0.0225541	70.9	23.1	3.069	<a href="#">1397184_at</a>	Transcribed locus, strongly similar to XP_137017.3 PREDICTED: hypothetical protein XP_137017 [Mus musculus]	<a href="#">Info</a>	
266	0.0006019	0.0225541	210.9	329.6	0.64	<a href="#">1383384_at</a>	TATA box binding protein-like 1 (predicted)	<a href="#">Info</a>	
267	0.0006022	0.0225541	16.6	26.9	0.617	<a href="#">1380397_at</a>	LOC499812	<a href="#">Info</a>	
268	0.0006036	0.0225541	34.1	14.6	2.336	<a href="#">1368393_at</a>	lymphocyte antigen 68	<a href="#">Info</a>	<a href="#">C1qr1</a>
269	0.0006043	0.0225541	16.1	76.4	0.211	<a href="#">1392870_at</a>		<a href="#">Info</a>	
270	0.0006067	0.0225541	41	16.4	2.5	<a href="#">1387365_at</a>	nuclear receptor subfamily 1, group H, member 3	<a href="#">Info</a>	<a href="#">Nr1h3</a>
271	0.0006153	0.0225541	14.1	8.3	1.699	<a href="#">1398479_at</a>	Transcribed locus, weakly similar to NP_996757.1 ryanodine receptor type 3 [Gallus gallus]	<a href="#">Info</a>	
272	0.0006156	0.0225541	80.6	191	0.422	<a href="#">1376470_at</a>	formin binding protein 4 (predicted)	<a href="#">Info</a>	<a href="#">Fbnp4_predicted</a>
273	0.0006206	0.0225541	28	60.8	0.461	<a href="#">1391731_at</a>	High mobility group box transcription factor 1	<a href="#">Info</a>	<a href="#">Hbp1</a>
274	0.0006223	0.0225541	134.3	16.3	8.239	<a href="#">1374474_at</a>	Transcribed locus, strongly similar to NP_080091.1 copine family member [Mus musculus]	<a href="#">Info</a>	
275	0.0006254	0.0225541	1486.2	873.9	1.701	<a href="#">1377742_at</a>	Transcribed locus	<a href="#">Info</a>	
276	0.0006314	0.0225541	178.5	43.9	4.066	<a href="#">1388166_at</a>	similar to Igh-6 protein /// similar to Ig H-chain V-region precursor /// similar to single chain Fv antibody fragment scFv 7-10A /// similar to Ig heavy chain V region MC101 precursor	<a href="#">Info</a>	<a href="#">RGD:1359202 ///</a> <a href="#">LOC299458 ///</a> <a href="#">LOC314509 ///</a> <a href="#">LOC366747</a>
277	0.0006316	0.0225541	1148.4	614.6	1.869	<a href="#">1371432_at</a>		<a href="#">Info</a>	
278	0.0006359	0.0225541	79.8	52.2	1.529	<a href="#">1380137_at</a>	Transcribed locus	<a href="#">Info</a>	
279	0.0006475	0.0225541	9.8	30.5	0.321	<a href="#">1381620_at</a>	Fat tumor suppressor homolog (Drosophila)	<a href="#">Info</a>	<a href="#">Fat</a>
280	0.0006478	0.0225541	204.9	120.7	1.698	<a href="#">1377669_at</a>	low Mr GTP-binding protein	<a href="#">Info</a>	<a href="#">Rab27a</a>
281	0.0006489	0.0225541	321.3	540.9	0.594	<a href="#">1388744_at</a>	minichromosome maintenance protein 7	<a href="#">Info</a>	<a href="#">RGD:1303018</a>
282	0.000649	0.0225541	70.9	172	0.412	<a href="#">1374799_at</a>	similar to mKIAA0159 protein	<a href="#">Info</a>	<a href="#">LOC362438</a>

283	0.0006493	0.0225541	298.3	137.6	2.168	<a href="#">1397300_at</a>	Transcribed locus	<a href="#">Info</a>	
284	0.00065	0.0225541	126.1	48	2.627	<a href="#">1394422_at</a>	similar to hypothetical protein FLJ23033	<a href="#">Info</a>	<a href="#">LOC310982</a>
285	0.000652	0.0225541	165.7	25.8	6.422	<a href="#">1378396_at</a>	Bone specific CMF608	<a href="#">Info</a>	<a href="#">Igsf10</a>
286	0.000653	0.0225541	97	34.8	2.787	<a href="#">1373979_at</a>	CDNA clone MGC:112715 IMAGE:7377326	<a href="#">Info</a>	
287	0.0006578	0.0225541	32.5	51.4	0.632	<a href="#">1380625_at</a>	CCR4-NOT transcription complex, subunit 4 (predicted)	<a href="#">Info</a>	
288	0.0006583	0.0225541	1115	303.6	3.673	<a href="#">1372168_s_at</a>	insulin-like growth factor binding protein 6	<a href="#">Info</a>	<a href="#">Igfbp6</a>
289	0.0006596	0.0225541	881.8	70.2	12.561	<a href="#">1393219_at</a>	complement component 2	<a href="#">Info</a>	<a href="#">C2</a>
290	0.0006612	0.0225541	95.9	20	4.795	<a href="#">1371014_at</a>	phospholipase C, beta 1	<a href="#">Info</a>	<a href="#">Plcb1</a>
291	0.0006631	0.0225541	94.8	26	3.646	<a href="#">1397537_at</a>		<a href="#">Info</a>	<a href="#">LOC363433 ///</a> <a href="#">LOC363434 ///</a> <a href="#">LOC367381 ///</a> <a href="#">LOC500070 ///</a> <a href="#">LOC501091 ///</a> <a href="#">LOC501092 ///</a> <a href="#">LOC501221 ///</a> <a href="#">LOC501222 ///</a> <a href="#">LOC501399</a>
292	0.0006642	0.0225541	135.4	15.5	8.735	<a href="#">1379482_at</a>	transmembrane 6 superfamily member 1 (predicted)	<a href="#">Info</a>	<a href="#">Tm6sf1_predicted</a>
293	0.0006652	0.0225541	2206.2	943.7	2.338	<a href="#">1372706_at</a>	hexosaminidase B (predicted)	<a href="#">Info</a>	<a href="#">Hexb_predicted</a>
294	0.000667	0.0225541	151.9	340.8	0.446	<a href="#">1371042_at</a>	mitogen-activated protein kinase kinase kinase 3	<a href="#">Info</a>	<a href="#">Map4k3</a>
295	0.0006673	0.0225541	207.8	136	1.528	<a href="#">1381297_at</a>	Rho guanine nucleotide exchange factor (GEF) 5	<a href="#">Info</a>	<a href="#">Arhgef5</a>
296	0.0006691	0.0225541	126.5	325.4	0.389	<a href="#">1384280_at</a>	Nucleolar and spindle associated protein 1 (predicted)	<a href="#">Info</a>	
297	0.0006709	0.0225541	427	269.7	1.583	<a href="#">1383982_at</a>	Transcribed locus	<a href="#">Info</a>	
298	0.0006747	0.0225541	242.4	412.4	0.588	<a href="#">1373194_at</a>	caspase 8 associated protein 2 (predicted)	<a href="#">Info</a>	<a href="#">Casp8ap2_predicte</a>
299	0.0006747	0.0225541	51.2	130.2	0.393	<a href="#">1382783_at</a>	Bloom syndrome (predicted)	<a href="#">Info</a>	<a href="#">Blm_predicted</a>
300	0.0006758	0.0225541	5145.2	3136	1.641	<a href="#">1368504_at</a>	lysosomal membrane glycoprotein 1	<a href="#">Info</a>	<a href="#">Lamp1</a>
301	0.0006762	0.0225541	5181.5	3251.7	1.593	<a href="#">1398892_at</a>	Niemann Pick type C2	<a href="#">Info</a>	<a href="#">Npc2</a>
302	0.0006766	0.0225541	560.2	95.1	5.891	<a href="#">1381993_at</a>	chloride intracellular channel 2 (predicted)	<a href="#">Info</a>	<a href="#">Clie2_predicted</a>
303	0.0006809	0.0226225	672.5	359.4	1.871	<a href="#">1391282_at</a>	Transcribed locus, moderately similar to XP_484071.1 PREDICTED: similar to Als2 protein [Mus musculus]	<a href="#">Info</a>	
304	0.0006857	0.022707	58.1	26.8	2.168	<a href="#">1376574_at</a>	Lymphocyte antigen 68	<a href="#">Info</a>	<a href="#">C1qr1</a>
305	0.0006962	0.0229792	22	51.3	0.429	<a href="#">1377410_at</a>	similar to hypothetical protein FLJ23311 (predicted)	<a href="#">Info</a>	<a href="#">RGD1308091_prec</a>
306	0.0006996	0.0230159	1398.5	2263	0.618	<a href="#">1371365_at</a>	similar to Ubiquitin-conjugating enzyme E2S	<a href="#">Info</a>	<a href="#">LOC292588</a>
307	0.0007034	0.0230656	525.7	850.5	0.618	<a href="#">1373217_at</a>	Transcribed locus	<a href="#">Info</a>	
308	0.0007069	0.0231051	241.2	933.6	0.258	<a href="#">1385871_at</a>	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	<a href="#">Info</a>	
309	0.0007107	0.023106	141	37.9	3.72	<a href="#">1368280_at</a>	cathepsin C	<a href="#">Info</a>	<a href="#">Ctsc</a>
310	0.0007133	0.023106	46.8	20.1	2.328	<a href="#">1385909_at</a>	Transcribed locus	<a href="#">Info</a>	

<b>311</b>	0.0007147	0.023106	541.6	343.3	1.578	<a href="#">1398254_at</a>	renin binding protein	<a href="#">Info</a>	<a href="#">Renbp</a>
<b>312</b>	0.0007164	0.023106	301.9	94	3.212	<a href="#">1398333_at</a>	Endothelial PAS domain protein 1	<a href="#">Info</a>	<a href="#">Epas1</a>
<b>313</b>	0.0007186	0.023106	191.1	79.2	2.413	<a href="#">1379402_at</a>	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	<a href="#">Info</a>	<a href="#">Abcc4</a>
<b>314</b>	0.0007207	0.023106	98.1	166	0.591	<a href="#">1373468_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>315</b>	0.0007238	0.0231317	1201.1	808.3	1.486	<a href="#">1379255_at</a>	ATPase, H+ transporting, lysosomal accessory protein 2	<a href="#">Info</a>	<a href="#">Atp6ap2</a>
<b>316</b>	0.0007274	0.0231732	31.2	118.5	0.263	<a href="#">1385185_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>317</b>	0.000738	0.0233245	40.6	84.2	0.482	<a href="#">1396645_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>318</b>	0.0007384	0.0233245	160.2	316.6	0.506	<a href="#">1374465_at</a>	similar to ubiquitously-expressed transcript isoform 1	<a href="#">Info</a>	<a href="#">RGD:1359326</a>
<b>319</b>	0.0007391	0.0233245	622.5	279.1	2.23	<a href="#">1390387_at</a>	Similar to SH3 domain protein D19 (predicted)	<a href="#">Info</a>	
<b>320</b>	0.0007434	0.0233869	44	84.4	0.521	<a href="#">1393168_at</a>	Similar to Mbt domain containing 1	<a href="#">Info</a>	
<b>321</b>	0.0007461	0.0233987	129.2	34.5	3.745	<a href="#">1372579_at</a>	Endoglin	<a href="#">Info</a>	
<b>322</b>	0.0007503	0.0234574	33.4	70.5	0.474	<a href="#">1369468_at</a>	frizzled homolog 4 (Drosophila)	<a href="#">Info</a>	<a href="#">Fzd4</a>
<b>323</b>	0.0007597	0.0235974	1684.3	1114.9	1.511	<a href="#">1382101_at</a>	heparan sulfate 2-O-sulfotransferase 1 (predicted)	<a href="#">Info</a>	<a href="#">Hs2st1_predicted</a>
<b>324</b>	0.0007622	0.0235974	88.6	172.6	0.513	<a href="#">1374225_at</a>	CDNA clone IMAGE:7389359	<a href="#">Info</a>	
<b>325</b>	0.000764	0.0235974	120.4	265.8	0.453	<a href="#">1398440_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>326</b>	0.0007645	0.0235974	43.1	90.6	0.476	<a href="#">1377718_at</a>	similar to CDNA sequence BC022692	<a href="#">Info</a>	<a href="#">LOC501552</a>
<b>327</b>	0.0007665	0.0235974	23.5	13	1.808	<a href="#">1370248_at</a>	FXYP domain-containing ion transport regulator 6	<a href="#">Info</a>	<a href="#">Fxyd6</a>
<b>328</b>	0.0007721	0.0235995	83.1	144.9	0.573	<a href="#">1390769_at</a>	Ribose-phosphate pyrophosphokinase I -like	<a href="#">Info</a>	<a href="#">LOC314140</a>
<b>329</b>	0.0007734	0.0235995	32.1	66.4	0.483	<a href="#">1393405_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>330</b>	0.0007736	0.0235995	77	228.7	0.337	<a href="#">1390891_at</a>	similar to Kinesin family member 11	<a href="#">Info</a>	<a href="#">LOC499350</a>
<b>331</b>	0.0007777	0.0236529	45	76.4	0.589	<a href="#">1394976_at</a>	Similar to HN1-like protein (predicted)	<a href="#">Info</a>	<a href="#">Hn11</a>
<b>332</b>	0.0007816	0.0236952	15.2	8.9	1.708	<a href="#">1397791_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>333</b>	0.0007838	0.0236952	157.3	23	6.839	<a href="#">1372926_at</a>	Synapsin III	<a href="#">Info</a>	<a href="#">Syn3</a>
<b>334</b>	0.0007943	0.0238693	56	856.5	0.065	<a href="#">1389581_at</a>	similar to RIKEN cDNA 9230117N10 (predicted)	<a href="#">Info</a>	<a href="#">RGD1311155_predicted</a>
<b>335</b>	0.0007943	0.0238693	39.9	87.7	0.455	<a href="#">1379562_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>336</b>	0.0007984	0.0239211	25.9	13.6	1.904	<a href="#">1378436_at</a>	Transcribed locus, weakly similar to XP_524755.1 PREDICTED: similar to RNA processing factor 1 [Pan troglodytes]	<a href="#">Info</a>	
<b>337</b>	0.0008053	0.0240268	38.2	23.6	1.619	<a href="#">1377632_at</a>		<a href="#">Info</a>	
<b>338</b>	0.0008067	0.0240268	45.3	88.1	0.514	<a href="#">1394839_at</a>	Phosphoribosylglycinamide formyltransferase (predicted)	<a href="#">Info</a>	
<b>339</b>	0.0008171	0.0242018	202.8	432.5	0.469	<a href="#">1377846_a_at</a>	mutS homolog 6 (E. coli) (predicted)	<a href="#">Info</a>	<a href="#">Msh6_predicted</a>
<b>340</b>	0.0008191	0.0242018	22.7	60.1	0.378	<a href="#">1395942_at</a>	Transcribed locus	<a href="#">Info</a>	
<b>341</b>	0.0008201	0.0242018	74.9	190.9	0.392	<a href="#">1370999_at</a>	sperm associated antigen 5	<a href="#">Info</a>	<a href="#">Spag5</a>
<b>342</b>	0.000823	0.0242018	179.6	34.7	5.176	<a href="#">1393084_at</a>		<a href="#">Info</a>	
<b>343</b>	0.000825	0.0242018	24.8	10.7	2.318	<a href="#">1368416_at</a>	integrin binding sialoprotein	<a href="#">Info</a>	<a href="#">Ibsp</a>
<b>344</b>	0.000827	0.0242018	275.3	412.2	0.668	<a href="#">1389131_at</a>	similar to C330027I04Rik protein	<a href="#">Info</a>	<a href="#">RGD:1359229</a>

345	0.0008353	0.0243546	22.9	15.8	1.449	<a href="#">1396345_at</a>		<a href="#">Info</a>	
346	0.0008393	0.0243546	83.1	32.4	2.565	<a href="#">1382311_at</a>	TRAF2 binding protein	<a href="#">Info</a>	<a href="#">RGD:1359151</a>
347	0.0008406	0.0243546	147.9	215	0.688	<a href="#">1382679_at</a>	similar to WD-repeat protein 43	<a href="#">Info</a>	<a href="#">LOC362703</a>
348	0.0008419	0.0243546	392.5	1234.5	0.318	<a href="#">1368565_at</a>	solute carrier family 1 (glial high affinity glutamate transporter), member 3	<a href="#">Info</a>	<a href="#">Slc1a3</a>
349	0.000845	0.0243743	160.8	236	0.681	<a href="#">1379097_at</a>	Transcribed locus	<a href="#">Info</a>	
350	0.000849	0.0244197	25.1	14	1.793	<a href="#">1370628_at</a>	granzyme B	<a href="#">Info</a>	<a href="#">Gzmb</a>
351	0.0008576	0.0245469	404.7	177.3	2.283	<a href="#">1370080_at</a>	heme oxygenase (decycling) 1	<a href="#">Info</a>	<a href="#">Hmox1</a>
352	0.0008583	0.0245469	129.7	226.4	0.573	<a href="#">1370075_at</a>	dihydrofolate reductase	<a href="#">Info</a>	<a href="#">Dhfr</a>
353	0.0008615	0.0245686	140.3	40.2	3.49	<a href="#">1387914_at</a>	cytochrome P450, family 27, subfamily a, polypeptide 1	<a href="#">Info</a>	<a href="#">Cyp27a1</a>
354	0.0008652	0.0246044	86.6	179.6	0.482	<a href="#">1374219_at</a>	dispatched homolog 1 (Drosophila) (predicted)	<a href="#">Info</a>	<a href="#">Disp1_predicted</a>
355	0.000873	0.0247563	67.8	46.2	1.468	<a href="#">1381475_at</a>	sidekick homolog 2 (chicken) (predicted)	<a href="#">Info</a>	<a href="#">Sdk2_predicted</a>
356	0.0008775	0.0247925	169	29.1	5.808	<a href="#">1385426_at</a>	similar to hypothetical protein FLJ20647 (predicted)	<a href="#">Info</a>	<a href="#">RGD1305326_prec</a>
357	0.0008792	0.0247925	64.6	180.3	0.358	<a href="#">1382183_at</a>	Transcribed locus	<a href="#">Info</a>	
358	0.0008873	0.024946	116.9	338.3	0.346	<a href="#">1398467_at</a>	hypothetical LOC360644	<a href="#">Info</a>	<a href="#">LOC360644</a>
359	0.0008896	0.024946	129.1	291.1	0.443	<a href="#">1392140_at</a>	Transcribed locus	<a href="#">Info</a>	
360	0.0008946	0.0250165	380.1	110.9	3.427	<a href="#">1379338_at</a>		<a href="#">Info</a>	
361	0.0009038	0.0252038	88.6	155	0.572	<a href="#">1396116_at</a>	serologically defined colon cancer antigen 1 (predicted)	<a href="#">Info</a>	<a href="#">Sdccag1_predicted</a>
362	0.0009291	0.0257262	524.1	224.4	2.336	<a href="#">1372132_at</a>	CNDP dipeptidase 2 (metallopeptidase M20 family) (predicted)	<a href="#">Info</a>	<a href="#">Cndp2_predicted</a>
363	0.0009298	0.0257262	28.3	15.1	1.874	<a href="#">1371942_at</a>	similar to Glutathione S-transferase, theta 3	<a href="#">Info</a>	<a href="#">LOC499422</a>
364	0.0009302	0.0257262	144.9	284.8	0.509	<a href="#">1370294_a_at</a>	cell division cycle 20 homolog (S. cerevisiae)	<a href="#">Info</a>	<a href="#">Cdc20</a>
365	0.0009329	0.0257301	62.5	20.3	3.079	<a href="#">1384544_at</a>	paraoxonase 3	<a href="#">Info</a>	<a href="#">RGD:1302965</a>
366	0.0009404	0.0258661	23.7	42.2	0.562	<a href="#">1393648_at</a>	BTB (POZ) domain containing 4 (predicted)	<a href="#">Info</a>	
367	0.0009457	0.0258722	450.3	682.1	0.66	<a href="#">1371064_at</a>	pericentriolar material 1	<a href="#">Info</a>	<a href="#">Pcm1</a>
368	0.0009465	0.0258722	325.2	209.6	1.552	<a href="#">1390851_at</a>		<a href="#">Info</a>	
369	0.0009503	0.0258722	71	125.5	0.566	<a href="#">1369018_at</a>	forkhead box M1	<a href="#">Info</a>	<a href="#">Foxm1</a>
370	0.0009509	0.0258722	533	1195.1	0.446	<a href="#">1368712_at</a>	zinc finger protein 386 (Kruppel-like)	<a href="#">Info</a>	<a href="#">Znf386</a>
371	0.0009577	0.0259481	6.5	11.1	0.586	<a href="#">1395372_at</a>	Transcribed locus	<a href="#">Info</a>	
372	0.0009622	0.0259481	125.8	229.6	0.548	<a href="#">1374181_at</a>	similar to heterogeneous nuclear ribonucleoprotein G - human	<a href="#">Info</a>	<a href="#">LOC302855</a>
373	0.0009638	0.0259481	70.5	157.7	0.447	<a href="#">1374805_at</a>	similar to hypothetical protein MGC5528	<a href="#">Info</a>	<a href="#">LOC299933</a>
374	0.000964	0.0259481	417.1	855.2	0.488	<a href="#">1383336_at</a>	similar to pinin	<a href="#">Info</a>	<a href="#">LOC368070</a>
375	0.0009739	0.0261287	95.8	64.3	1.49	<a href="#">1393229_at</a>	silver (predicted)	<a href="#">Info</a>	<a href="#">Si_predicted</a>
376	0.0009759	0.0261287	481.7	696.2	0.692	<a href="#">1373214_at</a>	KDEL (Lys-Asp-Glu-Leu) containing 1 (predicted)	<a href="#">Info</a>	<a href="#">Kdelc1_predicted</a>
377	0.0009845	0.026289	44.5	26.1	1.705	<a href="#">1383692_at</a>		<a href="#">Info</a>	
378	0.0009946	0.0264885	81.8	29.8	2.745	<a href="#">1376790_at</a>	Galactosylceramidase	<a href="#">Info</a>	<a href="#">Galc</a>

379	0.0009987	0.0265275	50.2	101.9	0.493	<a href="#">1391808_at</a>	Transcribed locus	<a href="#">Info</a>
-----	-----------	-----------	------	-------	-------	----------------------------	-------------------	----------------------

---



---

**Date and time of the analysis:**

Name of the project file: ProjectRMA\_BRB.xls

Time of the analysis: Fri Sep 22 04:36:37 2006

BRB-ArrayTools Version: 3.4

---

**Filtering parameters:**

- **Spot Filters: OFF**
  - **Normalization: OFF**
  - **Exclude a gene under any of the following conditions:**  
p-value of the log-ratio variation in greater than 0.05
  - **Gene Subsets: OFF**
- 

[View expression of significant genes.](#)