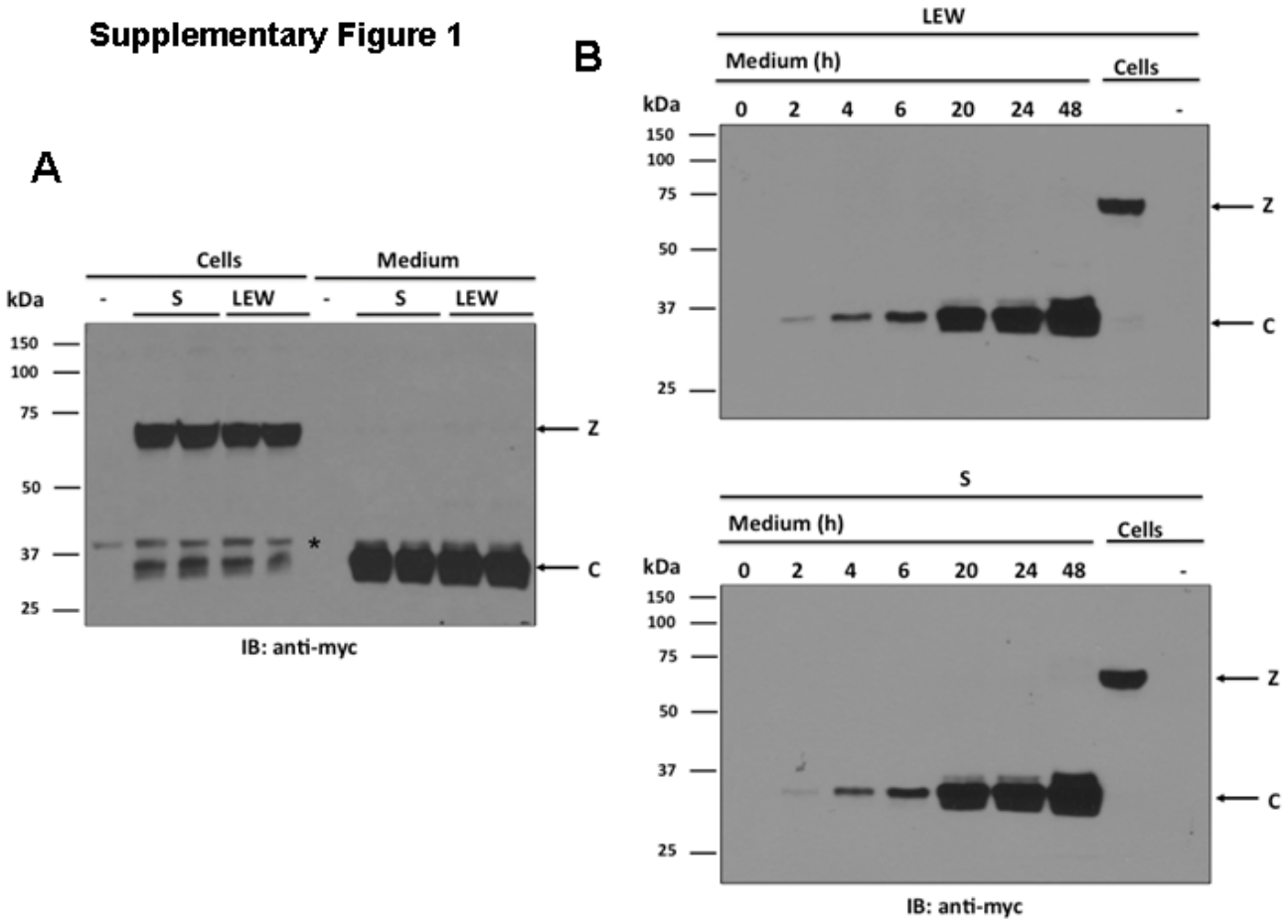
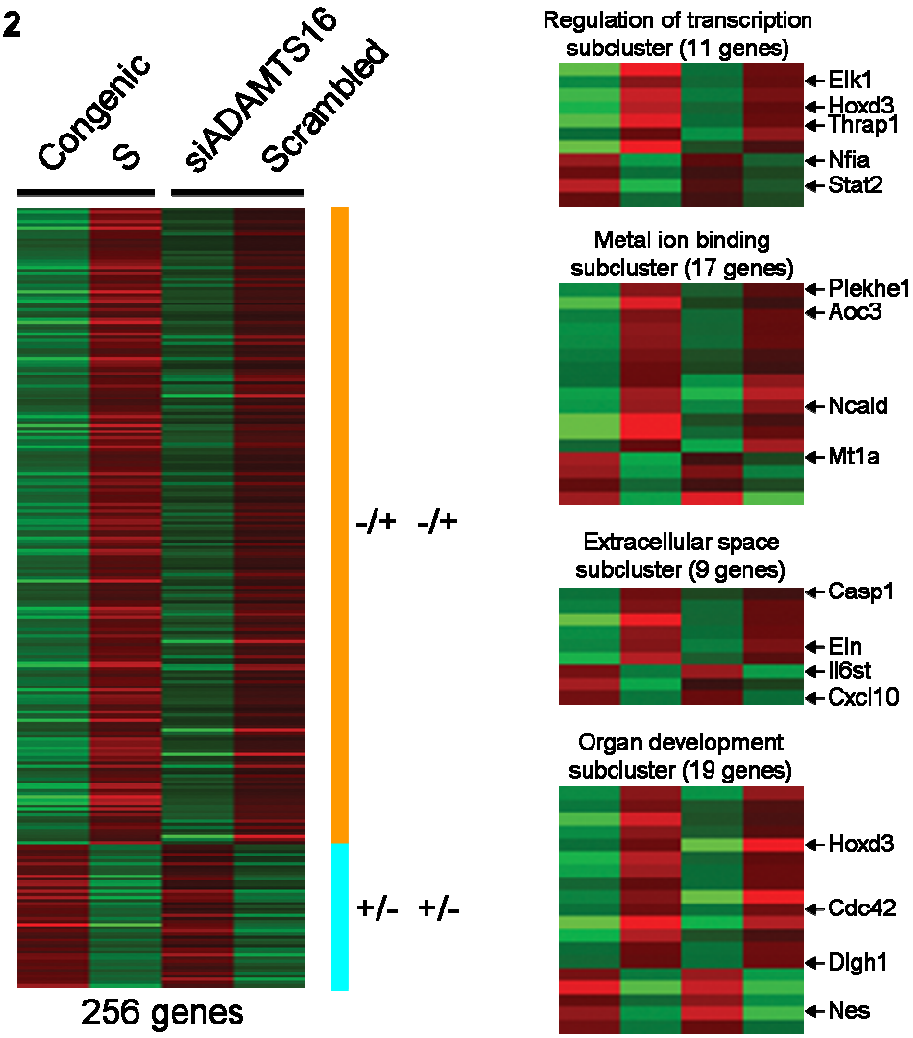
Supplementary Figure 1



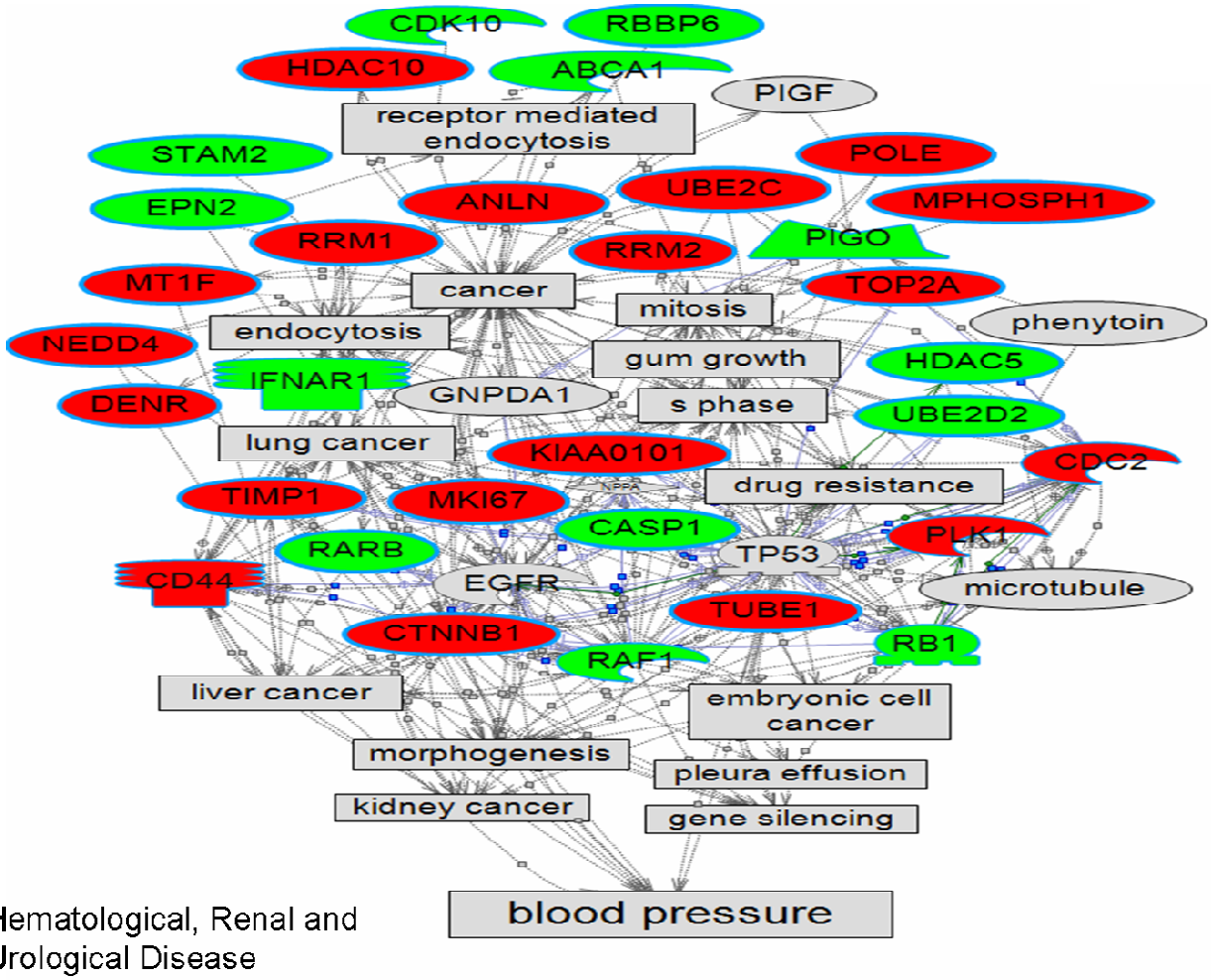
Furin-Cleavage analysis. HEK293F cells(Invitrogen) cultured in DMEM+10% FBS were transiently transfected with a vector control (-), or C-terminal myc-tagged ADAMTS16 Pro-Cat construct for the S and LEW variants using FuGene. Cells and conditioned medium was harvested after 48 h of culture in serum free DMEM (A) or medium was sampled at the indicated time points (B), and following reduction in Laemmli sample buffer, were electrophoresed by 7.5% SDS-PAGE. After electroblotting to polyvinyldifluoridine membrane, western blotting was done using anti-myc monoclonal 9E10 (Invitrogen) and enhanced chemiluminescence (ECL) for detection. In the cell lysate (cells), the dominant molecular form is the unprocessed zymogen (Z, 60 kDa). In cell lysate, some cleaved catalytic domain (C, 29 kDa) resulting from furin processing is also visualized. In the conditioned medium, no unprocessed zymogen was identified, suggesting efficient processing of both the S and LEW variants. As seen in panel B, there was no difference in the rate of secretion and processing of the S or Lew variants into the medium. The asterisk indicates a 42 kDa non-specific reactive protein species that is also seen in control cell lysate. Molecular weight markers are shown to the left of the gels.

Supplementary Figure 2



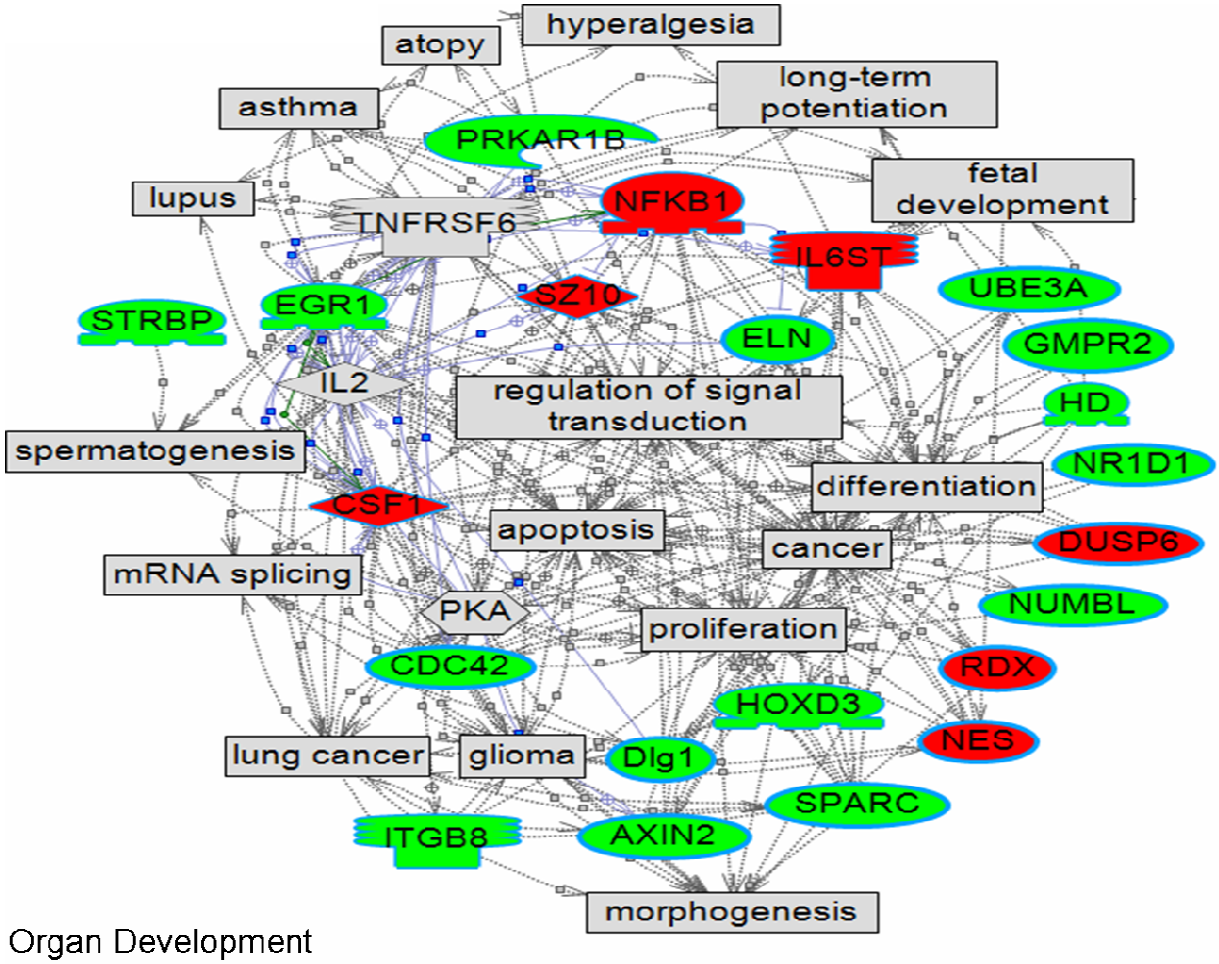
Microarray profiling and identification of genes downstream of *Adamts16*. (Left panel). Gene expressing profiling was performed in whole kidney comparisons of S.LEW(D1Mco4x1x3Bx1) congenic versus S rats. A corresponding comparison was performed in siRNA-mediated Adamts16 knockdowns in NRK-52E cells versus the same cells treated with a scrambled siRNA control. Depicted is a common set of 256 differentially expressed genes from the two comparisons representing candidate genes regulated by Adamts16. (Right panel). Gene ontology categories of interest in kidney function include regulation of transcription, metal ion binding, extracellular space, organ development. Each row in the cluster image represents the mean expression of an individual gene, and each column represents an individual experimental group. The relative transcript abundance of each gene is color coded. A red color indicates high expression, black indicates intermediate expression, and green indicates low expression.

Supplementary Figure 3



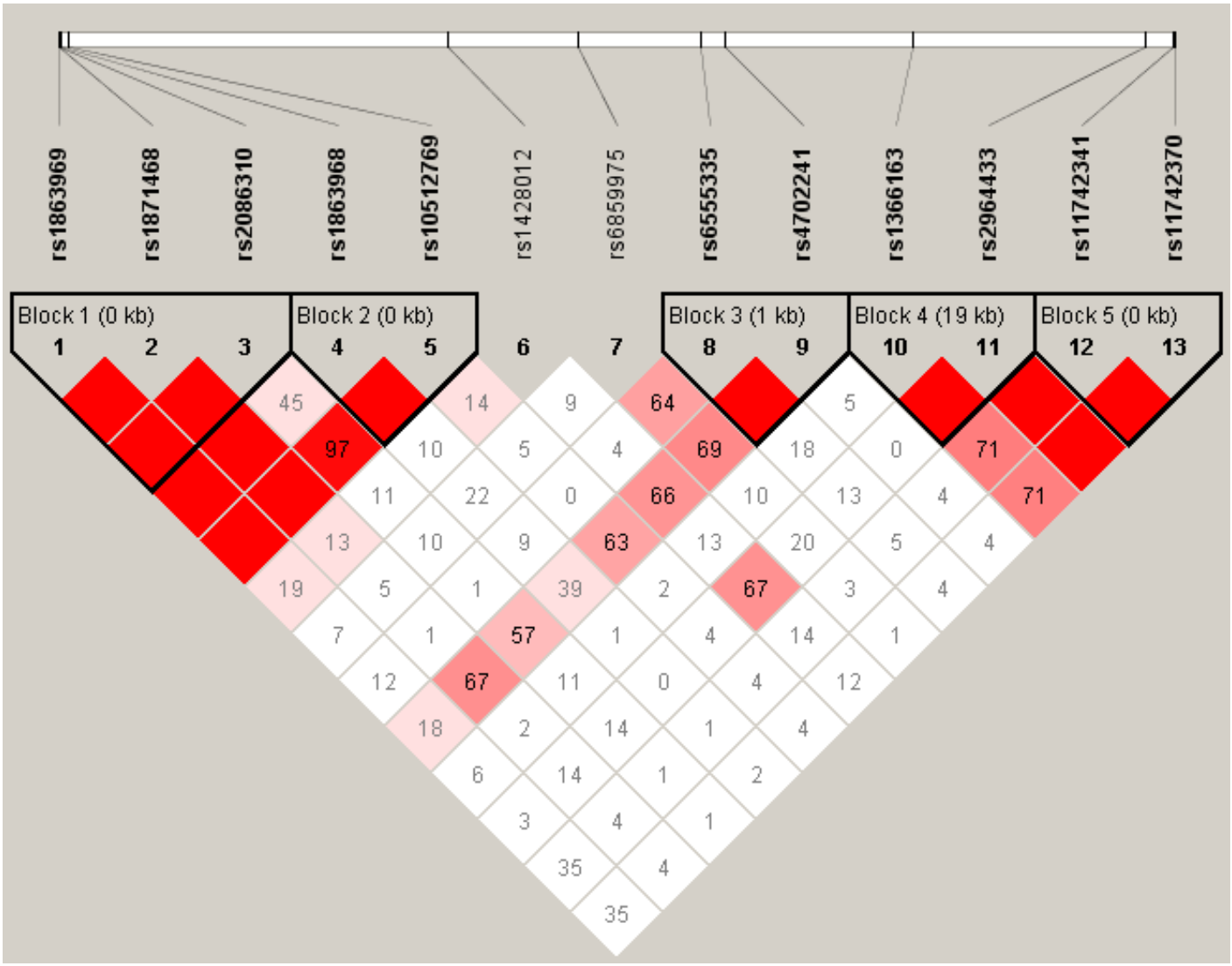
Gene network regulated by *Adamts16*. A gene regulatory network with renal, urological disease and blood pressure control as the associated biological theme was constructed from the overlapping gene set identified by expression profiling hypertensive S versus congenic animals and siRNA-mediated gene knockdown of *Adamts16* in rat kidney NRK-52E cells. Edges (lines) connecting nodes (genes) represent regulatory interactions such as regulation of gene expression, protein-protein interactions, protein-nucleic acid interactions, protein-hormone interactions. Genes up-regulated by *Adamts16* knockdown and congenic versus S comparisons are indicated in red and genes down-regulated by knockdown and congenic versus S comparisons in green. See Supplementary Table 3 for definition of gene symbol abbreviations.

Supplementary Figure 4



Organ development gene network. A gene regulatory network with organ development as the associated biological theme was constructed from the overlapping gene set identified by expression profiling S.LEW(D1Mco4x1x3Bx1) congenic animals versus hypertensive S and siRNA-mediated gene knockdown of *Adamts16* versus scrambled control siRNA in rat kidney NRK-52E cells. Edges (lines) connecting nodes (genes) represent regulatory interactions such as regulation of gene expression, protein-protein interactions, protein-nucleic acid interactions, protein-hormone interactions. Up-regulated genes are indicated in red and down-regulated genes are indicated in green. See Supplementary Tables 3 and 4 for definition of gene symbol abbreviations.

Supplementary Figure 5: LD Plot of associated SNPs in the QFS study



Supplementary Table 1. Regions of F2(S x LEW) linkage analysis that overlap with the regions of SNP association with hypertension in the WTCCC study.

Human Chr	Region (Mb)	SNP	Rat Chr	Region (Mb)	S.L QTL	Physical location of the rat QTL region (Mb)
HSA1q43	235.67-235.79	rs2820037	RNO17	69.28-69.35	D17Mit2-D17Mit5	38.35-82.13
HSA8q24	140.17-140.35	rs6997709	RNO7	109.82-110.00	D7Mit4-D7Wox3	100.27-123.64
HSA12q23	100.52-100.58	rs11110912	RNO7	25.24-25.30	D7Wox26-D7Uia3	22.93-44.70
HSA15q26	94.60-94.67	rs2398162	RNO1	125.30-125.37	D1Mco36-D1Mco101	122.99-130.39

All locations are in megabases (Mb) obtained from the Ensembl database (www.ensembl.org).

Supplementary Table 2: Variants of *Adamts16* in different inbred rat strains.

Chromosomal Location	2606898 (RNO17)	2629864 (RNO17)	2635933 (RNO17)	2637060 (RNO17)	2640570 (RNO17)	2652022 (RNO17)	2688316(RNO17)
Transcript Location	+820	+1482	+1785	+1926	+2226	+2646	+3508
RNO	1	1	1	1	1	1	1
EXON	5	10	12	13	15	17	22
Strain	**Variant 1**	**Variant 2**	**Variant 3**	**Variant 4**	**Variant 5**	**Variant 6**	**Variant 7**
S	T	C	T	A	C	C	T
WKY	T	C	T	A	C	C	T
R	T	C	C	A	T	C	T
SHR	T	C	C	A	T	C	T
MHS	T	C	C	A	T	C	T
LH	T	C	C	A	T	C	T
LN	T	C	C	A	T	C	T
LL	T	C	C	A	T	C	T
ACI	C	T	C	G	C	C	T
DA	C	T	C	G	C	C	T
COP	C	T	C	G	C	C	T
LEW	C	T	T	G	C	T	A
SBH	C	T	T	G	C	T	A
SBN	C	T	T	G	C	T	A
MNS	C	T	T	G	C	T	A
F344	C	T	T	G	C	T	A
AS	C	T	T	G	C	T	A
BN	C	T	T	G	C	T	A
LOU	C	T	T	G	C	T	A
MWF	C	T	T	G	C	T	A
SJH	C	T	T	G	C	T	A

Supplementary Table 3

Sl. No.	Probe Set ID	Mean log2 (congenic/S)	mean ratio value (congenics/S)	10%FDR	5%FDR	1%FDR	Transcript ID(Array Design)	Representative Public ID	UniGene ID	Gene Title
1	1379814_at	-1.865192531	0.27448657	yes	yes	yes	Rn.14694.1	AW532796	Rn.14694	CDNA clone IMAGE:7302159
2	1384795_at	-1.7800947	0.291164284	yes	yes	yes	Rn.52640.1	BE116205	Rn.15272	zinc finger, matrin-like (predicted)
3	1394721_at	-1.444990892	0.367294477	yes	yes	yes	Rn.62145.1	BF412697	---	---
4	1375816_at	-1.28974493	0.409023339	yes	yes	yes	Rn.73087.1	BI296706	Rn.32209	Similar to RIKEN cDNA 3110009E18
5	1394011_at	-1.267388511	0.415411047	yes	yes	yes	Rn.28442.2	BF543825	Rn.28442	Bardet-Biedl syndrome 7 (predicted)
6	1393224_at	-1.264467607	0.416252948	yes	yes	yes	Rn.43191.1	AW529774	Rn.87954	Transcribed locus
7	1397889_at	-1.233633359	0.425245136	yes	yes	yes	Rn.26698.1	BF402043	Rn.26698	Transcribed locus
8	1378123_x_at	-1.224360454	0.427987197	yes	yes	yes	Rn.23192.1	BI285319	---	---
9	1382422_at	-1.187719193	0.438996337	yes	yes	yes	Rn.9621.1	AA956340	Rn.15509	Transcribed locus, strongly similar to NP_115833.1 protocadherin 7 isoform c precursor; brain-heart protocadherin; protocadherin 7 [Homo sapiens]
10	1384267_at	-1.169235005	0.444657059	yes	yes	yes	Rn.20898.2	BF547003	Rn.124214	Transcribed locus
11	1382703_at	-1.168473807	0.444891732	yes	yes	yes	Rn.21696.1	BE099893	Rn.21696	Transcribed locus
12	1382675_at	-1.165947684	0.445671409	yes	yes	yes	Rn.23958.1	AA818193	---	---
13	1396250_at	-1.165732923	0.445737757	yes	yes	yes	Rn.72712.1	BF558291	Rn.45957	Similar to Coronin, actin binding protein 1C
14	1369120_a_at	-1.142093839	0.453101497	yes	yes	yes	Rn.10108.1	NM_012858	Rn.10108	luteinizing hormone beta
15	1371400_at	-1.117185772	0.460992194	yes	yes	yes	Rn.81140.2	AI169092	Rn.81140	thyroid hormone responsive protein
16	1378121_at	-1.11474992	0.461771193	yes	yes	yes	Rn.40525.1	AI600165	---	---
17	1376704_a_at	-1.113224376	0.46225974	yes	yes	yes	Rn.9406.1	BM390112	Rn.9406	necdin-like 2 (predicted)
18	1385407_at	-1.109185226	0.463555754	yes	yes	yes	Rn.73941.1	AI511405	Rn.24217	TCDD-inducible poly(ADP-ribose) polymerase (predicted)
19	1376659_at	-1.106728228	0.464345891	yes	yes	yes	Rn.13455.1	BF282469	Rn.13455	similar to hypothetical protein FLJ12660 (predicted)
20	1392872_at	-1.091536684	0.469261276	yes	yes	yes	Rn.58816.1	BF397413	---	---
21	1382789_at	-1.088643623	0.470203237	yes	yes	yes	Rn.64949.1	BM389812	Rn.64949	Transcribed locus
22	1388210_at	-1.077093379	0.473982803	yes	yes	yes	Rn.37524.1	Y09333	Rn.37524	mitochondrial acyl-CoA thioesterase 1

23	1370523_a_at	-1.067663541	0.477091027	yes	yes	yes	Rn.7390.2	AW142720	Rn.7390	ubiquitin-conjugating enzyme E2D 2
24	1394330_at	-1.061852394	0.479016616	yes	yes	yes	Rn.63834.1	BF544149	---	hypothetical protein LOC361915 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRGT00191 /// similar to LRRGT00191 /// similar to LRRGT00174 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRGT00150 /// similar to LRRGT00108 /// similar to LRRGT00014 /// similar to LRRGT00108 /// hypothetical protein LOC501130 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRG00135 /// similar to LRRG00135
25	1392317_at	-1.05918588	0.479902795	yes	yes	yes	Rn.75007.1	BI288026	Rn.75007	Transcribed locus
26	1386215_at	-1.054454876	0.481479115	yes	yes	yes	Rn.42465.1	AI101566	Rn.54975	geranylgeranyl diphosphate synthase 1
27	1393780_at	-1.040194317	0.486261975	yes	yes	yes	Rn.15308.1	AA924380	Rn.92641	zinc finger protein 131 (predicted)
28	1379602_at	-1.029745609	0.489796507	yes	yes	yes	Rn.17520.1	AI010055	---	---
29	1383946_at	-1.029306776	0.489945514	yes	yes	yes	Rn.27475.1	AI137640	Rn.24293	claudin 1
30	1375789_at	-1.023286809	0.491994192	yes	yes	yes	Rn.48025.3	BE100627	Rn.48025	Parathyroid hormone receptor 1
31	1375054_at	-1.022998816	0.492092415	yes	yes	yes	Rn.18197.1	AI233709	Rn.18197	Transcribed locus
32	1396539_at	-1.021996574	0.492434391	yes	yes	yes	Rn.53173.1	BE119221	Rn.6401	Actinin, alpha 1
33	1368271_a_at	-1.019012609	0.49345396	yes	yes	yes	Rn.4258.1	NM_053365	Rn.4258	fatty acid binding protein 4, adipocyte
34	1384361_at	-1.012330506	0.495744783	yes	yes	yes	Rn.81044.1	BF555523	Rn.103382	mal, T-cell differentiation protein 2
35	1382913_at	-1.003159845	0.498906079	yes	yes	yes	Rn.16244.1	BE114076	Rn.16244	cortactin binding protein 2
36	1383338_at	-1.002128823	0.49926275	yes	yes	yes	Rn.2822.1	AA875190	Rn.146915	Transcribed locus
37	1379116_at	-1.001838802	0.499363126	yes	yes	yes	Rn.51176.1	BM386353	Rn.102143	Developmentally regulated GTP binding protein 1 (predicted)
38	1392223_at	-1.000094298	0.49996732	yes	yes	yes	Rn.31647.1	AW521110	Rn.44273	Epsin 2
39	1384110_at	-0.998911345	0.500377442	yes	yes	yes	Rn.18309.1	AI045668	Rn.43956	similar to mKIAA0716 protein
40	1395782_at	-0.994586323	0.501879762	yes	yes	yes	Rn.13918.2	AW921463	Rn.103329	similar to glioma-amplified sequence-41 (predicted)
41	1390403_at	-0.982210652	0.506203486	yes	yes	yes	Rn.23416.1	BE108405	Rn.23416	similar to CG8312-PA (predicted)

42	1395962_at	-0.981978347	0.506285002	yes	yes	yes	Rn.51996.1	BI278960	---	---
43	1384260_at	-0.98030723	0.506871787	yes	yes	yes	Rn.20452.1	BE095699	Rn.146401	Transcribed locus
44	1397596_at	-0.978226157	0.507603472	yes	yes	yes	Rn.60320.1	H31511	Rn.16973	Transcribed locus, strongly similar to NP_032717.1 neurofilament 3, medium [Mus musculus]
45	1377531_at	-0.969533285	0.510671239	yes	yes	yes	Rn.60793.1	BF405592	Rn.60793	Transcribed locus
46	1375740_at	-0.966552601	0.511727404	yes	yes	yes	Rn.66309.1	BI296565	Rn.82734	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
47	1396863_at	-0.962263209	0.513251125	yes	yes	yes	Rn.48417.1	AW535061	Rn.48417	Similar to SPRY domain-containing SOCS box 4
48	1383824_at	-0.956246515	0.515396085	yes	yes	yes	Rn.7998.1	AI029445	Rn.94720	LIM domain binding 2 (predicted)
49	1393168_at	-0.955874682	0.515528938	yes	yes	yes	Rn.17921.1	BF398450	Rn.17921	Similar to Mbt domain containing 1
50	1386594_at	-0.953128398	0.516511223	yes	yes	yes	Rn.39317.3	BF558518	Rn.146599	Transcribed locus
51	1393652_at	-0.948302575	0.518241849	yes	yes	yes	Rn.59075.1	BF398438	Rn.127194	zinc finger and BTB domain containing 1
52	1383153_at	-0.940741259	0.520965139	yes	yes	yes	Rn.23647.1	AI555284	Rn.23647	Transcribed locus
53	1374786_at	-0.94013736	0.521183256	yes	yes	yes	Rn.67003.1	BI298817	Rn.50685	Cytotoxic granule-associated RNA binding protein 1 (predicted)
54	1377503_at	-0.939732967	0.521329366	yes	yes	yes	Rn.45186.1	BG371773	Rn.137079	RIO kinase 2 (yeast) (predicted)
55	1395896_at	-0.93815354	0.521900417	yes	yes	yes	Rn.37245.1	AI233009	Rn.12373	Transcribed locus
56	1378434_at	-0.930587621	0.524644606	yes	yes	yes	Rn.26737.1	BF400808	Rn.26737	Transcribed locus
57	1368527_at	-0.926657623	0.526075722	yes	yes	yes	Rn.44369.1	U03389	Rn.44369	prostaglandin-endoperoxide synthase 2
58	1395821_at	-0.921185675	0.528074845	yes	yes	yes	Rn.82160.1	BF524120	Rn.7308	core binding factor beta
59	1382286_at	-0.921172902	0.52807952	yes	yes	yes	Rn.12060.1	AA965275	Rn.43847	Similar to RIKEN cDNA 2610318K02 (predicted)
60	1385999_at	-0.919613565	0.528650604	yes	yes	yes	Rn.81249.1	AA849923	Rn.8153	YME1-like 1 (S. cerevisiae)
61	1396291_at	-0.916071313	0.529950195	yes	yes	yes	Rn.57488.1	BI290733	Rn.141203	Transcribed locus
62	1375314_at	-0.914543986	0.530511531	yes	yes	yes	Rn.35445.1	BF283490	Rn.7641	similar to Breast carcinoma amplified sequence 3 homolog (K20D4)
63	1378620_at	-0.912688153	0.531194402	yes	yes	yes	Rn.46275.1	BE104164	Rn.87834	Transcribed locus
64	1376892_at	-0.911887274	0.531489364	yes	yes	yes	Rn.13679.1	AI102061	Rn.13679	CDNA clone IMAGE:7313785
65	1389179_at	-0.911301705	0.531705131	yes	yes	yes	Rn.8171.1	BF284899	Rn.8171	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)

66	1390534_at	-0.910485965	0.532005857	yes	yes	yes	Rn.8034.1	BG374727	Rn.127947	Transcribed locus, strongly similar to XP_520066.1 PREDICTED: similar to SMC5 protein [Pan troglodytes]
67	1397957_at	-0.906263366	0.533565257	yes	yes	yes	Rn.73491.1	AA955460	Rn.73491	Transcribed locus
68	1370407_at	-0.902452394	0.534976567	yes	yes	yes	Rn.34505.1	AF332142	Rn.34505	chloride ion pump-associated 55 kDa protein
69	1397334_at	-0.90011399	0.535844392	yes	yes	yes	Rn.63663.1	BM385096	Rn.101656	Similar to SEC14-like 1
70	1391795_at	-0.898912337	0.536290894	yes	yes	yes	Rn.44937.1	AW535137	Rn.147793	Transcribed locus
71	1393708_at	-0.8983065	0.536516148	yes	yes	yes	Rn.52565.1	BE115766	Rn.21655	basic helix-loop-helix domain containing, class B5 (predicted)
72	1381434_s_at	-0.897093284	0.536967515	yes	yes	yes	Rn.44696.1	AW253721	Rn.145062	similar to nidogen 2
73	1386156_at	-0.895990903	0.537377975	yes	yes	yes	Rn.43703.1	AI639451	Rn.94023	thyroid hormone receptor associated protein 1 (predicted)
74	1385185_at	-0.895228588	0.537661998	yes	yes	yes	Rn.75369.1	BF388679	Rn.149253	Transcribed locus
75	1370034_at	-0.89363374	0.538256693	yes	yes	yes	Rn.11312.1	NM_133572	Rn.11312	cell division cycle 25 homolog B (S. cerevisiae)
76	1369696_at	-0.893004506	0.538491506	yes	yes	yes	Rn.11259.1	NM_053972	Rn.11259	Ras-related GTP binding B
77	1397335_at	-0.890080491	0.539584013	yes	yes	yes	Rn.47891.1	AW532165	Rn.147480	Transcribed locus
78	1392809_at	-0.889085859	0.539956145	yes	yes	yes	Rn.21763.1	AI072437	Rn.147170	Transcribed locus
79	1388077_a_at	-0.887621351	0.540504543	yes	yes	yes	Rn.10388.2	AF084975	Rn.10388	purinergic receptor P2X, ligand-gated ion channel, 3
80	1382263_at	-0.884745827	0.54158293	yes	yes	yes	Rn.34668.1	AI511280	Rn.139568	similar to DNA segment, Chr 3, ERATO Doi 250, expressed (predicted)
81	1385967_at	-0.88405401	0.541842698	yes	yes	yes	Rn.64471.3	BF389767	Rn.137783	Similar to nuclear prelamin A recognition factor isoform a (predicted)
82	1377728_at	-0.881906741	0.542649763	yes	yes	yes	Rn.29800.1	BI280802	Rn.145579	LOC499567
83	1368726_a_at	-0.878407826	0.543967429	yes	yes	yes	Rn.77686.2	AB047638	---	gonadotropin inducible ovarian transcription factor 2
84	1395139_at	-0.87761995	0.544264578	yes	yes	yes	Rn.82150.1	BM388214	Rn.7029	Kinesin family member 16B (predicted)
85	1384214_a_at	-0.873637465	0.545769068	yes	yes	yes	Rn.16225.1	AI045459	Rn.16225	Transcribed locus
86	1397045_at	-0.873336909	0.545882779	yes	yes	yes	Rn.62979.1	BF416297	---	---
87	1392042_at	-0.872877374	0.546056685	yes	yes	yes	Rn.62511.1	AI146029	Rn.98676	zinc finger protein 213 (predicted)
88	1370510_a_at	-0.869142748	0.547472063	yes	yes	yes	Rn.14532.1	AB012600	Rn.14532	aryl hydrocarbon receptor nuclear translocator-like

89	1393499_at	-0.868111172	0.547863664	yes	yes	yes	Rn.12063.1	AA964375	Rn.44193	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide
90	1382319_at	-0.867961029	0.547920684	yes	yes	yes	Rn.16653.1	BM389005	Rn.16653	G protein-coupled receptor 68 (predicted)
91	1395079_at	-0.861041072	0.550555125	yes	yes	yes	Rn.54762.1	AI454784	Rn.35112	Rho-related BTB domain containing 2 (predicted)
92	1398683_at	-0.852275487	0.553910393	yes	yes	yes	Rn.27126.3	BF553446	Rn.22759	similar to replication protein-binding trans-activator RBT1
93	1378931_at	-0.851934908	0.554041171	yes	yes	yes	Rn.45736.1	AW523881	Rn.87751	Transcribed locus
94	1385639_at	-0.851269436	0.554296792	yes	yes	yes	Rn.19029.2	AI058950	---	---
95	1393187_at	-0.850914481	0.554433186	yes	yes	yes	Rn.19349.1	BF417625	Rn.141231	Similar to Ifi204 protein
96	1390820_at	-0.847235867	0.555848695	yes	yes	yes	Rn.15558.1	BE108198	Rn.15558	zinc finger, CCHC domain containing 11 (predicted)
97	1385741_at	-0.844752544	0.556806306	yes	yes	yes	Rn.54308.2	BF566724	Rn.50425	similar to RIKEN cDNA 1700052N19 (predicted)
98	1394943_at	-0.843265899	0.557380371	yes	yes	yes	Rn.30141.1	AA893197	---	---
99	1367985_at	-0.84223852	0.557777437	yes	yes	yes	Rn.32517.1	NM_013197	Rn.32517	aminolevulinic acid synthase 2
100	1395551_at	-0.84004296	0.558626934	yes	yes	yes	Rn.76806.1	BG671371	Rn.100818	Similar to novel protein
101	1378058_at	-0.836956933	0.559823156	yes	yes	yes	Rn.23771.1	AI137429	Rn.98476	Double-stranded RNA-binding protein p74
102	1382989_at	-0.835299676	0.560466607	yes	yes	yes	Rn.52642.1	BE116242	---	---
103	1398273_at	-0.832823285	0.561429476	yes	yes	yes	Rn.8427.1	NM_053599	Rn.8427	ephrin A1
104	1375288_at	-0.831447803	0.561965004	yes	yes	yes	Rn.73053.1	BI299737	Rn.98494	GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)
105	1392613_at	-0.830872584	0.562189111	yes	yes	yes	Rn.22057.1	AA942745	Rn.149118	Transcribed locus
106	1382252_at	-0.82532676	0.564354366	yes	yes	yes	Rn.9295.1	BE099808	Rn.9295	Transcribed locus
107	1381324_at	-0.821822745	0.565726735	yes	yes	yes	Rn.68162.1	BM387030	Rn.146423	Transcribed locus
108	1379206_at	-0.820418587	0.566277618	yes	yes	yes	Rn.61676.1	BF410357	Rn.66154	similar to RIKEN cDNA 1110001E17 (predicted)
109	1396018_at	-0.818733312	0.566939498	yes	yes	yes	Rn.63157.1	BF416830	Rn.48797	Cullin 5
110	1379878_at	-0.817579092	0.567393256	yes	yes	yes	Rn.48230.1	AW533998	Rn.48230	Transcribed locus
111	1392617_at	-0.817364132	0.567477803	yes	yes	yes	Rn.64902.1	BI289715	Rn.118720	similar to hypothetical protein DKFZp761D0211 (predicted)
112	1392602_at	-0.817145105	0.567563963	yes	yes	yes	Rn.24675.1	BF290959	Rn.24675	CDC14 cell division cycle 14 homolog B (S. cerevisiae) (predicted)
113	1375067_at	-0.814004335	0.568800905	yes	yes	yes	Rn.35308.1	AI555354	Rn.20804	Transcribed locus
114	1383396_at	-0.812694217	0.56931767	yes	yes	yes	Rn.14851.1	AA894079	Rn.100627	fibronectin type III domain containing 3 (predicted)
115	1380849_at	-0.805434114	0.572189879	yes	yes	yes	Rn.69776.1	BI274299	Rn.140324	Similar to Poliovirus receptor-related 1
116	1370328_at	-0.804329719	0.572628064	yes	yes	yes	Rn.12516.1	AF245040	Rn.12516	Dickkopf homolog 3 (Xenopus laevis)

117	1374605_at	-0.804019286	0.572751293	yes	yes	yes	Rn.17269.1	AA818020	Rn.20164	similar to hypothetical protein MGC33214 (predicted)
118	1395215_at	-0.802854036	0.573214085	yes	yes	yes	Rn.60538.1	BF404567	Rn.148774	Transcribed locus
119	1373188_at	-0.802398377	0.573395156	yes	yes	yes	Rn.22230.1	AI137995	Rn.22230	sodium channel, voltage-gated, type IV, beta
120	1386911_at	-0.802176537	0.573483333	yes	yes	yes	Rn.1042.1	NM_012505	Rn.1042	ATPase, Na+/K+ transporting, alpha 2 polypeptide
121	1396755_at	-0.799902204	0.574388112	yes	yes	yes	Rn.48489.1	BF399394	Rn.140447	Transcribed locus
122	1385248_a_at	-0.79565184	0.576082828	yes	yes	yes	Rn.12119.3	AA997590	Rn.103114	osteoglycin (predicted)
123	1385261_s_at	-0.795405825	0.576181073	yes	yes	yes	Rn.50467.1	BE103057	Rn.125849	Transcribed locus
124	1393796_at	-0.79399197	0.576746013	yes	yes	yes	Rn.66357.1	BG375986	Rn.24594	similar to KIAA0912 protein (predicted)
125	1385728_at	-0.79189749	0.577583931	yes	yes	yes	Rn.51376.1	BE108006	Rn.1477	AE binding protein 2 (predicted)
126	1387371_at	-0.790934841	0.577969457	yes	yes	yes	Rn.11390.1	NM_133571	Rn.11390	cell division cycle 25 homolog A (S. cerevisiae)
127	1382715_at	-0.79022064	0.578255649	yes	yes	yes	Rn.16699.1	AA818382	Rn.7255	Deleted in liver cancer 1
128	1381644_at	-0.786185939	0.579875086	yes	yes	yes	Rn.49327.1	BE121056	Rn.17699	Transcribed locus
129	1394540_at	-0.784829383	0.580420595	yes	yes	yes	Rn.62750.1	BF387197	---	---
130	1374290_at	-0.782869728	0.581209533	yes	yes	yes	Rn.14810.1	AI408191	Rn.14810	Transcribed locus
131	1386252_at	-0.77939376	0.582611563	yes	yes	yes	Rn.54041.1	BE349825	Rn.54041	Transcribed locus
132	1385732_at	-0.777878379	0.583223849	yes	yes	yes	Rn.52556.1	BE115744	Rn.52556	Transcribed locus
133	1376390_at	-0.776757609	0.583677108	yes	yes	yes	Rn.12199.1	BF395317	Rn.101878	membrane-spanning 4-domains, subfamily A, member 11 (predicted)
134	1384956_at	-0.773914207	0.584828609	yes	yes	yes	Rn.39067.1	AI556490	Rn.41374	Similar to BC021442 protein
135	1379576_at	-0.768646534	0.586967881	yes	yes	yes	Rn.23764.1	AA848479	---	---
136	1385923_at	-0.765618939	0.588200967	yes	yes	yes	Rn.22987.1	AA944139	Rn.22987	Transcribed locus
137	1378365_at	-0.764785718	0.588540778	yes	yes	yes	Rn.41289.1	AW529483	Rn.138007	Transcribed locus
138	1376317_at	-0.762936697	0.58929556	yes	yes	yes	Rn.41300.1	BI282917	---	---
139	1387796_at	-0.762499966	0.589473978	yes	yes	yes	Rn.11318.1	NM_031010	Rn.11318	arachidonate 12-lipoxygenase
140	1397005_at	-0.760927405	0.590116865	yes	yes	yes	Rn.58160.1	BF393900	Rn.100042	Similar to RIKEN cDNA D130074J02 gene (predicted)
141	1393750_at	-0.760179825	0.590422733	yes	yes	yes	Rn.77445.1	BI303408	Rn.126080	Transcribed locus
142	1373433_at	-0.759401335	0.590741416	yes	yes	yes	Rn.6393.1	BE108745	Rn.6393	nucleosome binding protein 1 (predicted) /// similar to Nucleosome binding protein 1
143	1378117_at	-0.758968335	0.590918743	yes	yes	yes	Rn.64470.1	BF396269	Rn.153226	Transcribed locus
144	1381115_at	-0.757032816	0.591712051	yes	yes	yes	Rn.50794.1	AW536039	---	---
145	1393237_at	-0.756502396	0.59192964	yes	yes	yes	Rn.38101.1	AI577833	Rn.28553	Transcribed locus
146	1379474_at	-0.755132224	0.592492081	yes	yes	yes	Rn.46242.1	AW526574	Rn.11257	Early B-cell factor 1

147	1379412_at	-0.755058561	0.592522334	yes	yes	yes	Rn.25149.1	BF559875	Rn.25149	Transcribed locus
148	1385268_at	-0.754026394	0.592946402	yes	yes	yes	Rn.79004.1	BI289167	Rn.79004	hypothetical protein LOC304743
149	1368790_at	-0.753638568	0.593105819	yes	yes	yes	Rn.10502.1	NM_133617	Rn.10502	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10
150	1385401_at	-0.752672985	0.593502913	yes	yes	yes	Rn.79144.1	BI290381	---	---
151	1382201_at	-0.751469287	0.593998302	yes	yes	yes	Rn.8105.1	AA926250	Rn.47255	unc-5 homolog C (C. elegans)
152	1389290_at	-0.751196858	0.59411048	yes	yes	yes	Rn.8642.1	AI172034	Rn.8642	DnaJ (Hsp40) homolog, subfamily C, member 10 (predicted)
153	1390456_at	-0.749296235	0.594893684	yes	yes	yes	Rn.46564.1	AW524471	Rn.49278	Transcribed locus
154	1379727_at	-0.746008064	0.596251103	yes	yes	yes	Rn.24864.1	AI598320	Rn.11607	Bromodomain adjacent to zinc finger domain, 2A (predicted)
155	1393140_at	-0.745898992	0.596296183	yes	yes	yes	Rn.64897.1	AI574699	---	---
156	1377463_at	-0.745251291	0.596563952	yes	yes	yes	Rn.27085.1	BE099244	Rn.41796	Mannosidase 2, alpha 2 (predicted)
157	1398164_at	-0.742651958	0.597639762	yes	yes	yes	Rn.60917.1	BF406182	Rn.99617	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (predicted)
158	1398039_at	-0.74059586	0.598492113	yes	yes	yes	Rn.49878.1	BE110002	Rn.49878	Transcribed locus
159	1379544_at	-0.737638544	0.599720193	yes	yes	yes	Rn.44004.1	AI146108	Rn.147930	Transcribed locus
160	1374645_at	-0.736889363	0.600031704	yes	yes	yes	Rn.23413.1	AW535233	Rn.23413	Transcribed locus
161	1392875_at	-0.736627036	0.600140819	yes	yes	yes	Rn.11714.1	AA964134	Rn.12566	F-box and leucine-rich repeat protein 4 (predicted)
162	1382236_at	-0.735806328	0.600482319	yes	yes	yes	Rn.11480.1	BI288538	Rn.13205	Similar to hypothetical protein FLJ20272 (predicted)
163	1383326_a_at	-0.733215308	0.601561729	yes	yes	yes	Rn.39116.2	AI576297	Rn.122017	programmed cell death 4
164	1398122_at	-0.733124157	0.601599738	yes	yes	yes	Rn.47462.1	AW534158	Rn.20579	5'-nucleotidase, cytosolic II-like 1 (predicted)
165	1384542_at	-0.732510787	0.601855566	yes	yes	yes	Rn.6509.1	BE103021	Rn.153693	Transcribed locus
166	1388418_at	-0.732372971	0.601913062	yes	yes	yes	Rn.264.1	BG378875	Rn.264	Transcribed locus
167	1397283_at	-0.7319544	0.602087721	yes	yes	yes	Rn.55652.1	AI176618	Rn.14154	Transcribed locus
168	1384026_at	-0.729660503	0.603045807	yes	yes	yes	Rn.11612.1	AI070446	Rn.11612	Hypothetical protein LK44
169	1391738_at	-0.727062687	0.604132671	yes	yes	yes	Rn.56984.1	BF389673	Rn.148724	Transcribed locus
170	1397194_at	-0.723858715	0.605475834	yes	yes	yes	Rn.55320.1	BE119170	Rn.12542	similar to CG5554-PA (predicted)
171	1379424_at	-0.723603015	0.605583157	yes	yes	yes	Rn.43966.1	BE115825	Rn.43966	Similar to DKFZP434B168 protein (predicted)
172	1390900_at	-0.723009292	0.605832428	yes	yes	yes	Rn.43563.1	BI290628	Rn.147765	Transcribed locus

173	1379029_at	-0.722953748	0.605855753	yes	yes	yes	Rn.61329.1	BI284478	Rn.61329	Similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3)
174	1390981_at	-0.721629537	0.606412107	yes	yes	yes	Rn.18114.1	AI028965	Rn.3365	Polycystic kidney and hepatic disease 1-like 1 (predicted)
175	1377705_at	-0.721268105	0.606564048	yes	yes	yes	Rn.25559.1	BF549971	---	---
176	1395147_at	-0.720539069	0.60687064	yes	yes	yes	Rn.52695.1	BE116565	Rn.44012	Excision repair cross-complementing rodent repair deficiency, complementation group 3 (predicted)
177	1392548_at	-0.719727523	0.607212113	yes	yes	yes	Rn.51454.1	BF394282	---	similar to mKIAA1604 protein
178	1382025_at	-0.716841264	0.60842812	yes	yes	yes	Rn.23921.1	BG668084	Rn.23921	X-linked myotubular myopathy gene 1 (predicted)
179	1383579_at	-0.715967077	0.608796902	yes	yes	yes	Rn.12938.1	BE109121	Rn.12938	Similar to IKEN cDNA 6720480D16
180	1379238_at	-0.715679837	0.608918125	yes	yes	yes	Rn.52064.1	BE112261	---	---
181	1395063_at	-0.714846647	0.609269892	yes	yes	yes	Rn.35669.1	AA851300	Rn.149188	Transcribed locus
182	1386833_at	-0.71484187	0.609271909	yes	yes	yes	Rn.20865.2	BF554138	Rn.137148	Transcribed locus, strongly similar to XP_340831.2 PREDICTED: similar to BAZF [Rattus norvegicus]
183	1385837_at	-0.713843698	0.609693598	yes	yes	yes	Rn.9043.1	AA956624	Rn.100101	homeo box D3
184	1394420_at	-0.712181634	0.610396403	yes	yes	yes	Rn.55409.1	BF287027	Rn.91765	Transcribed locus
185	1383921_at	-0.710547178	0.611088324	yes	yes	yes	Rn.49250.1	AW916957	Rn.113924	Transcribed locus, strongly similar to XP_579758.1 PREDICTED: hypothetical protein XP_579758 [Rattus norvegicus]
186	1382578_at	-0.707943847	0.612192024	yes	yes	yes	Rn.29185.1	AI178173	Rn.89365	Transcribed locus
187	1397486_x_at	-0.7078171	0.61224581	yes	yes	yes	Rn.60538.1	BF404567	Rn.148774	Transcribed locus
188	1372660_at	-0.707016403	0.612585701	yes	yes	yes	Rn.9430.1	AI180420	Rn.99777	tubulin, gamma complex associated protein 3 (predicted)
189	1383055_at	-0.704627962	0.613600702	yes	yes	yes	Rn.22817.1	AW143805	Rn.22817	Guanine nucleotide binding protein, alpha q polypeptide
190	1370588_a_at	-0.704551886	0.613633059	yes	yes	yes	Rn.10419.1	U04933	Rn.118972	solute carrier family 8 (sodium/calcium exchanger), member 1
191	1395082_at	-0.704417193	0.613690352	yes	yes	yes	Rn.41662.1	AI763982	Rn.31840	Transcribed locus
192	1380311_at	-0.704343436	0.613721727	yes	yes	yes	Rn.34848.1	AI535528	Rn.51134	Protein phosphatase 1, regulatory (inhibitor) subunit 12A

193	1387054_at	-0.702178314	0.61464346	yes	yes	yes	Rn.8398.1	AI712719	Rn.8398	ATP-binding cassette, sub-family G (WHITE), member 1
194	1380969_at	-0.699698232	0.615700979	yes	yes	yes	Rn.58038.1	BE106363	Rn.106130	Similar to mKIAA0940 protein
195	1386261_x_at	-0.69967998	0.615708769	yes	yes	yes	Rn.22360.2	AI406385	Rn.81070	caveolin 2
196	1395372_at	-0.699589497	0.615747386	yes	yes	yes	Rn.72676.1	BG668993	Rn.72676	Transcribed locus
197	1377855_at	-0.698240248	0.616323519	yes	yes	yes	Rn.18672.1	BE111774	Rn.141032	similar to RIKEN cDNA 4921537D05
198	1385697_at	-0.69803979	0.616409162	yes	yes	yes	Rn.21407.3	BI302799	Rn.21407	Cyclin T2 (predicted)
199	1381814_at	-0.698012286	0.616420913	yes	yes	yes	Rn.15837.1	AI044216	Rn.72217	similar to KIAA0456 protein
200	1369864_a_at	-0.695122254	0.617656976	yes	yes	yes	Rn.9918.1	NM_053962	Rn.9918	serine dehydratase
201	1379594_at	-0.694522758	0.61791369	yes	yes	yes	Rn.42056.1	AW524408	Rn.93081	Transcribed locus, moderately similar to NP_080479.1 jouberin [Mus musculus]
202	1376425_at	-0.694519167	0.617915228	yes	yes	yes	Rn.28189.1	BF420705	Rn.24539	Transforming growth factor, beta 2
203	1397030_at	-0.693292353	0.618440903	yes	yes	yes	Rn.43776.1	AI406451	---	---
204	1368321_at	-0.692991	0.618570098	yes	yes	yes	Rn.9096.1	NM_012551	Rn.9096	early growth response 1
205	1396171_at	-0.692639304	0.61872091	yes	yes	yes	Rn.79868.1	BF552272	Rn.21237	peptidylprolyl isomerase (cyclophilin)-like 4 (predicted)
206	1381058_at	-0.690732274	0.619539308	yes	yes	yes	Rn.18180.1	AI548492	Rn.18180	Transcribed locus
207	1372180_at	-0.690706118	0.619550541	yes	yes	yes	Rn.11695.1	AI112985	Rn.10504	Syndecan 3
208	1385455_at	-0.689954811	0.619873266	yes	yes	yes	Rn.70810.1	BF397666	Rn.7210	similar to sarcoma antigen NY-SAR-27
209	1381902_at	-0.688927153	0.62031497	yes	yes	yes	Rn.50125.1	BE116321	Rn.106753	Zinc finger protein 292
210	1376218_a_at	-0.685281198	0.621884602	yes	yes	yes	Rn.24221.1	BI273855	Rn.20321	Atpase, class I, type 8B, member 2 (predicted)
211	1385986_at	-0.684131785	0.622380263	yes	yes	yes	Rn.57431.1	BF391203	Rn.57431	Transcribed locus
212	1384940_at	-0.683337782	0.622722891	yes	yes	yes	Rn.27199.1	AI136655	Rn.107229	similar to KIAA0335 (predicted)
213	1379881_at	-0.683191937	0.622785846	yes	yes	yes	Rn.13102.1	BI304043	Rn.119489	Transcribed locus, weakly similar to XP_125803.1 PREDICTED: hypothetical protein XP_125803 [Mus musculus]
214	1379153_at	-0.682668171	0.623011988	yes	yes	yes	Rn.63297.1	BF387484	Rn.57349	Similar to microfilament and actin filament cross-linker protein isoform a
215	1394992_at	-0.682632612	0.623027344	yes	yes	yes	Rn.57039.1	BF389891	Rn.57039	Transcribed locus
216	1392013_at	-0.682490891	0.623088549	yes	yes	yes	Rn.16756.1	AA819397	Rn.16756	DEP domain containing 2 (predicted)
217	1393322_at	-0.681337335	0.62358696	yes	yes	yes	Rn.39084.1	AI556910	Rn.72554	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)

218	1396939_at	-0.681194468	0.623648716	yes	yes	yes	Rn.28527.1	AI145547	Rn.146144	Transcribed locus
219	1397163_s_at	-0.680608527	0.623902058	yes	yes	yes	Rn.81244.1	BM392082	Rn.53471	Kinesin family member 9 (predicted)
220	1389664_at	-0.678504637	0.624812561	yes	yes	yes	Rn.22965.1	BM387379	Rn.49608	similar to hypothetical protein (predicted)
221	1377501_at	-0.676394223	0.625727223	yes	yes	yes	Rn.57387.1	BM383704	Rn.96156	similar to zinc finger protein 75
222	1378701_at	-0.675817641	0.625977349	yes	yes	yes	Rn.59798.1	BF401392	---	---
223	1370335_at	-0.674756697	0.626437856	yes	yes	yes	Rn.14323.1	AF236130	Rn.14323	disabled homolog 2 (Drosophila) interacting protein
224	1376983_at	-0.673590689	0.626944357	yes	yes	yes	Rn.9420.1	BF417687	---	---
225	1397209_at	-0.672940606	0.627226924	yes	yes	yes	Rn.48947.1	BE107268	---	---
226	1382902_at	-0.671012998	0.628065532	yes	yes	yes	Rn.7512.1	AA943147	Rn.107120	potential ubiquitin ligase
227	1390927_at	-0.668540574	0.629142805	yes	yes	yes	Rn.15642.1	AI176779	Rn.15642	Yes-associated protein (predicted)
228	1390525_a_at	-0.668500789	0.629160155	yes	yes	yes	Rn.12735.1	BI284420	Rn.12735	similar to retinoic acid-responsive protein; STRA6 (predicted)
229	1382125_at	-0.668161587	0.629308098	yes	yes	yes	Rn.8581.1	AI072976	---	---
230	1374500_at	-0.667869424	0.629435553	yes	yes	yes	Rn.7210.1	AI011571	Rn.7210	similar to sarcoma antigen NY-SAR-27
231	1374914_at	-0.667826234	0.629454397	yes	yes	yes	Rn.8864.1	AI230294	Rn.96181	Peroxisome proliferator activated receptor delta
232	1387374_at	-0.667040986	0.629797097	yes	yes	yes	Rn.9916.1	NM_013176	Rn.9916	transcription factor 12
233	1372469_at	-0.665897332	0.630296549	yes	yes	yes	Rn.7677.1	AI178901	Rn.147526	Transcribed locus
234	1393899_at	-0.66486096	0.63074949	yes	yes	yes	Rn.19493.2	AA901361	Rn.107132	guanosine monophosphate reductase 2
235	1384945_at	-0.663441641	0.631370325	yes	yes	yes	Rn.35357.1	AI501447	Rn.13677	similar to putative 40-2-3 protein (predicted)
236	1382684_at	-0.661355855	0.632283793	yes	yes	yes	Rn.72945.1	BI293639	Rn.148790	Transcribed locus
237	1381413_at	-0.660706331	0.632568521	yes	yes	yes	Rn.21720.1	AI547999	---	---
238	1395899_at	-0.659238008	0.633212654	yes	yes	no	Rn.65904.1	AW921250	---	---
239	1393369_at	-0.657211603	0.634102688	yes	yes	yes	Rn.66255.1	BI300502	Rn.146808	CDKN2A interacting protein
240	1392552_at	-0.656800962	0.634283201	yes	yes	yes	Rn.54954.1	BE109744	Rn.32193	similar to transcription repressor p66 (predicted)
241	1380699_at	-0.654486756	0.635301462	yes	yes	yes	Rn.48240.1	BE110761	Rn.59710	Zinc finger homeobox 1b (predicted)
242	1394828_at	-0.654169486	0.635441189	yes	yes	yes	Rn.37629.1	BF406986	Rn.148547	Transcribed locus
243	1384381_at	-0.65327505	0.63583527	yes	yes	yes	Rn.55270.1	BF284523	Rn.3724	ATP-binding cassette, sub-family A (ABC1), member 1 /// hypothetical gene supported by NM_178095
244	1375953_at	-0.650649612	0.636993426	yes	yes	yes	Rn.40486.1	AI012884	---	---
245	1387588_at	-0.648718115	0.637846811	yes	yes	yes	Affx.1.10	NM_138890	Rn.7771	EH-domain containing 3
246	1389460_at	-0.648612562	0.63789348	yes	yes	yes	Rn.16928.1	AI231787	Rn.16928	Transcribed locus

247	1398231_at	-0.647728207	0.638284621	yes	yes	yes	Rn.51171.1	BE107399	Rn.129584	Transcribed locus
248	1397149_at	-0.647646595	0.638320729	yes	yes	yes	Rn.58463.1	BF395834	Rn.58463	Transcribed locus
249	1374809_at	-0.645477194	0.639281304	yes	yes	yes	Rn.16806.1	BG672598	Rn.16806	Transcribed locus
250	1398355_at	-0.644051026	0.639913574	yes	yes	yes	Rn.20364.2	AI232142	Rn.86991	Similar to transient receptor potential phospholipase C interacting kinase
251	1382476_x_at	-0.643979624	0.639945245	yes	yes	no	Rn.21184.1	AI060133	Rn.79888	Similar to pellino 3 alpha (predicted)
252	1383463_at	-0.643689454	0.640073971	yes	yes	yes	Rn.8969.1	AW918514	Rn.1772	Zinc finger protein 91
253	1382183_at	-0.641426632	0.641078694	yes	yes	yes	Rn.21436.1	AA849479	Rn.21436	Transcribed locus
254	1372308_at	-0.641054401	0.641244121	yes	yes	yes	Rn.8110.1	BM386869	Rn.8110	CDNA clone IMAGE:7366335
255	1376120_at	-0.640693947	0.641404354	yes	yes	no	Rn.9399.1	BG671875	Rn.92162	similar to pancreatitis-induced protein 49 (predicted)
256	1381504_at	-0.639354008	0.642000351	yes	yes	no	Rn.43324.1	AI639412	Rn.45067	similar to asporin precursor
257	1384411_at	-0.639278444	0.642033978	yes	yes	yes	Rn.12168.1	AA962968	Rn.45039	Hypothetical LOC296884
258	1386807_at	-0.638823995	0.642236251	yes	yes	no	Rn.12718.2	BF556985	Rn.134460	wingless-related MMTV integration site 2
259	1389985_at	-0.637482935	0.64283352	yes	yes	yes	Rn.37778.1	BF415238	Rn.9231	similar to Tcfe3 protein
260	1388054_a_at	-0.637160297	0.642977297	yes	yes	no	Rn.35666.1	AF072892	Rn.35666	chondroitin sulfate proteoglycan 2
261	1383795_at	-0.637038635	0.643031521	yes	yes	yes	Rn.22181.3	BF521753	Rn.6374	CDNA clone IMAGE:7379585
262	1385765_at	-0.63609804	0.643450896	yes	yes	yes	Rn.60982.1	BF406563	Rn.35466	similar to lin-9 homolog (C. elegans)
263	1387322_at	-0.635609772	0.643668703	yes	yes	yes	Rn.14540.1	NM_053471	Rn.87343	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B
264	1380811_at	-0.634127214	0.644330497	yes	yes	yes	Rn.50814.1	BE105756	Rn.50814	Transcribed locus
265	1382639_at	-0.633736224	0.644505143	yes	yes	yes	Rn.55951.1	BF290625	Rn.55951	Transcribed locus
266	1368370_at	-0.632713679	0.644962113	yes	yes	yes	Rn.1904.1	NM_019285	Rn.1904	adenylate cyclase 4
267	1397786_at	-0.632612225	0.645007471	yes	yes	yes	Rn.57348.1	BF391927	Rn.41379	Similar to protein phosphatase 1, regulatory subunit 12C
268	1374399_at	-0.631221133	0.645629707	yes	yes	yes	Rn.4145.1	AA801107	Rn.7379	EH-domain containing 4
269	1387184_at	-0.631137601	0.64566709	yes	yes	yes	Rn.14542.1	NM_024355	Rn.14542	axin2
270	1395203_at	-0.631079903	0.645692913	yes	yes	yes	Rn.79192.1	BI290823	Rn.6421	Transcribed locus, moderately similar to XP_225891.2 PREDICTED: similar to hypothetical protein C630049M13 [Rattus norvegicus]
271	1385640_at	-0.631033239	0.645713798	yes	yes	yes	Rn.19195.1	AI059511	---	---
272	1385533_at	-0.629334248	0.646474671	yes	yes	yes	Rn.50882.1	BE106145	Rn.150956	Transcribed locus

273	1383666_at	-0.629184554	0.646541753	yes	yes	yes	Rn.48917.1	BG378435	Rn.34777	LOC362113 (predicted)
274	1396239_at	-0.628791659	0.646717852	yes	yes	yes	Rn.35597.1	AI502035	Rn.148264	Transcribed locus
275	1385956_at	-0.62852165	0.646838901	yes	yes	yes	Rn.25275.2	BF289086	Rn.119429	Transcribed locus
276	1396079_at	-0.626620096	0.647692034	yes	yes	no	Rn.53508.1	BF558358	---	---
277	1394501_at	-0.626391216	0.647794796	yes	yes	no	Rn.29166.1	BM390379	Rn.29166	sialic acid binding Ig-like lectin 10 (predicted)
278	1381875_at	-0.62606542	0.647941101	yes	yes	yes	Rn.18496.1	BM386847	Rn.18496	N-myc (and STAT) interactor (predicted)
279	1398321_a_at	-0.624945688	0.648444188	yes	yes	yes	Rn.11218.2	U57361	Rn.11218	procollagen, type XII, alpha 1
280	1379062_at	-0.624365337	0.64870509	yes	yes	no	Rn.72241.1	BI291230	Rn.135880	similar to Expressed sequence AU019823
281	1391690_at	-0.623348962	0.649162262	yes	yes	no	Rn.23563.1	AI171008	Rn.148568	Transcribed locus
282	1390498_at	-0.622964615	0.649335227	yes	yes	yes	Rn.23623.1	AI230554	Rn.147999	Transcribed locus
283	1395327_at	-0.622366348	0.649604554	yes	yes	yes	Rn.45365.1	AW522341	Rn.3957	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2
284	1383650_at	-0.622308593	0.64963056	yes	yes	no	Rn.3068.1	BI291080	Rn.38109	Transcribed locus
285	AFFX_Rat_Hexokinase_M_at	-0.622300379	0.649634259	yes	yes	no	AFFX_Rat_Hexokinase_M	AFFX_Rat_Hexokinase_M	Rn.11017	hexokinase 1
286	1389253_at	-0.621770331	0.649872979	yes	yes	yes	Rn.16319.1	BI289085	Rn.16319	vanin 1 (predicted)
287	1393371_at	-0.621580862	0.649958332	yes	yes	yes	Rn.66603.1	BG378781	Rn.146270	Transcribed locus
288	1370902_at	-0.621215619	0.650122902	yes	yes	yes	Rn.23676.1	AI233740	Rn.23676	aldo-keto reductase family 1, member B8
289	1392239_at	-0.621037386	0.650203224	yes	yes	yes	Rn.62463.1	BF386993	---	---
290	1373446_at	-0.620995875	0.650221932	yes	yes	yes	Rn.13782.1	AI102512	Rn.13782	PHD finger protein 13 (predicted)
291	1398368_at	-0.62099156	0.650223877	yes	yes	yes	Rn.16640.1	AI406502	Rn.16640	Transcribed locus
292	1391828_at	-0.620577405	0.650410564	yes	yes	yes	Rn.18608.1	AI030836	Rn.18608	Transcribed locus
293	1387337_at	-0.619398657	0.650942197	yes	yes	yes	Rn.10490.1	NM_012835	Rn.10490	cortistatin
294	1384695_at	-0.619396966	0.650942959	yes	yes	yes	Rn.81907.1	BM387108	Rn.81907	uroplakin 3A (predicted)
295	1390868_at	-0.618838498	0.651194989	yes	yes	yes	Rn.40331.1	BF403073	Rn.101917	similar to RIKEN cDNA 1200016B10 (predicted)
296	1385472_at	-0.617038111	0.652008143	yes	yes	no	Rn.11586.1	AA963583	Rn.82564	Zinc finger and BTB domain containing 8 (predicted)
297	1369177_at	-0.616329878	0.652328299	yes	yes	yes	Rn.64407.1	NM_053735	Rn.93583	phosphatidylinositol 4-kinase type 2 alpha
298	1398587_at	-0.615638038	0.652641196	yes	yes	yes	Rn.43360.1	AA860035	Rn.43360	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
299	1386947_at	-0.6147587	0.653039109	yes	yes	yes	Rn.1303.1	NM_031334	Rn.1303	cadherin 1

300	1371039_at	-0.614291361	0.653250686	yes	yes	yes	Rn.9863.1	L02315	Rn.9863	calcium channel, voltage-dependent, beta 4 subunit
301	1390800_a_at	-0.613653363	0.653539634	yes	yes	yes	Rn.22360.1	BE349669	Rn.81070	caveolin 2
302	1368634_at	-0.613193355	0.653748051	yes	yes	no	Rn.30034.1	NM_017108	Rn.144567	potassium voltage-gated channel, subfamily H (eag-related), member 3
303	1385711_at	-0.611750504	0.654402196	yes	yes	yes	Rn.25178.2	AW507178	Rn.25178	similar to RIKEN cDNA 1500031M22 (predicted)
304	1383934_at	-0.611258199	0.654625543	yes	yes	no	Rn.28721.1	BI299169	Rn.153521	Transcribed locus
305	1382826_at	-0.610310452	0.655055726	yes	yes	no	Rn.37167.1	AI230741	Rn.3244	Coatomer protein complex, subunit zeta 1 (predicted)
306	1384418_at	-0.610014196	0.655190255	yes	yes	no	Rn.38166.1	AI556531	Rn.138082	Transcribed locus, strongly similar to NP_060595.2 hypothetical protein FLJ10521 [Homo sapiens]
307	1398312_s_at	-0.609529705	0.65541032	yes	yes	yes	Rn.82694.1	AF042167	Rn.10157	solute carrier family 14 (urea transporter), member 2
308	1385408_at	-0.60913934	0.655587685	yes	yes	yes	Rn.78917.1	BI288589	Rn.78917	similar to mKIAA0518 protein
309	1396090_at	-0.609100844	0.655605179	yes	yes	no	Rn.72844.1	BF564059	---	---
310	1391536_at	-0.608499107	0.655878684	yes	yes	no	Rn.48994.1	AA892645	Rn.103328	similar to cDNA sequence BC020002 (predicted)
311	1387087_at	-0.607462996	0.65634989	yes	yes	yes	Rn.6479.1	NM_024125	Rn.6479	CCAAT/enhancer binding protein (C/EBP), beta
312	1386972_at	-0.605802253	0.657105875	yes	yes	yes	Rn.11305.1	NM_017228	Rn.11305	dentatorubral pallidoluysian atrophy
313	1394375_x_at	-0.604790771	0.657566738	yes	yes	no	Rn.20865.2	BF554138	Rn.137148	Transcribed locus, strongly similar to XP_340831.2 PREDICTED: similar to BAZF [Rattus norvegicus]
314	1379568_at	-0.604767631	0.657577285	yes	yes	no	Rn.6175.1	AI009765	Rn.6175	interferon-induced protein with tetratricopeptide repeats 2 (predicted)
315	1397294_at	-0.603596281	0.6581114	yes	yes	no	Rn.47215.1	AW529486	Rn.3437	Similar to small nuclear ribonucleoprotein B
316	1378010_at	-0.603134722	0.658321983	yes	yes	yes	Rn.45604.1	BG662522	Rn.98343	Origin recognition complex, subunit 4
317	1382153_at	-0.602769732	0.658488554	yes	yes	yes	Rn.24032.1	AI171821	Rn.24032	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6

318	1391730_at	-0.601360892	0.659131904	yes	yes	no	Rn.35488.1	AW433989	Rn.8013	Myeloid/lymphoid or mixed-lineage leukemia 2 (predicted)
319	1382653_at	-0.600961188	0.659314544	yes	yes	no	Rn.27121.1	AI136405	Rn.103515	similar to CG15929-PA (predicted)
320	1392170_at	-0.60058052	0.659488533	yes	yes	no	Rn.46581.1	BE121336	Rn.54470	RWD domain containing 3
321	1379884_at	-0.600518871	0.659516715	yes	yes	no	Rn.22695.1	AA799621	Rn.22695	Aspartate-beta-hydroxylase (predicted)
322	1383084_at	-0.600104468	0.659706183	yes	yes	yes	Rn.18376.1	BG671922	Rn.139571	Similar to hypothetical protein FLJ23033
323	1372831_at	-0.600001967	0.659753056	yes	yes	no	Rn.20180.1	BE349838	Rn.20180	Similar to leucine zipper, down-regulated in cancer 1; breast cancer, up-regulated 1 (predicted)
324	1383449_at	-0.599881149	0.659808309	yes	yes	yes	Rn.31888.1	AA801218	Rn.40130	RT1 class I, CE5
325	1383011_at	-0.599717895	0.659882976	yes	yes	yes	Rn.35294.1	AI501182	---	---
326	1368039_at	-0.599712858	0.659885281	yes	yes	no	Rn.6258.1	NM_022599	Rn.6258	synaptojanin 2 binding protein
327	1397006_at	-0.599519859	0.659973564	yes	yes	no	Rn.59834.1	BF401586	Rn.91118	Protein kinase C, beta 1
328	1394451_at	-0.599081806	0.660173985	yes	yes	no	Rn.63926.1	AI236455	Rn.1792	annexin A1
329	1397065_at	-0.598254499	0.660552667	yes	yes	no	Rn.59272.1	BF399120	Rn.148139	Transcribed locus
330	1370389_at	-0.598179961	0.660586796	yes	yes	no	Rn.8057.1	AB036421	---	hypothetical gene supported by NM_138846
331	1381989_at	-0.597647344	0.660830718	yes	yes	yes	Rn.17408.1	BI280114	---	---
332	1381616_at	-0.59718579	0.661042168	yes	yes	no	Rn.20073.1	AI072140	Rn.146996	Transcribed locus
333	1378531_at	-0.596170853	0.661507375	yes	yes	no	Rn.38591.1	AI555775	Rn.147356	Transcribed locus
334	1383606_at	-0.595991723	0.661589516	yes	yes	yes	Rn.43919.1	BI302544	Rn.43919	membrane targeting (tandem) C2 domain containing 1
335	1379265_at	-0.595754741	0.661698199	yes	yes	yes	Rn.7380.1	BF398764	Rn.7380	Transcribed locus
336	1382540_at	-0.595430291	0.661847027	yes	yes	yes	Rn.47926.1	BI296328	Rn.95204	Formin binding protein 3 (predicted)
337	1369723_at	-0.595154138	0.661973726	yes	yes	no	Rn.22727.1	NM_022296	Rn.22727	xylosyltransferase II
338	1383511_at	-0.594472327	0.662286645	yes	yes	no	Rn.24826.1	BF409024	Rn.24826	Transcribed locus
339	1392581_at	-0.594255841	0.662386033	yes	yes	no	Rn.63687.1	BF420172	Rn.13744	neurocalcin delta
340	1381558_at	-0.593950917	0.662526049	yes	yes	yes	Rn.76398.1	BG374759	Rn.19111	Similar to 4933427D14Rik protein (predicted)
341	1377550_at	-0.593471756	0.662746129	yes	yes	no	Rn.65355.1	BF405298	Rn.41	similar to RIKEN cDNA 2310067G05
342	1383164_at	-0.592932835	0.662993745	yes	yes	yes	Rn.7792.1	AW524366	Rn.7792	Transcribed locus
343	1387730_at	-0.591870972	0.663481906	yes	yes	no	Rn.10392.1	NM_031141	Rn.10392	paired box gene 8
344	1398382_at	-0.591698041	0.66356144	yes	yes	no	Rn.65040.1	AI175556	Rn.65040	Transcribed locus
345	1369417_a_at	-0.591697926	0.663561494	yes	yes	no	Rn.11366.1	NM_053848	Rn.11366	opioid-binding protein/cell adhesion molecule-like
346	1369002_at	-0.590637843	0.664049253	yes	yes	no	Rn.59.1	NM_031118	Rn.59	sterol O-acyltransferase

347	1374652_at	-0.590417015	0.664150905	yes	yes	no	Rn.16305.1	BF285372	Rn.96303	Solute carrier family 25, member 26 (predicted)
348	1380361_at	-0.590155383	0.664271359	yes	yes	no	Rn.38037.1	AI547532	Rn.66098	CDC16 cell division cycle 16 homolog (S. cerevisiae) (predicted)
349	1394827_at	-0.589440499	0.6646006	yes	yes	no	Rn.55468.1	AI012667	Rn.55468	similar to KIAA0240 (predicted)
350	1392354_at	-0.588945384	0.664828722	yes	yes	no	Rn.45016.1	AW529939	Rn.146138	Transcribed locus
351	1384298_at	-0.588771831	0.664908704	yes	yes	no	Rn.41734.1	AI764088	Rn.28908	myosin IF (predicted)
352	1385027_at	-0.588660385	0.664960069	yes	yes	no	Rn.73356.1	BG380549	Rn.148207	Transcribed locus
353	1395710_at	-0.588491243	0.665038034	yes	yes	no	Rn.39264.1	BI275003	Rn.36542	similar to mesoderm induction early response 1 (MI-ER1)
354	1392139_at	-0.587468113	0.665509833	yes	yes	yes	Rn.50821.1	BE105731	Rn.146614	Transcribed locus
355	1394094_at	-0.587415402	0.665534149	yes	yes	no	Rn.43463.1	AI412196	Rn.43463	Transcribed locus
356	1388142_at	-0.587354153	0.665562404	yes	yes	no	Rn.35666.2	AA850991	Rn.35666	chondroitin sulfate proteoglycan 2
357	1375788_at	-0.587129579	0.665666016	yes	yes	no	Rn.8562.3	BM388719	Rn.129121	Ribosomal protein L7
358	1383629_a_at	-0.586968685	0.665740257	yes	yes	yes	Rn.17587.1	BI289966	Rn.17587	CDNA clone IMAGE:7386859
359	1385100_at	-0.586704601	0.665862131	yes	yes	no	Rn.21839.1	AI073049	Rn.133488	Similar to RIKEN cDNA 1200014M14 (predicted)
360	1372664_at	-0.586633648	0.66589488	yes	yes	no	Rn.14615.1	BM384229	Rn.105232	Tnf receptor-associated factor 2 (predicted)
361	1392995_at	-0.586549047	0.665933929	yes	yes	no	Rn.16013.1	BG669396	Rn.16013	Transcribed locus
362	1397779_at	-0.586421374	0.665992865	yes	yes	yes	Rn.18540.1	BF562254	Rn.1779	Chromodomain helicase DNA binding protein 2 (predicted)
363	1388305_at	-0.585493407	0.666421381	yes	yes	yes	Rn.1714.2	AI176666	Rn.1714	v-raf oncogene homolog 1 (murine sarcoma 3611 virus)
364	1396341_at	-0.58534306	0.666490834	yes	yes	no	Rn.54344.1	BI276792	---	---
365	1397338_at	-0.584703463	0.666786378	yes	yes	no	Rn.27559.1	AI137999	Rn.119002	Transcribed locus
366	1383644_at	-0.584650382	0.666810912	yes	yes	no	Rn.21471.1	BM385202	Rn.21471	Transcribed locus
367	1398238_at	-0.584555323	0.666854849	yes	yes	no	Rn.51288.1	BE107786	Rn.51288	Transcribed locus
368	1393981_at	-0.583309275	0.667431057	yes	yes	yes	Rn.64256.2	BF567629	Rn.144424	similar to KIAA0423 (predicted)
369	1370953_at	-0.583197196	0.66748291	yes	yes	yes	Rn.38769.1	BE113639	---	---
370	1382059_at	-0.580823011	0.668582264	yes	yes	yes	Rn.29397.1	BI289529	Rn.29397	F-box only protein 30
371	1382671_at	-0.580099267	0.66891775	yes	yes	no	Rn.25451.1	AW920165	Rn.130959	Transcribed locus
372	1381347_at	-0.57907985	0.669390578	yes	yes	no	Rn.12899.1	AI178745	Rn.12899	Similar to Hypothetical protein KIAA0141
373	1385814_at	-0.578619679	0.669604125	yes	yes	no	Rn.32659.2	H32486	Rn.72680	mitogen activated protein kinase kinase kinase 3 (predicted)
374	1377133_at	-0.577732296	0.670016117	yes	yes	no	Rn.40935.1	BE100973	Rn.24858	Transcribed locus

375	1399099_at	-0.577583237	0.670085346	yes	yes	no	Rn.4170.1	BG381219	Rn.95170	heterogeneous nuclear ribonucleoprotein U-like 1 (predicted)
376	1381513_at	-0.577443252	0.670150368	yes	yes	no	Rn.18831.1	AI058295	Rn.18831	Transcribed locus
377	1376191_at	-0.577350096	0.670193641	yes	yes	no	Rn.6386.1	AA848820	Rn.6386	15-hydroxyprostaglandin dehydrogenase
378	1395840_at	-0.577330721	0.670202642	yes	yes	no	Rn.44976.1	AW520679	Rn.3361	eukaryotic translation initiation factor 1A (predicted)
379	1381508_at	-0.575830071	0.67090013	yes	yes	yes	Rn.49769.1	BE098143	Rn.49769	Transcribed locus
380	1392701_at	-0.57525667	0.671166833	yes	yes	no	Rn.18673.2	BI285572	Rn.102187	similar to GDP-mannose pyrophosphorylase B
381	1386029_at	-0.574013985	0.671745201	yes	yes	yes	Rn.55255.1	BF284035	---	---
382	1374204_at	-0.572866204	0.672279842	yes	yes	yes	Rn.18535.1	BM388946	Rn.18535	WD repeat and SOCS box-containing 1 (predicted)
383	1383819_at	-0.572756075	0.672331162	yes	yes	yes	Rn.11556.1	BI292866	Rn.11556	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)
384	1380907_at	-0.571946731	0.672708442	yes	yes	no	Rn.61733.1	BE109785	Rn.61733	Similar to Hypothetical protein KIAA0297/KIAA0329 (predicted)
385	1378216_at	-0.570828901	0.673229873	yes	yes	no	Rn.21695.1	BM387900	Rn.21695	Transcribed locus, weakly similar to NP_032201.1 granulin [Mus musculus]
386	1383410_at	-0.569642815	0.673783584	yes	yes	yes	Rn.14612.1	BI290777	Rn.24880	signal recognition particle 54
387	1386114_at	-0.568189687	0.674462582	yes	yes	no	Rn.3068.2	BF550033	Rn.38109	Transcribed locus
388	1379951_at	-0.567858988	0.674617202	yes	yes	no	Rn.50598.1	BE104039	Rn.2515	SNF2 histone linker PHD RING helicase (predicted)
389	1376383_at	-0.56635252	0.675322008	yes	yes	no	Rn.62167.1	BF403938	Rn.10961	Calcium/calmodulin-dependent protein kinase II gamma
390	1392575_at	-0.565035154	0.675938946	yes	yes	no	Rn.29452.1	BE108929	Rn.29452	Transcribed locus
391	1380162_at	-0.564521809	0.676179504	yes	yes	no	Rn.72896.1	BI274645	Rn.148244	Transcribed locus
392	1384198_at	-0.564227571	0.676317425	yes	yes	yes	Rn.20175.1	BF288648	Rn.20175	ecto-NOXdisulfide-thiolexchanger2
393	1371726_at	-0.564217781	0.676322014	yes	yes	yes	Rn.3000.1	AW433870	Rn.98492	Transcribed locus
394	1385595_at	-0.563283829	0.676759984	yes	yes	yes	Rn.53701.1	BE114414	---	---
395	1385546_at	-0.563255191	0.676773418	yes	yes	no	Rn.12902.1	AA998195	Rn.3917	similar to IQ motif and WD repeats 1
396	1386568_at	-0.562981279	0.676901923	yes	yes	no	Rn.12385.2	BF557891	Rn.12385	interferon regulatory factor 6 (predicted)
397	1391683_at	-0.562697264	0.677035194	yes	yes	no	Rn.7783.1	BF563946	Rn.7783	Transcribed locus, moderately similar to NP_065397.1 CSRP2 binding protein isoform a; CRP2 binding protein;

										cysteine rich protein 2 binding protein; CRP2 binding partner [Homo sapiens]
398	1367707_at	-0.562571525	0.677094204	yes	yes	no	Rn.9486.1	NM_017332	Rn.9486	fatty acid synthase
399	1386282_x_at	-0.561898048	0.677410358	yes	yes	no	Rn.36146.2	AA964809	Rn.10245	SNF related kinase /// hypothetical gene supported by NM_138833
400	1379251_at	-0.561870421	0.67742333	yes	yes	yes	Rn.24762.1	BF398485	Rn.24762	Transcribed locus
401	1393666_at	-0.559814634	0.678389322	yes	yes	no	Rn.50045.1	BE101321	Rn.6458	Transcribed locus
402	1375883_at	-0.559532868	0.678521828	yes	yes	no	Rn.59101.1	BI298766	---	---
403	1383445_at	-0.558077979	0.67920643	yes	yes	yes	Rn.44991.1	BG667490	Rn.44991	zinc finger protein 191
404	1376840_at	-0.55807163	0.679209419	yes	yes	no	Rn.22444.1	AI103040	Rn.22444	zinc finger protein 655
405	1383002_at	-0.557902778	0.679288917	yes	yes	no	Rn.12855.2	AA998043	Rn.22288	Similar to PHD finger protein 20-like 1 isoform 1
406	1394845_at	-0.557710256	0.679379572	yes	yes	no	Rn.37299.1	BF542618	Rn.37299	aquarius (predicted)
407	1386671_at	-0.557348944	0.679549739	yes	yes	yes	Rn.42665.1	AW921309	Rn.15267	Coiled-coil domain containing 2
408	1380660_at	-0.556868099	0.679776268	yes	yes	yes	Rn.52621.1	BI295181	Rn.147798	Transcribed locus
409	1391619_at	-0.556818998	0.679799404	yes	yes	yes	Rn.23774.1	AI137509	Rn.145765	LOC501623
410	1395460_at	-0.556818238	0.679799762	yes	yes	no	Rn.49381.1	BI290497	Rn.49669	cask-interacting protein 2 (predicted)
411	1375563_at	-0.555621326	0.680363982	yes	yes	no	Rn.24168.1	AA944394	Rn.95607	Similar to dendritic cell-derived ubiquitin-like protein (predicted)
412	1389369_at	-0.555501194	0.680420638	yes	yes	yes	Rn.35929.1	BF289017	Rn.124031	Transcribed locus, moderately similar to NP_076356.1 hypothetical protein LOC77547 [Mus musculus]
413	1377645_at	-0.555170399	0.680576669	yes	yes	yes	Rn.3653.1	AA892331	Rn.3653	similar to hypothetical protein /// hypothetical gene supported by BC083674
414	1377117_at	-0.555099542	0.680610096	yes	yes	no	Rn.60221.1	BF387780	Rn.136861	Transcribed locus
415	1391994_at	-0.554878131	0.680714558	yes	yes	yes	Rn.30602.1	AI408264	Rn.30602	Transcribed locus
416	1379747_at	-0.554611655	0.680840302	yes	yes	no	Rn.22637.1	AA866443	Rn.22637	Protease, serine, 35 (predicted)
417	1385857_at	-0.554194079	0.681037394	yes	yes	no	Rn.73624.1	AA998661	Rn.51010	oligophrenin 1
418	1381130_at	-0.553880917	0.681185242	yes	yes	no	Rn.77418.1	BF412056	Rn.70183	minichromosome maintenance deficient 8 (S. cerevisiae) (predicted)
419	1370145_at	-0.553123599	0.681542912	yes	yes	no	Rn.64579.1	NM_023988	Rn.64579	zinc finger protein 354C

420	1388097_at	-0.552927698	0.681635463	yes	yes	yes	Rn.81219.1	AF361342	Rn.81219	calcium channel, voltage-dependent, gamma subunit 5
421	1387029_at	-0.552554682	0.681811727	yes	yes	no	Rn.13111.1	NM_130409	Rn.101777	complement component factor H
422	1391647_at	-0.552063505	0.682043894	yes	yes	no	Rn.24665.1	AI232625	---	---
423	1378214_at	-0.55164275	0.682242838	yes	yes	yes	Rn.23884.1	AI101388	---	---
424	1397854_at	-0.551568269	0.682278061	yes	yes	no	Rn.26645.1	BI275309	Rn.26645	Transcribed locus
425	1380200_at	-0.551303177	0.682403439	yes	yes	no	Rn.16111.2	AI102906	Rn.10600	Transcription factor 8 (represses interleukin 2 expression)
426	1383114_at	-0.55116315	0.682469676	yes	yes	no	Rn.22821.1	BI296782	Rn.42926	Serine/threonine kinase
427	1374454_at	-0.549494799	0.683259349	yes	yes	yes	Rn.43517.1	BM388557	Rn.96446	Similar to RIKEN cDNA 5330414D10 (predicted)
428	1384098_at	-0.54850258	0.683729425	yes	yes	no	Rn.15586.1	AA925710	Rn.101837	ring finger protein 125 (predicted)
429	1380415_at	-0.547409234	0.684247785	yes	yes	no	Rn.33970.1	AI233027	---	---
430	1382881_at	-0.547399242	0.684252525	yes	yes	no	Rn.76083.1	BI290218	Rn.105739	similar to EXCretory canal abnormal EXC-7, ELAV type RNA binding protein (48.7 kD) (exc-7)
431	1383847_at	-0.54707235	0.684407583	yes	yes	yes	Rn.28057.1	BG379138	Rn.28057	Transcribed locus
432	1375218_at	-0.546221759	0.684811219	yes	yes	yes	Rn.76512.1	BI291250	Rn.3545	Similar to Transforming growth factor beta 1 induced transcript 4, isoform 1
433	1391985_at	-0.545827597	0.684998343	yes	no	no	Rn.50762.1	BI288541	Rn.15635	Transcribed locus
434	1382534_at	-0.545802836	0.6850101	yes	yes	yes	Rn.16900.1	BF284898	Rn.97951	Transcribed locus, weakly similar to NP_570953.1 CAMP [Mus musculus]
435	1378614_at	-0.545487391	0.685159893	yes	no	no	Rn.23736.1	BI274329	Rn.11193	Huntington disease gene homolog
436	1372604_at	-0.54511143	0.685338467	yes	yes	yes	Rn.2438.1	BI289459	---	similar to RIKEN cDNA 2210421G13
437	1381482_at	-0.544876403	0.685450123	yes	yes	no	Rn.26854.1	AI555166	Rn.12118	Transcribed locus, weakly similar to NP_795929.1 hypothetical protein LOC319587 [Mus musculus]
438	1387646_a_at	-0.544610405	0.685576515	yes	yes	no	Rn.44443.1	NM_022210	Rn.4210	Max protein
439	1375122_at	-0.544315508	0.685716666	yes	yes	no	Rn.3414.1	AI233235	Rn.7352	YY1 associated factor 2 (predicted)
440	1382296_at	-0.544061687	0.685837319	yes	yes	no	Rn.16839.1	BF291041	Rn.16839	Transcribed locus
441	1375404_at	-0.543857403	0.685934439	yes	no	no	Rn.52925.1	BF415963	Rn.98476	Double-stranded RNA-binding protein p74
442	1390985_at	-0.542993957	0.686345091	yes	yes	no	Rn.24958.1	AA956519	Rn.24958	Transcribed locus
443	1397709_at	-0.541856964	0.686886215	yes	yes	yes	Rn.40629.1	BG672259	Rn.3366	similar to PI-3-kinase-related kinase SMG-1 isoform 2

444	1383510_at	-0.541213439	0.687192674	yes	yes	yes	Rn.249.1	AI230360	Rn.249	Ubiquitin protein ligase E3A (predicted)
445	1380121_at	-0.540681795	0.687445956	yes	yes	yes	Rn.52796.1	BE117215	Rn.3649	Transcribed locus
446	1377114_at	-0.540646635	0.68746271	yes	yes	yes	Rn.3800.1	AI410861	---	---
447	1374103_at	-0.540098963	0.687723732	yes	yes	no	Rn.35282.2	BE102100	Rn.62653	Frequenin homolog (Drosophila)
448	1385063_at	-0.54000173	0.687770084	yes	yes	no	Rn.76433.1	BG377323	---	ELK1, member of ETS oncogene family
449	1378976_x_at	-0.539103714	0.688198325	yes	yes	no	Rn.19894.1	AI070952	Rn.120352	Transcribed locus
450	1387982_at	-0.538027713	0.688711794	yes	yes	no	Rn.14534.1	AF057025	Rn.14534	toll-like receptor 4
451	1368262_at	-0.537235288	0.689090184	yes	yes	no	Rn.41075.1	NM_021657	Rn.38371	pleckstrin homology domain containing, family E (with leucine rich repeats) member 1
452	1390400_a_at	-0.536711527	0.689340399	yes	no	no	Rn.227.1	BM390922	Rn.227	Transcribed locus
453	1391475_at	-0.535811733	0.689770468	yes	yes	no	Rn.14034.1	AI235307	Rn.101827	similar to 2810036L13Rik protein (predicted)
454	1397467_at	-0.535491451	0.689923616	yes	yes	no	Rn.45909.1	AW524703	Rn.148097	Transcribed locus
455	1388962_at	-0.535378036	0.689977855	yes	yes	no	Rn.11826.1	BI294621	Rn.11826	ring finger protein 110 (predicted)
456	1385953_at	-0.535117852	0.690102301	yes	yes	no	Rn.35070.2	AI454608	Rn.22828	Transcribed locus
457	1393772_at	-0.534420623	0.690435896	yes	yes	no	Rn.45588.1	AW523217	Rn.45588	Transcribed locus
458	1374879_x_at	-0.534271204	0.690507407	yes	yes	no	Rn.11463.2	AI228249	Rn.11463	Similar to expressed sequence AI256361 (predicted)
459	1373248_at	-0.534086711	0.690595716	yes	yes	no	Rn.18507.1	BI292079	Rn.114291	Similar to hypothetical protein FLJ20674
460	1379573_at	-0.533603254	0.690827178	yes	yes	no	Rn.16529.1	AA818730	---	---
461	1382210_at	-0.5334675	0.690892186	yes	no	no	Rn.28039.1	BE117392	Rn.11727	Strain Wistar Rap2a mRNA, 5' UTR
462	1385188_at	-0.532997087	0.691117499	yes	yes	no	Rn.66699.1	BG379787	Rn.153206	Transcribed locus
463	1376522_at	-0.532892365	0.691167667	yes	yes	no	Rn.73468.1	BI291288	Rn.32566	Fatty acid binding protein 3
464	1395965_at	-0.532845358	0.691190188	yes	yes	no	Rn.46860.1	BI298589	Rn.95305	Retinoblastoma binding protein 6 (predicted)
465	1385236_at	-0.532642568	0.69128735	yes	yes	no	Rn.2977.2	AA875617	Rn.139466	similar to RIKEN cDNA 4931408L03 (predicted)
466	1392593_a_at	-0.532301473	0.69145081	yes	yes	no	Rn.22234.2	AI555789	Rn.17162	similar to KIAA1205 protein (predicted)
467	1372690_at	-0.531664183	0.691756316	yes	yes	no	Rn.22361.1	AI137471	Rn.22361	Transcribed locus
468	1391347_at	-0.531648044	0.691764055	yes	yes	no	Rn.59159.1	BF398743	Rn.10995	RAB8B, member RAS oncogene family
469	1392015_at	-0.531058583	0.692046756	yes	yes	no	Rn.57803.1	BF392359	Rn.118099	Similar to RIKEN cDNA A930008G19 (predicted)
470	1380060_at	-0.531007043	0.692071479	yes	yes	no	Rn.31307.1	AI175848	Rn.31307	DNA topoisomerase I, mitochondrial
471	1392507_at	-0.529170554	0.692953018	yes	yes	no	Rn.17797.1	AI385280	Rn.17797	Transcribed locus
472	1377916_at	-0.528814369	0.693124121	yes	yes	no	Rn.34404.1	AW915529	Rn.105052	schlafen 2 (predicted)
473	1385322_at	-0.528289016	0.693376566	yes	yes	no	Rn.40150.1	AI602154	---	---

474	1395363_at	-0.527796019	0.693613547	yes	yes	no	Rn.23010.1	AI102047	Rn.140163	methionine-tRNA synthetase (predicted)
475	1383245_at	-0.527527325	0.693742741	yes	yes	no	Rn.24202.1	AI454309	Rn.24202	MAP3K12 binding inhibitory protein 1 (predicted)
476	1392979_at	-0.527364878	0.69382086	yes	yes	no	Rn.11540.2	AW918443	Rn.11540	similar to calcyclin binding protein
477	1393842_at	-0.527249514	0.693876343	yes	no	no	Rn.75489.1	BF391556	Rn.19815	similar to RIKEN cDNA 2700091N06 (predicted)
478	1377019_at	-0.525837035	0.69455602	yes	yes	no	Rn.31227.1	BF410042	Rn.153632	Transcribed locus
479	1386836_at	-0.525802755	0.694572523	yes	yes	no	Rn.15466.2	BF556285	Rn.15466	zinc finger protein 574 (predicted)
480	1368429_at	-0.525602784	0.694668804	yes	yes	no	Rn.11270.1	NM_133615	Rn.11270	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa
481	1375994_at	-0.525459963	0.694737577	yes	yes	no	Rn.23028.1	BE107324	Rn.55914	Transcribed locus
482	1381283_at	-0.525265689	0.694831137	yes	yes	no	Rn.50733.1	BE105217	Rn.15858	Zinc finger protein 346 (predicted)
483	1375950_a_at	-0.525194773	0.694865293	yes	yes	no	Rn.12955.1	BI294235	Rn.12955	Transcribed locus, weakly similar to XP_374936.1 PREDICTED: KIAA1052 protein [Homo sapiens]
484	1384101_at	-0.524424625	0.695236329	yes	yes	no	Rn.107.1	BM388523	Rn.31789	Type II keratin Kb1
485	1381822_x_at	-0.524389873	0.695253076	yes	yes	no	Rn.44939.1	AI711481	Rn.19574	TP53 regulating kinase (predicted) /// TP53 regulating kinase (predicted)
486	1398617_at	-0.523710406	0.695580597	yes	no	no	Rn.19839.1	BE098167	Rn.144605	Transcribed locus
487	1376672_at	-0.523640937	0.695614091	yes	yes	no	Rn.18056.1	AW533083	Rn.18056	Transcribed locus
488	1373126_at	-0.523271102	0.695792435	yes	yes	no	Rn.1563.1	AW918188	Rn.1563	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
489	1393813_at	-0.522826976	0.696006664	yes	yes	no	Rn.75377.1	BF388771	---	---
490	1392912_at	-0.522324529	0.696249104	yes	yes	no	Rn.11540.1	BG664561	Rn.11540	similar to calcyclin binding protein
491	1388111_at	-0.521166168	0.696808357	yes	yes	no	Rn.54384.1	J04035	Rn.54384	elastin
492	1373765_at	-0.520668426	0.697048803	yes	yes	no	Rn.17913.1	BG371708	Rn.17913	Transcribed locus
493	1375243_at	-0.520396064	0.697180409	yes	no	no	Rn.44877.1	BE113157	Rn.137561	Similar to BTB (POZ) domain containing 2
494	1372683_at	-0.5200415	0.697351773	yes	yes	no	Rn.51875.1	BI291252	Rn.51875	molybdenum cofactor sulfurase (predicted)
495	1375371_at	-0.519600836	0.697564808	yes	yes	no	Rn.52526.1	BI296662	Rn.101115	similar to Ran-binding protein 2
496	1383005_at	-0.519519198	0.697604282	yes	yes	no	Rn.9050.1	BM383579	Rn.109048	Vacuole membrane protein 1
497	1373839_at	-0.519013626	0.697848791	yes	yes	no	Rn.7944.1	BG372386	Rn.7944	Transcribed locus

498	1397041_at	-0.518284866	0.69820139	yes	yes	no	Rn.57280.1	BF404629	Rn.102748	Similar to hypothetical protein DKFZp564D0478 (predicted)
499	1371647_at	-0.518165782	0.698259024	yes	yes	no	Rn.6760.1	AA963367	Rn.17150	similar to transmembrane protein TM9SF3
500	1378928_at	-0.517170092	0.6987411	yes	yes	no	Rn.64318.1	BF387639	---	---
501	1383246_at	-0.517152026	0.69874985	yes	yes	no	Rn.19312.1	AI146111	Rn.144716	Similar to Hypothetical protein A630084C13 (predicted)
502	1385214_at	-0.516216609	0.699203054	yes	yes	no	Rn.57517.1	BF391513	Rn.95841	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
503	1393492_at	-0.515991487	0.699312168	yes	yes	no	Rn.51296.1	BE107812	Rn.31865	Similar to RIKEN cDNA 0610009F02
504	1396831_at	-0.515958669	0.699328076	yes	no	no	Rn.27194.1	AI501417	Rn.18357	Glutamine repeat protein 1 (predicted)
505	1374155_at	-0.515639378	0.699482865	yes	yes	no	Rn.33247.1	BF410502	Rn.33247	Transcribed locus
506	1398552_a_at	-0.515534291	0.699533818	yes	yes	no	Rn.48967.1	BG381450	Rn.123166	acrosin binding protein
507	1392708_at	-0.515068187	0.699759859	yes	no	no	Rn.28930.1	AI175745	Rn.91820	STAR-related lipid transfer (START) domain containing protein 6
508	1374299_at	-0.514718937	0.699929278	yes	yes	no	Rn.41553.1	BF398414	Rn.107359	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)
509	1397586_at	-0.514429405	0.70006976	yes	yes	no	Rn.76514.1	BI300588	---	---
510	1390743_at	-0.514394609	0.700086645	yes	yes	no	Rn.60798.1	BF405616	Rn.60798	Transcribed locus
511	1392220_at	-0.514296928	0.700134048	yes	yes	no	Rn.47987.1	AW532634	Rn.47987	Transcribed locus
512	1376891_at	-0.514070737	0.700243826	yes	yes	no	Rn.34212.1	AA818282	Rn.34212	Transcribed locus
513	1375193_at	-0.51381132	0.700369751	yes	yes	no	Rn.22159.1	BE095528	Rn.40930	low density lipoprotein receptor-related protein 11 (predicted)
514	1397876_at	-0.51347469	0.70053319	yes	yes	no	Rn.47639.1	AI549089	Rn.148047	Transcribed locus
515	1377237_at	-0.51334575	0.700595803	yes	yes	no	Rn.23759.1	AI137274	Rn.23759	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
516	1374981_at	-0.513313485	0.700611471	yes	yes	no	Rn.61766.1	BF399062	Rn.131889	similar to 2-aminoadipic 6-semialdehyde dehydrogenase (predicted)
517	1380818_at	-0.512556908	0.700978982	yes	no	no	Rn.66511.1	BE121297	Rn.2666	Similar to KIAA1838 protein (predicted)
518	1380693_at	-0.511911965	0.701292418	yes	yes	no	Rn.62888.1	BF415976	Rn.38550	Similar to ribosomal protein S6 kinase 2
519	1374111_at	-0.511611007	0.701438728	yes	yes	no	Rn.24288.1	BI301101	Rn.38987	similar to pinin
520	1378372_at	-0.511558348	0.701464331	yes	no	no	Rn.34650.1	AI574994	Rn.11055	Arginase 2
521	1379889_at	-0.511415546	0.701533768	yes	no	no	Rn.20276.1	AW527269	Rn.9278	lamimin, gamma 2
522	1385168_at	-0.511380883	0.701550624	yes	no	no	Rn.82110.1	BM387883	Rn.82110	similar to receptor-

										interacting factor 1 (predicted)
523	1369734_at	-0.511149073	0.701663357	yes	yes	no	Rn.10546.1	NM_053339	Rn.10546	acyl-Coenzyme A oxidase 3, pristanoyl
524	1392870_at	-0.510377655	0.702038641	yes	yes	no	Rn.64764.1	AI406729	---	---
525	1382118_at	-0.510377248	0.702038839	yes	yes	no	Rn.12821.1	BE104676	Rn.19473	paternally expressed 3 (predicted)
526	1381624_at	-0.510314126	0.702069556	yes	yes	no	Rn.64259.1	BF391717	Rn.120484	Nuclear protein in the AT region (predicted)
527	1391084_at	-0.510072092	0.702187348	yes	no	no	Rn.46224.1	AW528763	Rn.249	Ubiquitin protein ligase E3A (predicted)
528	1390433_at	-0.508329627	0.703035952	yes	yes	no	Rn.19335.1	AI102429	Rn.19335	Transcribed locus
529	1395126_at	-0.508201192	0.703098542	yes	yes	no	Rn.76819.1	AI011393	---	---
530	1380306_at	-0.507918408	0.70323637	yes	yes	no	Rn.54177.1	AW435415	Rn.54177	Transcribed locus
531	1382354_at	-0.50781261	0.703287943	yes	no	no	Rn.16093.1	BE099884	Rn.42579	Similar to Ab2-008 (predicted)
532	1397049_at	-0.507773949	0.70330679	yes	yes	no	Rn.60265.1	BF403412	Rn.138061	Transcribed locus, strongly similar to NP_081963.1 calcium-binding tyrosine-phosphorylation regulated protein [Mus musculus]
533	1377205_at	-0.507303555	0.703536142	yes	yes	no	Rn.49215.1	BE107410	Rn.49215	similar to KIAA0892 protein (predicted)
534	1397617_at	-0.507272431	0.70355132	yes	yes	no	Rn.8874.1	BM382925	Rn.134218	Similar to Retinoblastoma-binding protein 2 (RBBP-2)
535	1388899_at	-0.506734562	0.703813669	yes	no	no	Rn.25434.1	BE098818	Rn.25434	Transcribed locus
536	1389735_at	-0.506337363	0.704007468	yes	yes	no	Rn.51151.1	BE107296	Rn.51151	Transcribed locus
537	1391284_at	-0.505942888	0.70419999	yes	no	no	Rn.40795.1	BE099274	---	---
538	1393050_at	-0.505431688	0.704449558	yes	yes	no	Rn.11727.2	BG664069	Rn.11727	Strain Wistar Rap2a mRNA, 5' UTR
539	1369974_at	-0.504776301	0.704769648	yes	yes	no	Rn.31977.1	NM_012663	Rn.12939	vesicle-associated membrane protein 2
540	1371700_at	-0.504529306	0.704890318	yes	yes	no	Rn.12328.1	AI177059	Rn.12328	Microfibrillar-associated protein 4 (predicted)
541	1377920_at	-0.504456059	0.704926106	yes	yes	no	Rn.45015.1	AI413026	Rn.23400	Small glutamine rich protein with tetratricopeptide repeats 2
542	1380978_at	-0.503896035	0.705199797	yes	no	no	Rn.15924.1	AI044494	Rn.147477	Transcribed locus
543	1393171_at	-0.50366947	0.705310552	yes	yes	no	Rn.43134.1	BG664080	Rn.127766	Similar to transmembrane 4 superfamily member 10
544	1383818_at	-0.503366943	0.705458469	yes	no	no	Rn.47744.1	BF565324	Rn.46113	threonine synthase-like 1
545	1391710_at	-0.502522275	0.705871621	yes	yes	no	Rn.44668.1	AW251144	---	---
546	1369899_s_at	-0.502474358	0.705895066	yes	yes	no	Rn.2542.1	NM_013020	Rn.29434	Rab geranylgeranyl transferase, a subunit
547	1386725_at	-0.502185432	0.706036448	yes	no	no	Rn.45195.2	BF566582	Rn.45195	similar to DNA segment, Chr 19, ERATO Doi 386,

										expressed (predicted)
548	1389996_at	-0.501744486	0.706252275	yes	yes	no	Rn.7676.1	AI406369	Rn.7676	Transcribed locus
549	1387676_at	-0.501637936	0.706304436	yes	yes	no	Rn.21430.1	NM_053947	Rn.21430	MAP/microtubule affinity-regulating kinase 1
550	1387849_at	-0.501524362	0.706360042	yes	no	no	Rn.44273.1	NM_021852	Rn.44273	epsin 2
551	1378167_at	-0.501445136	0.706398833	yes	yes	no	Rn.35459.1	AI599898	Rn.101993	RNA (guanine-9-) methyltransferase domain containing 3 (predicted)
552	1389048_at	-0.501380218	0.70643062	yes	yes	no	Rn.9305.1	BI278614	Rn.9305	bone morphogenetic protein 1 (procollagen C-proetinase)
553	1375643_at	-0.500787658	0.706720833	yes	yes	no	Rn.8994.1	BM384259	Rn.99508	cytoskeleton-associated protein 4 (predicted)
554	1386535_at	-0.500709501	0.70675912	yes	yes	no	Rn.74085.1	BG667163	Rn.95841	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
555	1390689_at	-0.500702333	0.706762631	yes	yes	no	Rn.62050.1	BF401605	Rn.101893	ribosomal protein S6 kinase, polypeptide 1 (predicted)
556	1397911_at	-0.500350721	0.706934904	yes	yes	no	Rn.50847.1	BE115009	Rn.50847	Transcribed locus
557	1391427_at	-0.500116168	0.707049846	yes	yes	no	Rn.25178.1	AW254563	Rn.25178	Similar to RIKEN cDNA 1500031M22 (predicted)
558	1383561_at	-0.499933059	0.707139592	yes	yes	no	Rn.43328.1	BF550555	Rn.43328	Ligase IV, DNA, ATP-dependent (predicted)
559	1382306_at	-0.499147031	0.70752497	yes	yes	no	Rn.28200.1	AW919478	Rn.29865	Ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) (predicted)
560	1372615_at	-0.498356151	0.707912939	yes	yes	no	Rn.19962.1	AI070137	Rn.56603	amine oxidase, copper containing 3
561	1384144_at	-0.49782506	0.708173586	yes	no	no	Rn.18995.1	AI058824	Rn.105982	Nucleoredoxin (predicted)
562	1379495_at	-0.497179407	0.708490588	yes	no	no	Rn.19776.1	BM388504	Rn.19776	Transcribed locus
563	1373543_at	-0.496839656	0.708657455	yes	yes	no	Rn.15116.1	BI296461	Rn.15116	Transcribed locus, moderately similar to XP_573966.1 PREDICTED: similar to regulator of sex-limitation candidate 16 [Rattus norvegicus]
564	1392062_a_at	-0.496257158	0.708943638	yes	yes	no	Rn.24695.1	BE097702	---	---
565	1385050_at	-0.496020791	0.709059799	yes	no	no	Rn.75638.1	BF397804	Rn.106753	zinc finger protein 292
566	1376660_at	-0.496019514	0.709060427	yes	yes	no	Rn.43341.1	BG672127	Rn.43341	Transcribed locus
567	1395707_at	-0.495822066	0.709157476	yes	no	no	Rn.76540.1	BG670971	Rn.17648	Transcribed locus
568	1382131_at	-0.495792914	0.709171806	yes	no	no	Rn.20898.1	AW523674	Rn.124214	Transcribed locus
569	1392406_at	-0.495636115	0.709248886	yes	yes	no	Rn.47908.1	BE120827	Rn.47908	IAP promoted placental gene (predicted)
570	1386883_at	-0.495371613	0.709378931	yes	yes	no	Rn.36807.1	NM_017344	Rn.36807	Glycogen synthase

										kinase 3 alpha
571	1392149_at	-0.495343501	0.709392754	yes	no	no	Rn.79848.1	AA997766	Rn.95954	Eukaryotic translation initiation factor 4B (predicted)
572	1386507_at	-0.495295859	0.709416181	yes	no	no	Rn.6245.1	AA799858	---	---
573	1385978_at	-0.493835294	0.710134747	yes	yes	no	Rn.20262.2	AI072788	Rn.20262	Transcribed locus
574	1396830_at	-0.493802516	0.710150882	yes	yes	no	Rn.46332.1	AW527558	Rn.15233	LOC499979
575	1377337_at	-0.493624219	0.710238652	yes	no	no	Rn.53238.1	BE119412	Rn.95119	C-myc binding protein (predicted)
576	1389067_at	-0.49310871	0.710492482	yes	yes	no	Rn.8208.1	AI180349	Rn.67081	solute carrier organic anion transporter family, member 4a1
577	1381899_at	-0.493021073	0.710535643	yes	no	no	Rn.19154.1	AW534794	---	---
578	1393468_at	-0.491306009	0.711380824	yes	no	no	Rn.48907.2	BF556423	Rn.48907	mitochondrial ribosomal protein S2 (predicted)
579	1385901_at	-0.49124506	0.711410878	yes	no	no	Rn.24312.1	BE118197	Rn.130213	Transcribed locus
580	1371019_at	-0.490774825	0.711642795	yes	yes	no	Rn.64574.1	BM387324	Rn.24490	tribbles homolog 1 (Drosophila)
581	1398191_at	-0.489959583	0.712045045	yes	no	no	Rn.60303.1	BF403831	Rn.125162	RIM binding protein 2
582	1393690_at	-0.489698431	0.712173949	yes	yes	no	Rn.16736.1	AA818627	Rn.16736	insulin induced gene 2
583	1374643_at	-0.488994721	0.712521414	yes	yes	no	Rn.30629.1	BF288461	Rn.30629	similar to 6030410K14Rik protein
584	1383196_at	-0.488963067	0.712537048	yes	yes	no	Rn.20534.1	BI289677	Rn.20534	zinc finger protein 579 (predicted)
585	1380283_at	-0.488907242	0.71256462	yes	yes	no	Rn.23119.1	BF411100	Rn.23119	Serologically defined colon cancer antigen 33 (predicted)
586	1382963_at	-0.488768218	0.712633289	yes	yes	no	Rn.22937.2	BF416871	Rn.22937	ATP-binding cassette, sub-family B (MDR/TAP), member 10 (predicted)
587	1371472_at	-0.488767384	0.712633701	yes	yes	no	Rn.19113.1	BG380581	Rn.19113	Transcribed locus
588	1378766_at	-0.488688982	0.712672429	yes	no	no	Rn.25554.1	AI236320	Rn.25554	Transcribed locus
589	1392017_at	-0.48864642	0.712693454	yes	yes	no	Rn.58894.1	BF397766	Rn.134030	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (predicted)
590	1385213_at	-0.4886324	0.712700381	yes	no	no	Rn.45852.1	AW524454	Rn.45852	Similar to epithelial stromal interaction 1 isoform a
591	1385513_at	-0.488490703	0.712770383	yes	no	no	Rn.26838.1	AI112764	Rn.121336	Transcribed locus
592	1373061_at	-0.488438112	0.712796367	yes	no	no	Rn.6998.1	BE329329	Rn.137539	sorting nexin 17 (predicted)
593	1382599_at	-0.488176824	0.712925474	yes	yes	no	Rn.25124.3	BE103520	Rn.25124	Insulin-like growth factor I mRNA, 3' end of mRNA
594	1390538_at	-0.487857023	0.713083525	yes	yes	no	Rn.34156.1	BF414192	Rn.148039	Transcribed locus
595	1386002_at	-0.487817246	0.713103185	yes	no	no	Rn.25394.1	AI236841	Rn.25394	Transcribed locus, weakly similar to XP_128440.2 PREDICTED: RIKEN cDNA 4930432O21 [Mus musculus]

596	1380174_at	-0.487437916	0.713290707	yes	yes	no	Rn.34448.1	BE116115	Rn.34448	Transcribed locus
597	1385101_a_at	-0.487138562	0.713438728	yes	yes	no	Rn.21666.1	AI712625	Rn.21666	coiled-coildomaincontaining127
598	1393729_at	-0.487075652	0.713469839	yes	yes	no	Rn.69229.1	BE112114	Rn.96405	neuropilin (NRP) and tolloid (TLL)-like 2 (predicted)
599	1384747_at	-0.486811445	0.713600512	yes	yes	no	Rn.60453.1	BF404188	Rn.60453	transmembrane 7 superfamily member 1 (predicted)
600	1370992_a_at	-0.486052157	0.713976177	yes	no	no	Rn.5500.1	AI072045	Rn.139539	fibrinogen, alpha polypeptide
601	1393465_at	-0.485193272	0.714401358	yes	no	no	Rn.13545.2	BE103258	Rn.95697	Transcribed locus
602	1375420_at	-0.48511176	0.714441722	yes	no	no	Rn.22267.1	AI170535	Rn.22267	tumor protein p53 inducible protein 11 (predicted)
603	1393105_at	-0.484818618	0.714586905	yes	no	no	Rn.31727.2	BF288164	Rn.102011	similar to zinc finger protein
604	1382978_at	-0.484778939	0.714606559	yes	yes	no	Rn.8892.1	AA955691	Rn.8892	Transcribed locus
605	1385397_at	-0.484437247	0.714775828	yes	yes	no	Rn.16959.1	AA859085	Rn.16959	Ab1-219
606	1390856_at	-0.484342638	0.714822704	yes	yes	no	Rn.11631.1	BF289100	Rn.11631	Transcribed locus
607	1383430_at	-0.484086839	0.714949458	yes	no	no	Rn.45701.1	BF414509	Rn.45701	similar to hypothetical protein MGC2776 (predicted)
608	1398573_at	-0.48361278	0.715184423	yes	yes	no	Rn.8231.1	BE098868	Rn.8231	zinc finger protein 307 (predicted)
609	1376719_at	-0.482690549	0.715641745	yes	yes	no	Rn.22285.1	AI172189	Rn.22285	similar to hypothetical protein D4Ertd89e (predicted)
610	1398628_at	-0.482634302	0.715669647	yes	yes	no	Rn.19324.2	AI059960	---	---
611	1383895_at	-0.482176501	0.715896782	yes	no	no	Rn.27744.1	AI144946	Rn.27744	dynein, cytoplasmic, light chain 2B (predicted)
612	1381923_at	-0.481609857	0.716178018	yes	yes	no	Rn.37742.1	AI454658	Rn.22639	similar to LOC387763 protein
613	1372960_a_at	-0.48150062	0.716232247	yes	no	no	Rn.22727.2	AA892497	Rn.22727	xylosyltransferase II
614	1396643_at	-0.480960839	0.716500274	yes	yes	no	Rn.59232.1	BF400061	Rn.9903	C-terminal PDZ domain ligand of neuronal nitric oxide synthase
615	1383170_at	-0.480231159	0.716862754	yes	yes	no	Rn.7599.1	AW143788	Rn.7599	Transcribed locus
616	1383791_at	-0.47996104	0.716996986	yes	yes	no	Rn.13607.2	BG664616	Rn.108094	Similar to 2610030H06Rik protein
617	1384431_at	-0.479937221	0.717008824	yes	yes	no	Rn.19671.1	AI070150	Rn.135789	Similar to RIKEN cDNA 4930431B11 gene (predicted)
618	1393822_at	-0.479856884	0.717048752	yes	yes	no	Rn.15606.1	AA925789	Rn.19106	Transcribed locus
619	1367562_at	-0.479425278	0.717263301	yes	yes	no	Rn.31991.1	NM_012656	Rn.98989	secreted acidic cysteine rich glycoprotein
620	1386994_at	-0.478854124	0.717547318	yes	yes	no	Rn.27923.1	NM_017259	Rn.27923	B-cell translocation gene 2, anti-proliferative
621	1390681_at	-0.478852045	0.717548351	yes	no	no	Rn.11697.1	AA964074	Rn.11697	Similar to TGFB-induced factor 2
622	1374963_s_at	-0.47802057	0.717962018	yes	no	no	Rn.15248.1	BI290604	---	---

623	1372699_at	-0.477924074	0.718010042	yes	yes	no	Rn.22174.1	AI112403	Rn.22174	Similar to hypothetical protein C130032F08 (predicted)
624	1373651_at	-0.477739543	0.718101886	yes	yes	no	Rn.45576.1	BE103440	Rn.33919	Transcribed locus
625	1386716_at	-0.477272769	0.718334261	yes	no	no	Rn.74460.2	BF562934	Rn.17067	Similar to putative membrane steroid receptor (predicted)
626	1369247_at	-0.47715564	0.718392583	yes	yes	no	Rn.44609.1	NM_012655	Rn.44609	Sp1 transcription factor
627	1385859_at	-0.476615311	0.718661691	yes	yes	no	Rn.39317.2	AI059371	Rn.146599	Transcribed locus
628	1395471_at	-0.476536171	0.718701115	yes	no	no	Rn.34102.1	AW524834	Rn.34102	Transcribed locus
629	1381260_at	-0.476146466	0.718895279	yes	no	no	Rn.48973.1	AI764020	Rn.43808	Similar to RNA-binding protein Musashi2-S
630	1370492_a_at	-0.475359289	0.719287636	yes	no	no	Rn.10239.2	AF157595	Rn.10239	FMS-like tyrosine kinase 1
631	1368565_at	-0.475351334	0.719291602	yes	yes	no	Rn.34134.1	NM_019225	Rn.34134	solute carrier family 1 (glial high affinity glutamate transporter), member 3
632	1375488_at	-0.474859729	0.719536746	yes	no	no	Rn.73232.1	BI296702	Rn.73232	Transcribed locus
633	1397838_at	-0.474838779	0.719547195	yes	yes	no	Rn.61294.1	BF522792	Rn.8155	LOC499976
634	1395400_at	-0.474034425	0.71994848	yes	no	no	Rn.25006.1	AI178515	---	---
635	1391481_at	-0.473949618	0.719990803	yes	yes	no	Rn.44205.1	BE104424	---	---
636	1374842_at	-0.473760828	0.720085026	yes	yes	no	Rn.36685.1	BF287009	Rn.4019	CCAAT/enhancer binding protein zeta (predicted)
637	1383617_at	-0.473704329	0.720113227	yes	yes	no	Rn.17679.1	BF401603	Rn.16007	similar to RIKEN cDNA 4921511I16 (predicted)
638	1384678_at	-0.473320474	0.720304851	yes	no	no	Rn.9527.1	BF559356	Rn.147562	Transcribed locus
639	1367912_at	-0.47290233	0.720513651	yes	yes	no	Rn.40942.1	NM_021587	Rn.40942	latent transforming growth factor beta binding protein 1
640	1379902_at	-0.472705929	0.720611745	yes	yes	no	Rn.19055.1	BE108170	Rn.148941	Transcribed locus
641	1384296_at	-0.472375485	0.720776817	yes	no	no	Rn.27114.1	AI136388	Rn.144531	hypothetical LOC312654 (predicted)
642	1374793_at	-0.471896304	0.721016258	yes	no	no	Rn.12973.1	BE113663	Rn.12973	WD repeat domain 3 (predicted)
643	1392946_at	-0.471230337	0.721349166	yes	no	no	Rn.11575.1	AI029194	Rn.121260	Transcribed locus
644	1380997_at	-0.471004687	0.721461999	yes	yes	no	Rn.50277.1	BE103561	Rn.50277	Transcribed locus
645	1391744_at	-0.470816173	0.721556278	yes	yes	no	Rn.41758.1	AI548028	Rn.148269	Transcribed locus
646	1395704_at	-0.470591707	0.721668552	yes	yes	no	Rn.52959.1	BF561525	Rn.23284	Transcribed locus
647	1386069_at	-0.470534266	0.721697286	yes	yes	no	Rn.19192.1	BF549554	Rn.63937	Transcribed locus
648	1372629_at	-0.470041092	0.721944035	yes	yes	no	Rn.8477.1	BF285818	Rn.8477	similar to KIAA0925 protein
649	1377974_at	-0.46992884	0.722000209	yes	yes	no	Rn.24711.1	AI502837	Rn.72676	Transcribed locus
650	1390315_a_at	-0.469915381	0.722006945	yes	yes	no	Rn.24931.3	AA875438	Rn.24931	similar to KIAA0913 protein (predicted)
651	1377212_at	-0.469654376	0.722137578	yes	no	no	Rn.62985.1	BF416289	Rn.39281	Similar to Serologically defined colon cancer antigen 13

652	1383939_at	-0.469145755	0.722392212	yes	yes	no	Rn.23630.1	BG378849	Rn.23630	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
653	1389427_at	-0.468474223	0.722728543	yes	yes	no	Rn.13467.1	BM386487	---	---
654	1391976_at	-0.46833081	0.72280039	yes	no	no	Rn.12316.1	BI286417	Rn.12316	Transcribed locus
655	1397027_at	-0.468277615	0.722827042	yes	no	no	Rn.58511.1	BF396069	Rn.53998	Alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase
656	1383905_at	-0.468225485	0.722853161	yes	no	no	Rn.17596.1	BF401729	Rn.17596	Transcribed locus
657	1372272_at	-0.466688004	0.723623916	yes	yes	no	Rn.17306.1	BF394074	Rn.139064	Transcribed locus, strongly similar to NP_780454.1 hypothetical protein LOC76789 [Mus musculus]
658	1383378_at	-0.466156394	0.723890609	yes	yes	no	Rn.14926.1	BI298932	Rn.14926	Transcribed locus
659	1392596_at	-0.465868018	0.72403532	yes	no	no	Rn.19996.1	BF420447	Rn.19996	Transcribed locus
660	1391643_at	-0.465795571	0.724071679	yes	yes	no	Rn.79389.1	BI290758	---	---
661	1390886_at	-0.465470505	0.724234845	yes	yes	no	Rn.7030.1	BE111565	Rn.7030	Similar to hypothetical protein D3Ertd789e (predicted)
662	1392122_x_at	-0.465369506	0.724285548	yes	no	no	Rn.26793.2	BF559040	Rn.33401	similar to Btk-PH-domain binding protein
663	1375675_at	-0.46511986	0.72441089	yes	no	no	Rn.1940.1	AA892813	Rn.1940	Muscleblind-like 2 (predicted)
664	1368513_at	-0.46511879	0.724411428	yes	no	no	Rn.53979.1	AW144216	Rn.53979	glutamyl aminopeptidase
665	1387242_at	-0.465073531	0.724434154	yes	no	no	Rn.10022.1	NM_019335	Rn.10022	Protein kinase, interferon-inducible double stranded RNA dependent
666	1381118_at	-0.464775305	0.72458392	yes	yes	no	Rn.46278.1	AW526652	Rn.40865	similar to RIKEN cDNA 2700007P21 (predicted)
667	1373183_at	-0.46421669	0.724864535	yes	no	no	Rn.19806.1	AI229780	Rn.19806	Transcribed locus
668	1374546_at	-0.463342756	0.725303766	yes	no	no	Rn.25249.1	AW918040	Rn.34287	Protocadherin 17 (predicted)
669	1379970_at	-0.463316959	0.725316735	yes	yes	no	Rn.45963.1	AW525048	Rn.6202	similar to Eph receptor A4
670	1375870_a_at	-0.463261528	0.725344603	yes	yes	no	Rn.12152.1	BF420140	Rn.145202	RNA binding motif, single stranded interacting protein 1 (predicted)
671	1378717_at	-0.46322441	0.725363266	yes	no	no	Rn.57341.1	BF390952	Rn.57341	Transcribed locus
672	1382161_at	-0.463187355	0.725381896	yes	yes	no	Rn.16364.1	AA817668	Rn.103228	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (predicted)
673	1391866_at	-0.463145171	0.725403107	yes	yes	no	Rn.18968.1	AI014116	Rn.18968	Transcribed locus

674	1391143_at	-0.463107385	0.725422106	yes	no	no	Rn.51763.1	BF405315	Rn.138933	Similar to Pleckstrin homology domain containing, family A member 6
675	1372385_at	-0.463097642	0.725427005	yes	no	no	Rn.9237.1	AA957292	---	---
676	1369472_a_at	-0.463087347	0.725432182	yes	no	no	Rn.9825.1	NM_031018	Rn.9825	activating transcription factor 2
677	1384783_at	-0.462719486	0.725617177	yes	no	no	Rn.79083.1	BI289823	Rn.64095	zinc finger protein 161
678	1369066_at	-0.462566551	0.725694102	yes	no	no	Rn.6406.1	NM_053585	Rn.90117	MAP-kinase activating death domain
679	1383095_at	-0.462074528	0.725941638	yes	no	no	Rn.16886.1	BM387808	Rn.16886	Similar to RIKEN cDNA E230015L20 gene
680	1384362_at	-0.461683124	0.726138613	yes	no	no	Rn.43308.1	BF392187	Rn.43308	Transcribed locus
681	1384888_at	-0.461408554	0.726276823	yes	no	no	Rn.72499.1	AI547911	Rn.128305	suppressor of cytokine signaling 7 (predicted)
682	1384392_at	-0.461183568	0.726390093	yes	no	no	Rn.9325.1	BF397093	Rn.19898	cytochrome P450, family 26, subfamily b, polypeptide 1
683	1368190_at	-0.461128741	0.726417699	yes	yes	no	Rn.9831.1	J02941	Rn.9831	renin 1
684	1368171_at	-0.460470016	0.726749452	yes	no	no	Rn.11372.1	NM_017061	Rn.11372	lysyl oxidase
685	1395155_at	-0.460419925	0.726774686	yes	yes	no	Rn.74086.1	BF386083	Rn.44430	SEC10-like 1 (S. cerevisiae)
686	1389158_at	-0.460325257	0.726822377	yes	no	no	Rn.22482.1	BE329196	Rn.22482	Transcribed locus
687	1395114_at	-0.460054016	0.72695904	yes	no	no	Rn.79550.1	BI294247	Rn.148045	Transcribed locus
688	1382918_at	-0.459890596	0.727041391	yes	yes	no	Rn.8626.1	AA956561	Rn.147475	Transcribed locus
689	1397880_at	-0.459405763	0.727285761	yes	no	no	Rn.52531.1	BF389592	Rn.101953	Similar to serine/threonine kinase
690	1376379_a_at	-0.459399646	0.727288845	yes	yes	no	Rn.41221.1	AW252141	Rn.32842	similar to RIKEN cDNA 2310004I24 gene (predicted)
691	1385675_at	-0.45832215	0.727832233	yes	no	no	Rn.66437.1	BG376858	---	---
692	1387824_at	-0.458246767	0.727870265	yes	yes	no	Rn.53896.1	NM_020092	Rn.53896	splicing factor, arginine/serine-rich 12
693	1390811_at	-0.457904126	0.728043155	yes	no	no	Rn.23072.1	BI290344	Rn.99117	similar to Wdr8 protein
694	1382820_at	-0.456735781	0.728632988	yes	yes	no	Rn.40573.1	AI176342	Rn.40573	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
695	1391240_at	-0.455878734	0.729065968	yes	yes	no	Rn.18061.1	AI013954	---	---
696	1395222_at	-0.455848487	0.729081254	yes	no	no	Rn.33770.1	BF287049	Rn.4001	Similar to FCH domain only 2
697	1381163_at	-0.454973194	0.729523727	yes	yes	no	Rn.37378.1	AI229248	Rn.37378	Transcribed locus
698	1393428_at	-0.454949515	0.729535701	yes	yes	no	Rn.14806.1	BF398638	Rn.14806	Transcribed locus
699	1389159_at	-0.454863252	0.729579323	yes	yes	no	Rn.16626.1	BM385437	Rn.16626	Transcribed locus
700	1372760_at	-0.454761019	0.729631025	yes	no	no	Rn.22509.1	AI176579	Rn.119131	LOC499304
701	1393409_at	-0.454296373	0.729866053	yes	no	no	Rn.18723.1	AW143298	Rn.148983	Transcribed locus

702	1398427_at	-0.454210715	0.72990939	yes	no	no	Rn.46103.1	AW526160	Rn.89018	Myocyte enhancer factor 2D
703	1395374_at	-0.453558219	0.730239584	yes	yes	no	Rn.56110.1	BF548045	Rn.13544	Transcribed locus
704	1375990_a_at	-0.453315052	0.730362677	yes	yes	no	Rn.34609.2	BF284519	Rn.34609	Transcribed locus
705	1398487_at	-0.453311404	0.730364524	yes	yes	no	Rn.62666.1	BF419639	Rn.131549	pre-B-cell leukemia transcription factor 1 (predicted)
706	1368362_a_at	-0.452797565	0.730624701	yes	yes	no	Rn.9834.3	M16347	Rn.9834	asialoglycoprotein receptor 2
707	1388747_at	-0.452398812	0.73082667	yes	no	no	Rn.39119.1	BG381002	Rn.130261	leucine carboxyl methyltransferase 1
708	1384156_at	-0.452285372	0.730884137	yes	no	no	Rn.35244.1	BI293851	---	---
709	1389562_at	-0.452244523	0.730904832	yes	yes	no	Rn.43242.1	BF396686	Rn.43242	Transcribed locus
710	1373401_at	-0.452062555	0.730997028	yes	no	no	Rn.12723.1	AI176034	Rn.152256	Transcribed locus
711	1391444_at	-0.451483798	0.731290336	yes	yes	no	Rn.45255.1	BF285611	Rn.45255	Similar to teratocyte-specific carboxylesterase
712	1382212_at	-0.451376127	0.731344916	yes	yes	no	Rn.19027.1	AI385201	Rn.94884	Transcribed locus
713	1380466_at	-0.451319277	0.731373735	yes	yes	no	Rn.14723.1	BG670778	Rn.137505	Transcribed locus
714	1379565_at	-0.451175712	0.731446519	yes	yes	no	Rn.23031.1	AA956791	Rn.23031	cAMP responsive element binding protein 3-like 2 (predicted)
715	1388452_at	-0.451017992	0.731526487	yes	no	no	Rn.15590.1	AI716904	Rn.15590	LOC499428
716	1377889_at	-0.449979426	0.732053288	yes	yes	no	Rn.12586.1	BM388416	Rn.95642	similar to human mRNA for KIAA0539 protein
717	1384680_at	-0.449501962	0.732295603	yes	yes	no	Rn.23047.1	AA924336	Rn.95344	Mitochondrial tumor suppressor 1
718	1368373_at	-0.449256383	0.732420266	yes	no	no	Rn.21234.1	NM_019343	Rn.114591	regulator of G-protein signaling 7
719	1394077_at	-0.447620024	0.733251477	yes	yes	no	Rn.19396.1	BF548080	Rn.144843	ras homolog gene family, member E
720	1379306_at	-0.447377159	0.733374923	yes	yes	no	Rn.19759.1	BE111794	Rn.107172	mitochondrial ribosomal protein L48 (predicted)
721	1373473_a_at	-0.447148163	0.73349134	yes	yes	no	Rn.18480.2	BM386384	Rn.18480	nucleosome assembly protein 1-like 1
722	1372307_at	-0.44695853	0.733587759	yes	no	no	Rn.6554.1	BI275234	Rn.6554	Transcribed locus
723	1376992_a_at	-0.44676403	0.733686666	yes	yes	no	Rn.4112.1	AI058900	Rn.60855	forkhead box R1 (predicted)
724	1383398_at	-0.446721634	0.733708227	yes	yes	no	Rn.19084.1	AI059150	Rn.69726	Similar to integrin alpha 8
725	1397023_at	-0.446598305	0.73377095	yes	no	no	Rn.62501.1	BF414016	Rn.6107	Protein phosphatase 5, catalytic subunit
726	1397348_at	-0.446319538	0.733912748	yes	no	no	Rn.52992.1	BE118444	Rn.52992	Transcribed locus
727	1371771_at	-0.44596046	0.734095437	yes	yes	no	Rn.12602.1	BI274094	Rn.12602	Similar to novel protein
728	1377801_at	-0.445931029	0.734110413	yes	no	no	Rn.25408.1	AI237031	Rn.25408	Similar to BTB (POZ) domain containing 12
729	1379343_at	-0.445147859	0.734509034	yes	no	no	Rn.32655.1	BF404452	Rn.129346	similar to hypothetical protein FLJ22555
730	1388179_at	-0.44511434	0.7345261	yes	no	no	Rn.24240.1	AI548799	Rn.24240	activin receptor IIB
731	1385871_at	-0.445068096	0.734549645	yes	no	no	Rn.18656.1	AA859982	Rn.52518	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)

732	1368747_at	-0.444794402	0.734689009	yes	no	no	Rn.11324.1	NM_031074	Rn.11324	nucleoporin 98
733	1375519_at	-0.444432959	0.734873097	yes	no	no	Rn.11229.3	AI237401	Rn.108235	globin, alpha
734	1375428_at	-0.444342463	0.734919195	yes	no	no	Rn.8051.1	BE099979	Rn.8051	cellular repressor of E1A-stimulated genes (predicted)
735	1382664_at	-0.444334061	0.734923474	yes	no	no	Rn.16258.1	AW525662	Rn.13353	cell division cycle 27 homolog (S. cerevisiae) (predicted)
736	1394473_at	-0.444314966	0.734933202	yes	no	no	Rn.38338.1	AI716206	Rn.94638	PCTAIRE-motif protein kinase 2
737	1372423_at	-0.444234835	0.734974023	yes	no	no	Rn.8546.1	BI286396	Rn.101762	PERP, TP53 apoptosis effector (predicted)
738	1378467_at	-0.443994485	0.735096478	yes	no	no	Rn.6735.1	AA851361	Rn.6735	Transcribed locus
739	1369186_at	-0.44399375	0.735096853	yes	no	no	Rn.37508.1	D85899	Rn.37508	caspase 1
740	1370542_a_at	-0.443846516	0.735171877	yes	no	no	Rn.7728.2	AB030216	Rn.98640	E74-like factor 1
741	1393909_at	-0.443336284	0.735431928	yes	no	no	Rn.27855.1	BF544438	Rn.57428	similar to KIAA1841 protein (predicted)
742	1372977_at	-0.443223979	0.735489179	yes	no	no	Rn.66324.1	BI291366	Rn.145860	similar to mitogen-activated protein kinase kinase kinase kinase 5 isoform 2
743	1387099_at	-0.44297631	0.735615452	yes	no	no	Rn.32984.1	NM_053838	Rn.32984	natriuretic peptide receptor 2
744	1384901_at	-0.442859782	0.735674871	yes	no	no	Rn.38850.1	BF523017	Rn.6909	Zinc finger protein 451 (predicted)
745	1391127_at	-0.442276306	0.735972464	yes	no	no	Rn.24253.1	BF400818	Rn.60067	Cell division cycle 42 homolog (S. cerevisiae)
746	1397589_at	-0.442186977	0.736018035	yes	no	no	Rn.73063.1	BI296502	Rn.73063	Transcribed locus
747	1393817_at	-0.441713361	0.736259699	yes	no	no	Rn.19905.1	AI070991	Rn.151901	Transcribed locus
748	1395928_at	-0.441104326	0.736570577	yes	no	no	Rn.50316.1	BE102495	Rn.29848	Nuclear receptor subfamily 1, group D, member 1
749	1397541_at	-0.439990888	0.737139264	yes	no	no	Rn.38701.1	BG671148	Rn.8466	Transcribed locus
750	1376584_at	-0.439304518	0.737490046	yes	no	no	Rn.27685.1	BE116408	Rn.27685	Transcribed locus
751	1382748_at	-0.439283023	0.737501034	yes	no	no	Rn.54738.1	AI145481	---	---
752	1393156_at	-0.438658921	0.737820142	yes	no	no	Rn.45144.1	BI278333	Rn.45144	Mannan-binding lectin serine protease 2
753	1392564_at	-0.437761507	0.738279238	yes	no	no	Rn.20490.1	BI299176	Rn.106040	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) (predicted)
754	1384090_at	-0.43751773	0.738403998	yes	no	no	Rn.55666.1	AW920561	Rn.123611	phosphatidylinositol glycan anchor biosynthesis, class O
755	1380236_at	-0.435147031	0.739618373	yes	no	no	Rn.72013.1	BM390141	Rn.9198	Eomesodermin
756	1369682_at	-0.434745325	0.739824342	yes	no	no	Rn.11342.1	NM_013103	Rn.11342	transcription factor 2
757	1368246_at	-0.434709113	0.739842912	yes	no	no	Rn.11007.1	NM_133305	Rn.11007	adaptor-related protein complex 3, mu 2 subunit
758	1392559_at	-0.434390133	0.74000651	yes	no	no	Rn.56018.1	BM383442	Rn.56018	similar to mKIAA0701 protein

759	1381430_at	-0.434311131	0.740047034	yes	no	no	Rn.40471.1	AI010149	---	---
760	1387368_at	-0.434064142	0.74017374	yes	no	no	Rn.10641.1	NM_012981	Rn.10641	muscle and microspikes RAS
761	1381940_at	-0.433988851	0.740212369	yes	no	no	Rn.28619.1	AW527798	Rn.28619	Transcribed locus
762	1383336_at	-0.433913857	0.740250848	yes	no	no	Rn.38987.1	BF549763	Rn.38987	similar to pinin
763	1375004_at	-0.433405819	0.74051157	yes	no	no	Rn.18521.1	BF409055	Rn.18521	similar to KTSR5831
764	1394932_at	-0.432926429	0.740757673	yes	no	no	Rn.55065.1	AW534255	Rn.41269	Transcribed locus
765	1376414_x_at	-0.43052894	0.741989698	yes	no	no	Rn.24931.1	BE109634	Rn.24931	similar to KIAA0913 protein (predicted)
766	1386229_at	-0.430286016	0.742114646	yes	no	no	Rn.28069.1	AI101392	Rn.99641	similar to CBF1 interacting corepressor (predicted)
767	1386889_at	-0.430271793	0.742121962	yes	no	no	Rn.2627.1	BE107760	Rn.83595	stearoyl-Coenzyme A desaturase 2
768	1394984_at	-0.430227356	0.74214482	yes	no	no	Rn.79874.1	BI297127	Rn.6839	trinucleotide repeat containing 6 (predicted)
769	1377010_at	-0.429925445	0.742300145	yes	no	no	Rn.20937.1	BI274499	Rn.20937	similar to 2610317D23Rik protein
770	1386876_at	-0.429027469	0.742762318	yes	no	no	Rn.3313.1	NM_012821	Rn.3313	adenylate cyclase 6
771	1367740_at	-0.42900981	0.74277141	yes	no	no	Rn.1472.1	M14400	Rn.1472	creatine kinase, brain
772	1398594_at	-0.428907719	0.742823973	yes	no	no	Rn.22289.2	AI029767	Rn.22289	Tial1 cytotoxic granule-associated RNA binding protein-like 1
773	1392289_at	-0.42834074	0.74311596	yes	no	no	Rn.77549.1	BI276179	---	---
774	1396663_at	-0.428164447	0.743206772	yes	no	no	Rn.79905.1	BI300284	---	---
775	1387261_at	-0.428132025	0.743223474	yes	no	no	Rn.11063.1	NM_017042	Rn.11063	protein phosphatase 3, catalytic subunit, beta isoform
776	1377825_at	-0.427074982	0.743768224	yes	no	no	Rn.40256.1	AI411841	Rn.121336	Transcribed locus
777	1392997_at	-0.42687291	0.743872408	yes	no	no	Rn.6405.1	BF556742	Rn.11876	protein phosphatase 4, regulatory subunit 2 (predicted)
778	1380404_at	-0.426833029	0.743892971	yes	no	no	Rn.14586.1	H31722	---	---
779	1372275_at	-0.426254565	0.744191303	yes	no	no	Rn.11436.1	BI296757	Rn.11436	Transcribed locus
780	1395776_at	-0.425832046	0.744409284	yes	no	no	Rn.62780.1	BF396580	Rn.153884	Transcribed locus
781	1394388_at	-0.424142338	0.745281659	yes	no	no	Rn.34289.1	AA858844	Rn.149218	CDNA clone MGC:105701 IMAGE:7309421
782	1389252_at	-0.423838954	0.745438401	yes	no	no	Rn.16702.1	AI102190	Rn.92325	Transcribed locus
783	1381847_at	-0.423765564	0.745476323	yes	no	no	Rn.27472.1	AI137632	Rn.27472	Similar to BC021442 protein
784	1398434_at	-0.423740449	0.7454893	yes	no	no	Rn.8782.1	BE107465	Rn.8782	Death associated transcription factor 1 (predicted)
785	1373579_at	-0.422929687	0.745908366	yes	no	no	Rn.7908.1	AA945758	Rn.91057	retinoic acid receptor, alpha
786	1372725_at	-0.422837606	0.745955976	yes	no	no	Rn.1169.1	AI411594	Rn.105328	similar to phospholipid scramblase 2
787	1380402_at	-0.422660094	0.746047765	yes	no	no	Rn.1287.1	AA818127	Rn.145982	BCL2-associated athanogene 4

788	1369820_at	-0.421605676	0.746593226	yes	no	no	Rn.81062.1	NM_053951	Rn.81062	mcf.2 transforming sequence-like
789	1385314_at	-0.421379415	0.746710325	yes	no	no	Rn.5837.3	AA923974	Rn.147371	Transcribed locus
790	1381789_at	-0.421266511	0.746768764	yes	no	no	Rn.27809.1	BM384022	Rn.27809	similar to lysozyme homolog (predicted)
791	1368053_at	-0.421190414	0.746808154	yes	no	no	Rn.31803.1	NM_031235	Rn.31803	par-3 (partitioning defective 3) homolog (C. elegans)
792	1377849_at	-0.420506719	0.747162152	yes	no	no	Rn.22017.1	BI284363	Rn.21693	valosin-containing protein (p97)/p47 complex-interacting protein 135
793	1377992_at	-0.419723813	0.747567724	yes	no	no	Rn.26636.1	AI111775	Rn.26636	Transcribed locus
794	1383877_a_at	-0.419326241	0.747773764	yes	no	no	Rn.784.1	AW433647	Rn.95111	Transcribed locus
795	1373173_at	-0.41825975	0.748326749	yes	no	no	Rn.11919.1	BM390182	---	---
796	1390271_at	-0.417459611	0.748741897	yes	no	no	Rn.66183.1	BM392202	Rn.138933	similar to Pleckstrin homology domain containing, family A member 6
797	1389419_at	-0.417289546	0.748830163	yes	no	no	Rn.23543.1	BI296079	Rn.23543	Transcribed locus
798	1385757_at	-0.417001908	0.748979477	yes	no	no	Rn.58788.1	BF397258	Rn.133494	Activity and neurotransmitter-induced early gene 1 (ania-1) mRNA, 3'UTR
799	1380381_at	-0.416790005	0.749089495	yes	no	no	Rn.41558.1	AI709513	Rn.98222	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase) (predicted)
800	1384149_at	-0.41660216	0.749187036	yes	no	no	Rn.51825.1	H32531	Rn.57800	similar to hypothetical protein FLJ38348 (predicted)
801	1380496_at	-0.416503592	0.749238224	yes	no	no	Rn.44966.1	BF543485	Rn.102204	ubiquitin conjugation factor E4 A
802	1390983_at	-0.416409408	0.749287138	yes	no	no	Rn.22382.1	AA956823	Rn.22382	Integrin, alpha 6
803	1383896_at	-0.416294314	0.749346916	yes	no	no	Rn.42968.1	BM387943	Rn.116062	CDNA clone MGC:105591 IMAGE:7313723
804	1383603_at	-0.415562507	0.749727119	yes	no	no	Rn.24481.1	BM385552	Rn.24481	Transcribed locus, moderately similar to XP_579465.1 PREDICTED: DNA binding protein N5 [Rattus norvegicus]
805	1381838_at	-0.415446375	0.749787472	yes	no	no	Rn.17625.1	AI548281	Rn.17625	Transcribed locus
806	1395455_at	-0.415160026	0.749936306	yes	no	no	Rn.26836.1	AI713082	Rn.147253	Transcribed locus
807	1380692_at	-0.414457596	0.750301529	yes	no	no	Rn.50630.1	BM387127	Rn.148725	Transcribed locus
808	1396058_at	-0.414193542	0.750438868	yes	no	no	Rn.28439.1	BG669136	Rn.146940	Transcribed locus
809	1383428_at	-0.414061193	0.750507715	yes	no	no	Rn.8146.1	AA923920	Rn.8146	Similar to Thioredoxin domain containing protein 6 (Thioredoxin-

										like protein 2) (Txl-2)
810	1372487_at	-0.413867258	0.750608609	yes	no	no	Rn.3874.1	BI296006	---	hypothetical protein LOC619573
811	1394390_at	-0.413776308	0.75065593	yes	no	no	Rn.51029.1	BF394739	Rn.51029	Transcribed locus
812	1395548_at	-0.413196955	0.750957437	yes	no	no	Rn.52437.1	BG666506	Rn.22316	Epidermal growth factor receptor pathway substrate 15 (predicted)
813	1390590_at	-0.412960134	0.751080718	yes	no	no	Rn.30351.1	AA965207	Rn.11702	protein O-fucosyltransferase 2 (predicted)
814	1372396_at	-0.41286548	0.751129997	yes	no	no	Rn.21057.1	BE113316	Rn.21057	Similar to 2310047B19Rik protein (predicted)
815	1375862_at	-0.411914444	0.751625312	yes	no	no	Rn.40541.1	BM384701	---	---
816	1391862_at	-0.411325107	0.751932411	yes	no	no	Rn.66800.1	BG377635	Rn.54356	Transcribed locus
817	1388724_at	-0.411296975	0.751947074	yes	no	no	Rn.14862.1	BF284434	Rn.14862	cell division cycle 40 homolog (yeast) (predicted)
818	1369828_at	-0.409503304	0.752882534	yes	no	no	Rn.42930.1	NM_133555	Rn.42930	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage) /// hypothetical gene supported by NM_133555
819	1376411_at	-0.409401133	0.752935855	yes	no	no	Rn.30700.1	BE107062	Rn.30700	Transcribed locus
820	1394205_at	-0.409190344	0.753045872	yes	no	no	Rn.20789.2	AA955942	Rn.33275	LOC499369
821	1386632_at	-0.408407991	0.753454349	yes	no	no	Rn.16907.2	BF547901	Rn.16907	similar to RIKEN cDNA 2610319K07 (predicted)
822	1398398_at	-0.407929084	0.753704503	yes	no	no	Rn.852.1	BI295741	Rn.852	similar to Homeobox protein A10
823	1374971_at	-0.407912018	0.753713418	yes	no	no	Rn.16576.1	AA818954	Rn.16576	Transcribed locus
824	1372785_at	-0.407752372	0.753796828	yes	no	no	Rn.3979.3	BG671790	Rn.86973	Transcribed locus
825	1392404_at	-0.40768618	0.753831413	yes	no	no	Rn.79473.1	H33111	Rn.52228	Growth arrest specific 6
826	1379352_at	-0.406958126	0.754211929	yes	no	no	Rn.22148.1	BF406008	Rn.146140	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha (predicted)
827	1374093_at	-0.406865069	0.754260579	yes	no	no	Rn.23791.1	BE108840	Rn.23791	Transcribed locus
828	1374491_at	-0.406734803	0.754328687	yes	no	no	Rn.8312.1	AI408279	Rn.103184	chemokine-like factor super family 8
829	1374697_at	-0.406679955	0.754357365	yes	no	no	Rn.20730.1	AI178056	Rn.20730	neuronal RhoA GEF protein
830	1388755_at	-0.406513764	0.754444268	yes	no	no	Rn.7740.1	AI179139	Rn.7740	SEC23A (S. cerevisiae) (predicted)
831	1397135_at	-0.405836928	0.754798297	yes	no	no	Rn.49833.1	BE109290	Rn.89331	Discs, large homolog 1 (Drosophila)
832	1389226_at	-0.405725688	0.754856498	yes	no	no	Rn.27145.1	BI295219	Rn.136604	Transcribed locus
833	1397503_at	-0.405104918	0.755181371	yes	no	no	Rn.39286.1	AI555886	Rn.32931	Leucine-rich repeats and calponin homology (CH) domain containing 3

										(predicted)
834	1382955_at	-0.40506766	0.755200874	yes	no	no	Rn.12737.1	BI284296	Rn.100820	G protein-coupled receptor 126 (predicted)
835	1394555_at	-0.404976619	0.755248532	yes	no	no	Rn.36679.1	AI501080	Rn.22873	Similar to KIAA2010 protein (predicted)
836	1380017_at	-0.404769303	0.75535707	yes	no	no	Rn.34663.1	BE103930	Rn.153030	Transcribed locus
837	1389129_at	-0.404744008	0.755370314	yes	no	no	Rn.17377.1	BF282876	Rn.17377	similar to mKIAA0665 protein (predicted)
838	1382045_at	-0.403858952	0.755833856	yes	no	no	Rn.15910.1	BI304056	Rn.15910	TBC1 domain family, member 15 (predicted)
839	1375819_at	-0.403619021	0.755959567	yes	no	no	Rn.22071.1	BI299678	---	similar to RIKEN cDNA 1200011I18 (predicted)
840	1397706_at	-0.403502575	0.756020587	yes	no	no	Rn.48640.1	BF388794	Rn.48640	Transcribed locus
841	1387185_at	-0.4031953	0.756181626	yes	no	no	Rn.30067.1	NM_053957	Rn.30067	amyloid beta (A4) precursor protein-binding, family B, member 3
842	1388799_at	-0.403170476	0.756194638	yes	no	no	Rn.8854.1	BG374559	Rn.8854	kelch-like 7 (Drosophila) (predicted)
843	1388796_at	-0.402775307	0.756401796	yes	no	no	Rn.8228.1	AI169291	Rn.8228	Transcribed locus
844	1394182_at	-0.402560164	0.756514603	yes	no	no	Rn.47929.2	AI178892	Rn.2567	Myotubularin related protein 4 (predicted)
845	1383303_at	-0.402267515	0.756668077	yes	no	no	Rn.28004.1	BI282211	Rn.88644	SA rat hypertension-associated homolog
846	1391431_at	-0.402250808	0.756676839	yes	no	no	Rn.18247.1	AI712476	Rn.153891	Transcribed locus
847	1397529_at	-0.402146938	0.75673132	yes	no	no	Rn.49255.1	BI296754	Rn.105298	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (predicted)
848	1389367_at	-0.401876311	0.756873284	yes	no	no	Rn.22212.1	AI409747	Rn.22212	schwannomin interacting protein 1 (predicted)
849	1377730_at	-0.401116509	0.757272	yes	no	no	Rn.23702.1	BF290890	Rn.90167	similar to HSPC288 (predicted)
850	1379906_at	-0.401034146	0.757315233	yes	no	no	Rn.16400.1	BM385311	Rn.10624	ATPase, Na+/K+ transporting, beta 2 polypeptide
851	1393862_at	-0.400934788	0.757367391	yes	no	no	Rn.68012.1	AW530492	Rn.145636	similar to RIKEN cDNA 1700019G17
852	1387376_at	-0.400096445	0.757807622	yes	no	no	Rn.15681.1	NM_019363	Rn.15681	aldehyde oxidase 1
853	1389558_at	-0.400083872	0.757814226	yes	no	no	Rn.17799.1	BF281962	Rn.17799	Transcribed locus
854	1393438_at	-0.399923345	0.757898552	yes	no	no	Rn.40708.1	AI710341	Rn.40708	Zinc finger protein 316 (predicted)
855	1381705_at	-0.399859082	0.757932312	yes	no	no	Rn.49094.1	BE110067	Rn.13643	Pantothenate kinase 3 (predicted)
856	1379488_at	-0.399700771	0.758015487	yes	no	no	Rn.19574.1	BI274525	Rn.19574	TP53 regulating kinase (predicted)
857	1388540_at	-0.399626195	0.758054671	yes	no	no	Rn.11948.1	BM390828	---	---
858	1389463_at	-0.399490596	0.758125924	yes	no	no	Rn.14623.1	BG375376	Rn.145151	protein kinase, cAMP dependent regulatory, type I, beta
859	1394010_at	-0.398875044	0.758449461	yes	no	no	Rn.69014.2	H32100	Rn.23988	hepatitis B virus x associated protein

										(predicted)
860	1385506_at	-0.398418218	0.75868966	yes	no	no	Rn.74577.1	AW530507	Rn.153184	Transcribed locus
861	1372243_at	-0.398386118	0.758706542	yes	no	no	Rn.4011.1	BE112280	Rn.103055	calcium binding protein 39 (predicted)
862	1387598_at	-0.398371753	0.758714096	yes	no	no	Rn.10576.1	NM_031133	Rn.10576	thrombopoietin
863	1397565_at	-0.398366913	0.758716642	yes	no	no	Rn.32866.1	BI296579	Rn.1993	Syntaxin 7
864	1372995_at	-0.398307714	0.758747775	yes	no	no	Rn.15035.1	AI703715	Rn.15035	similar to protein kinase D2 (predicted)
865	1368009_at	-0.398100668	0.758856674	yes	no	no	Rn.18753.1	NM_053765	Rn.18753	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
866	1379261_at	-0.397983249	0.758918438	yes	no	no	Rn.12413.2	BE111490	Rn.40571	family with sequence similarity 33, member A (predicted)
867	1398595_at	-0.397835693	0.758996063	yes	no	no	Rn.21327.1	AI070585	Rn.17033	RNA binding motif protein 5 (predicted)
868	1389319_at	-0.397730615	0.759051346	yes	no	no	Rn.6624.1	AA800719	Rn.98517	Transcribed locus, strongly similar to NP_080446.1 hypothetical protein LOC67458 [Mus musculus]
869	1393792_at	-0.397673105	0.759081604	yes	no	no	Rn.65718.1	AI029501	Rn.65718	Similar to hypothetical protein FLJ23451
870	1395552_s_at	-0.397669413	0.759083547	yes	no	no	Rn.76806.1	BG671371	Rn.100818	Similar to novel protein
871	1392144_at	-0.397656202	0.759090498	yes	no	no	Rn.57536.1	BF391491	Rn.20579	5'-nucleotidase, cytosolic II-like 1 (predicted)
872	1390386_at	-0.397100114	0.759383147	yes	no	no	Rn.4185.1	BM387008	Rn.10562	caspase 3
873	1392818_at	-0.396638931	0.759625936	yes	no	no	Rn.81393.1	BM384139	Rn.145965	growth arrest specific 5
874	1389578_at	-0.396202185	0.759855931	yes	no	no	Rn.9475.1	AA850740	Rn.9475	ischemia/reperfusion inducible protein
875	1389210_at	0.395586523	1.315477454	yes	no	no	Rn.14256.1	BE109711	Rn.14256	lymphocyte cytosolic protein 1 (predicted)
876	1392090_at	0.396037143	1.315888403	yes	no	no	Rn.28330.1	BG377322	Rn.11698	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1 (predicted)
877	1377952_at	0.396297973	1.316126328	yes	no	no	Rn.50214.1	BE102146	Rn.66171	similar to RIKEN cDNA 2610017G09 (predicted)
878	1388946_at	0.397085216	1.316844702	yes	no	no	Rn.12301.1	AI233763	Rn.105128	similar to hypothetical p38 protein (predicted)
879	1379842_at	0.397118024	1.316874649	yes	no	no	Rn.48839.1	H33639	Rn.102337	suppression of tumorigenicity 7-like
880	1368397_at	0.397172809	1.316924657	yes	no	no	Rn.3686.1	NM_031980	Rn.92528	UDP-glucuronosyltransferase 2 family, member 5 /// UDP glycosyltransferase 2 family, polypeptide B4
881	1381811_at	0.397347726	1.317084335	yes	no	no	Rn.12335.1	BM385405	Rn.92548	Transcribed locus
882	1371451_at	0.399370428	1.318932222	yes	no	no	Rn.3693.1	AI010940	Rn.3693	ribonuclease H2, large subunit (predicted)

883	1397540_at	0.399997271	1.319505415	yes	no	no	Rn.26910.1	BF398168	Rn.146195	Transcribed locus
884	1367904_at	0.400085605	1.319586208	yes	no	no	Rn.2225.1	NM_019278	Rn.66430	regulated endocrine-specific protein 18
885	1390855_at	0.400473957	1.319941469	yes	no	no	Rn.25202.1	AI235923	Rn.11058	Prolyl endopeptidase
886	1372768_at	0.401656671	1.321023994	yes	no	no	Rn.22240.1	AW251331	Rn.22240	Similar to RIKEN cDNA 2010009L17 (predicted)
887	1383829_at	0.402122029	1.321450174	yes	no	no	Rn.51470.1	BF392234	Rn.113000	bobby sox homolog (Drosophila) (predicted)
888	1373778_at	0.402890269	1.322154039	yes	no	no	Rn.18425.1	BE349670	Rn.44359	Acetyl-Coenzyme A carboxylase beta
889	1388110_at	0.403047326	1.322297981	yes	no	no	Rn.965.1	X61043	Rn.145038	eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1
890	1371607_at	0.403105022	1.322350863	yes	no	no	Rn.16056.1	AI230787	Rn.91417	microtubule-associated protein 4
891	1382265_at	0.403632534	1.32283446	yes	no	no	Rn.29873.1	AI070061	Rn.96252	similar to KIAA1128 protein (predicted)
892	1368378_at	0.404129771	1.323290465	yes	no	no	Rn.2328.1	NM_022547	Rn.2328	formyltetrahydrofolate dehydrogenase
893	1367528_at	0.404790638	1.323896774	yes	no	no	Rn.812.1	BE103273	Rn.812	F-box and WD-40 domain protein 8 (predicted)
894	1373702_at	0.405148635	1.324225333	yes	no	no	Rn.17236.1	AI171798	---	---
895	1370988_at	0.405531619	1.324576914	yes	no	no	Rn.65184.1	BE349751	---	---
896	1373590_at	0.406714285	1.325663197	yes	no	no	Rn.16958.1	BI295949	Rn.16958	stomatin (predicted)
897	1377064_at	0.406823044	1.325763137	yes	no	no	Rn.13146.1	AI602811	Rn.4313	dual specificity phosphatase 6
898	1398585_at	0.407061465	1.325982252	yes	no	no	Rn.53854.1	BE111456	Rn.138796	F-box only protein 21 (predicted)
899	1379676_a_at	0.407125593	1.326041193	yes	no	no	Rn.23986.2	AW527320	Rn.23986	similar to RIKEN cDNA 2310005K03
900	1389816_at	0.407501728	1.326386959	yes	no	no	Rn.3807.1	AA926357	---	---
901	1386973_a_at	0.408559246	1.327359578	yes	no	no	Rn.44266.1	NM_053777	Rn.44266	mitogen activated protein kinase 8 interacting protein
902	1387135_at	0.409013925	1.327777974	yes	no	no	Rn.28393.1	NM_020308	Rn.98788	a disintegrin and metalloproteinase domain 15 (metargidin)
903	1368000_at	0.409019449	1.327783058	yes	no	no	Rn.11378.1	NM_016994	Rn.11378	complement component 3
904	AFFX-BioB-3_at	0.409933186	1.328624282	yes	no	no	AFFX-BioB-3	AFFX-BioB-3	---	biotin synthesis, sulfur insertion?
905	1370549_at	0.41065307	1.329287411	yes	no	no	Rn.9316.1	U81160	Rn.9316	vacuolar protein sorting 45 (yeast)
906	1387546_at	0.411002911	1.329609791	yes	no	no	Affx.1.1	NM_138916	Rn.48817	CDC2-related kinase 7
907	1387028_a_at	0.411522514	1.330088751	yes	no	no	Rn.2113.2	M86708	Rn.2113	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)
908	1393108_at	0.412033195	1.330559656	yes	no	no	Rn.25539.1	BM387813	Rn.116594	RT1 class I, A3

909	1397675_at	0.412107683	1.330628356	yes	no	no	Rn.79423.1	H31800	Rn.79423	eukaryotic translation initiation factor 4H
910	1369204_at	0.41256665	1.331051738	yes	no	no	Rn.10945.1	NM_013185	Rn.10945	hemopoietic cell kinase
911	1382471_at	0.412834011	1.331298432	yes	no	no	Rn.12878.1	AI709698	Rn.12878	similar to hypothetical protein MGC10993 (predicted)
912	1372002_at	0.41328392	1.331713667	yes	no	no	Rn.2731.1	AI411352	Rn.10346	gap junction membrane channel protein alpha 1
913	1385706_at	0.413870218	1.332254973	yes	no	no	Rn.9616.3	BI292758	Rn.44847	Similar to Testis derived transcript
914	1379497_at	0.413893316	1.332276302	yes	no	no	Rn.24928.1	BI275261	---	---
915	1384340_a_at	0.414532119	1.332866344	yes	no	no	Rn.12061.2	AA997134	Rn.12061	similar to N-acetyltransferase ARD1
916	1379114_at	0.415342545	1.333615285	yes	no	no	Rn.49081.1	BF412325	Rn.27737	Similar to KIAA0303 (predicted)
917	1395871_at	0.41610662	1.334321777	yes	no	no	Rn.82282.1	H31553	Rn.104585	similar to DNA topoisomerase (ATP-hydrolysing)
918	1377635_at	0.416548333	1.334730371	yes	no	no	Rn.3928.1	BM389350	Rn.3928	flavin containing monooxygenase 2
919	AFFX-ThrX-3_at	0.418141078	1.336204736	yes	no	no	AFFX-ThrX-3	AFFX-ThrX-3	---	---
920	1370031_at	0.41939903	1.337370343	yes	no	no	Rn.10734.1	NM_031685	Rn.13518	golgi SNAP receptor complex member 2
921	1398878_at	0.41958001	1.337538121	yes	no	no	Rn.22470.1	Y17326	Rn.142318	similar to CPSF4 protein
922	1382683_a_at	0.421937105	1.339725196	yes	no	no	Rn.3564.2	AA891943	---	---
923	1376501_at	0.422302059	1.340064144	yes	no	no	Rn.7830.1	AA945062	Rn.7830	Rho GTPase activating protein 8
924	1373746_at	0.422310746	1.340072213	yes	no	no	Rn.48631.1	BM390756	Rn.6558	similar to HSPC049 protein (predicted)
925	1377648_at	0.425681609	1.343206958	yes	no	no	Rn.2666.1	BF414047	Rn.2666	similar to KIAA1838 protein (predicted)
926	1397924_at	0.425778599	1.343297263	yes	no	no	Rn.45655.1	AW523490	Rn.141091	Transcribed locus, moderately similar to NP_666195.1 splicing factor, arginine/serine-rich 7 [Mus musculus]
927	1383808_at	0.425783657	1.343301973	yes	no	no	Rn.21877.1	AA818423	Rn.99535	tubulin tyrosine ligase-like 1 (predicted)
928	1390755_at	0.426043312	1.34354376	yes	no	no	Rn.12493.1	BE105876	Rn.136576	similar to Gnefr protein
929	1370207_at	0.426735493	1.344188525	yes	no	no	Rn.29258.1	AI170772	Rn.29258	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 /// similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
930	1369775_at	0.427128133	1.344554406	yes	no	no	Rn.21324.1	NM_022799	Rn.21324	nuclear ubiquitous casein kinase and cyclin-

										dependent kinase substrate
931	1374665_at	0.427323641	1.344736626	yes	no	no	Rn.53.1	BG057541	Rn.53	similar to Gem (nuclear organelle) associated protein 4
932	1387843_at	0.427798944	1.345179729	yes	no	no	Rn.22500.1	NM_012561	Rn.2743	follistatin
933	1391397_at	0.428040758	1.345405217	yes	no	no	Rn.20783.1	BF418393	Rn.20783	Transcribed locus
934	1372428_at	0.428648337	1.345971943	yes	no	no	Rn.20233.1	BG380252	Rn.91398	DnaJ (Hsp40) homolog, subfamily C, member 4 (predicted)
935	1383891_a_at	0.429146264	1.346436567	yes	no	no	Rn.12917.1	AA997097	Rn.12917	similar to RIKEN cDNA 2810417J12 gene (predicted)
936	1369964_at	0.429711729	1.346964407	yes	no	no	Rn.6990.1	NM_130411	Rn.6990	coronin, actin binding protein 1A
937	1367464_at	0.431549014	1.348680871	yes	no	no	Rn.21553.1	AI598391	Rn.96174	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1
938	1396559_at	0.43187372	1.348984452	yes	no	no	Rn.58781.1	BF396566	Rn.146976	Transcribed locus
939	1378131_at	0.433043078	1.350078297	yes	no	no	Rn.16082.1	AI045015	Rn.16082	Similar to solute carrier family 9 (sodium/hydrogen exchanger), isoform 9
940	1390164_at	0.433434948	1.35044506	yes	no	no	Rn.23225.1	BE099850	Rn.23225	Transcribed locus
941	1368550_at	0.433705139	1.350697997	yes	no	no	Rn.10101.1	NM_022858	Rn.10101	HNF-3/forkhead homolog-1 /// hypothetical gene supported by NM_022858
942	1385877_at	0.433851517	1.350835049	yes	no	no	Rn.16147.1	BI294012	Rn.86568	Transcribed locus
943	1370968_at	0.434521206	1.351462242	yes	no	no	Rn.2411.1	AA858801	Rn.2411	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105
944	1372207_at	0.435034401	1.35194307	yes	no	no	Rn.8076.1	AI549477	Rn.98723	bromodomain containing 8 (predicted)
945	1390288_at	0.435694821	1.352562088	yes	no	no	Rn.17994.1	AI013362	Rn.17994	protein serine kinase H1 (predicted)
946	1374332_at	0.436468302	1.35328744	yes	no	no	Rn.22269.1	AI171365	Rn.95332	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (predicted)
947	1374002_at	0.437213977	1.353987084	yes	no	no	Rn.18346.1	AI045904	---	---
948	1381363_at	0.437250167	1.35402105	yes	no	no	Rn.32960.1	BF388580	Rn.32960	Low density lipoprotein receptor-related protein 6 (predicted)
949	1375443_at	0.437347996	1.354112869	yes	no	no	Rn.22319.1	BF420090	---	---

950	1379332_at	0.437851147	1.354585208	yes	no	no	Rn.39063.1	AI556426	Rn.39063	Transcribed locus, strongly similar to XP_417265.1 PREDICTED: similar to F-box-WD40 repeat protein 6 [Gallus gallus]
951	1376431_at	0.439711433	1.356333007	yes	no	no	Rn.12585.1	BM387357	Rn.103851	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)
952	1397744_at	0.440177783	1.356771512	yes	no	no	Rn.27982.1	BI276183	Rn.87166	Dopamine beta hydroxylase
953	1374292_at	0.440200577	1.356792948	yes	no	no	Rn.21760.1	BF414124	Rn.153567	similar to RIKEN cDNA 1110031I02 (predicted)
954	1377869_at	0.442168492	1.358644951	yes	no	no	Rn.15040.1	BI284261	Rn.15040	similar to carbon catabolite repression 4 protein homolog
955	1397220_at	0.442691988	1.359138038	yes	no	no	Rn.72755.1	AW534601	---	---
956	1390739_at	0.44337834	1.359784792	yes	no	no	Rn.63559.1	BE118828	---	similar to zinc finger protein 609 /// similar to zinc finger protein 609
957	1395488_at	0.443504629	1.359903829	yes	no	no	Rn.57283.1	BF390807	Rn.57283	mutS homolog 3 (E. coli)
958	1396115_at	0.443668705	1.360058498	yes	no	no	Rn.76345.1	BF566051	Rn.6435	Similar to TRS85 homolog (predicted)
959	1380309_at	0.444001488	1.360372256	yes	no	no	Rn.27856.1	BI273829	Rn.63502	similar to mKIAA0804 protein (predicted)
960	1377772_at	0.444689528	1.36102119	yes	no	no	Rn.43072.1	BI295864	Rn.44829	Transmembrane protein with EGF-like and two follistatin-like domains 1
961	1386956_at	0.445417726	1.361708336	yes	no	no	Rn.3142.1	NM_031541	Rn.88169	scavenger receptor class B, member 1
962	1394241_at	0.445430473	1.361720368	yes	no	no	Rn.59906.1	BF401902	Rn.22069	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)
963	1392686_at	0.445614027	1.36189363	yes	no	no	Rn.20128.1	AI072336	Rn.144991	naked cuticle 2 homolog (Drosophila) (predicted)
964	1379910_at	0.44625664	1.362500388	yes	yes	no	Rn.23657.1	AI136097	---	similar to UDP-N-acteylglucosamine pyrophosphorylase 1 homolog
965	1379597_at	0.446401053	1.36263678	yes	no	no	Rn.24109.1	AI011037	Rn.24109	CDNA clone IMAGE:7301764
966	1397951_at	0.446805547	1.363018881	yes	no	no	Rn.69988.1	BI293109	---	---
967	1376256_at	0.448124774	1.36426582	yes	yes	no	Rn.8557.1	BE108131	Rn.8557	WD repeat and FYVE domain containing 1 (predicted)
968	1380041_at	0.44812822	1.36426908	yes	no	no	Rn.26624.1	BF396849	Rn.91999	Pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)
969	1384363_at	0.448266828	1.364400159	yes	no	no	Rn.19797.1	AI070597	Rn.107123	Shwachman-Bodian-Diamond syndrome (predicted)
970	1377904_at	0.448633713	1.364747177	yes	no	no	Rn.41047.1	BE109251	Rn.23978	Similar to SPT3-associated factor 42

										(predicted)
971	1392477_at	0.448859579	1.364960857	yes	yes	no	Rn.21155.1	AI059914	Rn.76536	ets variant gene 1 (predicted)
972	1373736_at	0.448943594	1.365040347	yes	yes	no	Rn.13717.1	AI178446	Rn.13717	Transcribed locus, weakly similar to NP_082606.1 hypothetical protein LOC72704 [Mus musculus]
973	1396194_at	0.449234436	1.365315562	yes	yes	no	Rn.54305.1	AW434492	Rn.54305	Similar to histone H2b-616
974	1371772_at	0.449402526	1.365474646	yes	yes	no	Rn.30490.1	AI410425	Rn.30490	similar to RIKEN cDNA 1810020C19 gene
975	1390801_at	0.450612408	1.366620249	yes	yes	no	Rn.23870.1	AI412174	Rn.23870	similar to hypothetical protein MGC34760
976	1374358_at	0.450812493	1.366809796	yes	yes	no	Rn.17341.1	BE098806	Rn.50057	similar to CG13901-PA (predicted)
977	1378515_at	0.450983834	1.366972134	yes	no	no	Rn.26529.1	BE116005	Rn.102356	Progesterone receptor membrane component 1
978	1373406_at	0.451407609	1.367373726	yes	yes	no	Rn.6487.1	BM384991	Rn.6487	Torsin family 1, member B (predicted)
979	1368567_at	0.45145809	1.367421571	yes	yes	no	Rn.6452.1	NM_022607	Rn.6452	MIPP65 protein
980	1371265_at	0.452473778	1.368384605	yes	yes	no	Rn.10535.1	X83264	Rn.44344	arginine vasopressin receptor 2
981	1394316_a_at	0.452900837	1.368789727	yes	yes	no	Rn.7077.2	AW920272	Rn.98240	transmembrane 4 superfamily member 9
982	1395886_at	0.452910874	1.368799249	yes	no	no	Rn.69784.1	H31273	Rn.103326	ARP3 actin-related protein 3 homolog (yeast)
983	1374304_at	0.452975105	1.368860192	yes	no	no	Rn.40979.1	AW526081	Rn.40979	X-ray repair cross complementing protein 4
984	1391644_at	0.453245423	1.3691167	yes	yes	no	Rn.49281.1	AW920336	Rn.101864	density-regulated protein
985	1389425_at	0.453916046	1.369753268	yes	no	no	Rn.12084.1	AI408674	Rn.12084	similar to 5(3)-deoxyribonucleotidase
986	1391148_at	0.453916065	1.369753286	yes	yes	no	Rn.9395.1	AA957886	Rn.9395	Transcribed locus
987	1383564_at	0.453925095	1.36976186	yes	yes	no	Rn.6246.1	BF411036	---	---
988	1373526_at	0.45434805	1.370163492	yes	yes	no	Rn.40171.1	AI105153	Rn.98385	similar to autophagy 5-like
989	1397412_at	0.45452531	1.370331851	yes	no	no	Rn.51112.1	BE107094	Rn.133235	Transcribed locus
990	1388157_at	0.455214387	1.37098652	yes	no	no	Rn.9560.1	BE111706	Rn.9560	myristoylated alanine rich protein kinase C substrate
991	1375596_at	0.457258125	1.372930052	yes	yes	no	Rn.73430.1	BI291219	Rn.137091	similar to transient receptor potential cation channel, subfamily M, member 1
992	1372134_at	0.457971576	1.37360917	yes	no	no	Rn.6212.1	AW918650	Rn.6212	coiled-coil-helix-coiled-coil-helix domain containing 6 (predicted)
993	1390813_at	0.458819639	1.37441686	yes	yes	no	Rn.43808.1	AI236624	Rn.43808	Similar to RNA-binding protein Musashi2-S
994	1387969_at	0.459275716	1.374851421	yes	yes	no	Rn.10584.1	U22520	Rn.10584	chemokine (C-X-C motif) ligand 10

995	1396309_at	0.462211124	1.377651637	yes	yes	no	Rn.46324.1	BI292839	Rn.46324	Similar to RIKEN cDNA 2810453K03 (predicted)
996	1390704_at	0.462781666	1.378196564	yes	no	no	Rn.61283.1	BF394953	Rn.12755	SDA1 domain containing 1
997	1373250_at	0.462825436	1.378238378	yes	no	no	Rn.14943.1	AI229404	---	anillin,actinbindingprotein
998	1392466_at	0.464011788	1.379372192	yes	yes	no	Rn.19940.1	BF416266	Rn.19940	similar to CG11737-PA (predicted) /// similar to RIKEN cDNA 2810439K08
999	1375411_at	0.464298979	1.379646805	yes	yes	no	Rn.3422.1	BI277002	Rn.3422	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)
1000	1376029_at	0.465107301	1.380420019	yes	no	no	Rn.11705.1	BI295991	Rn.107413	RAB2, member RAS oncogene family-like
1001	1371091_at	0.46568809	1.380975849	yes	yes	no	Rn.10718.1	BE118080	Rn.10718	unknown protein
1002	1378484_at	0.46782572	1.383023548	yes	no	no	Rn.46094.1	BI279720	Rn.147874	Transcribed locus
1003	1398772_at	0.469139726	1.384283779	yes	yes	no	Rn.2771.1	NM_031981	Rn.2771	NSFL1 (p97) cofactor (p47)
1004	1378575_at	0.469168774	1.384311651	yes	yes	no	Rn.60512.1	BF404457	Rn.60512	Transcribed locus
1005	1379854_at	0.469702826	1.384824185	yes	no	no	Rn.12459.1	AA996933	---	---
1006	1376971_at	0.470599596	1.385685251	yes	yes	no	Rn.41993.1	AI411341	Rn.21798	similar to autophagy 10-like
1007	1373671_at	0.47065925	1.385742549	yes	yes	no	Rn.83.1	AA944790	Rn.83	Hypothetical gene LOC554364
1008	1375707_at	0.471710483	1.386752651	yes	yes	no	Rn.22502.1	AA817993	---	---
1009	1399112_at	0.471841949	1.386879024	yes	yes	no	Rn.7122.1	AI599185	Rn.138027	superkiller viralicidic activity 2-like
1010	1370386_at	0.472824439	1.387823825	yes	yes	no	Rn.37500.2	AB002406	Rn.86410	RuvB-like protein 1
1011	1390139_a_at	0.47337488	1.388353432	yes	no	no	Rn.776.2	BE099622	Rn.776	similar to sallimus CG1915-PC (predicted)
1012	1385007_at	0.473825362	1.388787013	yes	no	no	Rn.77459.1	BI303672	Rn.145033	zinc finger, CCHC domain containing 9 (predicted)
1013	1370957_at	0.476273764	1.391145929	yes	yes	no	Rn.12138.1	BM383427	Rn.12138	interleukin 6 signal transducer
1014	1379646_at	0.476387906	1.391255996	yes	no	no	Rn.23486.1	AI229747	Rn.96035	Similar to CDNA sequence BC024479
1015	1394446_at	0.476448395	1.39131433	yes	no	no	Rn.44094.1	AW523015	Rn.87724	Transcribed locus
1016	1397112_at	0.477627203	1.39245162	yes	no	no	Rn.53698.1	BF415784	Rn.94638	PCTAIRE-motif protein kinase 2
1017	1390034_at	0.478178938	1.392984242	yes	no	no	Rn.25545.1	BF393945	Rn.53963	Transcribed locus
1018	1368159_at	0.478535633	1.393328689	yes	yes	no	Rn.54408.1	NM_080582	Rn.54408	ATP-binding cassette, sub-family B (MDR/TAP), member 6
1019	1383940_at	0.478584659	1.393376038	yes	no	no	Rn.41428.1	BG375704	Rn.41428	cell division cycle associated 1 (predicted)
1020	1389982_at	0.481117071	1.395824027	yes	no	no	Rn.48902.1	BF419586	Rn.127825	LIM homeobox protein 1
1021	1374315_at	0.481976875	1.396656145	yes	no	no	Rn.20014.1	AI228079	Rn.38221	Transcribed locus
1022	1376068_at	0.482434583	1.397099317	yes	yes	no	Rn.17162.1	BF283674	---	---

1023	1376247_at	0.483431982	1.398065528	yes	no	no	Rn.59912.1	BF403197	Rn.35508	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)
1024	1377793_at	0.48345124	1.398084191	yes	no	no	Rn.22781.1	BF407551	Rn.23554	similar to hypothetical protein MGC20460 (predicted)
1025	1383601_at	0.484482468	1.399083888	yes	no	no	Rn.17704.1	BI295614	Rn.130657	DUF729 domain containing 1 (predicted)
1026	1378196_at	0.485507159	1.400077957	yes	no	no	Rn.35465.1	BI290895	Rn.35465	solute carrier family 43, member 1 (predicted)
1027	1372718_at	0.487815681	1.402320078	yes	no	no	Rn.11602.1	AA799572	---	---
1028	1368437_at	0.487990594	1.402490107	yes	yes	no	Rn.9155.1	NM_019174	Rn.51389	carbonic anhydrase 4
1029	1391455_at	0.488197381	1.402691145	yes	no	no	Rn.36848.1	AI228280	Rn.36848	conserved nuclear protein Nhn1
1030	1382718_at	0.488431545	1.402918835	yes	no	no	Rn.15078.2	AA900547	Rn.55459	Nuclear transcription factor, X-box binding 1 (predicted)
1031	1374768_at	0.48860188	1.403084483	yes	no	no	Rn.34654.1	BI279857	Rn.34654	similar to NYD-SP28 protein
1032	1388233_at	0.489561887	1.404018443	yes	no	no	Rn.14523.1	AF065161	Rn.14523	cytokine inducible SH2-containing protein
1033	1398729_s_at	0.489925062	1.404371926	yes	yes	no	Rn.46039.1	AW525946	Rn.46039	Similar to Brain specific membrane-anchored protein precursor (predicted)
1034	1392652_at	0.490354674	1.404790189	yes	no	no	Rn.22782.1	AI060083	Rn.22782	Transcribed locus
1035	1389119_at	0.491378065	1.405787045	yes	no	no	Rn.27588.1	AI105018	Rn.27588	Cardiomyopathy associated 1 (predicted)
1036	1394732_at	0.491488654	1.405894809	yes	no	no	Rn.55738.1	BF289237	Rn.72491	G1 to S phase transition 1
1037	1369104_at	0.491911936	1.406307354	yes	no	no	Rn.44571.1	NM_019142	Rn.87789	protein kinase, AMP-activated, alpha 1 catalytic subunit
1038	1390941_at	0.492177947	1.40656668	yes	no	no	Rn.42854.1	BI277540	Rn.95305	retinoblastoma binding protein 6 (predicted)
1039	1382031_at	0.492646918	1.407023981	yes	yes	no	Rn.2564.1	AA859079	Rn.2564	Transcribed locus
1040	1384073_at	0.493047277	1.407414495	yes	yes	no	Rn.44252.1	BF543577	Rn.17173	alcohol dehydrogenase, iron containing, 1 (predicted)
1041	1372514_s_at	0.493941919	1.40828753	yes	no	no	Rn.3257.1	AA892303	Rn.3257	dynein, axonemal, light chain 4 (predicted)
1042	1392417_s_at	0.49402558	1.408369198	yes	no	no	Rn.44939.1	AI711481	Rn.19574	TP53 regulating kinase (predicted)
1043	1369427_at	0.49408512	1.408427323	yes	no	no	Rn.48702.1	NM_022617	Rn.4301	macrophage expressed gene 1
1044	1387345_at	0.49492059	1.409243184	yes	yes	no	Rn.16691.1	NM_023986	Rn.16691	proteasome (prosome, macropain) activator subunit 4
1045	1372630_at	0.49562375	1.409930207	yes	no	no	Rn.16629.2	AA891828	Rn.105419	RAD23a homolog (S. cerevisiae) (predicted)
1046	1395018_at	0.495774746	1.410077782	yes	no	no	Rn.69556.1	BE119004	Rn.7687	leucyl-tRNA synthetase (predicted)

1047	1381526_at	0.496470782	1.410758246	yes	yes	no	Rn.16053.1	BI293073	Rn.16053	par-6 (partitioning defective 6,) homolog alpha (C. elegans)
1048	1379759_at	0.497146377	1.41141904	yes	no	no	Rn.24864.2	BG377329	Rn.54352	Similar to hypothetical protein FLJ12118 (predicted)
1049	1395376_at	0.498743048	1.412981962	yes	no	no	Rn.33391.1	BE104111	Rn.33391	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (predicted)
1050	1376037_at	0.500244689	1.414453441	yes	yes	no	Rn.19210.1	BF283385	Rn.104730	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) (predicted)
1051	1370458_at	0.500817067	1.415014726	yes	no	no	Rn.17383.1	AF389347	Rn.17383	hepatoma-derived growth factor, related protein 3
1052	1373128_at	0.503890657	1.418032558	yes	yes	no	Rn.2997.1	BI278379	Rn.2997	reticulocalbin 3, EF-hand calcium binding domain
1053	1390113_a_at	0.50406536	1.418204285	yes	yes	no	Rn.24954.1	BI300539	Rn.98804	Similar to KIAA0731 protein (predicted)
1054	1385224_at	0.505585083	1.419698996	yes	yes	no	Rn.16855.1	AA819531	Rn.12627	T-cell, immune regulator 1
1055	1367602_at	0.506047742	1.420154354	yes	yes	no	Rn.31765.1	AI013390	Rn.31765	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
1056	1398661_at	0.50773244	1.421813698	yes	no	no	Rn.66907.1	BG372341	---	---
1057	1397552_at	0.507932097	1.422010479	yes	yes	no	Rn.22926.1	AA899923	Rn.22926	echinoderm microtubule associated protein like 4 (predicted)
1058	1390943_at	0.50860717	1.42267603	yes	yes	no	Rn.22531.1	BE096504	Rn.146065	similar to hypothetical protein dJ465N24.2.1
1059	1379078_at	0.510422379	1.424467177	yes	yes	no	Rn.50754.1	BE105838	Rn.132924	Transcribed locus
1060	1390701_at	0.510639707	1.424681775	yes	yes	no	Rn.15581.1	BG372551	Rn.15581	Transcribed locus
1061	1395968_at	0.510643098	1.424685124	yes	yes	no	Rn.52765.1	BI294877	Rn.127923	similar to mKIAA1783 protein
1062	1386218_at	0.511225693	1.425260563	yes	yes	no	Rn.43066.1	AI639301	Rn.43066	Transcribed locus
1063	1370267_at	0.511244723	1.425279363	yes	yes	no	Rn.10426.1	BF287444	Rn.10426	glycogen synthase kinase 3 beta
1064	1396683_at	0.51142324	1.425455735	yes	yes	no	Rn.49926.1	BE099973	Rn.96035	Similar to CDNA sequence BC024479
1065	1369989_at	0.512347106	1.426368854	yes	yes	no	Rn.6299.1	NM_022601	Rn.6299	pyridoxine 5'-phosphate oxidase
1066	1394112_at	0.513503224	1.427512347	yes	yes	no	Rn.7836.1	AA945123	Rn.126636	Hydroxyacid oxidase 1
1067	1372900_at	0.513528062	1.427536924	yes	yes	no	Rn.6001.1	BI274156	Rn.40489	phosphatidylinositol glycan, class T (predicted)
1068	1383283_at	0.514077057	1.428080255	yes	yes	no	Rn.36925.1	BM385645	Rn.36925	oculocerebrorenal syndrome of Lowe

1069	1384383_at	0.514987475	1.428981734	yes	yes	no	Rn.64031.1	BF557230	Rn.6835	similar to Putative lysophosphatidic acid acyltransferase (predicted)
1070	1391972_a_at	0.515431837	1.42942194	yes	yes	no	Rn.20813.1	BE108410	Rn.128757	zinc finger, SWIM domain containing 4 (predicted)
1071	1397564_at	0.515737598	1.42972492	yes	yes	no	Rn.56068.1	BF286959	Rn.89352	Transcribed locus
1072	1376136_at	0.516053505	1.430038021	yes	yes	no	Rn.12579.1	BI296118	---	---
1073	1371099_at	0.516437069	1.43041827	yes	yes	no	Rn.54456.1	U07886	Rn.107069	Polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence
1074	1368762_at	0.516522688	1.430503163	yes	yes	no	Rn.18473.1	NM_053299	Rn.18473	ubiquitin D
1075	1390606_at	0.516895927	1.430873296	yes	no	no	Rn.26680.1	BI289052	Rn.137981	similar to hedgehog-interacting protein
1076	1370892_at	0.517635248	1.431606747	yes	yes	no	Rn.30176.1	BI285347	Rn.81052	complement component 4a /// complement component 4, gene 2
1077	1370986_s_at	0.518244992	1.432211933	yes	yes	no	Rn.54043.1	AW535280	---	---
1078	1384036_s_at	0.51851622	1.432481215	yes	yes	no	Rn.12307.1	AW536030	Rn.23978	Similar to SPT3-associated factor 42 (predicted)
1079	1388340_at	0.519783949	1.433740522	yes	yes	no	Rn.7233.1	BF281153	Rn.7233	KIAA0101
1080	1382528_at	0.5199115	1.433867287	yes	yes	no	Rn.6365.2	BF406412	Rn.6365	similar to RIKEN cDNA 4933428G09 (predicted)
1081	1391418_at	0.520122222	1.434076734	yes	no	no	Rn.7508.1	AI072641	---	---
1082	1381809_at	0.520204891	1.434158913	yes	no	no	Rn.49713.1	BE097847	Rn.23844	ankyrin repeat domain 11 (predicted)
1083	1393451_at	0.521186719	1.435135263	yes	yes	no	Rn.65502.1	BI295149	Rn.65502	similar to RIKEN cDNA 2610510J17 (predicted)
1084	1389730_at	0.521787883	1.435733401	yes	yes	no	Rn.20365.1	AI176502	Rn.20365	Transcribed locus
1085	1395614_at	0.521955099	1.43589982	yes	yes	no	Rn.38986.1	AI407215	Rn.15383	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 (predicted)
1086	1382280_at	0.522120907	1.436064857	yes	yes	no	Rn.24696.1	BF290998	Rn.2334	ubiquinol-cytochrome c reductase core protein II
1087	1390799_at	0.522334389	1.436277374	yes	yes	no	Rn.24878.1	AI177748	Rn.24878	Transcribed locus
1088	1383864_at	0.522819704	1.436760611	yes	yes	no	Rn.18080.1	BF412512	---	---
1089	1375090_at	0.523206539	1.437145906	yes	yes	no	Rn.14814.1	AI579005	Rn.122206	Transcribed locus
1090	1381988_at	0.52439806	1.438333335	yes	yes	no	Rn.23356.1	AI029833	Rn.22817	Guanine nucleotide binding protein, alpha q polypeptide
1091	1392637_at	0.524531526	1.438466403	yes	no	no	Rn.2746.1	AA923988	Rn.2746	Similar to interferon-inducible GTPase (predicted)
1092	1382026_at	0.525249616	1.439182567	yes	yes	no	Rn.14833.2	BE116750	Rn.143729	Rho GTPase activating protein 9 (predicted)
1093	1377461_at	0.525318702	1.439251486	yes	no	no	Rn.25200.1	AI409983	Rn.25200	LOC499936
1094	1397410_at	0.525909883	1.439841377	yes	yes	no	Rn.46119.1	BI301687	Rn.46119	Similar to RIKEN cDNA

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1095	1370946_at	0.525934704	1.43986615	yes	yes	no	Rn.9647.1	BF420722	Rn.56776	nuclear factor I/X
1096	1398149_at	0.527415072	1.441344373	yes	yes	no	Rn.58255.1	BF402393	Rn.58255	Transcribed locus
1097	1389771_at	0.528563436	1.442492118	yes	yes	no	Rn.6634.1	AI013885	Rn.137623	Transcribed locus, strongly similar to XP_221913.3 PREDICTED: similar to Protein C7orf26 homolog [Rattus norvegicus]
1098	1369963_at	0.529803867	1.443732908	yes	yes	no	Rn.17971.1	NM_053654	Rn.17971	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit
1099	1391921_at	0.530332884	1.444262402	yes	yes	no	Rn.47583.1	AW530941	Rn.32402	RNA guanylyltransferase and 5'-phosphatase (predicted)
1100	1390240_at	0.531991327	1.445923602	yes	no	no	Rn.25146.1	BM389611	Rn.25146	Transcribed locus
1101	1370600_at	0.532343902	1.446277009	yes	no	no	Rn.29988.1	AF038388	Rn.29988	FYVE, RhoGEF and PH domain containing 4
1102	1377188_at	0.534913908	1.448855693	yes	yes	no	Rn.63575.1	BI296291	Rn.147846	Transcribed locus
1103	1380777_at	0.535058114	1.449000521	yes	yes	no	Rn.63026.1	BF399517	Rn.147957	Transcribed locus
1104	1383978_at	0.536814321	1.450765478	yes	no	no	Rn.34561.1	BM384029	Rn.34561	Huntingtin interactor protein E
1105	1389756_at	0.538635021	1.452597519	yes	yes	no	Rn.28232.1	BM390710	Rn.28232	maternal embryonic leucine zipper kinase (predicted)
1106	1371332_at	0.540081923	1.454055083	yes	yes	yes	Rn.3987.1	AA848821	Rn.3987	Histone 1, H4a (predicted)
1107	1393364_at	0.540839921	1.454819251	yes	yes	yes	Rn.15381.1	BM385460	Rn.15381	cation-chloride cotransporter 9
1108	1380285_at	0.541941849	1.455930863	yes	yes	yes	Rn.29459.1	AI171200	Rn.29459	chordin
1109	1375441_at	0.542992185	1.456991221	yes	yes	yes	Rn.12146.1	BI278468	Rn.73067	seryl-aminoacyl-tRNA synthetase 1
1110	1395448_at	0.544515809	1.458530756	yes	yes	yes	Rn.54293.1	BF415075	Rn.54315	similar to hypothetical protein FLJ13511 (predicted)
1111	1385916_at	0.544856947	1.458875679	yes	no	no	Rn.28835.1	AI639015	Rn.49264	Transcribed locus
1112	1370465_at	0.546528913	1.460567378	yes	yes	yes	Rn.54380.1	AF257746	Rn.107444	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
1113	1367601_at	0.546701632	1.460742247	yes	yes	yes	Rn.31765.1	NM_053698	Rn.31765	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
1114	1379467_at	0.546990123	1.461034376	yes	yes	yes	Rn.24761.1	BF284065	---	---
1115	1373006_at	0.548853378	1.462922536	yes	yes	no	Rn.32121.1	AI230091	Rn.102124	proline-rich protein PRP2
1116	1377619_at	0.549047802	1.463119699	yes	yes	no	Rn.24770.1	AI407932	Rn.23906	WD repeat domain 36 (predicted)
1117	1395636_at	0.550209244	1.464298058	yes	yes	no	Rn.30160.1	AI576368	---	---
1118	1385724_at	0.550471804	1.464564574	yes	yes	no	Rn.49586.1	BE097295	---	---
1119	1373393_at	0.551321234	1.465427134	yes	yes	no	Rn.35083.1	BM384468	Rn.106323	similar to Ext1

1120	1389693_at	0.553220571	1.467357669	yes	yes	yes	Rn.7748.1	AA944526	Rn.7748	similar to hypothetical protein 3010020C06 (predicted)
1121	1390513_at	0.554014418	1.468165309	yes	yes	no	Rn.37549.1	BI291604	---	---
1122	1392134_x_at	0.556683794	1.470884326	yes	yes	no	Rn.40795.2	BE099652	Rn.72217	similar to KIAA0456 protein
1123	1382435_at	0.557130407	1.471339736	yes	yes	no	Rn.41549.1	AA996835	Rn.12924	fizzy/cell division cycle 20 related 1 (Drosophila) (predicted)
1124	1374552_at	0.56014642	1.474418849	yes	yes	yes	Rn.24172.1	BF412718	Rn.24172	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
1125	1368234_at	0.560879704	1.475168448	yes	yes	yes	Rn.11058.1	NM_031324	Rn.11058	prolyl endopeptidase
1126	1381557_at	0.562111551	1.47642856	yes	yes	no	Rn.73873.1	BI289045	Rn.145901	TGFB inducible early growth response 3 (predicted)
1127	1372256_at	0.562706475	1.47703752	yes	yes	no	Rn.8405.1	BF550246	---	---
1128	1396928_at	0.562962371	1.477299531	yes	yes	no	Rn.34801.1	AI548614	Rn.147768	Transcribed locus
1129	1382811_at	0.562992276	1.477330154	yes	yes	no	Rn.14709.1	AA891721	Rn.101972	Mitochondrial ribosomal protein L16
1130	1397713_at	0.563942022	1.478303021	yes	yes	no	Rn.55237.1	AW917120	Rn.24369	Protein inhibitor of activated STAT 1 (predicted)
1131	1393238_at	0.563969786	1.47833147	yes	yes	no	Rn.8233.1	AA900649	Rn.43966	Similar to DKFZP434B168 protein (predicted)
1132	1384557_at	0.564395421	1.478767684	yes	yes	yes	Rn.6757.2	AI136444	Rn.6757	Transcribed locus
1133	1368008_at	0.565679	1.480083942	yes	yes	yes	Rn.43387.1	NM_021751	Rn.144589	prominin 1
1134	1396512_at	0.566252922	1.480672855	yes	yes	no	Rn.53310.1	BF393192	Rn.147717	Transcribed locus
1135	1393919_at	0.566328654	1.480750583	yes	yes	no	Rn.47831.1	AW535116	Rn.47831	similar to RIKEN cDNA 4933405A16 (predicted)
1136	1390469_at	0.566352623	1.480775184	yes	yes	yes	Rn.38521.1	BM391488	Rn.38521	nurim (nuclear envelope membrane protein)
1137	1387874_at	0.568329353	1.482805481	yes	yes	no	Rn.11274.1	AI230048	Rn.11274	D site albumin promoter binding protein
1138	1378655_at	0.56924797	1.483749938	yes	yes	no	Rn.59396.1	BF399516	Rn.59396	Transcribed locus
1139	1382151_at	0.569292794	1.483796039	yes	yes	yes	Rn.24324.1	AI145625	Rn.24324	TruB pseudouridine (psi) synthase homolog 1 (E. coli) (predicted)
1140	1393009_at	0.570413254	1.484948867	yes	yes	no	Rn.25446.1	AI535126	Rn.145001	similar to RIKEN cDNA 2410002F23 (predicted)
1141	1382346_at	0.570645755	1.485188197	yes	yes	no	Rn.13650.1	BF281960	Rn.13650	Transcribed locus
1142	1392594_at	0.571148432	1.48570577	yes	yes	no	Rn.23679.1	AI136409	Rn.16299	Sushi domain containing 2 (predicted)
1143	1386948_at	0.571541572	1.486110686	yes	yes	no	Rn.9701.1	NM_012987	Rn.9701	nestin
1144	1387377_a_at	0.572549053	1.487148848	yes	yes	no	Rn.9149.2	U23443	Rn.9149	p21 (CDKN1A)-activated kinase 1

1145	1369513_at	0.574965768	1.489642117	yes	yes	no	Rn.74257.1	NM_053700	Rn.74257	CC chemokine CCL28
1146	1395642_at	0.575463887	1.490156534	yes	yes	no	Rn.27851.1	BG372596	Rn.27851	similar to RIKEN cDNA 4632412I24
1147	1376768_at	0.576318165	1.491039177	yes	yes	no	Rn.8702.1	BM386807	Rn.8702	Transcribed locus
1148	1390742_at	0.576778667	1.491515187	yes	yes	no	Rn.60752.1	BF404359	---	---
1149	1386586_at	0.576808069	1.491545584	yes	yes	yes	Rn.25198.2	AA996838	Rn.115052	similar to PAK/PLC-interacting protein 1
1150	1392146_at	0.577617718	1.492382883	yes	yes	no	Rn.62900.1	BF418011	---	---
1151	1379999_at	0.579107057	1.493924311	yes	yes	no	Rn.47374.1	AW530087	Rn.47374	Microtubule associated monoxygenase, calponin and LIM domain containing 3
1152	1392738_at	0.579875317	1.494720063	yes	yes	no	Rn.64833.1	AI602954	Rn.23673	similar to KIAA1096 protein
1153	1385383_at	0.579991284	1.494840217	yes	yes	no	Rn.28599.1	AI145747	Rn.28599	similar to hypothetical protein 4933409I22
1154	1380529_at	0.58177955	1.496694268	yes	yes	no	Rn.38747.1	AI059721	Rn.102608	Zinc finger protein 207 (predicted)
1155	1368716_at	0.582600996	1.497546703	yes	yes	no	Rn.35234.1	NM_133425	Rn.87667	protein phosphatase 1, regulatory (inhibitor) subunit 14c
1156	1396521_at	0.583665037	1.498651607	yes	yes	no	Rn.57496.1	BF396135	Rn.57496	StAR-related lipid transfer (START) domain containing 4 (predicted)
1157	1391544_at	0.584655693	1.49968104	yes	yes	no	Rn.74079.1	BI285941	Rn.97779	Similar to adiponutrin
1158	1367977_at	0.585476393	1.5005344	yes	yes	yes	Rn.1827.1	NM_019169	Rn.1827	synuclein, alpha
1159	1370816_at	0.58803576	1.503198737	yes	yes	no	Rn.29848.1	M25804	Rn.29848	nuclear receptor subfamily 1, group D, member 1
1160	1388792_at	0.588631821	1.503819924	yes	yes	no	Rn.16950.1	AI599423	Rn.16950	growth arrest and DNA-damage-inducible 45 gamma (predicted)
1161	1392162_at	0.588946088	1.504147542	yes	yes	yes	Rn.35360.1	BF391447	---	---
1162	1377667_at	0.589469741	1.504693599	yes	yes	no	Rn.22569.1	AW141706	Rn.22569	gene trap locus 7 (predicted)
1163	1374334_at	0.590287038	1.505546261	yes	yes	yes	Rn.7881.1	AI412189	Rn.102149	Immunoglobulin heavy chain (alpha polypeptide)
1164	1373295_at	0.590332607	1.505593815	yes	yes	yes	Rn.15899.1	BI281889	Rn.15899	oligonucleotide/oligosaccharide-binding fold containing 1 (predicted)
1165	1395423_at	0.59165221	1.506971581	yes	yes	no	Rn.15182.1	AW920217	Rn.134121	Similar to C230080I20Rik protein
1166	1378431_at	0.593442218	1.508842499	yes	yes	yes	Rn.26650.1	BE095772	Rn.138055	serine/arginine-rich protein specific kinase 2 (predicted)
1167	1393992_at	0.593634325	1.509043428	yes	yes	no	Rn.33028.1	AA996507	---	homeo box A7
1168	1387019_at	0.593699807	1.509111923	yes	yes	yes	Rn.8069.1	NM_080481	Rn.66347	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
1169	1379575_at	0.595642745	1.511145677	yes	yes	no	Rn.55897.1	BF412271	Rn.10277	Arginine-glutamic acid dipeptide (RE) repeats

1170	1373403_at	0.596608557	1.512157651	yes	yes	yes	Rn.24073.1	AI230625	Rn.146058	Transcribed locus
1171	1369679_a_at	0.597040519	1.51261048	yes	yes	yes	Rn.10550.1	AB060652	Rn.10550	nuclear factor I/A
1172	1383972_at	0.59902241	1.514689844	yes	yes	yes	Rn.19836.1	AW524136	Rn.139918	Transcribed locus
1173	1379582_a_at	0.600446608	1.516185853	yes	yes	no	Rn.13094.2	AA998516	Rn.13094	cyclin A2
1174	1394216_at	0.602714501	1.518571146	yes	yes	no	Rn.29596.1	AI232395	Rn.105727	similar to RIKEN cDNA 2810055F11 (predicted)
1175	1393910_at	0.60347211	1.519368809	yes	yes	yes	Rn.47690.1	BF563961	Rn.47690	similar to Fam13a1 protein (predicted)
1176	1373189_at	0.603915938	1.519836297	yes	yes	no	Rn.17271.1	AW143154	Rn.106726	megakaryoblastic leukemia (translocation) 1 (predicted)
1177	1370910_at	0.60797155	1.524114775	yes	yes	yes	Rn.22905.1	BF283113	Rn.113319	replication factor C (activator 1) 2
1178	1372398_at	0.613366517	1.529824881	yes	yes	yes	Rn.23171.1	BG373314	Rn.23171	similar to Potassium channel tetramerisation domain containing 15
1179	1373750_at	0.615179212	1.53174826	yes	yes	yes	Rn.15264.1	BF406832	Rn.15264	leprecan-like 2 (predicted)
1180	1385944_at	0.616450778	1.533098911	yes	yes	no	Rn.2887.1	AA875348	Rn.40571	Family with sequence similarity 33, member A (predicted)
1181	1369737_at	0.617457429	1.534169015	yes	yes	yes	Rn.76185.1	NM_017334	Rn.10251	cAMP responsive element modulator
1182	1398171_at	0.619574425	1.536421891	yes	yes	no	Rn.60923.1	BF406300	Rn.52869	gametogenetin (predicted)
1183	1379679_at	0.620436702	1.537340462	yes	yes	yes	Rn.55946.1	BF290584	Rn.55946	Transcribed locus
1184	1387964_a_at	0.623241381	1.540332044	yes	yes	yes	Rn.64648.1	AY071924	Rn.64648	ERO1-like (S. cerevisiae)
1185	1375704_at	0.62676595	1.544099745	yes	yes	yes	Rn.22431.1	AA817860	Rn.98469	activating transcription factor 7 interacting protein (predicted)
1186	1389408_at	0.62778503	1.54519084	yes	yes	yes	Rn.14395.1	BG379338	Rn.101236	ribonucleotide reductase M2
1187	1368308_at	0.629660499	1.547200857	yes	yes	no	Rn.12072.1	NM_012603	Rn.12072	myelocytomatosis viral oncogene homolog (avian)
1188	1392736_at	0.63165762	1.549344128	yes	yes	yes	Rn.24679.1	AW532939	---	---
1189	1389234_at	0.633039435	1.550828802	yes	yes	yes	Rn.35561.1	BI298314	Rn.35561	von Willebrand factor
1190	1368545_at	0.63379774	1.551644159	yes	yes	yes	Rn.28010.1	NM_057138	Rn.28010	CASP8 and FADD-like apoptosis regulator
1191	1398637_at	0.634094983	1.551963882	yes	yes	yes	Rn.22742.1	AA893390	---	---
1192	1394923_at	0.634901384	1.552831602	yes	yes	no	Rn.76339.1	AW528728	Rn.52238	similar to neuronal interacting factor X 1 (NIX1)
1193	1382173_at	0.636955087	1.555043661	yes	yes	yes	Rn.22306.1	BF283569	Rn.51063	Transcribed locus
1194	1392506_at	0.640722693	1.559109973	yes	yes	no	Rn.44173.1	AI575645	Rn.44173	crystallin, zeta (quinone reductase)-like 1 (predicted)
1195	1375177_at	0.641522667	1.559974738	yes	yes	yes	Rn.7654.1	AI454932	Rn.22229	similar to BTEB3 protein
1196	1396588_at	0.642262072	1.560774456	yes	yes	yes	Rn.59561.1	BF405168	Rn.22981	Phosphatase and actin regulator 1
1197	1385521_at	0.64355948	1.562178684	yes	yes	yes	Rn.74051.2	AI603505	Rn.150075	Transcribed locus

1198	1392710_at	0.645036058	1.56377837	yes	yes	yes	Rn.31294.2	AI101727	Rn.8557	WD repeat and FYVE domain containing 1 (predicted)
1199	1368033_at	0.64904289	1.568127526	yes	yes	yes	Rn.9517.1	BI290791	Rn.9517	nucleolar and coiled-body phosphoprotein 1
1200	1389566_at	0.649723816	1.56886783	yes	yes	yes	Rn.23351.1	AW253821	Rn.6743	cyclin B2 (predicted)
1201	1377894_at	0.651846234	1.571177565	yes	yes	no	Rn.24183.1	BF404700	Rn.24183	Transcribed locus
1202	1371237_a_at	0.651994319	1.571338846	yes	yes	yes	Rn.54397.1	AF411318	Rn.16133	metallothionein1F
1203	1388398_at	0.653384709	1.572853946	yes	yes	yes	Rn.7303.1	BI282024	---	---
1204	1379631_at	0.654268574	1.573817847	yes	yes	no	Rn.17595.1	AI071665	Rn.83632	colony stimulating factor 1 (macrophage)
1205	1370540_at	0.655272823	1.574913751	yes	yes	yes	Rn.10055.1	U15660	Rn.10055	nuclear receptor subfamily 1, group D, member 2
1206	1391040_at	0.65557741	1.575246288	yes	yes	no	Rn.12500.1	AA997052	Rn.128724	similar to Retinoblastoma-binding protein 8 (RBBP-8) (CtBP interacting protein) (CtIP) (Retinoblastoma-interacting protein and myosin-like) (RIM) (predicted)
1207	1382551_at	0.656841943	1.576627608	yes	yes	yes	Rn.72639.1	BF417645	Rn.37673	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)
1208	1394107_at	0.657206162	1.57702569	yes	yes	no	Rn.63882.1	BF546029	Rn.148642	Transcribed locus
1209	1395559_at	0.65903884	1.579030284	yes	yes	no	Rn.39294.1	BF543323	Rn.67375	Tetratricopeptide repeat domain 3 (predicted)
1210	1370583_s_at	0.659613618	1.579659503	yes	yes	yes	Rn.82691.1	AY082609	Rn.107444	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 1A
1211	1381769_at	0.660187365	1.580287845	yes	yes	no	Rn.42314.1	AW251554	Rn.129550	Transcribed locus, strongly similar to NP_079716.1 mitochondrial ribosomal protein S16 [Mus musculus]
1212	1398015_at	0.660328331	1.580442263	yes	yes	yes	Rn.60527.1	BF404613	---	---
1213	1397855_at	0.66331787	1.583720636	yes	yes	yes	Rn.31289.1	BE096287	Rn.31289	Similar to cysteine sulfinic acid decarboxylase
1214	1374924_at	0.664340358	1.584843471	yes	yes	yes	Rn.24447.1	BE098025	---	---
1215	1370464_at	0.666360159	1.587063837	yes	yes	yes	Rn.54380.1	AF286167	Rn.107444	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
1216	1384759_at	0.666420204	1.587129892	yes	yes	yes	Rn.48234.1	AW534015	Rn.90858	PHD finger protein 17 (predicted)

1217	1383325_at	0.671208206	1.592405993	yes	yes	yes	Rn.23454.1	AI712781	---	---
1218	1385825_at	0.671393249	1.592610251	yes	yes	yes	Rn.55638.1	AW920445	Rn.64117	similar to mKIAA0256 protein
1219	1369110_x_at	0.671905586	1.593175927	yes	yes	yes	Rn.39743.1	NM_012645	Rn.40130	RT1 class Ib, locus Aw2
1220	1398686_at	0.672088666	1.593378116	yes	yes	yes	Rn.55182.1	BF288090	---	---
1221	1370824_at	0.6728561	1.59422593	yes	yes	yes	Rn.32067.1	AF273025	Rn.32067	solute carrier family 38, member 3
1222	1395399_at	0.674299747	1.595822007	yes	yes	yes	Rn.63831.1	BM387829	Rn.63831	similar to PS1D protein
1223	1375469_at	0.674983788	1.596578831	yes	yes	yes	Rn.23168.1	BE111847	Rn.23417	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
1224	1383560_at	0.681884936	1.60423438	yes	yes	yes	Rn.20177.1	BI303213	Rn.20177	Transcribed locus
1225	1387876_at	0.68616871	1.609004889	yes	yes	yes	Rn.54486.1	AI177626	---	signal transducer and activator of transcription 5B
1226	1377795_at	0.686420715	1.609285969	yes	yes	yes	Rn.25383.1	AI578745	Rn.25383	Transcribed locus
1227	1380527_at	0.686563141	1.609444849	yes	yes	yes	Rn.41125.1	AI454790	Rn.153615	Transcribed locus
1228	1397025_at	0.689248975	1.612443909	yes	yes	yes	Rn.59592.1	BF400595	Rn.10853	Transient receptor potential cation channel, subfamily C, member 4
1229	1390790_a_at	0.689442558	1.612660283	yes	yes	yes	Rn.12017.2	AA964219	---	hypothetical LOC361349
1230	1373751_at	0.690443392	1.613779415	yes	yes	yes	Rn.20626.1	BF396319	Rn.20626	Transcribed locus
1231	1389748_at	0.693748998	1.61748126	yes	yes	yes	Rn.18844.1	BE118122	Rn.147595	Transcribed locus
1232	1368125_at	0.695387535	1.619319354	yes	yes	yes	Rn.32091.1	NM_019229	Rn.32091	solute carrier family 12, member 4
1233	1385002_at	0.69739084	1.621569479	yes	yes	yes	Rn.35132.1	AI454867	Rn.147872	Transcribed locus
1234	1384445_at	0.704232028	1.629277141	yes	yes	yes	Rn.28812.3	BI288489	Rn.134687	similar to RIKEN cDNA 0610037D15
1235	1377329_at	0.712040749	1.638119664	yes	yes	yes	Rn.15241.1	BE113460	Rn.13196	Basic leucine zipper and W2 domains 2
1236	1378537_at	0.715637576	1.642208806	yes	yes	yes	Rn.61067.1	BI289126	Rn.61067	Transcribed locus
1237	1373685_at	0.716458913	1.643143993	yes	yes	yes	Rn.21120.1	BI291430	Rn.21120	similar to low density lipoprotein receptor-related protein binding protein
1238	1396468_at	0.716684386	1.643400813	yes	yes	yes	Rn.64029.1	BF556949	Rn.87212	glutathione S-transferase, theta 2
1239	1384903_at	0.723769055	1.65149094	yes	yes	yes	Rn.72502.1	AI535168	Rn.128759	glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)
1240	1384889_at	0.725934937	1.653972144	yes	yes	yes	Rn.34831.1	AI535467	Rn.124216	Transcribed locus
1241	1373670_at	0.727771475	1.656078977	yes	yes	yes	Rn.24237.1	AA799569	Rn.24237	Signal transducer and activator of transcription 2 (predicted)
1242	1379076_at	0.738842618	1.668836501	yes	yes	yes	Rn.12349.1	BE328961	Rn.12349	Transcribed locus
1243	1397275_at	0.744314785	1.675178446	yes	yes	yes	Rn.61568.1	BF386708	Rn.55975	similar to 60S ribosomal protein L7a

1244	1390325_at	0.746764985	1.678025902	yes	yes	yes	Rn.51774.1	BI289418	Rn.11414	CD38 antigen
1245	1368168_at	0.749305882	1.680983871	yes	yes	yes	Rn.16933.1	NM_053380	Rn.16933	solute carrier family 34 (sodium phosphate), member 2
1246	1389745_at	0.752420276	1.684616587	yes	yes	yes	Rn.15248.1	BI290604	---	---
1247	1372641_at	0.763519256	1.697626704	yes	yes	yes	Rn.23649.1	AW434261	Rn.68281	Similar to myocytic induction/differentiation originator (predicted)
1248	1381152_at	0.765407941	1.699850585	yes	yes	yes	Rn.63653.1	BF387456	Rn.12306	similar to RIKEN cDNA 2610205E22 (predicted) /// similar to RIKEN cDNA 2610205E22
1249	1382867_at	0.765545271	1.700012402	yes	yes	yes	Rn.6458.1	AA849390	Rn.6458	Transcribed locus
1250	1384960_at	0.766523925	1.701165998	yes	yes	yes	Rn.78169.1	BI281250	Rn.124539	Transcribed locus
1251	1389851_at	0.767255604	1.702028982	yes	yes	yes	Rn.22055.1	AA943730	Rn.22055	zinc finger protein 36, C3H type-like 2 (predicted)
1252	1381321_at	0.768251054	1.703203776	yes	yes	yes	Rn.52168.1	BE113257	Rn.102777	Similar to RIKEN cDNA D030060M11 (predicted)
1253	1397512_at	0.768465717	1.703457221	yes	yes	yes	Rn.78249.1	BI281965	Rn.6409	similar to Vps41 protein
1254	1383982_at	0.770728326	1.706130885	yes	yes	yes	Rn.9102.1	BE112063	Rn.9102	Transcribed locus
1255	1391485_at	0.772493041	1.708219112	yes	yes	yes	Rn.43745.1	BF290955	---	---
1256	1380443_at	0.773002612	1.708822575	yes	yes	yes	Rn.2684.1	AA899371	Rn.2684	similar to periodic tryptophan protein 1 homolog; periodic tryptophan protein 1 homolog (S. cerevisiae) (predicted)
1257	1394534_at	0.775091829	1.711298974	yes	yes	yes	Rn.64209.1	AW532329	Rn.22981	Phosphatase and actin regulator 1
1258	1383163_at	0.781528654	1.718951278	yes	yes	yes	Rn.17804.1	AA817898	Rn.17804	immunoglobulin joining chain (predicted)
1259	1377928_at	0.782083771	1.71961282	yes	yes	yes	Rn.6345.1	BM385993	---	---
1260	1398415_at	0.794452529	1.734419076	yes	yes	yes	Rn.22144.1	BG380708	Rn.22144	Transcribed locus
1261	1374799_at	0.796713462	1.737139317	yes	yes	yes	Rn.7870.1	AI407418	Rn.7870	similar to mKIAA0159 protein
1262	1386045_at	0.797164647	1.737682671	yes	yes	yes	Rn.13483.1	AA893205	Rn.143823	Transcribed locus
1263	1393576_at	0.806163821	1.748555782	yes	yes	yes	Rn.32972.1	AA963989	Rn.32972	Transcribed locus
1264	1378586_at	0.807297631	1.749930507	yes	yes	yes	Rn.56451.1	BI291842	Rn.14523	Cytokine inducible SH2-containing protein
1265	1372138_at	0.815301407	1.759665742	yes	yes	yes	Rn.22284.1	BM390477	Rn.10455	Cut-like 1 (Drosophila)
1266	1374030_at	0.816086644	1.760623762	yes	yes	yes	Rn.11451.1	BE100868	Rn.59795	Transcribed locus
1267	1385061_at	0.822387285	1.768329698	yes	yes	yes	Rn.28477.1	AI145445	Rn.28477	LOC500053
1268	1395219_at	0.828647516	1.776019615	yes	yes	yes	Rn.63713.1	BE096754	---	---
1269	1382193_at	0.838228224	1.787853128	yes	yes	yes	Rn.24858.1	BI294188	Rn.24858	Transcribed locus
1270	1375124_at	0.841713218	1.792177111	yes	yes	yes	Rn.23224.1	AW533917	Rn.7438	similar to OTTHUMP00000042400

1271	1384993_at	0.847357019	1.799201812	yes	yes	yes	Rn.73147.1	BG376804	Rn.73147	similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor; peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor protein-1 (predicted)
1272	1382668_at	0.848555881	1.800697548	yes	yes	yes	Rn.15368.1	AI232529	Rn.148144	Transcribed locus
1273	1374927_at	0.849110429	1.801389839	yes	yes	yes	Rn.14945.1	AI714124	Rn.14945	Transcribed locus
1274	1395944_at	0.857185076	1.81150034	yes	yes	yes	Rn.41999.1	AI548667	Rn.41999	Transcribed locus
1275	1368826_at	0.85960715	1.814544138	yes	yes	yes	Rn.220.1	NM_012531	Rn.220	catechol-O-methyltransferase
1276	1394068_x_at	0.864724558	1.820991967	yes	yes	yes	Rn.18297.2	BF288243	Rn.144973	Kruppel-like factor
1277	1380831_at	0.865853008	1.82241687	yes	yes	yes	Rn.39250.1	AI237035	Rn.39250	Transcribed locus
1278	1390504_at	0.887577293	1.850066711	yes	yes	yes	Rn.45222.1	AW524470	Rn.40573	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
1279	1390430_at	0.888576218	1.851348144	yes	yes	yes	Rn.24808.1	BF284190	Rn.10055	Nuclear receptor subfamily 1, group D, member 2
1280	1381121_at	0.892777967	1.856747927	yes	yes	yes	Rn.44962.1	AW533010	Rn.81055	Basic helix-loop-helix domain containing, class B2
1281	1375071_at	0.897765554	1.863178058	yes	yes	yes	Rn.58778.1	BE119719	Rn.91990	nucleoporin 133 (predicted)
1282	1375542_at	0.903766952	1.870944745	yes	yes	yes	Rn.7684.2	AI407092	Rn.18894	Radixin
1283	1370541_at	0.913694636	1.883863763	yes	yes	yes	Rn.10055.1	U20796	Rn.10055	nuclear receptor subfamily 1, group D, member 2
1284	1395416_at	0.934245143	1.910890544	yes	yes	yes	Rn.37137.1	BF546940	Rn.8482	nuclear receptor coactivator 5 (predicted)
1285	1376231_at	0.935885018	1.91306384	yes	yes	yes	Rn.18312.1	BF389244	Rn.117311	similar to Hypothetical UPF0080 protein KIAA0186
1286	1397878_at	0.940070238	1.918621645	yes	yes	yes	Rn.70053.1	BG671050	---	similar to crystallin, zeta (quinone reductase)-like 1
1287	1383025_at	0.941562935	1.920607791	yes	yes	yes	Rn.41557.1	BE097791	Rn.38577	meningioma expressed antigen 5 (hyaluronidase)
1288	1381553_at	0.96089738	1.946520286	yes	yes	yes	Rn.66865.1	BG371725	Rn.66865	Zinc finger and BTB domain containing 16
1289	1369341_a_at	0.999367517	1.999123384	yes	yes	yes	Rn.29998.2	AF130819	Rn.7033	activin receptor interacting protein 1
1290	1374164_at	1.039696483	2.055795106	yes	yes	yes	Rn.39004.1	BF410020	Rn.39004	Transcribed locus
1291	1384708_at	1.130086464	2.188718573	yes	yes	yes	Rn.58198.1	BF400572	Rn.9822	RAB3D, member RAS oncogene family

1292	1395994_at	1.198978866	2.295771196	yes	yes	yes	Rn.45199.1	BE116471	Rn.115701	Transcribed locus, moderately similar to XP_578397.1 PREDICTED: similar to sentrin 17 [Rattus norvegicus]
1293	1381048_at	1.280248398	2.428807917	yes	yes	yes	Rn.49956.1	BF398435	Rn.123710	Transcribed locus
1294	1385254_at	1.300207933	2.462643738	yes	yes	yes	Rn.50637.1	BE104427	Rn.13214	similar to 5-3 exonuclease (predicted)

Supplementary Table 4

Sl. No.	Affy_probe	Mean log2 (siADAMTS16/scrambled)	Mean ratio value (siADAMTS16/ scrambled)	10%FDR	5%FDR	1%FDR	Representative Public ID	UniGene ID	Gene Title
1	1377319_at	-1.2220647	0.428668793	yes	yes	yes	BF404163	Rn.116828	Spermatogenesis associated 5 (predicted)
2	1390085_at	-1.205408622	0.433646502	yes	yes	yes	BF406291	---	---
3	1398594_at	-1.185475422	0.439679623	yes	yes	yes	AI029767	Rn.22289	Transcribed locus
4	1395180_s_at	-1.167214591	0.445280213	yes	yes	yes	AW535140	Rn.2344	Prostaglandin E synthase 3 (cytosolic) (predicted)
5	1397259_at	-1.147622478	0.451368462	yes	yes	yes	BF291133	Rn.149172	similar to hypothetical protein D630010C10
6	1395215_at	-1.104898392	0.464935215	yes	yes	yes	BF404567	Rn.139712	Bromodomain adjacent to zinc finger domain, 2B (predicted)
7	1394555_at	-1.097557356	0.467307029	yes	yes	yes	AI501080	Rn.22873	Similar to KIAA2010 protein (predicted)
8	1384410_at	-1.076915042	0.474041397	yes	yes	yes	AA964404	Rn.2280	Sorting nexin 12 (predicted)
9	1382673_at	-1.062744197	0.478720603	yes	yes	yes	BE115812	Rn.16763	Nardilysin, N-arginine dibasic convertase 1
10	1375597_at	-1.028651982	0.490167935	yes	yes	yes	BI300655	Rn.47124	Inner membrane protein, mitochondrial
11	1391084_at	-1.027556852	0.490540156	yes	yes	yes	AW528763	Rn.162420	Ubiquitin protein ligase E3A (predicted)
12	1397481_at	-1.027013267	0.490725019	yes	yes	yes	BE120751	Rn.33283	Alstrom syndrome 1 (predicted)
13	1391557_at	-1.002881101	0.499002483	yes	yes	yes	AI009685	Rn.145250	SRY-box containing gene 15 (predicted)
14	1382982_at	-0.998226941	0.500614873	yes	yes	yes	AI230669	Rn.126047	Guanine nucleotide binding protein, beta 1
15	1381430_at	-0.992990685	0.502435154	yes	yes	yes	AI010149	Rn.15133	Numb-like
16	1392446_at	-0.986878963	0.504568146	yes	yes	yes	AI145435	Rn.11786	kelch-like 2, Mayven (Drosophila) (predicted)
17	1381077_at	-0.986429587	0.504725336	yes	yes	yes	AA996843	Rn.12430	Transcribed locus
18	1374872_at	-0.984654655	0.505346676	yes	yes	yes	AW532114	Rn.38473	RAS guanyl releasing protein 2 (calcium and DAG-regulated) (predicted)
19	1384748_at	-0.984153851	0.505522128	yes	yes	yes	BE106100	Rn.50873	mel transforming oncogene-like 1 (predicted)
20	1383691_at	-0.952268821	0.516819059	yes	yes	yes	BF415419	Rn.173720	Transcribed locus
21	1391344_at	-0.944204083	0.519716194	yes	yes	yes	AW527134	Rn.23420	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)
22	1382315_at	-0.937118982	0.522274807	yes	yes	yes	BF286388	Rn.21359	Similar to Hypothetical protein MGC28888
23	1391812_at	-0.929303961	0.525111625	yes	yes	yes	AI145876	Rn.103569	Similar to RIKEN cDNA E330026B02 (predicted)
24	1374543_at	-0.926944851	0.525970995	yes	yes	yes	AA858791	Rn.16899	Transcribed locus
25	1376865_at	-0.925782091	0.52639508	yes	yes	yes	AI228240	Rn.49261	Transcribed locus
26	1380644_at	-0.924550373	0.526844688	yes	yes	yes	AI178542	Rn.172971	Transcribed locus
27	1390723_at	-0.919620073	0.528648219	yes	yes	yes	BF386742	Rn.103790	Catenin (cadherin-associated protein), alpha 1
28	1368737_at	-0.911009867	0.531812699	yes	yes	yes	NM_022709	Rn.162774	SMR2
29	1381207_at	-0.901990071	0.535148032	yes	yes	yes	BE120425	Rn.10961	Calcium/calmodulin-dependent protein kinase II gamma
30	1379181_at	-0.900522491	0.535692688	yes	yes	yes	BF405290	---	---
31	1389923_at	-0.899616702	0.536029126	yes	yes	yes	BE104474	---	---
32	1396463_at	-0.897417092	0.536847008	yes	yes	yes	BE127046	Rn.38987	similar to pinin
33	1393674_at	-0.893352965	0.538361458	yes	yes	yes	BF396736	Rn.2428	Polyhomeotic-like 2 (Drosophila)
34	1379809_at	-0.888794279	0.540065285	yes	yes	yes	AI535522	Rn.11991	pleckstrin homology domain containing, family F (with FYVE domain) member 2 (predicted)
35	1380132_at	-0.865618311	0.548811147	yes	yes	yes	BI291804	Rn.31889	RAB3A interacting protein
36	1397112_at	-0.861940942	0.550211828	yes	yes	yes	BF415784	Rn.171772	Transcribed locus
37	1370828_at	-0.860687706	0.550689992	yes	yes	yes	AF228917	Rn.17310	zinc finger, DHHC domain containing 2
38	1378474_at	-0.856579011	0.552260554	yes	yes	yes	BF400707	Rn.52203	Transcribed locus
39	1375573_at	-0.849258102	0.555070105	yes	yes	yes	BE120038	Rn.106040	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)

40	1391898_at	-0.842652153	0.55761754	yes	yes	yes	AW524135	Rn.41955	Transcribed locus
41	1384406_at	-0.842019239	0.557862222	yes	yes	yes	AW527186	Rn.169598	Transcribed locus
42	1376410_at	-0.839768122	0.558733365	yes	yes	yes	BI291814	Rn.7971	Transcribed locus
43	1397859_x_at	-0.839202231	0.558952568	yes	yes	yes	BI291927	Rn.114328	Similar to T-cell receptor alpha chain (predicted)
44	1369594_at	-0.836435222	0.560025637	yes	yes	yes	NM_053903	Rn.10714	ephrin A5
45	1387571_at	-0.834460649	0.560792652	yes	yes	yes	NM_031130	Rn.89710	nuclear receptor subfamily 2, group F, member 1
46	1384859_at	-0.833424785	0.561195449	yes	yes	yes	AI045935	Rn.82705	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
47	1387491_at	-0.832603063	0.561515183	yes	yes	yes	NM_024381	Rn.44654	glycerol kinase
48	1397713_at	-0.832307325	0.561630299	yes	yes	yes	AW917120	Rn.24369	Protein inhibitor of activated STAT 1 (predicted)
49	1391979_at	-0.831246125	0.562043569	yes	yes	yes	AA851345	Rn.6731	Transcribed locus
50	1386641_at	-0.827849661	0.563368318	yes	yes	yes	BF546770	Rn.21134	Transcribed locus
51	1381078_at	-0.825138406	0.564428051	yes	yes	yes	BF409999	Rn.165945	Transcribed locus
52	1390280_at	-0.819417566	0.566670669	yes	yes	yes	BF396115	Rn.2280	Sorting nexin 12 (predicted)
53	1396214_at	-0.818914991	0.566868107	yes	yes	yes	BF562720	Rn.44216	kit ligand
54	1392795_at	-0.814431418	0.568632547	yes	yes	yes	AA963069	Rn.163377	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (predicted)
55	1380489_at	-0.814236572	0.56870935	yes	yes	yes	BF389269	Rn.7020	Similar to RIKEN cDNA G430041M01 (predicted)
56	1376124_at	-0.812127858	0.569541211	yes	yes	yes	BG375480	Rn.11866	Wiskott-Aldrich syndrome-like (human)
57	1398695_at	-0.812032553	0.569578836	yes	yes	yes	BF389056	Rn.2104	Amyloid beta (A4) precursor protein
58	1393878_at	-0.811717928	0.569703065	yes	yes	yes	BF416495	Rn.153668	Zinc finger and BTB domain containing 20 (predicted)
59	1386813_at	-0.80802209	0.571164378	yes	yes	yes	AA801454	Rn.164388	Transcribed locus
60	1380790_at	-0.807448318	0.57139158	yes	yes	yes	BF416414	Rn.63017	similar to mKIAA0376 protein
61	1395551_at	-0.802043721	0.573536131	yes	yes	yes	BG671371	Rn.100818	Transcribed locus
62	1378522_at	-0.799712636	0.574463591	yes	yes	yes	BG373062	Rn.32415	Similar to polycystic kidney disease 2 (predicted)
63	1377321_at	-0.794252678	0.576641799	yes	yes	yes	BF415831	Rn.106040	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
64	1378780_at	-0.791018578	0.577935911	yes	yes	yes	BF410325	Rn.141581	Exophilin 5 (predicted)
65	1389881_at	-0.790994281	0.577945644	yes	yes	yes	BI296516	Rn.176848	Transcribed locus
66	1372963_at	-0.789193555	0.578667468	yes	yes	yes	BG378723	Rn.163223	Kinesin-associated protein 3 (predicted)
67	1392354_at	-0.77438573	0.584637498	yes	yes	yes	AW529939	Rn.146138	Transcribed locus
68	1381448_at	-0.774312736	0.584667079	yes	yes	yes	AW535305	---	---
69	1392278_at	-0.773331408	0.585064907	yes	yes	yes	BF418109	Rn.163223	Kinesin-associated protein 3 (predicted)
70	1392704_at	-0.768337592	0.587093589	yes	yes	yes	AI029221	Rn.2645	Sorting nexin 4 (predicted)
71	1392392_at	-0.767970508	0.58724299	yes	yes	yes	AI012510	Rn.24948	Nuclear receptor co-repressor 1
72	1381483_at	-0.767908722	0.58726814	yes	yes	yes	BE118096	Rn.26922	Far upstream element (FUSE) binding protein 3
73	1375821_at	-0.767485597	0.587440404	yes	yes	yes	BF390754	---	---
74	1385497_x_at	-0.763515797	0.589059064	yes	yes	yes	AW522661	Rn.25032	ligand of numb-protein X 1 (predicted)
75	1381507_at	-0.76339879	0.589106841	yes	yes	yes	BE097981	Rn.169470	Transcribed locus
76	1394817_at	-0.762633825	0.589419287	yes	yes	yes	AI548775	Rn.99298	Nuclear factor of activated T-cells 5 (predicted)
77	1398197_at	-0.761704702	0.589799007	yes	yes	yes	BF390021	Rn.89428	Similar to Exocyst complex component Sec15B (predicted)
78	1391877_at	-0.760411104	0.59032809	yes	yes	yes	BF405044	Rn.46186	Transcribed locus
79	1368358_a_at	-0.75792953	0.591344384	yes	yes	yes	NM_053594	Rn.6277	protein tyrosine phosphatase, receptor type, R
80	1397915_at	-0.757457984	0.591537697	yes	yes	yes	AW526790	Rn.46323	Transcribed locus
81	1395319_at	-0.756056357	0.592112675	yes	yes	yes	BM383557	---	---
82	1382772_at	-0.750313945	0.59447418	yes	yes	yes	BF289261	Rn.61687	Phosphatidic acid phosphatase 2a
83	1392643_at	-0.748929184	0.595045056	yes	yes	yes	BF407212	Rn.3305	RAB5B, member RAS oncogene family (predicted)

84	1397032_at	-0.74620776	0.596168577	yes	yes	yes	BF404482	Rn.163182	Microrchidia 3 (predicted)
85	1394917_at	-0.745285473	0.596549818	yes	yes	yes	AI145806	Rn.46167	Centaurin, beta 2
86	1382421_at	-0.743960206	0.597098063	yes	yes	no	BI292508	---	---
87	1378808_at	-0.743336684	0.59735618	yes	yes	yes	AA925542	Rn.18925	Transcribed locus
88	1396775_at	-0.742615284	0.597654955	yes	yes	yes	BF403583	Rn.173236	Transcribed locus
89	1369771_at	-0.742246251	0.597807851	yes	yes	yes	NM_012969	Rn.10476	insulin receptor substrate 1
90	1395120_at	-0.737251501	0.599881107	yes	yes	yes	BF403704	Rn.2104	Amyloid beta (A4) precursor protein
91	1397316_at	-0.734812723	0.600896022	yes	yes	yes	AI179830	Rn.162886	NIMA (never in mitosis gene a)- related kinase 9 (predicted)
92	1383030_at	-0.734072961	0.601204219	yes	yes	yes	AI502367	Rn.11495	Amino-terminal enhancer of split
93	1394820_at	-0.731980149	0.602076975	yes	yes	yes	AI704849	Rn.21256	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
94	1395521_at	-0.731045905	0.602466988	yes	yes	yes	BI299174	Rn.103390	Anterior pharynx defective 1b homolog (C. elegans)
95	1380566_at	-0.729405078	0.603152584	yes	yes	yes	BI279622	Rn.57410	transmembrane protein 24
96	1390498_at	-0.728065555	0.603712863	yes	yes	yes	AI230554	Rn.22441	Carbonic anhydrase VB, mitochondrial
97	1384301_at	-0.72766234	0.603881616	yes	yes	no	BE113571	Rn.3665	Similar to Kelch-like protein 3 (predicted)
98	1380020_at	-0.727296697	0.604034686	yes	yes	yes	BF395860	Rn.10898	Peptidylprolyl isomerase G
99	1396763_at	-0.724142555	0.605356723	yes	yes	yes	BF412954	Rn.62204	Similar to ortholog of human amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19)
100	1396252_at	-0.723946697	0.605438911	yes	yes	yes	BE117174	---	---
101	1367598_at	-0.723616922	0.605577319	yes	yes	yes	NM_012681	Rn.1404	transthyretin
102	1378717_at	-0.723128781	0.605782253	yes	yes	yes	BF390952	Rn.57341	Transcribed locus
103	1396623_at	-0.718831907	0.607589184	yes	yes	yes	BF399568	Rn.60205	Transcribed locus
104	1394493_at	-0.718470139	0.607741561	yes	yes	yes	AW524359	Rn.23810	Casein kinase 1, alpha 1
105	1378866_at	-0.718008378	0.607936111	yes	yes	yes	BF401176	Rn.40404	Similar to actin-binding LIM protein 1 long isoform (predicted)
106	1376991_at	-0.717607899	0.608104892	yes	yes	yes	BE095620	Rn.25269	Transcribed locus
107	1398015_at	-0.716545512	0.60855286	yes	yes	no	BF404613	---	---
108	1377315_at	-0.715229458	0.609108247	yes	yes	yes	BF412662	Rn.47374	Similar to KIAA0819 protein (predicted)
109	1398613_at	-0.714489314	0.609420817	yes	yes	yes	AW532063	Rn.169951	Transcribed locus
110	1391558_at	-0.712207007	0.610385668	yes	yes	yes	BF290997	Rn.106300	Transcribed locus
111	1398704_at	-0.7121402	0.610413934	yes	yes	yes	BF391251	Rn.57442	Similar to Hypothetical protein C6orf60 (predicted)
112	1378646_at	-0.712060081	0.610447834	yes	yes	no	AW525661	Rn.4014	YTH domain family 3 (predicted)
113	1384333_at	-0.709316284	0.611609922	yes	yes	yes	AW920881	Rn.102249	ARP2 actin-related protein 2 homolog (yeast)
114	1380937_at	-0.709302185	0.611615899	yes	yes	yes	BE106331	Rn.11637	CDNA clone IMAGE:7461178
115	1374746_at	-0.707480383	0.612388721	yes	yes	yes	AA891922	Rn.3690	Ab1-152
116	1395102_at	-0.707469225	0.612393457	yes	yes	yes	AW528917	Rn.162642	potassium channel, subfamily T, member 1
117	1392945_at	-0.706642289	0.612744575	yes	yes	yes	BE115154	Rn.141084	Transcribed locus
118	1384120_at	-0.704363271	0.613713289	yes	yes	yes	BF386877	Rn.149983	Transcribed locus
119	1397851_at	-0.703701488	0.613994872	yes	yes	yes	BE102226	Rn.85462	Quaking homolog, KH domain RNA binding (mouse)
120	1376405_at	-0.703688687	0.61400032	yes	yes	no	BF404837	Rn.154631	Similar to KIAA0368 (predicted)
121	1392317_at	-0.703517445	0.614073204	yes	yes	yes	BI288026	Rn.95276	Solute carrier family 33 (acetyl-CoA transporter), member 1
122	1394888_at	-0.702678984	0.614430193	yes	yes	yes	AW920350	Rn.98522	RNA binding motif, single stranded interacting protein 1
123	1379117_at	-0.702564585	0.614478916	yes	yes	yes	BF415415	Rn.52558	Transcribed locus
124	1378604_at	-0.702036538	0.614703865	yes	yes	yes	BF396495	Rn.162165	Speckle-type POZ protein
125	1385250_at	-0.70134126	0.615000181	yes	yes	no	BF415132	Rn.43055	chromodomain helicase DNA binding protein 6 (predicted)
126	1373261_at	-0.697189326	0.61677264	yes	yes	yes	BF388657	Rn.156297	Transcribed locus
127	1393333_at	-0.694611813	0.617875548	yes	yes	yes	BF561617	---	---
128	1391312_at	-0.693214895	0.618474109	yes	yes	yes	BE108090	Rn.60475	inositol polyphosphate-5-phosphatase F (predicted)

129	1385204_at	-0.692189229	0.618913961	yes	yes	yes	AI639503	Rn.21777	similar to RIKEN cDNA 4833418A01 (predicted)
130	1395790_at	-0.691587135	0.619172312	yes	yes	yes	BF409032	---	---
131	1395092_at	-0.690574616	0.619607015	yes	yes	yes	BM388276	Rn.8555	RNA-binding region (RNP1, RRM) containing 2
132	1381414_at	-0.690179835	0.619776589	yes	yes	yes	AA964872	Rn.165086	Transcribed locus
133	1397716_at	-0.688800987	0.62036922	yes	yes	yes	AI547852	Rn.129179	Kelch domain containing 2
134	1397503_at	-0.686896982	0.621188496	yes	yes	yes	AI555886	Rn.32931	Leucine-rich repeats and calponin homology (CH) domain containing 3 (predicted)
135	1378004_at	-0.686632676	0.62130231	yes	yes	yes	BF287788	Rn.166203	Transcribed locus
136	1377329_at	-0.684227968	0.622338771	yes	yes	yes	BE113460	Rn.13196	Basic leucine zipper and W2 domains 2
137	1380844_at	-0.684038879	0.622420344	yes	yes	no	BE098337	Rn.144867	WW domain containing E3 ubiquitin protein ligase 1
138	1393546_at	-0.68396533	0.622452076	yes	yes	yes	BF394642	Rn.3455	Poly (A) polymerase alpha (predicted)
139	1381586_at	-0.683738308	0.622550032	yes	yes	yes	BI296171	Rn.162730	similar to mKIAA1386 protein
140	1399110_at	-0.682493956	0.623087226	yes	yes	yes	AW921218	Rn.17135	zinc finger protein 297
141	1380693_at	-0.681796156	0.623388672	yes	yes	yes	BF415976	Rn.38550	Similar to ribosomal protein S6 kinase 2 (predicted)
142	1393062_at	-0.680989498	0.623737326	yes	yes	yes	BI275419	Rn.14752	Transcribed locus
143	1397266_at	-0.68010068	0.624121718	yes	yes	yes	AA946437	Rn.18589	Transcription factor CP2-like 2
144	1380908_at	-0.678825583	0.624673579	yes	yes	no	AA924563	Rn.7085	Cd200 antigen
145	1382987_at	-0.678548683	0.624793486	yes	yes	no	AA874945	Rn.74539	Similar to RIKEN cDNA 5330414D10 (predicted)
146	1380652_at	-0.678296609	0.624902662	yes	yes	yes	BF396394	Rn.4226	Son of sevenless homolog 2 (Drosophila)
147	1396397_at	-0.677682135	0.625168878	yes	yes	yes	AW529321	Rn.46976	Transcribed locus
148	1398490_at	-0.675370352	0.626171455	yes	yes	yes	BM390414	Rn.172884	Transcribed locus
149	1396254_at	-0.674399967	0.626592772	yes	yes	yes	BF401989	Rn.49136	Nuclear receptor coactivator 2
150	1390292_at	-0.674027367	0.626754621	yes	yes	yes	AW527467	Rn.21890	transmembrane protein 8 (five membrane-spanning domains) (predicted)
151	1371109_at	-0.67216252	0.627565296	yes	yes	no	AA819870	Rn.110603	complement component 8, beta polypeptide (mapped)
152	1397618_at	-0.671809948	0.627718682	yes	yes	yes	BF559398	Rn.24583	sperm associated antigen 9 (predicted)
153	1379251_at	-0.669682398	0.628645065	yes	yes	yes	BF398485	Rn.24762	Transcribed locus
154	1393327_at	-0.66932012	0.628802945	yes	yes	yes	BG667328	Rn.21488	Transcribed locus
155	1397407_at	-0.668475587	0.629171145	yes	yes	no	AI137564	Rn.27457	Transcribed locus
156	1384078_at	-0.667843344	0.629446932	yes	yes	yes	AA875072	Rn.163704	Transcribed locus
157	1377332_at	-0.667521059	0.629587561	yes	yes	yes	BF403350	Rn.61756	Transcribed locus
158	1380625_at	-0.666220722	0.630155279	yes	yes	yes	BE109276	Rn.134425	CCR4-NOT transcription complex, subunit 4
159	1392017_at	-0.665655762	0.630402097	yes	yes	yes	BF397766	Rn.161793	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
160	1394107_at	-0.664825353	0.630765058	yes	yes	yes	BF546029	Rn.174564	Transcribed locus
161	1396138_at	-0.662562328	0.631755258	yes	yes	yes	BF544511	Rn.172976	Transcribed locus
162	1381498_at	-0.660463813	0.632674865	yes	yes	yes	AA956116	Rn.35935	ADP-ribosylation factor 4
163	1395032_at	-0.66019694	0.63279191	yes	yes	yes	AW531378	Rn.148911	Transcribed locus
164	1380038_at	-0.656631325	0.634357786	yes	yes	yes	BF393567	Rn.162986	similar to vacuolar protein sorting 13C protein (predicted)
165	1395667_at	-0.655574611	0.634822597	yes	yes	yes	BF418964	Rn.52592	similar to apurinic/apyrimidinic endonuclease 2 (predicted)
166	1388029_at	-0.654967435	0.635089826	yes	yes	yes	AF315467	Rn.30231	testis-specific gene including a ubiquitin-likely domain
167	1389767_at	-0.654274872	0.635394773	yes	yes	no	BE115349	Rn.34400	similar to hypothetical protein FLJ31364 (predicted)
168	1380807_at	-0.65248257	0.636184633	yes	yes	yes	AW529655	Rn.89331	Discs, large homolog 1 (Drosophila)
169	1390866_at	-0.651222008	0.636740746	yes	yes	yes	AI168981	Rn.146252	Transcribed locus
170	1387868_at	-0.650631504	0.637001421	yes	yes	yes	BF289368	Rn.48863	lipopolysaccharide binding protein
171	1379591_at	-0.64973756	0.637396252	yes	yes	yes	AI228518	---	---
172	1392214_at	-0.648330267	0.63801831	yes	yes	yes	AW532375	Rn.136438	Bromodomain and WD repeat domain containing 3 (predicted)
173	1368148_at	-0.648133701	0.638105246	yes	yes	no	NM_012610	Rn.10980	nerve growth factor receptor (TNFR superfamily, member 16)
174	1392199_at	-0.648097144	0.638121415	yes	yes	yes	BF398981	Rn.172452	Transcribed locus

175	1398059_at	-0.647491998	0.638389135	yes	yes	yes	AI501546	Rn.21519	Potassium channel regulator (predicted)
176	1395136_at	-0.647406552	0.638426945	yes	yes	yes	BE115145	Rn.52464	Transcribed locus
177	1377163_at	-0.646771603	0.638707987	yes	yes	yes	BM385741	Rn.35074	Transcribed locus
178	1392445_at	-0.646680672	0.638748245	yes	yes	yes	BE121428	Rn.61360	Transcribed locus
179	1377208_at	-0.644705391	0.639623393	yes	yes	yes	BI291457	Rn.1940	Muscleblind-like 2 (predicted)
180	1374685_at	-0.643868579	0.639994504	yes	yes	yes	BE117446	Rn.169246	Transcribed locus
181	1390503_at	-0.642936278	0.640408216	yes	yes	yes	BI301268	Rn.15352	Hypothetical LOC287306 (predicted)
182	1368775_at	-0.642396378	0.640647921	yes	yes	yes	NM_133563	Rn.107259	gonadotropin inducible ovarian transcription factor 1
183	1395185_at	-0.642316763	0.640683276	yes	yes	yes	BE115336	Rn.52500	Vesicle-associated membrane protein, associated protein B and C
184	1379917_at	-0.641455261	0.641065973	yes	yes	yes	AW528106	Rn.173203	Transcribed locus
185	1398595_at	-0.641326109	0.641123364	yes	yes	yes	AI070585	Rn.17033	RNA binding motif protein 5
186	1396570_at	-0.640315878	0.641572461	yes	yes	no	BF393250	Rn.132666	Transcribed locus
187	1373970_at	-0.639204795	0.642066755	yes	yes	yes	AI716248	Rn.106849	similar to RIKEN cDNA 9230117N10
188	1381141_at	-0.639181643	0.642077059	yes	yes	yes	BF396613	Rn.103225	Breast cancer 2
189	1380837_at	-0.638585496	0.642342431	yes	yes	yes	BE102082	Rn.19499	Similar to hypothetical protein A730008H23 (predicted)
190	1381527_at	-0.638435835	0.642409069	yes	yes	yes	AI535521	Rn.101986	Transcribed locus, strongly similar to NP_081306.1 histidine triad protein member 5 [Mus musculus]
191	1397969_at	-0.637068584	0.643018173	yes	yes	yes	BF401230	Rn.139546	Ash1 (absent, small, or homeotic)-like (Drosophila) (predicted)
192	1394997_at	-0.634661787	0.644091793	yes	yes	yes	AI409919	Rn.12683	Transcribed locus
193	1376451_at	-0.633279137	0.644709373	yes	yes	yes	BG377849	Rn.162726	similar to krev interaction trapped-1A
194	1374258_at	-0.633009839	0.644829727	yes	yes	yes	BF394021	Rn.58200	Similar to hypothetical protein MGC13138 (predicted)
195	1398565_at	-0.63191195	0.645320629	yes	yes	no	AW534457	Rn.113514	Similar to nemo like kinase (predicted)
196	1381719_at	-0.631811974	0.64536535	yes	yes	no	BE115752	Rn.1055	Cytochrome b-5
197	1379501_at	-0.631019598	0.645719903	yes	yes	no	AA963993	Rn.163395	Docking protein 4 (predicted)
198	1389785_at	-0.628549292	0.646826507	yes	yes	yes	AA892933	Rn.22552	aspartoacylase (aminoacylase) 3
199	1380924_at	-0.628499005	0.646849054	yes	no	no	BF395816	Rn.119102	Grainyhead-like 1 (Drosophila) (predicted)
200	1395047_at	-0.628467394	0.646863227	yes	yes	yes	BF397243	---	---
201	1397624_at	-0.628351467	0.646915208	yes	yes	no	BI300158	Rn.173174	Transcribed locus
202	1396325_at	-0.627662262	0.647224326	yes	yes	yes	BF413179	Rn.145000	similar to RIKEN cDNA 4933405K07
203	1396791_at	-0.625707824	0.648101724	yes	yes	no	BF392129	Rn.131185	Cdc42 GTPase-activating protein (predicted)
204	1391902_at	-0.624686705	0.648560603	yes	yes	yes	AW527377	Rn.9738	Phosphoglycerate mutase 2
205	1385108_at	-0.623809455	0.648955089	yes	yes	yes	AW524173	Rn.149172	Similar to hypothetical protein D630010C10
206	1385385_at	-0.623580759	0.649057969	yes	yes	yes	BE116745	Rn.48749	Wingless-type MMTV integration site 5A
207	1368322_at	-0.622949019	0.649342247	yes	yes	yes	NM_012880	Rn.10358	superoxide dismutase 3, extracellular
208	1395772_at	-0.620605183	0.650398041	yes	yes	yes	BF290181	---	---
209	1371081_at	-0.620336622	0.650519125	yes	yes	no	U78517	Rn.42890	Rap guanine nucleotide exchange factor (GEF) 4
210	1378759_at	-0.620192626	0.650584057	yes	yes	yes	BE102644	Rn.13214	5'-3' exoribonuclease 1 (predicted)
211	1381778_at	-0.620182081	0.650588812	yes	yes	no	BI273900	Rn.52469	Transcribed locus
212	1393746_at	-0.619698102	0.650807101	yes	yes	no	BE117730	Rn.157075	Transcribed locus, weakly similar to XP_219319.3 PREDICTED: similar to deleted in malignant brain tumors 1 [Rattus norvegicus]
213	1393608_at	-0.619297427	0.650987873	yes	yes	no	AW522185	Rn.76361	Transcribed locus
214	1396278_at	-0.617754019	0.651684678	yes	yes	yes	BF545212	Rn.13268	sorting nexin 11
215	1383750_at	-0.616665635	0.652176501	yes	yes	no	BF418523	Rn.11467	Transcribed locus
216	1385630_at	-0.616571105	0.652219235	yes	yes	yes	AA925114	---	---
217	1375187_at	-0.616358186	0.6523155	yes	yes	yes	BF281701	Rn.12112	Transcribed locus
218	1393337_at	-0.61610785	0.652428699	yes	yes	yes	AW524476	Rn.87419	Transcribed locus
219	1379602_at	-0.615368088	0.652763327	yes	yes	no	AI010055	---	---

220	1397608_at	-0.614902554	0.652973997	yes	yes	yes	BE107197	Rn.6839	Trinucleotide repeat containing 6 (predicted)
221	1389581_at	-0.614894087	0.652977829	yes	yes	yes	BF390510	Rn.106849	similar to RIKEN cDNA 9230117N10
222	1381386_at	-0.61303527	0.65381969	yes	yes	no	AI407297	Rn.168969	Transcribed locus
223	1370770_s_at	-0.612927307	0.65386862	yes	yes	yes	AF071205	Rn.44216	kit ligand
224	1398691_at	-0.612330326	0.654139244	yes	yes	yes	AI408578	Rn.43610	Similar to KIAA0669 gene product
225	1381503_at	-0.611496856	0.654517261	yes	yes	no	AI073168	---	---
226	1380701_at	-0.610932537	0.654773329	yes	yes	yes	BF400722	Rn.162666	Sperm specific antigen 2 (predicted)
227	1396072_at	-0.610455901	0.654989688	yes	yes	yes	BG662585	Rn.156667	Transcribed locus
228	1395716_at	-0.610249856	0.65508324	yes	yes	no	AW919386	Rn.21843	Similar to c-myc promoter binding protein (predicted)
229	1394759_at	-0.609738035	0.655315683	yes	yes	yes	BF289157	---	---
230	1387099_at	-0.609572904	0.655390695	yes	yes	yes	NM_053838	Rn.32984	natriuretic peptide receptor 2
231	1389714_at	-0.608304957	0.655966954	yes	yes	yes	AI103146	Rn.36807	Glycogen synthase kinase 3 alpha
232	1377138_at	-0.607428698	0.656365494	yes	yes	yes	AI709547	Rn.6524	Ataxin 10
233	1380851_at	-0.606688787	0.656702209	yes	yes	yes	BF417256	Rn.44951	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F (predicted)
234	1396098_at	-0.606410135	0.656829061	yes	yes	no	BG380369	Rn.97147	apoptotic chromatin condensation inducer 1
235	1394227_at	-0.606016415	0.657008338	yes	yes	no	AI237251	Rn.10830	dynamin 1-like
236	1382614_at	-0.605791351	0.657110841	yes	yes	yes	AI029732	Rn.78858	similar to Zinc finger, FYVE domain containing 16 (predicted)
237	1398523_a_at	-0.603823608	0.658007709	yes	yes	yes	AA900618	---	interferon (alpha and beta) receptor 1 (predicted)
238	1384542_at	-0.60305213	0.658359671	yes	yes	yes	BE103021	Rn.170862	Transcribed locus
239	1397999_at	-0.602580113	0.658575107	yes	yes	yes	BF386502	Rn.156286	Transcribed locus
240	1382839_at	-0.602577104	0.658576481	yes	yes	yes	AI009109	Rn.156695	Transcribed locus
241	1397786_at	-0.601933152	0.658870504	yes	yes	no	BF391927	Rn.41379	Similar to protein phosphatase 1, regulatory subunit 12C
242	1379001_at	-0.600915716	0.659335325	yes	yes	no	AA945695	Rn.11324	Nucleoporin 98
243	1387996_a_at	-0.599943469	0.659779808	yes	yes	yes	AF333326	Rn.17691	Hermansky-Pudlak syndrome 1 homolog (human)
244	1375602_at	-0.599394025	0.66003113	yes	yes	yes	BG378103	---	---
245	1374383_at	-0.599284496	0.660081241	yes	yes	yes	BE121006	Rn.156608	Transcribed locus
246	1391644_at	-0.59927583	0.660085206	yes	yes	yes	AW920336	Rn.101864	density-regulated protein
247	1381753_at	-0.599000557	0.660211166	yes	yes	yes	BF416214	Rn.45065	F-box and leucine-rich repeat protein 7 (predicted)
248	1376693_at	-0.598169229	0.66059171	yes	yes	yes	AA998964	Rn.13231	similar to OEF2 (predicted)
249	1381471_at	-0.597777951	0.660770896	yes	yes	yes	AI060117	Rn.21181	Transcribed locus
250	1391372_at	-0.597034597	0.661111449	yes	yes	yes	BF405555	Rn.7840	Dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)
251	1395148_at	-0.596395632	0.661404318	yes	yes	yes	BF388173	Rn.99077	Similar to protein tyrosine phosphatase, receptor type, D (predicted)
252	1375468_at	-0.595327272	0.661894289	yes	yes	yes	AW252983	---	---
253	1379228_at	-0.595265329	0.661922708	yes	yes	yes	BF418531	Rn.146209	similar to flt3 ligand (predicted)
254	1376677_a_at	-0.595141059	0.661979727	yes	yes	yes	BF282021	Rn.53921	Transcribed locus
255	1379815_at	-0.594978238	0.662054442	yes	yes	yes	AI713959	---	---
256	1369352_at	-0.594465349	0.662289849	yes	yes	yes	NM_031787	Rn.8099	homeodomain interacting protein kinase 3
257	1395436_at	-0.594249647	0.662388878	yes	yes	yes	BF415556	Rn.6866	Protein phosphatase 3, catalytic subunit, alpha isoform
258	1378291_at	-0.593784024	0.662602695	yes	yes	yes	BF549558	Rn.1464	FK506 binding protein 3 (predicted)
259	1380545_at	-0.593706568	0.66263827	yes	yes	yes	BF419027	Rn.63466	development and differentiation enhancing (predicted)
260	1378155_at	-0.593374216	0.662790939	yes	yes	yes	BI289641	Rn.131566	similar to KIAA1096 protein (predicted)
261	1383944_at	-0.59217767	0.663340874	yes	yes	yes	AI144970	Rn.3602	Sorting nexin 6 (predicted)
262	1388785_at	-0.59156025	0.66362482	yes	no	no	AA892303	Rn.3257	dynein, axonemal, light chain 4
263	1389871_at	-0.590967142	0.663897699	yes	yes	no	BI296539	Rn.98650	glutamate oxaloacetate transaminase 2, mitochondrial
264	1383084_at	-0.590492815	0.664116011	yes	yes	yes	BG671922	Rn.139571	Transcribed locus
265	1387338_s_at	-0.590320166	0.664195491	yes	yes	yes	NM_022612	Rn.82709	BCL2-like 11 (apoptosis facilitator)

266	1381714_at	-0.589780933	0.664443792	yes	yes	yes	BE105488	Rn.170953	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
267	1386962_at	-0.589778702	0.66444482	yes	no	no	NM_024353	Rn.6155	phospholipase C, beta 4
268	1390156_a_at	-0.58968003	0.664490265	yes	yes	yes	BF283671	Rn.85011	Transcribed locus
269	1378843_at	-0.588434262	0.665064301	yes	yes	yes	AW528827	Rn.129050	DnaJ (Hsp40) homolog, subfamily B, member 6
270	1390734_at	-0.58836891	0.665094428	yes	yes	yes	BI291369	Rn.176363	Transcribed locus
271	1371672_at	-0.588327361	0.665113583	yes	yes	yes	AI406275	Rn.12512	chromobox homolog 7
272	1380774_at	-0.588176609	0.665183087	yes	yes	yes	AI227918	Rn.171490	Transcribed locus
273	1380402_at	-0.588160394	0.665190563	yes	yes	yes	AA818127	Rn.1287	Transcribed locus
274	1381088_at	-0.588052378	0.665240368	yes	yes	yes	BE096686	---	---
275	1390719_at	-0.588008137	0.665260769	yes	yes	yes	BI294889	Rn.21735	Similar to DKFZP564P1916 protein (predicted)
276	1383061_at	-0.587735369	0.66538656	yes	yes	yes	AI070680	Rn.14666	Transcribed locus
277	1391912_at	-0.587013462	0.665719595	yes	yes	no	AI599382	Rn.166051	Transcribed locus
278	1378442_at	-0.586485625	0.665963205	yes	yes	yes	BF400763	Rn.89331	Discs, large homolog 1 (Drosophila)
279	1397795_at	-0.586023232	0.666176685	yes	yes	yes	AW533928	---	---
280	1377430_at	-0.585450365	0.666441264	yes	yes	yes	BF413556	Rn.19694	Transcribed locus
281	1382020_at	-0.583964622	0.667127944	yes	yes	yes	BE105500	---	---
282	1384624_at	-0.583738848	0.667232354	yes	no	no	AI233317	---	---
283	1397881_at	-0.583486178	0.667349222	yes	yes	yes	AI575768	Rn.168236	Transcribed locus
284	1380012_at	-0.583280755	0.667444251	yes	yes	yes	BF399592	Rn.60026	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19
285	1372254_at	-0.583257932	0.66745481	yes	yes	yes	AW915763	Rn.100285	serine (or cysteine) peptidase inhibitor, clade G, member 1
286	1368269_at	-0.582967673	0.66758911	yes	yes	yes	NM_012975	Rn.9656	lectin, galactose binding, soluble 4
287	1389722_at	-0.580998044	0.668501154	yes	yes	yes	BF408457	Rn.146811	Transcribed locus
288	1381888_x_at	-0.580457255	0.668751786	yes	yes	no	AA848451	Rn.6365	Similar to RIKEN cDNA 4933428G09 (predicted)
289	1391843_at	-0.580433531	0.668762783	yes	yes	yes	BF393134	Rn.133917	Similar to elongation protein 4 homolog (predicted)
290	1385677_s_at	-0.580349292	0.668801834	yes	yes	yes	BG372143	Rn.66895	Transcribed locus
291	1390956_at	-0.57940296	0.669240676	yes	yes	no	BI294909	Rn.35355	Transcribed locus
292	1381900_at	-0.579328108	0.6692754	yes	yes	yes	AI407705	Rn.27138	Transcribed locus
293	1388096_at	-0.579272887	0.669301018	yes	yes	yes	AF071204	Rn.44216	kit ligand
294	1382749_at	-0.578188106	0.669804463	yes	yes	no	BI293987	Rn.17033	RNA binding motif protein 5
295	1376817_at	-0.578121055	0.669835594	yes	yes	no	AA943165	Rn.105925	Transcribed locus
296	1386608_at	-0.57756591	0.670093394	yes	yes	no	BI395730	---	---
297	1397685_at	-0.576766677	0.670464719	yes	yes	no	BF553180	Rn.52800	Transcribed locus
298	1376284_at	-0.576527959	0.670575668	yes	yes	no	AI406517	Rn.27890	Similar to transcriptional intermediary factor 1 delta
299	1393495_at	-0.576505558	0.67058608	yes	yes	no	AI043752	Rn.147542	Transcribed locus
300	1381408_at	-0.575862853	0.670884886	yes	yes	no	BI275477	Rn.98296	OCIA domain containing 1
301	1392112_at	-0.575788559	0.670919435	yes	no	no	BF397377	Rn.168699	Transcribed locus, strongly similar to NP_071947.1 palmitoyl-protein thioesterase [Rattus norvegicus]
302	1369004_at	-0.575663543	0.670977576	yes	yes	no	NM_133580	Rn.10975	RAB26, member RAS oncogene family
303	1395993_at	-0.575658831	0.670979767	yes	yes	no	AI764408	---	---
304	1374717_at	-0.575420047	0.671090832	yes	yes	no	BI295624	Rn.10739	Calcium channel, voltage-dependent, beta 2 subunit
305	1384214_a_at	-0.574949504	0.671309748	yes	yes	no	AI045459	Rn.166129	Transcribed locus
306	1395762_at	-0.574884012	0.671340223	yes	yes	no	BG670091	Rn.8556	RNA binding motif protein 4 (predicted)
307	1369731_at	-0.574874963	0.671344434	yes	no	no	AF102854	Rn.42893	connector enhancer of kinase suppressor of Ras 2
308	1390259_at	-0.574562803	0.67148971	yes	yes	no	AI231279	Rn.24937	Transcribed locus
309	1378350_at	-0.574128858	0.671691716	yes	no	no	AA859902	Rn.156510	Transcribed locus
310	1375404_at	-0.573974789	0.671763452	yes	yes	no	BF415963	Rn.98476	Spermatid perinuclear RNA binding protein

311	1374744_at	-0.57320842	0.672120392	yes	yes	no	BF392285	Rn.92155	DnaJ (Hsp40) homolog, subfamily C, member 7
312	1374786_at	-0.572592089	0.672407588	yes	yes	no	BI298817	Rn.50685	Cytotoxic granule-associated RNA binding protein 1
313	1389603_at	-0.571705088	0.672821127	yes	yes	no	AA964544	---	---
314	1376966_at	-0.571689162	0.672828554	yes	yes	yes	BE108930	Rn.124042	Transcribed locus
315	1380952_at	-0.571266697	0.673025608	yes	yes	no	BF395639	Rn.23978	transcriptional adaptor 1 (HFI1 homolog, yeast) like
316	1369200_at	-0.571245397	0.673035544	yes	yes	yes	NM_021576	Rn.40132	5' nucleotidase, ecto
317	1375953_at	-0.570688197	0.673295535	yes	yes	no	AI012884	Rn.156340	Transcribed locus
318	1396315_at	-0.570291133	0.673480868	yes	yes	no	BF408941	---	---
319	1388185_at	-0.56982443	0.67369877	yes	yes	no	AI178012	Rn.55115	retinoblastoma 1
320	1381420_at	-0.568866752	0.674146127	yes	yes	no	BF397624	Rn.101536	Ubiquitin specific protease 47 (predicted)
321	1387328_at	-0.568751484	0.674199992	yes	yes	no	NM_019184	Rn.10870	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
322	1390402_at	-0.568225607	0.67444579	yes	no	no	AI172431	Rn.4080	Transcribed locus
323	1379648_at	-0.568166371	0.674473483	yes	yes	no	AA900610	Rn.99298	Nuclear factor of activated T-cells 5 (predicted)
324	1385260_at	-0.56772384	0.674680402	yes	yes	no	BE103057	Rn.125849	Transcribed locus
325	1374448_at	-0.566666965	0.675174834	yes	yes	no	AW523759	Rn.7365	reversion-inducing-cysteine-rich protein with kazal motifs (predicted)
326	1397310_at	-0.566549456	0.675229829	yes	yes	no	AI178436	Rn.29226	Transcribed locus
327	1385513_at	-0.566104455	0.675438137	yes	yes	no	AI112764	Rn.166628	Transcribed locus
328	1384207_at	-0.566052883	0.675462282	yes	yes	yes	AI028960	Rn.163065	Ngg1 interacting factor 3-like 1 (S. pombe)
329	1381899_at	-0.565862666	0.675551347	yes	yes	no	AW534794	Rn.156733	Transcribed locus
330	1391629_at	-0.565535265	0.675704672	yes	yes	no	BI290794	Rn.40729	RGD1563042 (predicted)
331	1395893_at	-0.565245079	0.675840598	yes	yes	yes	AW921408	Rn.1292	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
332	1399056_at	-0.565097583	0.675909697	yes	yes	no	AI716436	Rn.20063	similar to CG10585-PA
333	1380369_at	-0.564801455	0.676048448	yes	yes	yes	AI058315	Rn.20945	Transcribed locus
334	1394577_at	-0.564758522	0.676068567	yes	yes	no	BI279384	Rn.146573	Transcribed locus
335	1389252_at	-0.564375953	0.676247869	yes	yes	no	AI102190	Rn.92325	Zinc finger protein 238
336	1374817_at	-0.564054718	0.676398461	yes	yes	no	BE103235	Rn.19071	Transcribed locus
337	1392921_at	-0.563856229	0.676491528	yes	yes	no	BI294990	Rn.164392	Transcribed locus
338	1389742_at	-0.562845665	0.676965555	yes	yes	no	AW520758	Rn.65227	Transcribed locus
339	1390438_at	-0.562196766	0.677270111	yes	yes	yes	AW526136	---	histone deacetylase 5
340	1394430_at	-0.561755008	0.677477525	yes	yes	no	AI511275	Rn.168003	Transcribed locus
341	1393582_at	-0.561510921	0.677592156	yes	yes	no	AW529067	Rn.148912	Transcribed locus
342	1397274_at	-0.561471899	0.677610484	yes	yes	no	AI555780	Rn.23194	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
343	1380969_at	-0.561407418	0.67764077	yes	yes	no	BE106363	Rn.106130	Similar to mKIAA0940 protein (predicted)
344	1393870_at	-0.560588883	0.678025349	yes	yes	no	AA799465	Rn.6188	Transcribed locus
345	1390800_a_at	-0.560472535	0.678080032	yes	yes	no	BE349669	Rn.81070	caveolin 2
346	1382998_at	-0.559963651	0.678319254	yes	yes	no	AI044778	Rn.20871	RNA (guanine-7-) methyltransferase
347	1392277_at	-0.559585466	0.678497091	yes	yes	yes	BI303053	---	---
348	1369263_at	-0.559288499	0.678636768	yes	yes	no	NM_022631	Rn.48749	wingless-type MMTV integration site 5A
349	1390206_at	-0.559224737	0.678666762	yes	yes	no	AW434946	Rn.54341	Transcribed locus
350	1385231_at	-0.559199784	0.6786785	yes	yes	yes	AI044528	---	---
351	1390028_at	-0.55849485	0.679010199	yes	yes	no	BE096356	Rn.164476	Transcribed locus
352	1397362_at	-0.558317393	0.679093725	yes	yes	no	AI071343	Rn.153635	Hippyragranin
353	1381592_at	-0.558274542	0.679113896	yes	yes	no	AA926244	Rn.156726	Transcribed locus
354	1380016_at	-0.558180002	0.6791584	yes	yes	yes	BF389694	Rn.64856	Transcribed locus
355	1394785_at	-0.557671022	0.679398048	yes	yes	no	BE329290	Rn.54028	Transcribed locus

356	1378965_at	-0.557637862	0.679413664	yes	yes	yes	AA818967	Rn.33908	Transcribed locus
357	1368587_at	-0.557436742	0.679508385	yes	yes	yes	NM_012824	Rn.8887	apolipoprotein C-I
358	1381229_at	-0.557421256	0.679515679	yes	yes	yes	BE117665	Rn.14971	PR domain containing 2, with ZNF domain (mapped)
359	1380332_at	-0.557305138	0.679570373	yes	yes	no	BF411794	Rn.15395	Abhydrolase domain containing 6
360	1392723_at	-0.557188316	0.679625403	yes	yes	no	BF388065	Rn.8442	Similar to ankyrin repeat domain protein 17 isoform b (predicted)
361	1381175_at	-0.556938897	0.67974291	yes	yes	no	BE114469	---	---
362	1397201_at	-0.556338788	0.680025717	yes	yes	no	BE107286	Rn.92141	similar to KIAA1078 protein (predicted)
363	1390243_at	-0.556326753	0.68003139	yes	yes	no	AI535191	Rn.165990	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
364	1397492_at	-0.555554416	0.680395538	yes	yes	no	BF410962	---	---
365	1391115_at	-0.554737432	0.680780948	yes	yes	yes	BM390642	Rn.41478	similar to RIKEN cDNA 4930429O20
366	1396102_at	-0.554441596	0.680920562	yes	yes	no	BF406574	Rn.2022	UBX domain containing 2
367	1395519_at	-0.554210533	0.681029627	yes	yes	no	BG670960	Rn.92940	similar to B230212L03Rik protein
368	1397703_at	-0.554126481	0.681069306	yes	yes	yes	BF288942	---	---
369	1393782_at	-0.554013822	0.681122492	yes	yes	no	BF396790	Rn.6977	Pleiomorphic adenoma gene-like 1
370	1377296_at	-0.5531464	0.681532141	yes	yes	no	BF387370	Rn.162432	Transmembrane 6 superfamily member 1 (predicted)
371	1385074_at	-0.55235414	0.681906508	yes	yes	no	BE102268	Rn.94939	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
372	1370228_at	-0.552349709	0.681908603	yes	no	no	AA945178	Rn.91296	transferrin /// signal recognition particle receptor, B subunit
373	1392607_at	-0.551860741	0.682139759	yes	yes	no	BF391141	Rn.22747	Similar to erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) isoform 1 (predicted)
374	1391535_at	-0.551766573	0.682184286	yes	yes	no	BF284610	Rn.164131	Transcribed locus
375	1394200_at	-0.551425054	0.682345793	yes	yes	no	BF410146	---	heat shock 70kDa protein 2
376	1394912_at	-0.55107429	0.682511713	yes	yes	no	BG377129	Rn.125921	similar to DNA segment, Chr 6, Wayne State University 163, expressed (predicted)
377	1385927_at	-0.550197273	0.682926739	yes	yes	no	AA965251	Rn.12051	homeo box C4 (mapped)
378	1380154_at	-0.550077291	0.682983537	yes	no	no	BF410417	Rn.47124	inner membrane protein, mitochondrial
379	1378945_at	-0.549917634	0.683059124	yes	yes	no	AI638990	Rn.43737	Aconitase 2, mitochondrial
380	1391172_at	-0.549915964	0.683059915	yes	no	no	BE106088	Rn.148467	Transcribed locus
381	1398583_at	-0.54983824	0.683096715	yes	no	no	BE114791	---	---
382	1391006_at	-0.549331685	0.683336605	yes	yes	no	AI235353	Rn.73705	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)
383	1391980_at	-0.549188484	0.683404436	yes	yes	yes	BF394201	Rn.95507	similar to ubiquitin specific protease 34
384	1397320_at	-0.549071543	0.683459832	yes	yes	no	BI293372	Rn.83881	Similar to Progesterone-induced blocking factor 1 (predicted)
385	1375845_at	-0.548778173	0.683598827	yes	yes	yes	BI290029	Rn.14443	similar to Aig1 protein (predicted)
386	1385017_at	-0.54865169	0.683658762	yes	yes	yes	AW533683	Rn.37299	aquarius (predicted)
387	1393866_at	-0.548597466	0.683684458	yes	yes	no	AI137157	Rn.106560	similar to WSL-1-like protein
388	1373215_at	-0.548149956	0.683896563	yes	yes	no	BI282699	Rn.44897	active BCR-related gene (predicted)
389	1388044_at	-0.547861606	0.684033267	yes	yes	no	L27084	Rn.44844	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
390	1395554_at	-0.547763661	0.684079707	yes	yes	yes	BF405684	Rn.33262	V-raf-1 murine leukemia viral oncogene homolog 1
391	1390456_at	-0.546723153	0.684573261	yes	yes	yes	AW524471	Rn.169454	Transcribed locus
392	1379390_at	-0.546671507	0.684597768	yes	no	no	AA891414	Rn.53257	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
393	1392736_at	-0.546394334	0.684729306	yes	yes	no	AW532939	---	---
394	1390319_at	-0.546328518	0.684760545	yes	yes	no	BG378301	Rn.34047	Kinesin family member 13A (predicted)
395	1381057_at	-0.546047628	0.684893879	yes	yes	no	AW526130	Rn.145283	Similar to hypothetical protein MGC5391 (predicted)
396	1384062_at	-0.545569397	0.685120948	yes	yes	no	AI072443	Rn.14991	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide
397	1390574_at	-0.545094067	0.685346715	yes	yes	no	BE101126	Rn.16302	Transcribed locus

398	1391571_at	-0.545007736	0.685387727	yes	yes	no	BG666079	Rn.45627	Transcribed locus
399	1386029_at	-0.544340126	0.685704965	yes	yes	no	BF284035	---	---
400	1379646_at	-0.544165381	0.685788026	yes	yes	yes	AI229747	Rn.96035	Similar to CDNA sequence BC024479
401	1390016_at	-0.543448424	0.686128917	yes	no	no	BF415854	Rn.69854	Kelch repeat and BTB (POZ) domain containing 9 (predicted)
402	1379044_at	-0.543303085	0.686198043	yes	yes	no	AW534064	Rn.7988	Similar to RIKEN cDNA 1700108L22
403	1382975_at	-0.54261671	0.686524585	yes	yes	no	BE097239	Rn.91235	CEA-related cell adhesion molecule 1
404	1385970_at	-0.542508211	0.686576218	yes	yes	no	BF289079	Rn.102000	SH2 domain binding protein 1 (tetratricopeptide repeat containing)
405	1386474_at	-0.542346297	0.686653276	yes	no	no	H31753	Rn.132723	Transcribed locus
406	1379266_at	-0.54215845	0.686742688	yes	yes	no	AI235399	Rn.17705	Transcribed locus
407	1395241_at	-0.541955173	0.686839458	yes	yes	no	BF389686	Rn.93735	ADP-ribosylation factor 1
408	1381987_at	-0.541735266	0.686944159	yes	yes	no	AI175803	Rn.123918	Signal sequence receptor, alpha
409	1379280_at	-0.541730745	0.686946312	yes	yes	no	BF523849	Rn.24155	Transcribed locus
410	1370173_at	-0.541457969	0.687076208	yes	yes	no	BG671549	Rn.10488	superoxide dismutase 2, mitochondrial
411	1398265_at	-0.540972398	0.687307497	yes	yes	no	NM_013040	Rn.10528	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
412	1390198_at	-0.540496344	0.68753433	yes	yes	no	AW523642	Rn.165704	Transcribed locus
413	1373755_at	-0.538797289	0.688344512	yes	yes	no	AI717543	---	---
414	1382469_at	-0.538764186	0.688360307	yes	yes	no	AA900787	Rn.41046	Transcribed locus
415	1378000_at	-0.538688639	0.688396354	yes	yes	yes	AA801075	Rn.34520	Transcribed locus
416	1398440_at	-0.538572438	0.688451802	yes	yes	no	BI292166	Rn.164953	Transcribed locus
417	1380785_at	-0.537743579	0.688847446	yes	yes	no	BF405178	Rn.173324	Transcribed locus
418	1376332_at	-0.537698076	0.688869173	yes	yes	yes	BF396082	Rn.158172	Similar to AT motif-binding factor (predicted)
419	1397034_at	-0.537634665	0.688899452	yes	no	no	BE121170	Rn.18497	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) (predicted)
420	1394972_at	-0.537485896	0.688970494	yes	yes	no	BM390782	Rn.146598	Transcribed locus
421	1377782_at	-0.537413017	0.689005299	yes	yes	no	BF402614	Rn.165642	Transcribed locus
422	1375749_at	-0.537301693	0.689058467	yes	yes	yes	BF404853	Rn.163251	SEC3-like 1 (S. cerevisiae)
423	1391561_at	-0.536816844	0.689290079	yes	yes	yes	BE108893	Rn.28553	Transcribed locus
424	1395707_at	-0.536211943	0.689579149	yes	yes	no	BG670971	Rn.17648	Transcribed locus
425	1376794_at	-0.536171264	0.689598593	yes	yes	no	BF548418	Rn.11637	CDNA clone IMAGE:7461178
426	1372683_at	-0.536043908	0.689659471	yes	yes	yes	BI291252	Rn.51875	molybdenum cofactor sulfurase (predicted)
427	1373513_at	-0.536014017	0.68967376	yes	no	no	AI012419	Rn.163737	Transcribed locus
428	1382794_at	-0.535443608	0.689946496	yes	yes	no	AI179878	Rn.60224	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10
429	1377462_at	-0.535326034	0.690002726	yes	yes	no	BE111349	Rn.156502	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
430	1384775_s_at	-0.535300639	0.690014872	yes	yes	yes	AA925026	Rn.102783	transmembrane protease, serine 8 (intestinal)
431	1388747_at	-0.535056536	0.690131631	yes	yes	no	BG381002	Rn.162464	leucine carboxyl methyltransferase 1
432	1396310_at	-0.53496737	0.690174286	yes	yes	no	BF545380	Rn.137551	RNA binding motif protein 9 (predicted)
433	1376755_at	-0.534940019	0.690187371	yes	yes	no	BF419646	Rn.38896	retinoic acid receptor, beta
434	1391154_at	-0.534619828	0.690340568	yes	yes	no	BF394263	Rn.160261	Transcribed locus
435	1390366_at	-0.534447987	0.6904228	yes	yes	no	BI291884	Rn.162187	similar to PC-LKC gene product (predicted)
436	1392146_at	-0.534367135	0.690461494	yes	yes	no	BF418011	---	---
437	1388005_at	-0.534275359	0.690505419	yes	yes	yes	AF244920	Rn.18429	PRP18 pre-mRNA processing factor 18 homolog (yeast)
438	1380166_at	-0.534221022	0.690531426	yes	yes	no	BE101632	Rn.50095	Transcribed locus, strongly similar to XP_575581.1 PREDICTED: similar to hypothetical protein FLJ12056 [Rattus norvegicus]
439	1397152_at	-0.534153677	0.690563661	yes	yes	yes	BE108638	Rn.43612	Similar to KIAA1217 (predicted)
440	1390375_at	-0.532917083	0.691155825	yes	yes	no	BF414692	Rn.107308	A kinase (PRKA) anchor protein 8-like
441	1395941_at	-0.532482897	0.691363864	yes	yes	yes	BF542687	Rn.19263	potassium channel tetramerisation domain containing 3

442	1371011_at	-0.532300964	0.691451054	yes	yes	no	AW920487	Rn.111884	calcium-sensing receptor like 1 /// similar to putative pheromone receptor V2R2
443	1383659_a_at	-0.531971614	0.691608922	yes	yes	no	BG380561	---	---
444	1381247_at	-0.531797392	0.691692447	yes	yes	no	BE096812	Rn.168676	Transcribed locus
445	1375011_at	-0.531284429	0.691938428	yes	yes	no	AA818819	Rn.16544	Transcribed locus
446	1384058_at	-0.530850294	0.692146677	yes	yes	no	AI059089	Rn.21035	Transcribed locus
447	1390258_at	-0.530761462	0.692189297	yes	yes	no	AA893505	---	---
448	1376635_at	-0.53016343	0.692476285	yes	yes	no	BF283341	Rn.166636	Transcribed locus
449	1396147_at	-0.528699557	0.693179283	yes	yes	yes	BF394600	Rn.11071	Potassium voltage-gated channel, subfamily H (eag-related), member 1
450	1377195_at	-0.528335581	0.693354187	yes	yes	no	BF406252	Rn.5041	ATPase, Na+/K+ transporting, beta 3 polypeptide
451	1398057_at	-0.527668818	0.693674705	yes	yes	no	AI716292	Rn.26690	Excision repair cross-complementing rodent repair deficiency, complementation group 5 (mapped)
452	1394405_at	-0.527657736	0.693680033	yes	yes	no	AI232356	Rn.27737	Similar to KIAA0303 (predicted)
453	1373230_at	-0.527586797	0.693714143	yes	yes	yes	AI145851	Rn.95207	nudix (nucleoside diphosphate linked moiety X)-type motif 18
454	1386829_at	-0.526103803	0.694427602	yes	yes	yes	BF549319	Rn.130504	Mitogen activated protein kinase kinase kinase 10
455	1377758_at	-0.526067266	0.694445188	yes	yes	no	BF415386	Rn.25104	hydroxysteroid (17-beta) dehydrogenase 13
456	1378814_at	-0.525966516	0.694493686	yes	yes	no	BF387902	Rn.12390	Oxysterol binding protein-like 2
457	1370031_at	-0.52570582	0.694619193	yes	yes	no	NM_031685	Rn.13518	golgi SNAP receptor complex member 2
458	1380312_at	-0.525705309	0.694619439	yes	yes	yes	AA900436	Rn.146443	Similar to sperm antigen HCMOGT-1
459	1392007_at	-0.525456904	0.69473905	yes	yes	no	AI044568	Rn.129867	Transcribed locus, weakly similar to XP_214508.3 PREDICTED: similar to mKIAA0019 protein [Rattus norvegicus]
460	1378153_at	-0.525376243	0.694777894	yes	yes	yes	AI715156	Rn.147180	Transcribed locus
461	1372838_at	-0.525359056	0.694786171	yes	yes	no	AI227902	Rn.74447	Transcribed locus
462	1380397_at	-0.525107454	0.69490735	yes	yes	no	AI070744	Rn.43120	Transcribed locus
463	1394845_at	-0.524993813	0.69496209	yes	yes	yes	BF542618	Rn.37299	aquarius (predicted)
464	1397288_at	-0.524445565	0.695226238	yes	yes	no	BM390376	Rn.18174	Cleavage and polyadenylation specific factor 5
465	1373265_at	-0.524211453	0.695339064	yes	yes	no	BM383832	Rn.95210	Transcribed locus
466	1381561_at	-0.524201948	0.695343645	yes	yes	no	BI283817	Rn.11018	Calcium/calmodulin-dependent protein kinase I
467	1378547_at	-0.524107934	0.695388959	yes	yes	no	AI176027	Rn.149072	Transcribed locus
468	1382848_at	-0.524085541	0.695399753	yes	yes	no	BM383972	Rn.10470	Forkhead box A1
469	1380981_at	-0.524016754	0.69543291	yes	yes	yes	AW534519	Rn.162891	Stonin 2 (predicted)
470	1390985_at	-0.523966771	0.695457004	yes	yes	yes	AA956519	Rn.165041	Transcribed locus
471	1369768_at	-0.523417938	0.695721621	yes	yes	no	NM_133285	---	H1 histone family, member 4
472	1382148_at	-0.522781328	0.696028686	yes	yes	no	AA923980	Rn.24639	Transcribed locus
473	1378896_at	-0.522009783	0.696401018	yes	yes	no	BI277879	---	---
474	1394459_at	-0.521904991	0.696451604	yes	yes	no	AI715738	---	---
475	1392369_at	-0.521669154	0.696565462	yes	yes	no	BF388926	Rn.133954	Ischemia related factor NYW-1
476	1387052_at	-0.521439138	0.696676527	yes	yes	no	NM_031039	Rn.6318	glutamic pyruvic transaminase 1, soluble
477	1392581_at	-0.521186561	0.696798508	yes	yes	yes	BF420172	Rn.13744	neurocalcin delta
478	1373945_at	-0.520829502	0.696970983	yes	yes	no	AI012571	Rn.12319	similar to bruno-like 5, RNA binding protein (predicted)
479	1385467_at	-0.519783121	0.697476676	yes	yes	yes	BF388485	Rn.153008	Transcribed locus
480	1394756_at	-0.519771801	0.697482149	yes	yes	no	AA955494	Rn.28431	Similar to CG10084-PA
481	1391661_at	-0.518916231	0.697895904	yes	yes	no	AA945076	Rn.153497	Transcribed locus
482	1394808_at	-0.518875884	0.697915422	yes	yes	no	AW531925	Rn.98601	transmembrane 9 superfamily protein member 4
483	1380978_at	-0.518730999	0.697985514	yes	yes	yes	AI044494	Rn.147477	Transcribed locus
484	1382173_at	-0.518526671	0.698084377	yes	yes	yes	BF283569	---	---
485	1392249_at	-0.518215882	0.698234776	yes	yes	no	AI145746	Rn.1362	Similar to protein 4.1G (predicted)

486	1367926_at	-0.51757827	0.698543435	yes	yes	no	NM_031851	Rn.29754	prohibitin
487	1392792_at	-0.517536934	0.69856345	yes	yes	no	AI071152	Rn.40190	Transcribed locus
488	1397139_at	-0.517380644	0.698639131	yes	no	no	BF413644	Rn.22308	Protocadherin alpha 4
489	1377267_at	-0.517196717	0.698728205	yes	yes	no	BF402385	Rn.38053	melanoma antigen, family E, 1 (predicted)
490	1384193_at	-0.516955801	0.698844896	yes	no	no	AI235607	Rn.19609	Transcribed locus
491	1380340_at	-0.516703831	0.698966961	yes	yes	no	BF387865	Rn.63789	Transcribed locus
492	1385879_at	-0.515470389	0.699564803	yes	yes	no	AA893004	Rn.13465	Transcribed locus
493	1392846_at	-0.515373177	0.699611943	yes	yes	no	AA944574	Rn.38301	Zinc finger, MYND domain containing 11
494	1382388_at	-0.515143563	0.699723299	yes	yes	yes	AW533941	Rn.48200	Similar to hypothetical protein MGC27699 (predicted)
495	1383079_at	-0.514914816	0.699834254	yes	yes	no	AW916826	---	---
496	1389143_at	-0.514895855	0.699843451	yes	yes	yes	BF288139	Rn.165216	Transcribed locus
497	1379267_a_at	-0.513759482	0.700394917	yes	yes	yes	AA924312	Rn.8316	Transcribed locus
498	1397107_at	-0.513615604	0.700464769	yes	yes	no	BE114486	Rn.132347	Similar to D430018P08 protein (predicted)
499	1376554_at	-0.513039557	0.700744511	yes	yes	no	BE121079	Rn.79171	TatD DNase domain containing 1 (predicted)
500	1377618_at	-0.51260734	0.700954478	yes	yes	yes	AW534908	Rn.163076	Kruppel-like factor 7 (ubiquitous) (predicted)
501	1388639_at	-0.512214706	0.701145271	yes	yes	yes	BF284148	Rn.7641	Similar to Breast carcinoma amplified sequence 3 homolog (K20D4) (predicted)
502	1397937_at	-0.511673097	0.701408541	yes	no	no	BF409772	Rn.120717	Leucine rich repeat containing 35
503	1388152_at	-0.511672944	0.701408615	yes	yes	no	BG374290	Rn.10484	microtubule-associated protein 2
504	1391829_at	-0.511279626	0.701599864	yes	yes	no	AI105382	Rn.28335	Transcribed locus
505	1386733_at	-0.511065771	0.701703872	yes	yes	yes	BF544390	Rn.163266	Similar to hypothetical protein (predicted)
506	1382535_at	-0.511045583	0.701713692	yes	yes	yes	AI030942	Rn.164538	Transcribed locus
507	1378444_at	-0.510556812	0.701951466	yes	yes	yes	AI175473	Rn.28903	Transcribed locus
508	1390757_at	-0.510021807	0.702211823	yes	yes	no	BE116564	Rn.129782	similar to cell division cycle 2-like 1 (predicted)
509	1394716_at	-0.510003637	0.702220668	yes	yes	no	AI011137	Rn.102571	Lectin, mannose-binding 2-like (predicted)
510	1386097_at	-0.509571546	0.702431016	yes	yes	no	AW527230	Rn.94994	ankyrin repeat domain 12 (predicted)
511	1373510_at	-0.509165514	0.702628736	yes	yes	no	BF281373	Rn.31977	vesicle-associated membrane protein 1
512	1375320_at	-0.508600873	0.702903784	yes	yes	no	BI291436	Rn.18688	Similar to hypothetical protein DKFZp434H2010 (predicted)
513	1369539_at	-0.508232748	0.703083163	yes	yes	no	NM_031697	Rn.44390	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
514	1370122_at	-0.508155644	0.70312074	yes	yes	yes	NM_053459	---	similar to Ras-related protein Rab-27B
515	1378815_at	-0.508099777	0.703147968	yes	yes	no	BG372376	Rn.2813	similar to Gamma-tubulin complex component 4 (GCP-4) (predicted)
516	1383153_at	-0.507972639	0.703209937	yes	yes	no	AI555284	Rn.23647	Transcribed locus
517	1382820_at	-0.507876151	0.703256969	yes	yes	no	AI176342	Rn.165457	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
518	1377890_at	-0.507621739	0.703380996	yes	yes	no	AI411360	Rn.41920	Transcribed locus
519	1383871_at	-0.507195324	0.703588924	yes	no	no	BE120348	Rn.10121	Syntaxin binding protein 2
520	1378194_a_at	-0.50620613	0.70407151	yes	yes	yes	BG671338	Rn.40877	rap2 interacting protein x
521	1393938_at	-0.506029908	0.704157516	yes	yes	no	AI501880	Rn.167905	Transcribed locus
522	1395129_at	-0.505813355	0.70426322	yes	yes	no	BE107340	---	---
523	1382229_at	-0.505550248	0.70439167	yes	yes	no	AA998269	Rn.107975	Nexilin
524	1382859_at	-0.505089055	0.704616882	yes	no	no	AI043754	Rn.161790	similar to Rap1-interacting factor 1 (predicted)
525	1398406_at	-0.504903597	0.704707466	yes	yes	no	AI102382	Rn.127735	Transcribed locus
526	1375456_at	-0.504314705	0.704995178	yes	yes	no	AI007882	Rn.7522	Similar to Cgi67 serine protease precursor
527	1381153_at	-0.503939836	0.705178388	yes	yes	no	BF405492	Rn.41255	anaphase promoting complex subunit 4
528	1381146_at	-0.503614567	0.705337394	yes	yes	no	AW434387	Rn.148077	Transcribed locus
529	1391722_at	-0.503610641	0.705339314	yes	yes	yes	BI289088	Rn.161741	similar to heat shock transcription factor 2 binding protein (predicted)
530	1378732_at	-0.503056174	0.705610447	yes	no	no	BM387452	Rn.48835	Follistatin-like 3

531	1381091_at	-0.502939383	0.705667571	yes	yes	no	BE101556	Rn.170782	Transcribed locus
532	1396078_at	-0.502530597	0.705867549	yes	yes	no	BF389439	Rn.162726	similar to krev interaction trapped-1A
533	1396771_at	-0.502350824	0.705955512	yes	yes	no	BE107504	Rn.147314	Transcribed locus
534	1386252_at	-0.502290984	0.705984795	yes	yes	no	BE349825	Rn.54041	Transcribed locus
535	1386063_at	-0.502117994	0.706069452	yes	yes	no	BF559746	Rn.165284	Transcribed locus
536	1371714_at	-0.502092648	0.706081857	yes	yes	no	BG378760	Rn.2688	Serine/arginine-rich protein specific kinase 1
537	1381646_at	-0.501620612	0.706312918	yes	yes	no	BE101561	---	---
538	1391765_at	-0.501464811	0.706389199	yes	no	no	BM383632	Rn.137189	leucine rich repeat containing 48
539	1379225_at	-0.501411184	0.706415457	yes	yes	yes	AI071617	---	---
540	1387149_at	-0.501244863	0.706496901	yes	no	no	NM_030836	Rn.22516	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
541	1394732_at	-0.500725059	0.706751498	yes	yes	no	BF289237	Rn.72491	G1 to S phase transition 1
542	1397380_at	-0.500708424	0.706759647	yes	yes	no	BG376947	Rn.86175	PX domain containing serine/threonine kinase
543	1374957_at	-0.500679695	0.706773722	yes	yes	no	AI408197	Rn.160597	similar to ribosomal protein L27a (predicted)
544	1368218_at	-0.500101318	0.707057124	yes	no	no	U28830	Rn.7107	ralA binding protein 1
545	1383415_at	-0.499805692	0.707202024	yes	yes	no	AW531415	Rn.6866	Protein phosphatase 3, catalytic subunit, alpha isoform
546	1397698_at	-0.499604029	0.707300885	yes	yes	no	AW917627	Rn.171495	Transcribed locus
547	1393199_at	-0.499349066	0.707425895	yes	yes	no	AA955145	Rn.162314	similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted) /// similar to Jumonji/ARID domain-containing protein 1C (SmcX protein) (predicted)
548	1373084_at	-0.499251534	0.707473721	yes	yes	no	BI300912	Rn.17925	WD repeat domain 20
549	1373019_at	-0.498735065	0.707727035	yes	yes	no	AI172468	Rn.22316	Transcribed locus
550	1388843_at	-0.498585402	0.707800457	yes	yes	no	BI296771	Rn.60026	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19
551	1392421_at	-0.498480361	0.707851993	yes	yes	no	AW526570	Rn.139712	bromodomain adjacent to zinc finger domain, 2B (predicted)
552	1388073_a_at	-0.498429846	0.707876778	yes	no	no	AF000901	Rn.11099	nucleoporin like 1
553	1384293_at	-0.498323681	0.707928871	yes	yes	no	BE100543	Rn.24948	nuclear receptor co-repressor 1
554	1381893_at	-0.498224576	0.707977504	yes	yes	yes	BF396091	Rn.163434	similar to OTTHUMP00000040350 (predicted)
555	1394729_at	-0.498171924	0.708003342	yes	yes	no	AI714037	Rn.27409	Protein kinase, lysine deficient 1
556	1385166_at	-0.498053876	0.708061277	yes	yes	no	BF398185	Rn.48646	RGD1560390 (predicted)
557	1394624_at	-0.497598836	0.708284641	yes	yes	no	AW528017	Rn.106726	Megakaryoblastic leukemia (translocation) 1 (predicted)
558	1392932_at	-0.497548602	0.708309304	yes	yes	no	BI279191	Rn.170497	leukocyte receptor cluster (LRC) member 8
559	1386987_at	-0.497228767	0.708466348	yes	yes	no	NM_017020	Rn.1716	interleukin 6 receptor, alpha
560	1382872_at	-0.497096128	0.708531487	yes	yes	no	AA851616	Rn.65153	Similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - mouse (predicted)
561	1395057_at	-0.497063921	0.708547304	yes	yes	yes	BM389984	Rn.177844	Transcribed locus
562	1383517_at	-0.496790995	0.708681358	yes	yes	yes	AA998001	---	---
563	1381564_at	-0.496494096	0.708827216	yes	yes	yes	AI763657	Rn.44333	FKBP-associated protein
564	1367813_at	-0.4961011	0.70902033	yes	yes	no	NM_130403	Rn.73852	protein phosphatase 1, regulatory (inhibitor) subunit 14A
565	1368798_at	-0.495842415	0.709147473	yes	yes	yes	NM_023094	---	similar to N-acetylgalactosaminyltransferase A blood group-like enzyme (predicted)
566	1370266_at	-0.495133637	0.709495954	yes	yes	no	BE115857	---	---
567	1390557_at	-0.495116181	0.709504539	yes	yes	no	BF394809	Rn.21437	Transcribed locus
568	1390464_at	-0.495112665	0.709506268	yes	yes	no	BI291381	Rn.41044	FERM domain containing 4B
569	1382442_at	-0.495001343	0.709561017	yes	yes	yes	BF288000	Rn.48945	Similar to NF-kappa-B-repressing factor (Transcription factor NRF) (predicted)
570	1385585_at	-0.494161497	0.7099742	yes	yes	no	AI111674	Rn.21134	Transcribed locus
571	1372695_at	-0.494111947	0.709998584	yes	yes	yes	AI172165	Rn.18757	Fibronectin type III domain containing 5
572	1385814_at	-0.493393535	0.710352227	yes	yes	no	H32486	Rn.72680	mitogen activated protein kinase kinase kinase 3 (predicted)

573	1384255_at	-0.493328252	0.710384372	yes	yes	yes	AA956372	Rn.24090	N-ethylmaleimide-sensitive factor attachment protein, gamma
574	1385116_at	-0.49329076	0.710402833	yes	yes	yes	BF386807	---	---
575	1375484_at	-0.492594115	0.710745953	yes	yes	no	BG376458	Rn.166595	Transcribed locus
576	1386466_at	-0.492505193	0.710789762	yes	yes	no	H33093	Rn.135353	Transcribed locus
577	1397377_at	-0.492503419	0.710790636	yes	yes	no	AA955664	Rn.165274	Transcribed locus
578	1392526_at	-0.492422241	0.710830632	yes	yes	no	AA901274	Rn.96146	RGD1560866 (predicted)
579	1391230_at	-0.491965369	0.711055773	yes	yes	no	BF394904	Rn.11286	Sortilin 1
580	1380280_at	-0.491929059	0.71107367	yes	no	no	BE118420	Rn.24300	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
581	1397197_at	-0.49185821	0.71110859	yes	yes	no	BE120228	Rn.3775	Serine incorporator 3
582	1392311_at	-0.491669669	0.711201529	yes	yes	no	BF389762	Rn.22747	Similar to erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) isoform 1 (predicted)
583	1388157_at	-0.491220744	0.711422869	yes	yes	yes	BE111706	Rn.9560	myristoylated alanine rich protein kinase C substrate
584	1391413_at	-0.490745447	0.711657286	yes	yes	no	BM387140	Rn.22996	5'-nucleotidase, cytosolic II (predicted)
585	1395758_at	-0.490670218	0.711694396	yes	yes	no	AI548569	---	---
586	1396893_at	-0.490551908	0.711752762	yes	yes	no	AI576209	Rn.11283	Neural cell adhesion molecule 1
587	1393265_at	-0.490510969	0.71177296	yes	yes	no	BF546659	Rn.15186	Transcribed locus
588	1392162_at	-0.490415074	0.711820273	yes	yes	no	BF391447	---	---
589	1385667_x_at	-0.490262926	0.711895346	yes	no	no	AI029796	Rn.6374	CDNA clone IMAGE:7379585
590	1378431_at	-0.489995551	0.712027293	yes	yes	no	BE095772	Rn.138055	serine/arginine-rich protein specific kinase 2 (predicted)
591	1393135_at	-0.489985121	0.712032441	yes	yes	no	BM390238	Rn.7027	Transcribed locus
592	1393833_at	-0.489879481	0.712084581	yes	yes	yes	AI578461	Rn.135058	angel homolog 1 (Drosophila) (predicted)
593	1392389_at	-0.489720218	0.712163194	yes	yes	no	BF389942	Rn.105677	Similar to hypothetical protein FLJ34389 (predicted)
594	1390898_at	-0.489595042	0.712224988	yes	yes	no	BE111116	Rn.194997	Transcribed locus
595	1376441_at	-0.489476232	0.712283644	yes	yes	no	AI102249	Rn.8899	similar to chromosome 14 open reading frame 135 (predicted)
596	1395869_at	-0.488539601	0.712746226	yes	yes	no	BI296231	---	---
597	1384274_at	-0.48815395	0.712936777	yes	yes	yes	BG377595	Rn.20197	CDNA clone IMAGE:7300876
598	1397290_at	-0.488029057	0.712998498	yes	yes	no	AI408310	Rn.168130	Transcribed locus
599	1378121_at	-0.487925898	0.713049483	yes	yes	no	AI600165	---	---
600	1386120_at	-0.487883371	0.713070502	yes	yes	no	BF393607	Rn.118853	RGD1561595 (predicted)
601	1397283_at	-0.487680992	0.713170537	yes	yes	yes	AI176618	Rn.167263	Transcribed locus, weakly similar to XP_906839.1 PREDICTED: hypothetical protein [Mus musculus]
602	1372560_at	-0.487463099	0.713278257	yes	yes	no	AW522495	Rn.27177	Transcribed locus
603	1391126_at	-0.487461675	0.713278961	yes	yes	yes	BG379351	Rn.86466	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)
604	1384469_at	-0.486746669	0.713632553	yes	yes	no	AI502224	Rn.35782	ATP-binding cassette, sub-family A (ABC1), member 5
605	1381210_at	-0.48651457	0.71374737	yes	yes	no	AI639521	Rn.43708	Transcribed locus
606	1394674_at	-0.486118	0.713943593	yes	yes	yes	BG372056	Rn.25065	Synaptotagmin binding, cytoplasmic RNA interacting protein
607	1379494_at	-0.486018088	0.713993038	yes	yes	yes	AI012029	Rn.17793	Transcribed locus
608	1376568_at	-0.485907158	0.714047939	yes	yes	no	AI144997	Rn.166857	Transcribed locus
609	1379575_at	-0.485533562	0.714232871	yes	yes	no	BF412271	Rn.10277	Arginine-glutamic acid dipeptide (RE) repeats
610	1392774_at	-0.485489362	0.714254754	yes	yes	no	BF284310	Rn.148299	Transcribed locus
611	1392325_at	-0.485384668	0.714306588	yes	no	no	BF398187	Rn.161884	BTB (POZ) domain containing 4 (predicted)
612	1377389_at	-0.485324495	0.714336381	yes	yes	no	AI145613	Rn.166888	Transcribed locus
613	1382515_at	-0.485303632	0.714346712	yes	yes	no	AI059408	---	---
614	1392676_at	-0.485283709	0.714356576	yes	yes	no	AI548984	Rn.43493	myocardial ischemic preconditioning upregulated 1
615	1393829_at	-0.485129625	0.714432876	yes	yes	yes	AI639475	Rn.68658	FGFR1 oncogene partner 2
616	1375813_at	-0.484279285	0.714854094	yes	yes	no	BE102687	Rn.107308	A kinase (PRKA) anchor protein 8-like

617	1369412_a_at	-0.484014949	0.714985085	yes	yes	yes	NM_017299	Rn.9042	solute carrier family 19, member 1
618	1397780_at	-0.483944475	0.715020012	yes	yes	yes	BE096283	Rn.116762	similar to OTTHUMP00000040479 (predicted)
619	1390400_a_at	-0.483890323	0.715046851	yes	yes	no	BM390922	Rn.227	Transcribed locus
620	1372194_at	-0.48363816	0.715171842	yes	yes	yes	AI172035	Rn.22334	A kinase (PRKA) anchor protein 10 (predicted)
621	1393690_at	-0.483235992	0.715371232	yes	yes	yes	AA818627	Rn.16736	insulin induced gene 2
622	1376341_at	-0.48319011	0.715393983	yes	yes	no	BM388895	Rn.28603	Transcribed locus
623	1378835_at	-0.482771202	0.715601739	yes	yes	no	AI145398	Rn.160623	Rap guanine nucleotide exchange factor (GEF) 6 (predicted)
624	1392661_at	-0.482660778	0.715656513	yes	yes	no	AI228227	Rn.3830	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
625	1384151_at	-0.482410364	0.715780743	yes	yes	yes	AI578392	---	---
626	1392219_at	-0.482186426	0.715891856	yes	yes	no	AI145523	Rn.10485	Nuclear receptor subfamily 2, group C, member 2
627	1372989_at	-0.48167433	0.716146013	yes	yes	no	BI296586	Rn.18327	similar to zinc finger, DHHC domain containing 14
628	1379271_at	-0.481165399	0.716398688	yes	yes	no	AA925076	Rn.47568	similar to Suppressor of cytokine signaling 5 (predicted)
629	1371781_at	-0.480922107	0.71651951	yes	yes	no	BI285863	Rn.10247	signal transducer and activator of transcription 3
630	1376540_at	-0.479995519	0.716979851	yes	no	no	BE105373	Rn.163053	Similar to suppressor of Ty 3 homolog
631	1390629_at	-0.47996267	0.716996176	yes	no	no	BF400629	Rn.7758	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1` (predicted)
632	1392483_at	-0.479667635	0.717142819	yes	yes	no	AA892677	Rn.154718	Choline phosphotransferase 1
633	1390432_at	-0.47918456	0.717382989	yes	yes	no	AA997338	---	---
634	1383106_at	-0.479009574	0.717470006	yes	yes	no	BI295890	Rn.2970	cullin 2 (predicted)
635	1372754_at	-0.478902876	0.71752307	yes	yes	yes	BG666424	---	---
636	1391221_at	-0.478463725	0.717741515	yes	yes	yes	BE100776	---	---
637	1377746_at	-0.478270042	0.717837879	yes	yes	no	AI010418	---	RNA-binding protein 12
638	1383661_at	-0.478213135	0.717866194	yes	yes	no	AA926037	Rn.15645	Transcribed locus
639	1372756_at	-0.4780513	0.717946726	yes	yes	no	BG378166	Rn.18710	Transcribed locus
640	1373571_at	-0.477931578	0.718006307	yes	yes	yes	AI170276	Rn.11652	reticulon 3
641	1376386_at	-0.477866541	0.718038676	yes	yes	no	BF393799	Rn.62758	Transcribed locus
642	1382411_at	-0.477420558	0.718260679	yes	yes	no	BF288710	Rn.11713	Transcribed locus
643	1385728_at	-0.477144175	0.718398292	yes	no	no	BE108006	Rn.1477	AE binding protein 2 (predicted)
644	1378686_at	-0.477128027	0.718406333	yes	yes	yes	BF405626	Rn.27409	Protein kinase, lysine deficient 1
645	1395385_at	-0.47707885	0.718430821	yes	yes	no	BF548145	Rn.86984	GTPase activating RANGAP domain-like 1
646	1385096_at	-0.477071694	0.718434385	yes	no	no	BG380261	Rn.151464	Transcribed locus
647	1399109_at	-0.477015451	0.718462394	yes	yes	no	BI281673	Rn.101809	Transcribed locus
648	1392529_at	-0.476728045	0.718605536	yes	yes	yes	BI294478	Rn.146922	Transcribed locus
649	1391320_at	-0.476504766	0.71871676	yes	no	no	BF393578	Rn.37915	Hspb associated protein 1
650	1380900_at	-0.476472065	0.718733051	yes	no	no	BE120504	Rn.160168	Similar to KIAA1731 protein (predicted)
651	1391205_at	-0.476293397	0.718822067	yes	yes	no	AA818139	---	---
652	1393649_at	-0.476146496	0.718895264	yes	yes	no	BE108758	---	---
653	1385522_at	-0.476014786	0.718960898	yes	no	no	AI059490	Rn.92486	origin recognition complex, subunit 1-like (S.cereviaiae)
654	1396483_at	-0.475951573	0.718992401	yes	no	no	AW434740	Rn.161176	Transcribed locus
655	1385322_at	-0.475938745	0.718998793	yes	no	no	AI602154	Rn.156163	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]
656	1393584_at	-0.475417498	0.719258615	yes	no	no	AI045201	---	---
657	1392914_at	-0.475268875	0.719332716	yes	yes	yes	BI275467	---	---
658	1394776_at	-0.474654501	0.71963911	yes	no	no	AA899386	Rn.32385	Transcribed locus
659	1380551_at	-0.474566066	0.719683224	yes	yes	yes	AW254395	Rn.30028	Growth factor receptor bound protein 14
660	1376947_at	-0.474412979	0.719759595	yes	no	no	AI178158	Rn.95305	retinoblastoma binding protein 6
661	1396663_at	-0.474102246	0.719914636	yes	yes	yes	BI300284	Rn.107745	Component of oligomeric golgi complex 4 (predicted)

662	1393766_at	-0.473958033	0.719986603	yes	no	no	AI112375	---	---
663	1385627_at	-0.473948582	0.71999132	yes	yes	yes	BF407019	Rn.68084	B-cell leukemia/lymphoma 3 (predicted)
664	1395586_at	-0.47373807	0.720096385	yes	no	no	BF545930	Rn.163742	Transcribed locus
665	1395387_at	-0.473358148	0.720286042	yes	yes	yes	BI293317	Rn.47911	carnitine deficiency-associated gene expressed in ventricle 1
666	1393662_at	-0.47313394	0.720397989	yes	no	no	BF396974	---	---
667	1368778_at	-0.473104702	0.720412589	yes	yes	yes	NM_017206	Rn.9968	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
668	1395337_at	-0.473089665	0.720420098	yes	no	no	AW141192	Rn.101871	tight junction protein 1 (predicted)
669	1392267_at	-0.473047791	0.720441009	yes	no	no	BE102449	Rn.161825	similar to RIKEN cDNA B930096L08 (predicted)
670	1377556_at	-0.473023212	0.720453283	yes	no	no	AW535380	Rn.150634	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
671	1387495_at	-0.472609039	0.720660142	yes	no	no	NM_019141	Rn.162515	transducin-like enhancer of split 4, E(spl) homolog (Drosophila)
672	1384815_at	-0.472576096	0.720676598	yes	no	no	AI145507	Rn.6866	Protein phosphatase 3, catalytic subunit, alpha isoform
673	1376536_at	-0.472239022	0.720844998	yes	no	no	AW533496	Rn.47938	Transcribed locus
674	1375497_at	-0.471280853	0.721323908	yes	no	no	BE107853	Rn.171090	Transcribed locus
675	1385606_at	-0.470928027	0.721500337	yes	no	no	BF559626	Rn.17102	brain protein 16
676	1393700_at	-0.470862273	0.721533221	yes	no	no	AA875420	Rn.3424	Transcribed locus
677	1393279_at	-0.470771839	0.721578452	yes	no	no	AI070869	---	---
678	1396368_at	-0.470495182	0.721716837	yes	no	no	BF409869	Rn.61512	Transcribed locus
679	1368732_at	-0.470331438	0.721798756	yes	no	no	NM_032056	Rn.10372	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
680	1380091_at	-0.470317756	0.721805602	yes	no	no	BF287655	Rn.30231	Testis-specific gene including a ubiquitin-likely domain
681	1396965_at	-0.469852607	0.722038361	yes	no	no	BF406350	Rn.116108	Forkhead box O1A
682	1377216_at	-0.469635655	0.722146949	yes	yes	yes	BI295997	Rn.33757	Transcribed locus
683	1394727_at	-0.469614203	0.722157687	yes	no	no	AI407942	Rn.107176	Similar to ARG99 homolog (predicted)
684	1394939_at	-0.468848417	0.722541112	yes	no	no	BE116933	Rn.117902	protein phosphatase 1K (PP2C domain containing) (predicted)
685	1378518_at	-0.468552871	0.722689144	yes	no	no	BF394458	---	---
686	1394596_at	-0.467397892	0.72326794	yes	no	no	AW531463	Rn.160679	Transcribed locus
687	1367612_at	-0.467084365	0.723425137	yes	no	no	NM_134349	Rn.2580	microsomal glutathione S-transferase 1
688	1381798_at	-0.467010607	0.723462124	yes	no	no	BE114958	Rn.98417	LIM domain only protein 7
689	1373679_at	-0.466929204	0.723502946	yes	no	no	AA946467	Rn.35869	Transcribed locus
690	1377519_a_at	-0.466806565	0.723564451	yes	yes	yes	AI059932	Rn.37595	similar to SET binding factor 2 (predicted)
691	1387335_s_at	-0.465959874	0.723989222	yes	no	no	NM_023094	Rn.54025	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase) /// similar to N-acetylgalactosaminyltransferase A blood group-like enzyme (predicted)
692	1395837_at	-0.465379226	0.724280668	yes	no	no	BE119517	Rn.144260	General transcription factor II H, polypeptide 2 (predicted)
693	1384950_at	-0.465288418	0.724326258	yes	no	no	AI060149	Rn.21189	phosphatidylinositol 4-kinase type 2 beta
694	1391212_at	-0.464957929	0.724492204	yes	no	no	BF418812	Rn.41329	transcription elongation factor A (SII)-like 1
695	1381632_at	-0.46492547	0.724508505	yes	no	no	BF389481	---	---
696	1380311_at	-0.464723956	0.72460971	yes	no	no	AI535528	Rn.162937	Protein phosphatase 1, regulatory (inhibitor) subunit 12A
697	1380082_at	-0.464714666	0.724614376	yes	yes	yes	AA943616	Rn.7608	Transcribed locus
698	1376720_at	-0.464710122	0.724616658	yes	yes	yes	BG376414	Rn.3735	aarF domain containing kinase 2 (predicted)
699	1390534_at	-0.464660867	0.724641398	yes	no	no	BG374727	Rn.127947	SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (predicted)
700	1380099_at	-0.464389001	0.724777964	yes	yes	yes	BM391357	Rn.146732	Transcribed locus
701	1395371_at	-0.46423275	0.724856466	yes	yes	yes	AA957790	Rn.98280	similar to FLJ00052 protein (predicted)
702	1381125_at	-0.463934107	0.725006529	yes	no	no	AI229420	Rn.6087	Tetraspanin 8
703	1372536_at	-0.463579831	0.725184588	yes	no	no	AI105042	Rn.160865	chaperone, ABC1 activity of bc1 complex like (S. pombe)
704	1382789_at	-0.463405041	0.725272453	yes	no	no	BM389812	Rn.64949	Transcribed locus

705	1390053_at	-0.463359346	0.725295425	yes	yes	yes	BE099903	---	---
706	1392806_at	-0.463299385	0.72532557	yes	no	no	AI234807	Rn.163332	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)
707	1398415_at	-0.463152348	0.725399498	yes	no	no	BG380708	Rn.22144	Transcribed locus
708	1396863_at	-0.463119343	0.725416093	yes	no	no	AW535061	Rn.48417	SplA/ryanodine receptor domain and SOCS box containing 4 (predicted)
709	1379694_at	-0.462994208	0.725479016	yes	no	no	AI171596	Rn.23462	Enhancer of polycomb homolog 2 (Drosophila) (predicted)
710	1391422_at	-0.462961483	0.725495473	yes	no	no	BE100486	Rn.129050	DnaJ (Hsp40) homolog, subfamily B, member 6
711	1384243_at	-0.462632687	0.725660835	yes	yes	yes	AI111413	Rn.11581	Transcribed locus
712	1390654_at	-0.46247236	0.725741483	yes	yes	yes	AA874809	Rn.147940	Transcribed locus
713	1392368_at	-0.462199502	0.725878755	yes	no	no	BE117273	---	---
714	1396686_at	-0.462170852	0.725893171	yes	no	no	BF401617	Rn.103179	Myosin light chain, regulatory B
715	1394612_at	-0.46169588	0.726132192	yes	no	no	AW535206	Rn.19779	A disintegrin and metalloprotease domain 4
716	1375180_at	-0.461226608	0.726368423	yes	no	no	BF419280	Rn.1215	MARVEL (membrane-associating) domain containing 1
717	1380087_at	-0.460923714	0.72652094	yes	no	no	BE119409	Rn.20766	Ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)
718	1391899_at	-0.46073475	0.726616106	yes	yes	yes	BI303858	Rn.165121	Transcribed locus
719	1396255_at	-0.46053341	0.726717519	yes	yes	yes	BF420465	Rn.162692	kinesin family member 16B (predicted)
720	1382618_at	-0.460091222	0.726940292	yes	yes	yes	AI103100	Rn.23855	erythrocyte protein band 4.2 (predicted)
721	1396363_at	-0.45991427	0.72702946	yes	no	no	BF399356	Rn.160241	Transcribed locus
722	1397749_at	-0.459682222	0.727146407	yes	no	no	AI715712	Rn.46695	Neurofibromatosis 2
723	1390837_at	-0.459191781	0.727393641	yes	no	no	AI717114	Rn.168330	Transcribed locus
724	1369212_s_at	-0.459129013	0.727425289	yes	no	no	NM_021681	Rn.20361	erythrocyte protein band 4.1-like 1
725	1373952_at	-0.458771511	0.727605568	yes	yes	yes	AI409841	Rn.51208	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
726	1397743_at	-0.458656019	0.727663818	yes	no	no	BF410216	Rn.50770	Transcribed locus
727	1378515_at	-0.458466156	0.727759587	yes	no	no	BE116005	Rn.102356	Progesterone receptor membrane component 1
728	1377314_at	-0.457929904	0.728030146	yes	no	no	BE104391	Rn.161844	glutamine fructose-6-phosphate transaminase 1
729	1382286_at	-0.457612135	0.72819052	yes	no	no	AA965275	Rn.162672	Solute carrier family 12, member 6
730	1392730_at	-0.457083116	0.728457588	yes	no	no	AI144948	Rn.39034	Protein phosphatase 1, catalytic subunit, beta isoform
731	1378448_at	-0.45688584	0.728557205	yes	yes	yes	BI295914	Rn.29469	integrin beta 1 binding protein 1 (predicted)
732	1385043_at	-0.456777248	0.728612046	yes	yes	yes	AA924649	Rn.32617	Transcribed locus
733	1380777_at	-0.456177331	0.728915088	yes	no	no	BF399517	Rn.21970	TSC22 domain family 3
734	1377402_at	-0.455642026	0.729185599	yes	no	no	BI296989	Rn.20472	cyclin-dependent kinase (CDC2-like) 10
735	1387804_at	-0.455558781	0.729227675	yes	no	no	NM_080903	Rn.40636	tripartite motif protein 63
736	1392650_at	-0.455399733	0.729308072	yes	no	no	AI059349	---	---
737	1389368_at	-0.455386818	0.729314601	yes	no	no	AW253242	Rn.137681	Cnksr family member 3
738	1370463_x_at	-0.454677168	0.729673433	yes	yes	yes	U50449	---	RT1 class I, CE16
739	1376403_at	-0.454668034	0.729678053	yes	no	no	BE109059	---	---
740	1392120_at	-0.454235128	0.729897038	yes	no	no	AW526194	Rn.160913	Threonine synthase-like 1
741	1393762_at	-0.45417634	0.729926781	yes	no	no	AA901054	Rn.4126	p300/CBP-associated factor
742	1379873_at	-0.454098618	0.729966105	yes	no	no	BI276971	Rn.154013	Transcribed locus
743	1393039_a_at	-0.453735343	0.730149936	yes	no	no	AI547691	---	---
744	1396736_at	-0.453677749	0.730179085	yes	no	no	BF409344	Rn.153716	Transcribed locus
745	1391127_at	-0.453428802	0.730305094	yes	no	no	BF400818	Rn.60067	Cell division cycle 42 homolog (S. cerevisiae)
746	1369526_at	-0.453408956	0.73031514	yes	no	no	NM_013084	Rn.44423	acyl-Coenzyme A dehydrogenase, short/branched chain
747	1384692_at	-0.453377638	0.730330994	yes	yes	yes	AI172110	---	---
748	1393160_at	-0.45313702	0.730452811	yes	no	no	AA955879	Rn.95167	Transcribed locus, weakly similar to NP_035665.2 T-box 3 protein isoform 1 [Mus musculus]
749	1380997_at	-0.452881215	0.73058234	yes	no	no	BE103561	Rn.50277	Transcribed locus
750	1385493_at	-0.452878573	0.730583678	yes	no	no	AI639237	Rn.35526	THO complex 2 (predicted)

751	1374131_at	-0.452665204	0.730691736	yes	no	no	AI411971	Rn.34184	Transcribed locus
752	1398072_at	-0.452421421	0.730815217	yes	no	no	BF409833	Rn.195066	Transcribed locus
753	1373236_at	-0.451436383	0.731314371	yes	no	no	AI411422	Rn.16459	phosphopantothenoylcysteine decarboxylase (predicted)
754	1382587_at	-0.451220906	0.731423606	yes	no	no	AA901257	Rn.40571	Similar to RIKEN cDNA 1110001A07 gene
755	1385505_at	-0.450965217	0.731553248	yes	yes	yes	AI072068	Rn.166280	Transcribed locus
756	1385967_at	-0.450895601	0.731588549	yes	no	no	BF389767	Rn.44253	Forkhead box K2 (predicted)
757	1392768_at	-0.450782154	0.73164608	yes	no	no	AA900944	Rn.7111	Transcribed locus
758	1396872_at	-0.450773752	0.731650341	yes	no	no	AI555260	Rn.95239	Membrane associated guanylate kinase 1 b NT-short isoform
759	1390403_at	-0.450598337	0.731739307	yes	no	no	BE108405	Rn.23416	similar to CG8312-PA
760	1384314_at	-0.450533738	0.731772072	yes	no	no	BM383771	Rn.160632	mitochondrial translational initiation factor 2
761	1373336_at	-0.450416536	0.731831523	yes	no	no	AI411074	Rn.47330	Transcribed locus
762	1382655_at	-0.450073997	0.732005302	yes	no	no	AA964534	Rn.165290	Transcribed locus
763	1381098_at	-0.449978464	0.732053776	yes	no	no	BM384427	Rn.162860	similar to LOC398632 protein
764	1382428_at	-0.449777074	0.732155972	yes	no	no	AA925658	Rn.22314	taspase, threonine aspartase 1 (predicted)
765	1395340_at	-0.44959534	0.732248207	yes	no	no	AW918899	---	---
766	1397410_at	-0.448878919	0.732611921	yes	no	no	BI301687	Rn.46119	Similar to RIKEN cDNA 4631427C17 (predicted)
767	1376782_at	-0.448759383	0.732672624	yes	no	no	AW915083	Rn.147123	Transcribed locus
768	1376942_at	-0.44872919	0.732687958	yes	yes	yes	BF394140	Rn.65998	Tubulin, gamma complex associated protein 5 (predicted)
769	1381223_at	-0.448375467	0.732867622	yes	no	no	BG372869	Rn.73434	similar to Annexin A9 (Annexin 31) (Annexin XXXI) (predicted)
770	1397348_at	-0.448277729	0.732917273	yes	no	no	BE118444	Rn.171588	Transcribed locus
771	1388212_a_at	-0.447879194	0.733119765	yes	no	no	AJ243974	---	RT1 class Ib, locus S3
772	1389703_at	-0.447878535	0.7331201	yes	yes	yes	BI295225	Rn.24218	Zinc finger, ZZ-type with EF hand domain 1 (predicted)
773	1398187_at	-0.447720393	0.733200465	yes	no	no	BM391924	Rn.157556	Transcribed locus
774	1382989_at	-0.447297151	0.733415596	yes	yes	yes	BE116242	---	---
775	1387956_s_at	-0.44682456	0.733655884	yes	no	no	AF253064	Rn.81197	chemokine-like factor
776	1377825_at	-0.446450358	0.733846202	yes	no	no	AI411841	Rn.121336	Transcribed locus
777	1391699_at	-0.44635103	0.733896728	yes	yes	yes	AI556892	Rn.28212	polymerase (RNA) II (DNA directed) polypeptide F
778	1383311_at	-0.445808433	0.734172798	yes	no	no	AI716026	Rn.103871	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)
779	1397417_at	-0.445173215	0.734496125	yes	no	no	BG671626	Rn.76252	Transcribed locus
780	1374623_at	-0.445100487	0.734533153	yes	yes	yes	BF399447	Rn.15802	Transcribed locus
781	1388520_at	-0.444981297	0.73459384	yes	no	no	BI278854	Rn.164474	Transcribed locus
782	1392184_at	-0.44481931	0.734676325	yes	yes	yes	BI298049	Rn.75916	Similar to ALS2CR12 gene product
783	1375872_at	-0.444697025	0.7347386	yes	yes	yes	AI144944	Rn.100220	Fukuyama type congenital muscular dystrophy homolog (human) (predicted)
784	1395725_at	-0.444622334	0.73477664	yes	no	no	BF557088	Rn.162857	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)
785	1382451_at	-0.44452434	0.734826551	yes	no	no	BM385477	Rn.106778	heme binding protein 2 (predicted)
786	1383194_a_at	-0.444432956	0.734873098	yes	no	no	AI030349	Rn.6374	CDNA clone IMAGE:7379585
787	1394709_at	-0.444268259	0.734956995	yes	yes	yes	AI406967	Rn.11257	Early B-cell factor 1
788	1396326_at	-0.444231412	0.734975767	yes	no	no	BM390873	Rn.177896	Transcribed locus
789	1392360_at	-0.444059616	0.735063293	yes	no	no	BE119503	Rn.58939	Similar to homolog of Human holocarboxylase synthetase gene HLCS (predicted)
790	1396301_x_at	-0.444026098	0.735080371	yes	no	no	BI277442	---	---
791	1383826_at	-0.443405137	0.73539683	yes	yes	yes	AA924620	Rn.8397	Rab40b, member RAS oncogene family (predicted)
792	1377580_at	-0.443068765	0.735568312	yes	yes	yes	AA964744	Rn.44698	similar to mKIAA0738 protein (predicted)
793	1381837_at	-0.442721361	0.73574546	yes	no	no	AI502137	Rn.35623	Transcribed locus
794	1373569_at	-0.442640177	0.735786863	yes	yes	yes	AI013005	Rn.165774	Transcribed locus

795	1397745_at	-0.442544052	0.735835889	yes	yes	yes	BF414336	Rn.28794	Mindbomb homolog 1 (Drosophila) (predicted)
796	1395548_at	-0.442085052	0.736070036	yes	no	no	BG666506	Rn.171407	Transcribed locus
797	1393640_at	-0.442067609	0.736078935	yes	no	no	BF542956	Rn.40663	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
798	1376875_at	-0.441817245	0.736206685	yes	no	no	AI454691	---	---
799	1374918_at	-0.44133244	0.736454123	yes	yes	yes	BM392219	Rn.126386	Transcribed locus
800	1395021_at	-0.441240853	0.736500876	yes	no	no	AW533225	Rn.106278	Similar to myosin XVIIIa
801	1368641_at	-0.441180026	0.736531929	yes	yes	yes	NM_053402	Rn.34782	wingless-related MMTV integration site 4
802	1368346_at	-0.441124888	0.736560079	yes	yes	yes	NM_133553	Rn.24575	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4
803	1386154_at	-0.441119094	0.736563037	yes	no	no	AI639161	Rn.43059	similar to KIAA1411 protein (predicted)
804	1390981_at	-0.440781707	0.73673531	yes	no	no	AI028965	Rn.165836	Transcribed locus, moderately similar to XP_423294.1 PREDICTED: similar to dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 50k chain - chicken [Gallus gallus]
805	1388608_x_at	-0.440305806	0.736978376	yes	no	no	AI577319	Rn.107334	hemoglobin alpha, adult chain 1
806	1396227_at	-0.440274304	0.736994468	yes	yes	yes	BG374845	Rn.105234	mitochondrial ribosome recycling factor
807	1396485_at	-0.440174177	0.737045619	yes	yes	yes	AI705403	Rn.2717	BTB (POZ) domain containing 10
808	1395776_at	-0.440109201	0.737078815	yes	no	no	BF396580	Rn.20898	Rho GTPase activating protein 5
809	1397302_at	-0.439285115	0.737499965	yes	yes	yes	BF543495	Rn.38301	zinc finger, MYND domain containing 11
810	1395604_at	-0.439254269	0.737515733	yes	no	no	BF555073	Rn.154328	Transcribed locus
811	1391702_at	-0.439143859	0.737572177	yes	no	no	BM389392	Rn.66269	Transcribed locus
812	1391820_at	-0.438964809	0.737663722	yes	yes	yes	BE103427	Rn.167923	Transcribed locus, weakly similar to XP_418072.1 PREDICTED: similar to KIAA1636 protein [Gallus gallus]
813	1391251_at	-0.438862052	0.737716264	yes	no	no	BI290666	Rn.20351	Transcribed locus
814	1374454_at	-0.438770521	0.73776307	yes	no	no	BM388557	Rn.96446	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (predicted)
815	1382812_at	-0.438647312	0.737826079	yes	yes	yes	BE096595	Rn.160626	similar to Protein Njmu-R1 (predicted)
816	1373534_at	-0.438564366	0.737868501	yes	no	no	BE107209	Rn.8700	similar to SR rich protein
817	1382029_at	-0.438554391	0.737873603	yes	no	no	BE104800	Rn.19152	similar to CDNA sequence BC017647 (predicted)
818	1367545_at	-0.438406767	0.737949109	yes	no	no	AI710043	Rn.14944	Transcribed locus
819	1395060_at	-0.438402397	0.737951344	yes	yes	yes	AI764218	Rn.47124	Inner membrane protein, mitochondrial
820	1378255_at	-0.438338076	0.737984246	yes	yes	yes	BE111416	Rn.146857	Transcribed locus
821	1396559_at	-0.438282734	0.738012556	yes	no	no	BF396566	---	---
822	1377855_at	-0.43811082	0.738100504	yes	no	no	BE111774	Rn.45405	similar to RIKEN cDNA 4921537D05
823	1391134_at	-0.437865065	0.738226246	yes	no	no	BF404933	Rn.59630	transmembrane and coiled-coil domains 3 (predicted)
824	1379896_at	-0.437860341	0.738228663	yes	no	no	BM390256	Rn.154550	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (predicted)
825	1386102_at	-0.437811558	0.738253626	yes	no	no	AA851046	---	---
826	1382066_at	-0.437340879	0.73849452	yes	yes	yes	AI549105	Rn.33733	similar to mKIAA1002 protein
827	1391228_at	-0.437222726	0.738555003	yes	no	no	BE106353	Rn.14627	testis specific gene A2
828	1378143_at	-0.437128421	0.738603283	yes	no	no	AI170625	Rn.51153	phosducin-like
829	1381106_at	-0.437047239	0.738644846	yes	no	no	BE108055	Rn.24616	Dehydrodolichyl diphosphate synthase
830	1378602_at	-0.437044257	0.738646372	yes	no	no	BE098753	Rn.147328	Transcribed locus
831	1383467_at	-0.437032406	0.73865244	yes	no	no	AW918173	Rn.23462	enhancer of polycomb homolog 2 (Drosophila) (predicted)
832	1377793_at	-0.436756398	0.738793768	yes	no	no	BF407551	Rn.23554	similar to hypothetical protein MGC20460 (predicted)
833	1386818_at	-0.436517021	0.738916361	yes	yes	yes	AA848601	Rn.164405	Transcribed locus
834	1380745_at	-0.436475756	0.738937497	yes	no	no	AA900859	Rn.161764	Similar to Wilms tumor 1-associating protein (WT1-associated protein) homolog) (predicted)
835	1382340_at	-0.436410318	0.738971015	yes	no	no	AA924048	Rn.8048	similar to C630007L23Rik protein (predicted)
836	1391193_at	-0.436182808	0.739087558	yes	no	no	BI288564	Rn.170151	Transcribed locus

837	1368605_at	-0.436151352	0.739103673	yes	no	no	NM_053669	Rn.163202	adaptor protein with pleckstrin homology and src homology 2 domains
838	1369435_at	-0.435772834	0.739297616	yes	no	no	NM_013048	Rn.64565	tocopherol (alpha) transfer protein
839	1389399_at	-0.435642592	0.73936436	yes	no	no	BG372451	Rn.25199	similar to RIKEN cDNA 0610039J04
840	1377754_at	-0.435640032	0.739365672	yes	no	no	BF284038	Rn.15903	Transcribed locus
841	1397692_at	-0.43563563	0.739367928	yes	no	no	BE104820	Rn.50685	cytotoxic granule-associated RNA binding protein 1
842	1382846_at	-0.434894063	0.739748072	yes	no	no	AI501459	Rn.132779	Transcribed locus
843	1379248_at	-0.434434587	0.739983708	yes	no	no	AA926318	Rn.8457	Prolylcarboxypeptidase (angiotensinase C) (predicted)
844	1393151_at	-0.434369696	0.740016993	yes	no	no	BG668816	---	---
845	1372400_at	-0.434070088	0.74017069	yes	no	no	AI180403	Rn.1987	similar to cullin 4A (predicted)
846	1376808_at	-0.433814223	0.740301972	yes	no	no	BG672572	Rn.21871	Transcribed locus
847	1390753_at	-0.433804484	0.74030697	yes	no	no	BF419721	Rn.147551	Transcribed locus
848	1378691_at	-0.433799245	0.740309658	yes	yes	yes	AA893871	---	---
849	1372542_at	-0.433643151	0.740389761	yes	no	no	BE113281	Rn.85462	Quaking homolog, KH domain RNA binding (mouse)
850	1393676_at	-0.433521995	0.740451941	yes	no	no	BE106495	Rn.33321	Forkhead box P1
851	1395842_at	-0.433363732	0.740533172	yes	no	no	AI136504	Rn.30516	Periostin, osteoblast specific factor (predicted)
852	1397018_at	-0.433170064	0.740632588	yes	no	no	BF399590	Rn.28682	Protein kinase, cGMP-dependent, type 1 (mapped)
853	1389643_at	-0.433086649	0.740675412	yes	yes	yes	H31790	Rn.99647	widely-interspaced zinc finger motifs (predicted)
854	1393804_at	-0.43293738	0.740752051	yes	no	no	BF388537	Rn.34473	similar to hypothetical protein FLJ22490 (predicted)
855	1395964_at	-0.432930041	0.740755819	yes	yes	yes	BI301241	Rn.41069	Transcribed locus
856	1388982_at	-0.432855642	0.74079402	yes	yes	yes	BM389066	---	---
857	1379098_at	-0.432839753	0.740802179	yes	no	no	AI071602	---	---
858	1383002_at	-0.43281649	0.740814124	yes	no	no	AA998043	Rn.129730	Transcribed locus, strongly similar to XP_235292.3 PREDICTED: similar to PHD finger protein 20-like 1 isoform 1 [Rattus norvegicus]
859	1384494_at	-0.432754948	0.740845726	yes	no	no	BI303215	---	---
860	1377743_at	-0.432402784	0.74102659	yes	no	no	BI292687	Rn.22990	Sprouty protein with EVH-1 domain 1, related sequence
861	1397750_at	-0.432357236	0.741049985	yes	no	no	AI145087	Rn.149231	Transcribed locus
862	1382117_at	-0.43222356	0.741118652	yes	no	no	BF417345	Rn.18307	similar to hypothetical protein FLJ21148 (predicted)
863	1388213_a_at	-0.432115342	0.741174247	yes	no	no	AJ243973	---	RT1 class Ib, locus S3
864	1372673_at	-0.432015946	0.741225312	yes	no	no	AW433528	Rn.107603	Transcribed locus
865	1397135_at	-0.432002088	0.741232432	yes	no	no	BE109290	Rn.89331	Discs, large homolog 1 (Drosophila)
866	1377503_at	-0.43174414	0.741364973	yes	no	no	BG371773	Rn.137079	RIO kinase 2 (yeast)
867	1383001_at	-0.431715416	0.741379734	yes	no	no	AI178157	Rn.16708	RGD1560812 (predicted)
868	1380250_at	-0.431650525	0.741413081	yes	no	no	AI013978	Rn.23447	insulin responsive sequence DNA binding protein-1
869	1390840_at	-0.431620246	0.741428642	yes	no	no	BF398182	Rn.156518	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
870	1388829_at	-0.431594007	0.741442127	yes	no	no	AA946348	Rn.145173	similar to autoantigen
871	1394304_at	-0.431525141	0.74147752	yes	yes	yes	BF556357	---	---
872	1393369_at	-0.431155307	0.741667622	yes	no	no	BI300502	Rn.16007	CDKN2A interacting protein
873	1369817_at	-0.430634592	0.741935362	yes	no	no	NM_022696	Rn.41057	heart and neural crest derivatives expressed transcript 2
874	1380696_at	-0.430534937	0.741986613	yes	no	no	AW530527	Rn.15953	Similar to RIKEN cDNA C230093N12 (predicted)
875	1390431_at	-0.430438163	0.742036386	yes	yes	yes	AI111559	Rn.22062	Transcribed locus
876	1397277_at	-0.430371336	0.742070759	yes	no	no	AW920086	Rn.8048	Similar to C630007L23Rik protein (predicted)
877	1392524_at	-0.430319826	0.742097254	yes	no	no	AI234031	Rn.6763	tripartite motif protein 23
878	1378122_a_at	-0.430040038	0.742241186	yes	no	no	BI285319	---	---
879	1380163_at	-0.429875049	0.742326075	yes	no	no	BI302685	Rn.168120	SEC23 interacting protein
880	1396068_at	-0.429747518	0.742391698	yes	no	no	AA899954	Rn.162273	Similar to D1Ertd622e protein (predicted)
881	1384717_at	-0.429745842	0.74239256	yes	no	no	AA894199	Rn.63466	Development and differentiation enhancing (predicted)

882	1372824_at	-0.429725092	0.742403238	yes	no	no	AI103367	Rn.11991	pleckstrin homology domain containing, family F (with FYVE domain) member 2 (predicted)
883	1378338_at	-0.429416711	0.742561946	yes	no	no	BE103735	Rn.64258	similar to hypothetical protein MGC32132 (predicted)
884	1391155_at	-0.429365142	0.742588489	yes	no	no	AW528765	Rn.25032	Ligand of numb-protein X 1 (predicted)
885	1393678_at	-0.429174579	0.742686583	yes	no	no	BI275975	Rn.28431	similar to CG10084-PA
886	1390671_at	-0.428429976	0.743069997	yes	yes	yes	AI044666	Rn.10957	Insulin-like growth factor 1 receptor
887	1379695_at	-0.428371359	0.743100189	yes	no	no	AW915505	Rn.146468	Transcribed locus
888	1392949_at	-0.428328824	0.743122098	yes	yes	yes	BF420756	---	---
889	1370390_at	-0.428233376	0.743171264	yes	no	no	AF140359	Rn.28432	coronin, actin binding protein 6
890	1375392_at	-0.42812649	0.743226326	yes	no	no	BF405277	Rn.45546	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (predicted)
891	1391674_at	-0.427997239	0.743292915	yes	no	no	AA925120	Rn.15458	Transcribed locus
892	1382403_at	-0.427876577	0.743355084	yes	no	no	AA964146	Rn.11716	similar to RIKEN cDNA 2610019F03
893	1391404_at	-0.427822545	0.743382924	yes	yes	yes	BF402732	Rn.163442	stromal antigen 2 (predicted)
894	1383042_at	-0.427611692	0.74349158	yes	yes	yes	AA944383	Rn.3390	Similar to Dendritic cell protein GA17 (predicted)
895	1398409_at	-0.427467604	0.743565839	yes	no	no	AA850428	Rn.163705	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
896	1391569_at	-0.427297826	0.743653348	yes	no	no	BF406435	Rn.149230	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]
897	1394000_at	-0.426957285	0.743828904	yes	no	no	BM391003	---	---
898	1391788_at	-0.426765041	0.743928029	yes	yes	no	BF406814	Rn.74373	Sin3-associated polypeptide, 18kDa
899	1373765_at	-0.426652918	0.743985847	yes	no	no	BG371708	Rn.17913	Transcribed locus
900	1389641_at	-0.426564812	0.744031284	yes	no	no	BE349788	Rn.43354	small nuclear RNA activating complex, polypeptide 4 (predicted)
901	1398452_at	-0.426524106	0.744052277	yes	no	no	BI298587	Rn.15205	similar to chromosome 14 open reading frame 35 (predicted)
902	1385101_a_at	-0.42645983	0.744085428	yes	yes	yes	AI712625	Rn.21666	coiled-coildomaincontaining127
903	1377456_at	-0.426329182	0.744152814	yes	no	no	BE116775	Rn.160491	Transcribed locus
904	1389463_at	-0.426253367	0.744191921	yes	yes	no	BG375376	Rn.145151	protein kinase, cAMP dependent regulatory, type I, beta
905	1387237_at	-0.42621972	0.744209277	yes	no	no	BM388722	Rn.45761	exocyst complex component 7
906	1387029_at	-0.425903472	0.744372431	yes	no	no	NM_130409	Rn.101777	complement component factor H
907	1392559_at	-0.425836079	0.744407203	yes	yes	yes	BM383442	Rn.56018	similar to mKIAA0701 protein
908	1390743_at	-0.425616372	0.744520577	yes	no	no	BF405616	Rn.60798	Transcribed locus
909	1395578_at	-0.425593965	0.744532141	yes	no	no	BF419340	Rn.27883	Transcribed locus
910	1393246_at	-0.425560432	0.744549446	yes	yes	yes	BG378670	Rn.75726	zinc finger, MYND domain-containing 10
911	1389632_at	-0.425471609	0.744595288	yes	no	no	AA799294	Rn.3782	Transcribed locus, strongly similar to XP_228131.3 PREDICTED: similar to Rho-related BTB domain-containing protein 1 [Rattus norvegicus]
912	1383063_a_at	-0.42490917	0.744885627	yes	no	no	AI137878	Rn.164799	Transcribed locus
913	1378029_at	-0.424838931	0.744921893	yes	no	no	AI233769	Rn.6440	Transcribed locus
914	1393334_at	-0.424600292	0.745045122	yes	no	no	AW528448	Rn.17664	Transcribed locus
915	1386106_at	-0.424508606	0.745092473	yes	no	no	BF288435	Rn.9024	Transcribed locus, moderately similar to XP_511922.1 PREDICTED: similar to hypothetical protein DKFZp566I133 [Pan troglodytes]
916	1397238_at	-0.424374449	0.745161763	yes	no	no	AW524239	Rn.144757	Similar to RIKEN cDNA 8430426H19 (predicted)
917	1389989_at	-0.424255842	0.745223027	yes	yes	yes	BF397805	Rn.107838	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
918	1379103_at	-0.42410969	0.745298525	yes	yes	yes	BF406246	Rn.59850	Transcribed locus
919	1392259_at	-0.424096778	0.745305195	yes	yes	yes	AI574925	Rn.36797	similar to HECT domain containing 1 (predicted)
920	1379473_at	-0.423938432	0.745387003	yes	no	no	BI284815	Rn.7988	similar to RIKEN cDNA 1700108L22
921	1383931_at	-0.423932298	0.745390172	yes	no	no	AA901043	---	---
922	1387184_at	-0.423896314	0.745408764	yes	yes	yes	NM_024355	Rn.162212	axin2
923	1369696_at	-0.423648939	0.745536588	yes	no	no	NM_053972	Rn.11259	Ras-related GTP binding B

924	1397634_at	-0.423613465	0.74555492	yes	no	no	BE098186	---	---
925	1393298_at	-0.423581646	0.745571363	yes	no	no	BF566249	Rn.166843	Transcribed locus
926	1391543_at	-0.423558469	0.745583341	yes	yes	yes	BF406678	---	---
927	1374945_at	-0.423506489	0.745610205	yes	no	no	BI281827	Rn.54722	GCD14/PCMT domain containing protein RGD1359191
928	1382046_at	-0.42275706	0.745997624	yes	yes	yes	AA963495	Rn.72680	mitogen activated protein kinase kinase kinase 3 (predicted)
929	1375199_at	-0.422747426	0.746002605	yes	yes	yes	BG378641	Rn.168085	Transcribed locus
930	1384003_at	-0.422442769	0.746160157	yes	yes	yes	BF288235	Rn.93479	Similar to RIKEN cDNA 5230400G24
931	1374647_at	-0.422435667	0.74616383	yes	yes	yes	BI299718	Rn.38954	rosbin, round spermatid basic protein 1 (predicted)
932	1377633_a_at	-0.422339902	0.746213361	yes	yes	yes	AW918411	Rn.98525	Transcribed locus, weakly similar to NP_671483.1 hippyragranin [Rattus norvegicus]
933	1394779_at	-0.422191403	0.746290174	yes	yes	yes	AI717218	Rn.168649	Transcribed locus
934	1386507_at	-0.422191117	0.746290322	yes	yes	no	AA799858	---	---
935	1386477_at	-0.421927414	0.746426746	yes	yes	yes	AI170046	Rn.67055	Toll-like receptor adaptor molecule 2 (predicted)
936	1378754_at	-0.421697091	0.74654592	yes	yes	yes	BI274328	Rn.16196	Transcribed locus, weakly similar to XP_379479.2 PREDICTED: hypothetical protein XP_379479 [Homo sapiens]
937	1396291_at	-0.421469423	0.74666374	yes	yes	yes	BI290733	---	---
938	1386156_at	-0.421190488	0.746808116	yes	yes	yes	AI639451	Rn.94023	thyroid hormone receptor associated protein 1 (predicted)
939	1373525_at	-0.421146394	0.746830942	yes	yes	yes	AI113011	Rn.22096	Transcribed locus
940	1385239_at	-0.421042702	0.746884622	yes	yes	yes	AI045150	Rn.33362	Similar to hypothetical gene supported by AK044523 (predicted)
941	1392558_at	-0.420792202	0.747014317	yes	yes	yes	AI101600	Rn.162863	RGD1565142 (predicted)
942	1385261_s_at	-0.42070513	0.747059403	yes	yes	yes	BE103057	Rn.125849	Transcribed locus
943	1395898_at	-0.42044976	0.747191651	yes	yes	yes	BF396228	Rn.105907	Similar to RIKEN cDNA 1110001M20 (predicted)
944	1394672_at	-0.420355396	0.747240525	yes	yes	yes	BF414556	Rn.15351	Similar to U5 snRNP-specific protein (Prp8-binding) (predicted)
945	1384877_at	-0.420259099	0.747290404	yes	yes	yes	AI072405	Rn.20144	aquaporin 11
946	1383182_at	-0.419432052	0.747718922	yes	yes	yes	AW144184	Rn.2688	serine/arginine-rich protein specific kinase 1
947	1380763_at	-0.419370649	0.747750747	yes	yes	yes	AI101194	---	---
948	1380766_a_at	-0.419273453	0.747801125	yes	yes	yes	BF389689	Rn.137481	Transcribed locus
949	1376824_at	-0.419066322	0.747908497	yes	yes	yes	AI408131	Rn.168093	Transcribed locus, strongly similar to XP_233612.3 PREDICTED: similar to DNA-damage inducible protein 2 [Rattus norvegicus]
950	1372528_at	-0.418954005	0.747966725	yes	yes	yes	AI102069	Rn.13345	N-ethylmaleimide sensitive fusion protein
951	1378384_at	-0.418934966	0.747976596	yes	yes	yes	AW531141	Rn.139089	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26
952	1373123_at	-0.41889392	0.747997877	yes	yes	yes	BG372671	Rn.22107	similar to RIKEN cDNA 4932432N11 gene (predicted)
953	1394473_at	-0.418759892	0.74806737	yes	yes	yes	AI716206	Rn.17706	PCTAIRE-motif protein kinase 2
954	1391505_x_at	-0.418695262	0.748100882	yes	yes	yes	BI275261	Rn.177549	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]
955	1395147_at	-0.418684129	0.748106655	yes	yes	yes	BE116565	Rn.164573	Transcribed locus
956	1372872_at	-0.418489719	0.748207473	yes	yes	yes	BI291271	Rn.136946	Similar to mFLJ00191 protein
957	1373511_at	-0.418419928	0.748243669	yes	yes	yes	BI296596	Rn.164311	Transcribed locus
958	1388295_s_at	-0.418343716	0.748283197	yes	yes	yes	AI170571	Rn.195273	fibroblast growth factor receptor substrate 3
959	1397176_at	-0.418234195	0.748340004	yes	yes	yes	AI104417	Rn.29892	methyltransferase like 6
960	1380084_at	-0.418021968	0.748450096	yes	yes	yes	BF399367	Rn.17305	Similar to RIKEN cDNA C330005L02
961	1376835_at	-0.418012733	0.748454888	yes	yes	no	BI293600	Rn.129334	Solute carrier family 35, member B2
962	1393358_at	-0.417600238	0.748668916	yes	yes	no	AA957379	Rn.164771	Transcribed locus
963	1377316_at	-0.416658274	0.749157897	yes	yes	yes	BF397728	Rn.98615	Similar to RIKEN cDNA 2410006F12
964	1390500_at	-0.416443163	0.749269607	yes	yes	yes	BG375508	Rn.105388	similar to RIKEN cDNA 9130023F12 gene (predicted)
965	1396529_at	-0.416284472	0.749352028	yes	yes	yes	BF415512	Rn.173723	Transcribed locus
966	1388758_at	-0.415833905	0.749586095	yes	yes	yes	AI009074	Rn.163646	Transcribed locus
967	1394526_at	-0.415388942	0.749817321	yes	yes	yes	AI236935	Rn.34271	Transcribed locus

968	1395896_at	-0.415267009	0.749880697	yes	yes	yes	AI233009	---	---
969	1377002_at	-0.415134243	0.749949708	yes	yes	no	AA946209	Rn.105738	Transcribed locus, strongly similar to XP_213649.3 PREDICTED: similar to interferon alpha/beta receptor [Rattus norvegicus]
970	1381070_at	-0.414967665	0.750036305	yes	yes	yes	AI233106	---	---
971	1382131_at	-0.414697554	0.750176745	yes	yes	yes	AW523674	Rn.166138	Transcribed locus
972	1380174_at	-0.414369438	0.750347379	yes	yes	yes	BE116115	Rn.34448	Transcribed locus
973	1381590_at	-0.414313518	0.750376464	yes	yes	yes	BI295719	Rn.31803	Par-3 (partitioning defective 3) homolog (C. elegans)
974	1379164_at	-0.414159367	0.750456645	yes	yes	yes	BE117672	Rn.160662	Zinc finger protein 142 (clone pHZ-49) (predicted)
975	1380964_at	-0.413825624	0.750630271	yes	yes	yes	BF396607	Rn.170597	Transcribed locus
976	1380895_at	-0.413632065	0.750730985	yes	yes	yes	BE103215	Rn.1423	Amyloid beta (A4) precursor-like protein 2
977	1387519_at	-0.413613856	0.750740461	yes	yes	no	NM_013090	Rn.31977	vesicle-associated membrane protein 1
978	1383522_at	-0.413332852	0.750886702	yes	yes	yes	AI045086	Rn.105636	similar to Ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (predicted)
979	1382028_at	-0.413152537	0.750980558	yes	yes	yes	BE115406	---	similar to PxF protein
980	1392178_at	-0.413027647	0.751045571	yes	yes	no	BE106509	Rn.31034	SLIT and NTRK-like family, member 1 (predicted)
981	1378902_at	-0.412882467	0.751121153	yes	yes	yes	BF413695	Rn.163211	radical S-adenosyl methionine and flavodoxin domains 1 (predicted)
982	1378663_at	-0.412850154	0.751137977	yes	yes	yes	BF401737	---	---
983	1382551_at	-0.412454808	0.751343841	yes	yes	yes	BF417645	Rn.37673	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)
984	1385753_at	-0.412155149	0.751499918	yes	yes	yes	BF395818	Rn.172804	Transcribed locus
985	1392571_at	-0.411909952	0.751627652	yes	yes	yes	AA899216	Rn.14908	Transcribed locus
986	1391171_at	-0.411580505	0.751799309	yes	yes	no	AW534352	Rn.107335	Integral membrane protein 2B
987	1380975_at	-0.411506801	0.751837718	yes	yes	yes	AW534466	Rn.165669	Transcribed locus
988	1398089_at	-0.411340706	0.751924281	yes	yes	yes	BF401882	Rn.105397	Similar to Serine/threonine protein kinase 24 (predicted)
989	1381164_at	-0.411207195	0.751993869	yes	yes	yes	BF386935	Rn.116965	Golgi autoantigen, golgin subfamily a, 1 (predicted)
990	1388712_at	-0.410918432	0.752144399	yes	yes	yes	BM389186	Rn.10673	pleckstrin homology, Sec7 and coiled-coil domains 3
991	1384007_at	-0.410719219	0.752248266	yes	yes	yes	BG668983	Rn.135117	spastic paraplegia 3A homolog (human)
992	1384451_at	-0.410472955	0.752376683	yes	yes	yes	BE116574	Rn.161443	Transcribed locus
993	1394283_at	-0.410447038	0.7523902	yes	yes	yes	AW144132	Rn.18604	LUC7-like 2 (S. cerevisiae) (predicted)
994	1382609_at	-0.410074869	0.752584317	yes	yes	yes	AI058451	Rn.17318	Transcribed locus
995	1385063_at	-0.409969627	0.752639219	yes	yes	yes	BG377323	---	ELK1, member of ETS oncogene family
996	1378628_at	-0.409867757	0.752692365	yes	yes	yes	BF411451	Rn.61844	Transcribed locus
997	1377495_at	-0.409408179	0.752932178	yes	yes	yes	AA900220	Rn.15032	Transcribed locus
998	1368325_at	-0.40901646	0.753136641	yes	yes	yes	NM_012842	Rn.6075	epidermal growth factor
999	1390681_at	-0.408367239	0.753475633	yes	yes	yes	AA964074	Rn.11697	Transcribed locus
1000	1369157_at	-0.408224566	0.75355015	yes	yes	yes	NM_017229	Rn.10322	phosphodiesterase 3B
1001	1373350_at	-0.408182683	0.753572027	yes	yes	yes	H31668	Rn.93075	PC4 and SFRS1 interacting protein 1
1002	1391454_at	-0.40809501	0.753617823	yes	yes	yes	BF286105	---	---
1003	1378620_at	-0.407773483	0.753785797	yes	yes	yes	BE104164	Rn.156052	Transcribed locus
1004	1393613_at	-0.407771581	0.753786791	yes	yes	yes	BE117871	Rn.171579	Transcribed locus
1005	1382963_at	-0.407687276	0.75383084	yes	yes	yes	BF416871	Rn.22937	ATP-binding cassette, sub-family B (MDR/TAP), member 10
1006	1390547_at	-0.407205265	0.754082741	yes	yes	yes	BG375792	Rn.11757	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
1007	1390499_at	-0.406742646	0.754324586	yes	yes	yes	BG380393	Rn.118497	Transcribed locus
1008	1394436_at	-0.406410313	0.754498369	yes	yes	yes	BF560163	Rn.24583	sperm associated antigen 9 (predicted)
1009	1378334_a_at	-0.406405628	0.754500819	yes	yes	yes	BF417289	Rn.89152	Inositol 1,4,5-triphosphate receptor 2
1010	1391419_at	-0.406337175	0.754536619	yes	yes	no	BG376923	Rn.112088	AT hook, DNA binding motif, containing 1 (predicted)
1011	1378890_at	-0.40632044	0.754545372	yes	yes	yes	BF408090	Rn.33007	Transcribed locus, weakly similar to XP_574992.1 PREDICTED:

									hypothetical protein XP_574992 [Rattus norvegicus]
1012	1377333_at	-0.405798998	0.754818141	yes	yes	yes	BE114427	Rn.166868	Transcribed locus
1013	1396539_at	-0.405465943	0.754992415	yes	yes	yes	BE119221	Rn.6401	Actinin, alpha 1
1014	1388192_at	-0.405339779	0.755058443	yes	yes	yes	AI711028	Rn.54470	RWD domain containing 3
1015	1394699_at	-0.405003314	0.755234558	yes	yes	yes	BG671896	Rn.32723	Similar to transcription factor ONECUT2 (predicted)
1016	1393322_at	-0.404998446	0.755237106	yes	yes	yes	AI556910	Rn.72554	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)
1017	1372615_at	-0.40494664	0.755264227	yes	yes	yes	AI070137	---	amine oxidase, copper containing 3
1018	1383512_at	-0.404374184	0.755563972	yes	yes	yes	AW918674	Rn.3620	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
1019	1398264_at	-0.404305471	0.755599959	yes	yes	yes	NM_012890	Rn.11135	solute carrier family 30 (zinc transporter), member 2
1020	1386266_at	-0.404146271	0.755683344	yes	yes	yes	AI227948	Rn.162778	Similar to male sterility domain containing 1 (predicted)
1021	1376438_at	-0.403990244	0.755765075	yes	yes	yes	BF416513	Rn.15203	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
1022	1372874_at	-0.403614339	0.755962021	yes	yes	yes	BI299261	Rn.64427	Serologically defined colon cancer antigen 8
1023	1376177_at	-0.403490154	0.756027096	yes	yes	yes	AI179609	Rn.93919	similar to RIKEN cDNA 5730593F17 (predicted)
1024	1372939_at	-0.402670162	0.756456925	yes	yes	yes	AI010173	Rn.3419	NudC domain containing 2
1025	1377213_at	-0.402597902	0.756494814	yes	yes	yes	BI280353	Rn.14645	Transcribed locus
1026	1376659_at	-0.402009849	0.75680323	yes	yes	yes	BF282469	Rn.13455	nucleotide binding protein-like (predicted)
1027	1378844_at	-0.401924028	0.756848251	yes	yes	no	BE120931	Rn.53685	Transcribed locus
1028	1373078_at	-0.401639398	0.756997584	yes	yes	yes	AI409271	Rn.8222	Transcribed locus
1029	1391274_at	-0.401585288	0.757025977	yes	yes	yes	BI292056	Rn.91765	Transcribed locus
1030	1369919_at	-0.401472954	0.757084924	yes	yes	yes	NM_019194	Rn.59871	thyrotroph embryonic factor
1031	1388194_at	-0.401322643	0.757163808	yes	yes	yes	BI295900	Rn.15413	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
1032	1375217_at	-0.401296926	0.757177305	yes	yes	yes	BI296680	Rn.162539	Meningioma expressed antigen 5 (hyaluronidase)
1033	1376155_at	-0.401293778	0.757178957	yes	yes	no	BE113295	Rn.115871	similar to hypothetical protein 2BE2121 - Chinese hamster (fragment) (predicted)
1034	1392316_at	-0.401222747	0.757216237	yes	yes	yes	BI293349	Rn.146737	Transcribed locus
1035	1392929_at	-0.400869936	0.757401437	yes	yes	yes	BF416678	Rn.6943	RGD1565616 (predicted)
1036	1388471_at	-0.400778657	0.75744936	yes	yes	yes	AA800197	Rn.101085	t-complex 11 (mouse) like 2
1037	1388227_at	-0.400754842	0.757461863	yes	yes	yes	Y13972	Rn.163225	MHC class I-like sequence (mapped)
1038	1383170_at	-0.400739438	0.75746995	yes	yes	yes	AW143788	Rn.7599	Transcribed locus
1039	1368751_at	-0.400653242	0.757515208	yes	yes	yes	NM_031778	Rn.10878	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
1040	1397895_at	-0.40056673	0.757560634	yes	yes	yes	BI290793	---	---
1041	1392145_at	-0.400458497	0.75761747	yes	yes	no	BI281801	---	---
1042	1397960_at	-0.400448727	0.7576226	yes	yes	yes	AI030168	Rn.44741	similar to ALEX3 protein
1043	1372898_at	-0.400405918	0.757645082	yes	yes	yes	BI291248	Rn.27022	similar to 2700008B19Rik protein (predicted)
1044	1383840_at	-0.400405787	0.75764515	yes	yes	no	AA963833	Rn.162264	Similar to chondroitin beta1,4 N-acetylgalactosaminyltransferase (predicted)
1045	1379321_at	-0.400100675	0.7578054	yes	yes	no	AI180133	Rn.14721	X Kell blood group precursor related family member 6 homolog
1046	1379742_at	-0.399599677	0.758068605	yes	yes	yes	BI301216	---	similar to SP140 nuclear body protein isoform 1
1047	1383034_at	-0.399534816	0.758102687	yes	yes	yes	AA998572	Rn.33148	RING1 and YY1 binding protein (predicted)
1048	1377998_at	-0.399454426	0.758144931	yes	yes	yes	BI288705	Rn.19581	coproporphyrinogen oxidase
1049	1376840_at	-0.399347223	0.75820127	yes	yes	yes	AI103040	Rn.6640	zinc finger protein 655
1050	1381703_at	-0.399257098	0.758248636	yes	yes	yes	AW525915	Rn.19721	Glutathione reductase
1051	1378211_s_at	-0.399251159	0.758251757	yes	yes	yes	BE114473	Rn.172479	Transcribed locus
1052	1391906_at	-0.399124431	0.758318366	yes	yes	yes	BE113001	Rn.6526	kinesin family member 1B

1053	1391619_at	-0.399111805	0.758325002	yes	yes	yes	AI137509	Rn.43108	RGD1561917 (predicted)
1054	1389158_at	-0.398773361	0.758502919	yes	yes	yes	BE329196	Rn.98315	Similar to helicase-like protein NHL isoform 2
1055	1374339_at	-0.3987384	0.758521301	yes	yes	yes	BI303362	Rn.164881	Transcribed locus
1056	1378719_at	-0.398594104	0.758597171	yes	yes	no	BF411797	Rn.163381	Similar to hypothetical protein MGC28728 (predicted)
1057	1392811_at	-0.3980708	0.758872384	yes	yes	no	BI289490	Rn.9343	ubiquitin specific protease 40
1058	1376470_at	-0.397789135	0.759020557	yes	yes	yes	BG372703	Rn.66946	formin binding protein 4
1059	1398528_at	-0.397760971	0.759035375	yes	yes	yes	BE117514	Rn.128129	Transcribed locus
1060	1396692_at	-0.397703008	0.759065871	yes	yes	yes	BE115748	---	---
1061	1377623_at	-0.397245333	0.759306713	yes	yes	yes	AA925355	Rn.162915	ring finger (C3HC4 type) and KH domain containing 1 (predicted)
1062	1385815_at	-0.397222848	0.759318547	yes	yes	yes	AI072733	---	similar to striated muscle-specific serine/threonine protein kinase
1063	1387101_at	-0.397086036	0.759390557	yes	yes	yes	NM_053623	Rn.87821	acyl-CoA synthetase long-chain family member 4
1064	1393594_at	-0.396989539	0.759441352	yes	yes	yes	AI030196	Rn.103975	Pogo transposable element with ZNF domain (predicted)
1065	1384188_at	-0.396979342	0.759446719	yes	yes	yes	AW142766	---	---
1066	1388299_at	-0.396252703	0.759829324	yes	yes	yes	BF406304	Rn.172352	Transcribed locus
1067	1378261_at	-0.396156113	0.759880198	yes	yes	no	BE102806	Rn.156495	Transcribed locus
1068	1384043_at	-0.395878505	0.760026431	yes	yes	yes	BG667918	---	---
1069	1396217_at	-0.395132142	0.760419724	yes	yes	yes	BF542447	Rn.17309	Adaptor-related protein complex 1, sigma 2 subunit (predicted)
1070	1394970_at	-0.394791229	0.760599434	yes	yes	yes	BI279660	Rn.14865	cysteinyl-tRNA synthetase (predicted)
1071	1379303_at	-0.394366311	0.760823487	yes	yes	yes	AA964811	Rn.9570	ariadne homolog 2 (Drosophila) (predicted)
1072	1368487_at	-0.394089454	0.760969505	yes	yes	no	NM_021696	Rn.42912	serine (or cysteine) proteinase inhibitor, clade B, member 2
1073	1377960_at	-0.394028146	0.761001844	yes	yes	yes	BF407455	Rn.38402	Transcribed locus
1074	1368376_at	-0.393931703	0.761052718	yes	yes	yes	NM_057133	Rn.10712	nuclear receptor subfamily 0, group B, member 2
1075	1395015_at	-0.393920862	0.761058437	yes	yes	no	BE116550	Rn.95452	coagulation factor VIII
1076	1397907_at	-0.393845084	0.761098413	yes	yes	yes	BF553760	Rn.12130	Hypothetical protein LOC501546
1077	1392333_at	-0.393781203	0.761132114	yes	yes	no	BI277918	Rn.98695	peroxisome biogenesis factor 16
1078	1386296_at	-0.393776986	0.761134338	yes	yes	yes	AI639205	Rn.23507	septin 8 (predicted)
1079	1382489_at	-0.393670718	0.761190405	yes	yes	no	BE116698	Rn.23174	similar to WD repeat domain 11 protein (predicted)
1080	1376963_at	-0.393247348	0.761413815	yes	yes	no	BM388710	Rn.23189	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (predicted)
1081	1380024_at	-0.393142923	0.76146893	yes	yes	yes	BI282175	---	---
1082	1381108_at	-0.393104987	0.761488953	yes	yes	yes	BF387399	Rn.884	similar to hypothetical protein FLJ20436
1083	1395143_at	-0.392917752	0.761587787	yes	yes	no	BF389774	Rn.89229	U2AF homology motif (UHM) kinase 1
1084	1385837_at	-0.392822601	0.761638018	yes	yes	yes	AA956624	Rn.100101	homeo box D3 (mapped)
1085	1378998_at	-0.392622828	0.761743491	yes	yes	yes	AI071538	Rn.20558	Transcribed locus
1086	1389786_at	-0.392490533	0.761813346	yes	yes	yes	AA946272	Rn.51261	Similar to RIKEN cDNA 2410005O16
1087	1372696_at	-0.392478083	0.76181992	yes	yes	yes	AA893807	Rn.22756	Transcribed locus
1088	1385212_at	-0.392450642	0.76183441	yes	yes	yes	AI603192	Rn.154542	Ac1158
1089	1395127_at	-0.392424192	0.761848378	yes	yes	yes	AI176719	Rn.86072	Similar to RIKEN cDNA 4932438A13 (predicted)
1090	1375776_at	-0.392220792	0.761955795	yes	yes	yes	BF393112	Rn.9622	Transcriptional co-activator with PDZ-binding motif (TA)Z
1091	1383922_a_at	-0.391872011	0.762140026	yes	yes	yes	BG375634	Rn.12061	N-acetyltransferase ARD1 homolog (S. cerevisiae) (predicted)
1092	1397880_at	-0.391752403	0.762203214	yes	yes	yes	BF389592	Rn.101953	Similar to serine/threonine kinase
1093	1394009_at	-0.391362204	0.762409391	yes	yes	yes	BI288530	---	---
1094	1368342_at	-0.391308085	0.762437992	yes	yes	yes	NM_031544	Rn.11106	adenosine monophosphate deaminase 3
1095	1394869_at	-0.391303478	0.762440427	yes	yes	yes	BE104854	Rn.146659	Transcribed locus
1096	1394925_at	-0.391258515	0.762464189	yes	yes	yes	AI578037	Rn.38292	similar to RIKEN cDNA 2310035C23 (predicted)
1097	1379567_at	-0.39123264	0.762477864	yes	yes	yes	AI105643	Rn.94023	thyroid hormone receptor associated protein 1 (predicted)
1098	1379029_at	-0.391176014	0.762507792	yes	yes	yes	BI284478	Rn.163116	Similar to Zinc finger protein 62 homolog (Zfp-62) (ZT3) (predicted)

1099	1395274_at	-0.391126681	0.762533867	yes	yes	yes	AI235468	Rn.79807	dystonin (predicted)
1100	1383223_at	-0.391025074	0.762587573	yes	yes	yes	BG672206	Rn.12128	ubiquitin-like 3
1101	1374262_at	-0.390908405	0.762649245	yes	yes	yes	BF396371	Rn.32615	Transcribed locus
1102	1379020_at	-0.390852044	0.762679039	yes	yes	yes	AI454024	Rn.164815	Transcribed locus
1103	1380639_at	-0.390414789	0.762910229	yes	yes	yes	BI296446	Rn.5782	syntaxin 5a
1104	1387344_at	-0.390351835	0.76294352	yes	yes	yes	AI407458	Rn.2098	aldehyde dehydrogenase family 6, subfamily A1
1105	1393406_at	-0.390104519	0.76307432	yes	yes	yes	AI576602	Rn.8068	Ring-box 1
1106	1379415_at	-0.390055213	0.763100399	yes	yes	yes	AA998194	Rn.147786	Transcribed locus
1107	1374348_at	-0.389998572	0.76313036	yes	yes	yes	BG373082	Rn.103871	Similar to zinc finger protein Cezanne; cellular zinc finger anti-NF-kappaB Cezanne (predicted)
1108	1374199_at	-0.389474044	0.763407866	yes	yes	yes	BI282130	Rn.137473	similar to Disco-interacting protein 2 homolog
1109	1379680_at	-0.389471199	0.763409371	yes	yes	yes	AI030284	Rn.24305	Transcribed locus
1110	1380128_at	-0.38927214	0.763514711	yes	yes	yes	AI237408	Rn.61106	Leucine zipper-EF-hand containing transmembrane protein 2
1111	1384678_at	-0.389130357	0.76358975	yes	yes	yes	BF559356	Rn.147562	Transcribed locus
1112	1378167_at	-0.388958426	0.763680755	yes	yes	yes	AI599898	Rn.167959	Transcribed locus
1113	1370543_at	-0.388805855	0.763761522	yes	yes	yes	U76557	Rn.82705	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
1114	1369248_a_at	-0.388735594	0.763798719	yes	yes	yes	AF304333	Rn.91239	baculoviral IAP repeat-containing 4
1115	1377944_at	-0.388698568	0.763818322	yes	yes	yes	AW532214	---	---
1116	1383611_at	-0.38863055	0.763854334	yes	yes	yes	AI145497	Rn.23997	Transcribed locus
1117	1380452_at	-0.388352641	0.764001491	yes	yes	no	AA964564	Rn.11844	Transcribed locus
1118	1379583_at	-0.388306249	0.764026059	yes	yes	no	AI715295	Rn.41391	AFG3(ATPase family gene 3)-like 1 (yeast) (predicted)
1119	1381262_at	-0.388287362	0.764036061	yes	yes	no	BG374101	Rn.21294	Pre-B-cell leukemia transcription factor interacting protein 1
1120	1382948_at	-0.388242678	0.764059726	yes	yes	yes	BI296929	Rn.14693	similar to hypothetical protein E130310N06 (predicted)
1121	1375371_at	-0.388196419	0.764084225	yes	yes	no	BI296662	Rn.101115	similar to Ran-binding protein 2 (predicted)
1122	1371060_at	-0.38802955	0.764172608	yes	yes	yes	L04760	Rn.6763	tripartite motif protein 23
1123	1384519_at	-0.38785088	0.764267252	yes	yes	yes	BG377412	Rn.24233	SEC63-like (S. cerevisiae) (predicted)
1124	1384897_at	-0.387461303	0.764473659	yes	yes	yes	AA858696	Rn.16878	Transcribed locus
1125	1379244_at	-0.387225381	0.764598682	yes	yes	no	AW522926	Rn.13581	Transcribed locus
1126	1398430_at	-0.387174151	0.764625834	yes	yes	yes	AW524711	Rn.8814	Transcribed locus
1127	1372024_at	-0.387070616	0.764680709	yes	yes	yes	AI104846	Rn.23401	Transcribed locus
1128	1397731_at	-0.387043988	0.764694823	yes	yes	yes	AA998060	Rn.165471	Transcribed locus
1129	1386951_at	-0.386938972	0.764750488	yes	yes	yes	NM_012985	Rn.100240	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5
1130	1397902_at	-0.386737152	0.764857477	yes	yes	yes	BF548780	Rn.1309	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
1131	1380195_at	-0.386623063	0.764917965	yes	yes	yes	AI145357	Rn.7208	ATPase, Ca++ transporting, plasma membrane 1
1132	1384017_at	-0.386618832	0.764920208	yes	yes	yes	AI058817	Rn.18993	leucine-rich repeat kinase 1 (predicted)
1133	1384608_at	-0.386303054	0.765087653	yes	yes	yes	BF407962	---	---
1134	1392692_at	-0.386274957	0.765102553	yes	yes	yes	BE107050	Rn.170398	Transcribed locus
1135	1384286_at	-0.386253121	0.765114134	yes	yes	yes	BI285501	Rn.146558	Transcribed locus
1136	1377799_at	-0.386234168	0.765124186	yes	yes	yes	BE114159	Rn.37490	Microtubule-associated protein 6
1137	1377999_at	-0.385760048	0.765375673	yes	yes	yes	BE103242	Rn.26214	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
1138	1395602_at	-0.385642885	0.765437833	yes	yes	no	BF413296	Rn.37469	Striatin, calmodulin binding protein
1139	1396250_at	-0.385408781	0.76556205	yes	yes	yes	BF558291	Rn.45957	Similar to Coronin, actin binding protein 1C (predicted)
1140	1376533_at	-0.385213485	0.76566569	yes	yes	no	BF398368	Rn.139712	bromodomain adjacent to zinc finger domain, 2B (predicted)
1141	1376747_at	-0.385043895	0.7657557	yes	yes	yes	BE107075	Rn.95239	Membrane associated guanylate kinase 1 b NT-short isoform
1142	1388781_at	-0.385035178	0.765760326	yes	yes	yes	AW434329	---	---

1143	1373357_at	-0.384941123	0.765810251	yes	yes	yes	BI291467	Rn.74590	forkhead box D2 (predicted)
1144	1384256_at	-0.384915638	0.765823779	yes	yes	yes	BI293599	Rn.168323	CDNA clone MGC:95252 IMAGE:7133376
1145	1389589_at	-0.384679116	0.765949342	yes	yes	yes	BE105898	Rn.22273	Transcribed locus
1146	1373453_at	-0.384400472	0.766097293	yes	yes	yes	AA849756	Rn.164456	Transcribed locus
1147	1367755_at	-0.384340407	0.766129189	yes	yes	no	NM_052809	Rn.2589	cysteine dioxygenase 1, cytosolic
1148	1373415_at	-0.384038707	0.766289421	yes	yes	yes	AI407050	Rn.165854	Transcribed locus
1149	1395165_at	-0.384005415	0.766307104	yes	yes	no	BF397366	Rn.93075	PC4 and SFRS1 interacting protein 1
1150	1381090_at	-0.383957925	0.766332329	yes	yes	yes	BE096310	Rn.170576	Transcribed locus
1151	1378679_at	-0.383794447	0.76641917	yes	yes	yes	BG372484	Rn.23509	Ubiquitin specific protease 25 (predicted)
1152	1383561_at	-0.383705679	0.766466329	yes	yes	yes	BF550555	Rn.169228	Transcribed locus, strongly similar to XP_225045.1 PREDICTED: similar to ligase IV, DNA, ATP-dependent [Rattus norvegicus]
1153	1374170_at	-0.383346024	0.766657428	yes	yes	yes	AI172069	Rn.115091	similar to putative TRAF and TNF receptor associated protein
1154	1384006_at	-0.383330786	0.766665526	yes	yes	yes	AI045457	Rn.166128	Transcribed locus
1155	1393704_at	-0.383297797	0.766683057	yes	yes	no	AI136988	Rn.107738	CDNA clone IMAGE:7442534
1156	1378600_at	-0.383239699	0.766713932	yes	yes	yes	AI112986	Rn.137575	Josephin domain containing 3
1157	1395396_at	-0.38310624	0.766784862	yes	yes	yes	AA848942	Rn.98282	regulator of chromosome condensation 2 (predicted)
1158	1387063_at	-0.382878056	0.76690615	yes	yes	yes	NM_021660	Rn.112574	inositol hexaphosphate kinase 2
1159	1380289_at	-0.38285529	0.766918252	yes	yes	no	AA799834	Rn.35202	similar to part of a novel protein (predicted)
1160	1374598_at	-0.382346151	0.767188951	yes	yes	yes	AW914984	Rn.160441	Transcribed locus
1161	1385553_at	-0.382337233	0.767193694	yes	yes	yes	AI136699	Rn.3738	nuclear cap binding protein subunit 2 (predicted)
1162	1382270_at	-0.381900118	0.767426177	yes	yes	yes	BM384387	Rn.164820	Transcribed locus
1163	1382565_at	-0.381851594	0.76745199	yes	yes	yes	BE108260	Rn.20902	Similar to MAPK-interacting and spindle-stabilizing protein (predicted)
1164	1370751_at	-0.38184899	0.767453375	yes	yes	no	U77931	---	rRNA promoter binding protein
1165	1390297_at	-0.381767094	0.767496941	yes	yes	yes	BF395781	Rn.98359	nuclear protein UKp68
1166	1390611_at	-0.381758876	0.767501313	yes	yes	no	BF406297	Rn.61235	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)
1167	1371996_at	-0.38140156	0.767691426	yes	yes	yes	AI232384	Rn.1477	AE binding protein 2 (predicted)
1168	1392084_at	-0.381386548	0.767699414	yes	yes	yes	BE109244	Rn.12749	Transcribed locus
1169	1374574_at	-0.381025645	0.767891485	yes	yes	no	AI547611	Rn.23973	Similar to hypothetical protein MGC38960 (predicted)
1170	1384886_at	-0.380946482	0.767933622	yes	yes	yes	AW523423	Rn.141461	similar to hypothetical protein LOC168850 (predicted)
1171	1379126_at	-0.380399786	0.768224678	yes	yes	no	AI555608	Rn.146145	Transcribed locus
1172	1374974_at	-0.380378492	0.768236017	yes	yes	yes	BI299365	---	---
1173	1385202_at	-0.380173108	0.768345392	yes	yes	no	BE118820	Rn.151156	Transcribed locus
1174	1382057_at	-0.380096947	0.768385955	yes	yes	yes	AI058311	Rn.122028	similar to oocyte-testis gene 1 (predicted)
1175	1373773_at	-0.379600324	0.768650504	yes	yes	yes	BF394166	Rn.34370	glycoprotein m6a
1176	1393171_at	-0.379579361	0.768661673	yes	yes	yes	BG664080	Rn.127766	Transcribed locus
1177	1374500_at	-0.379250315	0.768837007	yes	yes	yes	AI011571	Rn.7210	similar to sarcoma antigen NY-SAR-27
1178	1370969_at	-0.379139898	0.768895852	yes	yes	yes	BE107303	Rn.8465	homeo box A5
1179	1373623_at	-0.379024261	0.768957484	yes	yes	no	BI278809	Rn.85907	inositol 1,4,5-trisphosphate 3-kinase C
1180	1376525_at	-0.378976789	0.768982788	yes	yes	no	BI296632	Rn.92643	KH-type splicing regulatory protein
1181	1397531_at	-0.378928078	0.769008752	yes	yes	yes	BF522208	Rn.38208	Transcribed locus
1182	1391456_at	-0.378865805	0.769041946	yes	yes	no	AA998207	Rn.104684	junctional adhesion molecule 3
1183	1375562_at	-0.378856226	0.769047052	yes	yes	yes	BF408460	Rn.34184	Transcribed locus
1184	1381903_at	-0.37805115	0.769476328	yes	yes	yes	AW533341	Rn.162867	F-box only protein 33 (predicted)
1185	1373892_at	-0.378009432	0.769498579	yes	yes	yes	AA945986	Rn.156574	Transcribed locus
1186	1383022_at	-0.377847518	0.769584945	yes	yes	yes	BF390046	Rn.59079	Transcribed locus
1187	1396759_at	-0.37783841	0.769589803	yes	yes	yes	BF393502	Rn.172725	Transcribed locus

1188	1385860_at	-0.37732721	0.769862546	yes	yes	yes	BF543907	Rn.46932	similar to SPla/RYanodine receptor SPRY (1J970) (predicted)
1189	1395132_at	-0.377292204	0.769881226	yes	yes	yes	BE115432	---	---
1190	1374618_at	-0.376990883	0.77004204	yes	yes	yes	BI279751	Rn.16122	AF4/FMR2 family, member 1 (predicted)
1191	1376129_at	-0.376975126	0.770050451	yes	yes	yes	BE108174	Rn.21609	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
1192	1378581_at	-0.376873098	0.770104911	yes	yes	yes	BI295536	Rn.138353	huntingtin interacting protein 1 related
1193	1388778_at	-0.376853881	0.770115169	yes	yes	yes	BF284876	Rn.17629	Transcribed locus
1194	1384219_at	-0.376823996	0.770131122	yes	yes	yes	BF522747	Rn.32015	Transcribed locus
1195	1369640_at	-0.376807646	0.77013985	yes	yes	yes	BG378227	Rn.10346	gap junction membrane channel protein alpha 1
1196	1397964_at	-0.376697548	0.770198625	yes	yes	yes	AI406662	Rn.24233	SEC63-like (S. cerevisiae) (predicted)
1197	1389107_at	-0.376539391	0.770283063	yes	yes	yes	AI008974	Rn.120904	Similar to KIAA1749 protein (predicted)
1198	1381081_at	-0.376412237	0.770350956	yes	yes	yes	AW523873	Rn.147885	Transcribed locus
1199	1377148_at	-0.376405085	0.770354775	yes	yes	yes	AI412344	---	---
1200	1382366_at	-0.376265242	0.77042945	yes	yes	yes	AI578786	Rn.165275	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide
1201	1389331_at	-0.3762392	0.770443358	yes	yes	yes	AI104371	Rn.22818	CDNA clone IMAGE:7313169
1202	1383981_at	-0.376148518	0.770491786	yes	yes	yes	BE102377	Rn.50333	transformation related protein 53 binding protein 2 (predicted)
1203	1385760_at	-0.376032326	0.770553843	yes	yes	yes	BF400633	Rn.147698	Transcribed locus
1204	1378007_at	-0.375754248	0.77070238	yes	yes	yes	BE103359	Rn.173383	Transcribed locus
1205	1385889_at	-0.375736268	0.770711986	yes	yes	yes	AA893212	Rn.3412	Ac2-193
1206	1396251_at	-0.375594194	0.770787888	yes	yes	yes	BF388318	Rn.6307	Adaptor-related protein complex AP-4, sigma 1 (predicted)
1207	1391758_at	-0.375509472	0.770833153	yes	yes	yes	BE109438	---	---
1208	1382920_at	-0.37509463	0.771054835	yes	yes	no	AA875002	Rn.33512	leucine-rich repeat-containing 8
1209	1370135_at	-0.374882632	0.771168147	yes	yes	no	NM_131914	Rn.81070	caveolin 2
1210	1373701_at	-0.374865645	0.771177227	yes	yes	no	BI275605	Rn.163696	Transcribed locus
1211	1382385_at	-0.374509255	0.771367756	yes	yes	yes	BE116344	Rn.103233	proteasome (prosome, macropain) 26S subunit, ATPase, 6
1212	1378540_at	-0.374267618	0.771496963	yes	yes	yes	BI294763	---	---
1213	1397153_at	-0.373776737	0.771759511	yes	yes	yes	BE115262	Rn.7990	LMBR1 domain containing 1
1214	1383533_at	-0.373746407	0.771775736	yes	yes	yes	AI715743	---	---
1215	1385533_at	-0.373735638	0.771781497	yes	yes	yes	BE106145	Rn.150956	Transcribed locus
1216	1397705_at	-0.373716214	0.771791889	yes	yes	yes	BF542792	Rn.55111	neuroligin 2
1217	1394891_at	-0.373366759	0.771978857	yes	yes	no	BF548290	Rn.40304	Similar to hypothetical protein FLJ22965 (predicted)
1218	1370933_at	-0.373070165	0.772137579	yes	yes	no	BI275813	Rn.8737	myosin IE
1219	1376888_a_at	-0.373037624	0.772154996	yes	yes	yes	AI501092	Rn.33401	similar to Btk-PH-domain binding protein
1220	1389134_at	-0.372504635	0.772440313	yes	yes	yes	BF551369	Rn.3805	Transcribed locus
1221	1391497_at	-0.372312282	0.772543309	yes	yes	yes	AA997515	Rn.23113	TBC1D12: TBC1 domain family, member 12 (predicted)
1222	1394120_a_at	-0.371993585	0.772713986	yes	yes	yes	AI176775	Rn.227	Transcribed locus
1223	1381478_at	-0.371720877	0.772860063	yes	yes	no	BF403155	Rn.161843	Histone cell cycle regulation defective interacting protein 5 (predicted)
1224	1384571_at	-0.371657238	0.772894155	yes	yes	no	BF398835	Rn.134685	zinc finger, SWIM domain containing 5 (predicted)
1225	1390990_at	-0.371094153	0.773195876	yes	yes	yes	AI409862	Rn.168114	Transcribed locus
1226	1374328_at	-0.37103148	0.773229465	yes	yes	yes	BF403886	Rn.48	similar to hypothetical protein (predicted)
1227	1380708_at	-0.37085186	0.773325741	yes	yes	no	BF396522	---	---
1228	1394932_at	-0.370616314	0.77345201	yes	yes	no	AW534255	Rn.170066	Transcribed locus
1229	1379649_at	-0.370408653	0.773563349	yes	yes	yes	BF394502	Rn.14826	Similar to CG9996-PA
1230	1377826_at	-0.370230969	0.773658628	yes	yes	yes	AI176721	Rn.17666	Transcribed locus
1231	1382668_at	-0.370187441	0.77368197	yes	yes	yes	AI232529	Rn.148144	Transcribed locus
1232	1378458_at	-0.370029956	0.77376643	yes	yes	no	BI281745	Rn.163233	Pre-B-cell leukemia transcription factor 1 (predicted)
1233	1370881_at	-0.370029475	0.773766688	yes	yes	yes	AI411117	Rn.6360	thiosulfate sulfurtransferase

1234	1378462_at	-0.369457747	0.774073386	yes	yes	yes	BE107396	Rn.36309	Similar to Cc1-6
1235	1396071_at	-0.369242204	0.774189044	yes	yes	yes	AI502944	Rn.32103	Plastin 3 (T-isoform)
1236	1395710_at	-0.369126865	0.77425094	yes	yes	yes	BI275003	Rn.36542	similar to mesoderm induction early response 1 (MI-ER1) (predicted)
1237	1378114_at	-0.368976356	0.774331718	yes	yes	yes	BF415965	Rn.163332	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)
1238	1375993_at	-0.368951707	0.774344948	yes	yes	yes	AW531919	Rn.40817	Transcribed locus
1239	1385542_at	-0.368934051	0.774354425	yes	yes	no	BF402259	Rn.153877	Transcribed locus
1240	1394118_at	-0.368653484	0.774505031	yes	yes	no	AA894340	Rn.40326	Arginine-tRNA-protein transferase 1 (predicted)
1241	1380023_at	-0.368286671	0.774701978	yes	yes	no	AA997863	Rn.165455	Transcribed locus
1242	1375176_at	-0.368006231	0.774852584	yes	yes	no	BF409908	Rn.109178	similar to Sperm 1 POU-domain transcription factor (SPRM-1) (predicted)
1243	1382674_a_at	-0.367973021	0.774870421	yes	yes	yes	AA818193	---	---
1244	1369236_at	-0.367891397	0.774914262	yes	yes	no	NM_133312	Rn.162921	PR domain containing 4
1245	1379368_at	-0.367775419	0.77497656	yes	yes	yes	AI237606	Rn.20571	B-cell leukemia/lymphoma 6 (predicted)
1246	1382423_at	-0.367665331	0.775035699	yes	yes	yes	AW920944	Rn.20338	Transcribed locus
1247	1368259_at	-0.367564593	0.775089819	yes	yes	yes	NM_017043	Rn.44404	prostaglandin-endoperoxide synthase 1
1248	1395139_at	-0.367530886	0.775107928	yes	yes	yes	BM388214	Rn.7029	Transcribed locus
1249	1389180_at	-0.367457163	0.775147538	yes	yes	yes	AI175035	Rn.6488	Phosphorylase kinase, beta
1250	1391850_at	-0.367260466	0.775253228	yes	yes	no	BE116159	Rn.52632	Serine (or cysteine) peptidase inhibitor, clade I, member 1
1251	1389779_at	-0.367174178	0.775299598	yes	yes	yes	AA800626	Rn.137349	SH2 domain containing 4A
1252	1376104_at	-0.367003764	0.775391183	yes	yes	yes	BG381010	Rn.24141	Similar to KIAA0802 protein (predicted)
1253	1383164_at	-0.366638674	0.775587429	yes	yes	yes	AW524366	Rn.7792	Transcribed locus
1254	1382137_at	-0.366586619	0.775615415	yes	yes	yes	BG662490	Rn.64445	abhydrolase domain containing 3 (predicted)
1255	1392324_at	-0.366575208	0.77562155	yes	yes	no	AI137983	Rn.23793	EPS8-like 2 (predicted)
1256	1386064_at	-0.366497906	0.775663109	yes	yes	yes	AI501693	Rn.165284	Transcribed locus
1257	1382030_at	-0.366395334	0.775718259	yes	yes	no	BF398500	Rn.144260	general transcription factor II H, polypeptide 2 (predicted)
1258	1382289_at	-0.365887156	0.775991548	yes	yes	no	BI291954	Rn.167665	Transcribed locus
1259	1380549_at	-0.365802008	0.776037349	yes	yes	no	AI555625	Rn.92786	similar to cell division cycle and apoptosis regulator 1 (predicted)
1260	1391828_at	-0.365795072	0.776041079	yes	yes	no	AI030836	Rn.18608	Transcribed locus
1261	1382913_at	-0.365730207	0.776075972	yes	yes	no	BE114076	Rn.16244	cortactin binding protein 2
1262	1380470_x_at	-0.365660486	0.776113478	yes	yes	no	BE105961	---	---
1263	1378777_at	-0.365573103	0.776160488	yes	yes	no	BF402045	Rn.172779	Transcribed locus
1264	1384883_at	-0.365327601	0.776292578	yes	yes	no	AA858571	Rn.146209	Similar to flt3 ligand (predicted)
1265	1393237_at	-0.365314271	0.776299751	yes	yes	no	AI577833	---	---
1266	1376869_at	-0.365283095	0.776316526	yes	yes	no	BE108193	Rn.53972	Transcribed locus
1267	1375121_at	-0.365273662	0.776321602	yes	yes	no	BI301428	Rn.42472	MAD homolog 6 (Drosophila) (predicted)
1268	1397226_at	-0.365198199	0.77636221	yes	yes	no	AI100942	Rn.43956	similar to mKIAA0716 protein (predicted)
1269	1379306_at	-0.36506699	0.776432821	yes	yes	no	BE111794	Rn.107172	mitochondrial ribosomal protein L48 (predicted)
1270	1370746_at	-0.365031389	0.776451982	yes	yes	no	D10770	Rn.3502	protein kinase, cAMP dependent, catalytic, beta (predicted)
1271	1397004_at	-0.364910715	0.77651693	yes	yes	no	BF394158	Rn.90070	Nuclear receptor subfamily 3, group C, member 1
1272	1374030_at	-0.364757029	0.776599655	yes	yes	no	BE100868	---	---
1273	1380711_at	-0.364705291	0.776627506	yes	yes	no	BF403307	Rn.49741	Ubinuclein 1 (predicted)
1274	1392487_at	-0.364631714	0.776667115	yes	yes	no	BI303896	Rn.25888	Transcribed locus
1275	1380374_at	-0.364495063	0.776740683	yes	yes	no	BI282293	Rn.146589	Death effector domain-containing
1276	1387737_at	-0.36435054	0.776818498	yes	yes	no	NM_134351	Rn.41420	methionine adenosyltransferase II, alpha
1277	1375493_at	-0.364089903	0.776958851	yes	yes	no	BE104373	Rn.19850	vang-like 2 (van gogh, Drosophila) (predicted)
1278	1394530_at	-0.363965594	0.7770258	yes	yes	no	AW535733	Rn.149084	Similar to hypothetical protein FLJ20259 (predicted)
1279	1379573_at	-0.363803048	0.77711335	yes	yes	no	AA818730	---	---

1280	1378643_at	-0.363801207	0.777114342	yes	yes	no	AI600226	---	---
1281	1374490_at	-0.363791974	0.777119316	yes	yes	no	AI177845	Rn.8277	thyroid hormone receptor interactor 12
1282	1390047_at	-0.363515627	0.777268186	yes	yes	no	BG378174	Rn.4181	RIO kinase 3 (yeast) (predicted)
1283	1370540_at	-0.363480227	0.777287259	yes	yes	no	U15660	Rn.10055	nuclear receptor subfamily 1, group D, member 2
1284	1388687_at	-0.363364927	0.777349382	yes	yes	no	BI274588	Rn.24616	dehydrodolichyl diphosphate synthase
1285	1389241_at	-0.363341147	0.777362195	yes	yes	no	AA800593	Rn.164349	Transcribed locus
1286	1392761_at	-0.363130117	0.777475912	yes	yes	no	BM389886	Rn.154345	Transcribed locus
1287	1392038_at	-0.363076595	0.777504756	yes	yes	no	BF387389	---	similar to PI-3-kinase-related kinase SMG-1 isoform 2 (predicted)
1288	1384518_at	-0.363047048	0.777520679	yes	yes	no	BE107536	Rn.117647	similar to PHD finger protein 14 isoform 1 (predicted)
1289	1385739_at	-0.362999162	0.777546487	yes	yes	no	BE120816	Rn.53919	Transcribed locus
1290	1395303_at	-0.362939988	0.77757838	yes	yes	no	BF397734	---	---
1291	1372951_at	-0.362871218	0.777615447	yes	yes	no	BI274172	Rn.21828	Transcribed locus
1292	1383096_at	-0.362829674	0.777637839	yes	yes	no	AI235240	Rn.1423	amyloid beta (A4) precursor-like protein 2
1293	1389672_at	-0.362698399	0.777708602	yes	yes	no	BI301467	Rn.56018	similar to mKIAA0701 protein
1294	1377463_at	-0.362673258	0.777722155	yes	yes	no	BE099244	Rn.41796	Mannosidase 2, alpha 2 (predicted)
1295	1387457_at	-0.362600869	0.777761179	yes	yes	no	NM_022248	Rn.52231	dual specificity phosphatase 12
1296	1381619_at	-0.362227808	0.777962323	yes	yes	no	BE116003	Rn.122003	A kinase (PRKA) anchor protein 5
1297	1395010_at	-0.362138641	0.778010407	yes	yes	no	AI102173	Rn.169451	Transcribed locus
1298	1392537_at	-0.361916893	0.77813	yes	yes	no	BM389666	---	---
1299	1382691_at	-0.361859693	0.778160852	yes	yes	no	AI234943	---	---
1300	1376996_at	-0.36181724	0.77818375	yes	yes	no	AI556018	Rn.42983	Transcribed locus
1301	1389052_at	-0.36155757	0.778323828	yes	yes	no	BI278584	Rn.98912	tetratricopeptide repeat domain 13
1302	1378578_at	-0.361474276	0.778368766	yes	yes	no	BE117291	Rn.52813	similar to chromosome X open reading frame 23 (predicted)
1303	1387379_at	-0.361433935	0.778390531	yes	yes	no	NM_013022	Rn.88642	Rho-associated coiled-coil forming kinase 2
1304	1397220_at	-0.361069527	0.778587168	yes	yes	no	AW534601	---	---
1305	1384128_at	-0.361060557	0.778592009	yes	yes	no	BF393261	Rn.25735	glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein
1306	1378590_at	-0.360951412	0.778650915	yes	yes	no	AW527807	Rn.89151	Transcribed locus
1307	1377283_at	-0.36093247	0.778661138	yes	yes	no	BI274486	---	---
1308	1394465_at	-0.360808283	0.778728168	yes	yes	no	BG381387	---	---
1309	1381474_at	-0.360751782	0.778758666	yes	yes	no	AI010322	Rn.105030	muscleblind-like 3 (Drosophila) (predicted)
1310	1375897_at	-0.360706805	0.778782945	yes	yes	no	AI101372	Rn.24732	Transcribed locus
1311	1389276_at	-0.360320985	0.778991243	yes	yes	no	BI275119	Rn.95421	L(3)mbt-like 3 (Drosophila) (predicted)
1312	1378168_at	-0.360257706	0.779025411	yes	yes	no	BG377391	Rn.13078	hypothetical LOC287534
1313	1392133_at	-0.360213782	0.77904913	yes	yes	no	AI502069	Rn.20902	Similar to MAPK-interacting and spindle-stabilizing protein (predicted)
1314	1391927_at	-0.360150531	0.779083286	yes	yes	no	BE100100	Rn.128652	Thioredoxin domain containing 5 (predicted)
1315	1394738_at	-0.360130983	0.779093842	yes	yes	no	AW531516	Rn.47738	Transcribed locus
1316	1378269_at	-0.359906646	0.779215	yes	yes	no	AI112113	Rn.156856	Transcribed locus
1317	1379691_at	-0.359893718	0.779221982	yes	yes	no	BM389372	Rn.7210	similar to sarcoma antigen NY-SAR-27
1318	1388862_at	-0.359893112	0.77922231	yes	yes	no	AI412143	Rn.164131	Transcribed locus
1319	1390913_at	-0.359698461	0.779327451	yes	yes	no	AW435463	Rn.25454	similar to RIKEN cDNA 4930506L13 (predicted)
1320	1383953_at	-0.3595079	0.779430396	yes	yes	no	BM384968	Rn.26690	excision repair cross-complementing rodent repair deficiency, complementation group 5 (mapped)
1321	1381234_at	-0.359488307	0.779440982	yes	yes	no	BF398454	---	---
1322	1395082_at	-0.359392085	0.779492969	yes	yes	no	AI763982	Rn.165149	Transcribed locus
1323	1381919_at	-0.359384736	0.77949694	yes	yes	no	BI290986	Rn.69203	Hermansky-Pudlak syndrome 6
1324	1375870_a_at	-0.359360855	0.779509843	yes	yes	no	BF420140	Rn.98522	RNA binding motif, single stranded interacting protein 1
1325	1368262_at	-0.359337845	0.779522276	yes	yes	no	NM_021657	Rn.163214	PH domain and leucine rich repeat protein phosphatase

1326	1372040_at	-0.359117653	0.77964126	yes	yes	no	BI296029	Rn.13745	calmodulin binding transcription activator 2 (predicted)
1327	1372397_at	-0.358953701	0.779729865	yes	yes	no	BE349744	---	---
1328	1368879_a_at	-0.358844925	0.779788657	yes	yes	no	AF413212	Rn.90161	guanine nucleotide binding protein, alpha o
1329	1393321_at	-0.358725563	0.779853177	yes	yes	no	AW525577	Rn.96357	kelch domain containing 1 (predicted)
1330	1373536_at	-0.358657445	0.779889999	yes	yes	no	AW525196	---	---
1331	1386711_a_at	-0.358537983	0.77995458	yes	yes	no	BF566761	Rn.66161	DnaJ (Hsp40) homolog, subfamily C, member 11 (predicted)
1332	1380848_at	-0.35833622	0.780063665	yes	yes	no	AI102396	Rn.110970	similar to DKFZP547E1010 protein /// similar to Protein HT031 homolog
1333	1367801_at	-0.358331177	0.780066392	yes	yes	no	NM_053596	Rn.7000	endothelin converting enzyme 1
1334	1371993_at	-0.358104303	0.780189073	yes	yes	no	AI237636	Rn.158920	Copine III (predicted)
1335	1381705_at	-0.358010765	0.780239658	yes	yes	no	BE110067	Rn.13643	Pantothenate kinase 3 (predicted)
1336	1370743_a_at	-0.357922056	0.780287635	yes	yes	no	AY079189	Rn.10614	leucyl/cystinyl aminopeptidase
1337	1370415_at	-0.357564924	0.780480816	yes	yes	no	AF002251	Rn.36106	Ras association (RalGDS/AF-6) domain family 5
1338	1395255_at	-0.357545607	0.780491266	yes	yes	no	AW526964	Rn.149098	Transcribed locus
1339	1378614_at	-0.357447819	0.780544171	yes	yes	no	BI274329	Rn.11193	Huntington disease gene homolog
1340	1394025_at	-0.357406848	0.780566338	yes	yes	no	AW434781	Rn.42472	MAD homolog 6 (Drosophila) (predicted)
1341	1391841_at	-0.35720884	0.780673477	yes	yes	no	BE103537	Rn.87540	Tropomyosin 1, alpha
1342	1374692_at	-0.357086521	0.780739669	yes	yes	no	BE107598	Rn.16406	Sorting nexin 14 (predicted)
1343	1393288_at	-0.356975207	0.780799911	yes	yes	no	BF560790	Rn.3305	RAB5B, member RAS oncogene family (predicted)
1344	1395063_at	-0.356941979	0.780817894	yes	yes	no	AA851300	Rn.35669	Mitochondrial ribosomal protein L14 (predicted)
1345	1369402_at	-0.356669251	0.780965514	yes	yes	no	NM_022681	Rn.48777	activity-dependent neuroprotective protein
1346	1392699_at	-0.356573861	0.781017153	yes	yes	no	BF411888	Rn.17764	Transcribed locus
1347	1382104_at	-0.35650621	0.781053778	yes	yes	no	AI113277	---	---
1348	1386716_at	-0.356057023	0.781296998	yes	yes	no	BF562934	Rn.17067	Similar to EF-hand domain (C-terminal) containing 1
1349	1369722_a_at	-0.355866872	0.781399982	yes	yes	no	NM_022296	Rn.22727	xylosyltransferase II
1350	1369026_at	-0.355779428	0.781447345	yes	yes	no	NM_021763	Rn.162603	ADP-ribosylation factor interacting protein 1
1351	1376896_at	-0.355724322	0.781477195	yes	yes	no	AI227699	Rn.12784	Similar to RIKEN cDNA 1810074P20 (predicted)
1352	1381567_at	-0.355335172	0.781688018	yes	yes	no	BG381715	Rn.3372	hypothetical LOC294390
1353	1395388_at	-0.355286345	0.781714474	yes	yes	no	BI282029	Rn.55992	Transcribed locus
1354	1372985_at	-0.354626526	0.782072074	yes	yes	no	BG378167	Rn.43215	zinc finger protein 444 (predicted)
1355	1396171_at	-0.354489393	0.782146416	yes	yes	no	BF552272	Rn.21237	peptidylprolyl isomerase (cyclophilin)-like 4 (predicted)
1356	1390460_at	-0.3544767	0.782153297	yes	yes	no	AI407307	Rn.20348	Transcribed locus
1357	1393241_at	-0.354289019	0.782255055	yes	yes	no	BI295197	---	---
1358	1374552_at	-0.354222864	0.782290926	yes	yes	no	BF412718	Rn.24172	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
1359	1380751_at	-0.354104835	0.782354929	yes	yes	no	AI639072	Rn.6589	Annexin A3
1360	1395071_at	-0.353887825	0.78247262	yes	yes	no	AI010512	Rn.39069	Transcribed locus
1361	1376811_a_at	-0.353757718	0.782543189	yes	yes	no	BE108383	Rn.162954	cleavage and polyadenylation specific factor 6, 68kDa (predicted)
1362	1367823_at	-0.353727743	0.782559448	yes	yes	no	BF523128	Rn.10161	tissue inhibitor of metalloproteinase 2
1363	1375006_at	-0.353703751	0.782572462	yes	yes	no	BE121050	Rn.23445	Similar to RIKEN cDNA B130055L09 (predicted)
1364	1375308_at	-0.353247593	0.782819939	yes	yes	no	BM383330	Rn.27282	Transcribed locus
1365	1393168_at	-0.353205084	0.782843005	yes	yes	no	BF398450	Rn.17921	Transcribed locus, strongly similar to NP_598773.1 mbt domain containing 1 [Mus musculus]
1366	1394714_at	-0.353162085	0.782866337	yes	yes	no	BF386268	Rn.7208	ATPase, Ca++ transporting, plasma membrane 1
1367	1386145_at	-0.353035095	0.78293525	yes	yes	no	AI236118	Rn.37802	phospholipid scramblase 4
1368	1374381_at	-0.352890038	0.783013975	yes	yes	no	BI296663	Rn.79904	Transcribed locus
1369	1374028_at	-0.352795367	0.783065359	yes	yes	no	AI412665	Rn.96035	similar to CDNA sequence BC024479
1370	1381248_at	-0.352360018	0.783301693	yes	yes	no	AI763874	Rn.168678	Transcribed locus, strongly similar to XP_215477.3 PREDICTED: similar

									to RIKEN cDNA 1500031M22 [Rattus norvegicus]
1371	1384948_at	-0.352356093	0.783303824	yes	yes	no	AI113157	Rn.26926	Transcribed locus
1372	1367815_at	-0.352331273	0.7833173	yes	yes	no	NM_130746	Rn.11105	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
1373	1390804_at	-0.352214587	0.783380658	yes	yes	no	AI176434	Rn.9545	Transcribed locus
1374	1396235_at	-0.351814212	0.783598091	yes	yes	no	AI137779	Rn.96967	WD repeat domain 32 (predicted)
1375	1383212_at	-0.351754636	0.78363045	yes	yes	no	AA925526	Rn.115473	CDNA clone IMAGE:7462850
1376	1396320_at	-0.351685863	0.783667807	yes	yes	no	BF396773	Rn.48817	Cdc2-related kinase, arginine/serine-rich
1377	1377141_at	-0.351620432	0.78370335	yes	yes	no	AI103397	Rn.24906	Similar to RIKEN cDNA 1110018J18
1378	1382199_at	-0.351361071	0.783844253	yes	yes	no	BF288776	Rn.41412	Microtubule-associated protein 1 light chain 3 beta
1379	1390863_at	-0.351031241	0.784023476	yes	yes	no	BF283298	Rn.19386	solute carrier family 19 (thiamine transporter), member 2
1380	1392082_a_at	-0.350988695	0.784046598	yes	yes	no	BI290548	Rn.8175	CD7 antigen (predicted)
1381	1374645_at	-0.350698312	0.784204425	yes	yes	no	AW535233	Rn.23413	Transcribed locus
1382	1369955_at	-0.350669817	0.784219914	yes	yes	no	NM_134452	Rn.117	Procollagen, type V, alpha 1
1383	1398536_at	-0.350584397	0.784266349	yes	yes	no	BI275768	Rn.6640	zinc finger protein 655
1384	1392890_at	-0.350531761	0.784294962	yes	yes	no	BG663460	Rn.5827	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
1385	1375627_at	-0.350406407	0.784363112	yes	yes	no	BF407856	Rn.3858	similar to hypothetical protein FLJ10342 (predicted)
1386	1391042_at	-0.350144431	0.784505556	yes	yes	no	BE107750	Rn.20300	metal response element binding transcription factor 2
1387	1373884_at	-0.35013599	0.784510146	yes	yes	no	BI298657	Rn.11786	kelch-like 2, Mayven (Drosophila) (predicted)
1388	1384607_at	-0.35012584	0.784515665	yes	yes	no	BE120546	Rn.60050	Transcribed locus
1389	1382355_at	-0.349935339	0.784619264	yes	yes	no	BM386420	Rn.48592	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)
1390	1369504_at	-0.349786159	0.7847004	yes	yes	no	NM_012775	Rn.44402	transforming growth factor, beta receptor 1
1391	1392108_at	-0.349638801	0.784780554	yes	yes	no	BF390648	Rn.166608	RM2 mRNA, partial sequence
1392	1392497_at	-0.349603789	0.7847996	yes	yes	no	BE104938	Rn.167724	Transcribed locus
1393	1387626_at	-0.349524592	0.784842683	yes	yes	no	NM_024158	Rn.10058	deoxycytidine kinase
1394	1390142_at	-0.349189939	0.785024759	yes	yes	no	BE111888	Rn.17121	Transcribed locus
1395	1392491_at	-0.34913244	0.785056047	yes	yes	no	AI072533	Rn.16560	Similar to RIKEN cDNA 2410127L17
1396	1380796_at	-0.348679318	0.785302656	yes	yes	no	AW521390	---	---
1397	1395207_at	-0.348654187	0.785316336	yes	yes	no	AW527787	Rn.168333	Transcribed locus
1398	1385181_at	-0.348646422	0.785320563	yes	yes	no	AI029337	Rn.77403	Transcribed locus
1399	1390727_at	-0.348425193	0.785440997	yes	yes	no	BF398618	Rn.147897	Transcribed locus
1400	1369826_at	-0.348334849	0.785490184	yes	yes	no	NM_021702	Rn.42932	ataxin 3
1401	1393382_at	-0.348275072	0.785522731	yes	yes	no	BE096740	Rn.47432	Transcribed locus
1402	1374588_at	-0.347905092	0.785724204	yes	yes	no	BM389462	Rn.17376	sulfatase modifying factor 1 (predicted)
1403	1380070_at	-0.347888215	0.785733396	yes	yes	no	BG377244	Rn.92965	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
1404	1382735_at	-0.347699503	0.78583618	yes	yes	no	BF563278	Rn.6224	autophagy-related 12 (yeast)
1405	1368227_at	-0.347670416	0.785852024	yes	yes	no	NM_031664	Rn.10140	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2
1406	1367753_at	-0.347491769	0.785949341	yes	yes	no	NM_033021	Rn.6322	SEC31-like 1 (S. cerevisiae)
1407	1370256_at	-0.347449171	0.785972548	yes	yes	no	AA944349	Rn.6575	frizzled homolog 1 (Drosophila)
1408	1384081_at	-0.347448029	0.78597317	yes	yes	no	BG372643	Rn.143980	similar to hypothetical protein MGC16491 (predicted)
1409	1378222_at	-0.347409813	0.78599399	yes	yes	no	BF389961	Rn.165641	Transcribed locus
1410	1370051_at	-0.347203156	0.786106587	yes	yes	no	NM_031659	Rn.10039	transglutaminase 1
1411	1397669_at	-0.347169332	0.786125018	yes	yes	no	BG666098	Rn.166829	CDNA clone MGC:116179 IMAGE:7455942
1412	1383187_a_at	-0.347100767	0.786162379	yes	yes	no	AA944136	Rn.24116	Transcribed locus, weakly similar to XP_234997.2 PREDICTED: similar

									to RIKEN cDNA E430026E19 [Rattus norvegicus]
1413	1389443_at	-0.346889321	0.786277611	yes	yes	no	AI236463	---	---
1414	1378118_at	-0.346740344	0.786358808	yes	yes	no	BI285675	Rn.32303	Similar to deaminase domain containing 1
1415	1398501_at	-0.346700604	0.786380469	yes	yes	no	BE102282	Rn.140918	similar to CDNA sequence BC027309 (predicted)
1416	1391537_at	-0.3465717	0.786450735	yes	yes	no	AW251654	Rn.101908	similar to SERTA domain containing 4 (predicted)
1417	1372199_at	-0.346505405	0.786486875	yes	yes	no	AI233191	Rn.103380	PTEN induced putative kinase 1 (predicted)
1418	1377169_at	-0.346436747	0.786524305	yes	yes	no	BI273710	---	---
1419	1389318_at	-0.346402404	0.786543028	yes	yes	no	BF282986	Rn.92012	Transcribed locus
1420	1378313_at	-0.346351914	0.786570555	yes	yes	no	BI299600	Rn.65153	Similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - mouse (predicted)
1421	1372855_at	-0.345905762	0.786813839	yes	yes	no	BF287135	Rn.167460	Transcribed locus
1422	1396028_at	-0.345751432	0.786898012	yes	yes	no	BF392616	Rn.147844	Transcribed locus
1423	1372941_at	-0.34555991	0.787002481	yes	yes	no	BI273897	Rn.101752	p53 and DNA damage regulated 1
1424	1383305_at	-0.345528116	0.787019825	yes	yes	no	AW530081	---	---
1425	1371588_at	-0.345469504	0.787051801	yes	yes	no	AA686007	Rn.92564	Transcribed locus
1426	1390919_at	-0.345461686	0.787056066	yes	yes	no	AI230176	Rn.12338	Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)
1427	1387500_at	-0.345409472	0.787084551	yes	yes	no	NM_022927	Rn.48730	midline 1
1428	1383239_at	-0.345265595	0.787163049	yes	yes	no	BF406915	Rn.56971	zinc finger, CCHC domain containing 7 (predicted)
1429	1382196_at	-0.345232248	0.787181245	yes	yes	no	BI293505	Rn.163173	Similar to hypothetical protein ET (predicted)
1430	1395574_at	-0.345122935	0.787240892	yes	yes	no	BE118358	Rn.171029	Transcribed locus
1431	1384292_at	-0.345120321	0.787242318	yes	yes	no	BI291018	Rn.117974	docking protein 1
1432	1368612_at	-0.344973906	0.787322217	yes	yes	no	NM_013180	---	integrin beta 4
1433	1376223_at	-0.344855252	0.787386973	yes	yes	no	BE120464	Rn.15757	similar to Ab2-095
1434	1386535_at	-0.344780117	0.78742798	yes	yes	no	BG667163	Rn.95841	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked
1435	1390796_at	-0.344731836	0.787454333	yes	yes	no	AA998424	Rn.164414	Transcribed locus
1436	1398683_at	-0.344645864	0.78750126	yes	yes	no	BF553446	Rn.22759	similar to replication protein-binding trans-activator RBT1
1437	1380027_at	-0.344645821	0.787501283	yes	yes	no	AW523502	---	---
1438	1385401_at	-0.344539733	0.787559194	yes	yes	no	BI290381	---	---
1439	1391475_at	-0.34450864	0.787576168	yes	yes	no	AI235307	Rn.161893	heterogeneous nuclear ribonucleoprotein L-like (predicted)
1440	1376751_at	-0.34417809	0.787756637	yes	yes	no	AI044250	Rn.17283	serine/threonine kinase 19
1441	1394822_at	-0.344167206	0.78776258	yes	no	no	BI275960	---	---
1442	1393104_at	-0.344099544	0.787799527	yes	yes	no	BI292315	Rn.16239	Transcribed locus
1443	1373079_at	-0.344047135	0.787828146	yes	yes	no	BI296427	Rn.8272	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]
1444	1381624_at	-0.343955773	0.787878039	yes	yes	no	BF391717	Rn.120484	Nuclear protein in the AT region (predicted)
1445	1371958_at	-0.34386522	0.787927493	yes	yes	no	BM392148	Rn.39199	poly(A) binding protein, nuclear 1
1446	1384039_at	-0.343829539	0.78794698	yes	yes	no	BF558912	Rn.92141	similar to KIAA1078 protein (predicted)
1447	1377715_at	-0.343820078	0.787952147	yes	yes	no	BI303075	Rn.19529	Transcribed locus
1448	1397217_at	-0.343766226	0.78798156	yes	yes	no	BF408757	Rn.162247	CUG triplet repeat, RNA binding protein 2
1449	1392452_at	-0.343726916	0.788003031	yes	yes	no	AI169548	---	---
1450	1390395_at	-0.343522084	0.788114919	yes	yes	no	BF284768	Rn.3812	Transcribed locus
1451	1392705_at	-0.343297439	0.788237647	yes	yes	no	AI412070	Rn.25009	solute carrier family 9 (sodium/hydrogen exchanger), member 6 (predicted)
1452	1380097_at	-0.343232652	0.788273045	yes	no	no	BE098726	Rn.108012	Lysosomal-associated protein transmembrane 4A
1453	1392701_at	-0.342732554	0.788546341	yes	yes	no	BI285572	Rn.102187	GDP-mannose pyrophosphorylase B (predicted)
1454	1376042_at	-0.342522351	0.788661242	yes	yes	no	BF284673	Rn.160697	FYVE, RhoGEF and PH domain containing 1

1455	1387813_at	-0.342505613	0.788670391	yes	yes	no	NM_017003	Rn.93966	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
1456	1393351_at	-0.342484464	0.788681953	yes	yes	no	BE109501	Rn.16968	Transcribed locus
1457	1381859_at	-0.342301824	0.788781804	yes	yes	no	BE097018	---	---
1458	1382524_at	-0.342239294	0.788815992	yes	yes	no	AA850361	Rn.95153	Transcribed locus
1459	1367805_at	-0.34214647	0.788866747	yes	yes	no	NM_012569	Rn.5762	glutaminase
1460	1390430_at	-0.342138052	0.78887135	yes	yes	no	BF284190	---	---
1461	1373618_at	-0.342025998	0.788932624	yes	yes	no	BE113210	Rn.107553	cAMP responsive element binding protein-like 2
1462	1382140_at	-0.341971952	0.788962179	yes	yes	no	AI012247	Rn.17823	Transcribed locus, weakly similar to NP_001003141.1 protein tyrosine kinase fer [Canis familiaris]
1463	1396076_at	-0.341730527	0.789094218	yes	yes	no	AW914907	Rn.43744	Transcribed locus
1464	1375056_at	-0.34152333	0.789207554	yes	yes	no	AA943310	Rn.105660	similar to OCIA domain containing 2 (predicted)
1465	1367515_at	-0.341470639	0.789236378	yes	yes	no	BE111850	Rn.101873	CCR4-NOT transcription complex, subunit 7 (predicted)
1466	1383698_at	-0.341348612	0.789303137	yes	yes	no	BF561717	Rn.3655	pyruvate dehydrogenase E1 alpha 1
1467	1383660_at	-0.341311927	0.789323207	yes	yes	no	AI713166	Rn.14604	Transcribed locus
1468	1397119_at	-0.341275012	0.789343405	yes	yes	no	BF563062	Rn.156025	Transcribed locus
1469	1380214_at	-0.340953849	0.789519142	yes	yes	no	BE118929	Rn.146890	Transcribed locus
1470	1375047_at	-0.340926987	0.789533843	yes	yes	no	BI295760	Rn.116828	spermatogenesis associated 5 (predicted)
1471	1397091_at	-0.340824933	0.789589695	yes	yes	no	BF411156	Rn.149069	Transcribed locus
1472	1391051_at	-0.340821097	0.789591795	yes	yes	no	AA997873	Rn.12796	Transcribed locus
1473	1378414_at	-0.340705039	0.789655317	yes	yes	no	BI300992	Rn.3346	Similar to hypothetical protein (predicted)
1474	1376409_at	-0.340613124	0.789705627	yes	yes	no	AI176677	Rn.24441	Transcribed locus
1475	1393585_at	-0.340589107	0.789718774	yes	yes	no	AI145951	Rn.148225	Transcribed locus
1476	1379727_at	-0.340559902	0.789734761	yes	yes	no	AI598320	Rn.162924	RGD1562336 (predicted)
1477	1384892_at	-0.340391404	0.789827002	yes	yes	no	AI029798	Rn.146636	Transcribed locus
1478	1375096_at	-0.3402958	0.789879344	yes	yes	no	BF418337	Rn.145079	stratifin (predicted)
1479	1378898_at	-0.340214765	0.789923712	yes	yes	no	BE109293	Rn.60026	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19
1480	1386899_at	-0.340207689	0.789927586	yes	yes	no	NM_012939	Rn.1997	cathepsin H
1481	1373180_at	-0.340119271	0.789976	yes	yes	no	AI227919	Rn.17029	Transcribed locus
1482	1382633_at	-0.340026902	0.79002658	yes	yes	no	BE120748	Rn.146928	Transcribed locus
1483	1384296_at	-0.339908726	0.790091297	yes	yes	no	AI136388	Rn.144531	hypothetical LOC312654 (predicted)
1484	1376448_at	-0.339873204	0.79011075	yes	yes	no	AI575081	Rn.8557	WD repeat and FYVE domain containing 1
1485	1384285_at	-0.339818894	0.790140495	yes	yes	no	BI298096	Rn.22418	membrane-associated ring finger (C3HC4) 3
1486	1397312_at	-0.339730948	0.790188662	yes	yes	no	AI574904	Rn.32535	exportin 7
1487	1385252_at	-0.339673881	0.79021992	yes	yes	no	BI280655	Rn.144794	Tripartite motif protein 34 (predicted)
1488	1373270_at	-0.339664964	0.790224804	yes	yes	no	AI233288	Rn.19813	WD repeat domain, phosphoinositide interacting 1 (predicted)
1489	1391630_at	-0.339592069	0.790264733	yes	yes	no	BF420033	Rn.161921	T-box18 (predicted)
1490	1384005_at	-0.339566896	0.790278522	yes	yes	no	BG662895	Rn.6666	down-regulator of transcription 1
1491	1380405_at	-0.339445967	0.790344767	yes	yes	no	BF549570	---	---
1492	1397764_at	-0.339422387	0.790357685	yes	yes	no	BG379719	Rn.161259	Transcribed locus
1493	1386217_at	-0.339400936	0.790369437	yes	yes	no	AI639048	Rn.144424	similar to KIAA0423 (predicted)
1494	1392815_at	-0.339315183	0.790416417	yes	yes	no	BE114489	Rn.106446	Centaurin, delta 1 (predicted)
1495	1369342_at	-0.339258765	0.790447328	yes	yes	no	NM_052803	Rn.10554	ATPase, Cu++ transporting, alpha polypeptide
1496	1378467_at	-0.339178948	0.79049106	yes	yes	no	AA851361	Rn.6735	Transcribed locus
1497	1385498_at	-0.339157244	0.790502953	yes	yes	no	AA848859	Rn.55926	hypothetical LOC316557
1498	1384854_at	-0.339099546	0.790534568	yes	yes	no	AI072679	Rn.3327	Transcribed locus
1499	1370925_at	-0.339068195	0.790551747	yes	yes	no	BG380816	Rn.40336	similar to Potential phospholipid-transporting ATPase IIB

1500	1395748_at	-0.338948705	0.790617226	yes	yes	no	AW528866	Rn.162672	Solute carrier family 12, member 6
1501	1393428_at	-0.338811656	0.790692335	yes	yes	no	BF398638	Rn.164207	Transcribed locus
1502	1391700_at	-0.338808389	0.790694125	yes	yes	no	BI294908	Rn.21199	Transcribed locus
1503	1373670_at	-0.338752875	0.790724551	yes	yes	no	AA799569	Rn.24237	Signal transducer and activator of transcription 2
1504	1389796_at	-0.33874317	0.790729871	yes	yes	no	BI298018	Rn.50018	Transcribed locus
1505	1377701_at	-0.338673778	0.790767905	yes	yes	no	AI012404	Rn.17844	similar to RIKEN cDNA 9330177P20 (predicted)
1506	1382940_at	-0.33862692	0.790793589	yes	yes	no	BI281084	---	---
1507	1390396_at	-0.338516651	0.790854034	yes	yes	no	AI101338	Rn.22427	Transcribed locus
1508	1378456_at	-0.33841983	0.790907111	yes	yes	no	AI411921	Rn.146546	Transcribed locus
1509	1382784_at	-0.338407796	0.790913708	yes	yes	no	AI058332	Rn.62	angel homolog 2 (Drosophila) (predicted)
1510	1373184_at	-0.338388911	0.790924061	yes	yes	no	BF410842	Rn.3853	Transcribed locus
1511	1382575_at	-0.338373904	0.790932288	yes	yes	no	BE118546	Rn.25306	Transcribed locus
1512	1389692_at	-0.338318633	0.790962591	yes	yes	no	BM391905	Rn.18186	Transcribed locus
1513	1395583_at	-0.338226878	0.791012897	yes	yes	no	BG664001	Rn.92906	Transcribed locus
1514	1392063_at	-0.338162219	0.791048349	yes	yes	no	BF395773	Rn.17933	PDZ and LIM domain 5
1515	1389500_at	-0.338055857	0.791106671	yes	yes	no	BM383122	---	---
1516	1374793_at	-0.33779897	0.791247548	yes	yes	no	BE113663	Rn.12973	WD repeat domain 3 (predicted)
1517	1393396_at	-0.33775261	0.791272975	yes	yes	no	AA964966	Rn.146929	Transcribed locus
1518	1381423_at	-0.337607362	0.791352643	yes	no	no	BI278770	---	---
1519	1374982_at	-0.337458482	0.791434311	yes	yes	no	BF412002	Rn.145223	protein phosphatase 1, regulatory (inhibitor) subunit 16A (predicted)
1520	1379927_at	-0.337457857	0.791434654	yes	yes	no	AI113197	Rn.162613	Tripartite motif protein 33 (predicted)
1521	1397078_at	-0.33743597	0.791446662	yes	yes	no	AI111920	Rn.148803	Transcribed locus
1522	1384224_at	-0.337394873	0.791469207	yes	yes	no	BE120549	---	---
1523	1375475_at	-0.33720594	0.791572863	yes	yes	no	BE111304	Rn.10877	Dual specificity phosphatase 5
1524	1374159_at	-0.337195884	0.791578381	yes	yes	no	BM388029	Rn.13298	Transcribed locus
1525	1379822_at	-0.336757088	0.791819176	yes	yes	no	BI294801	---	---
1526	1393326_s_at	-0.336699449	0.791850812	yes	yes	no	BG378917	Rn.98504	GTP binding protein 6 (putative) (predicted)
1527	1389764_at	-0.336503943	0.791958126	yes	yes	no	BG377235	Rn.22845	DNA methyltransferase 1-associated protein 1 /// similar to DNMT1 associated protein-1
1528	1392406_at	-0.336229761	0.792108651	yes	yes	no	BE120827	Rn.47908	IAP promoted placental gene (predicted)
1529	1379928_at	-0.336128548	0.792164224	yes	yes	no	AW529192	Rn.3963	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)
1530	1377649_at	-0.336081204	0.79219022	yes	yes	no	BM383391	Rn.16215	Transcribed locus
1531	1383150_at	-0.336045978	0.792209563	yes	yes	no	BE114751	---	---
1532	1376615_at	-0.335923219	0.792276975	yes	yes	no	BI289650	Rn.254	TEA domain family member 3
1533	1390619_at	-0.335915706	0.792281101	yes	yes	no	AI178473	Rn.24182	Hypothetical LOC315216 (predicted)
1534	1385901_at	-0.335909859	0.792284312	yes	yes	no	BE118197	Rn.130213	Transcribed locus
1535	1376486_at	-0.335903384	0.792287868	yes	yes	no	BG381092	Rn.26881	SH3-domain GRB2-like endophilin B2
1536	1377974_at	-0.335701656	0.792398659	yes	yes	no	AI502837	Rn.72676	Integrin beta 8 (predicted)
1537	1382924_at	-0.335672319	0.792414772	yes	yes	no	AA850195	Rn.6581	pantothenate kinase 1 (predicted)
1538	1376435_at	-0.335662731	0.792420039	yes	yes	no	BI303340	Rn.143739	Lysyl oxidase-like 4 (predicted)
1539	1393471_at	-0.335385061	0.792572567	yes	no	no	AI175908	Rn.102138	Sp3 transcription factor
1540	1394734_at	-0.335233078	0.792656067	yes	yes	no	BE120590	Rn.57036	acyl-Coenzyme A binding domain containing 3
1541	1371029_at	-0.335194431	0.792677301	yes	yes	no	AW916437	Rn.127770	polycystic kidney disease 1 homolog
1542	1384772_at	-0.335055871	0.792753435	yes	yes	no	BF400907	Rn.3502	protein kinase, cAMP dependent, catalytic, beta (predicted)
1543	1384198_at	-0.335042557	0.792760751	yes	yes	no	BF288648	Rn.20175	ecto-NOXdisulfide-thiolexchanger2
1544	1375302_at	-0.334871437	0.792854787	yes	yes	no	BM384146	Rn.15836	zinc finger and BTB domain containing 4 (predicted)

1545	1378110_at	-0.334566548	0.793022361	yes	yes	no	AI412190	Rn.164440	Transcribed locus
1546	1395007_at	-0.334471561	0.793074576	yes	yes	no	BE120572	Rn.52554	Zinc finger protein 612 (predicted)
1547	1391511_at	-0.334039715	0.793312005	yes	yes	no	AA997877	Rn.147945	Transcribed locus
1548	1392789_at	-0.333874765	0.793402712	yes	yes	no	BI296353	Rn.17305	Similar to RIKEN cDNA C330005L02
1549	1389638_at	-0.333639032	0.793532363	yes	yes	no	BG380701	Rn.23025	similar to 4632419K20Rik protein
1550	1373682_at	-0.333574259	0.793567991	yes	yes	no	BI290764	Rn.15921	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (predicted)
1551	1393517_at	-0.333285501	0.793726842	yes	yes	no	BE097991	---	---
1552	1384529_at	-0.33328077	0.793729444	yes	yes	no	BE104877	---	---
1553	1379659_at	-0.33323935	0.793752233	yes	yes	no	BF284068	Rn.103861	similar to BMP-2 inducible kinase
1554	1381008_at	-0.332977836	0.793896127	yes	yes	no	BF390077	Rn.147275	Transcribed locus
1555	1377399_at	-0.332937674	0.793918228	yes	yes	no	BF400800	Rn.147320	Transcribed locus
1556	1387452_a_at	-0.332677778	0.794061263	yes	yes	no	NM_031553	Rn.90077	nuclear transcription factor-Y beta
1557	1374182_at	-0.332580551	0.794114778	yes	yes	no	AA965063	Rn.94211	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 (predicted)
1558	1384187_at	-0.332443117	0.794190431	yes	yes	no	BF551686	Rn.17309	adaptor-related protein complex 1, sigma 2 subunit (predicted)
1559	1384945_at	-0.332348843	0.794242329	yes	yes	no	AI501447	Rn.162061	forty-two-three domain containing 1
1560	1381915_at	-0.332319182	0.794258659	yes	yes	no	AI111735	Rn.166590	Transcribed locus
1561	1374904_at	-0.332247534	0.794298105	yes	yes	no	AI175048	Rn.23396	sine oculis homeobox homolog 1 (Drosophila)
1562	1392546_at	-0.332236808	0.79430401	yes	yes	no	AI145332	---	---
1563	1373430_at	-0.332223945	0.794311092	yes	yes	no	BG378867	Rn.139712	bromodomain adjacent to zinc finger domain, 2B (predicted)
1564	1394797_at	-0.331904796	0.794486827	yes	yes	no	BI276075	Rn.169991	Transcribed locus
1565	1394599_at	-0.331359024	0.794787438	yes	yes	no	AA998165	Rn.144376	similar to cDNA sequence BC022133 (predicted)
1566	1393063_at	-0.330814498	0.795087477	yes	yes	no	BF409007	Rn.153832	Transcribed locus
1567	1388933_at	-0.330768054	0.795113073	yes	yes	no	AI233748	Rn.8858	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]
1568	1378381_x_at	-0.330714735	0.79514246	yes	yes	no	BF552442	Rn.156506	Transcribed locus
1569	1397326_at	-0.329984177	0.795545209	yes	yes	no	BE119158	---	---
1570	1375962_at	-0.329822056	0.795634613	yes	yes	no	BE102925	Rn.48946	Transcribed locus
1571	1393223_a_at	-0.329781784	0.795656822	yes	yes	no	BE115227	Rn.20168	similar to RIKEN cDNA 1110008J03 (predicted)
1572	1386725_at	-0.32975023	0.795674225	yes	yes	no	BF566582	Rn.45195	similar to DNA segment, Chr 19, ERATO Doi 386, expressed (predicted)
1573	1379666_at	-0.329638912	0.795735621	yes	yes	no	BF417824	Rn.38868	Transcribed locus
1574	1390689_at	-0.329608843	0.795752207	yes	no	no	BF401605	Rn.101893	ribosomal protein S6 kinase, polypeptide 1
1575	1369723_at	-0.329510227	0.795806602	yes	yes	no	NM_022296	Rn.22727	xylosyltransferase II
1576	1391814_at	-0.329487162	0.795819325	yes	yes	no	BI293690	Rn.149216	Transcribed locus
1577	1398366_at	-0.329454839	0.795837155	yes	yes	no	BF282644	Rn.156570	RGD1565074 (predicted)
1578	1371898_at	-0.329433213	0.795849085	yes	no	no	BI287946	Rn.23969	Transcribed locus
1579	1372552_at	-0.329401141	0.795866777	yes	yes	no	AI102273	Rn.57036	acyl-Coenzyme A binding domain containing 3
1580	1397356_at	-0.329354035	0.795892764	yes	no	no	AI234957	Rn.64898	Rho GTPase activating protein 1 (predicted)
1581	1398945_at	-0.329284619	0.79593106	yes	yes	no	AA851439	Rn.114358	Transcribed locus, strongly similar to XP_508798.1 PREDICTED: similar to probable RNA helicase (EC 3.6.1.-) RCK - human [Pan troglodytes]
1582	1383475_at	-0.329204926	0.795975027	yes	yes	no	AW521250	Rn.37403	Protein phosphatase 1A, magnesium dependent, alpha isoform
1583	1395835_at	-0.329187123	0.79598485	yes	yes	no	BE113328	Rn.60559	HD domain containing 2 (predicted)
1584	1370750_a_at	-0.32912135	0.79602114	yes	yes	no	U14010	Rn.9758	interleukin 1 receptor, type I
1585	1373293_at	-0.328991053	0.796093036	yes	yes	no	BM392010	Rn.41256	large subunit GTPase 1 homolog (S. cerevisiae)
1586	1393681_at	-0.328792398	0.796202663	yes	yes	no	BF390882	Rn.126315	testis-specific serine protease-5
1587	1377258_at	-0.328768462	0.796215873	yes	yes	no	BE107204	Rn.154647	Forkhead box R1 (predicted)
1588	1370544_at	-0.328595327	0.796311431	yes	yes	no	AF335571	Rn.76362	echinoderm microtubule associated protein like 2

1589	1374676_at	-0.328559621	0.79633114	yes	yes	no	AA818911	Rn.138163	Transcribed locus
1590	1380827_at	-0.328198157	0.796530684	yes	yes	no	AA819867	Rn.16683	similar to C1orf25
1591	1372027_at	-0.328105306	0.79658195	yes	yes	no	AI009713	Rn.7760	Transcribed locus
1592	1393772_at	-0.327907525	0.796691162	yes	yes	no	AW523217	Rn.45588	Transcribed locus
1593	1376383_at	-0.327809967	0.796745038	yes	yes	no	BF403938	Rn.10961	Calcium/calmodulin-dependent protein kinase II gamma
1594	1385339_at	-0.327765569	0.796769557	yes	no	no	BI304211	Rn.153485	Transcribed locus
1595	1391239_at	-0.327621757	0.796848985	yes	yes	no	BF412928	Rn.100769	Similar to hypothetical protein FLJ22175 (predicted)
1596	1395965_at	-0.327563298	0.796881275	yes	yes	no	BI298589	Rn.95305	Retinoblastoma binding protein 6
1597	1370129_at	-0.327471482	0.796931992	yes	yes	no	NM_131904	Rn.162539	meningioma expressed antigen 5 (hyaluronidase)
1598	1384995_at	-0.327456452	0.796940294	yes	yes	no	BM389881	Rn.82335	jerky homolog (mouse) (predicted)
1599	1377069_at	-0.327430659	0.796954542	yes	yes	no	BG379055	---	---
1600	1390096_at	-0.32735517	0.796996244	yes	yes	no	BF284481	Rn.1097	SH3-domain GRB2-like B1 (endophilin)
1601	1373838_at	-0.32720495	0.797079235	yes	yes	no	AI237192	Rn.44467	fucosyltransferase 4
1602	1394589_at	-0.327141162	0.797114478	yes	yes	no	AA892134	Rn.30125	Transcribed locus
1603	1373110_at	-0.326998338	0.797193395	yes	yes	no	AI407487	Rn.1452	Transcribed locus
1604	1384485_at	-0.326834787	0.797283774	yes	yes	no	BE116371	Rn.35625	protein tyrosine phosphatase, receptor type, U
1605	1381422_at	-0.326783697	0.797312009	yes	yes	no	AA817889	Rn.33733	Similar to mKIAA1002 protein
1606	1375647_at	-0.326710494	0.797352465	yes	yes	no	BG671943	Rn.164616	Transcribed locus
1607	1379817_at	-0.326691734	0.797362834	yes	yes	no	AI227924	Rn.88554	Transcribed locus
1608	1398547_at	-0.326675283	0.797371926	yes	yes	no	BE107624	Rn.153909	Transcribed locus
1609	1375490_at	-0.326582387	0.797423271	yes	yes	no	AI236283	Rn.39281	Similar to Serologically defined colon cancer antigen 13 (predicted)
1610	1379704_at	-0.326486012	0.797476542	yes	yes	no	BM383283	Rn.105662	zinc finger protein 143
1611	1373933_at	-0.32641485	0.797515879	yes	yes	no	BF407276	Rn.23121	Rap guanine nucleotide exchange factor (GEF) 2 (predicted)
1612	1399140_at	-0.326355386	0.797548752	yes	yes	no	AA965202	---	---
1613	1397240_at	-0.32599315	0.797749028	yes	yes	no	AA926273	---	---
1614	1389187_at	-0.325838493	0.797834551	yes	yes	no	BI286421	Rn.24486	Similar to RIKEN cDNA 1700088E04
1615	1393499_at	-0.325792823	0.797859808	yes	yes	no	AA964375	Rn.165275	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide
1616	1380197_at	-0.325568842	0.797983687	yes	yes	no	BE107160	Rn.68116	Protein phosphatase 1, regulatory (inhibitor) subunit 12B (predicted)
1617	1390451_at	-0.325530262	0.798005026	yes	yes	no	BM390195	Rn.146022	WD repeat domain 41 (predicted)
1618	1372314_at	-0.325507996	0.798017342	yes	yes	no	AI179677	Rn.18138	Transcribed locus
1619	1398679_at	-0.325466556	0.798040265	yes	yes	no	AI639098	Rn.11496	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
1620	1387078_at	-0.325421453	0.798065214	yes	yes	no	NM_031002	Rn.11215	inositol polyphosphate-4-phosphatase, type 1
1621	1377681_at	-0.325372226	0.798092446	yes	yes	no	AA925313	Rn.23380	Transcribed locus
1622	1373656_at	-0.325177547	0.798200149	yes	no	no	AI713313	Rn.165665	Transcribed locus
1623	1395404_at	-0.324873357	0.798368466	yes	yes	no	BE110529	Rn.130706	Similar to Hypothetical protein 9030012M21 (predicted)
1624	1382431_at	-0.324609044	0.798514747	yes	yes	no	AI103530	Rn.3724	Transcribed locus, strongly similar to XP_520163.1 PREDICTED: similar to ATP-binding cassette transporter 1 [Pan troglodytes]
1625	1381994_at	-0.324596896	0.798521471	yes	yes	no	BM385862	Rn.1477	AE binding protein 2 (predicted)
1626	1393115_at	-0.324527614	0.798559818	yes	yes	no	BI293687	Rn.165957	Transcribed locus
1627	1383236_at	-0.32451756	0.798565383	yes	yes	no	BE118678	Rn.94652	fragile X mental retardation gene 1, autosomal homolog
1628	1393561_at	-0.324506023	0.798571769	yes	yes	no	BF396511	Rn.147877	Transcribed locus
1629	1388630_at	-0.324503051	0.798573415	yes	yes	no	BI296506	Rn.129573	Transcribed locus
1630	1385024_at	-0.324494835	0.798577962	yes	yes	no	AW535558	Rn.13248	cutC copper transporter homolog (E.coli) (predicted)
1631	1388210_at	-0.324456898	0.798598962	yes	yes	no	Y09333	Rn.37524	mitochondrial acyl-CoA thioesterase 1
1632	1384254_at	-0.324408074	0.798625989	yes	yes	no	AI717553	Rn.41363	similar to OTU domain containing 1 (predicted)
1633	1383949_at	-0.324321603	0.798673858	yes	yes	no	AI703880	Rn.41407	Transcribed locus, moderately similar to XP_415884.1 PREDICTED: similar to Thyroid hormone receptor-associated protein complex 240 kDa

									component (Trap240) (Activator-recruited cofactor 250 kDa component) (ARC250) (Thyroid hormone receptor associated prote
1634	1372274_at	-0.3242172	0.798731657	yes	yes	no	AI009727	Rn.106040	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
1635	1382634_at	-0.324197295	0.798742677	yes	yes	no	AI044343	Rn.17025	similar to cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa (predicted)
1636	1378416_at	-0.324140059	0.798774367	yes	yes	no	AA892565	Rn.14768	Transcribed locus, strongly similar to XP_868417.1 PREDICTED: similar to tetratricopeptide repeat domain 8 isoform B isoform 2 [Canis familiaris]
1637	1382540_at	-0.324113148	0.798789267	yes	yes	no	BI296328	Rn.166742	Transcribed locus
1638	1395799_at	-0.323816943	0.798953285	yes	yes	no	AI177767	Rn.37673	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)
1639	1379493_at	-0.323332029	0.799221873	yes	yes	no	AW916067	Rn.161368	Transcribed locus
1640	1381336_at	-0.323287997	0.799246265	yes	yes	no	BF408248	Rn.14788	Transcribed locus
1641	1384067_at	-0.323266444	0.799258206	yes	yes	no	BF288361	Rn.4001	FCH domain only 2 (predicted)
1642	1383835_at	-0.323173031	0.799309958	yes	yes	no	BI303704	Rn.32756	Transcribed locus
1643	1379936_at	-0.323026478	0.799391159	yes	yes	no	AA875132	Rn.87540	Tropomyosin 1, alpha
1644	1383498_at	-0.322925735	0.799446982	yes	yes	no	BG373354	Rn.43744	Transcribed locus
1645	1397714_at	-0.322798598	0.799517436	yes	yes	no	BF565706	Rn.38292	similar to RIKEN cDNA 2310035C23 (predicted)
1646	1393372_at	-0.322535786	0.799663095	yes	yes	no	BG375691	---	---
1647	1380690_at	-0.322505412	0.799679931	yes	yes	no	AW534142	Rn.168007	Transcribed locus, strongly similar to NP_075544.1 leucine zipper- and sterile alpha motif-containing kinase isoform 1 [Mus musculus]
1648	1374115_at	-0.32246912	0.799700048	yes	yes	no	BG380595	Rn.15135	Solute carrier family 27 (fatty acid transporter), member 5
1649	1377207_at	-0.322194796	0.799852123	yes	no	no	BF404972	Rn.48840	Breast cancer 1
1650	1395318_at	-0.322187945	0.799855922	yes	no	no	BF397354	Rn.133004	similar to Probable chromodomain-helicase-DNA-binding protein KIAA1416
1651	1373721_at	-0.322088249	0.799911197	yes	yes	no	BI291360	Rn.139312	zinc finger, matrin type 2 /// similar to Histidyl-tRNA synthetase-like
1652	1394689_at	-0.321955469	0.799984821	yes	yes	no	BE117217	Rn.23810	Casein kinase 1, alpha 1
1653	1380627_at	-0.321901868	0.800014544	yes	no	no	BF404531	---	---
1654	1383416_at	-0.321887576	0.800022469	yes	yes	no	AA899304	Rn.4054	Acetyl-coenzyme A acetyltransferase 1
1655	1371018_at	-0.321614957	0.800173659	yes	yes	no	BF411765	Rn.168659	cadherin EGF LAG seven-pass G-type receptor 2
1656	1372392_at	-0.321613533	0.800174449	yes	yes	no	AI599125	Rn.15997	Transcribed locus
1657	1388830_at	-0.321607097	0.800178019	yes	yes	no	BM390687	Rn.30325	Transcribed locus
1658	1373014_at	-0.321552914	0.800208072	yes	yes	no	BE111966	Rn.2058	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) (predicted)
1659	1392246_at	-0.321434619	0.800273688	yes	yes	no	AA900645	Rn.164046	Transcribed locus
1660	1391499_at	-0.321084799	0.800467759	yes	yes	no	BF551074	Rn.13180	Transcribed locus
1661	1371038_at	-0.320835219	0.800606249	yes	yes	no	X64403	---	---
1662	1386348_at	-0.320801433	0.800624998	yes	yes	no	AI410655	---	---
1663	1392134_x_at	-0.320668675	0.800698676	yes	yes	no	BE099652	---	---
1664	1373880_at	-0.320576862	0.800749634	yes	yes	no	AI408513	Rn.16384	Transcribed locus, strongly similar to XP_344704.2 PREDICTED: similar to mKIAA1632 protein [Rattus norvegicus]
1665	1393707_at	-0.320563165	0.800757236	yes	yes	no	AW527957	Rn.44267	Bcl2-like 2
1666	1395794_at	-0.320396864	0.800849546	yes	no	no	BF395218	Rn.87540	tropomyosin 1, alpha
1667	1375885_at	-0.320353736	0.800873486	yes	no	no	AA925482	Rn.18311	myotubularin related protein 1 (predicted)
1668	1377877_at	-0.320349901	0.800875615	yes	yes	no	BF397870	---	---
1669	1395931_at	-0.320223287	0.800945905	yes	no	no	BF408949	Rn.154125	Transcribed locus
1670	1384602_at	-0.320173641	0.800973468	yes	no	no	AA943768	Rn.44529	G protein-coupled receptor 107 (predicted)
1671	1384446_at	-0.32002767	0.801054514	yes	yes	no	BF402271	Rn.146345	Transcribed locus
1672	1375450_at	-0.320024664	0.801056183	yes	yes	no	BF403864	Rn.135119	similar to serologically defined colon cancer antigen 1 isoform a

									(predicted)
1673	1374062_x_at	-0.319838877	0.801159348	yes	no	no	AA946204	Rn.154513	microtubule-associated protein, RP/EB family, member 3
1674	1376796_at	-0.319774022	0.801195364	yes	yes	no	BG372452	Rn.6008	RAB14, member RAS oncogene family
1675	1377004_at	-0.31977264	0.801196131	yes	no	no	AA800184	Rn.6294	Transcribed locus
1676	1371123_x_at	-0.319763055	0.801201455	yes	yes	no	AJ243973	---	RT1 class Ib, locus S3
1677	1396195_at	-0.319743419	0.801212359	yes	yes	no	BF550130	Rn.3722	ankyrin repeat domain 13
1678	1372926_at	-0.319698877	0.801237096	yes	yes	no	AI009159	Rn.119634	Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)
1679	1368169_at	-0.319696177	0.801238596	yes	yes	no	NM_053460	Rn.24750	protein interacting with C kinase 1
1680	1397709_at	-0.319374322	0.801417366	yes	yes	no	BG672259	---	similar to PI-3-kinase-related kinase SMG-1 isoform 2 (predicted)
1681	1390010_at	-0.319195328	0.801516804	yes	yes	no	AI454081	Rn.162849	nuclear receptor coactivator 1 (predicted)
1682	1372651_at	-0.319005692	0.801622167	yes	yes	no	AI144726	Rn.97686	CDW92 antigen
1683	1369783_a_at	-0.318878507	0.801692839	yes	yes	no	U02319	Rn.37438	neuregulin 1
1684	1367862_at	-0.318841649	0.801713321	yes	no	no	NM_053338	Rn.11189	Ras-related associated with diabetes
1685	1395994_at	-0.318658791	0.801814943	yes	yes	no	BE116471	Rn.115701	Transcribed locus, moderately similar to XP_578397.1 PREDICTED: similar to sentrin 17 [Rattus norvegicus]
1686	1372883_at	-0.318476862	0.801916061	yes	yes	no	BE109061	Rn.33056	centromere autoantigen B (predicted)
1687	1384381_at	-0.318453817	0.80192887	yes	yes	no	BF284523	Rn.148916	ATP-binding cassette, sub-family A (ABC1), member 1 /// hypothetical gene supported by NM_178095
1688	1376524_at	-0.318360637	0.801980666	yes	yes	no	BG378747	Rn.8478	hypothetical protein Dd25
1689	1385634_at	-0.318278638	0.80202625	yes	yes	no	AA817959	---	---
1690	1387406_at	-0.317993028	0.802185043	yes	yes	no	NM_017293	Rn.89229	U2AF homology motif (UHM) kinase 1
1691	1377180_at	-0.317969056	0.802198372	yes	yes	no	BF394102	Rn.52408	Transcribed locus, moderately similar to NP_998724.1 superkiller viralicidic activity 2-like [Rattus norvegicus]
1692	1377224_at	-0.317944055	0.802212274	yes	yes	no	BM391851	Rn.40190	Transcribed locus
1693	1383676_at	-0.317922056	0.802224507	yes	yes	no	AA996595	Rn.12338	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)
1694	1367542_at	-0.317855941	0.802261272	yes	yes	no	AI411793	Rn.6789	similar to RIKEN cDNA 5330440M15 /// similar to hypothetical protein SP192 (predicted) /// similar to 5330440M15Rik protein /// similar to 5330440M15Rik protein (predicted) /// similar to 5330440M15Rik protein /// similar to 5330440M15Rik protein (predict
1695	1368567_at	-0.317754339	0.802317773	yes	yes	no	NM_022607	Rn.6452	NADH dehydrogenase (ubiquinone) flavoprotein 3-like
1696	1381100_at	-0.317703437	0.802346081	yes	no	no	BE108751	Rn.129752	Rho guanine nucleotide exchange factor (GEF) 12
1697	1374326_at	-0.317394359	0.802517992	yes	yes	no	AI178019	Rn.144881	peter pan homolog (Drosophila)
1698	1395261_at	-0.317352765	0.802541129	yes	yes	no	BE097054	Rn.107060	U1 small nuclear ribonucleoprotein polypeptide A (predicted)
1699	1389405_at	-0.317347513	0.80254405	yes	yes	no	BG378880	Rn.165698	Transcribed locus
1700	1383593_at	-0.317292253	0.802574791	yes	yes	no	BE113211	Rn.107945	Transcribed locus
1701	1395289_at	-0.317207849	0.802621747	yes	yes	no	H33428	Rn.61419	similar to RIKEN cDNA 2310075A12
1702	1395821_at	-0.31713435	0.802662638	yes	yes	no	BF524120	Rn.7308	core binding factor beta
1703	1371675_at	-0.316831442	0.802831182	yes	yes	no	AA893193	Rn.1779	Transcribed locus
1704	1367527_at	-0.316655349	0.80292918	yes	yes	no	AI600258	---	---
1705	1399008_at	-0.316615853	0.802951162	yes	yes	no	AW434064	Rn.8442	similar to ankyrin repeat domain protein 17 isoform b (predicted)
1706	1396167_at	-0.316570315	0.802976508	yes	yes	no	BF555852	Rn.103296	acid phosphatase 6, lysophosphatidic
1707	1393922_at	-0.316432942	0.80305297	yes	yes	no	BF567535	Rn.162071	similar to CDNA sequence BC020077 (predicted)
1708	1376325_at	-0.316430609	0.803054269	yes	yes	no	BM388975	Rn.96240	Nuclear factor related to kappa B binding protein (predicted)
1709	1385933_at	-0.316346386	0.803101152	yes	yes	no	AI709424	Rn.19220	Transcribed locus
1710	1391732_at	-0.316334527	0.803107753	yes	yes	no	BI278779	Rn.148385	Transcribed locus
1711	1383337_at	-0.316318915	0.803116444	yes	yes	no	AA963875	Rn.44725	Similar to genetic suppressor element 1 (predicted)
1712	1385168_at	-0.31628938	0.803132886	yes	yes	no	BM387883	Rn.82110	similar to receptor-interacting factor 1

1713	1390391_at	-0.316220274	0.803171357	yes	yes	no	BF283381	Rn.25327	Transcribed locus
1714	1391670_at	-0.316108179	0.803233765	yes	yes	no	BI295819	Rn.38378	Transcribed locus
1715	1372826_at	-0.31610276	0.803236782	yes	yes	no	BI285718	---	---
1716	1371804_at	-0.316053223	0.803264363	yes	yes	no	AI172266	Rn.76647	cytidine and dCMP deaminase domain containing 1
1717	1376007_at	-0.31598556	0.803302037	yes	yes	no	AI411772	Rn.19429	Tp53rk binding protein
1718	1398557_at	-0.315975427	0.803307679	yes	yes	no	BF389362	Rn.16562	Similar to phosphoseryl-tRNA kinase (predicted)
1719	1378972_at	-0.31589547	0.803352201	yes	yes	no	AI071547	Rn.101912	Similar to KIAA0869 protein (predicted)
1720	1382099_at	-0.31585133	0.803376781	yes	yes	no	BI289595	Rn.3673	vacuolar protein sorting 26 (yeast)
1721	1381253_at	-0.315821769	0.803393242	yes	yes	no	BF398826	Rn.11523	Solute carrier family 12, member 2
1722	1378058_at	-0.315783802	0.803414385	yes	yes	no	AI137429	Rn.98476	Spermatid perinuclear RNA binding protein
1723	1393718_at	-0.315769448	0.803422379	yes	no	no	BE117189	Rn.21735	Similar to DKFZP564P1916 protein (predicted)
1724	1391916_at	-0.315711853	0.803454453	yes	no	no	BE116043	Rn.146945	Transcribed locus
1725	1377485_at	-0.315608854	0.803511817	yes	no	no	AI144646	---	gap junction protein, alpha 12, 47kDa (predicted)
1726	1374935_at	-0.315552547	0.803543177	yes	yes	no	AI412099	Rn.17648	Transcribed locus
1727	1381685_a_at	-0.315530749	0.803555319	yes	yes	no	BI276419	Rn.12453	Transcribed locus
1728	1383336_at	-0.315409626	0.803622785	yes	yes	no	BF549763	Rn.38987	similar to pinin
1729	1372563_at	-0.315267309	0.803702064	yes	yes	no	AA799488	---	similar to D330021B20 protein
1730	1392605_at	-0.315245261	0.803714346	yes	yes	no	AI071973	Rn.166493	Transcribed locus
1731	1376001_at	-0.315223671	0.803726374	yes	yes	no	BG380440	Rn.11499	polymerase (RNA) I associated factor 1 (predicted)
1732	1392192_at	-0.315168646	0.803757029	yes	no	no	BF413231	Rn.153421	Transcribed locus
1733	1379265_at	-0.315071331	0.803811247	yes	yes	no	BF398764	Rn.7380	Transcribed locus
1734	1379343_at	-0.31507047	0.803811727	yes	yes	no	BF404452	Rn.129346	similar to hypothetical protein FLJ22555
1735	1396511_at	-0.314887814	0.803913502	yes	no	no	AI763815	Rn.41386	RAD9 homolog B (S. cerevisiae)
1736	1370099_at	-0.314835447	0.803942683	yes	yes	no	NM_022272	Rn.18281	F-box and leucine-rich repeat protein 20
1737	1395372_at	-0.314831655	0.803944796	yes	yes	no	BG668993	Rn.72676	Integrin beta 8 (predicted)
1738	1373865_at	-0.314755179	0.803987413	yes	yes	no	BF281248	Rn.11022	synaptosomal-associated protein, 91kDa homolog (mouse)
1739	1374151_at	-0.314750507	0.803990017	yes	yes	no	BI289940	Rn.162432	Transmembrane 6 superfamily member 1 (predicted)
1740	1390067_at	-0.314748019	0.803991403	yes	yes	no	BF403821	Rn.2641	Myosin phosphatase-Rho interacting protein
1741	1386550_at	-0.314527976	0.804114039	yes	yes	no	BF563739	Rn.47535	Zinc finger protein, subfamily 1A, 5 (predicted)
1742	1372360_at	-0.314524791	0.804115815	yes	yes	no	AA817862	---	---
1743	1394388_at	-0.314521234	0.804117797	yes	yes	no	AA858844	Rn.34289	CDNA clone MGC:105701 IMAGE:7309421
1744	1382584_at	-0.314437928	0.804164231	yes	yes	no	BE116720	---	similar to mKIAA1321 protein (predicted)
1745	1392973_at	-0.314398875	0.804185999	yes	yes	no	AI073173	Rn.162418	RGD1566412 (predicted)
1746	1388036_a_at	-0.314336262	0.804220902	yes	no	no	U83231	Rn.58	afadin
1747	1398660_at	-0.31432378	0.80422786	yes	yes	no	BE102693	Rn.109807	Solute carrier family 35, member F2 (predicted)
1748	1386454_at	-0.314298303	0.804242063	yes	yes	no	AI639159	Rn.44148	solute carrier family 23 (nucleobase transporters), member 3 (predicted)
1749	1376139_at	-0.314272374	0.804256517	yes	yes	no	BI295513	Rn.21101	Plexin A3 (mapped)
1750	1390943_at	-0.314234954	0.804277377	yes	yes	no	BE096504	Rn.3870	similar to chromosome 1 open reading frame 63
1751	1393074_at	-0.314131959	0.804334797	yes	no	no	BF406819	Rn.9381	Similar to hypothetical protein FLJ38984 (predicted)
1752	1379554_at	-0.314094145	0.80435588	yes	yes	no	AW141639	Rn.41990	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)
1753	1397349_at	-0.314089651	0.804358385	yes	yes	no	BF394199	Rn.55611	UBX domain containing 6 (predicted)
1754	1383888_at	-0.313978081	0.804420593	yes	yes	no	AA998264	---	---
1755	1378705_at	-0.313977389	0.804420978	yes	yes	no	AW254450	Rn.49964	similar to mKIAA1757 protein (predicted)
1756	1382759_at	-0.313842286	0.804496313	yes	yes	no	AI454681	Rn.132931	Transcribed locus
1757	1379401_a_at	-0.313535951	0.804667154	yes	yes	no	AW918372	Rn.162867	F-box only protein 33 (predicted)
1758	1376194_at	-0.313526146	0.804672623	yes	yes	no	BM384889	Rn.25063	Transcribed locus

1759	1372176_at	-0.313511529	0.804680776	yes	yes	no	BF415343	Rn.86669	protein kinase C, alpha
1760	1370710_at	-0.313467662	0.804705243	yes	yes	no	L78306	Rn.10768	acetylserotonin O-methyltransferase
1761	1373506_at	-0.313327358	0.804783506	yes	yes	no	AA944568	---	---
1762	1369089_at	-0.313317543	0.804788981	yes	yes	no	NM_012628	Rn.9747	protein kinase C, gamma
1763	1389452_at	-0.313256764	0.804822886	yes	yes	no	AW528458	Rn.17261	zinc finger, DHHC domain containing 8
1764	1388685_at	-0.312975376	0.804979877	yes	yes	no	AI011749	Rn.6726	DiGeorge syndrome critical region gene 2
1765	1395343_at	-0.312702037	0.805132406	yes	yes	no	BF545305	Rn.17150	similar to transmembrane protein TM9SF3 (predicted)
1766	1379580_at	-0.312419438	0.805290133	yes	yes	no	BF398050	Rn.43055	chromodomain helicase DNA binding protein 6 (predicted)
1767	1384797_at	-0.312395434	0.805303532	yes	yes	no	BF404325	Rn.162491	similar to RIKEN cDNA 5730596K20 (predicted)
1768	1389774_at	-0.312130675	0.805451333	yes	yes	no	AI008371	Rn.6474	Transcribed locus
1769	1374516_at	-0.312071967	0.80548411	yes	yes	no	AI008492	Rn.3278	similar to RIKEN cDNA 5830457O10 (predicted)
1770	1389683_at	-0.311593884	0.805751077	yes	yes	no	AI170768	---	---
1771	1392329_at	-0.311114516	0.80601885	yes	no	no	BI295531	Rn.52743	homeodomain leucine zipper-encoding gene
1772	1395085_at	-0.311056843	0.806051072	yes	yes	no	BF386354	Rn.169795	Transcribed locus
1773	1394259_at	-0.311021858	0.806070619	yes	yes	no	AW920342	Rn.144007	Claudin 15 (predicted)
1774	1383280_at	-0.310968221	0.806100588	yes	yes	no	BG669130	Rn.107945	Transcribed locus
1775	1389212_at	-0.3109473	0.806112277	yes	yes	no	BI296278	Rn.11805	Casein kinase 1, epsilon
1776	1375067_at	-0.310900569	0.806138389	yes	yes	no	AI555354	Rn.167869	Transcribed locus
1777	1394833_at	-0.310754298	0.806220125	yes	yes	no	BE120930	---	---
1778	1387196_at	-0.310697843	0.806251675	yes	no	no	NM_022249	Rn.54682	KH domain containing, RNA binding, signal transduction associated 3
1779	1389545_at	-0.310674425	0.806264762	yes	yes	no	BF281994	Rn.17825	CDNA clone IMAGE:7307013
1780	1395353_at	-0.310473746	0.806376921	yes	no	no	AW144304	Rn.154631	similar to KIAA0368 (predicted)
1781	1383437_at	-0.310400738	0.806417729	yes	yes	no	AI547691	---	---
1782	1378806_at	-0.310230566	0.806512855	yes	no	no	BF392451	Rn.113514	Similar to nemo like kinase (predicted)
1783	1397977_at	-0.310172442	0.806545349	yes	no	no	AI548601	Rn.162275	Vesicle-associated membrane protein, associated protein a
1784	1379511_at	-0.310000389	0.806641542	yes	yes	no	AA875275	Rn.35732	Transcribed locus
1785	1384368_at	-0.309994826	0.806644652	yes	yes	no	AA900084	Rn.21448	DNA2 DNA replication helicase 2-like (yeast) (predicted)
1786	1375914_at	-0.309969557	0.806658781	yes	yes	no	BI285504	Rn.6775	multiple endocrine neoplasia 1
1787	1395552_s_at	-0.309945917	0.806671999	yes	yes	no	BG671371	Rn.100818	Transcribed locus
1788	1392743_at	-0.3097567	0.806777805	yes	yes	no	BI278157	Rn.77753	myc induced nuclear antigen
1789	1398596_at	-0.309736234	0.80678925	yes	yes	no	AA925896	Rn.3832	Transcribed locus
1790	1385066_a_at	-0.309730565	0.80679242	yes	yes	no	BM390527	Rn.95126	Similar to hypothetical protein FLJ13089
1791	1389919_at	-0.309722911	0.8067967	yes	yes	no	BI296756	Rn.16709	parvin, beta (predicted)
1792	1373528_at	-0.309662758	0.806830341	yes	no	no	AI407827	---	---
1793	1374024_at	-0.309619214	0.806854693	yes	yes	no	AA893640	---	---
1794	1383403_at	-0.309350619	0.807004924	yes	yes	no	AW523626	---	---
1795	1394041_at	-0.309148698	0.807117881	yes	yes	no	BI293870	Rn.11853	CDNA clone IMAGE:7131734
1796	1397644_at	-0.309022105	0.807188707	yes	yes	no	BI278369	---	---
1797	1379969_at	-0.308933831	0.807238098	yes	yes	no	AW529033	Rn.63642	Similar to fork head transcription factor Fhx (predicted)
1798	1383408_at	-0.308886573	0.80726454	yes	yes	no	BI276349	Rn.1854	Transcribed locus
1799	1368249_at	-0.3086884	0.807375437	yes	yes	no	NM_053536	Rn.22556	Kruppel-like factor 15
1800	1395327_at	-0.308618705	0.807414441	yes	yes	no	AW522341	Rn.163645	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
1801	1389232_at	-0.308516224	0.807471797	yes	yes	no	BI296464	Rn.162060	WD repeat domain 5B
1802	1383571_at	-0.308514886	0.807472546	yes	yes	no	BF411217	Rn.17949	hypothetical protein LOC303515
1803	1384816_at	-0.308451671	0.807507928	yes	yes	no	AI137518	Rn.113837	coxsackie virus and adenovirus receptor
1804	1379389_at	-0.308298126	0.807593875	yes	no	no	AI409738	Rn.11283	Neural cell adhesion molecule 1

1805	1375693_at	-0.308204512	0.80764628	yes	no	no	AI029772	---	---
1806	1391173_at	-0.308133383	0.8076861	yes	yes	no	BF389308	Rn.147729	Transcribed locus
1807	1378633_at	-0.308066477	0.807723558	yes	yes	no	BE106297	Rn.29200	leupaxin
1808	1375536_at	-0.307791315	0.807877628	yes	yes	no	BI287975	Rn.102078	Numb gene homolog (Drosophila)
1809	1378303_at	-0.30777964	0.807884166	yes	no	no	BE109416	Rn.147785	Transcribed locus
1810	1380890_at	-0.307380735	0.808107577	yes	yes	no	BE118102	---	---
1811	1396531_at	-0.307359939	0.808119226	yes	no	no	BF416287	Rn.98601	Transmembrane 9 superfamily protein member 4
1812	1389008_at	-0.307223462	0.808195676	yes	yes	no	AI409218	Rn.7582	Sprouty-related, EVH1 domain containing 2
1813	1371569_at	-0.307221536	0.808196755	yes	no	no	BI294976	Rn.22097	Transcribed locus
1814	1398225_at	-0.307146365	0.808238867	yes	no	no	BF413591	Rn.43055	chromodomain helicase DNA binding protein 6 (predicted)
1815	1376744_at	-0.307081536	0.808275187	yes	yes	no	BI289572	Rn.174769	Transcribed locus
1816	1382711_at	-0.306844997	0.80840772	yes	yes	no	AI030337	Rn.113295	zinc finger protein 36 (KOX 18)
1817	1392148_at	-0.306819557	0.808421975	yes	yes	no	BF391605	Rn.34800	Similar to mKIAA1107 protein (predicted)
1818	1389229_at	-0.306772415	0.808448392	yes	yes	no	AI113146	Rn.9589	acid phosphatase-like 2
1819	1383998_at	-0.306696695	0.808490824	yes	yes	no	BF545601	Rn.168765	Transcribed locus
1820	1392170_at	-0.306643069	0.808520877	yes	yes	no	BE121336	Rn.54470	RWD domain containing 3
1821	1393008_at	-0.306587192	0.808552192	yes	yes	no	BI290317	Rn.112577	CAMP-regulated phosphoprotein 19
1822	1398620_at	-0.306545198	0.808575728	yes	yes	no	BF397903	Rn.32662	Transcribed locus
1823	1367538_at	-0.306485506	0.808609184	yes	yes	no	BF284303	---	---
1824	1383772_at	-0.306391613	0.808661811	yes	yes	no	AA996760	Rn.165369	Transcribed locus
1825	1367975_at	-0.306363059	0.808677816	yes	yes	no	BF283732	Rn.6589	annexin A3
1826	1372371_at	-0.306241765	0.808745809	yes	yes	no	BI303031	Rn.164504	Transcribed locus
1827	1397071_at	-0.306205709	0.808766021	yes	yes	no	BF404434	Rn.24283	similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (predicted)
1828	1394948_at	-0.306204423	0.808766742	yes	yes	no	BI303527	Rn.4302	Transcribed locus
1829	1392123_at	-0.306160996	0.808791087	yes	no	no	BE114497	Rn.75037	SplA/ryanodine receptor domain and SOCS box containing 1 (predicted)
1830	1397767_at	-0.306136561	0.808804786	yes	yes	no	BG377356	Rn.41665	Transcribed locus
1831	1387039_at	-0.30599719	0.808882924	yes	no	no	NM_030828	Rn.7044	glypican 1
1832	1396645_at	-0.305949684	0.80890956	yes	yes	no	BE109893	Rn.171598	Transcribed locus
1833	1394778_at	-0.305946034	0.808911606	yes	yes	no	BE116111	Rn.9909	Nuclear factor I/B
1834	1392847_at	-0.305748527	0.809022355	yes	yes	no	BE118227	Rn.52970	Casitas B-lineage lymphoma-like 1 (predicted)
1835	1367996_a_at	-0.30560086	0.809105167	yes	yes	no	AF111099	Rn.10776	latrophilin 1
1836	1382907_at	-0.305476215	0.809175074	yes	yes	no	BI289723	Rn.162620	similar to 4930431B09Rik protein
1837	1390246_at	-0.305284288	0.809282729	yes	no	no	AI100769	Rn.22416	Transcribed locus
1838	1372700_at	-0.305233872	0.80931101	yes	yes	no	BI297236	Rn.48267	Transformation related protein 53 inducible nuclear protein 1
1839	1390429_at	-0.30512257	0.80937345	yes	yes	no	BF398114	Rn.165598	Transcribed locus, strongly similar to XP_862455.1 PREDICTED: similar to Axin 2 (Axis inhibition protein 2) (Conductin) (Axin-like protein) (Axil) isoform 2 [Canis familiaris]
1840	1387821_at	-0.30502294	0.809429346	yes	yes	no	NM_017313	Rn.31889	RAB3A interacting protein
1841	1378392_at	-0.305017827	0.809432215	yes	yes	no	BG377107	Rn.106362	DnaJ (Hsp40) homolog, subfamily A, member 3
1842	1397587_at	-0.304967686	0.809460347	yes	yes	no	BI300820	Rn.66254	Glucose 6 phosphatase, catalytic, 3
1843	1378246_at	-0.304944961	0.809473098	yes	yes	no	AW535196	Rn.7549	Transcribed locus
1844	1374299_at	-0.304929719	0.80948165	yes	yes	no	BF398414	Rn.107359	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (predicted)
1845	1382005_at	-0.304864378	0.809518312	yes	yes	no	BI280285	Rn.51103	Transcribed locus, weakly similar to NP_598738.1 transferrin [Mus musculus]
1846	1382487_at	-0.304844768	0.809529316	yes	no	no	AI500925	---	---
1847	1380011_at	-0.304798655	0.809555191	yes	yes	no	BM383573	Rn.147426	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]

1848	1384452_at	-0.304772341	0.809569958	yes	yes	no	AA924571	Rn.56971	zinc finger, CCHC domain containing 7 (predicted)
1849	1379369_at	-0.304765738	0.809573663	yes	yes	no	AI171526	Rn.86665	Prickle-like 1 (Drosophila)
1850	1381551_at	-0.30470827	0.809605912	yes	no	no	BG378461	Rn.107927	Transcribed locus
1851	1380490_at	-0.304686954	0.809617874	yes	yes	no	AW434884	---	---
1852	1397372_at	-0.304647798	0.809639848	yes	yes	no	BI289004	Rn.24123	similar to Mob4B protein
1853	1384104_at	-0.304610396	0.809660838	yes	yes	no	BE115892	Rn.134649	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
1854	1376023_at	-0.304594582	0.809669713	yes	yes	no	BM386555	Rn.10767	Integrin, beta 7
1855	1390856_at	-0.304573512	0.809681538	yes	yes	no	BF289100	Rn.11631	Transcribed locus
1856	1394038_at	-0.304470179	0.809739534	yes	yes	no	BG371654	Rn.47911	carnitine deficiency-associated gene expressed in ventricle 1
1857	1387855_at	-0.304465831	0.809741974	yes	yes	no	BI278628	Rn.4000	guanosine diphosphate dissociation inhibitor 1
1858	1369754_a_at	-0.304430429	0.809761844	yes	yes	no	NM_053295	Rn.17481	calpastatin
1859	1398663_at	-0.304372362	0.809794437	yes	yes	no	AI030120	Rn.122263	similar to zinc finger protein 61
1860	1385566_at	-0.304262845	0.809855913	yes	no	no	AI072144	Rn.162811	A kinase (PRKA) anchor protein 2
1861	1386817_at	-0.304245558	0.809865616	yes	yes	no	H32518	---	---
1862	1373117_at	-0.30421251	0.809884168	yes	yes	no	BI275765	Rn.2173	ubiquitin-like, containing PHD and RING finger domains 2 (predicted)
1863	1373092_at	-0.304205989	0.809887829	yes	yes	no	BE109587	Rn.8191	Transcribed locus
1864	1388453_at	-0.304138036	0.809925977	yes	yes	no	BI296048	Rn.106161	myeloid-associated differentiation marker
1865	1384277_at	-0.303962482	0.810024538	yes	yes	no	BM388018	Rn.177353	Transcribed locus
1866	1377674_at	-0.303787281	0.810122914	yes	yes	no	AI408930	Rn.22593	Similar to PHF21A protein (predicted)
1867	1376760_at	-0.303585361	0.810236307	yes	yes	no	BF402128	---	---
1868	1387510_at	-0.303554607	0.810253579	yes	yes	no	NM_022289	Rn.64585	sorting nexin 16
1869	1382572_at	-0.303309693	0.81039114	yes	no	no	AI577469	Rn.37924	Transcribed locus
1870	1386426_at	-0.303309054	0.810391499	yes	yes	no	AI137869	Rn.7208	ATPase, Ca++ transporting, plasma membrane 1
1871	1394774_at	-0.303069473	0.810526088	yes	yes	no	BI288920	Rn.97147	apoptotic chromatin condensation inducer 1
1872	1387507_at	-0.303064951	0.810528629	yes	no	no	NM_012968	Rn.10511	interleukin 1 receptor accessory protein
1873	1397211_at	-0.303030894	0.810547762	yes	yes	no	AA874782	Rn.63942	similar to Grb10 protein (predicted)
1874	1379485_at	-0.302963017	0.810585899	yes	no	no	BF389640	Rn.1644	eukaryotic translation initiation factor 3, subunit 10 (theta)
1875	1378937_at	-0.302897523	0.810622698	yes	no	no	BE349836	Rn.20575	Transcribed locus
1876	1393019_at	-0.302874929	0.810635393	yes	yes	no	BG372243	Rn.20287	Transcribed locus
1877	1381349_a_at	-0.302729866	0.810716906	yes	yes	no	AI231906	Rn.67473	similar to Ubr2 protein (predicted)
1878	1372463_at	-0.302645162	0.810764507	yes	yes	no	AI010084	---	---
1879	1383378_at	-0.302521797	0.810833838	yes	yes	no	BI298932	Rn.14926	Transcribed locus
1880	1374745_at	-0.302512985	0.810838791	yes	yes	no	BM391278	Rn.154619	Similar to sorting nexin 21 isoform a; sorting nexin L; sorting nexin 21 (predicted)
1881	1371538_at	-0.302503462	0.810844143	yes	yes	no	BF407786	Rn.168347	Transcribed locus
1882	1385859_at	-0.302487273	0.810853242	yes	yes	no	AI059371	Rn.17175	Glutaredoxin 2 (thioltransferase)
1883	1386069_at	-0.302469348	0.810863317	yes	no	no	BF549554	Rn.166268	Transcribed locus
1884	1380859_at	-0.302435513	0.810882334	yes	yes	no	AA891931	Rn.11518	Transcribed locus
1885	1378169_at	-0.302391265	0.810907204	yes	yes	no	BI295569	---	similar to peroxisomal long chain acyl-CoA thioesterase Ia (predicted)
1886	1395140_at	-0.30229687	0.810960263	yes	no	no	AW526814	Rn.11020	Retinoblastoma-like 2
1887	1393459_at	-0.302193269	0.811018501	yes	yes	no	AI705393	Rn.40595	fragile X mental retardation syndrome 1 homolog
1888	1383466_at	-0.302172218	0.811030335	yes	yes	no	BG667930	Rn.164410	Transcribed locus
1889	1375799_at	-0.30191569	0.811174558	yes	yes	no	AI763826	Rn.17349	similar to chromosome 14 open reading frame 80 (predicted)
1890	1382929_at	-0.301661698	0.811317382	yes	yes	no	BF386243	Rn.92802	leukocyte receptor cluster (LRC) member 9 (predicted)
1891	1385732_at	-0.30164978	0.811324084	yes	yes	no	BE115744	Rn.52556	Transcribed locus
1892	1391293_at	-0.301497075	0.811409965	yes	no	no	AI170038	Rn.16333	Transcribed locus

1893	1396264_at	-0.30147049	0.811424917	yes	no	no	BF397752	Rn.3738	Nuclear cap binding protein subunit 2 (predicted)
1894	1380358_at	-0.301288309	0.811527389	yes	yes	no	AW529415	Rn.22572	GPI-anchored membrane protein 1
1895	1384002_at	-0.300900563	0.811745528	yes	yes	no	BG663077	Rn.23898	similar to Potential phospholipid-transporting ATPase IF (ATPase class I type 11B) (ATPase IR)
1896	1380640_at	-0.300814011	0.811794229	yes	no	no	BM389373	Rn.49823	Transcribed locus
1897	1397757_at	-0.3008044	0.811799637	yes	yes	no	AW523345	Rn.12638	Similar to zinc finger protein 560 (predicted)
1898	1393780_at	-0.300771112	0.811818368	yes	yes	no	AA924380	Rn.92641	zinc finger protein 131
1899	1393439_a_at	-0.300757414	0.811826076	yes	no	no	AI045767	Rn.81030	progressive ankylosis homolog (mouse)
1900	1381638_at	-0.300561516	0.811936319	yes	yes	no	BM386607	Rn.173568	Transcribed locus
1901	1393125_a_at	-0.300529464	0.811954357	yes	yes	no	AA955445	---	---
1902	1371775_at	-0.300525453	0.811956615	yes	yes	no	AI172057	Rn.130237	Transcribed locus
1903	1390204_at	-0.30051457	0.81196274	yes	yes	no	AI227856	---	---
1904	1377858_at	-0.300431601	0.812009437	yes	yes	no	BE120443	Rn.14971	PR domain containing 2, with ZNF domain (mapped)
1905	1391736_at	-0.300416309	0.812018044	yes	yes	no	BG376666	Rn.162025	limb region 1-like homolog (mouse)
1906	1367704_at	-0.300389156	0.812033327	yes	yes	no	NM_080583	Rn.56138	adaptor-related protein complex 2, beta 1 subunit
1907	1372658_at	-0.30038872	0.812033573	yes	yes	no	BG373779	Rn.46362	desmuslin
1908	1388312_at	-0.300362166	0.812048519	yes	yes	no	BI274487	Rn.146338	Transcribed locus, moderately similar to XP_518086.1 PREDICTED: similar to arginyl-tRNA synthetase [Pan troglodytes]
1909	1388724_at	-0.300315141	0.812074988	yes	yes	no	BF284434	Rn.14862	cell division cycle 40 homolog (yeast) (predicted)
1910	1371975_at	-0.3002285	0.812123759	yes	no	no	BG377343	Rn.162924	RGD1562336 (predicted)
1911	1392116_at	-0.300212568	0.812132727	yes	yes	no	BE102137	Rn.9125	similar to RIKEN cDNA 5730470L24
1912	1394682_at	-0.300211122	0.812133541	yes	yes	no	BF290030	Rn.160331	AF4/FMR2 family, member 4 (predicted)
1913	1384106_at	-0.300202746	0.812138257	yes	yes	no	AW141276	Rn.67810	transmembrane protein 23
1914	1397355_at	-0.300191321	0.812144688	yes	yes	no	AW916626	---	---
1915	1397838_at	-0.300157837	0.812163538	yes	yes	no	BF522792	Rn.8155	RGD1564792 (predicted)
1916	1383405_at	-0.300075868	0.812209683	yes	yes	no	AW254703	Rn.15963	Transcribed locus, strongly similar to NP_001005420.1 hypothetical protein LOC241289 [Mus musculus]
1917	1380525_at	-0.30004657	0.812226178	yes	yes	no	AA849862	Rn.79118	arylsulfatase E (chondrodysplasia punctata 1)
1918	1397878_at	-0.300027568	0.812236875	yes	no	no	BG671050	Rn.44173	similar to crystallin, zeta (quinone reductase)-like 1
1919	1372635_at	-0.299816244	0.812355859	yes	no	no	BF282163	Rn.129499	Transcribed locus
1920	1377437_at	-0.299704355	0.812418865	yes	no	no	AI013299	Rn.158250	ventricular zone expressed PH domain homolog 1 (zebrafish)
1921	1369002_at	-0.299672456	0.812436828	yes	yes	no	NM_031118	Rn.59	sterol O-acyltransferase 1
1922	1388796_at	-0.299598062	0.812478723	yes	yes	no	AI169291	Rn.8228	Golgi SNAP receptor complex member 1
1923	1384387_at	-0.29948636	0.812541633	yes	yes	no	BE110061	Rn.17517	Transcribed locus
1924	1388022_a_at	-0.299121647	0.812747069	yes	yes	no	AF132727	Rn.10830	dynamin 1-like
1925	1390929_at	-0.299076379	0.812772571	yes	yes	no	BI275447	Rn.1761	Filamin, beta (predicted)
1926	1383769_at	-0.298847946	0.812901274	yes	yes	no	BF398206	Rn.163806	Transcribed locus, strongly similar to XP_217409.3 PREDICTED: bone morphogenic protein receptor, type II (serine/threonine kinase) [Rattus norvegicus]
1927	1377657_at	-0.298731128	0.812967099	yes	yes	no	AW525218	Rn.35504	Similar to mKIAA1417 protein (predicted)
1928	1373820_at	-0.298686052	0.8129925	yes	yes	no	AI179107	Rn.108036	similar to constitutive photomorphogenic protein 1
1929	1376071_at	-0.29859007	0.813046589	yes	yes	no	BM389326	Rn.3101	Transcribed locus
1930	1395901_at	-0.298546935	0.813070899	yes	yes	no	AW532049	Rn.167407	Transcribed locus
1931	1393170_at	-0.298433802	0.813134661	yes	yes	no	BF555514	Rn.162745	similar to homeobox-containing transcription factor (predicted)
1932	1376024_at	-0.298305619	0.813206911	yes	yes	no	AW914992	Rn.106771	stromal interaction molecule 1 (predicted)
1933	1383539_at	-0.298283594	0.813219326	yes	no	no	BG665568	Rn.147967	Transcribed locus
1934	1383743_at	-0.298244091	0.813241593	yes	yes	no	BI275464	Rn.40387	similar to RP23-462P2.7 (predicted)
1935	1385690_at	-0.298239069	0.813244424	yes	yes	no	BI293631	Rn.163055	similar to Mut protein (predicted) /// similar to Mut protein (predicted)

1936	1395273_at	-0.298220097	0.813255119	yes	yes	no	BE115782	Rn.162625	S-adenosylhomocysteine hydrolase-like 1 (predicted)
1937	1389682_at	-0.298164259	0.813286596	yes	yes	no	BF284967	Rn.113823	similar to RIKEN cDNA 2510006C20
1938	1367865_at	-0.298161579	0.813288106	yes	yes	no	NM_133421	Rn.27366	limkain b1
1939	1377043_at	-0.298022621	0.813366444	yes	yes	no	BF388434	Rn.107904	Transcribed locus
1940	1378783_at	-0.297671411	0.813564475	yes	yes	no	AI144739	Rn.166837	Transcribed locus
1941	1395580_at	-0.29752339	0.813647951	yes	no	no	BF546317	Rn.11218	procollagen, type XII, alpha 1
1942	1383276_at	-0.297506537	0.813657456	yes	yes	no	BG664988	Rn.104463	LanC (bacterial lantibiotic synthetase component C)-like 2 (predicted)
1943	1395923_at	-0.297424672	0.813703628	yes	yes	no	BF416343	Rn.11589	Nipped-B homolog (Drosophila)
1944	1373936_at	-0.297214699	0.813822065	yes	yes	no	AI407107	---	---
1945	1393107_at	-0.297192406	0.81383464	yes	yes	no	BI303078	Rn.17512	Transcribed locus
1946	1392639_at	-0.296870332	0.814016345	yes	yes	no	AI177281	Rn.7217	RGD1564971 (predicted)
1947	1376492_at	-0.296807218	0.814051956	yes	yes	no	AI548527	Rn.129828	similar to chromosome 16 open reading frame 28 (predicted)
1948	1389359_at	-0.296715119	0.814103926	yes	no	no	BE120823	---	---
1949	1389256_at	-0.296638274	0.81414729	yes	yes	no	BG381256	Rn.1630	Transcribed locus
1950	1372386_at	-0.296567645	0.814187149	yes	yes	no	AW530777	Rn.9367	SUMO/sentrin specific protease 2
1951	1376595_at	-0.29645071	0.814253144	yes	yes	no	BF282695	Rn.162727	similar to peroxisome biogenesis factor 1 (predicted)
1952	1374591_at	-0.296302113	0.814337016	yes	yes	no	AI409042	Rn.164138	Transcribed locus
1953	1372814_at	-0.296225829	0.814380076	yes	yes	no	BF283084	Rn.8424	similar to RIKEN cDNA 2010005O13
1954	1382075_at	-0.296215416	0.814385954	yes	yes	no	BF386499	Rn.2864	Prostate tumor over expressed gene 1
1955	1374751_at	-0.296170072	0.814411551	yes	yes	no	BM383668	---	---
1956	1377735_at	-0.296150467	0.814422618	yes	yes	no	AI176309	Rn.19854	Pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3
1957	1373859_at	-0.29607267	0.814466536	yes	yes	no	AA819884	Rn.2285	Transcribed locus
1958	1395277_at	-0.295717541	0.814667048	yes	yes	no	BF396535	Rn.148501	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]
1959	1371748_at	-0.295577543	0.814746106	yes	yes	no	BI284306	Rn.107348	1-acylglycerol-3-phosphate O-acyltransferase 1
1960	1384371_at	-0.295469266	0.814807257	yes	yes	no	AW921429	Rn.254	TEA domain family member 3
1961	1389681_at	-0.295393245	0.814850193	yes	yes	no	BI296388	Rn.7444	Poliovirus receptor-related 2 (herpesvirus entry mediator B)
1962	1377612_at	-0.295364617	0.814866363	yes	yes	no	BI289992	Rn.12587	NMDA receptor-regulated gene 1 (predicted)
1963	1381838_at	-0.295306954	0.814898933	yes	yes	no	AI548281	Rn.17625	Basic, immunoglobulin-like variable motif containing (predicted)
1964	1383488_at	-0.295239317	0.814937138	yes	yes	no	AA817785	---	---
1965	1373962_at	-0.295194583	0.814962407	yes	yes	no	AI178556	Rn.167394	Transcribed locus
1966	1374469_at	-0.295185535	0.814967518	yes	no	no	BG372375	Rn.22305	Similar to C20orf118 (predicted)
1967	1392109_at	-0.295179248	0.81497107	yes	yes	no	BG671422	Rn.66734	Similar to hypothetical protein FLJ21439 (predicted)
1968	1378543_at	-0.295028384	0.815056296	yes	yes	no	BE108222	Rn.162746	Nuclear factor, erythroid derived 2, like 3 (predicted)
1969	1393947_at	-0.295016381	0.815063078	yes	yes	no	BG377383	Rn.163331	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
1970	1385449_s_at	-0.294976184	0.815085788	yes	yes	no	BE115334	Rn.144032	vacuolar protein sorting 37B (yeast) (predicted)
1971	1397412_at	-0.294944744	0.815103551	yes	no	no	BE107094	Rn.107173	Similar to NICE-3
1972	1385876_at	-0.294740476	0.815218968	yes	no	no	AA817826	Rn.172879	Transcribed locus
1973	1369816_at	-0.294657251	0.815265997	yes	yes	no	NM_013018	Rn.44409	RAB3A, member RAS oncogene family
1974	1375728_at	-0.294616276	0.815289152	yes	yes	no	AI511102	Rn.34634	Ectonucleoside triphosphate diphosphohydrolase 4 (predicted)
1975	1384310_at	-0.294568183	0.81531633	yes	no	no	BM383081	Rn.23945	Transcribed locus
1976	1387716_at	-0.294458095	0.815378547	yes	yes	no	NM_013070	Rn.9901	utrophin
1977	1391944_at	-0.294429455	0.815394734	yes	yes	no	BI296237	Rn.57442	similar to Hypothetical protein C6orf60 (predicted)
1978	1392997_at	-0.294269762	0.815484996	yes	yes	no	BF556742	Rn.11876	protein phosphatase 4, regulatory subunit 2 (predicted)
1979	1387818_at	-0.294186454	0.815532087	yes	no	no	NM_053736	Rn.16195	caspase 4, apoptosis-related cysteine peptidase

1980	1383616_at	-0.29416017	0.815546945	yes	yes	no	AA997562	Rn.22261	similar to class II cytokine receptor 4 (predicted)
1981	1396749_at	-0.294073319	0.815596043	yes	yes	no	BF390144	Rn.23560	calcium binding protein 1
1982	1397210_at	-0.294056717	0.815605429	yes	no	no	BF396902	Rn.105849	Similar to TCF7L2 protein
1983	1373591_at	-0.29387899	0.81570591	yes	yes	no	BG375435	Rn.73878	ADP-ribosylation factor interacting protein 2
1984	1384258_at	-0.293846779	0.815724122	yes	no	no	AW920266	Rn.55566	Hypothetical protein LOC499120
1985	1373183_at	-0.293842698	0.81572643	yes	no	no	AI229780	Rn.19806	Transcribed locus
1986	1392919_at	-0.293814309	0.815742482	yes	yes	no	BI297513	---	---
1987	1384245_at	-0.2936829	0.815816788	yes	yes	no	AA997442	Rn.12701	Transcribed locus
1988	1374134_at	-0.293676555	0.815820376	yes	yes	no	BM384057	Rn.17706	PCTAIRE-motif protein kinase 2
1989	1393285_at	-0.293661263	0.815829023	yes	yes	no	BF561264	---	---
1990	1389386_at	-0.293581849	0.815873932	yes	yes	no	AI170759	Rn.20696	similar to hypothetical protein DKFZp313N0621 (predicted)
1991	1372956_at	-0.293494992	0.815923053	yes	yes	no	BF420425	Rn.155567	Bat4 gene
1992	1397734_at	-0.293490152	0.81592579	yes	yes	no	AW524780	Rn.102138	Sp3 transcription factor
1993	1383905_at	-0.29344941	0.815948832	yes	yes	no	BF401729	Rn.4050	Zinc finger protein 216 (predicted)
1994	1374674_at	-0.293437967	0.815955304	yes	yes	no	AW528792	Rn.164207	Transcribed locus
1995	1387493_at	-0.293345909	0.816007372	yes	yes	no	NM_133515	Rn.122003	A kinase (PRKA) anchor protein 5
1996	1392575_at	-0.293271977	0.81604919	yes	yes	no	BE108929	Rn.29452	Transcribed locus
1997	1382032_at	-0.293232242	0.816071666	yes	yes	no	AI407730	Rn.164681	Transcribed locus
1998	1369177_at	-0.293096587	0.816148404	yes	yes	no	NM_053735	Rn.162533	phosphatidylinositol 4-kinase type 2 alpha
1999	1382952_at	-0.292919511	0.816248584	yes	yes	no	C06972	Rn.73705	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)
2000	1396420_at	-0.292899989	0.816259629	yes	yes	no	BF395914	Rn.163203	Bromodomain adjacent to zinc finger domain protein 1B
2001	1381836_at	-0.292737899	0.816351343	yes	no	no	BF420334	Rn.140755	similar to GTP-binding protein RAB20
2002	1393944_at	-0.292723037	0.816359753	yes	yes	no	AI764505	---	---
2003	1374327_at	-0.292717184	0.816363065	yes	yes	no	AW531530	Rn.25002	Transcribed locus
2004	1397512_at	-0.292363369	0.816563299	yes	no	no	BI281965	Rn.6409	similar to Vps41 protein (predicted)
2005	1381775_at	-0.292353697	0.816568774	yes	no	no	BF391321	Rn.34703	RGD1566102 (predicted)
2006	1378330_at	-0.292353072	0.816569127	yes	no	no	BI273834	Rn.39156	Transcribed locus
2007	1391211_at	-0.292270893	0.816615642	yes	no	no	AI144936	---	---
2008	1375212_at	-0.292266225	0.816618284	yes	no	no	AA964250	Rn.8972	ankyrin repeat domain 52 (predicted)
2009	1370711_a_at	-0.292176485	0.816669082	yes	no	no	AF000900	Rn.11099	nucleoporin like 1
2010	1395414_at	-0.29206594	0.816731661	yes	no	no	BI296064	Rn.170753	Transcribed locus
2011	1385853_at	-0.291983394	0.816778393	yes	no	no	BF560180	Rn.162865	bromodomain adjacent to zinc finger domain, 1A (predicted)
2012	1394794_at	-0.291975215	0.816783023	yes	no	no	BF390257	Rn.145937	similar to hypothetical protein DKFZp434K1421
2013	1375943_at	-0.291872414	0.816841226	yes	no	no	BI288873	Rn.19479	Transcribed locus
2014	1390555_at	-0.29184247	0.81685818	yes	no	no	AW530876	Rn.47568	similar to Suppressor of cytokine signaling 5 (predicted)
2015	1383414_at	-0.291768195	0.816900236	yes	no	no	BG373072	Rn.104374	similar to 9930012K11Rik protein (predicted)
2016	1384213_at	-0.291744696	0.816913542	yes	no	no	AA955944	---	---
2017	1372751_at	-0.291695191	0.816941574	yes	no	no	BM390320	Rn.120538	RGD1560018 (predicted)
2018	1368818_at	-0.291533616	0.817033073	yes	no	no	AW531920	Rn.163607	proteasome (prosome, macropain) activator subunit 4
2019	1383482_at	-0.291324665	0.817151415	yes	no	no	AI578183	Rn.164773	Transcribed locus
2020	1376309_at	-0.291000746	0.817334906	yes	no	no	BI296018	Rn.7798	hypothetical LOC305452 (predicted)
2021	1389833_at	-0.290888222	0.817398657	yes	no	no	BF285924	Rn.17376	Sulfatase modifying factor 1 (predicted)
2022	1386026_at	-0.290862572	0.81741319	yes	no	no	BF287062	Rn.28221	Transcribed locus
2023	1393230_s_at	-0.29059457	0.817565051	yes	no	no	AI136714	Rn.12947	Similar to KIAA0564 protein (predicted)
2024	1380001_at	-0.290526878	0.817603412	yes	no	no	AW526140	Rn.38987	similar to pinin
2025	1380006_at	-0.290524777	0.817604602	yes	no	no	AW921301	Rn.156212	Transcribed locus, weakly similar to XP_486128.1 PREDICTED:

									hypothetical protein isoform 1 [Mus musculus]
2026	1384269_at	-0.290467349	0.817637149	yes	no	no	BF386887	Rn.7074	Transcribed locus
2027	1373600_at	-0.290371497	0.817691474	yes	no	no	AI412518	Rn.14826	Similar to CG9996-PA
2028	1375453_at	-0.290323618	0.817718612	yes	no	no	BM392052	---	---
2029	1367832_at	-0.290210442	0.817782762	yes	no	no	NM_013006	Rn.3594	lysophospholipase 1
2030	1392023_at	-0.290157015	0.817813047	yes	no	no	AW434002	Rn.162132	Leucine zipper and CTNNBIP1 domain containing
2031	1395571_at	-0.290083712	0.817854601	yes	no	no	BF557189	Rn.32563	ring finger protein 3 (predicted)
2032	1392755_at	-0.289935773	0.817938472	yes	no	no	AW920702	Rn.25285	leucine rich repeat containing 8 family, member C
2033	1389652_at	-0.289867685	0.817977075	yes	no	no	AI171655	Rn.106518	Similar to 2700029M09Rik protein (predicted)
2034	1372799_at	-0.289831597	0.817997536	yes	no	no	BF285179	Rn.6770	deoxyguanosine kinase (predicted)
2035	1368225_at	-0.289652905	0.81809886	yes	no	no	NM_134414	Rn.2869	exocyst complex component 2
2036	1382508_at	-0.289648784	0.818101196	yes	no	no	AI228722	Rn.72491	G1 to S phase transition 1
2037	1389525_at	-0.28948492	0.818194123	yes	no	no	AI171788	Rn.28251	ring finger protein 149
2038	1391780_at	-0.289472816	0.818200988	yes	no	no	BG373221	Rn.143980	similar to hypothetical protein MGC16491 (predicted)
2039	1371893_at	-0.289446182	0.818216093	yes	no	no	BE111640	Rn.164706	Transcribed locus
2040	1383213_at	-0.289295373	0.818301628	yes	no	no	BF393611	Rn.123609	epidermal growth factor receptor pathway substrate 8 (predicted) /// similar to Eps8
2041	1396274_at	-0.289137653	0.818391092	yes	no	no	AI111884	Rn.147953	Transcribed locus
2042	1381157_at	-0.289104325	0.818409998	yes	no	no	BF396928	Rn.148902	Transcribed locus
2043	1396877_at	-0.289010251	0.818463366	yes	no	no	AI715187	Rn.7145	Laminin, gamma 1
2044	1389700_at	-0.289002676	0.818467664	yes	no	no	H31078	Rn.22653	Transcribed locus
2045	1374949_at	-0.288964437	0.818489357	yes	no	no	BM385443	Rn.37288	similar to Zinc finger, FYVE domain containing 19
2046	1393760_at	-0.288943647	0.818501152	yes	no	no	BE116401	Rn.167224	Transcribed locus
2047	1393687_at	-0.288914147	0.818517889	yes	no	no	BE113870	Rn.148946	Transcribed locus
2048	1374130_at	-0.288832007	0.818564493	yes	no	no	BG373550	Rn.20576	Transcribed locus
2049	1393478_at	-0.288702554	0.818637946	yes	no	no	AI029492	Rn.147293	Transcribed locus
2050	1379642_at	-0.288619413	0.818685124	yes	no	no	BM386116	Rn.177650	Transcribed locus
2051	1373095_at	-0.288537122	0.818731824	yes	no	no	AI408081	Rn.93564	similar to nitric oxide synthase (predicted)
2052	1384380_at	-0.288466325	0.818772002	yes	no	no	AI535316	Rn.56971	Zinc finger, CCHC domain containing 7 (predicted)
2053	1379032_at	-0.288433275	0.818790759	yes	no	no	BG372658	Rn.11153	Phosphorylase kinase, gamma 2 (testis)
2054	1374462_at	-0.288207871	0.818918695	yes	no	no	AA850935	Rn.163223	kinesin-associated protein 3 (predicted)
2055	1370523_a_at	-0.288086763	0.818987443	yes	no	no	AW142720	Rn.7390	ubiquitin-conjugating enzyme E2D 2
2056	1392083_at	-0.288050741	0.819007892	yes	no	no	BF415852	Rn.106323	Similar to Ext1
2057	1394733_at	-0.287866972	0.819112223	yes	no	no	AW527528	Rn.173616	Transcribed locus
2058	1389100_at	-0.287644897	0.819238319	yes	no	no	BF409831	Rn.2561	EPM2A (laforin) interacting protein 1 (predicted)
2059	1395739_at	-0.287587652	0.819270826	yes	no	no	BG672302	Rn.21009	similar to RIKEN cDNA C920006C10 (predicted)
2060	1398213_at	-0.287558295	0.819287498	yes	no	no	BE116195	Rn.52637	Transcribed locus
2061	1388916_at	-0.287312662	0.819427002	yes	no	no	BE109616	Rn.17586	Transcribed locus
2062	1377443_at	-0.287276999	0.819447258	yes	no	no	BF401187	Rn.173133	Transcribed locus
2063	1384101_at	-0.287239185	0.819468736	yes	no	no	BM388523	---	---
2064	1380232_at	-0.287114289	0.819539682	yes	no	no	BE119516	Rn.171652	Transcribed locus, weakly similar to NP_035020.2 neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]
2065	1386022_at	-0.287105043	0.819544934	yes	no	no	AW921706	Rn.156183	Transcribed locus
2066	1395020_at	-0.287040974	0.81958133	yes	no	no	BI275435	Rn.35024	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)
2067	1396001_at	-0.28678123	0.819728902	yes	no	no	BF404704	Rn.53527	Transcribed locus
2068	1377762_at	-0.28674322	0.819750499	yes	no	no	BG381701	Rn.7020	Similar to RIKEN cDNA G430041M01 (predicted)

2069	1372544_at	-0.28663491	0.819812044	yes	no	no	AI410305	Rn.153608	Transcribed locus
2070	1380633_at	-0.286483895	0.819897863	yes	no	no	BG381596	Rn.107990	RNA polymerase 1-1
2071	1397484_at	-0.286455747	0.819913859	yes	no	no	BF394767	Rn.162872	similar to Cytosolic acyl coenzyme A thioester hydrolase, inducible (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) (LACH2) (ACH2) (predicted)
2072	1382521_at	-0.286401002	0.819944973	yes	no	no	AA925755	Rn.5762	glutaminase
2073	1380165_at	-0.286273281	0.820017565	yes	no	no	AI234713	Rn.8768	Non-catalytic region of tyrosine kinase adaptor protein 1 (predicted)
2074	1377992_at	-0.286218076	0.820048944	yes	no	no	AI111775	Rn.104502	Dual specificity phosphatase 7
2075	1393048_at	-0.286096572	0.820118012	yes	no	no	BF561277	---	---
2076	1383874_at	-0.285956014	0.820197917	yes	no	no	BG670036	Rn.16708	RGD1560812 (predicted)
2077	1371559_at	-0.28587208	0.820245637	yes	no	no	AI103384	Rn.28371	Transcribed locus
2078	1385306_at	-0.28563829	0.82037857	yes	no	no	BI288042	---	---
2079	1393152_at	-0.285606545	0.820396621	yes	no	no	AI007821	---	---
2080	1395395_at	-0.285555944	0.820425396	yes	no	no	BF291053	Rn.25550	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2081	1385543_at	-0.285495543	0.820459745	yes	no	no	BF413374	Rn.173632	Transcribed locus
2082	1392480_at	-0.285485705	0.82046534	yes	no	no	BE100901	Rn.39199	poly(A) binding protein, nuclear 1
2083	1398862_at	-0.285472599	0.820472794	yes	no	no	J04024	Rn.2305	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
2084	1370919_at	-0.285467382	0.820475761	yes	no	no	AI103467	Rn.10156	heterogeneous nuclear ribonucleoprotein M
2085	1382128_at	-0.285384979	0.820522625	yes	no	no	BI289196	---	---
2086	1394318_at	-0.285281152	0.820581679	yes	no	no	AW918228	---	---
2087	1391163_at	-0.285186766	0.820635365	yes	no	no	BM385306	Rn.137048	similar to Eftud1 protein (predicted)
2088	1379801_at	-0.285131697	0.820666691	yes	no	no	AI137954	Rn.23792	Transcribed locus, strongly similar to XP_580017.1 PREDICTED: hypothetical protein XP_580017 [Rattus norvegicus]
2089	1368012_at	-0.285070152	0.820701701	yes	no	no	NM_022591	Rn.5890	telomerase associated protein 1
2090	1380818_at	-0.285062796	0.820705885	yes	no	no	BE121297	Rn.2666	Transcribed locus, strongly similar to XP_218006.3 PREDICTED: similar to KIAA1838-like protein [Rattus norvegicus]
2091	1386392_at	-0.284972549	0.820757226	yes	no	no	AI104638	Rn.9619	anaphase promoting complex subunit 10 (predicted)
2092	1376656_at	-0.284909743	0.820792957	yes	no	no	BI274796	Rn.27074	ubiquitin specific protease 20 (predicted)
2093	1394818_at	-0.2847808	0.82086632	yes	no	no	AI176867	Rn.163606	Transcribed locus
2094	1368547_at	-0.284757935	0.82087933	yes	no	no	NM_130402	Rn.22573	osteoclast inhibitory lectin
2095	1378447_at	-0.284389886	0.821088773	yes	no	no	AA849989	Rn.94023	Thyroid hormone receptor associated protein 1 (predicted)
2096	1375859_a_at	-0.284355441	0.821108377	yes	no	no	BM386823	Rn.869	Similar to zinc finger protein 565 (predicted)
2097	1384700_at	-0.284275965	0.821153612	yes	no	no	BM390472	Rn.162406	Similar to chromosome 6 open reading frame 148 (predicted)
2098	1392102_at	-0.284258572	0.821163512	yes	no	no	BE118959	Rn.34447	Transcribed locus
2099	1367976_at	-0.284248261	0.82116938	yes	no	no	NM_031137	Rn.28991	tripeptidyl peptidase II
2100	1372442_at	-0.284123612	0.821240333	yes	no	no	BG673216	Rn.3887	Transcribed locus
2101	1393295_at	-0.283969074	0.821328307	yes	no	no	BF290301	Rn.11716	similar to RIKEN cDNA 2610019F03
2102	1393807_at	-0.283902972	0.82136594	yes	no	no	BF396605	Rn.107603	Transcribed locus
2103	1384638_at	-0.283766146	0.821443842	yes	no	no	AI030545	Rn.99039	Glutaryl-Coenzyme A dehydrogenase (predicted)
2104	1381143_at	-0.283677772	0.821494162	yes	no	no	AI029836	Rn.22860	Similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)
2105	1370531_a_at	-0.2836646	0.821501662	yes	no	no	U69550	Rn.11130	phospholipase D1
2106	1380078_at	-0.283543047	0.82157088	yes	no	no	AW144384	Rn.25351	Transcribed locus
2107	1383123_at	-0.283511332	0.821588942	yes	no	no	BF559503	Rn.164625	Transcribed locus
2108	1368748_at	-0.283322087	0.82169672	yes	no	no	NM_133396	Rn.144652	testis-specific kinase 2
2109	1377806_at	-0.283254541	0.821735192	yes	no	no	BF556273	Rn.84878	vascular endothelial zinc finger 1 (predicted)
2110	1375545_at	-0.28323087	0.821748675	yes	no	no	BE111095	Rn.137551	RNA binding motif protein 9 (predicted)

2111	1373757_at	-0.28309688	0.821824998	yes	no	no	AW529298	Rn.16272	FLN29 gene product
2112	1391023_at	-0.28308852	0.82182976	yes	no	no	AI548713	Rn.146327	Transcribed locus
2113	1384073_at	-0.283063919	0.821843775	yes	no	no	BF543577	Rn.17173	alcohol dehydrogenase, iron containing, 1
2114	1393800_at	-0.282997203	0.821881781	yes	no	no	AW526472	---	RGD1565777 (predicted)
2115	1377940_at	-0.282934423	0.821917546	yes	no	no	BF398271	Rn.13078	hypothetical LOC287534
2116	1389475_at	-0.282857242	0.821961518	yes	no	no	BF398112	Rn.44429	smoothened homolog (Drosophila)
2117	1372583_at	-0.282812991	0.82198673	yes	no	no	AI009094	Rn.13877	Transcribed locus
2118	1393757_at	-0.282802728	0.821992578	yes	no	no	BE105343	Rn.113220	similar to OTTHUMP00000018227
2119	1392485_at	-0.282782662	0.82200401	yes	no	no	BI290555	Rn.7322	similar to chromosome 1 open reading frame 50 (predicted)
2120	1391739_at	-0.282674715	0.822065518	yes	no	no	BF393038	Rn.162190	RUN domain containing 1 (predicted)
2121	1380517_at	-0.282468261	0.822183166	yes	no	no	BI288315	Rn.167936	zinc finger, MYM-type 3
2122	1379346_at	-0.282403873	0.822219861	yes	no	no	BI290578	Rn.162332	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
2123	1390336_at	-0.282369527	0.822239436	yes	no	no	BF408325	Rn.2895	similar to Protein C21orf63 homolog precursor (predicted)
2124	1392579_at	-0.282339615	0.822256484	yes	no	no	BI295501	Rn.21433	similar to 5830411E10Rik protein
2125	1384237_at	-0.282324542	0.822265075	yes	no	no	BF420822	---	---
2126	1382538_at	-0.282301911	0.822277973	yes	no	no	AI555902	---	---
2127	1383274_at	-0.282292114	0.822283558	yes	no	no	AA956005	Rn.107537	poly(rC) binding protein 3
2128	1386074_at	-0.282292085	0.822283574	yes	no	no	AA850705	Rn.77753	myc induced nuclear antigen
2129	1383205_at	-0.28222266	0.822323145	yes	no	no	BI288833	Rn.100050	dapper homolog 2, antagonist of beta-catenin (xenopus) (predicted)
2130	1368085_at	-0.282178385	0.822348382	yes	no	no	NM_133595	Rn.11137	GTP cyclohydrolase I feedback regulator
2131	1396116_at	-0.282046679	0.822423458	yes	no	no	BG669152	Rn.154516	serologically defined colon cancer antigen 1
2132	1397251_at	-0.281987633	0.822457119	yes	no	no	BF389812	Rn.64258	Similar to hypothetical protein MGC32132 (predicted)
2133	1382897_at	-0.281806181	0.822560568	yes	no	no	BF393872	---	---
2134	1390273_at	-0.281795249	0.822566801	yes	no	no	BE108849	Rn.55564	Zinc finger protein 532 (predicted)
2135	1386916_at	-0.281783178	0.822573684	yes	no	no	NM_017321	Rn.35934	aconitase 1
2136	1389406_at	-0.281779633	0.822575705	yes	no	no	BI296349	---	---
2137	1393480_at	-0.281599513	0.82267841	yes	no	no	AW919998	Rn.4016	protein phosphatase 1, regulatory (inhibitor) subunit 2
2138	1378791_at	-0.281479774	0.822746692	yes	no	no	BF398201	Rn.66100	mitogen activated protein kinase kinase kinase 4 (predicted)
2139	1383910_at	-0.281397479	0.822793625	yes	no	no	BF398220	Rn.34845	Transcribed locus, strongly similar to XP_218459.3 PREDICTED: similar to zinc finger protein 574 [Rattus norvegicus]
2140	1384349_at	-0.281358452	0.822815883	yes	no	no	AI577326	Rn.103975	pogo transposable element with ZNF domain (predicted)
2141	1393180_at	-0.281343505	0.822824408	yes	no	no	AI011492	Rn.163070	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
2142	1393983_at	-0.281311627	0.82284259	yes	no	no	AA998204	Rn.161931	exportin, tRNA (nuclear export receptor for tRNAs) (predicted)
2143	1387432_at	-0.281225386	0.822891779	yes	no	no	NM_031346	Rn.162818	ROD1 regulator of differentiation 1 (S. pombe)
2144	1383715_at	-0.281194534	0.822909376	yes	no	no	BI284371	Rn.22285	similar to hypothetical protein D4Ertd89e
2145	1392619_at	-0.281151861	0.822933717	yes	no	no	BE118107	Rn.22011	Transcribed locus
2146	1375635_at	-0.280979532	0.823032022	yes	no	no	AI406410	Rn.1619	Transcribed locus
2147	1376065_at	-0.280946072	0.82305111	yes	no	no	AI058889	Rn.15120	Transcribed locus
2148	1379746_at	-0.280931445	0.823059455	yes	no	no	AI101685	Rn.195274	JNK/SAPK-inhibitory kinase
2149	1394943_at	-0.280726889	0.823176163	yes	no	no	AA893197	---	---
2150	1372449_at	-0.280682393	0.823201552	yes	no	no	AW253616	Rn.935	Transcribed locus
2151	1397949_at	-0.280442917	0.823338208	yes	no	no	BE117532	---	---
2152	1373579_at	-0.280358314	0.823386492	yes	no	no	AA945758	---	---
2153	1391157_at	-0.280317842	0.823409591	yes	no	no	BE104457	Rn.8763	Similar to CG7744-PA (predicted)
2154	1371832_at	-0.280127334	0.823518329	yes	no	no	AW526333	Rn.43195	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)

2155	1384220_at	-0.28010288	0.823532288	yes	no	no	BE120941	Rn.18774	tubulin-specific chaperone c (predicted)
2156	1390463_at	-0.279947295	0.823621105	yes	no	no	BG378294	Rn.63780	Transcribed locus
2157	1378854_at	-0.279944555	0.82362267	yes	no	no	BF398480	Rn.59092	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
2158	1388002_at	-0.279938327	0.823626225	yes	no	no	AF084205	Rn.30050	TAO kinase 1
2159	1376679_at	-0.279927691	0.823632297	yes	no	no	AI556021	Rn.20956	Transcribed locus
2160	1385344_at	-0.279882304	0.823658209	yes	no	no	AW526794	Rn.1477	AE binding protein 2 (predicted)
2161	1381993_at	-0.279813214	0.823697655	yes	no	no	BI293548	Rn.103254	chloride intracellular channel 2
2162	1375965_at	-0.279710485	0.823756309	yes	no	no	AI229167	Rn.167445	Transcribed locus
2163	1381120_at	-0.279601006	0.823818822	yes	no	no	AI071248	Rn.166430	Transcribed locus, strongly similar to XP_216393.3 PREDICTED: similar to RP11-208F1.2 [Rattus norvegicus]
2164	1370106_at	-0.279591143	0.823824454	yes	no	no	NM_019199	Rn.44478	fibroblast growth factor 18
2165	1378098_at	-0.279472966	0.82389194	yes	no	no	AI406802	Rn.162012	Similar to CG4768-PA (predicted)
2166	1391370_at	-0.27931632	0.823981402	yes	no	no	AW532474	Rn.156016	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2167	1374753_at	-0.279250596	0.824018941	yes	no	no	AI105113	Rn.151634	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2168	1385460_at	-0.279235188	0.824027741	yes	no	no	AA956464	Rn.4063	WD repeat and SOCS box-containing 2
2169	1387126_at	-0.279181888	0.824058185	yes	no	no	NM_131907	Rn.5805	ATPase, Ca++-sequestering
2170	1373284_at	-0.279146588	0.824078349	yes	no	no	AI176607	Rn.14087	salvador homolog 1 (Drosophila) (predicted)
2171	1375880_at	-0.279076773	0.824118229	yes	no	no	AI170384	Rn.104856	Transcribed locus
2172	1374703_at	-0.279054829	0.824130763	yes	no	no	BI304209	Rn.164711	Transcribed locus
2173	1393066_at	-0.278831521	0.824258337	yes	no	no	AI070787	Rn.1303	Cadherin 1
2174	1393236_at	-0.278823545	0.824262894	yes	no	no	AI137233	Rn.166758	Transcribed locus
2175	1378610_at	-0.278676267	0.824347043	yes	no	no	BG378206	Rn.147204	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2176	1394400_at	-0.27858136	0.824401274	yes	no	no	BF542890	Rn.23078	Similar to myocardial ischemic preconditioning upregulated protein 2 (predicted)
2177	1397443_at	-0.27855108	0.824418577	yes	no	no	BF398770	Rn.42849	AT rich interactive domain 2 (Arid-rfx like) (predicted)
2178	1382183_at	-0.278444785	0.824479321	yes	no	no	AA849479	Rn.21436	Transcribed locus
2179	1385431_at	-0.278345605	0.824536003	yes	no	no	BF409456	---	similar to SH3-domain binding protein 3 (predicted)
2180	1372586_at	-0.278337457	0.82454066	yes	no	no	AI411995	Rn.2778	Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
2181	1373258_at	-0.278289669	0.824567973	yes	no	no	AI169359	Rn.25087	cathepsin F
2182	1385030_at	-0.278188959	0.824625535	yes	no	no	BE097270	Rn.96103	Similar to HTPAP protein (predicted)
2183	1373331_at	-0.278182873	0.824629014	yes	no	no	BM383310	Rn.61607	Similar to Leucine rich repeat and sterile alpha motif containing 1 (predicted)
2184	1394744_at	-0.278047339	0.824706487	yes	no	no	AI556327	Rn.43300	Eukaryotic translation elongation factor 1 gamma
2185	1397207_at	-0.27769852	0.824905911	yes	no	no	AI171260	Rn.22342	OTU domain containing 4
2186	1370968_at	-0.277694663	0.824908116	yes	no	no	AA858801	Rn.2411	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105
2187	1374714_at	-0.277556732	0.824986987	yes	no	no	BI284781	Rn.9345	Transcribed locus
2188	1379558_at	-0.27708852	0.825254771	yes	no	no	AA957033	Rn.9167	CDNA clone IMAGE:7930522
2189	1388856_at	-0.277037961	0.825283693	yes	no	no	BG374178	Rn.44216	kit ligand
2190	1394597_at	-0.276836834	0.825398754	yes	no	no	AI101356	Rn.163271	DDHD domain containing 1
2191	1373694_at	-0.276768817	0.825437669	yes	no	no	H33486	Rn.23316	WD repeat domain 79
2192	1368143_at	-0.276710668	0.82547094	yes	no	no	AI013902	Rn.106184	annexin A7
2193	1376101_at	-0.27658758	0.82554137	yes	no	no	AI228256	Rn.154628	Transcribed locus, strongly similar to NP_035543.1 sex-limited protein [Mus musculus]
2194	1383154_at	-0.276516477	0.825582058	yes	no	no	H34497	---	---
2195	1372444_at	-0.276468477	0.825609527	yes	no	no	AW918352	Rn.164126	Transcribed locus
2196	1378987_at	-0.276345836	0.825679713	yes	no	no	BE119446	Rn.44172	Similar to chromosome 10 open reading frame 42

2197	1396317_at	-0.276159587	0.825786313	yes	no	no	AI764350	Rn.43385	cell cycle progression 1 (predicted)
2198	1396279_at	-0.276019106	0.825866727	yes	no	no	BG663051	Rn.12944	ATPase, H+ transporting, lysosomal accessory protein 2
2199	1393395_at	-0.275902997	0.825933196	yes	no	no	BE120797	Rn.167790	Transcribed locus
2200	1398866_at	-0.275825326	0.825977664	yes	no	no	AF255614	Rn.162623	membrane associated guanylate kinase, WW and PDZ domain containing 3
2201	1388638_at	-0.275782576	0.82600214	yes	no	no	AW525725	Rn.8108	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)
2202	1390872_at	-0.275776023	0.826005891	yes	no	no	AI178134	Rn.6742	Intraflagellar transport 80 homolog (Chlamydomonas)
2203	1382455_at	-0.275704294	0.826046961	yes	no	no	BG379564	Rn.49234	Transcribed locus
2204	1375205_at	-0.27565613	0.826074538	yes	no	no	Z83046	Rn.4126	p300/CBP-associated factor
2205	1377820_a_at	-0.275618914	0.826095848	yes	no	no	BI276525	Rn.40326	Arginine-tRNA-protein transferase 1 (predicted)
2206	1372785_at	-0.275578152	0.826119189	yes	no	no	BG671790	Rn.86973	Transcribed locus
2207	1378607_at	-0.275540216	0.826140912	yes	no	no	BE098816	Rn.171415	Transcribed locus
2208	1393078_at	-0.275451819	0.826191533	yes	no	no	BG671648	Rn.12587	NMDA receptor-regulated gene 1 (predicted)
2209	1388064_a_at	-0.275446986	0.826194301	yes	no	no	AF265360	Rn.34134	solute carrier family 1 (glial high affinity glutamate transporter), member 3
2210	1377979_at	-0.275351322	0.826249087	yes	no	no	AW434228	Rn.20423	Transcribed locus
2211	1374324_at	-0.275343604	0.826253508	yes	no	no	AA945828	Rn.163625	Transcribed locus
2212	1380035_at	-0.275203914	0.826333514	yes	no	no	BF523119	Rn.9502	similar to RIKEN cDNA 5830433M19
2213	1367891_a_at	-0.275117567	0.826382973	yes	no	no	AF136232	Rn.1438	caspase 2
2214	1398607_at	-0.275054279	0.826419225	yes	no	no	AI717510	Rn.55468	Similar to KIAA0240 (predicted)
2215	1393606_at	-0.27494839	0.826479883	yes	no	no	AI137411	Rn.11612	hypothetical protein LK44
2216	1388633_at	-0.27482878	0.826548408	yes	no	no	BM388921	Rn.8265	similar to RIKEN cDNA 4930538D17
2217	1374179_at	-0.274781119	0.826575714	yes	no	no	BF285334	---	---
2218	1383594_at	-0.274751764	0.826592533	yes	no	no	AW914775	Rn.42180	similar to RIKEN cDNA 1810060J02
2219	1374773_at	-0.274700749	0.826621762	yes	no	no	BF398048	Rn.166573	Transcribed locus
2220	1393185_at	-0.274534917	0.826716785	yes	no	no	BF283249	Rn.162678	Similar to envelope (predicted)
2221	1378606_at	-0.274480726	0.826747839	yes	no	no	AI010216	Rn.25218	similar to hypothetical protein MGC37079 (predicted)
2222	1373581_at	-0.274393399	0.826797884	yes	no	no	BG380767	Rn.17471	Similar to KIAA0672 gene product
2223	1397011_at	-0.274192176	0.826913211	yes	no	no	BE108912	Rn.153647	Transcribed locus
2224	1380060_at	-0.274126949	0.826950598	yes	no	no	AI175848	Rn.31307	DNA topoisomerase I, mitochondrial
2225	1379031_at	-0.274097861	0.826967272	yes	no	no	BM390697	Rn.21437	Transcribed locus
2226	1374728_at	-0.273847752	0.827110649	yes	no	no	BG671786	Rn.9183	Transcribed locus
2227	1379881_at	-0.27383916	0.827115575	yes	no	no	BI304043	Rn.165504	Transcribed locus, weakly similar to XP_574512.1 PREDICTED: similar to LRRG00121 [Rattus norvegicus]
2228	1390978_at	-0.273823932	0.827124305	yes	no	no	BF406177	Rn.48887	Transcribed locus
2229	1373651_at	-0.273770771	0.827154784	yes	no	no	BE103440	Rn.169388	Transcribed locus
2230	1377785_at	-0.273537476	0.827288552	yes	no	no	BI275330	Rn.29182	DEAH (Asp-Glu-Ala-His) box polypeptide 40
2231	1376921_at	-0.273363951	0.827388063	yes	no	no	BG381722	---	FAD-dependent oxidoreductase domain containing 1 (predicted)
2232	1385974_at	-0.273356581	0.82739229	yes	no	no	BM384723	Rn.104110	par-6 partitioning defective 6 homolog gamma (C. elegans) (predicted)
2233	1371992_at	-0.273314345	0.827416513	yes	no	no	BG378110	Rn.74107	similar to RIKEN cDNA 5430437P03
2234	1369333_a_at	-0.273128567	0.827523067	yes	no	no	NM_053945	Rn.161948	regulating synaptic membrane exocytosis 2
2235	1392586_at	-0.272786248	0.827719443	yes	no	no	AI704512	Rn.162064	similar to RIKEN cDNA 4932432K03
2236	1382024_at	-0.272773073	0.827727002	yes	no	no	BM383877	Rn.129050	DnaJ (Hsp40) homolog, subfamily B, member 6 /// similar to mDj4 (predicted) /// similar to DnaJ homolog subfamily B member 6 (Heat shock protein J2) (predicted)
2237	1374171_at	-0.27273862	0.82774677	yes	no	no	AI170507	Rn.164431	Transcribed locus
2238	1372120_at	-0.272713546	0.827761156	yes	no	no	AI408025	Rn.18210	ubiquitin-activating enzyme E1-domain containing 1

2239	1391974_at	-0.272666183	0.827788331	yes	no	no	BF414433	Rn.99919	COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)
2240	1383168_at	-0.272628945	0.827809698	yes	no	no	BE102209	---	---
2241	1390441_at	-0.272606734	0.827822443	yes	no	no	AW527409	Rn.63466	Development and differentiation enhancing (predicted)
2242	1381424_at	-0.272540404	0.827860504	yes	no	no	AI535231	---	---
2243	1378152_at	-0.272486026	0.827891708	yes	no	no	AI170349	Rn.148001	Transcribed locus
2244	1393686_at	-0.272452941	0.827910694	yes	no	no	AA818655	Rn.16518	Similar to WAC (predicted)
2245	1374519_at	-0.272301027	0.827997876	yes	no	no	AI231782	---	---
2246	1383607_at	-0.272255264	0.828024142	yes	no	no	BG377487	Rn.154542	Ac1158
2247	1386088_at	-0.272148081	0.828085661	yes	no	no	AW141957	Rn.12583	similar to RIKEN cDNA 1200007B05 gene
2248	1380033_at	-0.271911795	0.828221296	yes	no	no	AI408858	Rn.167968	Transcribed locus
2249	1390132_at	-0.271818929	0.828274611	yes	no	no	BF282059	Rn.48189	Transcribed locus
2250	1375769_at	-0.271748997	0.82831476	yes	no	no	BI283106	Rn.79871	tripartite motif protein 41 (predicted)
2251	1385188_at	-0.271649538	0.828371867	yes	no	no	BG379787	Rn.4026	Similar to hypothetical protein BC011833 (predicted)
2252	1387759_s_at	-0.271435482	0.828494783	yes	no	no	J02612	Rn.26489	UDP glycosyltransferase 1 family, polypeptide A1 /// UDP glycosyltransferase 1 family, polypeptide A6 /// UDP glycosyltransferase 1 family, polypeptide A7 /// UDP glycosyltransferase 1 family, polypeptide A8 /// UDP glycosyltransferase 1 family polypeptid
2253	1383999_at	-0.271293916	0.828576084	yes	no	no	AW527651	Rn.167587	Transcribed locus
2254	1379662_a_at	-0.271266225	0.828591988	yes	no	no	AI011832	Rn.165314	Transcribed locus
2255	1372537_at	-0.271205012	0.828627145	yes	no	no	BI289642	---	---
2256	1372476_at	-0.271119907	0.828676027	yes	no	no	AW533321	Rn.35262	fatty acid desaturase 3
2257	1372888_at	-0.271087019	0.828694919	yes	no	no	BI294856	Rn.102204	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)
2258	1393098_at	-0.270900119	0.828802282	yes	no	no	BM386610	Rn.3360	Growth factor receptor bound protein 2
2259	1386876_at	-0.270789359	0.828865914	yes	no	no	NM_012821	Rn.3313	adenylate cyclase 6
2260	1382052_at	-0.270447501	0.829062344	yes	no	no	BF284373	Rn.162118	FUS interacting protein (serine-arginine rich) 1
2261	1390461_at	-0.270339867	0.829124199	yes	no	no	AI071102	Rn.160449	Transcribed locus
2262	1388202_at	-0.270275835	0.829161	yes	no	no	BI395698	Rn.145377	RT1 class Ib, locus Aw2
2263	1372719_at	-0.270225494	0.829189933	yes	no	no	BF283702	---	---
2264	1377755_at	-0.270160788	0.829227124	yes	no	no	AI179403	---	---
2265	1371603_at	-0.270022192	0.829306789	yes	no	no	BI291379	Rn.94992	proline-rich polypeptide 3
2266	1394726_at	-0.269618212	0.829539042	yes	no	no	AI412564	Rn.113837	Coxsackie virus and adenovirus receptor
2267	1369068_at	-0.269601143	0.829548857	yes	no	no	NM_022683	Rn.163001	cullin 5
2268	1374555_at	-0.269465626	0.829626782	yes	no	no	AI501425	Rn.27349	acyl-Coenzyme A binding domain containing 6
2269	1395621_at	-0.269237807	0.829757801	yes	no	no	H33102	Rn.110198	similar to Mitochondrial carrier triple repeat 1 (predicted)
2270	1391091_at	-0.269128521	0.829820658	yes	no	no	AI406286	Rn.128760	retinitis pigmentosa 1 homolog (human) /// similar to cylindromatosis (turban tumor syndrome) (predicted)
2271	1372358_at	-0.268978601	0.829906895	yes	no	no	AI012613	---	---
2272	1385581_at	-0.268926218	0.829937029	yes	no	no	BF551187	Rn.165449	Transcribed locus
2273	1389195_at	-0.268895224	0.829954859	yes	no	no	AI236726	Rn.6514	DNA fragmentation factor, alpha subunit
2274	1391786_at	-0.268576719	0.830138109	yes	no	no	BI297047	Rn.160642	Similar to Murine homolog of human ftp-3
2275	1372292_at	-0.268513154	0.830174686	yes	no	no	AI009732	Rn.164433	Transcribed locus
2276	1393231_at	-0.268432651	0.830221011	yes	no	no	BM386467	Rn.11876	protein phosphatase 4, regulatory subunit 2 (predicted)
2277	1383531_at	-0.268427535	0.830223955	yes	no	no	AA901061	---	---
2278	1392312_at	-0.26840891	0.830234673	yes	no	no	BG375255	---	---
2279	1372561_at	-0.268359768	0.830262954	yes	no	no	AI234095	Rn.106443	stromal membrane-associated protein 1-like
2280	1383025_at	-0.268299482	0.830297649	yes	no	no	BE097791	---	---
2281	1370930_at	-0.268187909	0.830361863	yes	no	no	BF417285	---	---

2282	1369414_at	-0.268156096	0.830380174	yes	no	no	NM_053637	Rn.64627	syntaxin binding protein 3
2283	1378512_at	-0.267994221	0.830473351	yes	no	no	BF396119	Rn.146462	Transcribed locus
2284	1395601_at	-0.267806864	0.830581208	yes	no	no	BI302615	Rn.44072	Transcribed locus
2285	1384356_at	-0.267764939	0.830605345	yes	no	no	AW141967	Rn.115871	similar to hypothetical protein 2BE2121 - Chinese hamster (fragment) (predicted)
2286	1377643_at	-0.267751761	0.830612932	yes	no	no	BI291489	Rn.194894	homeo box D10 (predicted)
2287	1391297_at	-0.267648609	0.830672323	yes	no	no	BI281108	Rn.79443	REST corepressor 1 (predicted)
2288	1386600_at	-0.267638459	0.830678167	yes	no	no	BF522129	Rn.1287	Transcribed locus
2289	1390338_at	-0.267599039	0.830700865	yes	no	no	BG373138	Rn.54347	similar to KIAA0556 protein
2290	1394413_at	-0.267480026	0.830769395	yes	no	no	AA819514	---	---
2291	1374624_at	-0.267329382	0.830856147	yes	no	no	AI179979	Rn.53789	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)
2292	1388938_at	-0.267048721	0.831017797	yes	no	no	AI411387	Rn.44078	ubiquitin specific protease 5 (isopeptidase T) (predicted)
2293	1390949_at	-0.266976767	0.831059245	yes	no	no	BE117624	Rn.87365	Transcribed locus
2294	1381454_at	-0.266960046	0.831068877	yes	no	no	AI144856	Rn.23078	Similar to myocardial ischemic preconditioning upregulated protein 2 (predicted)
2295	1388928_at	-0.266895667	0.831105964	yes	no	no	BF399310	Rn.101880	cofilin 2, muscle (predicted)
2296	1394931_at	-0.266798012	0.831162222	yes	no	no	AI180361	Rn.1940	muscleblind-like 2 (predicted)
2297	1386176_at	-0.266797687	0.83116241	yes	no	no	AA892868	Rn.124637	Transcribed locus
2298	1389996_at	-0.266744942	0.831192797	yes	no	no	AI406369	Rn.163326	NIMA (never in mitosis gene a)-related expressed kinase 1 (predicted)
2299	1369198_at	-0.266715043	0.831210024	yes	no	no	AF218388	Rn.64522	apoptotic peptidase activating factor 1
2300	1389014_at	-0.266711908	0.83121183	yes	no	no	BI297612	Rn.7264	pre-B-cell colony enhancing factor 1
2301	1371549_at	-0.26660638	0.831272632	yes	no	no	AI228630	Rn.16542	WD repeat domain 23
2302	1372616_at	-0.266520072	0.831322364	yes	no	no	AI144796	Rn.116146	Transcribed locus
2303	1374083_at	-0.2663992	0.831392017	yes	no	no	AA799740	Rn.3717	Transcribed locus
2304	1374906_at	-0.266295843	0.831451581	yes	no	no	BF407585	Rn.34457	similar to RIKEN cDNA 2810428C21
2305	1390915_at	-0.266277087	0.831462391	yes	no	no	BI275327	Rn.15934	Transcribed locus, strongly similar to XP_538131.2 PREDICTED: similar to MORC family CW-type zinc finger 4 (Zinc finger CW-type coiled-coil domain protein 2) [Canis familiaris]
2306	1380770_at	-0.266248902	0.831478635	yes	no	no	BF408818	Rn.61189	Transcribed locus
2307	1373149_at	-0.266193656	0.831510475	yes	no	no	BF285344	Rn.138455	similar to yippee-like 3 (predicted)
2308	1394086_at	-0.26616214	0.83152864	yes	no	no	AI069981	Rn.162010	SUMO1/sentrin specific protease 7 (predicted)
2309	1397847_at	-0.266124468	0.831550354	yes	no	no	AW921990	Rn.23514	CDNA clone IMAGE:7373898
2310	1398354_at	-0.266103687	0.831562331	yes	no	no	AI555457	Rn.33021	catenin (cadherin associated protein), alpha-like 1 (predicted)
2311	1381215_at	-0.266096168	0.831566666	yes	no	no	AA900967	Rn.15133	Numb-like
2312	1398555_at	-0.266022622	0.831609058	yes	no	no	AI549027	Rn.39287	Transcribed locus
2313	1392223_at	-0.265820097	0.831725807	yes	no	no	AW521110	Rn.44273	epsin 2
2314	1386621_at	-0.265817027	0.831727577	yes	no	no	AW142419	Rn.164736	Transcribed locus
2315	1389845_at	-0.265762484	0.831759023	yes	no	no	BI282224	Rn.106362	DnaJ (Hsp40) homolog, subfamily A, member 3
2316	1377677_a_at	-0.265670767	0.831811902	yes	no	no	AA900692	Rn.12094	Ubiquitin-conjugating enzyme E2R 2 (predicted)
2317	1375393_at	-0.265537987	0.831888462	yes	no	no	BG377970	Rn.48895	Beta-site APP cleaving enzyme 1
2318	1378036_at	-0.265394855	0.831971	yes	no	no	AI029387	Rn.17437	Transcribed locus
2319	1383933_at	-0.265351389	0.831996066	yes	no	no	AI136714	Rn.12947	Similar to KIAA0564 protein (predicted)
2320	1373729_at	-0.265195059	0.832086225	yes	no	no	BG376772	Rn.12551	Transcribed locus
2321	1378929_at	-0.26512959	0.832123986	yes	no	no	BE116137	Rn.16728	Chaperonin subunit 3 (gamma)
2322	1372978_at	-0.265062957	0.83216242	yes	no	no	BI291218	Rn.33902	Transcribed locus
2323	1368726_a_at	-0.264988047	0.83220563	yes	no	no	AB047638	Rn.127808	zinc finger protein 347
2324	1392044_at	-0.264986185	0.832206704	yes	no	no	BE117009	Rn.146484	Transcribed locus

2325	1379723_at	-0.264917971	0.832246053	yes	no	no	BG673264	Rn.35776	similar to tyrosine kinase-associated leucine zipper protein LAZipII (predicted)
2326	1383372_at	-0.264659549	0.832395142	yes	no	no	BF407234	Rn.10137	platelet-activating factor receptor
2327	1376602_a_at	-0.264654553	0.832398025	yes	no	no	AI030899	Rn.4284	F-box only protein 22
2328	1392493_at	-0.264640456	0.832406159	yes	no	no	AI501338	Rn.149611	Transcribed locus
2329	1393465_at	-0.264627206	0.832413804	yes	no	no	BE103258	Rn.95697	Transcribed locus
2330	1387083_at	-0.264588561	0.832436101	yes	no	no	NM_017129	Rn.10253	cardiotrophin 1
2331	1372821_at	-0.264345212	0.832576526	yes	no	no	AI236621	Rn.14926	Transcribed locus
2332	1374361_at	-0.264293112	0.832606593	yes	no	no	BI276503	Rn.23115	Similar to bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (variant 1) (predicted)
2333	1375939_at	-0.264252122	0.83263025	yes	no	no	BM391922	Rn.18063	Transcribed locus, strongly similar to XP_852159.1 PREDICTED: similar to GC-rich sequence DNA-binding factor homolog [Canis familiaris]
2334	1391723_at	-0.264233657	0.832640907	yes	no	no	BI291869	Rn.164573	Transcribed locus
2335	1382707_at	-0.264144296	0.832692482	yes	no	no	BM386762	---	---
2336	1368194_at	-0.264000703	0.832775365	yes	no	no	NM_133406	Rn.41595	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
2337	1382392_at	-0.263583536	0.833016204	yes	no	no	AI045633	Rn.102078	Numb gene homolog (Drosophila)
2338	1377551_at	-0.263465999	0.833084073	yes	no	no	BE118580	Rn.22576	Transcribed locus
2339	1374291_at	-0.263397491	0.833123633	yes	no	no	BI291937	Rn.41217	DnaJ (Hsp40) homolog, subfamily C, member 17 (predicted)
2340	1377949_s_at	-0.26326623	0.833199437	yes	no	no	AA899043	---	---
2341	1383664_a_at	-0.263250458	0.833208546	yes	no	no	AI172176	Rn.162513	similar to chromosome 11 open reading frame2 (predicted)
2342	1374027_at	-0.263242302	0.833213256	yes	no	no	AI071243	Rn.20480	Transcribed locus
2343	1378740_at	-0.26310664	0.83329161	yes	no	no	AI577567	Rn.66627	RAS protein activator like 2 (predicted)
2344	1387415_a_at	-0.263038227	0.833331126	yes	no	no	AF118889	Rn.96029	syntaxin binding protein 5 (tomosyn)
2345	1382235_at	-0.262779947	0.833480328	yes	no	no	BF549700	Rn.161785	similar to hypothetical protein FLJ30596 (predicted)
2346	1395086_at	-0.262742851	0.833501759	yes	no	no	BI293086	Rn.162495	similar to expressed sequence AV312086 (predicted)
2347	1383849_at	-0.262711676	0.83351977	yes	no	no	AW143311	Rn.58758	similar to hypothetical protein FLJ12994 (predicted)
2348	1380713_at	-0.262711654	0.833519783	yes	no	no	BG376879	Rn.161163	Transcribed locus
2349	1372191_at	-0.262710514	0.833520441	yes	no	no	BI303656	Rn.165910	Transcribed locus
2350	1393198_at	-0.262564507	0.833604802	yes	no	no	AW920606	Rn.74539	similar to RIKEN cDNA 5330414D10 (predicted)
2351	1379459_at	-0.262408016	0.833695229	yes	no	no	BI301276	Rn.162857	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)
2352	1385274_at	-0.26239328	0.833703744	yes	no	no	AW526381	---	---
2353	1381713_at	-0.262141035	0.833849525	yes	no	no	BE106279	Rn.21735	Similar to DKFZP564P1916 protein (predicted)
2354	1391187_at	-0.262081484	0.833883944	yes	no	no	BI303019	Rn.167598	Transcribed locus, strongly similar to XP_220174.3 PREDICTED: similar to periplakin [Rattus norvegicus]
2355	1376035_at	-0.262051714	0.833901152	yes	no	no	BI274308	Rn.64438	Tetratricopeptide repeat domain 7B (predicted)
2356	1389053_at	-0.262026254	0.833915868	yes	no	no	AI171280	---	---
2357	1388169_at	-0.261987409	0.833938322	yes	no	no	BE102096	Rn.99017	jumonji domain containing 1C
2358	1377801_at	-0.261944858	0.833962918	yes	no	no	AI237031	Rn.25408	Similar to BTB (PO)Z domain containing 12 (predicted)
2359	1370602_at	-0.261881619	0.833999475	yes	no	no	U15408	Rn.9986	ATPase, Ca++ transporting, plasma membrane 4
2360	1389352_at	-0.26185638	0.834014066	yes	no	no	BF281980	Rn.14154	Transcribed locus
2361	1379831_at	-0.261853561	0.834015695	yes	no	no	AW252506	Rn.145141	similar to multiple hat domains (predicted)
2362	1382242_at	-0.26182095	0.834034548	yes	no	no	BE105280	Rn.163059	zinc finger protein 451
2363	1379816_at	-0.261745967	0.834077897	yes	no	no	AI502578	Rn.24267	Similar to RIKEN cDNA 2410025L10 (predicted)
2364	1382334_at	-0.261691579	0.834109342	yes	no	no	AI170308	Rn.6650	Transcribed locus
2365	1390224_at	-0.26154972	0.834191363	yes	no	no	BM387978	---	---
2366	1383247_a_at	-0.261465305	0.834240175	yes	no	no	BI291029	Rn.159761	Transcribed locus, strongly similar to XP_848415.1 PREDICTED: similar to spinster-like [Canis familiaris]

2367	1392476_at	-0.261398637	0.834278726	yes	no	no	BE105480	Rn.10465	histone H4 variant H4-v.1 (predicted) /// similar to germinal histone H4 gene (predicted)
2368	1384172_at	-0.260842687	0.834600282	yes	no	no	BF398262	Rn.144424	Similar to KIAA0423 (predicted)
2369	1385521_at	-0.260650822	0.834711284	yes	no	no	AI603505	Rn.150075	Transcribed locus
2370	1376447_at	-0.260446806	0.834829331	yes	no	no	AI706850	Rn.68344	similar to hypothetical protein A430110N23 (predicted)
2371	1384124_at	-0.260387182	0.834863833	yes	no	no	AW534915	Rn.148509	Transcribed locus
2372	1395515_at	-0.2603695	0.834874066	yes	no	no	BG668905	Rn.154656	basic helix-loop-helix domain containing, class B, 9
2373	1371901_at	-0.260321306	0.834901956	yes	no	no	AI176646	Rn.3633	Transcribed locus
2374	1383017_at	-0.260240464	0.834948741	yes	no	no	AI639001	---	---
2375	1387451_at	-0.260084316	0.835039115	yes	no	no	NM_130419	Rn.157411	discoidin, CUB and LCCL domain containing 2
2376	1395704_at	-0.260041653	0.835063809	yes	no	no	BF561525	Rn.23284	Transcribed locus
2377	1371616_at	-0.259812437	0.835196495	yes	no	no	AW524495	Rn.23024	Transcribed locus
2378	1395779_at	-0.259655193	0.835287531	yes	no	no	BF523321	Rn.169067	Transcribed locus
2379	1393453_at	-0.259648297	0.835291523	yes	no	no	BI290287	Rn.14087	salvador homolog 1 (Drosophila) (predicted)
2380	1384179_at	-0.259542483	0.83535279	yes	no	no	BI294722	Rn.79618	Transcribed locus, moderately similar to NP_038871.1 zinc finger protein 53 [Mus musculus]
2381	1391101_at	-0.259512311	0.83537026	yes	no	no	AI407134	Rn.34541	Rho GTPase activating protein 12 (predicted)
2382	1389205_at	-0.2593838	0.835444676	yes	no	no	AI012582	Rn.6367	Transcribed locus
2383	1383423_at	-0.259313529	0.83548537	yes	no	no	BI295136	Rn.6470	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2384	1371689_at	-0.25921239	0.835543943	yes	no	no	BE107334	Rn.163742	Transcribed locus
2385	1397387_at	-0.259159852	0.835574372	yes	no	no	AA901254	Rn.32558	Transcribed locus
2386	1394079_at	-0.259044448	0.835641213	yes	no	no	AA944938	Rn.140831	transducin (beta)-like 1X-linked receptor 1 (predicted)
2387	1383237_at	-0.258932685	0.835705951	yes	no	no	BE098240	Rn.14610	Transcribed locus
2388	1382748_at	-0.25891171	0.835718101	yes	no	no	AI145481	---	---
2389	1376918_at	-0.258809657	0.83577722	yes	no	no	AI029930	Rn.11698	Serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1
2390	1375723_at	-0.258502998	0.835954892	yes	no	no	AI385171	Rn.167755	Transcribed locus
2391	1379528_at	-0.258472491	0.835972569	yes	no	no	BI284017	Rn.129894	Transcribed locus
2392	1393303_at	-0.258291939	0.836077197	yes	no	no	AW918896	Rn.30125	Transcribed locus
2393	1374803_at	-0.258290567	0.836077992	yes	no	no	BG374219	Rn.166834	Transcribed locus
2394	1374307_at	-0.258214284	0.836122201	yes	no	no	AI236027	Rn.164709	Transcribed locus
2395	1384383_at	-0.258120705	0.836176437	yes	no	no	BF557230	Rn.6835	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)
2396	1383089_at	-0.25782562	0.836347484	yes	no	no	BM386264	Rn.162952	RAB21, member RAS oncogene family
2397	1393490_at	-0.257769956	0.836379754	yes	no	no	AI501671	Rn.23781	component of oligomeric golgi complex 7
2398	1381144_at	-0.257561212	0.836500778	yes	no	no	AW524106	Rn.65720	Transcribed locus
2399	1392604_at	-0.257505081	0.836533325	yes	no	no	AA997187	Rn.164194	Transcribed locus
2400	1390442_at	-0.257421172	0.83658198	yes	no	no	BF284171	Rn.6429	Transcribed locus
2401	1385986_at	-0.257349194	0.836623719	yes	no	no	BF391203	Rn.173399	Transcribed locus
2402	1384765_at	-0.25734025	0.836628906	yes	no	no	BI289371	---	---
2403	1381376_at	-0.25732821	0.836635888	yes	no	no	AI103284	Rn.34387	Similar to [Mouse primary response gene B94 mRNA, 3end.], gene product
2404	1394472_at	-0.257301624	0.836651306	yes	no	no	BF282814	Rn.166902	Transcribed locus
2405	1379631_at	-0.257144226	0.836742589	yes	no	no	AI071665	Rn.83632	colony stimulating factor 1 (macrophage)
2406	1377704_at	-0.25711393	0.836760161	yes	no	no	BE117155	Rn.165026	Transcribed locus
2407	1384160_at	-0.256949863	0.836855325	yes	no	no	AI547837	Rn.7078	similar to Synaptopodin-2 (Myopodin) (predicted)
2408	1394991_at	-0.256810856	0.836935962	yes	no	no	BG376154	Rn.22238	interleukin-1 receptor-associated kinase 1 (predicted)

2409	1383869_at	-0.256763594	0.83696338	yes	no	no	AI071350	Rn.20510	Transcribed locus
2410	1374900_at	-0.256523652	0.837102591	yes	no	no	BM388807	Rn.13518	golgi SNAP receptor complex member 2
2411	1380155_at	-0.256424712	0.837160001	yes	no	no	AI137306	Rn.27384	Transcribed locus
2412	1398698_at	-0.256422733	0.83716115	yes	no	no	BG371721	Rn.66864	Caseinolytic peptidase X (E.coli)
2413	1379729_at	-0.256331988	0.837213809	yes	no	no	AI071906	Rn.162954	Cleavage and polyadenylation specific factor 6, 68kDa (predicted)
2414	1394761_at	-0.256319985	0.837220774	yes	no	no	BE114260	Rn.52342	similar to Rho-GTPase-activating protein 26 (Oligophrenin-1 like protein) (predicted)
2415	1376298_at	-0.256262583	0.837254086	yes	no	no	AW525099	Rn.29454	UPF3 regulator of nonsense transcripts homolog B (yeast) (predicted)
2416	1375213_at	-0.255854725	0.837490816	yes	no	no	BM384604	Rn.35508	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)
2417	1393213_at	-0.255821393	0.837510166	yes	no	no	BE098333	Rn.162156	cyclin L2
2418	1375934_at	-0.255663731	0.837601696	yes	no	no	BE112948	Rn.7002	similar to RIKEN cDNA D330045A20 (predicted)
2419	1382349_at	-0.255650938	0.837609124	yes	no	no	AI408238	Rn.23183	crystallin, gamma S
2420	1385615_at	-0.25564657	0.837611659	yes	no	no	BF550268	Rn.102204	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)
2421	1390830_at	-0.255621009	0.8376265	yes	no	no	BE113228	Rn.162574	hypothetical protein LOC499602
2422	1393336_at	-0.255425358	0.837740102	yes	no	no	BI274780	Rn.92644	SWAP complex protein (predicted)
2423	1382776_at	-0.255416626	0.837745173	yes	no	no	AI716936	Rn.14994	similar to O-acyltransferase (membrane bound) domain containing 1 (predicted)
2424	1385205_at	-0.25538935	0.837761012	yes	no	no	BF409092	Rn.173484	Transcribed locus
2425	1376059_at	-0.255297292	0.837814471	yes	no	no	AI716607	---	---
2426	1391978_at	-0.255104857	0.837926231	yes	no	no	AW531885	Rn.7967	Son cell proliferation protein
2427	1385561_at	-0.254767043	0.838122459	yes	no	no	BF561031	Rn.162727	similar to peroxisome biogenesis factor 1 (predicted)
2428	1397897_x_at	-0.25459058	0.838224979	yes	no	no	BI273954	Rn.136371	Transcribed locus
2429	1393572_at	-0.254586258	0.838227491	yes	no	no	AI229129	Rn.22944	Zinc finger protein 592 (predicted)
2430	1376235_at	-0.25452146	0.83826514	yes	no	no	BI289136	Rn.15451	Transcribed locus
2431	1382429_at	-0.25443905	0.838313025	yes	no	no	AI059574	---	---
2432	1390602_a_at	-0.254408815	0.838330594	yes	no	no	BG381320	Rn.116819	similar to RIKEN cDNA C430004E15
2433	1393580_at	-0.254379264	0.838347766	yes	no	no	AW531476	Rn.166371	Transcribed locus
2434	1389456_at	-0.254233718	0.838432346	yes	no	no	BI296591	Rn.17276	Transcribed locus
2435	1392464_at	-0.254232288	0.838433177	yes	no	no	BM392372	Rn.14600	RAE1 RNA export 1 homolog (S. pombe)
2436	1394247_x_at	-0.2541183	0.838499425	yes	no	no	AA799816	Rn.105740	Transcribed locus, strongly similar to XP_217044.2 PREDICTED: similar to lipocalin-interacting membrane receptor [Rattus norvegicus]
2437	1369220_at	-0.253846827	0.838657221	yes	no	no	NM_053655	Rn.10830	dynamin 1-like
2438	1375967_a_at	-0.253786531	0.838692273	yes	no	no	AI172067	Rn.162221	dual specificity phosphatase 22 (predicted)
2439	1383347_at	-0.253759425	0.838708031	yes	no	no	BM384011	Rn.94641	REV1-like (S. cerevisiae) (predicted)
2440	1391326_at	-0.253749996	0.838713512	yes	no	no	BE095733	Rn.47838	similar to homeotic protein Hox B5 - mouse (predicted)
2441	1396142_at	-0.253716933	0.838732733	yes	no	no	BI274476	Rn.13913	mitochondrial ribosomal protein S9
2442	1382214_at	-0.253686837	0.83875023	yes	no	no	AI029201	---	---
2443	1384127_at	-0.253649967	0.838771666	yes	no	no	AW917217	Rn.153603	CCAAT/enhancer binding protein (C/EBP), alpha
2444	1376032_at	-0.253634913	0.838780418	yes	no	no	BF283840	Rn.147189	Transcribed locus
2445	1382880_at	-0.253579359	0.838812718	yes	no	no	AI235339	Rn.136535	Transcribed locus, moderately similar to NP_005683.2 ATP-binding cassette, sub-family F, member 2 isoform b [Homo sapiens]
2446	1372690_at	-0.253535835	0.838838024	yes	no	no	AI137471	Rn.22361	Transcribed locus, strongly similar to NP_808376.1 reticulon 4 receptor-like 1 [Mus musculus]
2447	1377346_at	-0.253474238	0.83887384	yes	no	no	AI112098	Rn.129546	Transcribed locus, moderately similar to NP_001007591.1 hypothetical protein LOC433886 [Mus musculus]
2448	1391901_at	-0.253372569	0.838932959	yes	no	no	AA956085	Rn.18217	Transcribed locus
2449	1380486_at	-0.253357365	0.8389418	yes	no	no	BM383047	---	---
2450	1390552_at	-0.253276283	0.838988951	yes	no	no	AA859553	Rn.95239	membrane associated guanylate kinase 1 b NT-short isoform

2451	1370109_s_at	0.253179631	1.191830961	yes	no	no	NM_033539	Rn.156621	eukaryotic translation elongation factor 1 alpha 1
2452	1371041_at	0.25332543	1.191951414	yes	no	no	M22756	Rn.28882	NADH dehydrogenase (ubiquinone) flavoprotein 2
2453	1390967_a_at	0.253370151	1.191988363	yes	no	no	AW919980	Rn.98615	similar to RIKEN cDNA 2410006F12
2454	1369934_at	0.25348816	1.192085869	yes	no	no	NM_022536	Rn.1893	peptidylprolyl isomerase B
2455	1367586_at	0.253497843	1.192093869	yes	no	no	NM_017025	Rn.107896	lactate dehydrogenase A
2456	1368293_at	0.253581735	1.192163191	yes	no	no	NM_031766	Rn.11056	carboxypeptidase Z
2457	1373290_at	0.253587392	1.192167866	yes	no	no	AI012781	Rn.9027	similar to Ezh2 protein
2458	1371305_at	0.253743637	1.192296986	yes	no	no	AI409193	Rn.127774	ribosomal protein L8
2459	1367588_a_at	0.253749659	1.192301962	yes	no	no	NM_022179	Rn.92211	ribosomal protein L13A
2460	1367639_a_at	0.253911099	1.192435391	yes	no	no	U92700	Rn.2115	ribosomal protein S2
2461	1368051_at	0.253947122	1.192465165	yes	no	no	NM_032066	Rn.162663	hydroxysteroid (17-beta) dehydrogenase 12
2462	1389183_at	0.253947505	1.192465482	yes	no	no	BI281709	Rn.102072	postmeiotic segregation increased 2 (S. cerevisiae) (predicted)
2463	1377172_at	0.25412704	1.192613886	yes	no	no	BE117002	Rn.144235	similar to Pins (predicted)
2464	1391345_at	0.254127489	1.192614257	yes	no	no	BI293047	Rn.62611	BMP-binding endothelial regulator (predicted)
2465	1368507_at	0.254394394	1.192834917	yes	no	no	NM_017280	Rn.3997	proteasome (prosome, macropain) subunit, alpha type 3 /// proteasome subunit alpha type 3-like
2466	1389431_at	0.25441235	1.192849763	yes	no	no	BF400782	Rn.24110	protein kinase, DNA activated, catalytic polypeptide (predicted)
2467	1388587_at	0.254478963	1.192904841	yes	no	no	AI176519	Rn.23638	immediate early response 3
2468	1370250_at	0.254744073	1.19312407	yes	no	no	AA799453	Rn.2274	ubiquitin-conjugating enzyme E2I /// similar to RIKEN cDNA A930001M12 gene (predicted)
2469	1378501_at	0.254933042	1.19328036	yes	no	no	BE113386	---	---
2470	1383992_at	0.254995416	1.193331951	yes	no	no	BM383990	Rn.40467	Transcribed locus
2471	1374529_at	0.255070808	1.193394314	yes	no	no	AI406660	---	---
2472	1391649_a_at	0.255276537	1.193564504	yes	no	no	AW915522	Rn.128940	Transcribed locus
2473	1397641_at	0.255374459	1.19364552	yes	no	no	BF414999	Rn.153596	Transcribed locus
2474	1390244_at	0.255439744	1.193699536	yes	no	no	BF418231	Rn.52841	spermatogenesis associated, serine-rich 2 (predicted)
2475	1390542_at	0.255579931	1.193815534	yes	no	no	BE111757	Rn.160309	Similar to RAD51L2/RAD51C protein (predicted)
2476	1384707_at	0.255711681	1.193924561	yes	no	no	AI600020	Rn.168403	Transcribed locus
2477	1389433_at	0.255860713	1.194047901	yes	no	no	BI298816	Rn.8839	McKusick-Kaufman syndrome protein
2478	1398860_at	0.255880943	1.194064644	yes	no	no	AF095740	Rn.2079	neural precursor cell expressed, developmentally down-regulated gene 8
2479	1398974_at	0.255887434	1.194070016	yes	no	no	AI171615	Rn.36664	chromosome segregation 1-like (S. cerevisiae) (predicted)
2480	1372727_at	0.255939264	1.194112915	yes	no	no	BM384088	Rn.15045	Transcribed locus
2481	1367482_at	0.256421635	1.194512238	yes	no	no	AI172459	Rn.3964	similar to anaphase promoting complex subunit 11 homolog (predicted)
2482	1396984_at	0.256440946	1.194528227	yes	no	no	BM390248	Rn.13004	Transcribed locus, weakly similar to NP_703313.1 hypothetical protein [Plasmodium falciparum 3D7]
2483	1367562_at	0.256595852	1.194656494	yes	no	no	NM_012656	Rn.163095	secreted acidic cysteine rich glycoprotein
2484	1388306_at	0.256659055	1.194708832	yes	no	no	BM383758	Rn.2926	similar to RIKEN cDNA 1810042K04 (predicted)
2485	1371331_at	0.25684595	1.194863611	yes	no	no	BG665037	Rn.95652	follistatin-like 1
2486	1375526_at	0.256880381	1.194892128	yes	no	no	AI171327	---	similar to novel protein of unknown function (DUF423) family member (predicted)
2487	1375107_at	0.256903726	1.194911463	yes	no	no	AI170758	---	---
2488	1399031_at	0.257003531	1.19499413	yes	no	no	BM391360	Rn.163846	Transcribed locus, weakly similar to NP_594758.1 hypothetical protein SPAC4F10.15c [Schizosaccharomyces pombe 972h-]
2489	1375651_at	0.257035897	1.195020939	yes	no	no	AI230164	---	---
2490	1391425_at	0.257092525	1.195067846	yes	no	no	AW528585	Rn.90103	NCK interacting protein with SH3 domain (predicted)
2491	1385828_at	0.257248839	1.195197337	yes	no	no	BF559433	---	---
2492	1368204_at	0.257271118	1.195215795	yes	no	no	NM_030855	Rn.20467	ligase I, DNA, ATP-dependent
2493	1372105_at	0.257432214	1.195349264	yes	no	no	BF284932	Rn.64644	similar to Smhs2 homolog (predicted)

2494	1388923_at	0.257471081	1.195381467	yes	no	no	BG381657	Rn.106450	similar to 2410004L22Rik protein
2495	1371885_at	0.257519881	1.195421902	yes	no	no	BI282366	Rn.9550	cytoskeleton-associated protein 1 (predicted)
2496	1388158_at	0.257541088	1.195439474	yes	no	no	BG057565	---	HLA-B-associated transcript 1A
2497	1367625_at	0.257733637	1.195599034	yes	no	no	NM_031100	Rn.102157	ribosomal protein L10
2498	1398759_at	0.257938561	1.195768873	yes	no	no	NM_013043	Rn.3545	transforming growth factor beta 1 induced transcript 4
2499	1378638_a_at	0.257939441	1.195769601	yes	no	no	BM384709	Rn.106518	similar to 2700029M09Rik protein (predicted)
2500	1386080_at	0.258088529	1.195893179	yes	no	no	BE107815	Rn.98202	Hairy/enhancer-of-split related with YRPW motif 1
2501	1398850_at	0.258355631	1.196114608	yes	no	no	BG671399	Rn.1463	peptidylprolyl isomerase A
2502	1388931_at	0.258583998	1.196303958	yes	no	no	AA799440	Rn.107776	mitochondrial ribosomal protein L13
2503	1375157_at	0.258737008	1.196430844	yes	no	no	AA943117	Rn.162171	Myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog (Drosophila) (predicted)
2504	1369443_at	0.2587964	1.196480098	yes	no	no	NM_133569	Rn.162660	angiopoietin-like 2
2505	1381476_at	0.259037824	1.196680337	yes	no	no	BF416405	Rn.134531	Transcribed locus
2506	1375643_at	0.259107917	1.196738479	yes	no	no	BM384259	Rn.99508	cytoskeleton-associated protein 4 (predicted)
2507	1370145_at	0.259109429	1.196739733	yes	no	no	NM_023988	Rn.64579	zinc finger protein 354C
2508	1382307_at	0.259236913	1.196845487	yes	no	no	BF406594	Rn.162937	protein phosphatase 1, regulatory (inhibitor) subunit 12A
2509	1389073_at	0.259257097	1.196862233	yes	no	no	AA851248	Rn.6988	receptor accessory protein 4
2510	1383580_at	0.259270036	1.196872966	yes	no	no	AA859643	---	---
2511	1392746_x_at	0.259356459	1.196944666	yes	no	no	BF394189	Rn.163120	La ribonucleoprotein domain family, member 1 (predicted)
2512	1387778_at	0.259671569	1.197206129	yes	no	no	NM_130412	Rn.12964	stromal cell derived factor 4
2513	1398966_at	0.260367602	1.197783863	yes	no	no	AI169154	---	---
2514	1382093_at	0.260397583	1.197808755	yes	no	no	AI178038	Rn.156180	Similar to DKFZP434B168 protein (predicted)
2515	1384401_at	0.260542553	1.197929124	yes	no	no	AI059296	Rn.19125	Transcribed locus, weakly similar to XP_524118.1 PREDICTED: similar to zinc finger protein 433 [Pan troglodytes]
2516	1390590_at	0.260731466	1.198085996	yes	no	no	AA965207	Rn.11702	protein O-fucosyltransferase 2 (predicted)
2517	1398794_at	0.260793887	1.198137835	yes	no	no	NM_022593	Rn.48516	transcription elongation factor B (SIII), polypeptide 1
2518	1398884_at	0.260976546	1.19828954	yes	no	no	BM384924	Rn.3401	prefoldin 5 (predicted)
2519	1369930_at	0.261278888	1.198540689	yes	no	no	NM_017283	Rn.107278	proteasome (prosome, macropain) subunit, alpha type 6
2520	1388901_at	0.261306448	1.198563586	yes	no	no	AW534837	Rn.144288	FK506 binding protein 5
2521	1371936_at	0.261418928	1.198657036	yes	no	no	BI284436	Rn.91523	eukaryotic translation initiation factor 4A1
2522	1388960_at	0.261590374	1.198799489	yes	no	no	AI412958	Rn.106916	pyrophosphatase (mapped)
2523	1375411_at	0.262090821	1.199215405	yes	no	no	BI277002	Rn.3422	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)
2524	1367579_a_at	0.262149882	1.1992645	yes	no	no	BI285434	Rn.99661	tubulin, alpha 1 /// tubulin, alpha 6 /// similar to Tubulin alpha-2 chain (Alpha-tubulin 2) (predicted)
2525	1367634_at	0.262349804	1.199430699	yes	no	no	NM_022506	Rn.1101	ribosomal protein L31
2526	1388076_at	0.262400665	1.199472985	yes	no	no	AF388527	Rn.7370	Serpine1 mRNA binding protein 1
2527	1371396_at	0.262403024	1.199474946	yes	no	no	AI600035	---	---
2528	1388159_at	0.262697247	1.199719592	yes	no	no	AA849795	---	---
2529	1368052_at	0.262851832	1.199848149	yes	no	no	NM_133526	Rn.6087	tetraspanin 8
2530	1379441_at	0.263798217	1.200635488	yes	no	no	AA965092	Rn.44204	zinc finger protein 294
2531	1395331_at	0.264026669	1.200825626	yes	no	no	BF548263	Rn.102123	similar to hypothetical protein CL25084 (predicted)
2532	1371720_at	0.264028288	1.200826972	yes	no	no	AI599839	Rn.2913	similar to Mrpl20 protein (predicted)
2533	1374424_at	0.264103164	1.200889297	yes	no	no	BE112720	Rn.101808	protein arginine N-methyltransferase 5 (predicted)
2534	1368211_at	0.264169199	1.200944266	yes	no	no	NM_022672	Rn.36102	ribosomal protein S14
2535	1369621_s_at	0.26422369	1.200989627	yes	no	no	NM_053308	Rn.80611	FK506 binding protein 1a
2536	1375219_a_at	0.264321202	1.201070804	yes	no	no	AA944861	Rn.2115	ribosomal protein S2 /// similar to 40S ribosomal protein S2 (predicted) /// similar to ribosomal protein S2 (predicted) /// similar to ribosomal protein

									S2 (predicted)
2537	1372516_at	0.26453686	1.201250357	yes	no	no	AI317842	Rn.8601	kinesin family member 22
2538	1393689_at	0.264674638	1.201365083	yes	no	no	BE097322	Rn.49587	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (predicted)
2539	1375161_at	0.264714906	1.201398615	yes	no	no	BM386389	Rn.4271	mitochondrial ribosomal protein L55 (predicted)
2540	1372798_at	0.264760764	1.201436804	yes	no	no	BF282715	Rn.191489	membrane-associated DHHC16 zinc finger protein
2541	1379330_s_at	0.264840027	1.201502814	yes	no	no	AI600082	Rn.18796	Similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (predicted)
2542	1371573_at	0.265137933	1.201750941	yes	no	no	AW142090	Rn.23433	ribosomal protein L36a (predicted)
2543	1374210_at	0.265277386	1.20186711	yes	no	no	BM383870	Rn.17063	similar to RIKEN cDNA 2510027N19
2544	1398761_at	0.265419573	1.201985567	yes	no	no	NM_031099	Rn.92980	ribosomal protein L5
2545	1374734_at	0.265798128	1.202301003	yes	no	no	BE115842	Rn.76251	similar to RIKEN cDNA 2810025M15 (predicted)
2546	1390412_at	0.266011193	1.202478578	yes	no	no	AI229664	Rn.15324	Solute carrier family 39 (iron-regulated transporter), member 1
2547	1398871_at	0.266211963	1.20264593	yes	no	no	BG671311	Rn.34429	ribosomal protein L17
2548	1398917_at	0.266561097	1.202937008	yes	no	no	BF281221	Rn.129121	ribosomal protein L7
2549	1377359_at	0.266679011	1.20303533	yes	no	no	BM384440	Rn.140462	similar to protein P3
2550	1387995_a_at	0.266824527	1.203156678	yes	no	no	BI285494	Rn.145191	interferon induced transmembrane protein 3
2551	1389661_at	0.266968544	1.20327679	yes	no	no	AI599413	---	---
2552	1398852_at	0.267103782	1.20338959	yes	no	no	BF410811	Rn.4153	ribosomal protein S21
2553	1389655_at	0.267201363	1.203470988	yes	no	no	AA892330	Rn.13456	similar to A230072I16Rik protein
2554	1398839_at	0.267210221	1.203478377	yes	no	no	NM_053800	Rn.29777	thioredoxin 1
2555	1379506_at	0.267265098	1.203524155	yes	no	no	AA963909	Rn.12150	Transcribed locus
2556	1378367_at	0.267296918	1.203550701	yes	no	no	BF389087	Rn.61074	Transcribed locus
2557	1384462_at	0.26773821	1.203918899	yes	no	no	AA819526	Rn.82177	Transcribed locus
2558	1367500_at	0.267927767	1.204077094	yes	no	no	AI169461	---	---
2559	1373863_at	0.268001226	1.204138404	yes	no	no	BF398680	Rn.101820	mitogen-activated protein kinase kinase kinase kinase 4 (predicted)
2560	1386852_x_at	0.268150797	1.204263249	yes	no	no	D16554	Rn.1253	polyubiquitin
2561	1389956_a_at	0.268176022	1.204284306	yes	no	no	AI180257	---	---
2562	1371845_at	0.268269432	1.204362282	yes	no	no	BF287209	Rn.3013	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)
2563	1373574_at	0.268608065	1.204645007	yes	no	no	BI285607	Rn.6578	similar to hypothetical protein MGC40499 (predicted)
2564	1390046_at	0.26903748	1.205003619	yes	no	no	BI288110	Rn.138249	a disintegrin and metalloprotease domain 8 (predicted)
2565	1374897_at	0.269146591	1.205094758	yes	no	no	AI406842	---	---
2566	1369939_at	0.269656847	1.205521054	yes	no	no	AI104240	Rn.161841	cytochrome c, somatic
2567	1367610_at	0.269684947	1.205544535	yes	no	no	NM_031103	Rn.3384	ribosomal protein L19
2568	1368042_a_at	0.269963815	1.205777585	yes	no	no	AF275734	Rn.159876	high mobility group box 1 /// similar to High mobility group protein 1 (HMG-1) (predicted) /// similar to Hmgb1 protein (predicted) /// similar to High mobility group protein 1 (HMG-1) (predicted)
2569	1368123_at	0.270004719	1.205811772	yes	no	no	NM_052807	Rn.10957	insulin-like growth factor 1 receptor
2570	1372102_at	0.270086476	1.205880106	yes	no	no	BF390024	Rn.24948	nuclear receptor co-repressor 1
2571	1398827_at	0.270111558	1.205901072	yes	no	no	NM_013087	Rn.1975	CD 81 antigen
2572	1382783_at	0.270169385	1.205949409	yes	no	no	BF408187	Rn.162440	Bloom syndrome homolog (human) (predicted)
2573	1376368_at	0.270825662	1.206498115	yes	no	no	BE095878	Rn.19673	CUE domain containing 2 (predicted)
2574	1388479_at	0.270993589	1.206638558	yes	no	no	BI294841	Rn.93365	Dihydropyrimidinase-like 3
2575	1375525_at	0.27111147	1.206737154	yes	no	no	BI294783	Rn.7652	microtubule-associated protein, RP/EB family, member 1
2576	1374047_at	0.271201231	1.206812237	yes	no	no	BM390427	Rn.35239	similar to RIKEN cDNA 2400010D15
2577	1398868_at	0.271434781	1.207007618	yes	no	no	AI408157	Rn.2109	translocase of inner mitochondrial membrane 13 homolog (yeast)
2578	1371299_at	0.27146894	1.207036196	yes	no	no	BG665124	Rn.127805	ribosomal protein S3
2579	1371237_a_at	0.271500556	1.207062648	yes	no	no	AF411318	Rn.16133	metallothionein1F

2580	1374177_at	0.27198664	1.207469409	yes	no	no	AI230912	Rn.15054	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor (predicted)
2581	1367580_at	0.272056127	1.207527569	yes	no	no	NM_031065	Rn.2262	ribosomal protein L10A
2582	1398872_at	0.272326801	1.207754142	yes	no	no	BE107613	Rn.103229	ribosomal protein S13
2583	1388136_at	0.272358937	1.207781045	yes	no	no	BF282660	---	translocase of inner mitochondrial membrane 9 homolog (yeast)
2584	1369683_at	0.272364223	1.207785471	yes	no	no	AF136282	Rn.162782	BH3 interacting domain death agonist
2585	1387031_at	0.272421823	1.207833693	yes	no	no	U36482	Rn.32904	endoplasmic reticulum protein 29
2586	1385695_at	0.272562667	1.207951614	yes	no	no	BI274399	---	---
2587	1388715_at	0.272623567	1.208002606	yes	no	no	AA818089	Rn.3338	glycyl-tRNA synthetase
2588	1398770_at	0.272657987	1.208031427	yes	no	no	NM_031105	Rn.112597	large subunit ribosomal protein L36a
2589	1383404_at	0.272788509	1.208140724	yes	no	no	BI295203	Rn.168799	Transcribed locus
2590	1392527_at	0.272885774	1.208222178	yes	no	no	AI137840	---	---
2591	1371656_at	0.272904558	1.20823791	yes	no	no	BI283657	Rn.97889	chaperonin subunit 4 (delta)
2592	1370207_at	0.273065792	1.208372948	yes	no	no	AI170772	Rn.29258	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 /// similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (predicted)
2593	1398315_at	0.273203369	1.208488185	yes	no	no	AA800007	Rn.27505	ribosomal protein L15
2594	1392886_a_at	0.273211928	1.208495355	yes	no	no	AI453967	Rn.144949	similar to FCRL
2595	1373860_at	0.273334399	1.208597949	yes	no	no	BI297183	Rn.162218	SRY-box containing gene 4 (predicted)
2596	1388846_at	0.273443337	1.208689214	yes	no	no	AI227978	Rn.106127	BCL2-like 12 (proline rich) (predicted)
2597	1372450_at	0.273479731	1.208719705	yes	no	no	AW916609	---	---
2598	1375267_at	0.273555851	1.208783482	yes	no	no	BI291292	Rn.144176	peptidylprolyl isomerase C
2599	1379740_at	0.273578849	1.208802751	yes	no	no	AW521797	Rn.31250	Similar to chromosome 18 open reading frame 54
2600	1397668_at	0.273665513	1.208875368	yes	no	no	H34328	Rn.147455	Transcribed locus
2601	1393805_at	0.273683737	1.208890638	yes	no	no	BE106389	Rn.75037	splA/ryanodine receptor domain and SOCS box containing 1 (predicted)
2602	1369948_at	0.273817554	1.209002774	yes	no	no	NM_053401	Rn.3126	nerve growth factor receptor (TNFRSF16) associated protein 1
2603	1374639_at	0.273868878	1.209045784	yes	no	no	AA800800	Rn.1945	similar to Expressed sequence AI317223
2604	1387854_at	0.273977307	1.209136657	yes	no	no	BI282748	Rn.107239	procollagen, type I, alpha 2
2605	1384090_at	0.274006294	1.209160951	yes	no	no	AW920561	Rn.123611	phosphatidylinositol glycan anchor biosynthesis, class O
2606	1387361_s_at	0.274072379	1.20921634	yes	no	no	NM_053291	Rn.108127	phosphoglycerate kinase 1
2607	1386059_at	0.274109524	1.209247474	yes	no	no	BF284475	Rn.55181	Similar to histone H2b-613 (predicted)
2608	1372464_at	0.274116437	1.209253268	yes	no	no	BE109050	Rn.50150	coatomer protein complex, subunit gamma
2609	1387445_at	0.274615716	1.209671832	yes	no	no	NM_031573	Rn.10399	phosphorylase kinase gamma 1
2610	1384543_at	0.275289599	1.210237002	yes	no	no	BF406553	---	---
2611	1367560_at	0.275386961	1.210318679	yes	no	no	NM_022402	Rn.1079	acidic ribosomal phosphoprotein P0
2612	1371307_at	0.275393907	1.210324506	yes	no	no	AW914090	Rn.973	ribosomal protein, large, P1
2613	1367957_at	0.275409464	1.210337557	yes	no	no	NM_019340	Rn.53900	regulator of G-protein signalling 3
2614	1368931_at	0.275529759	1.210438482	yes	no	no	NM_031238	Rn.5909	SH3-domain GRB2-like 3
2615	1375431_at	0.275531951	1.210440321	yes	no	no	AW531861	Rn.1149	Transcribed locus
2616	1370682_at	0.275728755	1.210605454	yes	no	no	AF169636	Rn.145183	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
2617	1392194_at	0.275796488	1.210662291	yes	no	no	BE101986	Rn.50177	Transcribed locus
2618	1367570_at	0.275926316	1.210771244	yes	no	no	NM_031549	Rn.34397	transgelin
2619	1377689_at	0.276014449	1.210845211	yes	no	no	BF564273	Rn.47918	kinetochore associated 1 (predicted)
2620	1377112_at	0.276101394	1.210918185	yes	no	no	AA859352	Rn.6887	cytidine deaminase (predicted)
2621	1394598_at	0.276242801	1.211036881	yes	no	no	AA956038	Rn.146794	Transcribed locus
2622	1371310_s_at	0.276341615	1.211119831	yes	no	no	BI285495	Rn.98199	serine (or cysteine) proteinase inhibitor, clade H, member 1
2623	1376599_at	0.276410571	1.211177719	yes	no	no	AW915567	Rn.6690	ATPase family, AAA domain containing 2 (predicted)

2624	1373632_at	0.276494592	1.211248259	yes	no	no	AI172041	Rn.8139	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor
2625	1388303_at	0.276550756	1.211295414	yes	no	no	AI598536	Rn.144702	ribosomal protein L26
2626	1395464_at	0.276748923	1.211461807	yes	no	no	AI237163	Rn.25415	similar to hypothetical protein FLJ12242 (predicted)
2627	1367568_a_at	0.276839907	1.211538211	yes	no	no	NM_012862	Rn.2379	matrix Gla protein
2628	1371977_at	0.276849498	1.211546265	yes	no	no	BG381477	Rn.4233	actin related protein 2/3 complex, subunit 3 (predicted)
2629	1388372_at	0.277023811	1.211692659	yes	no	no	AW914118	Rn.3458	ribosomal protein L35
2630	1377967_at	0.277038904	1.211705335	yes	no	no	AI112987	Rn.8884	Retroviral integration site 2 (predicted)
2631	1375170_at	0.277146585	1.211795779	yes	no	no	BG378926	Rn.104930	S100 calcium binding protein A11 (calizzarin)
2632	1398972_at	0.277295101	1.211920532	yes	no	no	AW916366	Rn.3963	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)
2633	1397882_at	0.277619766	1.212193293	yes	no	no	BF559709	Rn.162105	zinc finger and BTB domain containing 8 (predicted)
2634	1393134_at	0.277639569	1.212209933	yes	no	no	BG375377	Rn.66307	Transcribed locus
2635	1377676_at	0.277729998	1.212285917	yes	no	no	AI599187	Rn.21324	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate
2636	1390345_at	0.277747648	1.212300748	yes	no	no	BG375523	---	---
2637	1398751_at	0.277811465	1.212354375	yes	no	no	NM_031570	---	similar to ribosomal protein S7
2638	1382656_at	0.278167763	1.212653824	yes	no	no	AW521183	Rn.23866	transcription termination factor, RNA polymerase II (predicted)
2639	1373767_at	0.278473844	1.212911127	yes	no	no	AI406908	Rn.19157	zinc finger, AN1-type domain 2A
2640	1382325_at	0.27859557	1.213013469	yes	no	no	AW525471	Rn.195267	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)
2641	1392967_at	0.278849183	1.213226725	yes	no	no	BF550692	Rn.12802	similar to RIKEN cDNA 2700062C07
2642	1372349_at	0.278913273	1.213280622	yes	no	no	AI703543	Rn.17090	similar to UCH37-interacting protein 1 (predicted)
2643	1367569_at	0.27923785	1.213553616	yes	no	no	NM_017138	Rn.161973	ribosomal protein SA
2644	1381018_a_at	0.279287647	1.213595505	yes	no	no	BG378709	Rn.63466	development and differentiation enhancing (predicted)
2645	1367582_at	0.279425365	1.213711359	yes	no	no	NM_017150	Rn.3973	ribosomal protein L29
2646	1382063_at	0.279462069	1.213742238	yes	no	no	BM385090	Rn.98982	galactosidase, alpha (mapped)
2647	1386882_at	0.279562465	1.213826704	yes	no	no	NM_031318	Rn.29901	t-complex testis expressed 1
2648	1394494_at	0.279615433	1.21387127	yes	no	no	AA963519	Rn.100374	Rho guanine nucleotide exchange factor (GEF) 19 (predicted)
2649	1391201_at	0.279653065	1.213902934	yes	no	no	AI012084	Rn.98955	WD repeat and HMG-box DNA binding protein 1 (predicted)
2650	1367979_s_at	0.279708414	1.213949506	yes	no	no	NM_012941	Rn.107152	cytochrome P450, subfamily 51
2651	1389483_at	0.279727498	1.213965564	yes	no	no	AI408686	Rn.22725	Dpy-19-like 1 (C. elegans) (predicted)
2652	1390836_at	0.279858481	1.214075785	yes	no	no	AI031048	---	---
2653	1370876_at	0.28006836	1.214252419	yes	no	no	BI285436	Rn.3048	neurofascin
2654	1388488_at	0.28018439	1.21435008	yes	no	no	AA943742	Rn.4333	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)
2655	1367597_at	0.280303546	1.214450381	yes	no	no	NM_031706	Rn.3198	ribosomal protein S8
2656	1383155_at	0.280615556	1.214713056	yes	no	no	AA945854	Rn.8070	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (predicted)
2657	1398853_at	0.280632136	1.214727017	yes	no	no	AI169273	Rn.94551	proteasome (prosome, macropain) subunit, beta type 3
2658	1372134_at	0.280718155	1.214799446	yes	no	no	AW918650	Rn.6212	coiled-coil-helix-coiled-coil-helix domain containing 6 (predicted)
2659	1369186_at	0.280736042	1.214814507	yes	no	no	D85899	Rn.37508	caspase 1
2660	1388404_at	0.280871546	1.214928613	yes	no	no	AA799724	---	---
2661	1377016_at	0.280872362	1.2149293	yes	no	no	BE106888	Rn.19198	cysteine-rich with EGF-like domains 2
2662	1385517_at	0.281008695	1.215044115	yes	no	no	AI715835	Rn.27575	general transcription factor II I
2663	1367969_at	0.281054352	1.215082568	yes	no	no	AF014009	Rn.42	peroxiredoxin 6
2664	1375377_at	0.281054897	1.215083027	yes	no	no	BE098713	Rn.166127	Transcribed locus
2665	1393847_at	0.281393453	1.215368203	yes	no	no	AI502379	Rn.98363	NFKB inhibitor interacting Ras-like protein 1 (predicted)
2666	1374397_at	0.281440997	1.215408256	yes	no	no	BE107498	Rn.133804	eukaryotic translation initiation factor 2, subunit 2 (beta)
2667	1370807_at	0.281545178	1.215496027	yes	no	no	AF411216	Rn.109048	transmembrane protein 49

2668	1385199_a_at	0.281667843	1.215599379	yes	no	no	AI073196	Rn.93968	RNA binding motif protein 34
2669	1370178_at	0.2818244	1.2157313	yes	no	no	BG373973	Rn.10739	calcium channel, voltage-dependent, beta 2 subunit
2670	1378537_at	0.281998842	1.215878308	yes	no	no	BI289126	Rn.61067	Transcribed locus
2671	1367499_at	0.282025841	1.215901061	yes	no	no	BM390900	Rn.3950	solute carrier family 35, member C1 (predicted)
2672	1370100_at	0.282088094	1.215953529	yes	no	no	NM_022185	Rn.22497	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2
2673	1371390_at	0.282121283	1.215981503	yes	no	no	AA892044	Rn.110562	tubulin, beta 2c
2674	1388436_at	0.282182074	1.216032742	yes	no	no	AI230728	Rn.9347	small nuclear ribonucleoprotein polypeptide A
2675	1388314_at	0.282222803	1.216067072	yes	no	no	BF281178	Rn.4120	high mobility group nucleosomal binding domain 1
2676	1367645_at	0.282301569	1.216133467	yes	no	no	NM_017152	Rn.6920	ribosomal protein S17
2677	1378979_x_at	0.282603664	1.216388148	yes	no	no	AW520354	Rn.17162	Similar to KIAA1205 protein (predicted)
2678	1392101_s_at	0.283175623	1.216870483	yes	no	no	AI175670	Rn.24732	Transcribed locus
2679	1389636_at	0.283238211	1.216923274	yes	no	no	AI231088	Rn.22493	similar to KIAA0833 protein
2680	1377790_at	0.283267732	1.216948176	yes	no	no	BE115859	Rn.49288	Transcribed locus
2681	1387890_at	0.283269769	1.216949895	yes	no	no	AI229633	Rn.34942	ribosomal protein S29
2682	1368564_at	0.28327245	1.216952156	yes	no	no	NM_053427	Rn.19372	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6
2683	1377338_at	0.283520619	1.217161511	yes	no	no	BF395193	Rn.27018	RAD1 homolog (S. pombe) (predicted)
2684	1388976_at	0.283919044	1.217497697	yes	no	no	AI178272	Rn.13809	similar to BolA domain-containing protein like (11.4 kD) (1P25) (predicted)
2685	1367494_at	0.28395624	1.217529088	yes	no	no	AW523764	Rn.1198	similar to CGI-35 protein (predicted)
2686	1367576_at	0.284057882	1.21761487	yes	no	no	S41066	Rn.11323	glutathione peroxidase 1
2687	1377976_at	0.284239816	1.217768428	yes	no	no	AI137539	---	---
2688	1379938_at	0.284658112	1.218121561	yes	no	no	BE109444	---	---
2689	1390827_at	0.284773812	1.218219254	yes	no	no	AA997679	Rn.10636	MAD homolog 3 (Drosophila)
2690	1369304_at	0.284871086	1.218301396	yes	no	no	NM_017220	Rn.87164	6-pyruvoyl-tetrahydropterin synthase
2691	1371761_at	0.285097564	1.218492663	yes	no	no	AI013910	Rn.2028	ribosomal protein L34 (predicted)
2692	1369081_at	0.285204147	1.218582685	yes	no	no	NM_031522	Rn.128560	neuraminidase 1
2693	1373490_at	0.285337615	1.218695426	yes	no	no	BG666787	Rn.15333	glia maturation factor, gamma
2694	1371316_at	0.285506532	1.218838124	yes	no	no	AI177362	Rn.5998	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) protein /// similar to Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)
2695	1380225_at	0.285601516	1.218918372	yes	no	no	BF396725	Rn.27009	Transcribed locus
2696	1398784_at	0.285644142	1.218954387	yes	no	no	NM_019259	Rn.2765	complement component 1, q subcomponent binding protein
2697	1370642_s_at	0.285647268	1.218957029	yes	no	no	BM389426	Rn.98311	platelet derived growth factor receptor, beta polypeptide
2698	1367557_s_at	0.28596724	1.219227408	yes	no	no	NM_017008	Rn.91450	glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// similar to glyceraldehyde-3-phosphate dehydrogenase (predicted) /// simila
2699	1398444_at	0.286027238	1.219278113	yes	no	no	BF405417	---	---
2700	1388354_at	0.286238769	1.2194569	yes	no	no	BE349703	Rn.76239	activating signal cointegrator 1 complex subunit 3-like 1
2701	1394005_s_at	0.286495636	1.219674039	yes	no	no	BE115762	Rn.6795	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae) (predicted)
2702	1393447_at	0.286603402	1.21976515	yes	no	no	BG380625	Rn.145008	kinesin family member 7 (predicted) /// similar to kinesin family member 7
2703	1398391_at	0.286665798	1.219817905	yes	no	no	BG379297	Rn.35325	guanine nucleotide binding protein-like 1
2704	1386890_at	0.286970178	1.220075289	yes	no	no	NM_031114	Rn.4083	S100 calcium binding protein A10 (calpactin)
2705	1392495_at	0.28707118	1.220160709	yes	no	no	BF408346	Rn.143440	similar to dJ202D23.2 (novel protein similar to C21ORF5 (KIAA0933)) (predicted)
2706	1388443_at	0.287190903	1.220261969	yes	no	no	AI177871	Rn.40447	CDK2 (cyclin-dependent kinase 2)-associated protein 1 (predicted)

2707	1367609_at	0.287195961	1.220266247	yes	no	no	NM_031051	Rn.2661	macrophage migration inhibitory factor
2708	1389126_at	0.287219631	1.220286268	yes	no	no	BG373580	Rn.2620	coiled-coil-helix-coiled-coil-helix domain containing 1 (predicted)
2709	1393750_at	0.287220247	1.220286789	yes	no	no	BI303408	Rn.126080	Similar to KIAA1333 protein (predicted)
2710	1375739_at	0.2873424	1.220390115	yes	no	no	BF395171	Rn.7379	EH-domain containing 4
2711	1372948_at	0.287538743	1.220556216	yes	no	no	BG376761	---	---
2712	1368079_at	0.287566775	1.220579931	yes	no	no	NM_053826	Rn.11185	pyruvate dehydrogenase kinase, isoenzyme 1
2713	1398830_at	0.287610874	1.220617242	yes	no	no	NM_022697	Rn.36614	ribosomal protein L28
2714	1386973_a_at	0.287769631	1.220751568	yes	no	no	NM_053777	Rn.44266	mitogen activated protein kinase 8 interacting protein
2715	1384019_a_at	0.288060157	1.220997424	yes	no	no	BM383449	Rn.14290	Transcribed locus
2716	1387357_at	0.288066688	1.221002952	yes	no	no	NM_133387	Rn.3607	trimethyllysine hydroxylase, epsilon
2717	1398789_at	0.288247377	1.221155885	yes	no	no	NM_031106	Rn.65053	ribosomal protein L37
2718	1376606_a_at	0.288268848	1.221174059	yes	no	no	BM387118	---	---
2719	1367581_a_at	0.288335645	1.221230601	yes	no	no	AB001382	Rn.8871	secreted phosphoprotein 1
2720	1367595_s_at	0.288486715	1.221358487	yes	no	no	NM_012512	Rn.1868	beta-2 microglobulin
2721	1386891_at	0.288550909	1.221412833	yes	no	no	NM_017236	Rn.29745	phosphatidylethanolamine binding protein 1
2722	1367505_at	0.28885221	1.221667947	yes	no	no	AW916491	Rn.8773	Zinc finger protein 644 (predicted)
2723	1373850_at	0.289028468	1.221817211	yes	no	no	AW251315	Rn.13596	X Kell blood group precursor related family member 8 homolog /// sphingomyelin phosphodiesterase, acid-like 3B
2724	1372543_at	0.289146903	1.221917517	yes	no	no	BI282107	Rn.12007	similar to RIKEN cDNA 2610029G23 (predicted)
2725	1369879_a_at	0.289229818	1.221987746	yes	no	no	NM_019381	Rn.107678	testis enhanced gene transcript
2726	1373644_at	0.28926006	1.222013362	yes	no	no	AW253720	Rn.40435	CDNA clone IMAGE:7308494
2727	1388296_at	0.289441245	1.222166841	yes	no	no	BF281388	Rn.42766	ribosomal protein S18
2728	1378357_at	0.289702973	1.222388582	yes	no	no	AI556522	Rn.167864	Transcribed locus
2729	1383083_at	0.289916802	1.222569772	yes	no	no	AI575458	Rn.55281	Btg3 associated nuclear protein (predicted)
2730	1380118_at	0.289990418	1.222632157	yes	no	no	BI275569	Rn.67727	similar to hypothetical gene supported by AK085276 (predicted)
2731	1388902_at	0.29011043	1.222733867	yes	no	no	AI599031	Rn.770	lysyl oxidase-like 1
2732	1371297_at	0.290447469	1.223019553	yes	no	no	BI281697	Rn.144857	ribosomal protein L7a (predicted)
2733	1367682_at	0.290497474	1.223061944	yes	no	no	NM_030859	Rn.17447	midkine
2734	1367945_at	0.290507897	1.223070781	yes	no	no	NM_053359	Rn.11992	ATX1 (antioxidant protein 1) homolog 1 (yeast)
2735	1395928_at	0.290543623	1.223101069	yes	no	no	BE102495	Rn.11307	Thyroid hormone receptor alpha
2736	1370158_at	0.290615191	1.223161745	yes	no	no	AA946388	Rn.98166	myosin, heavy polypeptide 10, non-muscle
2737	1370246_at	0.290654377	1.223194968	yes	no	no	AA943837	Rn.5968	calmodulin 2
2738	1373631_at	0.290725871	1.223255586	yes	no	no	BF284067	Rn.18036	RAP1, GTPase activating protein 1
2739	1369278_at	0.290727068	1.223256601	yes	no	no	NM_031034	Rn.10497	guanine nucleotide binding protein, alpha 12
2740	1388110_at	0.290757059	1.223282031	yes	no	no	X61043	Rn.159783	eukaryotic translation elongation factor 1 alpha 1 /// similar to eukaryotic translation elongation factor 1 alpha 1 (predicted)
2741	1370823_at	0.290924466	1.223423986	yes	no	no	AF387513	Rn.25267	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)
2742	1388900_at	0.291232744	1.223685437	yes	no	no	BG381414	Rn.128917	RGD1566118 (predicted)
2743	1371398_at	0.291275164	1.223721418	yes	no	no	BF281400	---	---
2744	1375340_at	0.29145244	1.223871796	yes	no	no	AI104151	---	---
2745	1367808_at	0.291520352	1.223929409	yes	no	no	NM_022541	Rn.3792	translocase of inner mitochondrial membrane 8 homolog b (yeast)
2746	1383306_at	0.291527537	1.223935504	yes	no	no	AI013468	Rn.22089	Activity and neurotransmitter-induced early gene 2 (ania-2) mRNA, 3'UTR
2747	1370020_at	0.291737408	1.224113565	yes	no	no	NM_133418	Rn.3631	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
2748	1367685_at	0.291831843	1.224193695	yes	no	no	NM_031113	Rn.106034	ribosomal protein S27a
2749	1377656_at	0.291863244	1.224220341	yes	no	no	BG375054	Rn.160904	RNA binding motif protein 13
2750	1398776_at	0.291948843	1.224292979	yes	no	no	NM_031698	Rn.2879	ribophorin II

2751	1379243_at	0.292150149	1.224463822	yes	no	no	AA819547	Rn.4013	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (predicted)
2752	1371412_a_at	0.292159269	1.224471563	yes	no	no	BE107450	Rn.162297	Neuronal regeneration related protein
2753	1379793_at	0.292188198	1.224496116	yes	no	no	AW535749	Rn.15726	similar to RIKEN cDNA 3110031B13
2754	1383684_at	0.292201033	1.22450701	yes	no	no	BI288761	Rn.899	ASF1 anti-silencing function 1 homolog B (S. cerevisiae) (predicted)
2755	1372718_at	0.292229257	1.224530966	yes	no	no	AA799572	---	---
2756	1395623_at	0.292238374	1.224538704	yes	no	no	AW521959	---	---
2757	1381526_at	0.292365365	1.224646497	yes	no	no	BI293073	Rn.16053	par-6 (partitioning defective 6,) homolog alpha (C. elegans)
2758	1392943_at	0.292367222	1.224648073	yes	no	no	BG665934	Rn.35322	O-acyltransferase (membrane bound) domain containing 2
2759	1382660_at	0.29266059	1.224897127	yes	yes	no	AA923866	Rn.8284	Similar to FLJ20298 protein isoform a (predicted)
2760	1378556_at	0.292782278	1.225000449	yes	yes	no	AI411989	Rn.167463	Transcribed locus
2761	1388341_at	0.292782855	1.225000939	yes	yes	no	BI285671	Rn.107099	RAN GTPase activating protein 1
2762	1399106_at	0.292783458	1.225001451	yes	yes	no	AI176121	---	---
2763	1399073_at	0.293200091	1.225355267	yes	no	no	BI274378	Rn.9218	OTU domain, ubiquitin aldehyde binding 1 (predicted)
2764	1370389_at	0.29325633	1.225403035	yes	yes	no	AB036421	Rn.153513	glycoprotein m6b
2765	1379764_at	0.293935162	1.22597976	yes	yes	no	AI555029	---	---
2766	1383127_at	0.29405002	1.226077369	yes	yes	no	BI295823	Rn.36437	CDNA clone IMAGE:7320912
2767	1384804_at	0.294257987	1.226254123	yes	yes	no	AI029751	Rn.92659	DNA methyltransferase 3A
2768	1395248_at	0.294458465	1.226424536	yes	yes	no	BF418342	Rn.8162	similar to mKIAA0212 protein (predicted)
2769	1371074_a_at	0.294499998	1.226459843	yes	yes	no	U17565	Rn.33226	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)
2770	1382326_at	0.294532934	1.226487843	yes	yes	no	AI555347	Rn.146589	Death effector domain-containing
2771	1398774_at	0.294659304	1.226595279	yes	yes	no	NM_022699	Rn.161950	ribosomal protein L30
2772	1388519_at	0.294701319	1.226631002	yes	yes	no	BI281906	Rn.103030	Sec61 beta subunit (predicted)
2773	1373387_at	0.294720701	1.226647481	yes	yes	no	BF558946	---	---
2774	1371982_at	0.294976787	1.226865237	yes	yes	no	AI411960	Rn.3297	AIP1
2775	1393880_at	0.295030473	1.226910892	yes	no	no	AI030169	Rn.145428	RGD1565240 (predicted)
2776	1389369_at	0.295370428	1.227200034	yes	no	no	BF289017	Rn.165141	Transcribed locus, weakly similar to XP_579981.1 PREDICTED: hypothetical protein XP_579981 [Rattus norvegicus]
2777	1373862_at	0.295480965	1.227294064	yes	yes	no	AI009673	Rn.67055	Toll-like receptor adaptor molecule 2 (predicted)
2778	1390126_at	0.295519266	1.227326647	yes	yes	no	BE112913	---	---
2779	1384032_at	0.2958178	1.227580641	yes	no	no	AI058837	Rn.97552	Transcribed locus
2780	1374725_at	0.295914291	1.227662747	yes	yes	no	AW252811	Rn.13838	similar to mKIAA1631 protein
2781	1389571_at	0.295917994	1.227665899	yes	yes	no	BG666368	Rn.24237	signal transducer and activator of transcription 2
2782	1370234_at	0.296061432	1.227787964	yes	yes	no	AA893484	Rn.1604	fibronectin 1
2783	1367661_at	0.296286345	1.227979388	yes	yes	no	AF140232	Rn.3233	S100 calcium binding protein A6 (calcyclin)
2784	1371696_at	0.296522841	1.228180703	yes	no	no	AI412938	Rn.1677	G protein-coupled receptor 56
2785	1371441_at	0.296606972	1.228252327	yes	yes	no	BG662875	Rn.155339	phosphoprotein enriched in astrocytes 15
2786	1398885_at	0.296670355	1.22830629	yes	yes	no	AA925327	Rn.103172	ribosomal protein L23
2787	1367476_at	0.296677589	1.228312449	yes	yes	no	AA799994	Rn.1668	signal recognition particle 14 (predicted)
2788	1373135_at	0.296720998	1.228349407	yes	yes	no	AW531123	Rn.153971	similar to hypothetical protein MGC2744
2789	1374517_at	0.296796342	1.228413559	yes	yes	no	AA891612	Rn.32182	RecQ protein-like
2790	1373674_at	0.296925795	1.22852379	yes	yes	no	BI283094	Rn.25217	microfibrillar associated protein 5 (predicted)
2791	1381217_at	0.297030964	1.228613349	yes	yes	no	AI639158	Rn.8742	similar to CGI-09 protein (predicted)
2792	1384186_at	0.297083042	1.2286577	yes	yes	no	AI556447	Rn.8162	similar to mKIAA0212 protein (predicted)
2793	1389361_at	0.297193964	1.22875217	yes	yes	no	AI012506	Rn.19522	similar to 2610111M03Rik protein
2794	1374246_at	0.297449013	1.228969416	yes	yes	no	BF402392	Rn.146581	Transcribed locus

2795	1378080_at	0.297483814	1.228999061	yes	no	no	BI274498	Rn.13276	similar to SCO cytochrome oxidase deficient homolog 1 (yeast) (predicted)
2796	1384263_at	0.29764263	1.229134361	yes	no	no	AI072473	Rn.20164	similar to hypothetical protein MGC33214 (predicted)
2797	1374249_at	0.297782484	1.229253518	yes	no	no	AI168962	Rn.2550	similar to Hypothetical protein MGC38513
2798	1390294_at	0.298150021	1.229566719	yes	yes	no	BE100986	Rn.26694	Ataxin 7-like 4 (predicted)
2799	1373009_at	0.298237741	1.229641483	yes	yes	no	AI176734	Rn.104738	similar to RIKEN cDNA 0610037L13
2800	1391936_a_at	0.298246095	1.229648603	yes	yes	no	BI289110	Rn.45026	Transcribed locus
2801	1383521_at	0.298524731	1.229886115	yes	no	no	AW915081	Rn.165361	Transcribed locus
2802	1392118_at	0.298615626	1.229963604	yes	no	no	BE099845	Rn.3109	Transcribed locus
2803	1371971_at	0.298715647	1.23004888	yes	yes	no	AI599676	---	---
2804	1381130_at	0.298730725	1.230061736	yes	yes	no	BF412056	Rn.70183	minichromosome maintenance deficient 8 (S. cerevisiae) (predicted)
2805	1382756_at	0.298770677	1.230095799	yes	no	no	AI101822	Rn.6272	karyopherin (importin) alpha 1
2806	1368188_at	0.299319932	1.230564204	yes	yes	no	NM_017233	Rn.3664	4-hydroxyphenylpyruvic acid dioxygenase
2807	1389166_at	0.299647888	1.23084397	yes	yes	no	BF403998	Rn.46320	calcium and integrin binding family member 2
2808	1398590_at	0.300062458	1.231197714	yes	yes	no	AA965286	Rn.148596	Transcribed locus
2809	1368862_at	0.300097835	1.231227905	yes	yes	no	NM_033230	Rn.11422	thymoma viral proto-oncogene 1
2810	1373609_at	0.300293644	1.231395024	yes	yes	no	AI232274	Rn.133208	mitochondrial ribosomal protein S21 (predicted) /// similar to chromosome 1 open reading frame 51 (predicted)
2811	1386898_at	0.300318622	1.231416344	yes	yes	no	NM_012966	Rn.106093	heat shock 10 kDa protein 1 (chaperonin 10)
2812	1383259_at	0.300377222	1.231466363	yes	yes	no	BF412819	Rn.16404	Transcribed locus
2813	1379399_at	0.300611164	1.23166607	yes	no	no	AI711484	Rn.21651	similar to cDNA sequence BC016188
2814	1397530_at	0.300674779	1.23172038	yes	no	no	BF550362	Rn.7232	Treacher Collins Franceschetti syndrome 1, homolog (predicted)
2815	1367618_a_at	0.300683626	1.231727933	yes	yes	no	NM_130734	Rn.154574	discs, large homolog 5 (Drosophila) (predicted)
2816	1380393_at	0.30085999	1.231878517	yes	yes	no	AI409083	Rn.6746	crystallin, zeta
2817	1367606_at	0.300876389	1.23189252	yes	yes	no	NM_017153	Rn.94935	ribosomal protein S3a
2818	1387011_at	0.30104288	1.232034692	yes	no	no	NM_130741	Rn.11303	lipocalin 2
2819	1367905_at	0.301069317	1.232057268	yes	yes	no	NM_019370	Rn.44	ectonucleotide pyrophosphatase/phosphodiesterase 3
2820	1382105_at	0.301230944	1.232195306	yes	no	no	AI603217	Rn.23042	guanine nucleotide binding protein, beta 5
2821	1380501_x_at	0.30128573	1.232242098	yes	no	no	BF561706	Rn.65866	FK506 binding protein 2 (predicted)
2822	1392479_at	0.301442466	1.232375978	yes	no	no	AA925694	Rn.80611	FK506 binding protein 1a
2823	1367640_at	0.30154548	1.232463978	yes	yes	no	NM_031709	Rn.8400	ribosomal protein S12
2824	1377706_x_at	0.302103331	1.23294063	yes	no	no	BF549971	Rn.158668	Transcribed locus, moderately similar to XP_574280.1 PREDICTED: similar to Ab2-143 [Rattus norvegicus]
2825	1378264_at	0.302192206	1.233016586	yes	yes	no	BG375928	Rn.48344	Nuclear autoantigenic sperm protein (histone-binding)
2826	1386888_at	0.302407522	1.233200622	yes	yes	no	NM_053857	Rn.11161	eukaryotic translation initiation factor 4E binding protein 1
2827	1395697_at	0.302649684	1.233407636	yes	yes	no	BF561171	Rn.9027	similar to Ezh2 protein
2828	1393491_at	0.303186455	1.233866625	yes	no	no	BF398496	Rn.163445	transducin (beta)-like 1 X-linked (predicted)
2829	1380187_at	0.303187145	1.233867216	yes	yes	no	BI286219	Rn.21037	similar to TNF intracellular domain-interacting protein
2830	1397974_at	0.303832321	1.234419126	yes	no	no	BE110207	---	---
2831	1399004_at	0.304313493	1.234830902	yes	yes	no	BM986309	---	---
2832	1368652_at	0.304416517	1.234919086	yes	yes	no	AF262319	Rn.32199	caspase 9
2833	1398304_at	0.304471288	1.234965969	yes	yes	no	L02530	Rn.92324	frizzled homolog 2 (Drosophila)
2834	1379235_x_at	0.304760822	1.235213839	yes	yes	no	AI179539	Rn.98535	similar to CDC45L
2835	1374366_at	0.304970951	1.235393762	yes	no	no	AI556941	Rn.7960	solute carrier family 39 (zinc transporter), member 4 (predicted)
2836	1371023_at	0.305055181	1.235465891	yes	yes	no	AW524873	Rn.21378	EGF-like-domain, multiple 4
2837	1388371_at	0.305184577	1.235576706	yes	yes	no	AI008784	Rn.104417	Protein kinase C substrate 80K-H (predicted)
2838	1367578_at	0.305250738	1.235633369	yes	yes	no	NM_017169	Rn.2511	peroxiredoxin 2

2839	1368321_at	0.305433316	1.235789753	yes	no	no	NM_012551	Rn.9096	early growth response 1
2840	1371295_at	0.305502126	1.235848696	yes	yes	no	AW914097	Rn.103133	ribosomal protein S20
2841	1370864_at	0.3056756	1.235997307	yes	yes	no	Z78279	Rn.2953	procollagen, type 1, alpha 1
2842	1393990_at	0.305697851	1.23601637	yes	yes	no	AA956230	Rn.37928	zinc finger protein 503 (predicted)
2843	1395770_at	0.305715745	1.236031701	yes	yes	no	BM391695	Rn.176376	Transcribed locus
2844	1373147_at	0.305917471	1.236204542	yes	yes	no	AI145387	Rn.36356	F-box and leucine-rich repeat protein 3
2845	1383945_at	0.305961767	1.236242499	yes	yes	no	AA859827	Rn.24811	uridine monophosphate kinase (predicted)
2846	1371683_at	0.306000662	1.236275828	yes	yes	no	AI103250	Rn.27306	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)
2847	1384759_at	0.30660283	1.236791946	yes	no	no	AW534015	Rn.90858	PHD finger protein 17 (predicted)
2848	1383678_at	0.306733634	1.236904087	yes	no	no	BE102294	Rn.154712	similar to RIKEN cDNA 1810007P19
2849	1371595_at	0.306900831	1.237047443	yes	no	no	BM384301	Rn.153998	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2850	1392906_at	0.30710629	1.237223627	yes	yes	no	AW528860	Rn.163454	ubiquitin-like 4a (predicted)
2851	1387390_at	0.307309459	1.237397873	yes	no	no	NM_017119	Rn.11190	granzyme K
2852	1368679_a_at	0.307615569	1.237660451	yes	yes	no	L14782	Rn.4338	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog
2853	1377167_at	0.30762583	1.237669254	yes	no	no	AA964494	Rn.165176	Transcribed locus
2854	1384605_at	0.307679584	1.23771537	yes	yes	no	BF419162	Rn.170876	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
2855	1370999_at	0.308334305	1.238277194	yes	yes	no	AF111111	Rn.154430	sperm associated antigen 5
2856	1394995_at	0.308681037	1.238574833	yes	no	no	BM385139	Rn.161796	Cobl-like 1 (predicted)
2857	1397556_at	0.308928453	1.238787262	yes	yes	no	BF563329	Rn.137798	Mak3 homolog (S. cerevisiae) (predicted)
2858	1372219_at	0.309021538	1.238867193	yes	yes	no	AA012755	Rn.17580	similar to tropomyosin 1, embryonic fibroblast - rat
2859	1374902_at	0.30907531	1.238913368	yes	no	no	AI071398	Rn.17539	IQ motif containing GTPase activating protein 3 (predicted)
2860	1370010_at	0.309166817	1.238991952	yes	yes	no	NM_017068	Rn.1722	lysosomal membrane glycoprotein 2
2861	1369966_a_at	0.309188743	1.239010783	yes	yes	no	BG375811	Rn.979	ribosomal protein S24
2862	1369970_at	0.30934681	1.239146541	yes	yes	no	NM_031827	Rn.82672	vesicle-associated membrane protein 8
2863	1371808_at	0.309473591	1.239255439	yes	yes	no	AI012747	Rn.100672	bleomycin hydrolase
2864	1383137_at	0.310281466	1.239949587	yes	yes	no	AA956294	Rn.162218	SRY-box containing gene 4 (predicted)
2865	1392460_at	0.310297704	1.239963543	yes	yes	no	BF283685	---	---
2866	1367574_at	0.310607308	1.24022967	yes	yes	no	NM_031140	Rn.2710	vimentin
2867	1379058_at	0.310760812	1.240361638	yes	no	no	AA900904	Rn.5854	Transcribed locus
2868	1368268_at	0.310871521	1.240456824	yes	yes	no	NM_053729	Rn.98685	thymine-DNA glycosylase
2869	1373448_at	0.311300055	1.240825341	yes	yes	no	AI413052	Rn.3465	acylphosphatase 1, erythrocyte (common) type (predicted)
2870	1367559_at	0.311349381	1.240867765	yes	yes	no	L01122	Rn.1905	ferritin light chain 1
2871	1368953_at	0.31136165	1.240878318	yes	yes	no	NM_133596	Rn.162227	UDP-glucose ceramide glucosyltransferase-like 1
2872	1388618_at	0.311500702	1.240997924	yes	yes	no	BM389302	Rn.98892	nidogen 2
2873	1383900_at	0.31171396	1.241181381	yes	no	no	BG377183	---	---
2874	1367757_at	0.311855455	1.241303118	yes	yes	no	NM_019360	Rn.846	cytochrome c oxidase, subunit VIc
2875	1374216_at	0.311911695	1.241351508	yes	yes	no	BI280277	Rn.24598	Transcribed locus
2876	1369238_at	0.312015732	1.241441029	yes	yes	no	NM_031815	Rn.30020	inhibin beta E /// hypothetical gene supported by NM_031815
2877	1382620_at	0.312026826	1.241450576	yes	no	no	BF523248	Rn.23844	ankyrin repeat domain 11 (predicted)
2878	1397105_at	0.312362307	1.241739293	yes	yes	no	BE095920	Rn.63749	transcriptional regulator, SIN3A (yeast) (predicted)
2879	1374308_at	0.312392952	1.241765669	yes	no	no	AI575603	Rn.46850	SEC14-like 2 (S. cerevisiae)
2880	1385262_at	0.31257304	1.241920686	yes	no	no	BF387891	---	---
2881	1388325_at	0.312739286	1.242063804	yes	yes	no	BF281358	Rn.161955	ATPase, H+ transporting, V1 subunit D
2882	1368146_at	0.312852319	1.242161122	yes	yes	no	U02553	Rn.98260	dual specificity phosphatase 1

2883	1367561_at	0.313050552	1.242331812	yes	yes	no	NM_022514	Rn.1254	ribosomal protein L27
2884	1377749_at	0.313127302	1.242397905	yes	no	no	BE112621	Rn.160479	Transcribed locus
2885	1370220_at	0.313158676	1.242424923	yes	yes	no	BI283159	Rn.2108	serine carboxypeptidase 1
2886	1386420_at	0.313169714	1.242434429	yes	no	no	AI178749	Rn.167323	Transcribed locus
2887	1374340_at	0.313618601	1.242821067	yes	no	no	AA848536	Rn.17175	Glutaredoxin 2 (thioltransferase)
2888	1381513_at	0.313963259	1.24311801	yes	no	no	AI058295	Rn.29899	Similar to RIKEN cDNA 1300017J02
2889	1378137_at	0.314026292	1.243172324	yes	yes	no	BG379788	Rn.2783	leucine rich repeat containing 59
2890	1373408_at	0.314191163	1.243314402	yes	yes	no	BI282062	Rn.185799	tubulin cofactor a
2891	1396302_at	0.31422513	1.243343675	yes	no	no	BM389727	Rn.79053	Transcribed locus
2892	1367868_at	0.314432391	1.24352231	yes	no	no	NM_031708	Rn.9320	adhesion regulating molecule 1
2893	1389576_at	0.314432805	1.243522667	yes	yes	no	AA944322	Rn.7712	U2 small nuclear ribonucleoprotein B (predicted)
2894	1384107_at	0.314518146	1.243596228	yes	no	no	AI071397	Rn.20525	Transcribed locus
2895	1373841_at	0.314535663	1.243611328	yes	no	no	AI177431	Rn.3700	Transcribed locus
2896	1386935_at	0.314656014	1.243715075	yes	no	no	NM_024388	Rn.10000	nuclear receptor subfamily 4, group A, member 1
2897	1390098_at	0.314787844	1.243828728	yes	yes	no	AA955687	Rn.7240	similar to RIKEN cDNA 2510005D08 (predicted)
2898	1390109_at	0.314906893	1.243931372	yes	yes	no	BI303073	---	---
2899	1384878_at	0.314913852	1.243937371	yes	yes	no	AI501085	Rn.162255	N-myristoyltransferase 2
2900	1370284_at	0.315040026	1.244046168	yes	yes	no	AF010323	Rn.3454	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
2901	1367624_at	0.315205484	1.244188851	yes	yes	no	NM_024403	Rn.2423	activating transcription factor 4
2902	1367630_at	0.315406948	1.244362607	yes	yes	no	NM_031110	Rn.2177	ribosomal protein S11
2903	1391512_at	0.315578048	1.244510194	yes	yes	no	AI029734	Rn.18311	Myotubularin related protein 1 (predicted)
2904	1379628_at	0.315757497	1.244665002	yes	yes	no	AI070862	Rn.21362	Transcribed locus
2905	1387884_at	0.315807408	1.244708062	yes	yes	no	AI011191	Rn.1276	proteasome (prosome, macropain) subunit, alpha type 5
2906	1383741_at	0.316030103	1.244900211	yes	yes	no	BE100721	Rn.9410	Transcribed locus
2907	1367766_at	0.31620745	1.245053253	yes	yes	no	NM_031833	Rn.927	expressed in non-metastatic cells 2
2908	1390615_at	0.316282187	1.245117753	yes	yes	no	BI281629	Rn.146478	Transcribed locus
2909	1393301_at	0.316516823	1.245320272	yes	no	no	AI555172	Rn.12950	Similar to mKIAA0534 protein (predicted)
2910	1398410_at	0.316585655	1.245379689	yes	yes	no	AW535349	---	---
2911	1393290_at	0.316625412	1.245414009	yes	yes	no	AW142022	Rn.162435	similar to myocyte enhancer factor 2C
2912	1398777_at	0.316800203	1.245564907	yes	yes	no	NM_057099	Rn.8118	proteasome (prosome, macropain) subunit, beta type 6
2913	1372577_at	0.317053934	1.245783987	yes	yes	no	AI411582	---	actin related protein 2/3 complex, subunit 4 (predicted)
2914	1373372_at	0.317094013	1.245818596	yes	yes	no	BM389227	Rn.994	similar to lymphocyte antigen 6 complex, locus E ligand
2915	1372643_at	0.317172992	1.2458868	yes	yes	no	BE110569	Rn.1362	similar to protein 4.1G (predicted)
2916	1386926_at	0.317183472	1.24589585	yes	yes	no	NM_053607	Rn.105862	acyl-CoA synthetase long-chain family member 5
2917	1372701_at	0.317442587	1.246119639	yes	yes	no	AI237597	Rn.119867	heat shock protein 1, alpha
2918	1377173_at	0.317478862	1.246150972	yes	yes	no	BE104535	Rn.8670	Similar to Drctnnb1a (predicted)
2919	1387879_a_at	0.317687711	1.246331382	yes	no	no	AF090695	Rn.162247	CUG triplet repeat, RNA binding protein 2
2920	1370276_at	0.317738312	1.246375096	yes	yes	no	D13127	Rn.1817	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit
2921	1389686_at	0.31831306	1.246871732	yes	yes	no	BF408898	Rn.16741	protein kinase, X-linked
2922	1385191_at	0.318373176	1.246923689	yes	yes	no	AA997253	Rn.147561	Transcribed locus
2923	1383555_at	0.318551221	1.247077583	yes	yes	no	AW525704	Rn.145152	similar to RIKEN cDNA 4930579G22 (predicted)
2924	1396054_at	0.318721149	1.247224479	yes	yes	no	BF399535	Rn.173058	Transcribed locus, strongly similar to XP_575473.1 PREDICTED: similar to PALS2-alpha splice variant [Rattus norvegicus]
2925	1389967_at	0.318943677	1.247416871	yes	yes	no	AA892386	Rn.3366	ADP-ribosylation factor-like 6 interacting protein 1
2926	1382760_at	0.318962691	1.247433312	yes	no	no	AA899481	Rn.22915	Transcribed locus
2927	1374727_at	0.31907569	1.247531021	yes	yes	no	AF244895	Rn.20419	similar to DnaJ (Hsp40) homolog, subfamily B, member 12

2928	1368124_at	0.319214267	1.247650858	yes	no	no	NM_133578	Rn.10877	dual specificity phosphatase 5
2929	1384548_at	0.319421856	1.247830395	yes	yes	no	BM388159	Rn.162903	ribosomal protein L32
2930	1373977_at	0.319527908	1.247922125	yes	yes	no	BE108253	Rn.50843	Kinesin family member 5C (predicted)
2931	1383559_at	0.31954536	1.247937222	yes	yes	no	AI144819	Rn.60026	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19
2932	1392481_at	0.319722146	1.248090151	yes	yes	no	BG057566	Rn.22860	similar to DNA segment, Chr 1, Brigham & Womens Genetics 0212 expressed (predicted)
2933	1388525_at	0.319787143	1.248146383	yes	yes	no	BE112999	Rn.138969	similar to HGFL protein
2934	1386263_at	0.319895166	1.248239841	yes	yes	no	AI227677	Rn.99540	neural precursor cell expressed, developmentally down-regulated gene 4A
2935	1396205_at	0.320183587	1.248489413	yes	yes	no	BI303419	Rn.42381	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
2936	1369431_at	0.320221691	1.248522388	yes	yes	no	NM_022926	Rn.144577	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7
2937	1391817_at	0.320237827	1.248536352	yes	yes	no	AA901178	Rn.15144	Transcribed locus
2938	1383598_at	0.32043869	1.248710195	yes	yes	no	AI136294	Rn.23670	Transcribed locus
2939	1393205_at	0.320451282	1.248721094	yes	no	no	AA997182	Rn.9160	Similar to polymerase (RNA) II (DNA directed) polypeptide H (predicted)
2940	1392228_at	0.320531423	1.248790461	yes	yes	no	BI294408	Rn.163715	Transcribed locus
2941	1398909_at	0.320534947	1.248793512	yes	yes	no	AA849634	---	similar to QIL1
2942	1367951_at	0.320640363	1.248884763	yes	yes	no	NM_017328	Rn.9738	phosphoglycerate mutase 2
2943	1389875_at	0.320806965	1.249028992	yes	no	no	AI227951	---	---
2944	1390019_at	0.320880967	1.249093062	yes	yes	no	BM390456	Rn.124815	H3 histone, family 3B
2945	1395105_at	0.321191968	1.249362357	yes	yes	no	AW527267	Rn.90283	CWF19-like 2, cell cycle control (S. pombe) (predicted)
2946	1392875_at	0.321261086	1.249422214	yes	yes	no	AA964134	Rn.12566	F-box and leucine-rich repeat protein 4 (predicted)
2947	1398617_at	0.321477793	1.249609904	yes	yes	no	BE098167	Rn.144605	Transcribed locus, strongly similar to NP_062613.2 ubiquitin C [Mus musculus]
2948	1376381_at	0.321654688	1.249763133	yes	yes	no	AW252094	Rn.33372	XK-related protein 5
2949	1386901_at	0.322168409	1.250208234	yes	no	no	NM_031561	---	similar to fatty acid translocase/CD36 (predicted)
2950	1367983_at	0.322678207	1.250650091	yes	yes	no	NM_053430	Rn.16664	flap structure-specific endonuclease 1
2951	1368199_at	0.322698155	1.250667385	yes	yes	no	NM_053616	Rn.11042	nucleoporin 88
2952	1391518_at	0.322773576	1.250732768	yes	yes	no	AI579823	---	---
2953	1377616_at	0.323338273	1.251222423	yes	yes	no	BE114214	Rn.92601	similar to RIKEN cDNA 6720467C03 (predicted)
2954	1377600_at	0.323593747	1.251444011	yes	yes	no	BF419034	Rn.20401	similar to KIAA1285 protein (predicted)
2955	1371445_at	0.32378897	1.251613365	yes	yes	no	BF285649	Rn.2783	leucine rich repeat containing 59
2956	1392796_at	0.323867078	1.25168113	yes	yes	no	AI231609	Rn.16306	Transcribed locus
2957	1391236_at	0.324021177	1.251814834	yes	yes	no	BG380318	Rn.21174	similar to RIKEN cDNA 5730469D23 (predicted)
2958	1390741_at	0.324324198	1.25207779	yes	yes	no	BI294610	Rn.41117	similar to KIAA1086 protein (predicted)
2959	1375368_at	0.324350169	1.25210033	yes	yes	no	BF420654	Rn.163107	similar to RIKEN cDNA 1700012G19 gene (predicted)
2960	1376912_at	0.32455636	1.252279294	yes	yes	no	BI290097	Rn.82639	hypothetical LOC287388 (predicted)
2961	1374149_at	0.324856636	1.252539965	yes	yes	no	AW144301	Rn.8938	Transcribed locus
2962	1387795_at	0.325164183	1.252807004	yes	yes	no	NM_053480	Rn.91557	polymerase (DNA directed), alpha 2
2963	1385323_at	0.325643465	1.253223271	yes	no	no	AW532389	Rn.169976	Transcribed locus
2964	1395348_at	0.325747501	1.253313648	yes	no	no	AW143673	Rn.37666	tweety homolog 3 (Drosophila) (predicted)
2965	1382441_at	0.32605728	1.253582791	yes	yes	no	AI556402	Rn.22598	AT rich interactive domain 1B (Swi1 like)
2966	1370253_at	0.326078001	1.253600796	yes	yes	no	AI228150	Rn.21738	ribosomal protein L22
2967	1370931_at	0.326113068	1.253631268	yes	yes	no	AA893188	Rn.52078	X-ray repair complementing defective repair in Chinese hamster cells 5
2968	1372157_at	0.327448677	1.254792383	yes	yes	no	AI232807	Rn.13864	bolA-like 1 (E. coli) (predicted)
2969	1371521_at	0.327659027	1.25497535	yes	yes	no	BI284797	---	---
2970	1371578_at	0.327816006	1.255111911	yes	yes	no	AW915101	Rn.20	protein kinase, cAMP-dependent, catalytic, alpha

2971	1371869_at	0.327857012	1.255147586	yes	yes	no	BF282262	Rn.105784	proteasome (prosome, macropain) subunit, alpha type 7
2972	1372597_at	0.32791357	1.255196792	yes	yes	no	BE113348	Rn.35669	mitochondrial ribosomal protein L14 (predicted)
2973	1370062_at	0.327990651	1.255263857	yes	yes	no	NM_080902	Rn.2084	hypoxia induced gene 1
2974	1398324_at	0.328107918	1.255365893	yes	yes	no	BI279866	Rn.105821	similar to 60S ribosomal protein L18a
2975	1369588_a_at	0.328515645	1.255720728	yes	yes	no	NM_012915	Rn.1658	ATPase inhibitory factor 1
2976	1379360_at	0.328625199	1.255816087	yes	yes	no	AI013789	Rn.42741	similar to Putative protein 15E1.2 (predicted)
2977	1377914_at	0.329218288	1.256332457	yes	yes	no	AI059437	Rn.39266	serine/arginine repetitive matrix 1 (predicted)
2978	1387446_at	0.32935071	1.256447778	yes	yes	no	NM_022950	Rn.37669	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase
2979	1376084_a_at	0.329389531	1.256481589	yes	yes	no	AI385371	Rn.135286	extra spindle poles like 1 (S. cerevisiae) (predicted)
2980	1368320_at	0.329453276	1.256537107	yes	yes	no	NM_031521	Rn.11283	neural cell adhesion molecule 1
2981	1384762_at	0.329454935	1.256538551	yes	yes	no	BE103873	Rn.147915	Similar to shugoshin-like 1
2982	1394010_at	0.329588687	1.256655051	yes	yes	no	H32100	Rn.23988	hepatitis B virus x associated protein (predicted)
2983	1383596_at	0.329623937	1.256685755	yes	yes	no	AA956300	Rn.25170	similar to RIKEN cDNA 5830446M03
2984	1386860_at	0.329870139	1.256900232	yes	yes	no	NM_012811	Rn.3742	milk fat globule-EGF factor 8 protein
2985	1374799_at	0.33016553	1.257157608	yes	yes	no	AI407418	Rn.7870	similar to mKIAA0159 protein (predicted)
2986	1371300_at	0.330211753	1.257197888	yes	yes	no	AA892367	Rn.107726	ribosomal protein L3
2987	1398350_at	0.330373293	1.257338665	yes	yes	no	BG380454	Rn.37779	brain abundant, membrane attached signal protein 1
2988	1378977_at	0.330420645	1.257379934	yes	yes	no	AI178197	Rn.102063	Mediator of RNA polymerase II transcription, subunit 8 homolog (yeast) (predicted)
2989	1393730_at	0.330638484	1.257569806	yes	yes	no	BI277836	Rn.150301	Transcribed locus
2990	1373250_at	0.330676305	1.257602774	yes	yes	no	AI229404	---	anillin,actinbindingprotein
2991	1387074_at	0.331196968	1.25805672	yes	yes	no	AY043246	Rn.1892	regulator of G-protein signaling 2
2992	1393252_at	0.33148276	1.258305961	yes	yes	no	AA996804	Rn.165372	Transcribed locus
2993	1373223_at	0.331513931	1.258333148	yes	yes	no	AI101361	Rn.22383	Transcribed locus
2994	1371321_at	0.331558879	1.258372353	yes	yes	no	AI230604	Rn.6009	similar to Cytochrome c oxidase polypeptide VIb (Cytochrome c oxidase subunit AED) (predicted)
2995	1388532_at	0.331575719	1.258387041	yes	yes	no	AI599496	Rn.54973	similar to hypothetical protein
2996	1368192_at	0.331605727	1.258413216	yes	yes	no	NM_053415	Rn.24787	chemokine (C-X-C motif) receptor 3
2997	1389778_a_at	0.33172536	1.258517572	yes	yes	no	AI233115	Rn.37427	transcription elongation factor B (SIII), polypeptide 3
2998	1371539_at	0.331933567	1.258699212	yes	yes	no	AW921151	Rn.4216	nucleolar protein family A, member 2 (predicted)
2999	1375414_at	0.331981657	1.258741169	yes	yes	no	AA944572	Rn.8139	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor
3000	1379546_at	0.332146516	1.258885016	yes	no	no	AA875623	---	---
3001	1391600_at	0.332266512	1.258989728	yes	yes	no	BE118049	Rn.41977	Transcribed locus
3002	1370235_at	0.332290568	1.259010721	yes	yes	no	AI175009	Rn.3285	diazepam binding inhibitor
3003	1367594_at	0.332305139	1.259023437	yes	yes	no	NM_017087	Rn.783	biglycan
3004	1395045_at	0.33233553	1.259049959	yes	yes	no	BM384525	Rn.3422	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)
3005	1367860_a_at	0.33248007	1.259176106	yes	yes	no	X83537	Rn.10371	matrix metallopeptidase 14 (membrane-inserted)
3006	1379423_at	0.332506943	1.259199561	yes	yes	no	AA963364	Rn.11453	Transcribed locus, strongly similar to XP_418627.1 PREDICTED: similar to Ras suppressor protein 1 (Rsu-1) (RSP-1) [Gallus gallus]
3007	1380717_at	0.33296119	1.259596095	yes	yes	no	BF397758	Rn.58892	Zinc finger protein 626 (predicted)
3008	1371860_at	0.333101964	1.259719009	yes	yes	no	AA944016	Rn.1896	similar to RIKEN cDNA 1110059P08
3009	1371428_at	0.333584907	1.260140771	yes	yes	no	AI170002	---	---
3010	1389858_at	0.333851959	1.260374052	yes	yes	no	BM389006	---	---
3011	1373185_at	0.334653766	1.261074726	yes	yes	no	BE329347	Rn.17458	signal sequence receptor, beta (predicted)
3012	1393441_at	0.334719412	1.261132109	yes	yes	no	BI395605	Rn.185816	similar to cyclin-dependent kinase inhibitor 2D

3013	1391118_at	0.334940727	1.261325587	yes	yes	no	BI280337	Rn.33391	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (predicted)
3014	1367839_at	0.334948968	1.261332792	yes	yes	no	NM_019238	Rn.154404	farnesyl diphosphate farnesyl transferase 1
3015	1372013_at	0.335231053	1.261579439	yes	yes	no	BG380285	Rn.22087	interferon induced transmembrane protein 1 (predicted)
3016	1397686_at	0.335296617	1.261636774	yes	yes	no	BF566984	---	---
3017	1375661_at	0.335312266	1.261650459	yes	yes	no	BE104180	Rn.165233	Transcribed locus
3018	1386031_at	0.335358356	1.261690766	yes	yes	no	BF288135	Rn.3990	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3019	1370226_at	0.33562221	1.261921537	yes	yes	no	AI409867	Rn.1233	cystatin B
3020	1383558_at	0.335624221	1.261923296	yes	yes	no	BI290282	Rn.11965	similar to MJ0495-like protein SelB (predicted)
3021	1375220_at	0.335879232	1.262146374	yes	yes	no	AA818971	Rn.96380	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11
3022	1389339_at	0.335941779	1.262201094	yes	yes	no	BF284062	Rn.23323	Arylsulfatase A
3023	1389561_at	0.336025551	1.262274387	yes	yes	no	BE110624	Rn.105997	similar to RIKEN cDNA 1810021J13
3024	1378916_at	0.336072395	1.262315374	yes	no	no	AI029234	---	---
3025	1371335_at	0.3363502	1.262558468	yes	yes	no	AA944393	Rn.107458	similar to CG6105-PA
3026	1369858_at	0.336804386	1.262956007	yes	yes	no	NM_012706	Rn.10316	gastrin releasing peptide receptor
3027	1384289_at	0.337405751	1.26348256	yes	yes	no	BI281651	Rn.145169	similar to RIKEN cDNA 4631403P03
3028	1384050_at	0.337776436	1.26380724	yes	no	no	AI454535	Rn.6897	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)
3029	1383665_at	0.338069319	1.264063833	yes	yes	no	BE096055	---	---
3030	1378477_a_at	0.338859598	1.264756451	yes	yes	no	BI281796	Rn.105655	similar to Formin homology 2 domain containing 1
3031	1371313_at	0.339049129	1.264922617	yes	yes	no	AI172199	Rn.6018	similar to 60S ribosomal protein L23a (predicted)
3032	1386662_at	0.339093597	1.264961606	yes	no	no	BF553981	---	---
3033	1386854_at	0.339114134	1.264979613	yes	yes	no	AW535877	Rn.40291	Transcribed locus
3034	1397476_at	0.339319443	1.265159644	yes	yes	no	BM383386	Rn.107533	Ttk protein kinase (predicted)
3035	1371604_at	0.33953922	1.265352391	yes	yes	no	AA858969	Rn.2509	mitochondrial ribosomal protein L34
3036	1372653_at	0.33996672	1.265727396	yes	yes	no	BI276210	---	FK506 binding protein 11
3037	1389059_at	0.34007324	1.265820853	yes	yes	no	BI278651	Rn.165675	Transcribed locus, weakly similar to XP_359938.1 hypothetical protein MG11009.4 [Magnaporthe grisea 70-15]
3038	1388414_at	0.340163653	1.265900184	yes	yes	no	AI410498	Rn.162835	NADH dehydrogenase (ubiquinone) Fe-S protein 5b, 15kDa (NADH-coenzyme Q reductase)
3039	1388318_at	0.340364069	1.266076052	yes	yes	no	BI279760	Rn.108127	phosphoglycerate kinase 1
3040	1367946_at	0.340513295	1.266207017	yes	yes	no	NM_017365	Rn.11170	PDZ and LIM domain 1 (elfin)
3041	1384720_at	0.340723702	1.266391698	yes	yes	no	AI232723	---	---
3042	1387891_at	0.341354145	1.266945218	yes	yes	no	BI282076	Rn.17958	peroxiredoxin 4
3043	1388163_at	0.341369112	1.266958362	yes	yes	no	AI012445	Rn.102263	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
3044	1377959_at	0.341397055	1.266982902	yes	yes	no	BF397523	Rn.7484	similar to RIKEN cDNA 2510049I19 (predicted)
3045	1384988_at	0.341676958	1.267228738	yes	yes	no	BM385403	Rn.81585	F-box only protein 5 (predicted)
3046	1388391_at	0.341938838	1.267458788	yes	yes	no	AA996544	Rn.3640	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (predicted)
3047	1370290_at	0.342222654	1.267708155	yes	yes	no	AB011679	Rn.2458	tubulin, beta 5
3048	1373993_at	0.342569224	1.268012725	yes	no	no	AA799470	Rn.3573	Transcribed locus
3049	1376052_at	0.342799708	1.268215318	yes	yes	no	AW525031	Rn.39053	similar to hypothetical protein FLJ20512 (predicted)
3050	1375266_at	0.34355225	1.268877021	yes	yes	no	BG380633	---	---
3051	1398442_at	0.34355429	1.268878814	yes	yes	no	BF418993	Rn.17349	similar to chromosome 14 open reading frame 80 (predicted)
3052	1370962_at	0.343792373	1.269088231	yes	yes	no	AI136555	Rn.127830	castration induced prostatic apoptosis-related protein 1
3053	1393655_at	0.343831697	1.269122823	yes	yes	no	BF397746	Rn.134695	RAD54 like (S. cerevisiae) (predicted)
3054	1382736_at	0.343874829	1.269160767	yes	no	no	AI407047	Rn.20430	Similar to Zinc finger protein 198 (Fused in myeloproliferative disorders protein) (Rearranged in atypical myeloproliferative disorder protein) (predicted)

3055	1372640_at	0.343914166	1.269195372	yes	yes	no	BI277758	Rn.9448	RGD1563171 (predicted)
3056	1391477_at	0.343936577	1.269215088	yes	yes	no	BF396595	Rn.146152	Transcribed locus, moderately similar to NP_446319.1 tumor protein, translationally-controlled 1 [Rattus norvegicus]
3057	1372958_at	0.344106043	1.269364185	yes	yes	no	BE111986	Rn.9218	OTU domain, ubiquitin aldehyde binding 1 (predicted)
3058	1384857_at	0.344709712	1.269895438	yes	yes	no	AI145240	Rn.57458	A kinase (PRKA) anchor protein (yotiao) 9
3059	1389457_at	0.344989768	1.270141974	yes	yes	no	BF281184	Rn.20824	myeloblastosis oncogene-like 2 (predicted)
3060	1382768_at	0.345527802	1.270615745	yes	yes	no	BF289486	---	---
3061	1388879_at	0.34595986	1.270996326	yes	yes	no	BG669292	---	---
3062	1394478_at	0.346010918	1.271041308	yes	yes	no	BF388080	Rn.3730	Similar to expressed sequence AU040320 (predicted)
3063	1371417_at	0.346011807	1.271042091	yes	yes	no	AI233054	Rn.3472	low molecular mass ubiquinone-binding protein
3064	1389075_at	0.346067035	1.271090749	yes	yes	no	AI600221	Rn.164336	Transcribed locus
3065	1398906_at	0.346156007	1.271169141	yes	yes	no	BM391354	---	---
3066	1398439_a_at	0.346917504	1.271840279	yes	yes	no	AI070593	Rn.41300	origin recognition complex, subunit 6-like (S. cerevisiae)
3067	1389671_at	0.347062637	1.27196823	yes	yes	no	AW252088	Rn.48766	transient receptor potential cation channel, subfamily C, member 2
3068	1384231_at	0.347209993	1.272098155	yes	yes	no	BE108276	---	---
3069	1375981_a_at	0.347211245	1.272099259	yes	yes	no	AA997899	Rn.98526	suppressor of variegation 3-9 homolog 1 (Drosophila) (predicted)
3070	1398919_at	0.34755833	1.272405338	yes	yes	no	BI296033	Rn.1434	similar to Hypothetical protein CGI-99
3071	1376013_at	0.348021981	1.272814328	yes	yes	no	BF282700	Rn.8149	similar to mKIAA0227 protein (predicted)
3072	1381958_at	0.348025565	1.27281749	yes	yes	no	BE107587	Rn.21056	similar to mKIAA0259 protein (predicted)
3073	1388666_at	0.348095429	1.272879129	yes	yes	no	AI179988	Rn.3039	ectodermal-neural cortex 1
3074	1367726_at	0.348958458	1.2736408	yes	yes	no	NM_031134	Rn.11307	thyroid hormone receptor alpha
3075	1367623_at	0.348962858	1.273644685	yes	yes	no	NM_031102	Rn.484	ribosomal protein L18
3076	1369639_at	0.349281269	1.273925817	yes	yes	no	NM_012567	Rn.10346	gap junction membrane channel protein alpha 1
3077	1376684_at	0.349586473	1.274195346	yes	yes	no	AA874827	Rn.3137	discs, large homolog 7 (Drosophila) (predicted)
3078	1390170_at	0.349680534	1.274278423	yes	yes	no	BI287343	---	---
3079	1395745_at	0.349768498	1.274356122	yes	yes	no	AI113308	Rn.166667	Transcribed locus
3080	1374377_at	0.350249418	1.274780996	yes	yes	no	AA799657	---	---
3081	1374927_at	0.350574216	1.275068024	yes	yes	no	AI714124	Rn.14945	Transcribed locus
3082	1383436_at	0.350613677	1.2751029	yes	yes	no	BG376768	---	---
3083	1388339_at	0.350637253	1.275123738	yes	yes	no	BE112895	Rn.155339	phosphoprotein enriched in astrocytes 15
3084	1393643_at	0.350909556	1.275364435	yes	yes	no	AI112962	Rn.103345	reticulocalbin 1 (predicted)
3085	1390188_at	0.351078905	1.275514151	yes	yes	no	BF419327	Rn.154504	mitochondrial ribosomal protein L51 (predicted)
3086	1371344_at	0.351164077	1.275589456	yes	yes	no	AI177054	Rn.2722	ribosomal protein L27a (predicted)
3087	1387651_at	0.351508837	1.275894319	yes	yes	no	L07268	Rn.1618	aquaporin 1
3088	1387863_at	0.351891467	1.276232755	yes	yes	no	BE099415	Rn.3562	upstream of NRAS
3089	1371256_at	0.352570945	1.276833975	yes	yes	no	BM386565	Rn.9310	protein tyrosine phosphatase, non-receptor type 18
3090	1378453_at	0.353026668	1.277237369	yes	yes	no	BM389035	---	---
3091	1395361_at	0.353052201	1.277259973	yes	yes	no	AW142913	Rn.6102	Deoxyuridine triphosphatase
3092	1373296_a_at	0.35313443	1.277332775	yes	yes	no	AA800001	Rn.6268	similar to RIKEN cDNA 3200002M19 (predicted)
3093	1388304_at	0.353400112	1.277568027	yes	yes	no	BI281307	Rn.3367	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (predicted)
3094	1372665_at	0.353564757	1.277713835	yes	yes	no	AI230228	Rn.100813	phosphoserine aminotransferase 1
3095	1376078_at	0.353983658	1.278084886	yes	yes	no	BI296274	Rn.22415	Transcribed locus
3096	1385640_at	0.354407472	1.278460398	yes	yes	no	AI059511	Rn.19195	proprotein convertase subtilisin/kexin type 9
3097	1398279_at	0.354510361	1.278551577	yes	yes	no	NM_053787	Rn.137513	transient receptor potential cation channel, subfamily V, member 5
3098	1377299_at	0.354618288	1.278647229	yes	yes	no	AI137618	Rn.48344	nuclear autoantigenic sperm protein (histone-binding)
3099	1376342_at	0.355002622	1.278987906	yes	yes	no	BI295185	---	---
3100	1369779_at	0.3556521	1.279563815	yes	yes	no	NM_012983	Rn.10376	myosin ID

3101	1398426_at	0.35667674	1.280472918	yes	yes	no	AI409065	Rn.162334	similar to RIKEN cDNA B130052G07 (predicted)
3102	1380236_at	0.356978251	1.280740554	yes	yes	no	BM390141	Rn.9198	Integrin alpha 9
3103	1372389_at	0.357068675	1.28082083	yes	yes	no	BF420059	Rn.4298	immediate early response 2
3104	1383926_at	0.357183335	1.280922629	yes	yes	no	BF557145	Rn.49845	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)
3105	1389041_at	0.35723666	1.280969975	yes	yes	no	BF408597	Rn.46366	Vac14 homolog (S. cerevisiae)
3106	1387889_at	0.357733284	1.281411003	yes	yes	no	AI233882	Rn.6912	folate receptor 1 (adult)
3107	1393581_at	0.357829721	1.281496663	yes	yes	no	AW528001	Rn.55479	asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted)
3108	1383568_at	0.358073534	1.281713251	yes	yes	no	BF523441	Rn.101545	tubulin, epsilon 1 (predicted)
3109	1388116_at	0.358816722	1.282373681	yes	yes	no	BI285575	Rn.2953	procollagen, type 1, alpha 1
3110	1398967_at	0.359010299	1.282545758	yes	yes	no	AI410050	Rn.7360	thyroid hormone receptor associated protein 4
3111	1371354_at	0.359683673	1.283144523	yes	yes	no	AI710682	Rn.15460	troponin C type 1 (slow)
3112	1395981_at	0.360149303	1.283558725	yes	yes	no	AW919934	Rn.24209	activating signal cointegrator 1 complex subunit 3 (predicted)
3113	1393647_at	0.36023856	1.283638139	yes	yes	no	BI285581	Rn.139751	histone aminotransferase 1
3114	1398754_at	0.360517672	1.283886503	yes	yes	no	NM_031687	Rn.4300	ubiquitin A-52 residue ribosomal protein fusion product 1
3115	1393238_at	0.360753177	1.284096101	yes	yes	no	AA900649	---	---
3116	1396049_x_at	0.360935014	1.284257959	yes	yes	no	BG057530	Rn.107726	ribosomal protein L3
3117	1396114_at	0.361628788	1.284875691	yes	yes	no	BF416488	Rn.162867	F-box only protein 33 (predicted)
3118	1395467_at	0.361694437	1.284934159	yes	yes	no	AI145705	---	similar to N-copine
3119	1387017_at	0.361704504	1.284943126	yes	yes	no	NM_017136	Rn.33239	squalene epoxidase
3120	1389160_at	0.36186102	1.285082535	yes	yes	no	AI230287	Rn.136569	erythroid associated factor (predicted)
3121	1376120_at	0.361866148	1.285087103	yes	yes	no	BG671875	Rn.92162	similar to pancreatitis-induced protein 49
3122	1376476_at	0.36193169	1.285145486	yes	yes	no	BI279598	Rn.34729	similar to 1200003M09Rik protein (predicted)
3123	1375191_at	0.363257915	1.286327423	yes	yes	no	AI230379	Rn.4131	RGD1564011 (predicted)
3124	1392287_at	0.363697108	1.286719074	yes	yes	no	AW523201	Rn.18215	Transcribed locus
3125	1371701_at	0.363845101	1.286851073	yes	yes	no	BG666921	Rn.22045	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (predicted)
3126	1370075_at	0.364018883	1.287006093	yes	yes	no	NM_130400	Rn.133502	dihydrofolate reductase
3127	1376780_at	0.364603836	1.287528026	yes	yes	no	AI172311	---	---
3128	1390335_at	0.365073433	1.287947184	yes	yes	no	AW252589	Rn.168533	Transcribed locus
3129	1399102_at	0.365703192	1.288509516	yes	yes	no	BG377901	Rn.18664	similar to hypothetical protein MGC15523
3130	1382280_at	0.365970329	1.288748125	yes	yes	no	BF290998	Rn.2334	ubiquinol cytochrome c reductase core protein 2
3131	1368307_at	0.366895497	1.289574836	yes	yes	yes	NM_130423	Rn.15462	gamma-glutamyltransferase-like 3
3132	1398587_at	0.367005891	1.289673517	yes	yes	no	AA860035	Rn.43360	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3133	1367960_at	0.367254595	1.28989586	yes	yes	yes	NM_019186	Rn.9258	ADP-ribosylation factor-like 4A
3134	1370238_at	0.367265859	1.289905932	yes	yes	yes	AA891707	Rn.15277	upregulated during skeletal muscle growth 5
3135	1382980_at	0.367331382	1.289964517	yes	yes	no	AA964943	Rn.147566	Transcribed locus
3136	1396086_at	0.367656716	1.290255442	yes	yes	yes	H31931	Rn.20057	transmembrane protein 97
3137	1394518_at	0.367728984	1.290320076	yes	yes	no	BF284436	Rn.162758	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)
3138	1367690_at	0.368094944	1.290647426	yes	yes	yes	NM_017199	Rn.1999	signal sequence receptor 4
3139	1379234_a_at	0.368401595	1.290921787	yes	yes	no	AI179539	Rn.98535	similar to CDC45L
3140	1382284_at	0.368520843	1.291028495	yes	yes	no	AW525175	Rn.45730	NIMA (never in mitosis gene a)-related expressed kinase 3 (predicted)
3141	1372406_at	0.368633189	1.291129034	yes	yes	yes	BM383428	Rn.12916	minichromosome maintenance deficient 3 (S. cerevisiae) (predicted) /// similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3)
3142	1395530_at	0.368726339	1.2912124	yes	yes	no	AI555739	Rn.14633	CD2 antigen (cytoplasmic tail) binding protein 2 (predicted)
3143	1398892_at	0.368735941	1.291220994	yes	yes	yes	BI287960	Rn.3491	Niemann Pick type C2

3144	1394746_at	0.368764482	1.291246539	yes	yes	no	AI180352	Rn.77165	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)
3145	1371368_at	0.369149619	1.291591292	yes	yes	yes	BI279499	Rn.47029	Sec61 alpha 1 subunit (S. cerevisiae)
3146	1390469_at	0.369265281	1.291694844	yes	yes	no	BM391488	Rn.38521	nurim (nuclear envelope membrane protein)
3147	1385220_at	0.36975387	1.292132369	yes	yes	yes	BG377563	---	---
3148	1368712_at	0.369931608	1.292291567	yes	yes	yes	NM_019620	Rn.10663	zinc finger protein 386 (Kruppel-like)
3149	1381089_at	0.370259329	1.292585156	yes	yes	no	BE114458	Rn.147596	Transcribed locus
3150	1369679_a_at	0.370279543	1.292603267	yes	yes	yes	AB060652	Rn.10550	nuclear factor I/A
3151	1399139_at	0.370658129	1.292942511	yes	yes	no	BF551251	Rn.43960	Similar to hypothetical protein FLJ11305 (predicted)
3152	1382636_at	0.371043895	1.293288281	yes	yes	no	AA899383	Rn.164585	Transcribed locus
3153	1371497_at	0.37121126	1.293438321	yes	yes	no	BF393085	Rn.160607	ankyrin repeat and SOCS box-containing protein 6
3154	1389501_at	0.37135785	1.293569753	yes	yes	no	BG371889	---	---
3155	1390233_at	0.371616251	1.293801465	yes	yes	no	BE107321	Rn.38778	Transcribed locus
3156	1367973_at	0.372274201	1.294391645	yes	yes	no	NM_031530	Rn.4772	chemokine (C-C motif) ligand 2
3157	1375576_at	0.372318257	1.294431173	yes	yes	no	BE113025	Rn.140812	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28 (predicted)
3158	1380162_at	0.372724811	1.294795998	yes	yes	yes	BI274645	Rn.72896	RDCR-0918-3 protein
3159	1368822_at	0.372742993	1.294812316	yes	yes	yes	BI290885	Rn.95652	follistatin-like 1
3160	1384174_at	0.372944921	1.294993558	yes	yes	yes	AI028874	---	---
3161	1368260_at	0.373184302	1.295208449	yes	yes	yes	NM_053749	Rn.10865	aurora kinase B
3162	1371540_at	0.373331505	1.295340611	yes	yes	yes	AI102711	Rn.103147	keratinocyte associated protein 2 (predicted)
3163	1380799_at	0.373459601	1.295455628	yes	yes	no	BF388208	Rn.62391	Transcribed locus
3164	1370241_at	0.374157766	1.29608269	yes	yes	yes	AA800502	Rn.1247	cytochrome P450, family 2, subfamily c, polypeptide 7
3165	1371552_at	0.374223428	1.296141681	yes	yes	yes	BF400684	Rn.41520	Transcribed locus
3166	1373671_at	0.374543825	1.296429564	yes	yes	yes	AA944790	Rn.83	Hypothetical gene LOC554364
3167	1390832_at	0.374825882	1.296683049	yes	yes	yes	BI294696	Rn.19106	Transcribed locus
3168	1381282_at	0.375039044	1.296874652	yes	yes	no	BF416808	Rn.63148	similar to cDNA sequence BC026432 (predicted)
3169	1378163_at	0.375199139	1.297018574	yes	yes	yes	AA817956	Rn.16419	Transcribed locus
3170	1373126_at	0.375253707	1.297067632	yes	yes	no	AW918188	Rn.1563	Hook homolog 3 (Drosophila)
3171	1386874_at	0.375724569	1.297491034	yes	yes	yes	NM_017151	Rn.3391	ribosomal protein S15
3172	1384812_at	0.376039995	1.297774744	yes	yes	no	AI229409	Rn.147831	Transcribed locus
3173	1395628_at	0.376226656	1.297942666	yes	yes	no	AW434310	Rn.147027	Transcribed locus
3174	1378072_at	0.376651477	1.298324918	yes	yes	yes	BE115405	Rn.51222	similar to novel protein (predicted)
3175	1375988_at	0.377065781	1.298697817	yes	yes	yes	AW914928	---	---
3176	1371015_at	0.377174692	1.298795861	yes	yes	no	X52711	Rn.10373	myxovirus (influenza virus) resistance 1
3177	1372042_at	0.377512929	1.299100396	yes	yes	yes	BI294844	Rn.15332	CKLF-like MARVEL transmembrane domain containing 3 (predicted)
3178	1395229_at	0.378000029	1.299539089	yes	yes	no	BG375118	Rn.129752	Rho guanine nucleotide exchange factor (GEF) 12
3179	1382314_at	0.378349016	1.299853484	yes	yes	yes	BE096523	---	interferon, alpha-inducible protein (clone IFI-15K) (predicted)
3180	1384652_at	0.378466078	1.299958961	yes	yes	no	AI555485	Rn.140508	HIV TAT specific factor 1 (predicted)
3181	1379619_at	0.378744385	1.300209757	yes	yes	yes	BE104952	Rn.27422	Transcribed locus
3182	1368233_at	0.379100265	1.300530528	yes	yes	yes	NM_031042	Rn.11000	general transcription factor IIF, polypeptide 2
3183	1394155_at	0.379500419	1.300891301	yes	yes	no	AI010943	Rn.22366	RNA binding motif protein 7 (predicted)
3184	1382896_at	0.3797311	1.301099325	yes	yes	no	BI291999	Rn.177350	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
3185	1371556_at	0.379874483	1.301228641	yes	yes	no	BE108748	Rn.12810	protein inhibitor of activated STAT, 4
3186	1382468_at	0.380109625	1.301440743	yes	yes	yes	AW143385	---	similar to CG9752-PA
3187	1381035_at	0.380215638	1.30153638	yes	yes	no	AI235476	Rn.10526	Peptidase (prosome, macropain) 26S subunit, ATPase 1
3188	1381399_at	0.38076514	1.302032211	yes	yes	no	BG381338	Rn.65053	ribosomal protein L37 /// similar to ribosomal protein L37 (predicted) ///

									similar to ribosomal protein L37 (predicted)
3189	1386571_at	0.380971924	1.302218847	yes	yes	no	BF567145	Rn.27435	similar to adaptor molecule SRCASM (predicted)
3190	1397173_at	0.381036098	1.302276774	yes	yes	yes	BE109095	Rn.31723	Transcribed locus
3191	1378555_at	0.381457367	1.302657096	yes	yes	no	BE107055	Rn.16888	Transcribed locus
3192	1380009_at	0.381491793	1.302688181	yes	yes	yes	BM392230	Rn.92083	vaccinia related kinase 1
3193	1397704_at	0.38170054	1.302876683	yes	yes	yes	BF407449	Rn.145486	similar to establishment of cohesion 1 homolog 2 (predicted)
3194	1397341_at	0.381793435	1.302960578	yes	yes	yes	BG663837	Rn.137333	PDZ binding kinase (predicted)
3195	1394926_at	0.382771713	1.303844403	yes	yes	no	AW527214	Rn.20389	Spectrin beta 3
3196	1395358_at	0.382901404	1.303961617	yes	yes	no	BF562492	Rn.53889	Rho-related BTB domain containing 3 (predicted)
3197	1393706_at	0.383177847	1.304211501	yes	yes	no	BE109939	Rn.51773	six transmembrane epithelial antigen of the prostate 1 (predicted)
3198	1378906_at	0.383522794	1.304523374	yes	yes	yes	BE098141	Rn.14573	Similar to hypothetical protein FLJ25416 (predicted)
3199	1393982_at	0.383849121	1.304818481	yes	yes	yes	AI070935	Rn.34652	polymerase (DNA directed), epsilon 2 (p59 subunit) (predicted)
3200	1384828_at	0.384522953	1.305428058	yes	yes	no	AI058952	Rn.145008	Kinesin family member 7 (predicted)
3201	1368716_at	0.384534132	1.305438174	yes	yes	no	NM_133425	Rn.87667	protein phosphatase 1, regulatory (inhibitor) subunit 14c
3202	1391399_at	0.385183222	1.306025642	yes	yes	no	AW524037	Rn.129744	Transcribed locus
3203	1371854_at	0.385194111	1.306035499	yes	yes	yes	BG374451	---	---
3204	1389326_at	0.38527973	1.30611301	yes	yes	yes	AI103093	Rn.3711	replication factor C (activator 1) 3
3205	1391578_at	0.385947583	1.306717776	yes	yes	no	BF397936	---	---
3206	1367866_at	0.386247761	1.30698969	yes	yes	yes	NM_019153	Rn.1699	fibulin 5
3207	1389481_at	0.386257091	1.306998142	yes	yes	yes	BI282891	Rn.104274	similar to GI:13385412-like protein splice form I
3208	1375632_at	0.386316716	1.30705216	yes	yes	yes	H35210	---	similar to 60S ribosomal protein L38 (predicted)
3209	1388850_at	0.386451886	1.307174628	yes	yes	yes	BG671521	Rn.119867	heat shock protein 1, alpha
3210	1370230_at	0.386675077	1.307376869	yes	yes	yes	BG666602	Rn.5790	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
3211	1374193_at	0.387074302	1.307738698	yes	yes	yes	BI303636	Rn.167718	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3212	1389319_at	0.387199032	1.307851765	yes	yes	yes	AA800719	Rn.98517	Transcribed locus
3213	1390939_at	0.387431935	1.308062916	yes	yes	yes	AA944518	Rn.174745	Transcribed locus
3214	1373910_at	0.387437915	1.308068339	yes	yes	no	BG373576	Rn.18530	Transcribed locus, weakly similar to NP_473118.2 hypothetical protein [Plasmodium falciparum 3D7]
3215	1373893_at	0.388171739	1.308733854	yes	yes	no	BI291309	---	---
3216	1385830_at	0.388739898	1.309249358	yes	yes	yes	BE110287	Rn.47098	similar to hypothetical protein FLJ31606 (predicted)
3217	1369590_a_at	0.390683438	1.311014314	yes	yes	yes	NM_024134	Rn.11183	DNA-damage inducible transcript 3
3218	1372125_at	0.390729526	1.311056197	yes	yes	yes	BF408445	Rn.4130	glutathione peroxidase 7 (predicted)
3219	1376048_at	0.390777537	1.311099828	yes	yes	yes	BG373370	Rn.38113	Transcribed locus
3220	1385086_at	0.391269758	1.311547227	yes	yes	yes	BF388785	Rn.56816	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)
3221	1374772_at	0.391781611	1.312012632	yes	yes	no	BE100409	Rn.15872	similar to Chromosome 13 open reading frame 21 (predicted)
3222	1379249_at	0.391925444	1.312143443	yes	yes	no	AA900400	Rn.164627	Transcribed locus
3223	1385068_at	0.393033407	1.313151533	yes	yes	yes	BF397283	Rn.147678	Transcribed locus
3224	1374840_at	0.393083887	1.31319748	yes	yes	yes	BG377716	Rn.107310	Similar to CG2919-PA (predicted)
3225	1381393_at	0.393274252	1.31337077	yes	yes	no	BI301735	Rn.146443	Similar to sperm antigen HCMOGT-1
3226	1374802_at	0.393470351	1.313549302	yes	yes	yes	AI010721	Rn.17621	similar to chromosome 14 open reading frame 94
3227	1380707_at	0.393930883	1.313968676	yes	yes	no	BE113229	Rn.9525	similar to 2010321M09Rik protein
3228	1375179_at	0.394045293	1.314072881	yes	yes	no	AI231282	---	---
3229	1373363_at	0.394376846	1.314374909	yes	yes	no	BI281702	Rn.98152	microtubule-associated protein 1b
3230	1392139_at	0.394376878	1.314374939	yes	yes	no	BE105731	Rn.146614	Transcribed locus
3231	1394873_at	0.394494441	1.31448205	yes	yes	no	AI454447	---	---

3232	1382197_at	0.394528603	1.314513176	yes	yes	no	AA955648	Rn.25197	ras homolog gene family, member D (predicted)
3233	1374426_at	0.394826945	1.314785039	yes	yes	yes	BG670074	Rn.129215	ubiquinol-cytochrome c reductase binding protein (predicted)
3234	1375868_at	0.395342321	1.315254805	yes	yes	yes	BI282767	Rn.43179	Transcribed locus
3235	1390802_at	0.395734702	1.315612574	yes	yes	yes	AI170769	Rn.106153	similar to RIKEN cDNA 5033414D02 (predicted)
3236	1377678_at	0.395851111	1.315718734	yes	yes	yes	BI283757	Rn.11630	Transcribed locus
3237	1375686_at	0.395924421	1.315785593	yes	yes	yes	AI706907	Rn.14747	peptidylprolyl isomerase (cyclophilin)-like 3
3238	1367911_at	0.396307126	1.316134679	yes	yes	yes	NM_053638	Rn.95104	isocitrate dehydrogenase 3 (NAD+) alpha
3239	1385538_at	0.39636805	1.31619026	yes	yes	yes	AI059209	---	---
3240	1377853_at	0.396435165	1.316251491	yes	yes	yes	AI599177	Rn.9411	Zinc finger protein 537 (predicted)
3241	1367780_at	0.396588947	1.316391802	yes	yes	yes	NM_022391	Rn.271	pituitary tumor-transforming 1
3242	1389998_at	0.396601716	1.316403453	yes	yes	yes	BE113958	Rn.17815	Nuclear receptor subfamily 2, group F, member 2
3243	1376222_at	0.397851281	1.317544127	yes	yes	yes	AI710677	Rn.38645	similar to HCDI protein (predicted)
3244	1394075_at	0.397904805	1.317593009	yes	yes	no	AI059004	Rn.163415	Fanconi anemia, complementation group A (predicted)
3245	1385594_at	0.398689602	1.318309947	yes	yes	no	AW144020	Rn.118218	Transcribed locus
3246	1377446_at	0.398819197	1.318428375	yes	yes	no	BF409122	Rn.23848	similar to phosphoinositol 4-phosphate adaptor protein-2 (predicted)
3247	1389651_at	0.398950214	1.318548112	yes	yes	yes	AI177057	Rn.22847	apelin, AGTRL1 ligand
3248	1387151_at	0.399469545	1.319022838	yes	yes	yes	NM_053830	Rn.11398	nucleoporin 107
3249	1371462_at	0.399681839	1.319216948	yes	yes	no	BE108969	Rn.160666	insulin-like growth factor binding protein 4
3250	1390982_at	0.39986063	1.319380447	yes	yes	yes	BM389435	Rn.159953	chromatin assembly factor 1, subunit B (p60)
3251	1367641_at	0.399982532	1.319491935	yes	yes	yes	NM_017050	Rn.6059	superoxide dismutase 1
3252	1379957_at	0.400477247	1.319944479	yes	yes	yes	BE107457	Rn.137139	schlafen 8
3253	1371387_at	0.40048401	1.319950667	yes	yes	yes	AA866477	Rn.2026	cytochrome c oxidase subunit VIIb
3254	1387592_at	0.401071979	1.320488721	yes	yes	no	NM_031575	Rn.10506	thymoma viral proto-oncogene 3
3255	1394419_at	0.401194907	1.320601241	yes	yes	yes	BE109109	Rn.51673	similar to RIKEN cDNA 6530401L14 gene
3256	1389621_at	0.401227352	1.320630941	yes	yes	yes	BE113454	Rn.138993	FIP1 like 1 (S. cerevisiae)
3257	1371843_at	0.401322661	1.320718188	yes	yes	yes	AI234128	Rn.7575	Yip1 domain family, member 5
3258	1370324_at	0.401608661	1.320980034	yes	yes	no	AF120492	Rn.10025	ATPase, Cu++ transporting, beta polypeptide
3259	1371381_at	0.401972486	1.321313206	yes	yes	yes	AI007981	Rn.141267	similar to TBC1 domain family member 4 (predicted)
3260	1374166_at	0.402188633	1.321511183	yes	yes	yes	AW252076	Rn.140754	Transcribed locus
3261	1373082_at	0.402370277	1.321677579	yes	yes	yes	AA893743	Rn.164219	Transcribed locus
3262	1397218_at	0.402454473	1.321754715	yes	yes	yes	BF420803	Rn.93365	Dihydropyrimidinase-like 3
3263	1387892_at	0.402478485	1.321776714	yes	yes	yes	BI285440	Rn.2458	tubulin, beta 5
3264	1397586_at	0.403486893	1.322700926	yes	yes	yes	BI300588	---	---
3265	1379524_at	0.403673908	1.322872398	yes	yes	yes	AI136576	Rn.116904	WD repeat domain 34
3266	1394501_at	0.403798157	1.322986332	yes	yes	no	BM390379	Rn.29166	sialic acid binding Ig-like lectin 10 (predicted)
3267	1394510_at	0.403834544	1.3230197	yes	yes	yes	BF290684	Rn.56130	Transcribed locus
3268	1369960_at	0.404015626	1.323185772	yes	yes	yes	NM_031648	Rn.3828	FXYD domain-containing ion transport regulator 1
3269	1376185_at	0.405086031	1.324167871	yes	yes	yes	AW253880	Rn.38181	kinesin family member C1
3270	1374922_at	0.405402733	1.324458585	yes	yes	yes	AI013096	Rn.32671	ATP binding domain 1 family, member B (predicted)
3271	1382591_at	0.405609614	1.324648526	yes	yes	no	AI045562	Rn.23346	Transcribed locus
3272	1369076_at	0.406733683	1.325681021	yes	yes	yes	NM_021671	Rn.12122	transmembrane protein 33
3273	1371323_at	0.406755569	1.325701132	yes	yes	yes	BG666002	---	---
3274	1376176_at	0.40730916	1.326209928	yes	yes	yes	AI145586	Rn.140743	Transcribed locus, moderately similar to XP_533875.2 PREDICTED: similar to microtubule associated serine/threonine kinase 2 [Canis familiaris]
3275	1388661_at	0.407328606	1.326227804	yes	yes	yes	AA943734	Rn.106244	mitochondrial protein, 18 kDa
3276	1374632_at	0.407678056	1.326549082	yes	yes	yes	AI232697	Rn.19923	phosphatidylserine receptor

3277	1367590_at	0.407755954	1.326620711	yes	yes	yes	NM_053439	Rn.107698	RAN, member RAS oncogene family
3278	1371605_at	0.407818045	1.326677807	yes	yes	yes	AI710281	Rn.86466	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (predicted)
3279	1374887_at	0.408004535	1.326849311	yes	yes	no	AA894189	---	---
3280	1372471_at	0.408114794	1.326950721	yes	yes	yes	BI283728	Rn.13004	Transcribed locus, weakly similar to NP_703313.1 hypothetical protein [Plasmodium falciparum 3D7]
3281	1392037_at	0.408202624	1.327031507	yes	yes	no	BM383048	Rn.43297	Transcribed locus
3282	1381795_at	0.408283819	1.327106194	yes	yes	no	AA963295	Rn.147524	Transcribed locus
3283	1377718_at	0.408292958	1.327114601	yes	yes	yes	BI302694	Rn.136497	similar to CDNA sequence BC022692 (predicted)
3284	1374780_at	0.408345073	1.327162542	yes	yes	yes	AI232806	Rn.165115	Transcribed locus
3285	1376039_at	0.408481539	1.327288086	yes	yes	yes	AA996882	Rn.161874	serine/threonine kinase 6
3286	1382203_at	0.409695358	1.328405276	yes	yes	yes	AI549010	Rn.144974	growth differentiation factor 1 (predicted)
3287	1373520_at	0.410121221	1.32879746	yes	yes	yes	BI285960	Rn.94887	CDNA clone IMAGE:7367270
3288	1378055_at	0.410621595	1.329258411	yes	yes	yes	BI296430	Rn.13989	Transforming, acidic coiled-coil containing protein 2
3289	1382649_at	0.410809946	1.329431963	yes	yes	yes	AI030649	Rn.163805	Transcribed locus, strongly similar to NP_112381.2 Sjogren syndrome antigen B [Rattus norvegicus]
3290	1382592_at	0.410873637	1.329490656	yes	yes	yes	AI059054	Rn.54949	similar to RIKEN cDNA 2600001J17
3291	1382234_at	0.410993854	1.329601444	yes	yes	yes	BI286950	Rn.2260	Hypothetical protein LOC311254
3292	1390147_at	0.411203801	1.329794947	yes	yes	yes	AI549079	Rn.102580	similar to mKIAA1429 protein (predicted)
3293	1396389_at	0.411351335	1.329930943	yes	yes	yes	AW522358	---	---
3294	1389137_at	0.411385203	1.329962163	yes	yes	yes	AA957183	Rn.89069	Citron
3295	1370004_at	0.411647154	1.330203668	yes	yes	yes	M99065	Rn.11098	H2A histone family, member Y
3296	1397485_at	0.411652803	1.330208876	yes	yes	yes	BI298636	Rn.176861	Transcribed locus
3297	1372440_at	0.411787821	1.330333373	yes	yes	yes	BI275818	Rn.2271	serine (or cysteine) proteinase inhibitor, clade E, member 2
3298	1385781_at	0.411825887	1.330368475	yes	yes	yes	BF397986	Rn.72855	similar to SNF2/RAD54 family protein (predicted)
3299	1381529_at	0.41211169	1.330632052	yes	yes	no	AA997407	Rn.98494	GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)
3300	1378296_at	0.412688245	1.331163928	yes	yes	yes	AI012651	---	---
3301	1370861_at	0.412841576	1.331305413	yes	yes	yes	BI282326	Rn.880	cytochrome c oxidase, subunit VIa, polypeptide 1
3302	1398886_at	0.412934521	1.331391184	yes	yes	yes	BI285703	Rn.63	similar to Selenoprotein H (predicted)
3303	1376228_at	0.413289768	1.331719064	yes	yes	yes	BF419434	Rn.43445	Catalytic/ protein phosphatase type 2C
3304	1381396_s_at	0.413914813	1.332296155	yes	yes	yes	AA998067	Rn.22556	Kruppel-like factor 15
3305	1389088_at	0.414401309	1.332745498	yes	yes	yes	AI600029	Rn.48777	activity-dependent neuroprotective protein
3306	1369665_a_at	0.414723967	1.333043599	yes	yes	yes	AJ222813	Rn.11118	interleukin 18
3307	1383686_at	0.414918997	1.333223819	yes	yes	yes	BE111537	---	---
3308	1375952_at	0.415042829	1.333338259	yes	yes	yes	AI178495	---	---
3309	1369380_at	0.415660292	1.33390904	yes	yes	yes	NM_134472	Rn.152404	kinesin family member 2C
3310	1392899_at	0.416028011	1.334249075	yes	yes	yes	BI284262	Rn.138438	protein regulator of cytokinesis 1 (predicted)
3311	1368707_at	0.416733165	1.334901382	yes	yes	no	NM_019369	Rn.11308	inter alpha-trypsin inhibitor, heavy chain 4
3312	1377809_at	0.41700047	1.335148738	yes	yes	yes	BE111879	---	---
3313	1373658_at	0.418183262	1.336243808	yes	yes	yes	AI409259	Rn.101301	Rac GTPase-activating protein 1 (predicted)
3314	1370422_at	0.418297596	1.33634971	yes	yes	yes	AF036537	Rn.7110	receptor-interacting serine-threonine kinase 3
3315	1377197_at	0.418577749	1.336609237	yes	yes	yes	BE108892	Rn.146957	Transcribed locus
3316	1374912_at	0.418737374	1.336757132	yes	yes	yes	BI274467	Rn.152404	kinesin family member 2C
3317	1398831_at	0.419073017	1.337068165	yes	yes	yes	NM_031629	Rn.6169	proteasome (prosome, macropain) subunit, beta type 4
3318	1395870_at	0.419865164	1.337802517	yes	yes	no	BF403357	Rn.60258	HpaII tiny fragments locus 9c
3319	1373341_at	0.420727439	1.338602338	yes	yes	no	AI231183	---	---
3320	1376485_at	0.421146873	1.338991565	yes	yes	yes	BG377082	Rn.8891	TRAF-interacting protein (predicted)

3321	1387969_at	0.421209359	1.339049561	yes	yes	yes	U22520	Rn.10584	chemokine (C-X-C motif) ligand 10
3322	1384946_at	0.421310845	1.33914376	yes	yes	yes	AI070419	---	---
3323	1371446_at	0.421380634	1.339208541	yes	yes	yes	BI283703	Rn.6276	MAP kinase-activated protein kinase 2
3324	1368886_at	0.422228276	1.339995611	yes	yes	yes	NM_013055	Rn.146082	mitogen activated protein kinase kinase kinase 12
3325	1367629_at	0.422691624	1.340426045	yes	yes	yes	NM_022503	Rn.1745	cytochrome c oxidase, subunit VIIa 2
3326	1368189_at	0.423946503	1.341592476	yes	no	no	NM_022389	Rn.228	7-dehydrocholesterol reductase
3327	1381103_a_at	0.424009223	1.341650802	yes	no	no	AA996485	---	---
3328	1392128_at	0.424163297	1.341794093	yes	no	no	BE104541	Rn.51222	Similar to novel protein (predicted)
3329	1384900_at	0.424350434	1.341968153	yes	yes	yes	AW530806	Rn.9147	MOB1, Mps One Binder kinase activator-like 2B (yeast) (predicted)
3330	1368454_at	0.424807583	1.342393452	yes	no	no	NM_053364	Rn.15366	proliferin related protein
3331	1393848_at	0.425187568	1.342747065	yes	no	no	AA957260	Rn.144946	ribonucleotide reductase M2 (mapped)
3332	1375994_at	0.425252817	1.342807795	yes	yes	yes	BE107324	Rn.10686	Neurofibromatosis 1
3333	1371780_at	0.425491412	1.343029888	yes	no	no	AA850164	Rn.4066	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
3334	1393195_at	0.425870875	1.343383184	yes	yes	no	AI045632	---	---
3335	1389555_at	0.425949264	1.343456179	yes	no	no	BM387190	Rn.14867	transcription factor 19
3336	1372269_at	0.426178494	1.343669658	yes	no	no	AI229534	Rn.97814	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (predicted)
3337	1370213_at	0.426292932	1.343776245	yes	no	no	BI282111	Rn.110976	Y box protein 1 related, pseudogene 3 /// similar to nuclease sensitive element binding protein 1 (predicted) /// Y box protein 1
3338	1383537_at	0.427576166	1.344972025	yes	no	no	BF522715	Rn.84878	Vascular endothelial zinc finger 1 (predicted)
3339	1373323_at	0.427610402	1.345003943	yes	no	no	BF397730	Rn.20801	similar to Epidermal growth factor receptor substrate 15-like 1 (Eps15-related protein) (Eps15R) (Epidermal growth factor receptor pathway substrate 15 related sequence) (Eps15-rs)
3340	1373557_at	0.427640855	1.345032334	yes	no	no	AI145081	---	---
3341	1391751_at	0.427766348	1.345149337	yes	yes	no	BE107919	---	---
3342	1386062_at	0.427856886	1.345233756	yes	no	no	AI060227	Rn.25153	Rho family GTPase 3
3343	1370672_a_at	0.427888252	1.345263003	yes	yes	no	D14076	Rn.11191	dynamin 3
3344	1379668_at	0.42789531	1.345269585	yes	yes	yes	BI296117	Rn.37199	similar to hypothetical protein B230397C21 (predicted)
3345	1370898_at	0.428271407	1.34562033	yes	no	no	BF288101	Rn.6147	stannin
3346	1388744_at	0.428374624	1.345716604	yes	no	no	AI599678	Rn.113	minichromosome maintenance deficient 7 (S. cerevisiae)
3347	1397748_at	0.428610717	1.345936846	yes	yes	no	AW521583	Rn.43486	Transcribed locus
3348	1370155_at	0.428955281	1.346258339	yes	no	no	BM388837	Rn.107239	procollagen, type I, alpha 2
3349	1378617_at	0.429000221	1.346300276	yes	yes	no	BM390846	Rn.91677	transcriptional regulating factor 1 (predicted)
3350	1376989_at	0.429053197	1.346349713	yes	yes	yes	BE099568	Rn.14653	Transcribed locus
3351	1385904_at	0.429401145	1.346674464	yes	yes	no	BG153342	Rn.28931	cold inducible RNA binding protein
3352	1384344_at	0.429521717	1.346787015	yes	no	no	AI060231	Rn.82775	FK506 binding protein 7 (predicted)
3353	1381421_at	0.429637847	1.346895429	yes	no	no	AA899688	---	---
3354	1395647_at	0.431210968	1.348364891	yes	yes	no	AA684690	Rn.48850	Tu translation elongation factor, mitochondrial (predicted)
3355	1380529_at	0.431498853	1.34863398	yes	no	no	AI059721	Rn.102608	Transcribed locus
3356	1375773_at	0.431617549	1.348744941	yes	no	no	BG379365	Rn.4018	Transcribed locus
3357	1394066_at	0.431644044	1.348769712	yes	no	no	AA875609	Rn.94939	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
3358	1373822_at	0.432016816	1.34911826	yes	no	no	BI275708	Rn.137099	similar to RIKEN cDNA 1110025L05 (predicted)
3359	1367712_at	0.432496406	1.349566817	yes	no	no	NM_053819	Rn.25754	tissue inhibitor of metalloproteinase 1
3360	1383460_at	0.432759544	1.349812991	yes	no	no	AI058976	Rn.6638	uroplakin 3B (predicted)
3361	1393816_at	0.432943323	1.34998495	yes	no	no	AI555801	---	---
3362	1393578_at	0.433009744	1.350047103	yes	no	no	AA892301	---	---

3363	1379195_s_at	0.433111106	1.350141959	yes	no	no	AI556346	Rn.20467	ligase I, DNA, ATP-dependent
3364	1393243_at	0.433277989	1.350298146	yes	no	no	BG372316	Rn.159977	CDNA clone MGC:94716 IMAGE:7193261
3365	1378507_at	0.433364184	1.350378822	yes	no	no	BE108914	Rn.88974	Transcribed locus
3366	1370294_a_at	0.433371448	1.350385622	yes	no	no	U05341	Rn.9262	cell division cycle 20 homolog (S. cerevisiae)
3367	1373176_at	0.433462156	1.350470529	yes	no	no	AA943208	Rn.45023	Transcribed locus
3368	1395944_at	0.433663856	1.350659348	yes	no	no	AI548667	Rn.161307	Transcribed locus
3369	1370094_at	0.434074354	1.351043713	yes	yes	yes	NM_021747	Rn.42946	acrosomal vesicle protein 1
3370	1396500_at	0.434588229	1.351525028	yes	no	no	BE120381	Rn.51400	Transcribed locus
3371	1372538_at	0.434827407	1.35174911	yes	no	no	BM389148	Rn.94733	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 (predicted)
3372	1387020_at	0.434841845	1.351762639	yes	no	no	BG664123	Rn.107152	cytochrome P450, subfamily 51
3373	1372760_at	0.43533804	1.352227638	yes	no	no	AI176579	Rn.119131	CDNA clone IMAGE:7321089
3374	1380433_at	0.435490093	1.352370164	yes	no	no	AI229240	Rn.22923	Transcribed locus
3375	1380546_at	0.435723554	1.352589026	yes	no	no	AA926048	Rn.8436	similar to hypothetical protein FLJ10986 /// similar to hypothetical protein FLJ10986
3376	1372332_at	0.436473331	1.353292158	yes	no	no	AI170687	Rn.13655	Transcribed locus
3377	1369642_at	0.436884575	1.353677972	yes	no	no	BM392366	Rn.24751	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit
3378	1393261_at	0.436924206	1.353715158	yes	no	no	AI058850	Rn.2153	Similar to protein phosphatase 2A B56 regulatory subunit gamma 3 isoform (predicted)
3379	1370074_at	0.437225358	1.353997766	yes	no	no	NM_057196	Rn.95155	brain-specific angiogenesis inhibitor 1-associated protein 2
3380	1391148_at	0.437230639	1.354002722	yes	no	no	AA957886	Rn.9395	Transcribed locus
3381	1376165_at	0.438510438	1.355204376	yes	yes	yes	BE098153	Rn.45360	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
3382	1373919_at	0.438539329	1.355231515	yes	no	no	AA943801	Rn.156379	Transcribed locus, weakly similar to XP_342574.1 PREDICTED: similar to Csr1 [Rattus norvegicus]
3383	1393277_at	0.439313988	1.355959406	yes	no	no	AI579547	---	---
3384	1372896_at	0.439491935	1.356126665	yes	no	no	BM390440	Rn.16961	Transcribed locus
3385	1388458_at	0.439626636	1.356253288	yes	no	no	BI291451	Rn.17046	replication factor C (activator 1) 4 (predicted)
3386	1367479_at	0.439729759	1.356350237	yes	no	no	AI599994	---	---
3387	1389428_at	0.440440298	1.357018414	yes	no	no	AI104431	---	---
3388	1383152_at	0.440827897	1.357383044	yes	no	no	BF544427	Rn.162505	similar to Cc1-9
3389	1371017_at	0.441178726	1.357713167	yes	yes	yes	Z27087	Rn.10427	T-cell receptor gamma chain
3390	1381633_at	0.441389437	1.357911481	yes	yes	yes	BE116563	Rn.163448	Zinc finger protein X-linked (predicted)
3391	1377153_a_at	0.441451382	1.357969787	yes	no	no	AI178384	Rn.137232	kelch-like 6 (Drosophila) (predicted)
3392	1396381_at	0.441635768	1.358143355	yes	yes	yes	BE097451	Rn.72979	CDNA clone MGC:114512 IMAGE:7456844
3393	1376456_at	0.441846139	1.358341412	yes	no	no	BE114264	Rn.145458	similar to nicotinamide nucleotide adenylyltransferase 2 (predicted)
3394	1391552_at	0.441993853	1.358480496	yes	yes	yes	BM391661	Rn.25189	Transcribed locus
3395	1390175_at	0.442078376	1.358560088	yes	no	no	AI072997	Rn.22113	similar to Delta-interacting protein A (Hepatitis delta antigen interacting protein A) (predicted)
3396	1370218_at	0.442334505	1.358801302	yes	no	no	AA848319	Rn.1785	lactate dehydrogenase B
3397	1377442_at	0.442520635	1.358976619	yes	no	no	BF409997	Rn.45278	Transcribed locus
3398	1373246_at	0.443192293	1.359609449	yes	yes	yes	BF397920	Rn.139314	CDC23 (cell division cycle 23, yeast, homolog)
3399	1375538_at	0.44322781	1.35964292	yes	no	no	AI230737	Rn.164613	Transcribed locus
3400	1372411_at	0.443230693	1.359645638	yes	no	no	BE110638	---	---
3401	1390282_at	0.443606467	1.359999826	yes	no	no	BI274639	Rn.6389	Transcribed locus
3402	1393899_at	0.443975117	1.36034739	yes	no	no	AA901361	Rn.178689	guanosine monophosphate reductase 2
3403	1388067_a_at	0.444238615	1.36059587	yes	yes	yes	AF205779	Rn.40949	glucocorticoid modulatory element binding protein 2
3404	1390113_a_at	0.444245198	1.360602078	yes	no	no	BI300539	Rn.163120	La ribonucleoprotein domain family, member 1 (predicted)

3405	1372792_at	0.444641343	1.360975733	yes	no	no	BI279648	Rn.107346	similar to hypothetical protein MGC15677
3406	1398282_at	0.444724542	1.361054222	yes	no	no	NM_053902	Rn.10575	kynureninase (L-kynurenine hydrolase)
3407	1388316_at	0.444858352	1.361180465	yes	no	no	BG668062	Rn.4025	RGD1566320 (predicted)
3408	1368978_at	0.445034391	1.361346568	yes	yes	yes	NM_033499	Rn.7724	scrapie responsive gene 1
3409	1374919_at	0.445720306	1.361993961	yes	no	no	BE103543	Rn.103272	Replication factor C 1
3410	1385218_at	0.445952522	1.362213204	yes	no	no	AI044551	---	---
3411	1397049_at	0.446571295	1.362797584	yes	yes	yes	BF403412	Rn.154363	Transcribed locus
3412	1371698_at	0.446648137	1.362870172	yes	yes	yes	BF282614	Rn.62495	elongation factor Tu GTP binding domain containing 2
3413	1377835_at	0.446859064	1.363069444	yes	no	no	BM390876	Rn.167758	similar to dedicator of cytokinesis 8
3414	1376393_at	0.446992457	1.36319548	yes	no	no	BI296409	Rn.138900	Ral GEF with PH domain and SH3 binding motif 2
3415	1387562_at	0.447749728	1.36391121	yes	no	no	NM_017230	Rn.32094	peptidyl arginine deiminase, type III
3416	1381923_at	0.447930369	1.364081997	yes	yes	yes	AI454658	Rn.22639	similar to LOC387763 protein (predicted)
3417	1393032_x_at	0.447961955	1.364111862	yes	no	no	BI290033	---	---
3418	1379386_at	0.448473682	1.364595801	yes	yes	yes	BE107238	Rn.162961	similar to B99 protein (predicted)
3419	1377966_at	0.448533308	1.3646522	yes	no	no	BI275560	Rn.22923	Transcribed locus
3420	1384259_at	0.449087458	1.365176474	yes	no	no	BF559151	Rn.101301	Rac GTPase-activating protein 1 (predicted)
3421	1371484_at	0.449841128	1.365889835	yes	no	no	BM390252	---	---
3422	1385965_at	0.450094558	1.366129793	yes	no	no	AI045533	Rn.11853	CDNA clone IMAGE:7131734
3423	1368429_at	0.450450966	1.366467328	yes	no	no	NM_133615	Rn.11270	TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa
3424	1378333_at	0.450639968	1.366646355	yes	yes	yes	BI284174	Rn.50362	Transcribed locus
3425	1385870_at	0.451280606	1.367253359	yes	no	no	AA997980	Rn.22691	Zinc finger protein 281
3426	1386583_at	0.451586329	1.367543125	yes	no	no	AA859497	Rn.238	Transcribed locus
3427	1384084_at	0.451619184	1.367574269	yes	yes	yes	AW433952	Rn.16874	LOC361719 (predicted)
3428	1382493_at	0.451702855	1.367653585	yes	no	no	BG377427	Rn.41236	Transcribed locus, strongly similar to XP_223060.3 PREDICTED: similar to LEK1 [Rattus norvegicus]
3429	1389746_at	0.452162876	1.368089749	yes	no	no	BM386322	Rn.9000	similar to Naglu (predicted)
3430	1375073_at	0.452606778	1.36851076	yes	no	no	BE107313	Rn.144385	similar to sterile alpha motif domain containing 11 (predicted)
3431	1379542_at	0.452617439	1.368520873	yes	no	no	BF522334	Rn.14918	similar to Small nuclear ribonucleoprotein F (snRNP-F) (predicted) /// small nuclear ribonucleoprotein polypeptide F (predicted)
3432	1377751_at	0.454235257	1.370056374	yes	yes	yes	AI233227	Rn.24708	Transcribed locus
3433	1380854_at	0.454337855	1.37015381	yes	no	no	BF396482	---	---
3434	1389543_at	0.454345124	1.370160713	yes	yes	yes	BE111083	Rn.131140	mannan-binding lectin serine peptidase 1
3435	1371221_at	0.454580219	1.370384006	yes	no	no	AF053095	Rn.107103	sequestosome 1
3436	1385893_at	0.454729576	1.370525885	yes	no	no	AA874903	Rn.32193	Transcribed locus, moderately similar to XP_515015.1 PREDICTED: similar to immunoglobulin lambda light chain [Pan troglodytes]
3437	1387826_at	0.455050247	1.370830549	yes	no	no	NM_031769	Rn.154694	similar to pyridoxal (pyridoxine, vitamin B6) kinase (predicted)
3438	1382539_at	0.455106532	1.37088403	yes	no	no	AI171022	---	---
3439	1398602_at	0.455252157	1.371022414	yes	no	no	AW143296	Rn.19771	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (predicted)
3440	1378855_a_at	0.455665591	1.371415365	yes	yes	yes	BE097672	Rn.28648	similar to transcription elongation factor A (SII)-like 3 (predicted)
3441	1376513_a_at	0.45577961	1.371523755	yes	no	no	BE098803	---	---
3442	1384572_at	0.457355484	1.373022706	yes	no	no	AI716028	Rn.21291	Similar to mKIAA0704 protein (predicted)
3443	1375382_at	0.457527671	1.373186587	yes	yes	yes	BE120346	Rn.106312	mediator of DNA damage checkpoint 1
3444	1377986_at	0.458029166	1.373664004	yes	no	no	AI029749	Rn.18315	short coiled-coil protein /// similar to short coiled-coil protein
3445	1380200_at	0.458066987	1.373700015	yes	yes	yes	AI102906	Rn.166094	Transcribed locus
3446	1387474_at	0.458116881	1.373747524	yes	yes	yes	J05097	Rn.89609	tachykinin receptor 1
3447	1376127_at	0.458642329	1.374247951	yes	no	no	BE117201	Rn.165276	Transcribed locus
3448	1388058_at	0.45876375	1.374363617	yes	yes	yes	D49446	Rn.102447	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated

									factor
3449	1398326_at	0.458910326	1.374503258	yes	no	no	BI282332	Rn.2281	similar to Nur77 downstream protein 2
3450	1373803_a_at	0.459135989	1.374718271	yes	yes	yes	AI170771	Rn.2178	growth hormone receptor
3451	1383767_at	0.459597639	1.375158239	yes	yes	yes	AW524430	Rn.163683	Transcribed locus
3452	1389566_at	0.459662505	1.37522007	yes	no	no	AW253821	Rn.6743	cyclin B2
3453	1382605_at	0.46015523	1.375689831	yes	no	no	AI234026	Rn.11455	Transcribed locus
3454	1390983_at	0.460223213	1.375754658	yes	yes	yes	AA956823	Rn.22382	Transcribed locus
3455	1374164_at	0.461050709	1.376543984	yes	yes	yes	BF410020	Rn.39004	Transcribed locus
3456	1380269_at	0.461374264	1.376852738	yes	yes	yes	AA859619	Rn.162118	FUS interacting protein (serine-arginine rich) 1
3457	1368963_at	0.461664787	1.37713003	yes	yes	yes	NM_013160	Rn.37510	Max interacting protein 1
3458	1388010_at	0.461774788	1.377235037	yes	no	no	AF303035	Rn.160145	Antisense RNA overlapping MCH protein
3459	1386744_x_at	0.461946305	1.37739878	yes	no	no	BF544149	Rn.157549	Transcribed locus, strongly similar to XP_574268.1 PREDICTED: similar to LRRGT00194 [Rattus norvegicus]
3460	1378322_at	0.462434879	1.37786532	yes	no	no	BM385592	---	---
3461	1377920_at	0.464422295	1.379764737	yes	yes	yes	AI413026	Rn.23400	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta
3462	1381220_at	0.464534489	1.379872042	yes	yes	yes	BM383968	Rn.161783	activin receptor IIA
3463	1374961_at	0.464889366	1.380211507	yes	no	no	BI274511	---	---
3464	1376055_at	0.465872862	1.381152728	yes	no	no	AA859768	Rn.123	Transcribed locus
3465	1368294_at	0.466206914	1.381472568	yes	no	no	NM_053907	Rn.29996	deoxyribonuclease I-like 3
3466	1388927_at	0.466233043	1.381497588	yes	no	no	BE109617	Rn.9036	RAB, member of RAS oncogene family-like 4 (predicted)
3467	1384095_at	0.467365668	1.382582594	yes	yes	yes	BF524140	Rn.161974	myosin VIIA and Rab interacting protein
3468	1384325_at	0.467759329	1.382959904	yes	no	no	BF546645	Rn.19272	palate, lung, and nasal epithelium carcinoma associated
3469	1384004_at	0.467944614	1.383137528	yes	no	no	AI030360	Rn.146822	Transcribed locus
3470	1381163_at	0.468432916	1.383605752	yes	no	no	AI229248	Rn.37378	Transcribed locus
3471	1394087_at	0.468823439	1.38398033	yes	yes	yes	BF561962	Rn.162478	Zinc finger, RAN-binding domain containing 1 (predicted)
3472	1377554_at	0.46937773	1.384512165	yes	yes	yes	BF394106	Rn.185237	tumor necrosis factor (ligand) superfamily, member 9
3473	1385926_at	0.469908824	1.385021934	yes	no	no	BF550565	Rn.23216	Transcribed locus
3474	1376503_a_at	0.470015966	1.385124797	yes	no	no	BE104991	Rn.22366	RNA binding motif protein 7 (predicted)
3475	1394181_at	0.470527298	1.385615812	yes	no	no	AI176506	Rn.9406	Necdin-like 2
3476	1373663_at	0.470892766	1.385966864	yes	yes	yes	AI102482	Rn.12825	similar to 1110014F24Rik protein (predicted)
3477	1381758_at	0.47178887	1.386828	yes	yes	yes	AI535566	Rn.34858	similar to MDM2 Binding protein (predicted)
3478	1382829_at	0.471879418	1.386915045	yes	yes	yes	AI137187	Rn.23530	Transcribed locus
3479	1398382_at	0.472216818	1.387239437	yes	no	no	AI175556	Rn.65040	Transcribed locus
3480	1390481_a_at	0.472220639	1.387243111	yes	no	no	AW531714	Rn.18835	ubiquitin-conjugating enzyme E2T (putative) (predicted)
3481	1392598_at	0.472736198	1.387738943	yes	no	no	AA899326	Rn.164582	Transcribed locus
3482	1398338_at	0.473192484	1.388177917	yes	yes	yes	AI716099	Rn.20372	Transcribed locus
3483	1377720_x_at	0.473237328	1.388221067	yes	no	no	AA892765	---	---
3484	1383536_at	0.47326682	1.388249446	yes	no	no	AI712541	Rn.24681	Transcribed locus, strongly similar to NP_569084.1 dihydrofolate reductase [Rattus norvegicus]
3485	1389020_at	0.473303503	1.388284745	yes	yes	yes	BM389149	---	---
3486	1392498_at	0.473747366	1.388711934	yes	no	no	BG670494	Rn.2153	similar to protein phosphatase 2A B56 regulatory subunit gamma 3 isoform (predicted)
3487	1384972_at	0.474167778	1.389116673	yes	yes	yes	BF399656	Rn.154546	topoisomerase (DNA) III alpha (predicted)
3488	1377729_at	0.474322088	1.389265261	yes	yes	yes	BG668988	Rn.7567	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (predicted)
3489	1384904_at	0.475018263	1.389935815	yes	no	no	AW527233	Rn.161719	neuropilin (NRP) and tolloid (TLL)-like 2 (predicted)
3490	1374776_at	0.476084863	1.39096379	yes	yes	yes	BG380430	Rn.13814	Transcribed locus
3491	1370903_a_at	0.476089024	1.390967801	yes	yes	yes	AI146115	Rn.93910	similar to Ndr3 protein

3492	1375687_at	0.476294661	1.391166079	yes	yes	no	BE097926	Rn.163656	Transcribed locus
3493	1381364_at	0.476303339	1.391174447	yes	yes	no	BE116070	Rn.56083	transportin 1
3494	1370047_at	0.477139336	1.391980823	yes	yes	no	NM_053535	Rn.1199	ectonucleotide pyrophosphatase/phosphodiesterase 1
3495	1389573_at	0.47767971	1.3925023	yes	yes	no	AI170665	Rn.23367	ChaC, cation transport regulator-like 1 (E. coli) (predicted)
3496	1371712_at	0.477965546	1.392778218	yes	yes	no	AI176503	---	similar to snRNP core protein SMX5d (predicted)
3497	1373787_at	0.47842055	1.393217549	yes	yes	no	AA943735	Rn.32110	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9
3498	1369012_at	0.478604459	1.393395162	yes	no	no	NM_017128	Rn.9874	inhibin beta-A
3499	1388268_at	0.478849565	1.393631912	yes	no	no	AF053361	Rn.37575	tropomyosin 3, gamma
3500	1377814_at	0.479414252	1.394177502	yes	no	no	AA926368	Rn.13040	Similar to Nedd4-binding brain specific protein BEAN (predicted)
3501	1379480_at	0.479470957	1.394232301	yes	yes	yes	BG380938	---	similar to diacylglycerol kinase iota-1
3502	1380611_at	0.479483309	1.394244239	yes	yes	no	BI284255	Rn.144288	FK506 binding protein 5
3503	1373747_at	0.479495662	1.394256176	yes	yes	no	BG381691	Rn.18785	cornichon homolog 2 (Drosophila)
3504	1375572_at	0.479744386	1.39449657	yes	yes	no	BE100602	Rn.195042	Ultraviolet B radiation-activated UV98 mRNA, partial sequence
3505	1375664_at	0.480006705	1.394750148	yes	yes	yes	BI294732	Rn.6839	Trinucleotide repeat containing 6 (predicted)
3506	1375523_at	0.480747539	1.395466546	yes	yes	no	BE108178	Rn.163463	Transcribed locus
3507	1367671_at	0.48076874	1.395487053	yes	yes	no	NM_022381	Rn.223	proliferating cell nuclear antigen
3508	1375122_at	0.480798866	1.395516194	yes	yes	no	AI233235	Rn.7352	YY1 associated factor 2 (predicted)
3509	1375178_at	0.481511531	1.396205724	yes	no	no	BE111601	Rn.11422	Thymoma viral proto-oncogene 1
3510	1377733_at	0.481707583	1.396395471	yes	yes	yes	AA944531	---	---
3511	1397628_at	0.482392792	1.397058848	yes	yes	no	BM390965	Rn.159917	similar to RIKEN cDNA 2900092E17
3512	1381940_at	0.482516448	1.397178598	yes	yes	no	AW527798	Rn.28619	Transcribed locus
3513	1392544_at	0.482574713	1.397235025	yes	yes	no	AI044879	Rn.18033	rcd1 (required for cell differentiation) homolog 1 (S. pombe)
3514	1383142_at	0.482833379	1.397485563	yes	yes	no	BI289244	Rn.165780	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3515	1389334_at	0.483394449	1.398029157	yes	yes	no	BI277594	Rn.102304	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 /// NADH dehydrogenase 1 alpha subcomplex 10-like protein
3516	1391317_at	0.483643021	1.398270053	yes	yes	no	BE109802	Rn.106906	similar to RIKEN cDNA 2810433K01 (predicted)
3517	1397779_at	0.483947002	1.398564705	yes	no	no	BF562254	Rn.162437	Chromodomain helicase DNA binding protein 2 (predicted)
3518	1383211_at	0.484842888	1.399433456	yes	yes	yes	BE109736	Rn.168687	Transcribed locus
3519	1375093_at	0.484952936	1.399540209	yes	yes	no	AI236089	Rn.145214	ribokinase (predicted)
3520	1380277_at	0.484980502	1.399566951	yes	yes	yes	AI639142	Rn.42022	Transcribed locus
3521	1385224_at	0.485139155	1.399720869	yes	yes	no	AA819531	Rn.12627	T-cell, immune regulator 1
3522	1377696_at	0.486086549	1.400640344	yes	yes	yes	AI407755	Rn.162446	mesoderm development candidate 1
3523	1372188_at	0.48667322	1.40121003	yes	yes	no	BM392171	Rn.4227	Similar to hypothetical protein D15Ertd785e
3524	1387019_at	0.486747572	1.401282245	yes	yes	no	NM_080481	Rn.66347	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e
3525	1381960_at	0.487563013	1.402074503	yes	yes	no	BI288014	---	---
3526	1376318_at	0.489076407	1.403546058	yes	yes	yes	BE113300	Rn.160479	Transcribed locus
3527	1368773_at	0.48928289	1.403746952	yes	yes	yes	NM_012955	Rn.10411	FSH primary response 1
3528	1388111_at	0.489865712	1.404314154	yes	yes	no	J04035	Rn.54384	elastin
3529	1393924_s_at	0.490554802	1.404985072	yes	yes	no	BF553036	Rn.113170	similar to mdgl-1 (predicted)
3530	1372886_at	0.490980644	1.405399844	yes	yes	no	AI556917	Rn.58838	transforming, acidic coiled-coil containing protein 3
3531	1395953_at	0.491386527	1.405795291	yes	yes	yes	AA955517	Rn.8838	Transcribed locus
3532	1370139_a_at	0.491455243	1.405862251	yes	yes	no	AB051214	Rn.105986	transient receptor potential cation channel, subfamily C, member 6
3533	1370269_at	0.492214759	1.406602571	yes	yes	no	X00469	Rn.10352	cytochrome P450, family 1, subfamily a, polypeptide 1
3534	1368574_at	0.492384692	1.406768262	yes	no	no	NM_016991	Rn.10032	adrenergic receptor, alpha 1b
3535	1384280_at	0.492420477	1.406803157	yes	yes	no	AA964152	Rn.165257	Transcribed locus
3536	1388151_at	0.49265953	1.407036282	yes	yes	yes	AI008369	Rn.13808	coronin 7

3537	1378801_at	0.493049598	1.407416759	yes	yes	yes	AI599072	Rn.168129	Transcribed locus
3538	1398526_at	0.493670765	1.408022868	yes	yes	yes	BE102813	Rn.154049	Transcribed locus
3539	1382395_at	0.493905162	1.40825165	yes	yes	no	AA963192	Rn.23187	Transcribed locus
3540	1384208_at	0.494392023	1.408726968	yes	yes	yes	BM385222	Rn.17804	immunoglobulin joining chain
3541	1378752_at	0.494407615	1.408742192	yes	yes	yes	BF413430	Rn.152948	Similar to cajalin 2 isoform a (predicted)
3542	1394031_at	0.494693817	1.409021687	yes	yes	no	AA800742	Rn.55931	similar to Protein C20orf129 homolog (predicted)
3543	1384246_at	0.495476782	1.409786584	yes	yes	yes	AA996404	Rn.163398	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)
3544	1380608_at	0.495572671	1.40988029	yes	yes	no	BM386241	Rn.107028	histone deacetylase 10
3545	1384156_at	0.496272054	1.41056393	yes	yes	yes	BI293851	---	---
3546	1390509_a_at	0.497201038	1.411472517	yes	yes	no	BI294860	Rn.118218	Transcribed locus
3547	1395686_at	0.497725675	1.411985893	yes	yes	yes	BE096030	Rn.31965	Activating transcription factor 7 (predicted)
3548	1379424_at	0.497819957	1.412078171	yes	yes	no	BE115825	Rn.156180	Similar to DKFZP434B168 protein (predicted)
3549	1387925_at	0.497942233	1.412197858	yes	yes	no	U07202	Rn.11172	asparagine synthetase
3550	1389974_at	0.498040466	1.412294017	yes	yes	no	BF555171	Rn.163729	Transcribed locus
3551	1398710_at	0.498129702	1.412381375	yes	yes	no	BF392959	Rn.161862	cytochrome P450, family 2, subfamily u, polypeptide 1
3552	1370393_at	0.498608576	1.412850266	yes	yes	no	BF418951	Rn.163388	coiled-coil domain containing 5
3553	1382419_at	0.498894255	1.413130062	yes	yes	no	BI276776	Rn.40474	SoxLZ/Sox6 leucine zipper binding protein in testis (predicted)
3554	1377714_at	0.499209135	1.413438523	yes	yes	no	AI030979	Rn.138771	Poliovirus receptor-related 3 (predicted)
3555	1385733_at	0.499299532	1.413527089	yes	yes	no	BE116198	Rn.52638	exonuclease 1 (predicted)
3556	1389354_at	0.499449445	1.413673979	yes	yes	no	BF285490	Rn.20103	similar to semaF cytoplasmic domain associated protein 2
3557	1380243_at	0.499676776	1.413896755	yes	yes	no	BE098614	Rn.23932	similar to CG14803-PA (predicted)
3558	1380775_at	0.500533528	1.414736655	yes	yes	no	BE110723	Rn.138477	M-phase phosphoprotein 1 (predicted)
3559	1369310_at	0.500756395	1.41495522	yes	yes	no	NM_022300	Rn.37779	brain abundant, membrane attached signal protein 1
3560	1368440_at	0.501422367	1.415608537	yes	yes	yes	NM_017216	Rn.11196	solute carrier family 3, member 1
3561	1389818_at	0.501554527	1.415738221	yes	yes	no	AA997712	Rn.166407	Transcribed locus
3562	1392065_at	0.501721646	1.415902227	yes	yes	no	BE116803	Rn.35496	Similar to Kinesin family member 18A (predicted)
3563	1384774_at	0.502807635	1.416968449	yes	yes	yes	AA925026	Rn.102783	transmembrane protease, serine 8 (intestinal)
3564	1368878_at	0.503624164	1.417770645	yes	yes	no	NM_053539	Rn.10780	isopentenyl-diphosphate delta isomerase
3565	1377839_at	0.504257777	1.418393448	yes	yes	yes	BG378776	---	---
3566	1370461_at	0.504683961	1.418812515	yes	yes	no	AF336825	Rn.92304	hyaluronan mediated motility receptor (RHAMM)
3567	1383068_at	0.505066005	1.419188284	yes	yes	no	BI290898	Rn.95	deoxythymidylate kinase (predicted)
3568	1390531_at	0.505223473	1.419343195	yes	yes	no	BE098021	Rn.47450	Similar to Peroxisomal proliferator-activated receptor A interacting complex 285 kDa protein (PPAR-alpha interacting complex protein 285) (predicted)
3569	1392151_at	0.505493199	1.41960858	yes	no	no	AW526257	Rn.46139	Transcribed locus
3570	1383784_at	0.505540053	1.419654685	yes	yes	yes	BI289438	---	---
3571	1379378_at	0.505621405	1.41973474	yes	yes	no	AI071605	Rn.105741	mitochondrial ribosomal protein S18C (predicted)
3572	1392440_at	0.506632067	1.420729666	yes	yes	no	AI072122	Rn.121380	Transcribed locus, weakly similar to XP_520576.1 PREDICTED: similar to clathrin, light polypeptide A isoform a; clathrin light chain LCA [Pan troglodytes]
3573	1384801_at	0.506877501	1.420971383	yes	yes	no	AA963592	Rn.11589	Nipped-B homolog (Drosophila)
3574	1389542_at	0.507098563	1.421189134	yes	yes	yes	BE108837	Rn.44998	centromere protein E (predicted)
3575	1390247_at	0.507154874	1.421244606	yes	no	no	BI275999	Rn.18259	Transcribed locus
3576	1381924_at	0.508188783	1.422263508	yes	yes	no	BF412180	Rn.47098	similar to hypothetical protein FLJ31606 (predicted)
3577	1381335_at	0.508471729	1.422542474	yes	yes	yes	BE349658	Rn.177224	Transcribed locus
3578	1374055_at	0.508618361	1.422687065	yes	yes	no	BF285169	Rn.9093	Ets2 repressor factor (predicted)
3579	1386008_at	0.509159327	1.423220629	yes	no	no	AW914833	Rn.117988	Transcribed locus

3580	1385434_at	0.509352901	1.423411603	yes	yes	yes	AI705087	Rn.162044	Prostaglandin E receptor 2, subtype EP2
3581	1379996_at	0.509514119	1.423570675	yes	yes	no	AI411753	Rn.164361	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3582	1384238_at	0.509548168	1.423604273	yes	yes	no	BM385249	Rn.16666	Transcribed locus
3583	1388292_at	0.509609806	1.423665097	yes	yes	no	U91449	Rn.9809	potassium inwardly-rectifying channel, subfamily J, member 3
3584	1373497_at	0.509845582	1.423897781	yes	yes	yes	BE109208	Rn.8042	Transcribed locus
3585	1380728_at	0.509853155	1.423905256	yes	yes	no	BE118404	Rn.2889	Dihydropyrimidinase-like 2
3586	1377114_at	0.509868981	1.423920875	yes	yes	no	AI410861	---	---
3587	1375151_at	0.510498275	1.424542116	yes	yes	yes	BF284007	Rn.8473	Similar to RAP2A, member of RAS oncogene family (predicted)
3588	1384326_at	0.510628637	1.424670844	yes	yes	no	BF560443	Rn.99540	Neural precursor cell expressed, developmentally down-regulated gene 4A
3589	1375194_at	0.511362816	1.425396035	yes	yes	yes	AI231460	Rn.12107	Transcribed locus
3590	1392342_at	0.51217979	1.426203441	yes	no	no	AI709861	---	---
3591	1391584_at	0.512581234	1.426600352	yes	yes	yes	AA850595	Rn.164498	Transcribed locus
3592	1382372_at	0.512583036	1.426602134	yes	yes	no	AA858521	Rn.174710	Transcribed locus
3593	1372156_at	0.512947346	1.426962425	yes	yes	no	BF414018	Rn.20057	transmembrane protein 97
3594	1392592_at	0.512986766	1.427001416	yes	yes	yes	AI137045	Rn.166746	Transcribed locus
3595	1388484_at	0.513121372	1.427134563	yes	yes	no	BI296084	Rn.3102	ubiquitin-conjugating enzyme E2C (predicted)
3596	1393158_at	0.513197671	1.427210042	yes	yes	no	BI298434	Rn.155071	similar to 2610528M18Rik protein
3597	1385342_at	0.513327989	1.427338967	yes	yes	yes	AA998932	Rn.13221	Transcribed locus
3598	1367683_at	0.513392712	1.427403002	yes	yes	no	NM_053483	Rn.2949	karyopherin (importin) alpha 2
3599	1391290_at	0.513639592	1.427647286	yes	no	no	BF401802	Rn.171136	Transcribed locus
3600	1388313_at	0.513743583	1.427750196	yes	yes	yes	BM389289	Rn.60855	ribosomal protein s25
3601	1395342_at	0.513760515	1.427766953	yes	yes	no	AI598942	Rn.99508	cytoskeleton-associated protein 4 (predicted)
3602	1390415_at	0.514071415	1.428074669	yes	yes	no	BM392319	Rn.11751	thyroid hormone receptor interactor 13
3603	1392732_at	0.514658415	1.428655839	yes	yes	no	AI711233	Rn.106933	nucleolar and spindle associated protein 1 (predicted)
3604	1386861_at	0.515095279	1.429088517	yes	yes	no	NM_022674	Rn.112573	H2A histone family, member Z
3605	1370008_at	0.516156909	1.430140521	yes	yes	yes	NM_134458	Rn.144650	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein
3606	1393943_at	0.516700661	1.430679644	yes	no	no	AI716693	Rn.41528	Transcribed locus
3607	1378934_at	0.516706204	1.43068514	yes	yes	no	BE116059	Rn.171457	Transcribed locus, strongly similar to XP_511078.1 PREDICTED: DEAD (Asp-Glu-Ala-As) box polypeptide 19 [Pan troglodytes]
3608	1389421_at	0.517197488	1.431172417	yes	yes	no	BE101140	Rn.40977	polymerase (DNA directed), epsilon (mapped)
3609	1391599_at	0.517340276	1.431314072	yes	yes	yes	AA875010	Rn.163701	Transcribed locus
3610	1370072_at	0.517567931	1.431539949	yes	yes	no	NM_012608	Rn.33598	membrane metallo endopeptidase
3611	1380758_at	0.518188553	1.432155905	yes	yes	yes	BF412419	Rn.145315	Similar to RIKEN cDNA 2610528A15
3612	1382778_at	0.518230033	1.432197082	yes	yes	no	AI231350	Rn.4313	Dual specificity phosphatase 6
3613	1369495_at	0.519164143	1.433124696	yes	yes	yes	NM_022714	Rn.10023	corticotropin releasing hormone receptor 2
3614	1372596_at	0.519893764	1.43384966	yes	yes	no	BI284774	Rn.102176	similar to RIKEN cDNA 1110007L15 (predicted)
3615	1386857_at	0.520858479	1.43480878	yes	yes	no	NM_017166	Rn.555	stathmin 1
3616	1382050_at	0.521095992	1.435045014	yes	yes	no	AI410262	Rn.7315	Transcribed locus
3617	1379179_at	0.521180382	1.435128959	yes	no	no	BF413722	Rn.74021	similar to novel protein similar to multidomain presynaptic cytomatrix protein piccolo (presynaptic cytomatrix protein) (predicted)
3618	1383119_at	0.522351126	1.436294037	yes	yes	yes	BF554283	Rn.35627	opioid growth factor receptor-like 1
3619	1389440_at	0.522607118	1.436548915	yes	yes	no	AI178476	Rn.16546	Transcribed locus
3620	1378076_at	0.522690441	1.436631886	yes	yes	no	AA963273	Rn.11429	Transcribed locus
3621	1391677_at	0.523077574	1.437017443	yes	yes	yes	AA900618	Rn.105738	Transcribed locus, strongly similar to XP_213649.3 PREDICTED: similar to interferon alpha/beta receptor [Rattus norvegicus]

3622	1396792_at	0.523767433	1.437704752	yes	yes	no	BF392277	---	---
3623	1374449_at	0.523853038	1.437790063	yes	yes	no	BF417638	Rn.3246	cell division cycle associated 3 /// similar to cell division cycle associated 3 (predicted)
3624	1378892_at	0.524096587	1.438032804	yes	yes	yes	BF564915	Rn.88925	Bone morphogenetic protein receptor, type 1A
3625	1379192_at	0.524366797	1.438302166	yes	yes	no	AW528096	Rn.163427	ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (predicted)
3626	1383526_at	0.524686532	1.438620963	yes	yes	no	AA957027	Rn.146377	Transcribed locus
3627	1372629_at	0.525329438	1.439262197	yes	yes	yes	BF285818	Rn.8477	similar to KIAA0925 protein
3628	1384000_at	0.525445986	1.439378472	yes	yes	no	BF560932	Rn.15099	Transcribed locus
3629	1392071_at	0.52552461	1.439456917	yes	yes	no	BF392945	Rn.7596	Synaptotagmin I
3630	1375654_at	0.526773831	1.440703874	yes	yes	no	BI278813	Rn.99508	cytoskeleton-associated protein 4 (predicted)
3631	1372584_at	0.527104492	1.441034117	yes	yes	yes	BG672517	Rn.8173	similar to DKFZP566K1924 protein
3632	1389103_at	0.527281054	1.441210486	yes	yes	yes	BM391005	Rn.103411	similar to RIKEN cDNA 2810037C03
3633	1382597_at	0.527888948	1.441817883	yes	yes	yes	BF288069	---	---
3634	1385619_at	0.528185451	1.442114236	yes	yes	no	BF562797	Rn.58850	similar to Kinesin family member 11 (predicted)
3635	1371703_at	0.528600916	1.442529594	yes	yes	no	AI407114	Rn.112831	AHNAK nucleoprotein (desmoyokin)
3636	1374306_at	0.528743611	1.442672279	yes	yes	no	BF394933	Rn.34857	zinc finger, DHHC domain containing 18
3637	1370103_at	0.528778736	1.442707404	yes	yes	no	NM_053375	Rn.21408	hyperpolarization-activated cyclic nucleotide-gated potassium channel 1
3638	1385977_at	0.529406522	1.443335332	yes	yes	yes	BF557320	Rn.8773	Zinc finger protein 644 (predicted)
3639	1372186_a_at	0.529799707	1.443728745	yes	yes	no	BM385445	Rn.90996	topoisomerase (DNA) 2 alpha
3640	1373067_at	0.529860182	1.443789265	yes	yes	no	AI102738	Rn.112601	Catenin (cadherin associated protein), beta 1
3641	1378757_at	0.53045346	1.444383115	yes	yes	no	BG375931	Rn.161177	Transcribed locus
3642	1389300_at	0.530763822	1.444693873	yes	yes	yes	AI410415	Rn.22356	similar to RIKEN cDNA 4930404J24 (predicted)
3643	1391036_at	0.530923735	1.444854017	yes	yes	yes	BG376106	---	IQ motif and Sec7 domain 3
3644	1369167_at	0.531205309	1.44513604	yes	yes	no	NM_012750	Rn.90137	glial cell line derived neurotrophic factor family receptor alpha 2
3645	1373035_at	0.531213329	1.445144073	yes	yes	no	AI031032	---	---
3646	1376914_at	0.531485783	1.445417016	yes	yes	no	AW253690	Rn.27037	DEP domain containing 1a (predicted)
3647	1395423_at	0.531813848	1.445745737	yes	yes	yes	AW920217	Rn.134121	Similar to C230080I20Rik protein (predicted)
3648	1381026_at	0.532183118	1.446115835	yes	yes	no	BF391155	Rn.50159	Transcribed locus
3649	1392221_at	0.533113804	1.447049029	yes	no	no	BE114215	Rn.141320	Similar to GREB1 protein isoform a (predicted)
3650	1372662_at	0.53517414	1.449117059	yes	yes	yes	AI176698	Rn.137885	F-box only protein 34 (predicted)
3651	1395480_at	0.535181245	1.449124196	yes	yes	yes	BI303370	Rn.103858	Transcribed locus
3652	1370346_at	0.53542616	1.449370223	yes	yes	no	X64589	Rn.9232	cyclin B1
3653	1392213_at	0.536497218	1.450446636	yes	yes	yes	BM389936	Rn.19412	Similar to novel protein (predicted)
3654	1371862_at	0.536596171	1.450546125	yes	yes	no	AI412015	Rn.162454	ribonucleotide reductase M1 (mapped)
3655	1383361_at	0.536635721	1.45058589	yes	yes	no	BM383741	---	---
3656	1376346_at	0.536666256	1.450616592	yes	yes	no	BM392156	---	---
3657	1380487_at	0.537279382	1.451233216	yes	yes	yes	BE105524	Rn.50789	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hypothetical protein PB402898.00.0 [Rattus norvegicus]
3658	1397486_x_at	0.537469398	1.451424369	yes	yes	no	BF404567	Rn.139712	Bromodomain adjacent to zinc finger domain, 2B (predicted)
3659	1391200_at	0.538055992	1.452014632	yes	yes	no	AW530290	Rn.151033	Transcribed locus
3660	1379320_at	0.538864364	1.452828454	yes	yes	no	AI102591	Rn.18606	Small nuclear ribonucleoprotein D1 (predicted)
3661	1382480_at	0.540115235	1.454088658	yes	yes	no	AI060139	Rn.166331	Transcribed locus
3662	1369037_at	0.540437306	1.454413309	yes	yes	no	NM_019349	Rn.33275	serine/threonine kinase 2
3663	1382413_at	0.540604181	1.454581549	yes	yes	yes	AA874825	Rn.11328	Nucleoporin 155
3664	1389533_at	0.541182697	1.455164948	yes	yes	yes	AA944398	Rn.7350	fibulin 2
3665	1382654_at	0.541309999	1.455293356	yes	yes	no	AA859319	Rn.175480	Transcribed locus
3666	1382911_at	0.541504227	1.455489293	yes	yes	yes	BE105150	Rn.157510	Transcribed locus, weakly similar to XP_574807.1 PREDICTED: similar

									to HORMA domain containing 1 [Rattus norvegicus]
3667	1384260_at	0.541512402	1.45549754	yes	yes	no	BE095699	---	---
3668	1373754_at	0.543199282	1.457200386	yes	yes	no	AI599232	Rn.1545	Golgi phosphoprotein 2 (predicted)
3669	1371756_at	0.543376566	1.457379463	yes	yes	no	BI286411	Rn.162014	Keratin complex 2, basic, gene 5
3670	1376669_at	0.544068	1.458078102	yes	yes	yes	BF283340	Rn.166103	Transcribed locus
3671	1392866_at	0.544548553	1.45856386	yes	yes	no	AI044609	Rn.20780	LOC360791 (predicted)
3672	1375426_a_at	0.545187901	1.459210384	yes	yes	no	BI295086	Rn.92643	KH-type splicing regulatory protein
3673	1374695_at	0.545338724	1.459362941	yes	yes	yes	BF564593	Rn.32816	Chromobox homolog 1 (Drosophila HP1 beta) (predicted)
3674	1375892_at	0.54568595	1.459714221	yes	yes	no	BF559812	Rn.73705	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)
3675	1383958_at	0.546861686	1.460904312	yes	yes	no	BG381524	Rn.49950	cell division cycle associated 2
3676	1389755_at	0.547131226	1.461177279	yes	no	no	BM391858	---	similar to transcription factor RAM2
3677	1368745_at	0.547850373	1.461905821	yes	no	no	NM_017222	Rn.85891	solute carrier family 10, member 2
3678	1395560_at	0.547953274	1.462010096	yes	no	no	BF522151	Rn.24173	Transcribed locus
3679	1375427_at	0.548537067	1.462601825	yes	yes	yes	AI411580	Rn.13052	RAN binding protein 1 (predicted)
3680	1384166_a_at	0.54917935	1.463253116	yes	yes	no	AW522260	---	---
3681	1385254_at	0.549275887	1.463351031	yes	yes	no	BE104427	Rn.13214	5'-3' exoribonuclease 1 (predicted)
3682	1368001_at	0.549366925	1.463443376	yes	yes	yes	NM_012905	Rn.11313	aortic preferentially expressed gene 1
3683	1387883_a_at	0.54945628	1.463534018	yes	yes	no	BG668902	Rn.23434	thymosin, beta 4
3684	1378983_at	0.550020302	1.464106299	yes	yes	no	AA997020	Rn.146007	Similar to translin-associated factor X (Tsnax) interacting protein 1 (predicted)
3685	1388946_at	0.550078965	1.464165834	yes	yes	yes	AI233763	Rn.105128	similar to hypothetical p38 protein (predicted)
3686	1377064_at	0.550195274	1.464283879	yes	yes	no	AI602811	Rn.4313	dual specificity phosphatase 6
3687	1377350_at	0.551014415	1.465115514	yes	yes	no	AA859898	Rn.809	Transcribed locus, weakly similar to XP_577997.1 PREDICTED: similar to exo-alpha-sialidase (EC 3.2.1.18) - Trypanosoma cruzi [Rattus norvegicus]
3688	1376051_at	0.551564461	1.465674214	yes	yes	yes	BI293393	Rn.57632	crystallin, lamda 1
3689	1381817_at	0.55253611	1.466661672	yes	yes	no	AI044318	Rn.166043	Transcribed locus
3690	1373026_at	0.552763031	1.466892381	yes	yes	yes	BI303598	Rn.162984	spindle pole body component 24 homolog (S. cerevisiae) (predicted)
3691	1379624_at	0.55284165	1.466972321	yes	yes	yes	AA964442	Rn.22683	CCR4-NOT transcription complex, subunit 8
3692	1379010_at	0.554342125	1.468498839	yes	yes	no	AA956727	Rn.9002	Splicing factor, arginine/serine-rich 3 (SRp20) (predicted)
3693	1378302_at	0.555026351	1.469195468	yes	yes	no	BF403965	---	---
3694	1374332_at	0.555884754	1.470069898	yes	yes	no	AI171365	Rn.95332	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (predicted)
3695	1368799_at	0.557106632	1.47131549	yes	yes	no	NM_022274	Rn.54471	baculoviral IAP repeat-containing 5
3696	1369018_at	0.557540163	1.471757688	yes	yes	yes	NM_031633	Rn.10665	forkhead box M1
3697	1381617_at	0.558946311	1.473192861	yes	yes	yes	BE102030	Rn.104893	Phosphatidylserine synthase 2 (predicted)
3698	1382092_at	0.558954909	1.473201641	yes	yes	no	AA965250	---	---
3699	1389850_at	0.559380293	1.473636083	yes	yes	no	AA900926	Rn.61077	AT rich interactive domain 1A (Swi1 like) (predicted)
3700	1389756_at	0.560889768	1.475178738	yes	yes	no	BM390710	Rn.28232	maternal embryonic leucine zipper kinase (predicted)
3701	1386956_at	0.560972305	1.475263136	yes	yes	yes	NM_031541	Rn.88169	scavenger receptor class B, member 1
3702	1394935_at	0.561471491	1.475773679	yes	yes	no	AI175684	Rn.162111	WAS protein family, member 2
3703	1374354_at	0.56157203	1.475876528	yes	yes	no	BE349704	Rn.48468	RGD1564003 (predicted)
3704	1376037_at	0.562723767	1.477055225	yes	yes	no	BF283385	Rn.104730	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) (predicted)
3705	1376625_at	0.563292427	1.477637542	yes	yes	yes	BI296015	---	---
3706	1376930_at	0.56366232	1.478016443	yes	yes	no	BI294860	Rn.118218	Transcribed locus
3707	1399024_at	0.563780193	1.478137207	yes	yes	no	AI180441	Rn.143751	SCY1-like 1 (S. cerevisiae)
3708	1379297_at	0.564438757	1.478812104	yes	yes	no	AI556361	Rn.1269	Myelin basic protein expression factor 2, repressor

3709	1378317_at	0.564475974	1.478850253	yes	yes	no	BI282595	Rn.40671	type II keratin Kb40
3710	1371229_at	0.564667098	1.47904618	yes	yes	no	M35300	Rn.1658	ATPase inhibitory factor 1
3711	1397737_at	0.564994233	1.479381596	yes	yes	no	BF391084	Rn.61385	Similar to RIKEN cDNA C130096D04 gene (predicted)
3712	1382529_at	0.565100165	1.479490226	yes	yes	yes	AW531626	Rn.169927	Transcribed locus, strongly similar to NP_032644.2 malate dehydrogenase 1, NAD (soluble) [Mus musculus]
3713	1385427_at	0.566756981	1.481190274	yes	yes	yes	BE118330	Rn.163145	similar to RNA-binding protein Musashi2-S (predicted)
3714	1394362_at	0.566816075	1.481250946	yes	yes	no	BF546803	Rn.38655	similar to intracellular protein transport like (XM453) (predicted)
3715	1382220_at	0.567192747	1.481637734	yes	yes	no	AI180454	---	---
3716	1385172_at	0.567463631	1.481915957	yes	yes	no	BF389065	Rn.158476	Transcribed locus, weakly similar to XP_576359.1 PREDICTED: similar to LRRGT00073 [Rattus norvegicus]
3717	1375697_at	0.567769649	1.482230328	yes	yes	no	AI407016	Rn.162140	similar to Hypothetical protein KIAA0152
3718	1391626_at	0.56846876	1.482948771	yes	yes	yes	BF288218	Rn.42077	similar to RIKEN cDNA 2610034E18 gene (predicted)
3719	1369116_a_at	0.568633383	1.483117996	yes	yes	no	NM_017338	Rn.90085	calcitonin/calcitonin-related polypeptide, alpha
3720	1395713_at	0.569376172	1.483881794	yes	yes	no	AI136510	Rn.27154	Endosulfine alpha
3721	1373470_at	0.569932017	1.484453618	yes	yes	no	BM388896	---	---
3722	1379138_at	0.57002615	1.484550479	yes	yes	yes	BF391688	Rn.31803	Par-3 (partitioning defective 3) homolog (C. elegans)
3723	1370462_at	0.571280162	1.485841433	yes	yes	no	AI171185	Rn.92304	hyaluronan mediated motility receptor (RHAMM)
3724	1398345_at	0.571758257	1.486333909	yes	yes	no	BM389225	---	---
3725	1374716_at	0.573985129	1.48862991	yes	yes	no	AI411620	Rn.137835	similar to RIKEN cDNA 2810430M08
3726	1374794_at	0.573989559	1.488634481	yes	yes	no	BF396282	---	---
3727	1368903_at	0.578372205	1.493163559	yes	yes	no	NM_053416	Rn.98476	spermatid perinuclear RNA binding protein
3728	1397164_at	0.578585085	1.493383902	yes	yes	yes	AI175779	Rn.153998	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3729	1369067_at	0.579489699	1.494320593	yes	yes	no	NM_031628	Rn.62694	nuclear receptor subfamily 4, group A, member 3
3730	1383701_at	0.580051725	1.494902844	yes	yes	yes	BM385937	Rn.19653	Mitogen activated protein kinase kinase 4
3731	1381273_at	0.580387774	1.495251095	yes	yes	no	AW532624	Rn.169983	Transcribed locus
3732	1396289_at	0.582720901	1.497671172	yes	no	no	BI283720	Rn.133657	MAM domain containing glycosylphosphatidylinositol anchor 1 (predicted)
3733	1393673_at	0.583472382	1.498451493	yes	yes	yes	BE120005	Rn.38645	similar to HCDI protein (predicted)
3734	1388650_at	0.583489063	1.498468818	yes	yes	yes	BM385445	Rn.90996	topoisomerase (DNA) 2 alpha
3735	1392951_at	0.585291137	1.500341728	yes	yes	yes	AW521231	Rn.164642	Transcribed locus
3736	1382651_at	0.585433871	1.500490173	yes	yes	no	AA998677	Rn.165520	Transcribed locus
3737	1395822_at	0.58555095	1.500611947	yes	no	no	BE098563	Rn.49293	tripartite motif protein 28
3738	1393345_at	0.586425848	1.501522245	yes	yes	yes	BF561145	Rn.22695	Aspartate-beta-hydroxylase (predicted)
3739	1397267_at	0.58692513	1.502041975	yes	no	no	BF410275	---	---
3740	1395612_at	0.587682912	1.502831137	yes	yes	yes	BI297603	Rn.79888	pellino homolog 3 (Drosophila) (predicted)
3741	1394840_at	0.588278048	1.503451207	yes	yes	no	AI511432	Rn.123716	Transcribed locus
3742	1395567_at	0.589462274	1.504685812	yes	yes	no	BF287710	---	---
3743	1381833_at	0.590288123	1.505547393	yes	yes	yes	AW532628	Rn.49950	cell division cycle associated 2
3744	1377245_a_at	0.591666103	1.506986092	yes	yes	yes	AI146147	Rn.160168	similar to KIAA1731 protein (predicted)
3745	1388250_at	0.592542184	1.507901493	yes	yes	yes	AB012232	Rn.9909	nuclear factor I/B
3746	1387122_at	0.592627143	1.507990294	yes	yes	yes	NM_012760	Rn.6977	pleiomorphic adenoma gene-like 1
3747	1376430_at	0.592675241	1.50804057	yes	yes	yes	AA925921	Rn.163649	Transcribed locus
3748	1379714_at	0.593406258	1.508804891	yes	no	no	AI230650	---	---
3749	1376262_at	0.594362855	1.509805655	yes	yes	yes	BM385390	Rn.3037	UDP-glucuronate decarboxylase 1
3750	1375458_at	0.595415041	1.510907187	yes	yes	yes	AI232205	Rn.22774	Asparaginase like 1
3751	1368290_at	0.595509514	1.511006131	yes	yes	yes	NM_031327	Rn.22129	cysteine rich protein 61
3752	1391434_at	0.595728362	1.511235359	yes	no	no	BF389910	Rn.44409	RAB3A, member RAS oncogene family

3753	1380410_at	0.598146201	1.513770188	yes	yes	yes	AI043958	Rn.96000	Similar to GLI pathogenesis-related 2
3754	1379762_at	0.598218374	1.51384592	yes	yes	no	AA849027	Rn.156069	Transcribed locus
3755	1395499_at	0.598283656	1.513914422	yes	yes	yes	BF392443	Rn.30310	Transcribed locus
3756	1388340_at	0.599089346	1.514760122	yes	yes	yes	BF281153	Rn.7233	KIAA0101
3757	1373782_a_at	0.600518307	1.516261206	yes	yes	yes	AW253957	Rn.154936	similar to LOC495800 protein
3758	1372922_at	0.600744698	1.516499159	yes	yes	yes	BI292045	Rn.15352	hypothetical LOC287306 (predicted)
3759	1386669_at	0.601388851	1.517176417	yes	yes	no	BF565188	---	---
3760	1370957_at	0.601967357	1.517784911	yes	yes	yes	BM383427	Rn.12138	interleukin 6 signal transducer
3761	1386277_at	0.602249424	1.518081688	yes	yes	yes	AI177396	Rn.98275	ubiquitin-activating enzyme E1-like (predicted)
3762	1398566_at	0.602959446	1.518828995	yes	yes	yes	AW526014	Rn.161133	Transcribed locus
3763	1387283_at	0.60313271	1.519011414	yes	yes	no	NM_134350	Rn.10374	myxovirus (influenza virus) resistance 2
3764	1384354_at	0.604169033	1.520102949	yes	yes	no	BI288653	Rn.154477	similar to X-linked lymphocyte regulated gene 4 (predicted)
3765	1379046_at	0.606114411	1.522154088	yes	yes	yes	BI290140	Rn.162140	similar to Hypothetical protein KIAA0152
3766	1380143_at	0.606881293	1.522963423	yes	yes	yes	AI029786	Rn.165884	Transcribed locus
3767	1370345_at	0.606979428	1.523067022	yes	yes	yes	L11995	Rn.9232	cyclin B1
3768	1372551_at	0.608095011	1.524245208	yes	yes	yes	AI227743	Rn.7680	Fas-activated serine/threonine kinase
3769	1372903_at	0.608098497	1.524248892	yes	yes	yes	AI410054	Rn.112739	similar to 3000004C01Rik protein
3770	1394026_at	0.608381479	1.524547899	yes	yes	yes	AA875227	Rn.19220	Transcribed locus
3771	1383599_at	0.608402347	1.524569952	yes	yes	yes	BE101133	---	---
3772	1383421_at	0.608961028	1.525160453	yes	yes	yes	BM386110	Rn.223	Proliferating cell nuclear antigen
3773	1374389_at	0.609001942	1.525203707	yes	yes	yes	BF399387	Rn.87228	guanylate cyclase 1, soluble, beta 3
3774	1385706_at	0.609147279	1.525357363	yes	yes	yes	BI292758	Rn.177359	Transcribed locus
3775	1390569_at	0.609751536	1.525996376	yes	yes	no	AI231438	Rn.15548	carnosine dipeptidase 1 (metallopeptidase M20 family)
3776	1374775_at	0.610363834	1.526644166	yes	yes	yes	AI714002	Rn.159784	antigen identified by monoclonal antibody Ki-67 (predicted) /// similar to Mki67 protein (predicted) /// similar to Ki-67 (predicted)
3777	1380453_at	0.611466349	1.52781128	yes	yes	yes	AW530611	Rn.134685	zinc finger, SWIM domain containing 5 (predicted)
3778	1390962_at	0.611568535	1.5279195	yes	yes	yes	BM385344	Rn.167071	Transcribed locus
3779	1369525_at	0.611823075	1.528189099	yes	yes	yes	NM_133293	Rn.92350	GATA binding protein 3
3780	1373278_at	0.614046404	1.530545999	yes	yes	yes	BM391303	Rn.21931	nuclear factor, erythroid derived 2,-like 1 (predicted)
3781	1391418_at	0.614531195	1.531060397	yes	yes	yes	AI072641	---	---
3782	1383842_at	0.614636333	1.531171979	yes	yes	yes	BG380618	Rn.94899	Transcribed locus, strongly similar to XP_343596.1 PREDICTED: similar to hypothetical protein FLJ10415 [Rattus norvegicus]
3783	1381990_at	0.616597058	1.533254365	yes	yes	yes	AA963979	Rn.165154	Transcribed locus
3784	1382799_at	0.618113601	1.53486695	yes	yes	no	AA998800	Rn.41192	Transcribed locus
3785	1392767_at	0.618835249	1.535634895	yes	yes	yes	AI502349	---	---
3786	1398209_at	0.620814607	1.537743211	yes	yes	no	BF413358	Rn.92051	Leucine-rich PPR-motif containing
3787	1390678_at	0.62104742	1.537991383	yes	yes	yes	AA955527	Rn.98833	Transcribed locus, strongly similar to XP_578163.1 PREDICTED: similar to hypothetical protein, expressed [Rattus norvegicus]
3788	1385265_a_at	0.621084698	1.538031124	yes	yes	yes	AW528215	---	---
3789	1385315_at	0.621354971	1.538319284	yes	yes	yes	AI145941	Rn.101261	Similar to actin monomer-binding protein (predicted)
3790	1373530_at	0.622146343	1.53916334	yes	yes	yes	AW913890	Rn.15455	cyclin E
3791	1389852_at	0.622435892	1.539472282	yes	yes	yes	AI598316	Rn.11654	similar to proliferation associated nuclear element 1 isoform 1 (predicted)
3792	1379483_at	0.623962994	1.541102686	yes	yes	yes	AI548256	Rn.81055	Basic helix-loop-helix domain containing, class B2
3793	1385872_at	0.624430388	1.541602042	yes	yes	yes	AI237532	Rn.162589	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)
3794	1375629_at	0.625791419	1.543057068	yes	yes	yes	AI230371	---	---
3795	1379448_at	0.627660253	1.545057203	yes	yes	yes	BE110883	---	---
3796	1375310_at	0.627747513	1.545150658	yes	yes	no	AI409746	---	---

3797	1386073_at	0.62869641	1.546167276	yes	yes	yes	AI043800	Rn.161794	Similar to T-Brain-1
3798	1388777_at	0.6314761	1.549149203	yes	yes	yes	BE113224	Rn.3264	signal sequence receptor, gamma
3799	1369097_s_at	0.631723225	1.549414585	yes	yes	yes	NM_012769	Rn.87228	guanylate cyclase 1, soluble, beta 3
3800	1381298_at	0.632245332	1.549975414	yes	yes	yes	AI103253	Rn.137948	Minichromosome maintenance deficient 10 (S. cerevisiae) (predicted)
3801	1388822_at	0.63284506	1.550619873	yes	yes	yes	AI409077	Rn.18315	short coiled-coil protein /// similar to short coiled-coil protein
3802	1392895_at	0.633136482	1.550933127	yes	yes	yes	BE101114	---	---
3803	1389846_at	0.633250412	1.551055609	yes	yes	yes	BE104273	Rn.37575	Tropomyosin 3, gamma
3804	1390137_at	0.63333836	1.551150166	yes	yes	yes	BM388478	Rn.20235	TRAF4 associated factor 1
3805	1385961_at	0.633345573	1.551157922	yes	yes	yes	BF561079	Rn.8954	Kruppel-like factor 5
3806	1397609_at	0.633474505	1.551296552	yes	yes	yes	BF287466	Rn.20235	TRAF4 associated factor 1
3807	1376231_at	0.63354971	1.551377422	yes	yes	yes	BF389244	Rn.117311	similar to Hypothetical UPF0080 protein KIAA0186 (predicted)
3808	1385424_at	0.633652938	1.551488429	yes	yes	no	AA900738	Rn.164651	Transcribed locus
3809	1368921_a_at	0.634719977	1.552636358	yes	yes	yes	NM_012924	Rn.1120	CD44 antigen
3810	1393200_at	0.635053034	1.552994837	yes	no	no	AI500827	Rn.23430	Transcribed locus
3811	1392500_at	0.635294785	1.553255093	yes	yes	yes	AA957990	Rn.165165	Transcribed locus
3812	1371472_at	0.636109872	1.554132892	yes	yes	yes	BG380581	Rn.19113	Transcribed locus
3813	1390891_at	0.636903656	1.554988225	yes	yes	yes	BE116384	Rn.58850	similar to Kinesin family member 11 (predicted)
3814	1397421_at	0.64167174	1.560135938	yes	yes	no	AI549253	Rn.168795	Transcribed locus
3815	1376862_at	0.643430934	1.562039498	yes	yes	yes	BI296848	Rn.19289	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (predicted)
3816	1367776_at	0.64345181	1.562062101	yes	yes	yes	NM_019296	Rn.6934	cell division cycle 2 homolog A (S. pombe)
3817	1369777_a_at	0.644745972	1.56346397	yes	yes	no	NM_133440	Rn.14545	SH3/ankyrin domain gene 2
3818	1385536_at	0.646828444	1.565722396	yes	yes	no	AI454433	Rn.138175	Similar to zinc finger protein ZFP235 (predicted)
3819	1396026_at	0.647175897	1.566099523	yes	yes	yes	BE108856	Rn.170643	Transcribed locus
3820	1393712_at	0.648180543	1.567190484	yes	yes	no	BF419515	Rn.155831	Transcribed locus
3821	1367811_at	0.648711727	1.567767613	yes	yes	yes	NM_031620	Rn.6872	3-phosphoglycerate dehydrogenase
3822	1372641_at	0.649696418	1.568838036	yes	yes	yes	AW434261	Rn.68281	Transcribed locus
3823	1383486_at	0.653614232	1.573104196	yes	yes	yes	AA926109	Rn.35842	Transcribed locus
3824	1374805_at	0.654196585	1.573739318	yes	yes	yes	AW251849	Rn.8559	similar to hypothetical protein MGC5528 (predicted)
3825	1385887_at	0.654257061	1.573805288	yes	yes	yes	BE107316	Rn.10455	Cut-like 1 (Drosophila)
3826	1392149_at	0.65570655	1.5753873	yes	yes	yes	AA997766	Rn.165448	Transcribed locus
3827	1395943_at	0.655781629	1.575469286	yes	yes	no	AI502219	Rn.91605	zinc finger CCCH-type containing 7B (predicted)
3828	1381002_at	0.659220198	1.579228792	yes	yes	yes	AI711108	---	---
3829	1379581_at	0.659906186	1.579979879	yes	yes	yes	BI288586	Rn.22587	Transcribed locus
3830	1387005_at	0.660971127	1.581146589	yes	yes	yes	NM_017320	Rn.11347	cathepsin S
3831	1372685_at	0.663648949	1.58408412	yes	yes	yes	BE113362	Rn.107220	cyclin-dependent kinase inhibitor 3 (predicted)
3832	1371279_at	0.668891213	1.589850614	yes	yes	yes	U95113	---	Histone H2a (predicted)
3833	1383209_at	0.672046047	1.593331047	yes	yes	yes	AW916721	Rn.4177	similar to RIKEN cDNA A630054L15; hypothetical protein MGC38041 (predicted)
3834	1382915_at	0.67622875	1.597957181	yes	yes	yes	AI237079	Rn.15945	Transcribed locus
3835	1391663_at	0.676390087	1.598135891	yes	yes	yes	AI511259	---	---
3836	1378240_at	0.676983712	1.598793611	yes	yes	yes	AI031007	Rn.32370	Fanconi anemia D2 protein
3837	1388604_at	0.678329852	1.600286098	yes	yes	yes	BI276959	---	---
3838	1374750_at	0.680889217	1.603127552	yes	yes	yes	AI172313	Rn.6257	Transcribed locus
3839	1370240_x_at	0.682009217	1.604372582	yes	yes	yes	AI179404	Rn.107334	hemoglobin alpha, adult chain 1 /// hemoglobin alpha 2 chain
3840	1388985_at	0.683143676	1.605634673	yes	yes	yes	AI012869	---	hypothetical protein LOC310926 /// LOC501211
3841	1380773_at	0.684314551	1.606938316	yes	yes	yes	BI288767	Rn.155429	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]

3842	1373169_at	0.686360149	1.609218411	yes	yes	yes	AI175416	Rn.15556	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted)
3843	1368324_at	0.688002796	1.611051705	yes	yes	yes	NM_031542	Rn.103225	breast cancer 2
3844	1381159_at	0.690377343	1.613705535	yes	yes	yes	AI548586	Rn.6535	Similar to 1300014I06Rik protein
3845	1386282_x_at	0.69318493	1.616848978	yes	yes	yes	AA964809	---	---
3846	1370297_at	0.693191678	1.616856541	yes	yes	yes	U10188	Rn.11034	polo-like kinase 1 (Drosophila)
3847	1397065_at	0.69537193	1.619301839	yes	yes	yes	BF399120	Rn.148139	Transcribed locus
3848	1397546_at	0.697537433	1.621734256	yes	yes	yes	BF567095	Rn.52841	spermatogenesis associated, serine-rich 2 (predicted)
3849	1397195_at	0.698212445	1.622493214	yes	yes	yes	AI110520	Rn.165547	Transcribed locus
3850	1371130_at	0.698619201	1.622950728	yes	yes	yes	X63744	Rn.34134	solute carrier family 1 (glial high affinity glutamate transporter), member 3
3851	1389668_at	0.6995405	1.623987469	yes	yes	yes	AI408269	Rn.16268	spindle pole body component 25 homolog (S. cerevisiae)
3852	1382216_at	0.699952662	1.62445149	yes	yes	yes	BF283004	Rn.108103	gem (nuclear organelle) associated protein 6
3853	1393844_at	0.70523871	1.630414413	yes	yes	yes	AW525736	Rn.128609	similar to myeloid leukemia factor 1 interacting protein
3854	1378286_at	0.705713168	1.630950694	yes	yes	yes	BI294238	Rn.73847	neurobeachin-like 2 (predicted)
3855	1396684_at	0.705752034	1.630994632	yes	yes	yes	BE120966	Rn.162643	neuropathy target esterase like 1
3856	1370308_at	0.70843755	1.634033488	yes	yes	yes	AY029335	Rn.8733	RS21-C6 protein
3857	1370621_at	0.710090961	1.635907257	yes	yes	yes	D13555	Rn.9997	CD3 antigen, zeta polypeptide
3858	1379741_at	0.710273655	1.636114431	yes	yes	no	BG377116	Rn.154498	ATPase, H+ transporting, lysosomal V0 subunit A isoform 4 (predicted)
3859	1379622_at	0.711274671	1.637250046	yes	yes	yes	BF405145	Rn.28061	Transcribed locus
3860	1368310_at	0.712664472	1.638828028	yes	yes	yes	NM_017115	Rn.9465	myogenin
3861	1393571_at	0.714011632	1.640359048	yes	yes	yes	AA963158	Rn.165009	Transcribed locus
3862	1375354_at	0.716658985	1.643371878	yes	yes	yes	BE098366	Rn.22682	Similar to HT014 (predicted)
3863	1371480_at	0.718443783	1.645406198	yes	yes	yes	AI407985	Rn.119060	RGD1561797 (predicted)
3864	1380504_at	0.718827528	1.64584392	yes	yes	no	BI282488	---	---
3865	1387059_at	0.720148477	1.647351566	yes	yes	no	NM_019362	Rn.34414	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)
3866	1383162_at	0.72415785	1.651936064	yes	yes	yes	AI008646	---	---
3867	1391395_at	0.72489266	1.652777661	yes	yes	yes	AI170715	Rn.98470	Transcribed locus, strongly similar to XP_342143.2 PREDICTED: similar to nucleolar protein GU2 [Rattus norvegicus]
3868	1384359_at	0.727407644	1.655661385	yes	yes	yes	BF407520	Rn.173430	Transcribed locus, moderately similar to XP_618803.1 PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G [Mus musculus]
3869	1385088_at	0.729430233	1.657984171	yes	yes	yes	AA891356	Rn.40355	hypothetical LOC304650 (predicted)
3870	1388253_at	0.732365412	1.661360792	yes	yes	yes	M15114	Rn.83595	Stearoyl-Coenzyme A desaturase 2
3871	1397338_at	0.732478371	1.661490876	yes	yes	no	AI137999	---	---
3872	1389356_at	0.73399719	1.663240957	yes	yes	yes	AW915885	Rn.106230	Kinesin 2
3873	1393612_a_at	0.734024447	1.663272382	yes	yes	yes	AI059270	Rn.97407	similar to Hypothetical protein MGC19163
3874	1370312_at	0.737902129	1.667748946	yes	yes	no	M88469	Rn.7546	spondin 1
3875	1385325_at	0.745835969	1.676945693	yes	yes	yes	BM389545	Rn.82263	syntrophin, gamma 2 (predicted)
3876	1379874_at	0.746313479	1.677500828	yes	yes	yes	BE107929	Rn.118218	Transcribed locus
3877	1392658_at	0.747550592	1.678939904	yes	yes	yes	AI230409	Rn.154851	Similar to transcription elongation factor IIS - mouse
3878	1377413_at	0.751313372	1.683324564	yes	yes	yes	BF548480	Rn.163733	Transcribed locus
3879	1392370_at	0.751505983	1.683549316	yes	yes	yes	BF392339	Rn.101545	tubulin, epsilon 1 (predicted)
3880	1398390_at	0.754247838	1.686751959	yes	yes	yes	AA892854	Rn.6917	similar to Small inducible cytokine B13 precursor (CXCL13) (B lymphocyte chemoattractant) (CXC chemokine BLC)
3881	1390540_at	0.754899629	1.687514185	yes	yes	yes	BF400717	Rn.50326	Transcribed locus
3882	1375532_at	0.755043673	1.687682681	yes	yes	yes	AI008792	Rn.164123	Transcribed locus
3883	1383161_a_at	0.75660886	1.689514649	yes	yes	yes	AI008646	---	---

3884	1389930_at	0.758479034	1.691706197	yes	yes	yes	AI598451	Rn.7535	Heat shock 70kDa protein 9A (predicted)
3885	1386517_at	0.760991193	1.694654524	yes	yes	yes	AI233363	---	---
3886	1381931_at	0.761899441	1.69572173	yes	yes	no	AI229552	Rn.40404	similar to actin-binding LIM protein 1 long isoform (predicted)
3887	1373823_at	0.763980501	1.698169541	yes	yes	yes	AA944180	Rn.6116	similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2) (predicted)
3888	1367971_at	0.764356043	1.698611642	yes	yes	yes	NM_053475	Rn.167750	protein tyrosine phosphatase 4a2
3889	1393335_at	0.765407654	1.699850248	yes	yes	yes	BF418373	Rn.21946	EGF-like-domain, multiple 6
3890	1375612_at	0.765782844	1.700292371	yes	yes	yes	AA965147	Rn.151553	Transcribed locus
3891	1377962_at	0.771572413	1.707129393	yes	yes	yes	AI549424	Rn.20824	Myeloblastosis oncogene-like 2 (predicted)
3892	1381322_at	0.772763607	1.708539506	yes	yes	yes	BF402728	---	---
3893	1383940_at	0.775914879	1.71227554	yes	yes	yes	BG375704	Rn.41428	cell division cycle associated 1
3894	1380582_at	0.780142639	1.717300654	yes	yes	yes	AW535553	Rn.83632	colony stimulating factor 1 (macrophage)
3895	1375360_at	0.782844997	1.720520398	yes	yes	yes	BE099437	---	---
3896	1395659_at	0.783394618	1.721175988	yes	yes	yes	AI715999	---	---
3897	1375104_at	0.786062351	1.724361612	yes	yes	yes	AI408517	Rn.2773	Protein phosphatase 1, regulatory (inhibitor) subunit 14B
3898	1387617_at	0.786696317	1.725119518	yes	yes	yes	NM_057208	Rn.37575	tropomyosin 3, gamma
3899	1375542_at	0.787446681	1.726017008	yes	yes	yes	AI407092	Rn.27421	Radixin
3900	1374473_at	0.788232907	1.726957892	yes	yes	yes	BI282910	Rn.156197	Transcribed locus
3901	1376972_at	0.788240363	1.726966817	yes	yes	yes	AI407028	Rn.15324	Solute carrier family 39 (iron-regulated transporter), member 1
3902	1373432_at	0.790570374	1.729758192	yes	yes	yes	BE111604	Rn.9560	myristoylated alanine rich protein kinase C substrate
3903	1369410_at	0.791129758	1.730429012	yes	yes	yes	NM_053584	---	---
3904	1377954_at	0.792513664	1.732089723	yes	yes	yes	AA900691	Rn.15097	Transcribed locus
3905	1374600_at	0.794526908	1.734508497	yes	yes	yes	BM986536	Rn.1659	germinal histone H4 gene
3906	1375860_at	0.795184386	1.735299143	yes	yes	yes	AI011063	---	---
3907	1371979_at	0.795963983	1.73623711	yes	yes	yes	AI170663	Rn.41063	sterol regulatory element binding factor 2 (predicted)
3908	1374297_at	0.796804972	1.737249507	yes	yes	yes	BE100843	---	---
3909	1386948_at	0.799407989	1.740386812	yes	yes	yes	NM_012987	Rn.9701	nestin
3910	1393138_at	0.799893392	1.740972473	yes	yes	yes	BE329377	Rn.46225	Jun D proto-oncogene
3911	1375921_at	0.801410566	1.742804286	yes	yes	yes	BF281577	Rn.103345	Reticulocalbin 1 (predicted)
3912	1391839_at	0.816931323	1.761654886	yes	yes	yes	AA891521	Rn.9217	Spermatogenesis associated 9 (predicted)
3913	1380477_at	0.818624837	1.763724026	yes	yes	yes	BE112382	Rn.167687	Transcribed locus, moderately similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3914	1379525_at	0.819693289	1.765030715	yes	yes	yes	BF559514	Rn.35982	similar to chromosome 20 open reading frame 155
3915	1369426_at	0.820966887	1.766589555	yes	yes	yes	NM_022933	Rn.98337	chromodomain helicase DNA binding protein 8
3916	1378066_at	0.821242169	1.766926673	yes	yes	yes	AI103699	Rn.167859	Transcribed locus
3917	1397758_at	0.824104728	1.770436044	yes	yes	yes	BI301535	Rn.135561	Similar to mKIAA1208 protein (predicted)
3918	1372778_at	0.825650498	1.772333988	yes	yes	yes	AA799420	Rn.43952	Transcribed locus
3919	1380314_at	0.82853195	1.775877354	yes	yes	yes	BI290787	Rn.9381	similar to hypothetical protein FLJ38984 (predicted)
3920	1370169_at	0.839056789	1.788880218	yes	yes	yes	BI289608	Rn.3562	upstream of NRAS
3921	1375676_at	0.840358198	1.790494637	yes	yes	yes	AA956897	Rn.9461	Transcribed locus
3922	1394019_at	0.841103223	1.791419509	yes	yes	yes	BI283971	---	---
3923	1380888_at	0.846781416	1.798484114	yes	yes	yes	AI176481	Rn.3987	histone 1, H2ai (predicted) /// histone 1, H4a (predicted)
3924	1370745_at	0.847777007	1.79972566	yes	yes	yes	AB013454	Rn.92022	solute carrier family 34 (sodium phosphate), member 1
3925	1381384_at	0.848490912	1.800616459	yes	yes	yes	AW530069	Rn.168043	Transcribed locus, moderately similar to XP_223005.2 PREDICTED: similar to Mdes protein [Rattus norvegicus]
3926	1375937_a_at	0.852205217	1.805258227	yes	yes	yes	BE104344	Rn.195269	similar to RIKEN cDNA G630055P03 gene
3927	1392813_at	0.856119975	1.810163453	yes	yes	yes	AI548994	Rn.76633	Similar to SRY sex determining region Y-box 9 protein (predicted)

3928	1393451_at	0.859780507	1.81476219	yes	yes	yes	BI295149	Rn.65502	similar to RIKEN cDNA 2610510J17
3929	1377719_a_at	0.864987958	1.821324464	yes	yes	yes	AA892765	---	---
3930	1379008_at	0.865327293	1.821752907	yes	yes	yes	BE104149	---	---
3931	1371776_at	0.8684312	1.825676563	yes	yes	yes	AA819268	Rn.163585	Transcribed locus, strongly similar to XP_424759.1 PREDICTED: similar to 3-phosphatidylinositol kinase (EC 2.7.1.-) 85K chain alpha - bovine [Gallus gallus]
3932	1384298_at	0.868856708	1.826215107	yes	yes	yes	AI764088	---	myosin IF (predicted)
3933	1377840_at	0.87129994	1.829310458	yes	yes	yes	BF415080	---	---
3934	1372336_at	0.873163113	1.831674453	yes	yes	yes	BE115454	---	---
3935	1380395_at	0.874988834	1.833993891	yes	yes	yes	AI230394	Rn.3287	Transcribed locus
3936	1386038_x_at	0.880931713	1.841564226	yes	yes	yes	BF288392	---	---
3937	1398108_at	0.881570545	1.842379859	yes	yes	yes	AW532298	Rn.1801	Rho GDP dissociation inhibitor (GDI) alpha
3938	1389408_at	0.882786052	1.843932765	yes	yes	yes	BG379338	Rn.144946	ribonucleotide reductase M2 (mapped)
3939	1370953_at	0.893600741	1.857807138	yes	yes	yes	BE113639	---	---
3940	1381309_at	0.896098201	1.861025987	yes	yes	yes	AI453886	Rn.34540	Transcribed locus
3941	1376083_at	0.896683645	1.861781343	yes	yes	yes	BE112924	Rn.22312	Similar to RIKEN cDNA 0610016J10 gene
3942	1372357_at	0.898160969	1.863688788	yes	yes	yes	BI281833	Rn.1185	TBC1 domain family, member 20
3943	1385964_at	0.899290061	1.865147933	yes	yes	yes	AI237569	---	---
3944	1397208_at	0.900939195	1.867281188	yes	yes	yes	AI409411	Rn.9218	OTU domain, ubiquitin aldehyde binding 1 (predicted)
3945	1373021_at	0.902158155	1.868859556	yes	yes	yes	AI171823	Rn.163210	Transcribed locus
3946	1393373_at	0.909141032	1.877927064	yes	yes	yes	BI289640	Rn.15626	similar to encephalopsin
3947	1375141_at	0.910443052	1.879622643	yes	yes	yes	AI574962	Rn.91533	Similar to HOX11L2 (predicted)
3948	1375675_at	0.918371717	1.889980981	yes	yes	yes	AA892813	Rn.1940	Muscleblind-like 2 (predicted)
3949	1373722_at	0.927668639	1.902199602	yes	yes	yes	BE111697	Rn.101107	kinesin family member 20A (predicted)
3950	1389905_at	0.931467256	1.907214694	yes	yes	yes	AI175728	---	---
3951	1389239_at	0.935661104	1.912766946	yes	yes	yes	BM384377	Rn.128124	Transcribed locus
3952	1390077_at	0.958547892	1.943352877	yes	yes	yes	AA956421	Rn.158941	Translocation associated membrane protein 1
3953	1392543_at	0.96296072	1.949306188	yes	yes	yes	BI293462	Rn.162104	similar to retinoblastoma binding protein 4 (predicted) /// retinoblastoma binding protein 4 (predicted)
3954	1388994_at	0.971681543	1.961125066	yes	yes	yes	AW917849	Rn.2740	Frizzled homolog 6 (Drosophila)
3955	1375591_at	0.975445283	1.96624798	yes	yes	yes	AI101245	Rn.30004	Transcribed locus
3956	1384971_at	0.976434691	1.967596905	yes	yes	yes	BI289108	Rn.97407	similar to Hypothetical protein MGC19163
3957	1395951_at	0.980497109	1.973145178	yes	yes	yes	BF289714	---	---
3958	1377006_at	0.983420888	1.977148027	yes	yes	yes	AA875047	Rn.33807	Chaperonin subunit 6a (zeta)
3959	1389944_at	0.991369445	1.988071227	yes	yes	yes	AI014155	Rn.67055	Toll-like receptor adaptor molecule 2 (predicted)
3960	1381898_at	0.993323223	1.990765407	yes	yes	yes	AI576907	---	---
3961	1372905_at	0.994843982	1.992864999	yes	yes	yes	AW433888	---	---
3962	1399048_at	0.997030156	1.995887156	yes	yes	yes	BI274121	Rn.94869	protein arginine N-methyltransferase 4
3963	1386941_at	1.008970442	2.012474414	yes	yes	yes	NM_022401	Rn.1085	plectin 1
3964	1374458_at	1.009129374	2.012696128	yes	yes	yes	AI600031	Rn.17432	Transcribed locus, strongly similar to NP_573483.1 serum/glucocorticoid regulated kinase 3 [Mus musculus]
3965	1380886_at	1.009969634	2.013868711	yes	yes	yes	AI145907	Rn.58553	Transcribed locus
3966	1377088_at	1.010699627	2.014887972	yes	yes	yes	BI275952	Rn.14715	similar to RIKEN cDNA 2310046K01
3967	1387313_at	1.014588719	2.02032686	yes	yes	yes	NM_030865	Rn.30051	myocilin
3968	1375127_at	1.014676965	2.020450441	yes	yes	yes	BI395849	---	---
3969	1371700_at	1.022630888	2.031620432	yes	yes	yes	AI177059	Rn.12328	microfibrillar-associated protein 4
3970	1375652_at	1.043555377	2.061301269	yes	yes	yes	BI285910	Rn.3264	signal sequence receptor, gamma
3971	1373811_at	1.044414983	2.062529827	yes	yes	yes	AA942728	Rn.161872	similar to heat shock protein 8 (predicted)

3972	1375712_at	1.048502897	2.068382347	yes	yes	yes	AI600090	Rn.22227	Similar to RIKEN cDNA 1500006O09 (predicted)
3973	1374186_at	1.050235262	2.07086752	yes	yes	yes	BE109362	Rn.160689	Transcribed locus
3974	1370704_at	1.051898474	2.073256296	yes	yes	yes	AB073756	Rn.10185	potassium inwardly-rectifying channel, subfamily J, member 6
3975	1371205_at	1.074002534	2.105266007	yes	yes	yes	AF230638	Rn.10157	Solute carrier family 14 (urea transporter), member 2
3976	1390100_s_at	1.093231875	2.13351444	yes	yes	yes	BG371810	Rn.40130	RT1 class Ib, locus Aw2
3977	1371406_at	1.1055049	2.151741694	yes	yes	yes	BG664147	Rn.13589	Transcribed locus
3978	1385800_at	1.106167453	2.152730102	yes	yes	yes	AW531915	---	---
3979	1375268_at	1.109653874	2.157938686	yes	yes	yes	AA858591	Rn.34330	Transcribed locus, strongly similar to XP_853191.1 PREDICTED: similar to 40S ribosomal protein S27-like protein [Canis familiaris]
3980	1368057_at	1.15338938	2.224358583	yes	yes	yes	NM_012804	Rn.7024	ATP-binding cassette, sub-family D (ALD), member 3
3981	1369957_at	1.165840703	2.243639213	yes	yes	yes	NM_019341	Rn.1150	regulator of G-protein signaling 5
3982	1376166_at	1.18948947	2.280720205	yes	yes	yes	AW528438	Rn.46881	LOC361192 (predicted)
3983	1390936_at	1.217471123	2.325387463	yes	yes	yes	BE120691	Rn.143830	Leucine-rich repeat LGI family, member 4
3984	1383036_at	1.228096353	2.342576811	yes	yes	yes	AI137547	Rn.166786	Transcribed locus, weakly similar to XP_125510.6 PREDICTED: hypothetical protein LOC73112 [Mus musculus]
3985	1396152_s_at	1.25601941	2.388358507	yes	yes	yes	BF399783	Rn.1593	insulin-like growth factor binding protein 5
3986	1386242_at	1.409619578	2.656671002	yes	yes	yes	AI179722	---	---
3987	1397466_at	1.480100558	2.78968177	yes	yes	yes	BI292573	---	---
3988	1388763_at	1.481273311	2.791950398	yes	yes	yes	AI230762	Rn.43993	Transcribed locus, strongly similar to NP_031751.1 calponin 2 [Mus musculus]
3989	1390717_at	1.528454957	2.884767317	yes	yes	yes	BM391963	Rn.35982	similar to chromosome 20 open reading frame 155
3990	1375788_at	1.554829585	2.937990204	yes	yes	yes	BM388719	Rn.129121	Ribosomal protein L7
3991	1367731_at	1.648125801	3.134262039	yes	yes	yes	NM_030987	Rn.126047	guanine nucleotide binding protein, beta 1
3992	1382278_at	1.64922213	3.136644725	yes	yes	yes	BI278180	Rn.21549	Transcribed locus, weakly similar to XP_580018.1 PREDICTED: hypothetical protein XP_580018 [Rattus norvegicus]
3993	1372467_at	1.735853157	3.330764049	yes	yes	yes	AA943794	Rn.163751	Transcribed locus
3994	1375850_at	2.1315638	4.381921988	yes	yes	yes	BG371810	Rn.40130	RT1 class Ib, locus Aw2