

# Table S1

AFID	GeneSymbol	GeneName	ContigStart	ContigEnd	AssayEffect	ContigStart/AssayEffect	FoldChange
1435494_a_at	Ddp	desmoplamin	7.8082E-13	0.0269849	0.0762722	0.0380440	0.0380440
1419093_a_at	Tol2	tryptophan 2,3-dioxygenase	2.58935E-12	0.0222035	0.140441	0.09183759	0.09183759
1452107_a_at	Npat	neptunium	4.88022E-11	0.0237779	0.232854	0.15621508	0.15621508
1435493_a_at	Ddp	desmoplamin	2.09973E-10	0.6083208	0.35077	0.036149346	0.036149346
1433681_a_at	CAPN3	CALPAIN 3	3.45309E-10	0.1529352	0.2590779	0.400097718	0.400097718
1419353_a_at	NIH1H	NEBESCENT HELIX LOOP HELIX 1	5.09421E-10	0.6557419	0.1809421	0.606206172	0.606206172
1440849_a_at	6330417G04RIK	RIKEN CDNA 6330417G04 GENE	2.61509E-09	0.08842818	0.1563052	0.617701168	0.617701168
1448738_a_at	Calb1	calbindin-28K	2.85029E-09	0.004076686	0.9237763	0.541333043	0.541333043
1450954_a_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	3.2861E-09	0.2501676	0.399841	0.485892327	0.485892327
1437125_a_at	Cam2a	calcium/calmodulin-dependent protein kinase II alpha	5.14192E-09	0.0332322	0.741775	0.557552024	0.557552024
1457366_a_at	4931407K02RIK	RIKEN CDNA 4931407K02 GENE	5.42526E-09	0.0151514	0.0177448	0.37503591	0.37503591
1437226_a_at	Marcks1	MARCKS-like 1	6.20397E-09	1.21985E-05	0.3843127	0.464735895	0.464735895
1425053_a_at	Isoe1	isochorismatase domain containing 1	8.51862E-09	0.3058534	0.4995614	0.541751189	0.541751189
1448950_a_at	IL1R1	INTERLEUKIN 1 RECEPTOR, TYPE I	1.94144E-08	0.0100275	0.06881165	0.193789662	0.193789662
1422711_a_at	DNCK	pregnancy upregulated non-abruptly expressed CaM kinase	2.01359E-08	0.941677	0.468097	0.95269617	0.95269617
1428809_a_at	1810010H24RIK	RIKEN CDNA 1810010H24 GENE	2.16699E-08	0.4806871	0.1636789	0.366818765	0.366818765
1449854_a_at	A1838259	EXPRESSED SEQUENCE A1838259	2.5192E-08	0.8249145	0.1467698	0.482725912	0.482725912
1419355_a_at	Smoc2	SPARC-related modular calcium binding 2	3.61754E-08	0.9553183	0.4829796	0.682937906	0.682937906
1431362_a_at	Smoc2	SPARC-related modular calcium binding 2	5.27571E-08	0.4286949	0.231905	0.410280495	0.410280495
1436532_a_at	DCAMK1.3	DOUBLECORTIN AND CAM KINASE-LIKE 3	6.15391E-08	0.1007432	0.236967	0.508840335	0.508840335
1429355_a_at	130609K11RIK	RIKEN CDNA 130609K11 GENE	8.2977E-08	0.3581192	0.0799313	1.89525709	1.89525709
1444150_a_at	Epb4.1	erythrocyte protein band 4.1	2.00194E-07	0.8057454	0.480825	2.452332943	2.452332943
1418110_a_at	INPP5D	INOSITOL POLYPHOSPHATE-5-PHOSPHATASE 4	2.39076E-07	0.00386617	0.2986411	1.514745934	1.514745934
1437991_a_at	ACCN4	AMILORIDE-SENSITIVE CATION CHANNEL 4, PITUITARY	2.82406E-07	0.9173669	0.181897	1.708657524	1.708657524
1426601_a_at	SCL37A1	SOLUTE CARRIER FAMILY 37 (GLYCEROL-3-PHOSPHATE TRANSPORTER), MEMBER 1	5.49997E-07	0.3082207	0.1370467	2.364293397	2.364293397
1436127_a_at	CRHRP	CORTICOTROPIN RELEASING HORMONE BINDING PROTEIN	6.14282E-07	0.306857	0.9208977	0.52481244	0.52481244
1429162_a_at	1500015A07RIK	RIKEN CDNA 1500015A07 GENE	6.21154E-07	0.4452592	0.231881	0.496739883	0.496739883
1417391_a_at	Ifi16	interferon 16	7.34573E-07	0.001492084	0.6991007	0.52278757	0.52278757
145145_a_at	---	---	7.51534E-07	0.2222331	0.6077884	0.619888207	0.619888207
141414_a_at	ntng1	netrin G1	1.14888E-06	0.1134961	0.2497985	0.95798957	0.95798957
142278_a_at	Dgat2	diacylglycerol O-acyltransferase 2	1.13174E-06	0.0106925	0.7783189	0.538616367	0.538616367
1431946_a_at	Apa42p	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein	1.41164E-06	0.174008	0.212282	2.327988901	2.327988901
1437965_a_at	Sytn13	synaptotagmin 13	1.5136E-06	0.000170011	0.472751	1.711818481	1.711818481
1455401_a_at	Camk2b	calcium/calmodulin-dependent protein kinase kinase 2, beta	1.62224E-06	0.0782373	0.4999253	1.516324078	1.516324078
1424674_a_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	1.72099E-06	0.0597446	0.778477	0.498328603	0.498328603
1434129_a_at	Ihpk2	lipoma HMGIC fusion partner-like 2	1.92298E-06	0.0776529	0.648051	0.64805159	0.64805159
1425863_a_at	Ptpn22	protein tyrosine phosphatase, receptor type, O	2.51724E-06	9.4225E-09	0.189927	1.37879731	1.37879731
1416072_a_at	CD34	CD34 ANTIGEN	2.53628E-06	0.000856461	0.2862298	1.58295522	1.58295522
1418809_a_at	FR3A	PAIRED-GL-LIKE RECEPTOR A1	2.60244E-06	0.1681435	0.1078049	0.18722786	0.18722786
1425232_a_at	Ar2	arrestin 3, retinal	2.97602E-06	0.9702853	0.5481091	0.47538628	0.47538628
1483310_a_at	---	---	3.10494E-06	0.2043566	0.7407074	0.481302606	0.481302606
1416251_a_at	Mcm6	minichromosome maintenance deficient 6 (MISS homolog, S. pombe) (S. cerevisiae)	3.17964E-06	0.00025121	0.240123	1.582450003	1.582450003
1460043_a_at	---	---	3.41445E-06	0.01072407	0.626092	0.957780102	0.957780102
1460437_a_at	PRC2	PLECKSTRIN HOMOLOG, SECT AND COILED-COIL DOMAINS 4	3.55702E-06	0.00178774	0.0738535	0.475429166	0.475429166
1424255_a_at	GRP	GASTRIN RELEASING PEPTIDE	3.8937E-06	0.9191378	0.4079159	3.07325791	3.07325791
1448823_a_at	CXCL12	CHEMOKINE (C-C motif) RANTES	4.11537E-06	0.6771474	0.0731131	1.779142828	1.779142828
1457213_a_at	Dgkq	diacylglycerol kinase, eta	4.20891E-06	0.00148591	0.1814887	0.621852678	0.621852678
1440030_a_at	KCNT2	POTASSIUM CHANNEL, SUBFAMILY T, MEMBER 2	4.74741E-06	0.00444551	0.3763487	2.243666984	2.243666984
1480219_a_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	5.02181E-06	0.6102558	0.5450719	0.545071923	0.545071923
1459525_a_at	PRDM8	PR DOMAIN CONTAINING 8	5.60895E-06	0.3823469	0.1309853	0.547159897	0.547159897
1417777_a_at	LTB4HD1	LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE	6.8071E-06	0.121652	0.3300815	0.55243446	0.55243446
1434013_a_at	Alms1a3	alms1 binding LIM protein family, member 3	6.80977E-06	0.7487033	0.6480813	0.648081367	0.648081367
1455082_a_at	Chb	Casitas B-lineage lymphoma b	8.5433E-06	0.02358481	0.697795	0.585212724	0.585212724
1424675_a_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	9.44505E-06	0.00023991	0.1315532	0.653235998	0.653235998
1450329_a_at	Ar2	arrestin 3, retinal	9.74891E-06	0.2232856	0.23981	1.487125419	1.487125419
1451804_a_at	LRRFC16	LEUCINE RICH REPEAT CONTAINING 16	1.03541E-05	0.6702009	0.4539123	0.759082193	0.759082193
1439378_a_at	Lsm11	U7 snRNP-specific Sm-like protein LSM11	1.05261E-05	0.967071	0.9431416	1.461096612	1.461096612
1440761_a_at	SSBP2	U7 snRNP-STRANDED DNA-BINDING PROTEIN 2	1.07582E-05	0.00802744	0.0861375	0.479202864	0.479202864
1439327_a_at	Csbn1	collagen and calcium binding EGF domains 1	1.07872E-05	0.2876069	0.4668348	0.733230339	0.733230339
1429402_a_at	G08d2	glycyltransferase 8 domain containing 2	1.14727E-05	0.0949919	0.6704487	0.542805203	0.542805203
1423915_a_at	OLEML2B	OLEFACTOMYELIN-LIKE 2B	1.27725E-05	0.0157589	0.0962076	0.684164121	0.684164121
1416658_a_at	Frzb	frizzled-related protein	1.29668E-05	0.01585719	0.622829	0.55597676	0.55597676
1443876_a_at	Camk2a	Calcium/calmodulin-dependent protein kinase II alpha	1.33961E-05	0.00416932	0.5472887	0.523393387	0.523393387
1419322_a_at	Marcks1	MARCKS-like 1	1.43481E-05	0.3215486	0.1992545	0.67039513	0.67039513
1449337_a_at	Tol2	tryptophan 2,3-dioxygenase	1.43995E-05	0.2172683	0.368353	0.845791156	0.845791156
1438007_a_at	A1831790	EXPRESSED SEQUENCE A1831790	1.60133E-05	0.000213598	0.352793	0.673431713	0.673431713
1416266_a_at	PDYN	PRODYNORPHIN	1.66676E-05	0.1619489	0.6768647	1.699686621	1.699686621
1426277_a_at	Dgat2	diacylglycerol O-acyltransferase 2	1.72824E-05	0.0471127	0.9901446	0.9901446	0.9901446
1426712_a_at	SLLCA15	SOLUTE CARRIER FAMILY 6 (NEUROTRANSMITTER TRANSPORTER), MEMBER 15	1.76109E-05	0.6700746	0.1279997	0.711545032	0.711545032
1423494_a_at	2310042I22RIK	RIKEN CDNA 2310042I22 GENE	1.81197E-05	0.3257314	0.192636	2.09567208	2.09567208
1433898_a_at	At2p2c	AT2p2c C++ transmembrane plasma membrane 2	1.82046E-05	0.7480794	0.12972496	1.2972496	1.2972496
1456656_a_at	Lin7a	lin-7 homolog A (C. elegans)	2.04534E-05	0.02926636	0.7919776	1.583414364	1.583414364
1436858_a_at	MBNL1	MUSCLE-BINDING-LIKE 2	2.08747E-05	2.79143E-12	0.4221382	1.0846619	1.0846619
1419230_a_at	Kat5	katana 1	2.14864E-05	0.0898405	0.7699254	1.957100255	1.957100255
1457311_a_at	Cam2a	calcium/calmodulin-dependent protein kinase II alpha	2.15093E-05	0.514289	0.5180424	0.54550081	0.54550081
1438019_a_at	IPPK	INOSITOL 1,3,4,5,6-PENTAKISPHOSPHATE 2-KINASE	2.28765E-05	0.002148871	0.0975466	0.75486655	0.75486655
1423233_a_at	C/EBPD	C/CAAT-ENHANCER BINDING PROTEIN (C/EBP), DELTA	2.30643E-05	0.08577387	0.5107893	0.5107893	0.5107893
1445124_a_at	A930009L07RIK	RIKEN CDNA A930009L07 GENE	2.48877E-05	0.02757881	0.5508991	0.66165234	0.66165234
1428397_a_at	R3gap5	UDP-Gal beta(6)GlcNAc beta 1,3-galactosyltransferase, polypeptide 5	2.6742E-05	0.0348475	0.9144667	0.722238905	0.722238905
1450195_a_at	Ndel1	N-decylglycyl-N-sulfotransferase (heparan glucosaminyl) 4	2.8449E-05	0.0424969	0.1431482	0.4742799	0.4742799
1451753_a_at	Ptxn2	ptx2n A2	3.06327E-05	0.02522E-05	0.112631	1.250933101	1.250933101
1440099_a_at	---	---	3.22951E-05	0.00109391	0.0760926	0.336751923	0.336751923
1459626_a_at	G08d2	glycyltransferase 8 domain containing 2	3.31418E-05	0.1243535	0.0992328	1.213746379	1.213746379
1429403_a_at	G08d2	glycyltransferase 8 domain containing 2	3.49897E-05	0.281869	0.366182	0.530489975	0.530489975
1435705_a_at	LOC232875	SIMILAR TO HYPOPHYSALIN PROTEIN FLJ12895	3.62199E-05	0.1875445	0.4534812	0.675737377	0.675737377
1429191_a_at	Dlx3	DLX3 (Asp-Glu-Ala-His) box polypeptide 33	3.66729E-05	0.0433907	0.1736216	0.630481735	0.630481735
1451547_a_at	0610009A07RIK	RIKEN CDNA 0610009A07 GENE	3.72976E-05	0.00271349	0.286474	0.604340175	0.604340175
1431230_a_at	Ptxn2	PTB (POZ) domain containing 9	3.75617E-05	3.83021E-08	0.2864805	0.629897112	0.629897112
1448473_a_at	Ar2 // Dhrs2	5-azacytidine induced gene 2 // DIRAS family, GTP-binding RAS-like 2	3.88424E-05	0.000499719	0.1423418	1.5804349	1.5804349
1438852_a_at	Mcm6	minichromosome maintenance deficient 6 (MISS homolog, S. pombe) (S. cerevisiae)	3.88843E-05	0.4745971	0.7699254	0.957780102	0.957780102
1437075_a_at	FRMD3	FERM DOMAIN CONTAINING 3	4.09977E-05	0.319474	0.936535	2.56703778	2.56703778
1456651_a_at	Drd1a	dequamine receptor 1A	4.39717E-05	0.924668	0.06431629	1.91917514	1.91917514
1455721_a_at	ALKK3B1	ALKK3 ALKYLATION REPAIR HOMOLOG 3 (E. COLI)	4.61193E-05	0.05782602	0.3280749	0.55895874	0.55895874
1448246_a_at	HIDAC1	HISTONE DEACETYLASE 1 PSEUDOGENE	4.64543E-05	0.5066967	0.761297	0.7101007	0

1417355_at	PEG3	PATERNALLY EXPRESSED 3	0.0002062016	0.05291179	0.1889134	1.218296896
1414245_at	261020170717R1K	RIKEN cDNA 261020170717	0.000206789	9.49313E-05	0.2398047	0.6236958
1456093_at	ZFP536	ZINC FINGER PROTEIN 536	0.00020204	0.2270198	0.3588086	1.46097566
1454966_at	Igfb3	integrin alpha 8	0.000206307	0.0118105	0.6133862	0.574379585
1452703_at	4631427C17R1K	RIKEN cDNA 4631427C17	0.000206550	0.2425378	0.6483187	0.68381194
1441166_at	A330050F15R1K	RIKEN cDNA A330050F15	0.000202624	0.2647657	0.802525	0.724306381
1429022_at	ADCYAP1R1	ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE 1 RECEPTOR 1	0.000202361	0.9115902	0.3494843	0.74535617
1416156_at	DNAH11	DNAH1 (IRP49)/HOMOLOG, SUBFAMILY B, MEMBER 1	0.000202458	0.3317747	0.1873575	1.2506207
1447340_at	4631408O11R1K	RIKEN cDNA 4631408O11	0.000302296	0.2195051	0.06031197	2.062618622
1448608_at	Ccnd1	cyclin D1	0.000302403	0.393879	0.7540753	1.3760863
1423596_at	Nck6 // LOC674247	NIMA (never in mitosis gene a)-related expressed kinase 6 // similar to NIMA (never in mitosis gene a)-related expressed kinase 6	0.000306777	0.00723489	0.7444122	0.71409482
1451354_at	SCGN	SIGNAL CELL GROWTH FACTOR-INDUCED CYCLIN BINDING PROTEIN	0.000317693	0.0789603	0.6362326	0.661131168
142157_at	A930041H05R1K	RIKEN cDNA A930041H05	0.000301041	0.002763003	0.1362671	1.441245159
1457558_at	A330050F15R1K	RIKEN cDNA A330050F15	0.000303041	0.28354059	0.4543908	0.56222826
1447491_at	LRRC2D	LEUCINE RICH REPEAT CONTAINING RD	0.000317316	0.009276419	0.1578963	1.801824396
1428602_at	Kcnp9	potassium inwardly-rectifying channel, subfamily J, member 9	0.000317425	0.02328887	0.087541	1.3312311
1438326_at	A330001M20R1K	RIKEN cDNA A330001M20	0.000338007	8.18806E-09	0.2939136	0.765387133
1416793_at	Tfcd1	TROPOCALCIN 1	0.000342519	4.27467E-06	0.9121351	0.779442328
1444422_at	Pcdh19	protocadherin 19	0.000348332	0.1025842	0.9653787	0.749036762
1459619_at	EPHA11.2	ERYTHROCYTE PROTEIN BAND 4.1-LIKE 2	0.000350994	0.6647238	0.7158628	1.47049762
1419730_at	4631427C17R1K	RIKEN cDNA 4631427C17	0.000356659	0.2005454	0.7105472	0.650281127
1440656_at	Flsht7	F-box only protein 7	0.000357627	0.5241263	0.7801649	0.667134382
1435111_at	LRG1	LEUCINE-RICH ALPHA-2-GLYCOPROTEIN 1	0.000364407	0.2667043	0.391235	1.361893487
1417290_at	PRSS35	PROTEASE, SERINE, 35	0.000370403	0.0825122	0.828202	3.89275294
1434195_at	CMKOR1	CHEMOKINE ORPHAN RECEPTOR 1	0.000372919	0.5365725	0.572982	0.656345332
1417625_x_at	GLE3A4	GLI3 ACTOMERIN 4	0.000384652	0.5330373	0.7121008	0.616383672
1437960_at	Apod4l	adenomatous polyposis coli down-regulated 1	0.000390853	0.7797704	0.494543	0.625849096
1449070_x_at	Ln7a	lin-7 homolog (A. elegans)	0.000405235	0.00345898	0.2586282	0.6832348
1438450_at	Ln7a	lin-7 homolog (A. elegans)	0.00041516	0.3593095	0.0886646	1.459101335
142009_at	NWCC1	CINA SEQUENCE BINDING PROTEIN 8	0.000446985	0.8091927	0.2482287	1.248228747
1438075_at	FEM1C	FEM-1 HOMOLOG C (C. ELEGANS)	0.000448166	0.1587452	0.1464097	1.283708176
1437568_at	MMP16	MATRIX METALLOPROTEINASE 16	0.000448307	0.94702E-05	0.6664409	0.727551022
1438304_at	PCDH21	PROTOCOLADHERIN 21	0.00045411	0.2810025	0.5333385	0.902212374
1431393_at	SEMO181	RIKEN cDNA 492150402 GENE	0.000458129	0.00632623	0.5107176	0.657898618
1431905_x_at	4933427G17R1K	RIKEN cDNA 4933427G17	0.000458758	0.1262748	0.8708775	0.559363798
1432225_at	ACVRC1	ACTIVIN A RECEPTOR, TYPE 1C	0.000460009	0.9352097	0.705102	1.7698907
1433939_at	A73004616	HYPOPHYSICAL PROTEIN A73004616	0.000460733	0.26094673	0.6483187	1.31765128
1421471_at	NPY1R	NEUROPEPTIDE Y RECEPTOR Y1	0.000467232	0.4101227	0.8948635	1.631051881
1439689_at	903022AM15R1K	RIKEN cDNA 903022AM15	0.00046992	0.01180232	0.0560524	1.33392111
1426146_at	Itihg	interleukin 1 receptor accessory protein	0.000476572	0.07927656	0.697048429	0.744384427
1428657_at	Reb1	retinoblastoma 1 receptor accessory protein 1	0.00048732	0.2699668	0.8661403	0.577384327
1457729_at	GRP12	G-PROTEIN COUPLED RECEPTOR 12	0.000495968	0.9066335	0.4783524	0.72022285
1442931_at	Gc1d3	keratin 12	0.000511281	0.792136	0.1878262	1.740404103
1440215_at	C130086A10	HYPOPHYSICAL PROTEIN C130086A10	0.000517376	0.03162541	0.0605104	0.710720872
1443196_at	---	---	0.000523461	0.009679651	0.1188838	1.66151737
1439019_at	Frsd1	Frsr syndrome 1 homolog (human)	0.000525375	0.8039165	0.147698967	1.476709895
1451972_at	Glc1c1	glucocorticoid induced transcript 1	0.000526784	0.7234774	0.7650407	1.349952898
1424042_at	Alp2b2	ATPase, Ca++ transporting, plasma membrane 2	0.00052826	0.00150443	0.206829	1.58026223
1438399_at	Myo1b	myosin IB	0.000535424	0.30921	0.3184134	1.811793991
1427450_x_at	Myo1b	myosin IB	0.00054444	0.07649313	0.3184134	1.514965066
1454818_at	GMB2B	GLUCOCORTICOID MODULATORY ELEMENT BINDING PROTEIN 2	0.000557182	0.9529894	0.3157971	1.247374057
1437375_at	1429591	0 day neonatal thymus cDNA, RIKEN full-length cDNA library, clone A30010E21 product-unclassified, full insert sequence	0.00055808	0.3820729	0.615714	0.802729749
1429591_at	TACC1	TRANSFERRIN, ACIDIC COILED-COIL CONTAINING PROTEIN 1	0.000572051	8.16425E-05	0.7377905	1.29900573
1445297_at	---	---	0.000575949	0.1113447	0.1891607	1.224837951
1458010_at	---	---	0.000576339	0.603577188	0.3756734	1.544224137
1456722_at	Chd1l	chordin-like 1	0.000587863	0.7627504	0.5689023	1.844246463
1437247_at	FOSL2	FOS-LIKE ANTIGEN 2	0.000587934	0.5597199	0.4454171	1.798587386
1438382_at	Apod4l	adenomatous polyposis coli down-regulated 1	0.00058983	0.6193384	0.6029865	0.7151574555
1418310_at	Ch1c1	cholecystokinin releasing hormone receptor 1	0.00059948	0.6500034	0.4078906	1.571115114
1441610_at	N28178	expressed sequence N28178	0.000595041	0.7968254	0.7866748	1.218206338
142174_x_at	Tspn18	tetraspanin 18	0.00059779	0.1446278	0.3534409	0.862158994
1417676_at	Rarb2	retinoblastoma tyrosine phosphatase, receptor type, O	0.000609238	0.000514671	0.5886915	1.281444177
1429123_at	RAB27A	RAB27A, MEMBER RAS ONCOGENE FAMILY	0.000602793	0.7988219	0.728725	0.630781819
1444492_at	PTPRD	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, D	0.000606742	0.04267448	0.1569284	1.56922739
1448929_at	Myo1b	myosin IB	0.000614678	0.02372215	0.1589023	0.91261497
1426972_at	SEC24D	SEC24 RELATED GENE FAMILY, MEMBER D (S. CEREVISIAE)	0.00061969	0.0882915	0.0810835	0.658666594
1439130_at	BC052046	cDNA sequence BC052046	0.000625838	0.0345614	0.2902352	0.657992563
1435276_at	A330211H01R1K	RIKEN cDNA A330211H01	0.00062586	0.154908	0.3190482	1.740404103
1417300_at	SMPD3.3B	SPHINGOMYELIN PHOSPHODIESTERASE, ACID-LIKE 3B	0.00062848	0.7741984	0.7602493	0.531146654
1402317_at	CLDN22	CLAUDIN 22	0.000638248	0.5325018	0.9598387	0.662004293
1450712_at	Kcnp9	potassium inwardly-rectifying channel, subfamily J, member 9	0.000645581	0.31646965	0.15466437	1.51466437
1429982_at	4933426K21R1K	RIKEN cDNA 4933426K21	0.000647113	0.05212072	0.86106	0.659822201
1439170_at	E3300619R1K	RIKEN cDNA E3300619	0.000646573	0.2148221	0.1961828	1.3721187
1452110_at	AT8R	TRIS(1,4)ETHYLENEBIS(2-AMINOETHYL)HOMOCYSTEINE METHYLTRANSFERASE REDUCTASE	0.000646573	0.01681263	0.147698967	1.476709895
1460353_at	TMEM48	TRANSMEMBRANE PROTEIN 48	0.000661049	0.00977746	0.752787	0.78031516
201002040R1K	RIKEN cDNA 201002040	RIKEN cDNA 201002040 GENE	0.000667145	0.9393164	0.1547886	0.788381582
1449048_at	RANBP5	RAS ASSOCIATION (B) DOMAIN (RAF-6) DOMAIN FAMILY 5	0.000681456	0.16623766	0.648039856	0.658039856
1426083_x_at	Rgi1	B-cell translocation gene 1, anti-proliferative	0.00072815	0.4067262	0.2059762	0.618457638
1426167_at	Camk4	calcium/calmodulin-dependent protein kinase IV	0.000720995	0.03167661	0.1627457	1.354461238
1452363_at	MAK10	MAK10 HOMOLOG, AMINO-ACID N-ACETYLTRANSFERASE SUBUNIT, (S. CEREVISIAE)	0.000747576	0.00080344	0.1379038	1.146545558
1418743_x_at	Tesc	teskalin	0.000762746	0.5381729	0.2028326	1.412664931
1441608_at	---	---	0.000770032	0.1580723	0.0796021	1.36697908
1458177_at	EBPL	EMPOPHILIN BINDING PROTEIN-LIKE	0.000771717	0.3252991	0.1033491	0.626284032
1459602_at	CN11	CYCLIN 11	0.000778714	0.237446	0.09997429	1.36389945
1446332_at	Pcdhgc3	Protocadherin gamma subfamily C, 3	0.000779902	0.210633	0.2295728	1.554208568
1456397_at	Cdh4	cadherin 4	0.000800952	0.8647289	0.3462504	0.7114149
1459020_at	CACNG3	CALCIUM CHANNEL, VOLTAGE-DEPENDENT, GAMMA SUBUNIT 3	0.000803362	0.01417108	0.0779062	1.258001475
1444338_at	---	---	0.000848265	0.002769319	0.1686604	1.865171001
1438138_x_at	SLC25A29	SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, PALMITOYL-CARNITINE TRANSPORTER), MEMBER 29	0.00085135	7.34486E-06	0.9966446	0.842992748
1427870_at	Glc1c1	glucocorticoid induced transcript 1	0.000864449	0.8996362	0.063638	0.620638
1426218_at	Glc1c1	glucocorticoid induced transcript 1	0.000868661	0.6055454	0.2295962	1.411001585
1439358_at	Pip2	Phosphatidylinositol 2	0.000880943	0.00302325	0.1706165	0.688100209
1444835_at	BC030409	CINA SEQUENCE BINDING PROTEIN 8	0.000884683	0.4336973	0.531121	1.224052352
1417215_at	RAB27B	RAB27B, MEMBER RAS ONCOGENE FAMILY	0.000886661	0.8083673	0.8953132	0.688614762
1439748_at	ABC2D	ATP-BINDING CASSETTE, SUB-FAMILY D (ALD), MEMBER 2	0.000909902	0.01275477	0.3348173	1.247978557
1422825_at	CART	COCaine AND AMPHETAMINE REGULATED TRANSCRIPT	0.000911957	0.1099084	0.1845212	0.920851321
1444956_at	---	---	0.000924746	0.9072413	0.3961552	0.738422586
1441693_at	ADAMTS3	ADAM METALLOPROTEINASE WITH THROMBOSPONDIN TYPE 1 MOTIF 3	0.00097849	0.00316611	0.4835131	0.71604599
1447807_at	Aphap2b	Aphap2b like (A4) domain containing protein-binding, family A, member 1 binding protein	0.00098392	0.1488984	0.1892245	0.832934625
1453211_at	FNDC1	FIBRONECTIN TYPE III DOMAIN CONTAINING 1	0.000985838	0.4910492	0.2392053	0.683814124
1460619_at	4931419K03R1K	RIKEN cDNA 4931419K03	0.000996462	0.62524239	0.9171043	0.752370651
1444633_at	---	---	0.001019597	0.7379793	0.1945432	1.544224137
1456200_at	LNORF3	LON PEPTIDASE N-TERMINAL DOMAIN AND RING FINGER 3	0.001031352	0.9121484	0.8039901	0.79396473
1446802_at	---	---	0.001031493	0.01498977	0.08872428	1.212302926
1433558_at	DAB2IP	DISABLED HOMOLOG 2 (DROSOPHILA) INTERACTING PROTEIN	0.001033356	5.49321E-06	0.4431257	1.344244928
1449205_at	OYV2L2	RIKEN cDNA 1809107D21 GENE	0.001048296	0.003816281	0.0663176	1.468091901
1427049_at	SMO	SMOOTH ENDED HOMOLOG (DROSOPHILA)	0.001050125	0.533677	0.9547994	0.747461136
1416623_at	THBS3	THROMBOSPONDIN 3	0.001055748	5.54418E-07	0.1487456	0.608509771
1429916_at	PFP40A</					

143782_at	Acv2a	Activin receptor 1A	0.001679687	0.04003979	0.73557	0.66644821
143783_at	Kcch1	potassium voltage gated channel, Shal-related subfamily, member 1	0.00175528	0.494451	0.448177	1.377454151
1447493_at	AS30088108R1K	RIKEN cDNA AS30088108 GENE	0.001739215	0.116369	0.559078	0.671127354
1437306_at	C130092011R1K	RIKEN cDNA C130092011 GENE	0.001746823	0.9943533	0.06938976	1.37200521
1453236_at	Pfna2	pflin2	0.001751353	0.1140773	0.2992017	1.24545397
1429906_at	AY900351E12R1K	RIKEN cDNA AY900351E12 GENE	0.001783319	8.27359E-05	0.176933	1.469990979
1433699_at	TNFAP3	TUMOR NECROSIS FACTOR, ALPHA-INDEUCIBLE PROTEIN 3	0.00182239	0.408289	0.6129667	0.764642987
1439073_at	ZPPI60	RIKEN cDNA ZP6480D16 GENE	0.001825262	0.6024086	0.329893	1.335043577
1457496_at	---	---	0.001825464	0.005051657	0.1282663	1.581004519
1433792_at	Nrip2	nuclear receptor interacting protein 2	0.001831938	0.8315431	0.5822663	0.678171351
1436011_at	ELMO2	RIKEN cDNA F19000224 GENE	0.001849156	0.1386772	0.7880814	0.715474386
1437339_at	Pc45	progesterone corepressor subunit kcn type 5	0.001852366	0.9748423	0.243955	0.510970972
1442603_at	P61	Polybromo 1	0.001862726	0.9587058	0.9589642	0.710964739
1444305_at	LOC381400	SIMILAR TO MYH7B PROTEIN	0.001866114	0.9390687	0.6052182	1.497084659
143015608R1K	931015608R1K	progesterone corepressor subunit kcn type 5	0.001880347	0.2898359	0.649577	1.817495972
1427416_x_at	LOC674944	similar to dual specificity phosphatase 7	0.001886665	0.2378063	0.4529707	1.381492971
1447399_at	LTK	LEUKOCYTE TYROSINE KINASE	0.001904364	0.0358879	0.09104937	1.259478148
1437199_at	Ccnd1	cyclin D1	0.001923435	0.9184858	0.501764	1.389226218
1433716_x_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	0.00194143	0.6441185	0.9761226	0.589642247
1441730_at	TMC1	HYPOPHYSEAL PROTEIN LOC212904	0.001947073	0.008094833	0.3070752	1.324933469
1449552_at	DHDWG0951E	DNA SEGMENT, CHR 4, BIRG1A4 & WOMEN'S GENETICS 0951 EXPRESSED	0.001969892	0.3433088	0.6623628	0.665619834
1425688_at	SCN1A	SODIUM CHANNEL, NONVOLTAGE-GATED, TYPE 1, ALPHA	0.001982165	0.001043262	0.3088074	0.665908904
1455250_at	Sb3hp4	Sb3-domain binding protein 4	0.001987874	3.002513	0.118991	1.251138571
1451421_x_at	FKBP5	FKBP51	0.001991383	0.00335685	0.3075704	0.723821092
1423395_at	Tmx3	translin-associated factor X	0.001997468	0.01499031	0.1661533	1.311403876
1433893_x_at	Spag5	sperm associated antigen 5	0.002003174	0.4575088	0.5020399	1.451442549
1428946_at	UBE1L2	UBQUITIN-ACTIVATING ENZYME E1-LIKE 2	0.002008689	0.06547071	0.948077	1.35920604
1440765_at	Fra1	Fraser syndrome 1 homolog (human)	0.002044737	0.7797992	0.4975831	1.963584532
1429125_at	Mgk11	mitogen-activated protein kinase 11	0.002088871	0.2244072	0.7796736	1.431623477
1457196_at	Nipi	neurapilin	0.002097462	0.001245739	0.065248279	0.789036062
1426611_at	PRKACB	PROTEIN KINASE, CAMP DEPENDENT, CATALYTIC, BETA	0.002115789	0.1391557	0.2325005	1.11996859
1424341_x_at	PCFHA9	PROTOPACHIERIN ALPHA 9	0.002122168	0.3835737	0.1656558	0.9093538
1453554_at	C230878M08R1K	RIKEN cDNA C230878M08R1K GENE	0.002126732	0.02216122	0.2023162	0.78905725
1426098_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	0.002142316	0.4654404	0.4462413	1.13248362
1432228_at	4933406B15R1K	RIKEN cDNA 4933406B15 GENE	0.002185774	0.2533959	0.4701839	0.57561987
1401847_at	ARG2	ARGINASE, TYPE II	0.002199091	0.3186883	0.164491	0.602254994
1440721_at	9304031N17R1K	RIKEN cDNA 9304031N17 GENE	0.002200888	0.1858383	0.3681731	1.475232608
1426797_at	Z700094F01R1K	RIKEN cDNA Z700094F01 GENE	0.002212024	0.9275622	0.6104745	0.800664296
1494236_x_at	CCL21C	CHEMOKINE (C-C MOTIF) LIGAND 21A	0.002212423	0.00469359	0.06686577	1.257463178
1456759_at	LRRC4C	LEUCINE RICH REPEAT CONTAINING 4C	0.00221461	0.4091444	0.4013162	0.60341595
1448686_at	Ifi16	interferon 16	0.002226614	0.4718047	0.6928443	0.616264149
1440455_at	AB48899	EXPRESSED SEQUENCE AB48899	0.002247425	0.7609111	0.5163439	1.254294094
1450842_at	CENPA	CENTROMERE AUTOANTIGEN A	0.002254832	0.09196765	0.4930178	1.579245138
1445118_at	---	---	0.002279182	0.790276	0.5984705	0.32736631
1457137_at	---	---	0.002282962	0.8011371	0.2632338	1.380720997
1428909_at	---	---	0.002286537	0.0280853	0.3081734	1.808641244
1427975_at	---	---	0.002315581	0.0134933	0.9859467	0.710429032
1424310_at	MOC52	MOULDBLENDED COFACTOR SYNTHESIS 2	0.002326232	0.0908444	0.3114025	0.827162368
1435559_at	Adh3p15	ADH3 (GTPase activating protein) 5	0.002325882	0.06734582	0.468870713	0.5552227
1430407_at	3110035C09R1K	RIKEN cDNA 3110035C09 GENE	0.002362953	0.2779883	0.5129998	1.590698228
1427242_at	KLF6	KRUPPEL-LIKE FACTOR 6	0.002371487	0.002319291	0.52528169	1.1868683
1438611_at	TUBA7	TUBULIN, ALPHA 3	0.002374251	0.4640408	0.4098162	1.444895558
14161818_at	Parva	parvin, alpha	0.002381097	0.008516735	0.2905245	1.42062797
1428006_at	FGF16	FIBROBLAST GROWTH FACTOR 16	0.002426912	0.4261487	0.6289859	1.403279081
1420647_at	Dac2b	deaf-2b, C2, beta	0.002430234	0.1554317	0.616310432	0.616310432
1433833_at	Fad3cb	fibronectin type III domain containing 3B	0.002432995	0.108788	0.1120496	1.181289738
1421991_x_at	Igf8p4	insulin-like growth factor binding protein 4	0.002476039	0.0656398	0.7200266	1.356177625
1426411_at	STRIP	SUPERMIMETIC FIBRINOLYTIC RAS BINDING PROTEIN	0.002479264	0.2977965	0.1111478	1.090304997
1431098_at	Ran	ras (Ras) oncogene cell-expressed intermediate filament-associated protein	0.002485466	0.0512478	0.09270319	1.97951387
1418881_at	EFCB2	EF HAND CALCIUM BINDING PROTEIN 2	0.002507072	0.01494399	0.6156661	1.408683762
1448303_at	GNPMB	GLYCOPROTEIN (TRANSMEMBRANE) NMB	0.002518961	0.7179739	0.3333386	0.628089784
1429487_at	5430455Z22R1K	RIKEN cDNA 5430455Z22R1K GENE	0.002525357	0.197255	0.6156662	1.389283216
1433758_at	NISCH1	IMIDAZOLINE RECEPTOR 1-LIKE PROTEIN	0.002529478	2.4958E-08	0.1152466	0.78928748
1409286_at	Nng1	neurin G1	0.002564994	0.827615	0.1270329	1.494316035
1455868_at	TUBGCP2	TUBULIN, GAMMA COMPLEX ASSOCIATED PROTEIN 2	0.002599971	0.00808076	0.4613172	0.735282693
1453444_at	AW49418	EXPRESSED SEQUENCE AW49418	0.002606251	0.2321098	0.601785	0.787928748
1433577_at	DAB1	DISABLED HOMOLOG 1 (DROSOPHILA)	0.002610985	0.1561446	0.5692791	1.23809734
1421896_at	ELK1	ELK1, member of ETS oncogene family	0.002614348	0.2344454	0.2031218	0.634627217
1448445_at	Rage2	Ras-related GTP binding 2	0.002618702	0.5133508	0.521022	1.253485655
1440555_at	6631427C17R1K	RIKEN cDNA 6631427C17R1K GENE	0.002623665	0.00492608	0.2931255	1.2767023
1420340_at	4930413O22R1K	RIKEN cDNA 4930413O22 GENE	0.002627497	0.06881979	0.686081	0.834567836
1422552_at	RPRM	RPRM10, TP53 DEPENDENT G2 ARREST MEDIATOR CANDIDATE	0.002742006	0.1872118	0.3135224	0.741515193
1434909_at	LYCAT	LYSINE CARDIOLIPIN ACYLTRANSFERASE	0.002748119	0.3716402	0.9187874	1.12231407
1421821_at	LDLR	LOW DENSITY LIPOPROTEIN RECEPTOR	0.002770765	0.4789911	0.206769	1.19833807
1427685_x_at	Synj2	synaptojanin 2	0.002791243	0.03214055	0.3202033	1.341507722
1456129_at	R308033G06R1K	RIKEN cDNA R308033G06R1K GENE	0.002802832	0.977968	0.6134845	0.392913766
1425934_at	BG4L14	UDP-GAL-BETA-GALACTOSYL BETA 1-4-GALACTOSYLTRANSFERASE, POLYPEPTIDE 4	0.002803544	0.00356542	0.5732844	0.72824747
1451964_at	MA2	MELANOMA INHIBITOR ACTIVITY 2	0.002819707	0.2799629	0.2331639	2.301042477
1425052_at	---	---	0.002819952	0.28671029	0.6295714	0.710363182
1441018_at	USP24	UBQUITIN SPECIFIC PROTEINASE 24	0.00284575	0.3471024	0.7409226	1.35198367
1438523_x_at	1500001A10R1K	RIKEN cDNA 1500001A10 GENE	0.002858532	0.2099917	0.7998469	0.47679978
1428396_at	Pdgfra5	UDP-GAL-4-epimerase 5	0.002872781	0.05283085	0.6395714	0.784302137
1430703_at	LOC546515	SIMILAR TO KERATIN ASSOCIATED PROTEIN 9-1	0.002898796	0.210209	0.09418322	0.28518005
1427401_at	Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	0.002899101	0.1387745	0.822963	0.66686132
1491722_at	KLK8	PROTEASE, SERINE, 19 (NEUROPSIN)	0.002910979	0.01643689	0.7605146	1.403909389
1419592_at	UNC5C	UNC-5 HOMOLOG C (C. ELEGANS)	0.00291111	0.00047912	0.896131	1.437906213
1455629_at	Drd1a	dopamine receptor 1A	0.002914916	0.5967964	0.078413	0.834325514
1457193_at	---	---	0.002920767	0.6767904	0.229907	1.22796873
1435445_at	MMD	MONOCYTE TO MACROPHAGE DIFFERENTIATION-ASSOCIATED	0.002926645	0.1592673	0.1986405	0.6766195
1435847_at	CDC42BP4	EXPRESSED SEQUENCE A462003	0.002944464	0.02718867	0.3494781	1.129914876
1428991_at	HRASL5	HRAS-LIKE SUPPRESSOR	0.002970996	0.4972422	0.5988169	0.71079541
1434852_at	PLA2G2F	PHOSPHOLIPASE A2, GROUP IIF	0.002984579	0.3462078	0.3525629	1.063467217
1456242_at	---	---	0.00298491	0.0588951	0.2284971	0.362290461
1448496_x_at	DNG1	INHIBITOR OF GROWTH FAMILY, MEMBER 1	0.002998381	2.19812E-08	0.1218883	1.071427468
1417111_at	Man1a	mannosidase 1, alpha	0.003004849	0.02336604	0.7183784	1.311586169
1428535_at	9430020K01R1K	RIKEN cDNA 9430020K01 GENE	0.003016259	0.1056557	0.7043294	1.578963887
1449175_at	GNR65	G-PROTEIN COUPLED RECEPTOR 65	0.003033385	0.7190088	0.06420755	2.444651606
1427038_at	PENK1	PROENKEPHALIN 1	0.003034664	0.22232	0.7183784	1.688256734
1427186_x_at	Mez2a	myocyte enhancer factor 2A	0.003037817	0.900066	0.025638	0.812567834
1438539_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	0.003040693	0.03973051	0.9578223	1.358878469
1439715_at	150001106R1K	RIKEN cDNA 150001106R1K GENE	0.003042151	0.01807443	0.5611447	0.609510262
1437857_at	Dpy193	dpy-19-like 3 (C. elegans)	0.003066528	0.2170245	0.3233033	1.37710879
1429249_at	4833424O15R1K	RIKEN cDNA 4833424O15 GENE	0.003073392	5.47808E-05	0.3033078	1.241136415
1437654_at	SST	SEROTONIN	0.003079157	0.015791	0.5661447	0.609510262
1448249_at	Gpdi1	glycerol-3-phosphate dehydrogenase 1 (soluble)	0.003077571	0.1888997	0.7207397	1.271984209
1418790_at	ZPPI2	ZINC FINGER PROTEIN 312	0.003081384	0.1132621	0.5299336	1.331702517
1451469_at	1250905L17R1K	RIKEN cDNA 1250905L17R1K GENE	0.003084337	0.003714741	0.06364482	0.869484562
1439647_at	LOC433698	HYPOPHYSEAL LOC433698 GENE	0.003093695	0.4321166	0.4323937	1.199463685
1425606_at	SLC5A8	SOLUTE CARRIER FAMILY 5 (IODIDE TRANSPORTER), MEMBER 8	0.003099857	0.9131834	0.7273167	2.984182824

1427196_at	WNK4	WNK LYSINE DEFICIENT PROTEIN KINASE 4	0.004001409	0.8349315	0.711122	1.7918384
1434051_s_at	Hsp90a2	heat shock protein 90A class B member 2	0.004008756	0.5447309	0.711122	1.21151314
1425413_t	Rfx3	regulatory factor X, 3 (influences HLA class II expression)	0.004003118	0.3978921	0.066258529	0.72900018
1438702_at	---	---	0.004016134	0.003167681	0.241812	1.259830656
1430996_s_at	D14Etd581e	---	0.00411237	0.1855833	0.65492279	0.718037277
1429725_at	STX17	SYNTAXIN 17	0.00411221	0.2895206	0.4639702	0.72667522
1428384_at	D4Bdg9951e	---	0.004116906	0.0584922	0.8342578	0.67038683
1447025_at	UBE2E2	UBQUITIN-CONJUGATING ENZYME E2E 2 (UBC45 HOMOLOG, YEAST)	0.004120787	0.05453038	0.5151224	1.31588881
1458620_at	LOC312993	SIMILAR TO UBQUITIN-A5 RESIDUE RIBOSOMAL PROTEIN FUSION PROTEIN	0.004128331	0.5620697	0.5876269	0.33442906
1419638_t	Efnb2	efrin B2	0.004133247	0.3182625	0.50295	1.34366053
1457528_at	Slc6a7	solute carrier family 6, sodium bicarbonate cotransporter, member 7	0.00417394	0.00026293	0.7067562	0.61777437
1426115_s_at	Keap1	potassium inwardly-rectifying channel, subfamily 1, member 9	0.004178037	0.8012154	0.829082	1.759440715
1457505_s_at	ABC8	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTRMRP), MEMBER 8	0.004208127	0.00638697	0.5138617	0.676975609
1424095_at	Ax33	additional sex combs like 3 (Drosophila)	0.004229411	0.2684004	0.0780893	1.1921268
1424237_at	---	---	0.004252799	0.62464109	0.39837	0.838500676
1422540_at	FBLN1	FIBULIN 1	0.004289857	0.003829405	0.8851269	0.614152771
1427177_at	Ftyc1	FYVE and coiled-coil domain containing 1	0.004294494	0.9952577	0.4433076	0.79914202
1434153_at	SHB	SRC HOMOLOGY 2 DOMAIN-CONTAINING TRANSFORMING PROTEIN	0.004302764	0.8580033	0.90638	1.48578369
1452161_at	TIPARP	TCDD-INDUCIBLE POLY(ADP-RIBOSE) POLYMERASE	0.004307401	0.006390009	0.1978319	1.206061258
1431496_at	LOC3104F01R1K	RIKEN CDNA B23014F01 GENE	0.004326662	0.1001636	0.0847249	0.507065888
1427728_at	CHRN3	CHOLINEERGIC RECEPTOR, NICOTINIC, GAMMA POLYPEPTIDE	0.004348294	0.6161636	0.1102239	2.79378562
1453800_at	9130022K13R1K	RIKEN CDNA 9130022K13 GENE	0.004361579	0.9265856	0.6326760	0.260075283
1451871_s_at	GHR	GROWTH HORMONE RECEPTOR	0.004394831	0.0131566	0.8143499	1.56447954
1452524_at	Lrrn6l	leucine rich repeat transmembrane neuronal 1	0.004410201	1.7536849	0.0985806	0.758830796
1422088_t	Mylc1	v-myc myelocytomatous viral oncogene homolog 1, lung carcinoma derived (avian)	0.00442022	0.02137007	0.1554219	0.644792514
1446237_at	Akap9	A kinase (PRK) anchor protein (yt9a9)	0.004436014	0.946461	0.305646	0.76726905
1456769_at	PSMA4	PROTEASOME (PROSOM, MACROPAIN) SUBUNIT, ALPHA TYPE 1	0.004445471	0.9747684	0.8292038	0.539337173
1427665_s_at	NFIC	NUCLEAR FACTOR 1C	0.00445666	0.6058722	0.4727632	0.913454325
1422221_at	HAND2	HEART AND NEURAL CREST DERIVATIVES EXPRESSED TRANSCRIPT 2	0.004471885	0.4005059	0.3870322	2.452813166
1454763_at	ANKRD17	ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 17	0.004485994	0.0332724	0.5640821	1.138344643
1456532_at	GNB5	GUANINE NUCLEOTIDE BINDING PROTEIN, BETA 5	0.004541135	0.529984	0.3452762	1.440083954
1418995_at	---	---	0.004550313	0.423604	0.591077	0.690217887
1456759_at	PSME4	PROTEASOME (PROSOM, MACROPAIN) ACTIVATOR, SUBUNIT 4	0.004591058	0.2213532	0.0642952	0.642392818
1426383_at	CRY2	CRYPTOCHROME 2 (PHOTOLYASE-LIKE)	0.004598424	0.477643	0.6846672	1.181726829
1434431_s_at	ADORA2B	ADENOSINE A2B RECEPTOR	0.004598378	0.2416206	0.2585774	0.719331205
1444169_at	3110952M02R1K	RIKEN CDNA 3110952M02 GENE	0.00460571	0.2614884	0.6879995	1.46491081
1453777_s_at	RNF13	RIKEN CDNA 4921310F01 GENE	0.004636019	0.8797167	0.828912	0.93119546
1446673_t	YAF2	YY1 ASSOCIATED FACTOR 2	0.004638485	0.00023877	0.05706189	0.520415832
1454529_at	4930518C04R1K	RIKEN CDNA 4930518C04 GENE	0.004647408	0.7702303	0.0582453	2.17661075
1449491_at	CARD10	CASPASE RECRUITMENT DOMAIN FAMILY, MEMBER 10	0.004759033	0.0911053	0.8800194	1.26641817
1428372_t	ST5	SUPPRESSION OF TUMORIGENICITY 5	0.00475725	0.2115799	0.3450327	0.732028375
1446255_at	KCNQ1	POTASSIUM VOLTAGE-GATED CHANNEL, SUBFAMILY Q, MEMBER 1	0.004767956	0.1744414	0.1700572	1.55910764
142474_s_at	Camk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	0.004791302	0.2903213	0.943021	0.802399096
1438213_t	AKS0018L16R1K	RIKEN CDNA AKS0018L16 GENE	0.004842968	0.3216865	0.9343686	0.776900923
1440506_at	SLC7A2	SOLUTE CARRIER FAMILY 7 (CATIONIC AMINO ACID TRANSPORTER, Y+ SYSTEM), MEMBER 2	0.004861527	0.9779995	0.0618137	0.63411475
1458151_at	KLHL2	KELCH LIKE 2, MAYVAIN (DROSOPHILA)	0.004877338	0.974768	0.146605	0.81746038
1440325_at	SMARCA2	SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY A, MEMBER 2	0.00487402	0.7602567	0.2990749	1.20742377
1430316_at	493079E17R1K	RIKEN CDNA 493079E17 GENE	0.004904702	0.7175509	0.81413	0.823574224
1456395_at	hred1	head end containing 1	0.004906279	4.12076e-05	0.74421	1.39654448
1456596_at	643050I02R1K	EXPRESSED SEQUENCE AW260253	0.00498224	0.000524296	0.0654959	0.669684143
1431864_at	FBOXD2	F-BOX ONLY PROTEIN 24	0.004989122	0.2058865	0.00715273	0.505066723
1439041_at	SLC39A10	SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 10	0.004989758	0.00031511	0.117292049	0.891292949
1437082_at	Akap9	A kinase (PRK) anchor protein (yt9a9)	0.005023017	0.01305182	0.3498189	1.176781125
1439754_t	SOX12	SOX-BOX CONTAINING GENE 12	0.005028449	0.0566366	0.0624533	0.633399964
1418392_at	GRP4	GLYCYLATE NUCLEOTIDE BINDING PROTEIN 4	0.005066811	0.1739975	0.1378226	0.618460662
1421530_s_at	GRM8	GLUTAMATE RECEPTOR, METABOTROPIC 8	0.005067801	0.7561452	0.3537733	1.42341819
1424241_at	KALRN	RIKEN CDNA 2210407G14 GENE	0.00506974	0.0013261	0.905579	1.464349001
1427600_at	MMPK3	PROTEIN KINASE, MITOGEN ACTIVATED KINASE 3	0.005070022	0.0602224	0.4577927	0.615834447
1431014_t	C12C2	CAT EYE SYNDROME CHROMOSOME REGION, CANDIDATE 2 HOMOLOG (HUMAN)	0.005080106	0.3244484	0.4466205	0.692287123
1444683_at	---	---	0.00510448	0.3462227	0.0960744	0.62105327
1425248_s_at	Tyros3	TYRO3 protein tyrosine kinase 3	0.005107816	0.2896242	0.926668	1.398709867
1427212_at	---	Transcribed locus	0.00512598	0.2735117	0.146605	0.480738825
1427738_at	DDK12	DNA SEGMENT, KIST 2	0.005151203	0.5414169	0.0595922	0.48459386
1416305_at	SKS2BP	SH3-DOMAIN BINDING PROTEIN 4	0.005162017	0.730101	0.0962075	1.345125414
1448546_at	Rasaf1	RAS-ASSOCIATION (RABGAP1-6) DOMAIN FAMILY 3	0.005164649	0.5571273	0.2042128	0.732198554
1421488_at	Rabgap11	RAB GTPASE INTERACTING PROTEIN 1-LIKE	0.005186091	0.00020249	0.345198	0.76256487
1441024_at	STIM2	FASL SIGNALING MOLECULE 2	0.00518752	0.0584426	0.5717998	0.651167366
1450139_at	Rd11b	R-cell leukemia lymphoma 11B	0.005200022	0.060823295	0.4780794	0.645814017
1447952_at	AUH	AU RNA BINDING PROTEIN/ENOYL-COENZYME A HYDRATASE	0.005202039	0.4213596	0.0962197	1.327525266
1442119_at	AI449212	EXPRESSED SEQUENCE AI449212	0.005248949	0.6504306	0.369954	0.77668418
1458499_at	Pde1a	phosphodiesterase 10A	0.005252192	0.6263479	0.4180227	0.8180227
1440113_at	MTA1	METASTASIS ASSOCIATED 1	0.005258732	0.02008804	0.2159561	0.463634852
1442050_at	Zfp608 // D430007A19R1K	zinc finger protein 608 // RIKEN cDNA D430007A19 gene	0.005280892	1.0440311	0.1240171	1.207742962
1458582_at	ZHWI1C15	ZINC FINGER, DREAM DOMAIN CONTAINING 15	0.005286444	0.00442568	0.707145143	0.61581143
1421834_at	Pgk5l1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.005312821	0.005251164	0.5773443	0.807114576
1440990_at	BC096349	CDNA SEQUENCE BC096349	0.005333486	0.1786648	0.4499974	0.787815256
1440613_at	PERL1D	PERL-LIKE DOMAIN CONTAINING 1	0.005335633	0.3730538	0.408429	0.243635448
1454549_at	4930480R2K1K	RIKEN CDNA 4930480R2K GENE	0.00535704	0.0871007	0.0781479	2.86312803
1424674_at	---	---	0.005394734	0.4060016	0.06789738	0.68507183
1417310_s_at	PACSIN2	PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS 2	0.005399887	0.5604695	0.666902457	0.669024757
1419754_at	---	Transcribed locus	0.005405149	0.0992376	0.2136229	0.42382522
1418271_t	BHLHB5	BASIC HELIX-LOOP-HELIX DOMAIN CONTAINING, CLASS B5	0.005413308	0.1149079	0.4466327	0.661742066
1457287_at	IRF6	INTERFERON REGULATORY FACTOR 6	0.005413401	0.05066757	0.1798261	0.833855532
1448510_t	C8163	EXPRESSED SEQUENCE C8163	0.005439075	0.3997485	0.1725436	2.021083379
1449428_t	CLDN18	CLAUDIN 18	0.005475912	0.08608799	0.1087346	2.966535036
1426338_t	Ning1	neirin G1	0.005492406	0.9873319	0.383038	1.59817892
1414388_at	---	---	0.005515515	0.062806453	0.933701	0.757606494
1436012_s_at	SCR2N	SCRIBIN 2	0.005575258	0.6719427	0.0589909	0.608852463
1458536_at	PAPPLA	POLY (A) POLYMERASE ALPHA	0.005588645	0.000920887	0.2032004	1.15477092
1430359_at	Pgk5l1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.005614645	0.3992819	0.7204769	0.8909139
1421992_s_at	Ighp4	immunoglobulin heavy chain binding protein 4	0.005676891	0.734703	0.9000421	1.40076989
1452424_at	Gpr23	G protein-coupled receptor 23	0.005692563	0.5228424	0.08044831	0.703907552
1448967_at	NIPSNAP3A	NIPSNAP HOMOLOGY 3A (C. ILEGNAS)	0.005703073	0.279174	0.3291376	0.73240746
1441531_at	PLC4A	PHOSPHOLIPASE C, BETA 4	0.005745859	0.9892666	0.4782513	1.57419803
1446309_at	5830483C08R1K	RIKEN CDNA 5830483C08 GENE	0.005767372	0.6462055	0.104764	0.408168062
145129_at	CALB2	CALBINDIN 2	0.005772721	0.9002358	0.1924127	1.311778867
1443216_at	TBC1D15	TBC1 DOMAIN FAMILY, MEMBER 5	0.005800485	0.033448689	0.0814203	0.642131082
1431651_at	C330001K17R1K	RIKEN CDNA C330001K17 GENE	0.005898404	0.8699784	0.3840667	1.7787771
1458483_at	TBC1D26	TBC1 DOMAIN FAMILY, MEMBER 8	0.005908004	0.9324195	0.14543117	1.214401197
1457391_at	VAMP3	VESICLE-ASSOCIATED MEMBRANE PROTEIN 3	0.005909972	0.7887013	0.9673007	3.53349433
1446942_at	---	---	0.005934768	0.4599237	0.4030151	2.58720604
1458449_at	P90002H16R1K	HYPOTHETICAL PROTEIN LOC54241	0.005956174	0.1841568	0.121440197	1.214401197
1456874_at	Fhl2	fibronectin leucine rich transmembrane protein 2	0.005995465	0.08484813	0.1378313	1.20643191
1434948_at	RAB11FP2	RAB11 FAMILY INTERACTING PROTEIN 2 (CLASS 1)	0.006015805	0.1114777	0.079723	0.78249968
1424278_s_at	---	---	0.006031929	0.1239146	0.064515219	0.645132519
1454073_at	493045D15R1K	RIKEN CDNA 493045D15 GENE	0.006034242	0.31639479	0.0602386	1.486615611
1427410_at	DLI12	DELETED IN LYMPHOCTIC LEUKEMIA 2	0.006088899	0.2599242	0.8329006	0.57890649
1455819_at	Rodi	RODI regulator of differentiation 1 (S. pombe)	0.00612525	0.1503841	0.0432274	0.83272362
1437769_at	EPIDRMAL	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY SUBSTRATE 15-LIKE 1	0.006134319	0.8748785		

1449422_at	Cd8a	cd8alpha 4	0.006904786	0.1547909	0.9027728	1.469933291
1449435_at	EST		0.006909815	0.9751701	0.9734023	0.451632118
1446209_at	USP40	UBIQUITIN SPECIFIC PEPTIDASE 40	0.006914489	0.3928723	0.0925498	0.82193471
1432219_at	NOL9	NUCLEOLAR PROTEIN 9	0.006914772	0.0827243	0.7154579	0.563052594
1420238_at	ECTONUCLEOTIDIC PHOSPHATASE 1	ectonucleotidic phosphatase 1	0.006914917	0.0827308	0.0827308	2.480390004
1434049_at	ENTPD3	ECTONUCLEOTIDIC PHOSPHATASE 3	0.00691792	0.9306409	0.3306669	0.746652943
1458205_at	---	---	0.006919879	0.2666164	0.8301647	1.520639228
1425201_at	HY11	HYDROXYPRUVATE ISOMERASE HOMOLOG (L. COLI)	0.006922227	0.2413584	0.625010716	0.7943593
1455225_at	PAQR9	PROGESTIN AND ADIPOU RECEPTOR FAMILY MEMBER IX	0.006926626	0.2644281	0.7495527	0.862512628
1456773_at	NUP12	NUCLEOPORIN LIKE 2	0.00694474	0.1668417	0.1668417	0.76274132
1436652_at	ABC5	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTRMRP), MEMBER 5	0.006946804	0.00211238	0.3209479	0.729683769
1436447_at	AS5002N12R1K	RIKEN CDNA AS5002N12R1K	0.007007768	0.0129824	0.6482606	0.802476178
1458114_at	SAMD12	STERILE ALPHA MOTIF DOMAIN CONTAINING 12	0.00705429	0.1937525	0.7920953	1.3848455
1457409_at	FUT9	FUCOSYLTRANSFERASE 9	0.007062036	0.0471627	0.5457826	1.218953435
1428292_at	SIROH1720R1K	RIKEN CDNA SIROH1720R1K	0.007063343	0.004661752	0.630317	0.843766706
1417933_at	IGFBP6	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 6	0.007094081	0.5560857	0.4583711	1.328700654
1440250_at	COL4A4	COLLAGEN, TYPE IV, ALPHA 4	0.007133571	0.1134811	0.3131689	2.014964511
1431601_at	Prk4	protein tyrosine phosphatase, receptor type, K	0.007174783	0.2823546	0.3751991	1.179492038
1449800_at	GABRD	GAMMA-AMINO-BUTYRIC ACID (GABA-) RECEPTOR, SUBUNIT DELTA	0.007181606	0.04107823	0.2641572	1.337365112
1440587_at	---	---	0.007183332	0.000183732	0.1040437	0.679796607
1429076_at	Man1a2	mannosidase, alpha, class 1A, member 2	0.007193738	0.01204148	0.620317	1.251464749
1423630_at	CYGB	STELLATE CELL ACTIVATION ASSOCIATED PROTEIN	0.00721435	0.0173972	0.7588963	0.742395123
1453946_at	SCPCAG8	RIKEN CDNA 5730470G24 GENE	0.007242107	2.49082266	0.424258	1.211652796
1453791_at	PPP1R1A	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 1A	0.007304426	0.001967042	0.8610148	0.693891361
1453533_at	4913403008R1K	RIKEN CDNA 4913403008 GENE	0.007335231	0.7714802	0.6311808	0.727299552
1424007_at	GDF10	GROWTH DIFFERENTIATION FACTOR 10	0.007338877	0.1830775	0.189002	3.36588553
1450440_at	Gfzl1	glial cell line derived neurotrophic factor family receptor alpha 1	0.007344236	0.001967042	0.8610148	0.693891361
1453682_at	GABRP2	GA REPEAT BINDING PROTEIN, BETA 2	0.007378877	0.1830775	0.8479208	0.641622534
1436652_at	583041808R1K	RIKEN CDNA 583041808 GENE	0.007409393	0.48975	0.1117227	0.767799994
1439264_at	SCN5A	SODIUM CHANNEL, VOLTAGE-GATED, TYPE II, ALPHA	0.007409846	0.6161013	0.723898276	0.623898276
1439723_at	573059019R1K	RIKEN CDNA 573059019 GENE	0.007429916	0.760052	0.1057512	0.621545263
1455424_at	---	---	0.007457173	0.2093484	0.105414	0.702077058
1422353_at	PRK4E3	PROU DOMAIN, CLASS 4, TRANSCRIPTION FACTOR 3	0.007478205	6.767322745	0.5337273	1.698262112
1429537_at	573040606R1K	RIKEN CDNA 573040606 GENE	0.007528175	0.2477173	0.4570599	1.25412784
1445394_at	---	---	0.007533778	0.4585504	0.5272905	1.586158867
1424605_at	Prk45	proteinase convertase subunit kexin type 5	0.007579398	0.1349809	0.136558	0.711510313
1458656_at	AW50198	EXPRESSED SEQUENCE AW50198	0.007584741	0.00904596	0.9033099	0.75126186
1449206_at	SYPL2	SYNAPOTOPHYSIN-LIKE 2	0.007585852	0.1976434	0.13624919	1.451612377
1437791_at	---	---	0.007592198	0.7711823	0.1444279	0.506885261
1428236_at	MBNL3	MUSCULIN-LIKE 3 (DROSOPHILA)	0.007597254	0.0352181	0.8823745	0.285937675
1439616_at	---	---	0.007625274	0.3885251	0.5274222	0.54926151
1422208_at	Gnb5	guanine nucleotide binding protein, beta 5	0.007627874	0.08941653	0.3040789	1.237665708
1435131_at	478054121R1K	RIKEN CDNA 478054121R1K	0.007678752	0.2839031	0.6301504	0.792134481
1443618_at	PDZD2	PDZ DOMAIN CONTAINING 2	0.007631083	0.2040155	0.4128052	2.767286898
1459679_at	Myo1b	myosin II	0.007669349	0.1777886	0.2904401	1.511761639
1425600_at	FLC3B1	FRODOPHILINASE C, BETA 1	0.007723938	0.0001402	0.15254188	0.6301504
1435608_at	Zarf1 // LOC631806	zinc and ring finger 3 // similar to Goliath homolog precursor (Ring finger protein 130) (R-goliath)	0.007733432	0.16775309	0.5193117	0.781454923
1417149_at	PAH2A	PROCOLLAGEN-PROLINE, 2-OXOGLUTARATE-4-OXYGENASE (PROLINE 4-HYDROXYLASE), ALPHA 1 POLYPEPTIDE	0.007784709	0.2899668	0.1140307	1.262435706
1437763_at	DCTN1D3	DEFECTIVE IN COULI NEURONITIS 1	0.007789848	0.5502901	0.227787466	0.9033099
1425051_at	loc1	isochromatid domain containing 1	0.00780368	0.02029273	0.6574329	0.789022812
1427149_at	PLEKH16A	HYPOTHETICAL PROTEIN BC031133	0.007821571	0.06454198	0.2795887	1.337455403
1456648_at	Man1a	mannosidase 1, alpha	0.007849886	0.4379848	0.3399422	1.233438744
1434186_at	Cpr23	G protein-coupled receptor 23	0.007953949	0.8614117	0.7089966	0.60662875
1438431_at	Grit	Rho GTPase-activating protein	0.007978166	0.0005411	0.1540918	1.14235706
1438439_at	RIKEN CDNA 1700016G14R1K	RIKEN CDNA 1700016G14 GENE	0.008002319	0.8257489	0.405076948	0.805076948
1448327_at	ACTN2	ACTIN ALPHA 2	0.008006363	0.5380552	0.9672326	0.821425542
1417967_at	MMS19L	MMS19 (MEI-TS1, CERVISIAE)-LIKE	0.008037683	0.1161892	0.550007	0.818469566
1439665_at	MM2	G protein-coupled receptor 2	0.008041993	0.1482931	0.5521721	0.609548307
1418061_at	LTRP2	LATENT TRANSMEMBRANE GROWTH FACTOR BETA BINDING PROTEIN 2	0.008046605	0.04286238	0.3412427	1.99593485
1434313_at	6330407D12R1K	RIKEN CDNA 6330407D12 GENE	0.008055855	0.7796855	0.4099508	0.609665447
1433169_at	583045623R1K	RIKEN CDNA 583045623 GENE	0.008079102	0.00065786	0.1927962	0.740994277
1439608_at	---	---	0.008087928	0.6285067	0.695035	0.745201131
1448914_at	Csf1	colony stimulating factor 1 (macrophage)	0.00813638	0.9980167	0.253456	0.791371963
1455074_at	EFCAB1	EF HAND CALCIUM BINDING DOMAIN 1	0.008150894	0.4957243	0.2315038	0.767892529
1456591_at	AKAP3	AKINASE (PKA) ANCHOR PROTEIN 3	0.008152225	0.4609395	0.375491	0.754780576
1423235_at	AP3B1	ADAPTOR-RELATED PROTEIN COMPLEX 3, BETA 1 SUBUNIT	0.008152543	0.0519994	0.8078833	0.818662504
1434760_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	0.008195586	0.7671032	0.4415741	1.389034991
1429613_at	PANK1	PANTOTHENATE KINASE 1	0.008252602	0.3989817	0.466478755	0.805076948
1435607_at	GRM2	G PROTEIN-COUPLED RECEPTOR, FAMILY C, GROUP 1, MEMBER B	0.008262655	0.0189381	0.8601461	0.735642886
1451406_at	Prk45	proteinase convertase subunit kexin type 5	0.008265029	0.8070914	0.3928511	0.619071576
1454011_at	PRK2	PROTEIN KINASE 2	0.008266001	0.00042988	0.717193037	0.695035
1446353_at	TUBB6	TUBULIN, BETA 6	0.008317564	0.02429681	0.5593976	0.76179581
1445427_at	NLK	NEMO LIKE KINASE	0.008332603	0.0470269	0.85544	1.618718777
1448744_at	GALNS	GALACTOSAMINE (N-ACETYL)-6-SULFATE SULFATASE	0.008337436	0.23848	0.628428	0.787898187
1424963_at	RPIH1	RETINETS PIGMENTOSA 1 HOMOLOG (HUMAN)	0.008402466	0.2146266	0.561245	0.397555268
1441142_at	2700081122R1K	RIKEN CDNA 2700081122 GENE	0.008417595	0.3457895	0.7701847	0.697525838
1458742_at	LPH3	LACTOPHILIN 3	0.008422566	0.5887265	0.4786684	1.229575021
1448797_at	ELK3	ELK3, MEMBER OF ETS ONCOGENE FAMILY	0.00842799	0.0818405	0.304266	0.751030488
1451627_at	SLC12A2	SOLITE CARRIER FAMILY 1 (GLIAL HIGH AFFINITY GLUTAMATE TRANSPORTER), MEMBER 2	0.008440962	0.1332844	0.2401468	1.179999799
1450045_at	SNR11	SNRIN-LIKE 1	0.008445086	0.03035547	0.6039187	1.113393914
1448901_at	CPXM1	CARBOXYPEPTIDASE X1 (M14 FAMILY)	0.008448442	0.00100278	0.0784653	1.12684713
1426608_at	---	---	0.008448893	0.75179	0.102405	0.56878069
1458433_at	993345106R1K	RIKEN CDNA 993345106 GENE	0.008476647	0.4777715	0.4933274	0.808998123
145892_at	Ax31	axonal semaphorin 3 (Drosophila)	0.00848125	0.01028027	0.0624934	1.54176585
1453713_at	4930546H06R1K	RIKEN CDNA 4930546H06 GENE	0.008511452	0.0401839	0.1510929	1.248971939
1436299_at	Clb5	glutaminase	0.008530788	0.1511925	0.46136	0.702920376
1438476_at	CHD4	CHROMATIN REMODELING 4	0.008543234	0.0489403	0.28391	1.330474895
1456871_at	PHF20L1	PHD FINGER PROTEIN 20-LIKE 1	0.008546681	0.00017564	0.08451474	1.096811174
1431337_at	1810055112R1K	RIKEN CDNA 1810055112 GENE	0.00855999	0.0470633	0.3050572	0.859953713
1440001_at	LOC311480	HYPOTHETICAL LOC311480	0.008560497	0.2114927	0.33230246	0.73520246
1439697_at	Il1rap	interleukin 1 receptor accessory protein	0.00858601	0.00914225	0.986754	0.701656569
1436234_at	4732471D19R1K	RIKEN CDNA 4732471D19 GENE	0.008617343	0.8901586	0.7998522	0.785588777
1439141_at	AKZ20484	CDNA SEQUENCE AKZ20484	0.008681181	0.8292599	0.375491	0.737648663
1440032_at	E130008017R1K	RIKEN CDNA E130008017 GENE	0.008688106	0.00232362	0.2432511	1.315568416
1460220_at	Csf1	colony stimulating factor 1 (macrophage)	0.008694793	0.5975261	0.7611148	0.772211122
1453710_at	MEM116	RIKEN CDNA 4930513P12 GENE	0.008701855	0.5827109	0.628401776	0.628401776
1426560_at	Nptx	neuropilin	0.008715761	0.7615768	0.4793632	0.61533869
1431871_at	TNXCDC3	THIOREDOXIN DOMAIN CONTAINING 3 (SPERMATOZOEA)	0.00871967	0.0642027	0.6293458	0.42350323
1417626_at	Hsd4dp	STEREO-O-ACYLTRANSFERASE 1 (myogmatid)	0.008722797	0.4112809	0.6293458	0.296798628
1434761_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	0.008775104	0.8152745	0.7440047	0.43103336
1429183_at	Prp2	plakophilin 2	0.00878133	4.2997765	0.8383278	0.74247857
1438096_at	99334918R1K	RIKEN CDNA 99334918 GENE	0.008834289	0.0243826	0.628401776	0.628401776
1434889_at	PLEKH17	PLECKSTRIN HOMOLOGUY DOMAIN CONTAINING, FAMILY A MEMBER 7	0.0088424	0.7051713	0.911013	1.48736009
1432746_at	6030442121R1K	RIKEN CDNA 6030442121 GENE	0.008908806	0.5091955	0.1642426	0.719948419
1425272_at	EMP2	EPITHELIAL-MEMBRANE PROTEIN 2	0.008910297	0.0320319	0.810591	1.269157592
1437858_at	Dysp193	dysp19-like 3 (C. elegans)	0.008948078	0.3246398	0.866994	1.259931902
1435310_at	4930589M24R1K	RIKEN CDNA 4930589M24R1K	0.008972021	0.0381051	0.7184091	0.808005145
1425581_at	Galn7	UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetyl-galactosyltransferase 7	0.008973631	0.3308477	0.107558905	0.644760736
1422255_at	KCN4A	POTASSIUM VOLTAGE-GATED CHANNEL, SHAKER-RELATED SUBFAMILY, MEMBER 4	0.008987567	0.07946182	0.3706519	1.270113479
1437256_at	KCNJND5	---	0.009086153	0.0116625	0.6345039	0.808477017
1424708_at	---	---	0.00913782	0.0438424	0.109173	1.295297376
1436134_at	DM32	GENE MODEL 632 (NCBI)	0.009229634	0.0235799	0.4842044	0.808441062
1436177_at	KCNJ2	transiently associated	0.009233465	0.05609003	0.8591316	0.816784571
1457152_at	KCNB2	POTASSIUM VOLTAGE GATED CHANNEL, SHAB-RELATED SUBFAMILY, MEMBER 2	0.009263847	0.00014839	0.6174124	0.367722582
1417800_at	PARP2	POLY (ADP-RIBOSE) POLYMERASE FAMILY MEMBER 2	0.009266755	0.1257564	0.8332738	0.797254013
1436714_at	LPP	LIM DOMAIN CONTAINING PREFERRED TRANSLATION PARTNER IN LIPOMA	0.009301955	0.00813335	0.1574878	0.823262572
1433325_at	9330154F10R1K	RIKEN CDNA 9330154F10 GENE	0.009448344	0.2353659	0.9484249	1.362217734
1438364_at	CNCG2	CYCLIN G2	0.009472471	0.0007216		

1418639_at	SFTPC	SURFACTANT ASSOCIATED PROTEIN C	0.01034834	0.1213087	0.1159914	0.839444169
1419325_at	FADS2	FATTY ACID DESATURASE 2	0.01032385	0.80052414	1.11448989	0.7866487
1419971_at	---	---	0.01037531	0.2275356	0.8498135	1.997119516
1441055_at	R75368	EXPRESSED SEQUENCE R75368	0.0104231	0.0288314	0.4702256	0.7493488
1455700_at	MTEF3D3	MTEF1 DOMAIN CONTAINING 3	0.01045027	0.9514537	0.622318999	0.731814507
1437095_at	Tpsta18	tetraepin 18	0.01045558	0.9792629	0.9467906	0.390002894
1438275_at	C130046Z22RK	RIKEN CDNA C130046Z22 GENE	0.01047562	0.318181	1.020234	1.29829073
1422616_at	MUT1H	MUT1 HOMOLOG (FOXO, CXX1)	0.01048202	0.2654607	0.4447375168	0.4603348
1441251_at	201000141RK	RIKEN CDNA 201000141 GENE	0.01048453	0.1778707	1.024071	1.386916689
1439524_at	DNAB74	DNAB (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 4	0.0104892	0.2976703	0.83170274	0.83170274
1450522_at	H110	H1 HISTONE FAMILY, MEMBER 0	0.01052352	0.80039044	0.2237754	0.789377461
1451498_at	BC004853	CDNA SEQUENCE BC004853	0.01059113	0.9569107	0.65262318	0.65262318
1458633_at	SNX8	SORTING NEXIN 8	0.01062554	0.275177	0.676396	1.565806203
1452824_at	493041212RK	RIKEN CDNA 493041212 GENE	0.01063373	0.5134213	1.083398	0.448900045
1419794_at	S110089E131RK	RIKEN CDNA S110089E131 GENE	0.01064262	0.8462752	0.5986642	0.558066489
1457181_at	ARHGFE11	RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 11	0.01066952	0.1293303	1.0200275	0.807720383
1456114_at	CDS1	CDP-DIACYLGLYCEROL SYNTHASE 1	0.01071725	0.1247904	0.3018718	1.122899647
1457000_at	BC060207	CDNA SEQUENCE BC060207	0.01070725	0.9854839	0.925276	1.714781359
1433466_at	A1467606	EXPRESSED SEQUENCE A1467606	0.01078665	0.5182186	0.3329924	0.635199275
1416403_at	Absc10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	0.01079979	0.00757413	0.7095446	0.716820413
1455965_at	NAV2	NAV2 ONCOGENE	0.01080294	0.391782	0.800992	0.723925175
1425709_at	Raf17	raf ring finger protein 17	0.01091426	0.3649866	0.3271822	1.898165565
1445055_at	---	---	0.01092756	0.4176985	0.2036165	0.365599723
1452278_at	U1-CE1	HECT DOMAIN AND ANKYRIN REPEAT CONTAINING, EU3 UBIQUITIN PROTEIN LIGASE 1	0.01092284	0.0975687	0.4007167	0.739086669
1418631_at	MPDZ	MULTIPLE PDZ DOMAIN PROTEIN	0.01096294	0.1786143	0.1545866	1.24194177
1436587_at	1700123D08RK	RIKEN CDNA 1700123D08 GENE	0.01097554	0.811347	0.06708753	1.309446332
1444937_at	---	---	0.01101897	0.4021398	0.2587451	2.158136097
1423786_at	8430410A17RK	RIKEN CDNA 8430410A17 GENE	0.0110113	0.2532223	0.0956537	1.109760876
1421520_at	Jph1	junctionphi 1	0.01102413	0.001021108	0.5532901	0.667897173
1434315_at	SFM0B2	RIKEN CDNA D33000906 GENE	0.01103365	0.0404545	0.700202291	0.700202291
1433702_at	D19WSU112E	DNA SEGMENT, CHR. 19, WAYNE STATE UNIVERSITY 12, EXPRESSED	0.01102925	0.0824922	0.5112609	0.757777072
1453016_at	2900042B11RK	RIKEN CDNA 2900042B11 GENE	0.01108889	0.3404909	0.783899	0.816256997
1450663_at	SPTZ	SPTZ ADENOSINE ZIP 1	0.01108849	0.2726277	0.1752224	2.504974012
1456960_at	ADK	ADENOSINE KINASE	0.01108892	0.099461193	0.3832622	0.649649093
1459336_at	GLUCY1A2	GUANYLATE CYCLASE 1, SOLUBLE, ALPHA 2	0.01109812	0.4375056	0.3104261	1.886058041
1418753_at	GPFT2	GLUTAMINE FRUCTURYL-6-PHOSPHATE TRANSAMINASE 2	0.01109897	0.5442221	0.2881065	1.211231251
1464627_at	ADAM28	ADENYLETIRIN AND METALLOPEPTIDASE DOMAIN 28	0.01103278	0.441273	0.7102764	0.492608674
1458976_at	C23003316RK	RIKEN CDNA C23003316 GENE	0.0111129	0.795688	0.8014815	0.61291946
1437287_at	SETDB1	SET DOMAIN CONTAINING 16	0.011147	0.478676-05	0.5372679	0.820400499
1417922_at	SLC17A7	SIGNAL TRANSDUCING ADAPTOR MOLECULE (SH3 domain and ITAM motif) 7	0.0111827	0.3433898	0.4717075	0.492608674
1416975_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0.01123585	0.001690013	0.2302767	1.612127905
1427647_at	BC022150	CDNA SEQUENCE BC022150	0.01124059	0.09890485	0.1694537	1.914042425
1427198_at	BC022960	CDNA SEQUENCE BC022960	0.0112961	0.107323	0.7331254	0.61341721
1418237_x_at	COL18A1	PROCOLLAGEN, TYPE XVIII, ALPHA 1	0.01132114	0.2761782	0.8002139	2.487343723
1434925_at	4833424015RK	RIKEN CDNA 4833424015 GENE	0.01132419	0.4024032	0.1050575	1.18618341
1430864_at	TTL19	TITRIN TYROSINE LIKASE LIKE FAMILY 9	0.01135542	0.1012119	0.7315165	1.651368475
1460448_x_at	Tcl14	tetratricopeptide repeat domain 14	0.01141797	0.001267684	0.4690196	0.806307804
1436407_at	943009097RK	RIKEN CDNA 943009097 GENE	0.01146449	0.8524252	0.3099961	0.752269137
1422292_at	RCTD1	POTASSIUM CHANNEL TETRAMERISATION DOMAIN CONTAINING 1	0.01146774	0.807595848	0.2309451	0.729087626
1435808_at	A230051G13RK	RIKEN CDNA A230051G13 GENE	0.01153606	0.644522	0.3996815	0.870854235
1424813_at	DGKI	DIACYLGLYCEROL KINASE, IOTA	0.01163317	0.1063697	0.2820211	1.237232331
1430844_at	1700018M17RK	RIKEN CDNA 1700018M17 GENE	0.01163469	0.02104835	0.167682478	0.53332106
1418141_at	DCX	DOUBLECORTIN	0.01166534	0.6994953	0.266642	1.202735821
1430088_at	3000020J31RK	RIKEN CDNA 3000020J31 GENE	0.01171093	0.5796435	0.8346046	0.831751499
1445095_at	ATXN1	ATAXIN 1	0.01171942	0.4090984	0.1329378	1.414331204
1453755_at	Lsm11	U7 snRNP-specific Sm-like protein LSM11	0.01172717	0.7627368	0.9173647	1.380106141
1434506_at	ARID2	AT RICH INTERACTING DOMAIN 2 (ARID-REFX LIKE)	0.0117424	0.00747552	0.1574817	1.075764056
1448312_at	Pfak2	proteomim convariant substitution/keum type 2	0.01174943	0.0334148	0.14809951	1.144699541
1442598_at	---	---	0.01176371	0.1660262	0.458239	1.419506792
1440092_at	SERAC1	DNA SEGMENT, CHR 17, ERATO DOI 141, EXPRESSED	0.01178038	0.2261766	0.5468789	1.263678148
1425275_at	Asph	aspartate-beta-hydroxylase	0.01180459	0.0477687	0.1227291	0.792625384
1434955_at	Mem81	MEMBRANE ASSOCIATED RING FINGER (CHRC4) 1	0.0119647	0.8624759	0.1642616	0.799898075
1452675_at	RBM22	RNA BINDING MOTIF PROTEIN 22	0.0119781	0.4322899	0.5184226	0.719355662
1460144_at	BC052040	CDNA SEQUENCE BC052040	0.01198893	0.1660718	0.2247996	0.68291989
1428623_at	PFXNA1	PFXNA1	0.0119748	0.5898255	0.121451184	0.8087327
1422492_at	CPOX	COPROPORPHYRINOGEN OXIDASE	0.0120276	0.0117468	0.8117526	0.812938346
1429881_at	Ahgep15	Rho GTPase activating protein 15	0.012063	0.009774056	0.4845403	0.548441638
1428852_at	DOCK3	REGULATOR OF CYTOKINESIS 3	0.01208976	0.2071816	0.3087327	1.214383535
1416812_at	THA1	CYTOTOXIC GRANULE-ASSOCIATED RNA BINDING PROTEIN 1	0.01209346	1.222931-06	0.3142259	0.7700092
1453596_at	ID2	INHIBITOR OF DNA BINDING 2	0.012124	0.002063004	0.1101049	1.009292327
1458182_at	RBM18	RNA BINDING MOTIF PROTEIN 18	0.01225667	0.9024916	0.855488074	0.855488074
1438183_x_at	SYND	SORBITOL DEHYDROGENASE	0.01229553	0.4123898	0.3619913	0.733981401
1427045_at	SORP	RIKEN CDNA 9030217H11 GENE	0.01231766	0.3791388	0.685056	1.32828962
1455097_at	130101E033RK	RIKEN CDNA 130101E033 GENE	0.01232541	0.066693419	0.151398452	1.151398452
1429772_at	Pfna2	pflxin A2	0.01233122	0.174314	0.1950314	1.27465191
1433495_at	GLT25D1	GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	0.01240157	0.5386101	0.5755797	0.773519431
1439757_at	EphA4	Eph receptor A4	0.01242375	0.0985708	0.6950996	0.728687609
1450788_at	SAA1	SERUM AMYLOID A 1	0.01242508	0.9436224	0.539847	2.70002197
1443075_at	---	---	0.01249197	1.237146-08	0.3303045	1.137925324
1421604_at	Ki67	Ki67-like factor 3 (basic)	0.01252311	0.04339326	0.6950996	0.728687609
1453424_at	Fyvol	FYVE and coiled-coil domain containing 1	0.01254979	0.00239498	0.417057	0.808553393
1418092_x_at	TRF10	TRIFLAVIN HOMONE RECEPTOR INTERACTOR 10	0.01256603	0.1361371	0.4195562	1.389709239
1419315_at	ICRFP3B161405.5	ICRFP3B161405.5 GENE	0.01259014	0.05099662	0.356978	2.451834829
1418754_at	ADCY8	ADENYLYLATE CYCLASE 8	0.01259883	0.5658471	0.7291411	1.425502206
1441267_at	RSRC1	ARGININE/SERINE-RICH COILED-COIL 1	0.01265857	0.01500432	0.44024	0.587086095
1444341_at	8030451F13RK	RIKEN CDNA 8030451F13 GENE	0.0126806	0.1027779	0.4203061	0.68686967
1424208_at	PTGRL4	PROSTAGLANDIN E RECEPTOR 4 (SUBTYPE 4)	0.01269693	0.4603968	0.3178257	1.59380638
1442308_at	SMYD4	SET AND MYND DOMAIN CONTAINING 4	0.01271032	0.9838952	0.4187257	0.788026174
1439189_at	D630023B12RK	RIKEN CDNA D630023B12 GENE	0.01271178	0.0995241	0.7099966	0.810666628
1446791_at	---	---	0.01271989	0.064215441	0.786155577	0.6468491
1446748_at	2010007H06 GENE	RIKEN CDNA 2010007H06 GENE	0.01275959	0.7765871	0.3346684	2.30645616
1434087_at	MTHFR	5,10-METHYLENTETRAHYDROFOLATE REDUCTASE	0.01278597	0.3675277	0.6658009	0.83748331
1419205_at	HTFPC	HTF PIV TINY FRAGMENTATION LOCUS 9C	0.01281733	0.1411713	0.1734476	0.73243352
1435634_at	Pfcm11	protein-L-isopartate (D-aspartate) O-methyltransferase domain containing 1	0.01280421	0.0449151	0.5910635	0.794608823
1419194_x_at	GMPG	GLIA MATURATION FACTOR, GAMMA	0.01280897	0.7684855	0.3353537	0.721153896
1429085_at	VEZF1	VASCULAR ENDOTHELIAL ZINC FINGER 1	0.01285012	0.5059662	0.338813	0.755679739
1417783_at	Als2	amyotrophic lateral sclerosis 2 (gavene1) homolog (human)	0.01294882	0.1771731	0.881201	0.789773508
1421929_at	EphA4	Eph receptor A4	0.01303247	3.52601E-05	0.3479267	1.190462293
1420183_at	Lam	Lamin	0.01303683	0.84405984	0.6497272424	0.6497272424
1446374_at	ARHGFE10	RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 10	0.01307983	0.0303855	0.0527030	0.849646985
1438765_at	Dlx33	DLX3 (Asp-Glu-Ala-His) box polyprotein 33	0.01308264	0.0883874	0.0772348	0.711516743
1452593_at	SNX19	RIKEN CDNA 352401K01 GENE	0.01312444	0.3840151	0.8171527	0.59380638
1424859_at	HOMER3	HOMER HOMOLOG 3 (DIROSOPHILA)	0.01316961	0.00899007	0.66730009	0.824553025
1436045_x_at	STIM1	STROMAL INTERACTION MOLECULE 1	0.01317349	0.01429928	0.6132626	0.712113158
1430369_at	EphA1	Eph receptor A1	0.01321629	0.7697523	0.2981724	1.474306325
1440271_at	---	Transcribed locus	0.01326244	0.0641831	0.0774537	1.206990931
1457030_at	MIRG	MIRNA CONTAINING GENE	0.01329095	0.7859758	0.3299725	1.23057394
1455644_at	MAPP3K9	MIRNA-ACTIVATED PROTEIN KINASE KINASE 9	0.01331831	0.33378	0.238622873	0.238622873
1435880_at	ANKRD50	ANKYRIN REPEAT DOMAIN 50	0.01336553	0.6514272	0.6897443	1.284733654
1441728_at	SCN1A	SODIUM CHANNEL, VOLTAGE-GATED, TYPE I, ALPHA	0.01337888	0.9013822	0.15	

1452484_at	CAR7	CARBONIC ANHYDRASE 7	0.01431174	1.6345E-05	0.7514179	1.14096883
1459169_at	MAPK6	MITOGEN ACTIVATED PROTEIN KINASE 4	0.01431187	0.04708881	0.1764794	1.19240937
1460321_at	CNTN4	AXONAL-ASSOCIATED CELL ADHESION MOLECULE	0.01431785	0.179471	0.09829315	1.188097283
1444742_at	ASB14	ANKRYRN REPEAT AND SOCS BOX-CONTAINING PROTEIN 14	0.01434356	0.001030666	0.6487709	0.484564309
1422755_at	CD84	CD84 ANTIGEN	0.01439118	0.1992265	0.13981866	0.828186924
1457446_at	OPCML	OPIOD BINDING PROTEIN/CELL ADHESION MOLECULE-LIKE	0.01444036	0.8030494	0.4204454	1.104101047
1427344_at	RASD2	RASD FAMILY, MEMBER 2	0.01447291	0.1717629	0.8071305	1.34278223
1424296_at	PPP2R2C	PROTEIN PHOSPHATASE 2, REGULATORY SUBUNIT B (B56), GAMMA ISOFORM	0.01447325	0.000403757	0.5998043	0.78076308
1440116_at	DR040512R1K	RKIN CDNA D6040512 GENE	0.01448594	0.264442	0.3893249	1.131795313
1420863_at	DCTN4	DYNACTIN 4	0.01448687	1.2720E-06	0.06585429	1.067049891
1429528_at	RAE1	RAE1 RNA EXPORT 1 HOMOLOG (S. POMBE)	0.01449422	0.000031838	0.130666	0.72743407
1441472_x_at	---	---	0.01449887	0.04852794	0.2163956	0.802258285
1431096_at	---	---	0.01452173	0.4639346	0.7658116	1.214202141
1451114_at	UNG2	URACIL DNA GLYCOSYLASE 2	0.01459454	0.7170304	0.3995528	0.730796308
1423585_at	ACTBP1	ATP/GTP BINDING PROTEIN 1	0.01462944	2.06832E-07	0.6307203	1.072378078
1426228_at	KRAS	V-KI-RAS2 KIRSTEN RAT SARCOMA VIRAL ONCOGENE HOMOLOG	0.01463681	0.1633777	0.1137849	0.27714895
1444857_at	C83712	EXPRESSED SEQUENCE C83712	0.01469541	0.1319629	0.2955202	0.32698207
1444730_at	Nrcx3	Neurexin III	0.01471879	0.0100275	0.560898	1.753430199
1440034_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0.01473302	0.8209325	0.3644538	1.48668684
1429943_at	CTBS	CHITINASE, DE-N-ACETYL-	0.01474353	0.00046217	0.0735709	0.741681334
1423503_at	JAM3	RKIN CDNA 1110002E2 GENE	0.01477894	0.04578748	0.0512059	1.16217038
1416562_at	Gad1	glutamic acid decarboxylase 1	0.01486335	0.002307308	0.9763202	0.77319249
1457995_at	---	---	0.01489246	0.879279	0.3091364	2.21078839
1429429_at	Ptenad1	protein-L-isoopartate (D-apartate) O-methyltransferase domain containing 1	0.01490564	0.2384762	0.0603377	0.820918131
1425388_at	TPK1	THIAMIN PYROPHOSPHOKINASE	0.01489723	0.8199376	0.4403206	0.803283868
1439101_at	DR0300702R1K	RKIN CDNA DR0300702 GENE	0.01489964	0.06077438	0.2661805	0.607030132
1417878_at	E2F1	E2F TRANSCRIPTION FACTOR 1	0.01490231	0.1685346	0.2004586	1.650828737
1456967_at	TRIM66	KIAA0298 HYPOTHETICAL PROTEIN (HUMAN)	0.01492154	0.1807018	0.339114	1.346434297
1431749_x_at	Ragap1	RA5 guanyl releasing protein 1	0.01492451	6.48451E-05	0.8605856	1.241384893
1456166_at	Cmp1	Cyprin-like	0.01495803	0.19546377	0.3762566	0.272980699
1421595_at	9630031F12R1K	RKIN CDNA 9630031F12 GENE	0.01497003	0.02158468	0.0735401	0.80373569
1423218_at	RAD18	RAD18 HOMOLOG (S. CEREVISIAE)	0.01501785	0.0414371	0.6917924	0.540957312
1454212_at	49304509R1K	RKIN CDNA 49304509 GENE	0.01503881	0.5730356	0.1339813	0.584838656
1457166_at	AA536749	EXPRESSED SEQUENCE AA536749	0.01504068	0.0023649	0.0864146	1.315544385
1452117_at	FYB	FYB BINDING PROTEIN	0.01504985	0.0760122	0.3289472	1.448382732
1457615_at	---	---	0.01506807	0.8268608	0.9275171	0.541770103
1446609_at	Albin3	Actin binding LIM protein family, member 3	0.0151077	0.0401133	0.0583161	0.686019183
1453250_at	4921511C04R1K	RKIN CDNA 4921511C04 GENE	0.0151112	0.7075807	0.796177	0.431458103
1442581_at	KSR1	KINASE SUPPRESSOR OF RAS 1	0.01512604	0.1347556	0.1570192	0.818979994
1454593_at	SYN1	SYNAPTOBULBIN-1/CLYXOPE 1	0.01512662	0.6339084	1.261484241	0.6190866
1426934_at	NHSL1	NHSL-LIKE 1	0.01519089	0.00812816	0.6323646	0.697033257
1443359_at	ODZ4	ODD OZ/TEN-5 HOMOLOG 4 (DROSOPHILA)	0.01524488	0.07037986	0.1410952	1.449165718
1423740_at	SMYD2	RKIN CDNA 1110002E2 GENE	0.01527200	0.1856611	0.0728279	1.222787877
1441735_at	LRG1	LEUCINE-RICH REPEATS AND IMMUNOGLOBULIN-LIKE DOMAINS 1	0.01528303	0.9164515	0.5899939	1.799015497
1424035_at	Chrm5	cholinergic receptor, nicotinic, alpha polypeptide 5	0.01530184	0.4003324	0.5980455	0.736297259
1452777_at	63304012F12R1K	RKIN CDNA 63304012F12 GENE	0.01530777	0.1613927	0.3316784	1.083078713
1434321_at	6620401K05R1K	RKIN CDNA 6620401K05 GENE	0.01531368	0.196225	0.0582521	1.216024306
1426832_at	6330405F04R1K	RKIN CDNA 6330405F04 GENE	0.01538948	0.0146948	0.802342	0.784711998
1456949_at	RKIC2	PHOSPHATIDYLINOSITOL 3-KINASE, CATALYTIC, BETA POLYPEPTIDE	0.01539738	0.066825308	0.8022562	1.191702899
1445217_at	A730073F16R1K	RKIN CDNA A730073F16 GENE	0.01541555	0.0176697	0.2043241	0.600757575
1440277_at	AL0041474	EXPRESSED SEQUENCE AL0041474	0.01543996	0.0340467	0.1449159	0.842885074
1446206_at	TDRD5	TDRD DOMAIN CONTAINING 5	0.01548804	0.2085974	0.545700842	0.6194842
1449978_x_at	Cncl	cyclin J-like	0.01550218	0.5748562	0.9105308	0.75240145
1440932_at	TRIM17	TRIPARTITE MOTIF PROTEIN 17	0.01552962	0.9372151	0.4004027	0.777947833
1423111_at	4930452D17R1K	RKIN CDNA 4930452D17 GENE	0.01554567	0.04333607	0.769665532	0.646578028
1416136_at	SLC27A2	SOLUTE CARRIER FAMILY 27 (FATTY ACID TRANSPORTER), MEMBER 2	0.01556671	0.2449473	0.1123171	0.473647753
1419966_at	TUBB2B	TUBULIN, BETA 2B	0.01562189	0.2328009	0.09628279	1.603817284
1441178_at	DTXD2	DTXD DOMAIN CONTAINING 2	0.01564788	0.31819682	0.3918324	0.603053054
1454075_at	NUD1F1	NUDX (NUCLEOSIDE DIPHOSPHATE LINKED MOEITY X)-TYPE MOTIF 13	0.01568349	0.3676165	0.1642058	0.848414477
1427946_x_at	DPYD	DIHYDROPYRIMIDINE DEHYDROGENASE	0.01572054	0.9152999	0.408219	0.817879648
1426983_at	CNO176	CCR4-NOT TRANSCRIPTION COMPLEX, SUBUNIT 6	0.01575219	0.8796225	0.4228852	1.138945437
1421094_at	ZNF16	ZINC FINGER AND FIBRIN DOMAIN CONTAINING 13	0.01579898	0.0151471	0.0728279	1.402752884
1451793_at	TPPI	TISSUE FACTOR PATHWAY INHIBITOR	0.01579318	0.0578822	0.3250552	0.829542009
1410383_at	syndecan 2	adomatosis protein coxsii down-regulated 1	0.01579922	0.001695823	0.1092744	0.70716455
1417011_at	Sema2	Sema domain, immunoglobulin domain (GG), short basic domain, secreted, (SEMAPHORIN 3A)	0.0158007	0.00218757	0.0654159	1.447931619
1420416_at	SEMA3A	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (GG), SHORT BASIC DOMAIN, SECRETED, (SEMAPHORIN 3A)	0.01582739	0.000811971	0.3420789	1.201629872
1431615_at	TMEM117	TRANSMEMBRANE PROTEIN 117	0.01583049	0.3832041	0.1792634	0.644272715
1450193_at	RKX1	RYR-RELATED KINETIN-ACTIVATED, CYCLIC NUCLEOTIDE-GATED K+ 1	0.01583642	0.00317397	0.684801	1.107466274
1453287_at	573057B15R1K	RKIN CDNA 573057B15 GENE	0.01588959	0.05821053	0.2038449	1.187563163
1434098_at	GLRA2	GLYCINE RECEPTOR, ALPHA 2 SUBUNIT	0.01592045	0.1470627	0.1828674	0.730751688
1426223_at	210419102R1K	RKIN CDNA 210419102 GENE	0.01594669	0.2372752	0.614329	0.708280557
1459906_at	Dgk8	Diacylglycerol kinase, eta	0.01603166	0.5078008	0.2866179	0.730719341
1421973_at	Gria1	glial cell line derived neurotrophic factor family receptor alpha 1	0.01605719	0.263157	0.1780897	0.682118704
1429011_at	SNRP70	70 S SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE A	0.01606241	0.182808	0.363166	0.750610118
1454666_at	KID	Kruppel factor 3 (basic)	0.01609457	0.9540296	0.813613	0.759610118
1459746_at	R3hdml1	R3H domain 1 (binds single-stranded nucleic acids)	0.01613615	0.000554198	0.3252642	1.200664192
1427526_at	Epha7	Eph receptor A7	0.01614762	0.000154018	0.8980862	0.666578028
1427735_x_at	ACTA1	ACTIN, ALPHA 1, SKELETAL MUSCLE	0.01620608	0.01723737	0.3619712	1.205873983
1427155_x_at	STSS1AS	SHALYTRANSFERASE 8 (ALPHA-2, S-SALYTRANSFERASE) E	0.01620855	0.0954948	0.2621539	1.151557479
1460591_at	ESR1	ESTROGEN RECEPTOR 1 (ALPHA)	0.01622409	0.192405	0.0923403	0.662315354
1430733_at	4932441P12R1K	RKIN CDNA 4932441P12 GENE	0.01627777	0.2094016	0.6979604	0.540991604
1452344_at	Synj2	synapjanin 2	0.01632672	0.7451598	0.3027498	1.235917178
1438815_at	HIST2AA1	HISTONE 2, 2AA1A	0.01635555	0.03917298	0.9232403	0.728727282
1453407_at	1700018L24R1K	RKIN CDNA 1700018L24 GENE	0.01644994	0.01418599	0.2029402	0.740170171
1430353_at	GLIS3	GLIS FAMILY ZINC FINGER 3	0.01645526	0.7419447	0.7248987	0.678262779
1415861_at	TYRP1	TYROSINASE-RELATED PROTEIN 1	0.01646533	0.2727063	0.7099485	0.597193976
1440077_at	6330490D2R1K	RKIN CDNA 6330490D2 GENE	0.01647839	0.2924998	0.633600979	0.63049207
1424249_at	SLC6A2	SOLUTE CARRIER FAMILY 6 (NEUROTRANSMITTER TRANSPORTER, NORADRENALIN, MEMBER 2)	0.01650081	0.4121415	0.9381406	0.597193976
1447112_x_at	CRYL1	CRYSTALLIN, LAMDA 1	0.01662036	0.721475	0.1156236	0.717282717
1458839_at	Cd6b	calbindin-D28k	0.01663489	0.01524355	0.040462454	0.6194842
1430045_at	Tnax	translin-associated factor X	0.01662183	0.2599799	0.9574008	1.506232366
1430416_at	ZNR2	ZINC AND RING FINGER 2	0.01662336	0.00299084	0.1101133	0.823638588
1429296_at	913040119R1K	RKIN CDNA 913040119 GENE	0.01666489	0.5601591	0.7510361	1.774662698
1453126_at	LRFN2	LEUCINE RICH REPEAT AND FIBRONECTIN TYPE III DOMAIN CONTAINING 2	0.01668157	0.996656	0.2912194	1.237670691
1429327_at	USP29	UBQUITIN SPECIFIC PEPTIDASE 29	0.01672061	0.003150871	0.3626081	1.297525248
1450083_at	A113524	EXPRESSED SEQUENCE A113524	0.01676167	0.002832808	0.0874029	1.121478029
1452983_at	CEP57	RKIN CDNA 4921511C04 GENE	0.01676979	0.0132504	0.5781276	0.785004514
1436450_at	---	---	0.01683888	0.3467999	0.3444766	1.115395222
1427496_x_at	Spag5	spem associated antigen 5	0.01691875	0.4778448	0.6054736	1.603472369
1431380_at	5730409L17R1K	RKIN CDNA 5730409L17 GENE	0.01697102	0.0765586	0.256042	1.402907518
1418600_at	MAPK7	MITOGEN ACTIVATED PROTEIN KINASE 7	0.01707227	0.0714782	0.578978	0.599941402
1451544_at	GNAI7	GNAI7 MOLECULE 47, (NON)BIOPHILIN	0.01709404	0.626338	0.187501083	0.87501083
1430106_at	1700126L10R1K	RKIN CDNA 1700126L10 GENE	0.0171548	0.1889752	0.6087901	1.964073747
1434754_at	GARNA4	GTPASE ACTIVATING RANGAP DOMAIN-LIKE 4	0.01716358	0.6522329	0.1750043	0.773372318
1427609_at	Hhcx2b	Hedgehog protein 2b	0.01716929	0.03857524	0.2121865	1.150391735
1451355_at	ASAH1L	RKIN CDNA 241011605 GENE	0.0171984	0.003413011	0.2571287	0.86020449
1438105_at	LOC62687	HYPOTHETICAL PROTEIN LOC62686	0.0174267	0.722355	0.1750495	0.748504474
1427439_at	PRMT5	PROTEIN ARGININE-S-METHYLTRANSFERASE 5	0.01731837	0.9501491	0.2270821	1.116600564
1441628_at	DIAP3	DIAPHANOUS HOMOLOG 3 (DROSOPHILA)	0.0173423	0.002730623	0.5877269	0.405666015
1416561_at	Gad1	glutamic acid decarboxylase 1	0.01733459	0.3499238	0.3340359	0.761336232
1447101_at	RNF122	RING FINGER PROTEIN 122	0.01734843	0.000495335	0.2096847	0.575800521
1431109_at	SLC49A0M13R1K	RKIN CDNA 5430004G1 GENE	0.01737874	0.3307901	0.618139419	1.181394139
1421225_at	Ap3a2	adaptor-related protein complex 3, mu 2 subunit	0.01739489	0.4860998	0.800546	0.444323259
1417343_at	FXYD6	FXYD DOMAIN CONTAINING ION TRANSPORT REGULATOR 6	0.0174097	0.1068963	0.1809908	2.09158443
1454785_at	DRBP11	DIAL SYMBIOTIC PHOSPHATASE 11 (RNA-RNP COMPLEX 1-INTERACTING)	0.01743406	0.001798407	0.0827133	0.735232855
1440838_at	ALS2264	EXPRESSED SEQUENCE ALS2264	0.01743422	0.2569977	0.807891	1.261429059
1424519_at	MTG1	MITOCHONDRIAL GPASE 1 HOMOLOG (S. CEREVISIAE)	0.01744866	0.2151717	0.4848991	0.8007185
1423290_at	Epha7	Eph receptor A7	0.01745089	0.6232407</		

142859_u	PAOX	POLYAMINE OXIDASE (EXO-N4-AMINO)	0.01823749	0.08577803	0.6878419	0.73758119
142101_u	L6b2	L10 domain binding 2	0.01823749	0.290424	0.242712	1.133206454
1454030_u	SAPS3	SAPS DOMAIN MEMBER 3	0.01827146	0.0170514	0.4599935	1.17175756
1419167_u	PRAP1	PROLINE-RICH ACIDIC PROTEIN 1	0.01828251	0.2227828	0.0672343	0.7481639
1419994_u	---	---	0.01828259	0.3089617	0.4690964	0.777929035
1414660_u	EIF3S10	---	0.01829943	1.248986-06	0.07427238	1.05691321
1458186_u	---	---	0.01831199	0.7878885	0.3793665	0.85304608
1421457_u	SAMSN1	SAM DOMAIN, SH3 DOMAIN AND NUCLEAR LOCALIZATION SIGNALS, 1	0.01834855	0.104854	0.0122529	0.78783046
1457935_u	TS122	SEROLOGICALLY DEFINED COLON CANCER-LIKE 3 LIKE	0.01838124	0.16578209	0.2995518	0.425012886
1456482_u	PK3R3	PHOSPHATIDYLINOSITOL 3 KINASE, REGULATORY SUBUNIT, POLYPEPTIDE 3 (P55)	0.01842876	0.00012386	0.1293815	1.082325465
1443589_u	---	---	0.01844252	0.00069431	0.284183	1.18981165
1416600_u	TF1c	PEPTIDYL LEUCYL ISOMERASE F (CYCLOPHILIN F)	0.01847919	0.04216518	0.709292	0.855282412
1439764_u	C330012H03RIK	RIKEN CDNA C330012H03 GENE	0.01849834	0.6343072	0.563307	2.175914309
1443589_u	DXERTD242E	DNA SEGMENT, CHR X, ERATO DOJ 242, EXPRESSED	0.01850068	0.1386918	0.4520099	1.361778935
1449020_u	CYP19A1	CYP19A1 (P450) FAMILY 19, SUBFAMILY A, POLYPEPTIDE 1	0.01851931	0.1053265	0.282489	0.498696264
1427748_u	IGK-V1	IMMUNOGLOBULIN KAPPA CHAIN VARIABLE 1 (V1)	0.01851313	0.4124349	0.3607899	0.487628797
1458180_u	---	---	0.01854075	0.0396164	0.7854399	1.50092707
1435655_u	---	---	0.01855886	0.335023	0.649089	0.848376575
1440343_u	RPS6A5	RIBOSOMAL PROTEIN S6 KINASE, POLYPEPTIDE 5	0.0185655	0.0167605	0.122354	0.700042526
1447120_u	BTIC	BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN	0.01858908	0.0413628	0.2395764	1.289778215
1440340_u	---	---	0.01864415	0.04359851	0.6156775	0.735021122
1457229_u	GPR173	G-PROTEIN COUPLED RECEPTOR 173	0.01866779	0.0927871	0.608574	0.789811036
1454822_u	ApoJ1	adenomatous polyposis coli down-regulated 1	0.01868536	0.6066306	0.4263041	0.609872882
1451284_u	111007014H1RIK	RIKEN CDNA 111007014 GENE	0.01874509	0.06661608	0.420095	0.759474669
1449677_u	TMEM38B	TRANSMEMBRANE PROTEIN 38B	0.01879477	0.1041784	0.2259673	0.899717731
1429790_u	KLRK16	KILLER CELL LECTIN-LIKE RECEPTOR, SUBFAMILY A, MEMBER 16	0.01879971	0.6179097	0.897976	0.682481258
1419483_u	IFIP1	INTERFERON INDUCIBLE GTPASE 1	0.01881709	0.8469935	0.212837	2.211737573
1440063_u	FARSLA	PHENYLALANINE-TRNA SYNTHETASE-LIKE, ALPHA SUBUNIT	0.0189026	0.0887275	0.652925	2.33646548
1460490_u	MRP15	MITOCHONDRIAL RIBOSOMAL PROTEIN L15	0.01892049	0.4448971	0.1667158	0.811654731
1427194_u	KLR3C	KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY C, MEMBER 3	0.01893388	0.3952305	0.18182	2.64523814
1448469_u	ND1	ND1	0.01897389	0.00025497	0.3306007	0.775862122
1429712_u	LOC262308	ETHANOL INDUCED 1	0.01898373	0.0395378	0.2526786	1.144462568
1450949_u	KAT5A1	KAT5/NIN PRO1 (ATPASE CONTAINING) SUBUNIT A1	0.01899484	0.007940052	0.2607995	1.286554328
1433300_u	Z900004RIK	RIKEN CDNA Z900004 GENE	0.01899889	0.1059774	0.80099792	0.643110827
1430710_u	---	---	0.01906339	0.7204962	0.1534982	1.203090972
1415144_u	CN3M3	heparan sulfate 6-O-sulfotransferase 2	0.01909249	0.7908552	0.22900254	1.22900254
1450047_u	H662	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 2 LIKE 1	0.01909661	0.0041812	0.4230385	0.809058331
1440120_u	GNB2L1	---	0.01910397	0.7949096	0.2607881	1.52664206
1424004_u	AW56556	EXPRESSED SEQUENCE AW56556	0.01914166	0.455427	0.551144092	0.8949898
1425236_u	Neucl1	neural cell adhesion molecule 1	0.0191584	0.1579441	0.1656367	1.13346274
1424161_u	DDX27	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 27	0.01917082	0.6418098	0.758766	2.14906414
1412194_u	SPEER7-PS1	SPERMATOGENESIS ASSOCIATED GLUTAMATE (E)-RICH PROTEIN 7, PSEUDOGENE 1	0.01919322	0.5104626	0.84391289	0.84391289
1445870_u	C13C2P2	RIKEN CDNA 111008006 GENE	0.01919754	0.000217458	0.3470676	1.10213786
1447204_u	Mpkl5	Mitogen-activated protein kinase kinase kinase 5	0.01930691	0.0015247	0.9008677	1.30949193
1437573_u	PR2	PROPHOSPHATASE (INORGANIC) 2	0.01932159	0.2885072	0.668280545	0.668280545
1433141_u	4921504P05RIK	RIKEN CDNA 4921504P05 GENE	0.01932803	0.3311669	0.5608005	0.758480169
1439673_u	E230008015RIK	RIKEN CDNA E230008015 GENE	0.01933061	0.02407488	0.823973236	0.823973236
1419990_u	---	---	0.01933507	0.1237443	0.5030212	1.163579991
1415909_u	ST1P1	STRESS-INDUCED PHOSPHOPROTEIN 1	0.01939674	0.3226089	0.64624	0.672512314
1421481_u	TNFRSF9	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 9	0.01941053	0.001864993	0.094654993	1.59062958
1457992_u	---	---	0.0194528	0.4267932	0.7921742	0.66528542
1445855_u	AO3000717RIK	RIKEN CDNA AO3000717 GENE	0.01945848	0.0127694	0.07313051	1.196974912
1440751_u	EP400	E1A BINDING PROTEIN P400	0.01949411	0.2072425	0.5435446	0.874107369
1435874_u	---	---	0.01950576	0.2295646	0.3201689	1.37272354
1447123_u	---	---	0.01950853	0.00737862	0.1922667	1.13489149
1423785_u	A445040	expressed sequence A445040	0.01952023	0.1468881	0.094654993	0.710371037
1425211_u	CEP27	CENTROSOMAL PROTEIN 27	0.01952386	0.6794484	0.3701077	1.16809993
1430849_u	CORGF1	CELL GROWTH REGULATOR WITH RING FINGER DOMAIN 1	0.01956242	0.1818337	0.2217677	0.818648388
1455095_u	H1S1212BE	SYMBOL TO HISTONE H2B-616	0.0195808	0.8522606	0.3999993	1.60741738
1431433_u	SRF2	MYOTUBULARIN RELATED PROTEIN 13	0.01958731	0.641246-05	0.7905294	0.80103885
1428748_u	CS8428123RIK	CNA SEQUENCE BC025757	0.01961413	0.0947632	0.05176088	0.456400812
1433113_u	4921504P20RIK	RIKEN CDNA 4921504P20 GENE	0.0196385	0.3146257	0.601024	1.44358394
1445062_u	ELOW16	ELOW FAMILY MEMBER 6, ELONGATION OF LONG CHAIN FATTY ACIDS (YEAST)	0.0196774	0.0786452	0.4961774	0.787037594
1427225_u	---	---	0.01968582	0.2344514	0.1783657	0.7451115
1449141_u	FLB1M1	FILAMIN BINDING LIM PROTEIN 1	0.01972372	0.625996	0.1084929	1.32026347
1429760_u	RPS6A6	RIBOSOMAL PROTEIN S6 KINASE POLYPEPTIDE 6	0.01977107	0.00083283	0.58411	0.82444999
1440848_u	---	---	0.0197868	0.8771729	0.7873208	0.633701121
1460570_u	PGBD5	PIGGYBAC TRANSPOSABLE ELEMENT DERIVED 5	0.01979807	0.1013621	0.9422745	0.82177631
1458731_u	---	---	0.01983932	0.0243878	0.4998844	0.901414289
1460105_u	BGALNT2	UDP-GALNAC-BETA(1-6) GALACTOSAMINYLTRANSFERASE, POLYPEPTIDE 2	0.01986148	0.3389674	0.6822635	2.971798596
1439799_u	ZCC1C2	ZINC FINGER, C2CH DOMAIN CONTAINING 2	0.01992923	0.4409319	0.0689786	1.528108427
1428276_u	1110065107RIK	RIKEN CDNA 1110065107 GENE	0.01994417	0.7405248	0.7834217	0.874327594
1439543_u	1110064423RIK	RIKEN CDNA 1110064423 GENE	0.01996891	0.5982409	0.5294927	0.5294927
1423401_u	ETV6	ETS VARIANT GENE (A TEL ONCOGENE)	0.01999499	0.0272672	0.08721028	0.81140779
1433122_u	Igf5	insulin-like growth factor 5	0.02001037	0.0121489	0.5087962	0.508796169
1432131_u	---	---	0.02004442	0.4089222	0.26591	0.79267002
1458606_u	---	---	0.02008465	0.1944433	0.05990091	1.939198185
1437052_u	SC2A3	sialate carrier family 2 (sialinated glucose transporter) member 3	0.02008814	0.1262378	0.8201016	0.820101547
1423353_u	CRISPLD1	CYSTEINE-RICH SECRETORY PROTEIN LCC1 DOMAIN CONTAINING 1	0.02010196	0.145471	0.372132	1.17911986
1430073_u	1430073RIK	RIKEN CDNA 290014801 GENE	0.02015798	0.6980706	0.3492827	1.410625949
1456099_u	D93001703RIK	RIKEN CDNA D93001703 GENE	0.02016927	0.3225094	0.7916346	0.400303524
1448478_u	TRF7	TRF (TATA BINDING PROTEIN-RELATED FACTOR)-PROXIMAL PROTEIN HOMOLOG (DROSOPHILA)	0.02020009	0.8296767	0.0720245	0.78663466
1418131_u	SAMHD1	SAM DOMAIN AND HHD DOMAIN, 1	0.02020655	0.08836287	0.9734223	0.83263403
1460073_u	---	---	0.02020709	0.0995552	0.1602352	0.881428227
1418493_u	SNCA	SYNUCLEIN, ALPHA	0.02025004	0.0568424	0.8488417	0.752997744
1421018_u	111001818RIK	RIKEN CDNA 111001818 GENE	0.02031317	0.4189331	0.223555	1.236506121
1444424_u	270092106RIK	RIKEN CDNA 270092106 GENE	0.02036182	0.3014489	0.3476221	0.726270964
1438577_u	BRK1	RYTHER LECTIN-1 RECEPTOR-ASSOCIATED KINASE 1	0.02041882	0.0031187	0.829144601	0.829144601
1453017_u	DSER12S85E	DNA SEGMENT, CHR 5, ERATO DOJ S85, EXPRESSED	0.02044003	0.141495	0.2576573	1.160896829
1449593_u	DI7ERTD191E	DNA SEGMENT, CHR 17, ERATO DOJ 191, EXPRESSED	0.02044096	0.4623955	0.2771658	0.595302777
1455185_u	PRF16	PROTEIN F16	0.02046395	0.8009611	0.54117	0.773488153
1455373_u	---	---	0.02047563	0.0662018	0.2071783	1.251599777
1418831_u	PKP3	PLAKOPHILIN 3	0.02047851	0.4013533	0.05900294	0.774933397
1451624_u	PRO39P02	PROTEINASE, ORPHAN 2	0.02052352	0.1210077	0.15586647	1.15586647
1416081_u	FOXO1	FORKHEAD BOX O1	0.02053078	0.342918	0.3230763	1.16454159
1443868_u	ATP13A3	ATPASE TYPE 13A3	0.02057612	0.1733088	0.2473732	0.418884001
1437248_u	2700049A03RIK	RIKEN CDNA 2700049A03 GENE	0.02059352	0.5792749	1.5543043	1.5543043
1430853_u	3110045G13RIK	RIKEN CDNA 3110045G13 GENE	0.02062133	0.4445954	0.3908144	0.527837438
1416490_u	TME4D	TRANSMEMBRANE EMP24 METAL TRANSPORT DOMAIN CONTAINING 6	0.02062987	0.8117087	0.1494577	2.23021577
1437506_u	ADAMTS5	A DISINTEGRIN-LIKE AND METALLOPEPTIDASE (REPROLYSIN TYPE) WITH THROMBOSPONDIN TYPE 1 MOTIF, 6	0.02066974	0.02263268	0.1676382	1.725191922
1446347_u	---	---	0.0206959	0.8169594	0.0684278	1.476778957
1428618_u	H6c2	host cell factor 2	0.02070142	0.00576026	0.7860073	0.78232264
1459129_u	TIC7	RIKEN CDNA 111003402 GENE	0.02070765	0.0703412	0.33101	0.497678871
1416287_u	RGS4	REGULATOR OF G-PROTEIN SIGNALING 4	0.02071291	0.04330961	0.5956269	1.24602379
1454418_u	5330421C15RIK	RIKEN CDNA 5330421C15 GENE	0.02071309	0.1021767	0.569246	1.246022171
1415191_u	Dnaj1	DnaJ (Hsp40) homolog, subfamily A, member 4	0.0207402	0.6097783	0.1209576	1.199871468
1457388_u	AK5080801RIK	RIKEN CDNA AK5080801 GENE	0.02074854	0.8832785	0.9005778	2.9251824
1444337_u	GM761	GENE MODEL 761, (NCBI)	0.02080457	0.3928341	0.1376649	0.618218897
1439804_u	2110015A10RIK	RIKEN CDNA 2110015A10 GENE	0.02081966	0.5754527	0.0370088	0.804357697
1431404_u	TBC1D19	TBC1 DOMAIN FAMILY MEMBER 9	0.02084059	0.8508499	0.2605223	1.210128495
1						



1438827_at	Gls	Glutaminase	0.02224072	0.00317981	0.1206682	1.718841197
1455876_at	270021E23RK	RIKEN CDNA 270021E23 GENE	0.02225336	0.03165533	0.97657377	0.780501759
1456854_at	NEURL	NEURALIZED-LIKE HOMOLOG (DROSOPHILA)	0.02226148	0.063980975	0.8565982	1.186392255
1462222_at	10H1CR2A	LOSS OF HETEROZYGOSITY 11, CHROMOSOMAL REGION 2, GENE A HOMOLOG (HUMAN)	0.02229385	0.3297865	0.05835083	1.265492425
1425282_at	311055A05G	RIKEN CDNA 311055A05 GENE	0.02229542	0.3296668	0.3286668	1.422323909
1449502_at	DAZL	DELETED IN AZOOSPERMIA-LIKE	0.02232827	0.06698227	0.3950868	0.751635332
1444884_at	PPT1	PALMITOYL-PROTEIN THIOESTERASE 1	0.02237307	0.8985487	0.1099257	0.811387333
1430689_at	281006C22RK	RIKEN CDNA 281006C22 GENE	0.02244083	0.11491304	0.3662454	0.785153233
1456236_s_at	COMM10	COMM DOMAIN CONTAINING 10	0.02250133	0.7622555	0.3820854	0.77444923
1448898_at	CCL9	CHEMOKINE (C-C MOTIF) LIGAND 9	0.02252203	0.07890362	0.6751509	0.71731557
1418173_at	SRXN4	SIDEROFLIXIN 4	0.02258554	0.8635011	0.3132847	0.785722263
1442409_at	DRETT27SE	DNA SEGMENT, CHR 9, ERATO DOI 278, EXPRESSED	0.02258719	0.0852319	0.0597624	0.511241076
1458982_at	ALU014965	EXPRESSED SEQUENCE ALU014965	0.02259817	0.9776944	0.0849601	0.542088898
1425972_at	QR	QUAKING	0.0226189	0.0110777	0.8454564	1.118166861
1422598_at	310485I05RK	RIKEN CDNA 310485I05 GENE	0.02262067	0.1416219	0.930335	0.900485068
1441543_at	EYA3	EYES ABSENT 3 HOMOLOG (DROSOPHILA)	0.02264461	0.4439303	0.8490011	1.942865656
142776_s_at	FGFR4	FIBROBLAST GROWTH FACTOR RECEPTOR 4	0.02264922	0.0698676	0.1813978	1.953778931
1444815_at	CR328	EXPRESSED SEQUENCE CR328	0.02265485	0.3459441	0.625735	0.668268426
1440055_at	AI84810	EXPRESSED SEQUENCE AI84810	0.02267211	0.01142127	0.6053169	0.668395679
1436915_x_at	LAPTM4B	LYSOSOMAL-ASSOCIATED PROTEIN TRANSMEMBRANE 4B	0.02270925	0.00165622	0.3413247	0.779092335
1445944_at	EXOSC1	EXOSOME COMPONENT 1	0.02272361	0.8711425	0.5714452	1.071924608
1444215_at	---	---	0.02273092	0.9067858	0.7353354	0.841955972
1425937_at	ANKRD39	RIKEN CDNA 913014A05 GENE	0.02273233	0.6312114	0.480561	0.789421447
1420280_x_at	COL9A3	PROCOLLAGEN, TYPE IX, ALPHA 3	0.02275887	0.0897618	0.0981449	0.842328375
1442921_at	MMP24	MATRIX METALLOPROTEINASE 24	0.02279076	0.8426051	0.5603101	2.260946461
1416204_at	GpII	glycosyl 3-phosphatidylglycerol 1 (soluble)	0.02284271	0.923845	0.7171904	1.423793999
1452435_at	Wdr22	WD repeat domain 22	0.02289059	0.1994407	0.2962613	1.142869322
1430190_at	1700041C02RK	RIKEN CDNA 1700041C02 GENE	0.02290126	0.9377018	0.1116886	0.813314459
1456097_at	Hg879	hepatitis B 3 binding protein (hep-3-endonuclease)	0.02292031	0.1230741	0.1278184	0.723657615
1425206_at	DNAI1A1	DNAI (HSP40) HOMOLOG, SUBFAMILY A, MEMBER 1	0.02294261	0.4894838	0.1193777	1.268383374
1453931_at	COL14A1	PROCOLLAGEN, TYPE XIV, ALPHA 1	0.02294678	0.165166	0.0732456	0.663034626
1424229_at	DYRK3	DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE 3	0.02295432	0.05560315	0.4291123	1.139434665
1424297_s_at	Tam2	topoisomerase II, alpha	0.02301511	0.1712955	0.620209	0.675078274
1457837_at	BC033606	PHOSPHOLIPASE B1	0.02302541	0.2050943	0.2050733	0.670317801
1429447_at	EVC2	ELLIS VAN CREVELD SYNDROME 2 HOMOLOG (HUMAN)	0.02303518	0.13109578	0.312916	0.808060717
1421176_at	Ragap1	RAS guanine releasing protein 1	0.02305664	0.41932336	0.278676	1.921789872
1427043_x_at	COVA1	CYTOSOLIC OVARIAN CARCINOMA ANTIGEN 1	0.02309362	0.3625534	0.8940571	0.719862715
1416396_at	SNX4	SORTING NEXIN 4	0.02310423	0.00712884	0.6117475	0.859091561
1447474_at	Hs162	heparan sulfate glycosaminoglycan 3-O-sulfotransferase 2	0.02314863	0.0780847	0.48166882	1.48166882
1418734_at	BE136769	EXPRESSED SEQUENCE BE136769	0.02318554	0.36288	0.09138047	0.434683799
1448573_x_at	CLACAM10	CLA-RELATED CELL ADHESION MOLECULE 10	0.02318391	0.3071879	0.9486636	2.422389811
1429445_at	310109A09RK	RIKEN CDNA 310109A09 GENE	0.02324221	0.2779794	0.5590112	1.391498505
1424243_at	Per3	perla homolog 3 (Drosophila)	0.02323832	0.6208494	0.1382249	1.198025389
1440126_at	BC037704	CDNA SEQUENCE BC037704	0.02327787	0.5099958	0.09954625	0.661782977
1445200_at	---	---	0.02332221	0.1045221	0.9225567	0.9225567
1451475_at	PLXND1	PLEXIN D1	0.02329858	0.1585437	0.2900665	1.24441231
1437604_x_at	Apcd1	adenomatous polyposis coli down-regulated 1	0.02331037	0.0747052	0.3945335	0.732092339
1425421_at	RBBP6	RETINOBLASTOMA BINDING PROTEIN 6	0.02333736	0.08920496	0.071205566	0.771205566
1416527_at	RAB32	RAB32, MEMBER RAS ONCOGENE FAMILY	0.02336555	0.1763344	0.641259	0.6793904
1429875_at	170004305RK	RIKEN CDNA 170004305 GENE	0.02338272	0.98607	0.1988083	0.52413452
142315_s_at	ASB1	ANKRYN REPEAT AND SOCS BOX-CONTAINING PROTEIN 11	0.02340271	0.4808853	0.727876	0.719332366
1445465_at	N28178	expressed sequence N28178	0.02341082	0.2419908	0.2442798	1.171483737
1457056_at	FTCD	FORMININOTRANSFERASE CYCLODEAMINASE	0.02341784	0.5460602	0.2199728	2.276276233
1421518_at	BC14	BLASTIC LEUKEMIA 14 PROPHILA 4	0.02343676	0.9901726	0.3610721	0.780670262
1429629_at	ZH1	ENHANCER OF ZESTE HOMOLOGY 1 (DROSOPHILA)	0.0234422	0.2240255	0.5619771	1.163762252
1460133_at	---	---	0.02351299	0.6279378	0.0930299	1.596988241
1434646_at	EXOSC8	EXOSOME COMPONENT 8	0.02353798	0.4787116	0.6487112	0.831191658
1424248_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	0.02353897	0.4991034	0.2545575	1.255168409
1430572_at	1810042K04RK	RIKEN CDNA 1810042K04 GENE	0.02359328	0.419023	0.0746653	1.63431729
1452783_at	Fdc3b	fibronectin type III domain containing 3B	0.02359779	0.0114288	0.331534	1.173866229
1453653_at	310103A11RK	RIKEN CDNA 310103A11 GENE	0.02360834	0.8329707	0.8549113	0.9718268118
1450957_s_at	SQSTM1	SQSTM1	0.02362409	0.7320797	0.5915405	1.066898658
1426206_at	FBXO10	F-box protein 10	0.02365614	0.1180741	0.966805	0.75063633
1448133_at	NR237	NR2 REPEAT DOMAIN 27	0.02372984	0.65329669	0.1466239	1.901560972
1431001_at	903062A402RK	RIKEN CDNA 2610029J22 GENE	0.02373336	0.8648729	0.3615929	2.201563634
1432299_at	492151108RK	RIKEN CDNA 492151108 GENE	0.02381809	0.219229	0.0915947	0.534626201
1433357_at	3730422I09RK	RIKEN CDNA 3730422I09 GENE	0.02382327	0.5558469	0.7903887	2.351668242
1416914_x_at	MTVR2	MAMMARY TUMOR VIRUS RECEPTOR 2	0.02382631	0.01064205	0.5397272	1.177509767
1441300_at	KCNF1	POTASSIUM VOLTAGE-GATED CHANNEL, SUBFAMILY F, MEMBER 1	0.02383862	0.3071964	0.4016422	1.544228911
1417235_at	SHD3	SH3-DOMAIN CONTAINING 3	0.02384648	0.5491969	0.9303112	0.799857074
1436537_at	ZFP629	ZINC FINGER PROTEIN 629	0.02387462	0.1613557	0.871858	0.820209987
1446994_at	EXOSC2	EXOSOME COMPONENT 2	0.02387855	0.729254	0.1748826	2.424954811
1454770_at	CKKBR	CHOLECYSTOKININ B RECEPTOR	0.02390417	0.6311711	0.1942638	1.1942638
1438565_at	AK8001M20RK	EXPRESSED SEQUENCE AK8001M20	0.02391924	0.0003252	0.7041547	1.12720459
1425833_x_at	HPC4	HIPPOCAMPIN	0.02392542	0.00673859	0.5919145	1.134646521
1455856_at	---	---	0.02392955	0.2820789	0.6567082	0.656707706
1460233_at	GUCA2B	GUANYLATE CYCLASE ACTIVATOR 2B (RETINA)	0.02400555	0.1466555	0.9012465	0.580640954
1459768_at	DLG1B	DISCS, LARGE HOMOLOG 1 (DROSOPHILA)	0.02403939	0.5611963	0.7193547	1.205315785
1418230_at	LIMS1	RIKEN CDNA 492151A02 GENE	0.02404135	0.060392312	0.060392312	1.086826223
1441848_at	---	---	0.02413731	0.2468342	0.9058387	1.351796596
1453772_at	KIF21B	KINESIN FAMILY MEMBER 21B	0.02421936	0.3137274	0.9689241	1.275899154
1422258_at	CR3A3	CHOLESTEROL RECEPTOR, MUSCARINIC 3, CARDIAC	0.02423418	0.01607961	0.6176129	0.753564229
1444082_at	A73001C20RK	RIKEN cDNA A73001C20 GENE	0.02424407	0.7668341	0.3192514	0.761464677
1441397_at	PARD3	DNA SEGMENT, CHR 8, ERATO DOI 580, EXPRESSED	0.02424967	0.193142	0.3312718	0.731810483
1448805_at	KCNH3	POTASSIUM VOLTAGE-GATED CHANNEL, SUBFAMILY H (EAG-RELATED), MEMBER 3	0.02425332	0.8952085	0.861523	1.384713604
1481133_at	---	---	0.02438799	0.7738149	0.5642486	0.851308872
1457054_x_at	DJ1002I05RK	RIKEN CDNA DJ1002I05 GENE	0.02440989	0.1426742	0.620213	0.732200674
1424220_x_at	PORCN	PORCUPINE HOMOLOG (DROSOPHILA)	0.02442256	0.0670580	0.991139	0.767286401
1426850_at	MARCK6	MITOGEN-ACTIVATED PROTEIN KINASE 6	0.02444035	0.82997161	0.8008245	0.800768474
1446637_at	PRDM10	PR DOMAIN CONTAINING 10	0.02446423	0.5792204	0.9457037	2.064857025
1431469_at	CXNC5	CXCR FINGER 5	0.02446625	0.113422	0.0881611	1.151829902
1424229_at	RIN2	RAS AND RAB1 INTERACTOR 2	0.02446646	0.0475173	0.9303112	1.995411191
1420461_at	MSTR1	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)	0.02447079	0.4533267	0.5421922	1.860201196
1421922_at	SH3BP5	SH3-DOMAIN BINDING PROTEIN 5 (BTK-ASSOCIATED)	0.02447402	0.001534888	0.637853	0.792106174
1453401_at	170007G11RK	RIKEN CDNA 170007G11 GENE	0.02451622	0.5520344	0.2688956	2.6889956
1422737_at	NCOA3	NUCLEAR RECEPTOR COACTIVATOR 3	0.02452468	0.01947548	0.1761461	1.124144845
1445740_at	MASS1	MONOGENIC, AUTODIGENIC SEIZURE SUSCEPTIBILITY 1	0.02452538	0.00237364	0.2976891	1.574984611
1454055_at	1600029D15RK	RIKEN CDNA 1600029D15 GENE	0.02453796	0.01819689	0.617852	0.810842403
1437151_at	USP22	UBOQUITIN SPECIFIC PEPTIDASE 22	0.02457568	6.4016E-05	0.1864809	0.814565314
1429767_at	281003P96RK	RIKEN CDNA 281003P96 GENE	0.02457877	0.4661835	0.7052198	0.801731213
1449113_at	FP2	ZINC FINGER PROTEIN 2	0.02460435	0.0012029	0.0012029	0.800768474
1451059_at	493349D10RK	RIKEN CDNA 493349D10 GENE	0.02464645	0.5158011	0.955785	2.099293813
1456000_at	---	---	0.02467319	0.06392541	0.2176024	1.18003341
1428144_at	311035I14RK	RIKEN CDNA 311035I14 GENE	0.02470465	0.06914632	0.8119766	1.231228944
1438543_at	Spat13	Spermatogenesis associated 13	0.02474368	0.139331	0.6373263	0.513262063
1418084_at	Np1	neuropilin 1	0.02481817	0.00758669	0.7319888	0.772023405
1450253_at	Mmp14	matrix metalloproteinase kinase kinase 4	0.02483728	0.00189963	0.7809987	0.805379252
1445398_at	373241D22RK	RIKEN CDNA 373241D22 GENE	0.02485832	0.02742409	0.1948449	0.65565619
1429041_at	LOC436177	SIMILAR TO CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OSF-4)	0.02486246	0.2643033	0.2102306	0.854662434
1443818_at	---	---	0.024			

1483831_at	YYPEL2	YYPEL-LIKE 2 (DRÖSOPHILA)	0.02628811	0.03708494	0.1327741	1.183492433
1483799_at	CDC43D3	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 3	0.02628559	0.03142378	0.1326449	0.757781512
1486459_u_at	INRPA1	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1	0.02631016	0.8989618	0.3248372	0.69806861
1489813_at	1700012D01RIK	RIKEN CDNA 1700012D01 GENE	0.02631379	0.150065	0.3800639	1.247002777
1446912_at	---	---	0.02624936	0.5556424	0.05943723	1.195578485
1448397_at	DDIT3	DNA-DAMAGE INDUCIBLE TRANSCRIPT 3	0.02626237	0.1603979	0.6693483	0.52840339
1488743_at	NK38483C08RIK	RIKEN cDNA NK38483C08 GENE	0.02626491	0.1281019	0.3404989	0.457723659
1449399_at	NEK2	NIMA INVERSE IN MITOSIS GENE(A)-RELATED EXPRESSED KINASE 2	0.02626592	0.127884	0.6811564	0.670888527
1440179_u_at	brca1	BRCA1 domain containing 1	0.02644831	0.9487208	0.0479205	1.352999095
1437480_at	RIKEN CDNA 1110001A07 GENE	RIKEN CDNA 1110001A07 GENE	0.02645965	0.2465091	0.3271134	0.792924459
1453233_u_at	OACT1	O-ACYLTRANSFERASE (MEMBRANE BOUND) DOMAIN CONTAINING 1	0.02646164	0.4778784	0.2296797	0.769181508
1425284_at	RIKEN CDNA 1110004M10RIK	RIKEN CDNA 1110004M10 GENE	0.02646481	0.2784891	0.8814191	0.915847322
1430033_at	RIKEN CDNA 5330431K02RIK	RIKEN CDNA 5330431K02 GENE	0.02648866	1.07839E-05	0.1061905	0.78332533
1435511_at	SYN2	SYNAPSIN II	0.02649023	0.2920195	0.4328866	0.823771104
1435550_at	TRAF6	TNF RECEPTOR-ASSOCIATED FACTOR 6	0.02650297	0.8255188	0.789245572	1.138108485
1440581_at	AS30088H08RIK	RIKEN cDNA AS30088H08 GENE	0.02651028	0.3271257	0.0870163	0.69533337
1421252_u_at	Mez2	myocyte enhancer factor 2A	0.02654181	0.2597204	0.2009622	0.808017745
1429191_at	6833421H05RIK	RIKEN CDNA 6833421H05 GENE	0.02655551	0.1116855	0.3211527	0.789245572
1429122_u_at	170004003RIK	RIKEN CDNA 170004003 GENE	0.02660763	0.7665851	0.4646549	1.232922246
1446380_at	9430076C15RIK	RIKEN CDNA 9430076C15 GENE	0.02666891	0.3265822	0.05184005	0.589651611
149141_at	RIKEN CDNA 1810008M10RIK	RIKEN CDNA 1810008M10 GENE	0.02670001	0.8160038	0.2507422	0.566718061
1453807_at	6330563C09RIK	RIKEN CDNA 6330563C09 GENE	0.02670329	0.0733042	0.3236027	1.173228855
1447941_u_at	BRAF	BRAF TRANSFORMING GENE	0.02671369	0.1445554	0.07601548	1.13357953
1424382_at	RCN3	RETICULOCALBIN 3; EF-HAND CALCIUM BINDING DOMAIN	0.02674451	0.00874997	0.4992055	0.730264506
1432223_at	4930552N02RIK	RIKEN CDNA 4930552N02 GENE	0.02683633	0.6896833	0.9005044	4.062061047
1428207_at	BCL7A	B-CELL CLL LYMPHOMA 7A	0.02688935	0.0792521	0.5448005	0.857383854
1444409_at	RBP17A	RABPHILIN 3-LIKE (WITHOUT C2 DOMAINS)	0.02690938	0.062368	0.7094607	0.748195114
1450323_at	5730493B19RIK	RIKEN CDNA 5730493B19 GENE	0.02692614	0.1268134	0.2010628	1.49152415
1446409_at	GITDC1	GLYCOSYLTRANSFERASE-LIKE DOMAIN CONTAINING 1	0.02696949	0.3405633	0.2010628	0.736418391
1424245_at	C130075A20RIK	RIKEN CDNA C130075A20 GENE	0.02701302	0.00959849	0.176680401	1.176680401
1445452_at	4930579C12RIK	RIKEN CDNA 4930579C12 GENE	0.02708041	0.1398133	0.3171761	1.786898584
1444904_at	CBFA2T1H	CBFA2T1 IDENTIFIED GENE HOMOLOG (HUMAN)	0.02712077	0.9892325	0.05290933	1.329236888
1455555_at	CD3C67	COILED-COIL DOMAIN CONTAINING 67	0.02715435	0.7843625	0.8394761	0.569309894
1449091_at	Yiel	Yamaguchi sarcoma viral (y-v) oncoprotein homolog 1	0.02715445	0.3315001	0.830669	0.70532829
1452653_at	SLC25A22	SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, GLUTAMATE), MEMBER 22	0.02717683	0.0468722	0.773748	0.751786905
1442380_at	LCN4	LIPICALIN 4	0.02719281	0.1762895	0.0663991	0.618119536
1420236_at	CRAMP1L	CRAL CRAMP-LIKE (DRÖSOPHILA)	0.02720717	0.3917238	0.86072334	0.86072334
1416622_at	WBSRC16	WILLIAMS-BEUREN SYNDROME CHROMOSOME REGION 16 HOMOLOG (HUMAN)	0.02734077	0.001499114	0.05171627	1.033267211
1428141_at	GG2	GOLGI ASSOCIATED, GAMMA ADAPTIN EAR CONTAINING, ARF BINDING PROTEIN 2	0.02734322	0.1662849	0.6322652	1.29765387
1422638_at	PLZ2	PROLIFERIN-LIKE 2	0.02737497	0.1253732	0.8544119	1.81617826
1439105_at	CDAD1C	CYTIDINE AND DCMP DEAMINASE DOMAIN CONTAINING 1	0.02737451	0.5795671	0.0545432	0.900433405
1438169_at	Frm4b	FERM domain containing 4b	0.02746414	0.708717	0.5454221	0.618029941
1424812_at	RCN715S	CINA SEQUENCE BOUND PROTEIN C substrate	0.02747831	0.4278768	0.821516	0.85849358
1454972_at	ATCAY	ATAXIA, CEREBELLAR, CAYMAN TYPE HOMOLOG (HUMAN)	0.02750694	0.1355888	0.7229931	1.185790557
1449252_u_at	Lin7b	lin 7 homolog C (C. elegans)	0.02758348	1.75625E-06	0.8887706	0.718313878
1453244_u_at	5830416P10RIK	RIKEN CDNA 5830416P10 GENE	0.02759378	0.0416615	0.0416615	0.85849358
1419705_at	CARS5	CARBONIC ANHYDRASE 5B, MITOCHONDRIAL	0.02760815	0.1982852	0.4066689	0.68538472
1446605_u_at	BCL2L11	BCL2-LIKE 11 (APOPTOSIS FACILITATOR)	0.02762811	0.0276441	0.0620748	1.141667268
1455038_at	SLC30A3	SOLUTE CARRIER FAMILY 30 (ZINC TRANSPORTER), MEMBER 3	0.02762566	0.9749951	0.249187	0.546873819
1446654_at	2110057K04RIK	RIKEN CDNA 2110057K04 GENE	0.02768539	0.8172696	0.1681884	1.319195952
1446793_at	RIKEN CDNA 1110057K04 GENE	RIKEN CDNA 1110057K04 GENE	0.02774118	0.9158436	0.1345822	0.806797716
1440387_at	RIKEN CDNA 2610091F11 GENE	RIKEN CDNA 2610091F11 GENE	0.02774263	0.7732131	0.0561771	1.8162826261
1431297_u_at	4933436C20RIK	RIKEN CDNA 4933436C20 GENE	0.02774891	0.2586408	0.6391515	0.64012162
1453565_at	---	---	0.02775278	0.1838527	0.16172329	1.25716632
1457946_at	COXV	COX HOMEOBOX GENE	0.02775676	0.030214	0.06321318	1.098131255
1491924_at	2210010105RIK	RIKEN CDNA 2210010105 GENE	0.02778191	0.0590636	0.1606832	1.15020255
1444345_at	---	---	0.02780911	0.7725292	0.4854881	1.478276449
1424740_u_at	rib2	ribin 2	0.02781407	0.3801725	0.4040103	1.513374209
1435930_at	ZFP291	RIKEN CDNA D530014003 GENE	0.02781593	0.1936661	0.4737513	0.784806609
1445359_at	ADCV1	ADENYLATE CYCLASE 1	0.02783848	0.02201534	0.8468609	1.314215302
1447174_at	DACH1	DACHSHUND 1 (DRÖSOPHILA)	0.02784889	0.08816881	0.6134526	0.680212017
1444164_at	PRF9	PRF9 PRE-MRNA PROCESSING FACTOR 39 HOMOLOG (YEAST)	0.02784866	0.8557588	0.9180788	0.849117244
1424247_at	ADCVAP1	ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE 1	0.02789827	0.1787896	0.8435914	1.424584802
1416124_at	CNCD2	CYCLIN D2	0.02797243	0.1099922	0.1570218	1.18669552
1458453_at	LM107	LIM DOMAIN ONLY 7	0.02818492	0.1191204	0.1581419	1.158141939
1455702_at	---	---	0.02819681	0.7955148	0.1644258	0.91551697
1429168_at	BTBD4	RIKEN CDNA 4934306L5 GENE	0.02811331	0.8594866	0.171878	1.32951584
142121_at	Appp21	cytoic AMP-regulated phosphoprotein 21	0.02814594	9.98986E-06	0.944119	1.206170174
1439008_at	ZKSCAN1	ZINC FINGER WITH KRAB AND SCAN DOMAINS 1	0.0281877	0.00013647	0.0610184	1.058419604
1443595_at	CNO74	CCR-NOT TRANSCRIPTION COMPLEX, SUBUNIT 6-LIKE	0.02818792	0.16492589	0.09052131	0.668272575
1427954_at	RCN5403	RIKEN CDNA 5830416P10 GENE	0.02819938	0.09709398	0.8006939	0.85849358
1417262_at	FIG2	PROSTAGLANDIN-ENDOPEROXIDASE SYNTHASE 2	0.0282431	0.4324683	0.5577079	1.51279887
1449276_u_at	ENPP1	ECTONUCLEOTIDIC PYROPHOSPHATASE/PHOSPHODIESTERASE 1	0.0282493	0.2348191	0.1613038	1.199466878
1456072_at	Man2c	1,6-mannosylidene dihydroxyacetone C substrate	0.02825233	0.0298824	0.60177881	0.60177881
1421622_u_at	Ragg4f	Rap guanine nucleotide exchange factor (GEF) 4	0.0282704	0.09721107	0.8223147	0.759239884
1423542_at	KLK7	KALLIKREIN 7 (CHYMOTRYPSIN, STRIPAN CORNEUM)	0.02827828	0.2453622	0.1620241	0.564578787
1423753_at	RAMBI	RAMP AND ACTIVIN MEMBRANE-BINDING INHIBITOR, HOMOLOG (XENOPUS LAEVIS)	0.02831364	0.0306951	0.722646678	0.722646678
1433683_at	RBMS5B	RNA BINDING MOTIF PROTEIN 5B	0.02833033	0.9546075	0.837179	2.639759968
1423254_u_at	231004007RIK	RIKEN CDNA 231004007 GENE	0.02838255	0.01392439	0.7456554	0.815509499
1438384_at	943008034RIK	RIKEN CDNA 943008034 GENE	0.02838426	0.7237884	0.951481	0.789292552
1428569_at	B320171C12RIK	RIKEN CDNA B320171C12 GENE	0.02840996	0.3984444	0.1065815	1.404881348
1437396_at	CREB3L2	CAMP RESPONSIVE ELEMENT BINDING PROTEIN 3-LIKE 2	0.02841595	0.2609736	0.1327753	1.159821771
1451008_at	STSSA3	STYLAIPALIN-ACTIVIN-RECEPTOR-ASSOCIATED 3	0.02841927	0.1637984	0.6703821	1.208351187
1429654_at	DDPA2	DEVELOPMENTAL PL10-PROTEIN ASSOCIATED 2	0.02842075	0.2871306	0.272118	2.206154784
1439731_at	RIKEN cDNA E130309F12 GENE	RIKEN cDNA E130309F12 GENE	0.02846126	0.8347113	0.1515768	1.194145061
1421302_u_at	GNAS1	GUANINE NUCLEOTIDE BINDING PROTEIN, ALPHA 15	0.02846268	0.1480909	0.05601144	0.853461601
1424116_at	PRK1	PROLINE SERINE-RICH COILED-COIL 1	0.02847281	0.0763129	0.1799818	1.1799818
1429606_at	4930572B16RIK	RIKEN CDNA 4930572B16 GENE	0.02850549	0.1716932	0.4499558	1.288528626
1421833_at	Pp61a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.02852333	0.771789	0.3302626	0.877554136
1424096_at	PHK87	PHOSPHOINOSITIDE 3-OH DEHYDROXYLASE	0.02853666	0.6140848	0.8467186	1.0467186
1428195_at	4631427C17RIK	RIKEN cDNA 4631427C17 GENE	0.02860157	0.159951105	0.6288016	0.752831068
1426005_at	DMP1	DENTIN MATRIX PROTEIN 1	0.02860367	0.477993	0.1205708	0.732957978
1458421_at	Egfs	transforming growth factor alpha	0.02872783	0.00292842	0.86240364	0.86240364
1452474_u_at	ART3	ADEN-TRIBOSYLTRANSFERASE 3	0.02876239	0.8919958	0.09329204	1.240276469
1428497_at	SECSB2	SECS BINDING PROTEIN 2	0.0287838	0.2394883	0.8156219	1.187464224
1446300_at	---	---	0.0288559	0.08196272	0.6835299	1.358520996
1441843_u_at	5230400M03RIK	RIKEN CDNA 5230400M03 GENE	0.02888634	0.4677496	0.08228236	1.525086992
1445463_at	9430099H24RIK	RIKEN CDNA 9430099H24 GENE	0.02892566	0.4009779	0.3739663	2.304992226
1453703_at	AKT2	PROTEIN KINASE C-ALPHA GENE 2	0.02893945	0.7007042	0.1312123387	1.312123387
1435500_u_at	RA26	RA26, MEMBER RAS ONCOGENE FAMILY	0.02894044	0.2283889	0.7411815	0.781013873
1447865_u_at	PZFD1	PZD DOMAIN CONTAINING 11	0.02897326	0.0147963	0.1040935	0.861136627
1450972_at	RIKEN CDNA 1110040N11RIK	RIKEN CDNA 1110040N11 GENE	0.0289861	0.6286125	0.878763524	0.878763524
1430357_at	HJ3B	H3 HISTONE, FAMILY 3A	0.02903716	0.8066295	0.2127476	1.35207725
1437250_at	WD12	WHN-DEPENDENT TRANSCRIPT 2	0.0290918	0.472715	0.6386353	0.76353384
1455449_at	TYC3	TYRINATRIPEPTIDE REPEAT DOMAIN 9	0.02907558	0.00974695	0.10037105	1.10037105
1492726_at	A430107D22RIK	RIKEN CDNA A430107D22 GENE	0.0290788	0.1795731	0.5266907	2.143464452
1433661_at	BC034204	CINA SEQUENCE BOUND PROTEIN				

1434442_at	DSHRTD593E	DNA SEGMENT, CHR 5, ERATO DOI 593, EXPRESSED	0.03037271	0.5724891	0.4689454	1.271882412
1432834_at	C308002073RJK	RIKEN CDNA C308002073 GENE	0.03044422	0.06812207	0.8032322	1.087434904
1435324_at	633059M23RJK	RIKEN CDNA 633059M23 GENE	0.03052875	0.6913863	0.57959	0.821496753
1436838_at	BC072620	CDNA SEQUENCE BC072620	0.03060997	0.07782224	0.9823758	1.210982802
1439532_at	GRM7	GLUTAMATE RECEPTOR METABOTROPIC 7	0.03063126	0.01696811	0.9585	1.309291817
1439081_at	ATG10	AUTOPLAGY-RELATED 10 (YEAST)	0.0306523	0.6964258	0.7063499	0.710006738
1448650_at	POLE	POLYMERASE (DNA DIRECTED), EPSILON	0.03071251	0.04128191	0.1922769	0.510094594
1435340_at	PABPC1	POLY(A) BINDING PROTEIN, CYTOSOLIC 1	0.03072717	0.1110428	0.1110428	0.8141451012
1437241_at	LRRK4C	LEUCINE RICH REPEAT CONTAINING 48	0.03075167	0.6219162	0.6219162	0.549266646
1417699_at	GIT2F1	RIKEN CDNA 2810405L04 GENE	0.03079854	6.31051E-07	0.0850538	1.016737227
1422168_at	Rblp	brain derived neurotrophic factor	0.03080196	0.1390533	0.9832214	1.328692047
1436473_at	ARE2	ADENOSINE RIBOSYLATION FACTOR 2	0.03083759	0.4220078	0.0557263	1.131848024
1423904_at	PVR	POLIOVIRUS RECEPTOR	0.03092701	0.8304499	0.8953158	0.823571328
1419929_at	D15HRTD55E	DNA SEGMENT, CHR 15, ERATO DOI 55, EXPRESSED	0.03099976	0.7213788	0.2525854	1.228851988
1438717_at	OSM2F6	OSYSTEIN BINDING PROTEIN, CYTOSOLIC 6	0.03098773	0.08438625	0.1302146	1.211701766
1423839_at	6430598H11RJK	RIKEN CDNA 6430598H11 GENE	0.03098109	0.003365673	0.1635255	1.123884976
1436411_at	RCDD1	RC1 DOMAIN CONTAINING 1	0.03099857	0.0843517	0.9687664	0.766656597
1431618_at	D14I46481E	DNA SEGMENT, CHR 14, ERATO D04 881, EXPRESSED	0.03099887	0.6139992	0.718581	0.855496234
1421155_at	BGAL16	UDP-GAL-BETAGAL BETA 1,3-GALACTOSYLTRANSFERASE, POLYPEPTIDE 6	0.03100382	0.2961159	0.3856761	0.825627538
1448616_at	DVL2	DISHVEILED 2, DSH HOMOLOG (DROSOPHILA)	0.03100802	0.7160406	0.1971251	1.418461166
1426539_at	ICSP11	ICPULVIN SPECIFIC FACTOR 11	0.03102127	0.2051984	0.741781	0.883128061
1434720_at	953003124RJK	RIKEN CDNA 953003124 GENE	0.0311025	0.5893303	0.2955581	0.81641823
1446861_at	GNS	GLUCOSAMINE (N-ACETYL)-6-SULFATASE	0.03112942	0.7580105	0.08817099	0.844620724
1442309_at	Big1	B-cell translocation gene 1, anti-proliferative	0.03113214	0.06441998	0.324839	1.305388232
1449085_at	PHF10	PHD FINGER PROTEIN 10	0.03112738	0.2050186	0.322917	0.624381296
1442135_at	GM237	GENE MODEL 237, (NCBI)	0.03112786	0.060990547	0.3105624	1.090118001
1420977_at	Man1a2	mannosidase, alpha, class 1A, member 2	0.03123936	0.5491586	0.1757548	0.708166898
1457762_at	TTIC15	TETRAICICLOPEPTIDE REPEAT DOMAIN 15	0.03134348	0.05138673	0.1459759	0.841264184
1436601_at	TBR2	TRANSFORMER BETA 2	0.03151808	0.17795308	0.6825431	0.832443341
1449747_at	BCDIN3	BIN, BICOID-INTERACTING 3, HOMOLOG (DROSOPHILA)	0.03138064	0.04044382	0.5427921	0.604103939
1451397_at	TNR3C5	RIKEN CDNA 261004H01 GENE	0.03139347	3.83638E-05	0.2174569	1.0707971
1435114_at	WDHD1	WD REPEAT AND HMG BOX DNA BINDING PROTEIN 1	0.03142432	0.05175173	0.5070761	0.835346463
14318159_at	TCTP2	TRANSCRIPTION FACTOR CP2	0.0314557	0.0339139	0.8427372	0.831342303
1416545_at	ZDHHC7	ZINC FINGER, DHHC DOMAIN CONTAINING 7	0.03146288	0.08833976	0.3969911	1.183258628
1431904_at	4933427G17RJK	RIKEN cDNA 4933427G17 GENE	0.03146797	0.8713679	0.9088416	0.54971184
1438715_at	STK38L	SERINE/THREONINE KINASE 38 LIKE	0.03147401	0.8889877	0.3191767	0.515292023
1435577_at	CI30089N23RJK	RIKEN CDNA CI30089N23 GENE	0.03150664	0.000344993	0.2940046	1.074536029
1435579_at	CI1000409RJK	RIKEN CDNA CI1000409 GENE	0.03154391	0.218193	0.29996	1.183559117
1452576_at	Hcf2	host cell factor 2	0.03156532	0.0796238	0.91567	1.173290978
1438328_at	GALNTL2	UDP-N-ACETYL-L-ALPHA-D-GALACTOSAMINE-POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE-LIKE 2	0.03158644	0.2243732	0.973171	0.828574901
1429235_at	MEF2D	MYOCTYL ENHANCER FACTOR, MYOGENESIS 2	0.03159883	0.1640824	0.100098	1.352288326
1434487_at	AB48149	EXPRESSED SEQUENCE AB48149	0.03164845	0.8956967	0.916587	0.695427675
1455489_at	LRRMT2	LEUCINE RICH REPEAT TRANSMEMBRANE NEURONAL 2	0.03168259	0.0567274	0.4888948	1.183703886
1439476_at	Dag2	delta2	0.0316883	0.000262469	0.60411859	1.11219033
1438991_at	CTNND2	CATENIN (CADHERIN ASSOCIATED PROTEIN), DELTA 2	0.03169422	0.530713	0.3460926	0.655231594
1437355_at	ZCCHC5	ZINC FINGER, CTCF DOMAIN CONTAINING 5	0.0317482	0.8283647	0.976292	1.240191722
1428800_at	Pc17	peacock/late synaptic protein homolog 5, cerevisiae-like	0.03174995	0.192816	0.581586	0.347699731
1431612_at	170000710RJK	RIKEN CDNA 170000710 GENE	0.03175339	0.0797516	0.6151124	0.832443341
1435100_at	AI3004220RJK	RIKEN CDNA AI3004220 GENE	0.03176565	0.4539628	0.90087265	1.982036653
1440106_at	CTCA	TRANSCRIPTION FACTOR 4	0.031770069	0.2063585	0.842418	0.671905963
1430401_at	6330406005RJK	RIKEN CDNA 6330406005 GENE	0.03184522	0.0501813	0.11909161	0.6151124
1427592_at	PCD17	PROTODCADHERIN 7	0.03188319	0.3144853	0.5544736	1.267100325
1431464_at	PRM2	PROPHOSPHATINOMYLASE 2	0.03190216	0.002170475	0.1366964	1.423132505
1454330_at	4933415D04RJK	RIKEN CDNA 4933415D04 GENE	0.03192455	0.06601808	0.6232366	1.193567759
1447364_at	Mylv1b	myosin IIb	0.03197283	0.000586316	0.0591986	0.492390687
1441994_at	PCDH16	PROTODCADHERIN BETA 16	0.03199798	0.1158481	0.8013172	1.611386461
1450172_at	PKNOX1	PREX-KNOTTED 1 (HOMEBOX)	0.03202865	0.6555105	0.0541128	0.835964402
1416823_at	OSBP1A	OXYSTEROL BINDING PROTEIN-LIKE 1A	0.03208172	0.0678401	0.3661162	0.61326891
1455800_at	RAPGEF5	RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 5	0.03211797	0.048317515	0.9504426	0.863493438
1439843_at	Gamb4	glycine calcium-dependent protein kinase 4	0.03214217	0.2952491	0.242146	0.711039859
1431511_at	A1747699	EXPRESSED SEQUENCE A1747699	0.03217191	0.8340157	0.3424783	0.606211505
1434909_at	Rngp	Ras-related GTP binding 9	0.0321773	0.2357366	0.2639043	1.261125287
1432595_at	DHHC10E	DNA SEGMENT, CHR 5, BUCAN 30 EXPRESSED	0.0322358	0.3141249	0.91617	0.855662431
1457876_at	DHHC10E	DNA SEGMENT, CHR 9, ERATO D01 496, EXPRESSED	0.03224007	0.1485661	0.392302	2.578991928
1458754_at	---	---	0.03224353	0.3148941	0.5260082	1.05029464
1425279_at	PHK1	PLD1M1 INTERACTING KINASE 1 LIKE	0.03225669	0.0848016	0.916587	1.116152828
1431869_at	5730419F03RJK	RIKEN CDNA 5730419F03 GENE	0.03226135	0.3019443	0.4382975	0.559725768
1420563_at	GRIA3	GLUTAMATE RECEPTOR, IONOTROPIC, AMPA3 (ALPHA 3)	0.03226265	0.0094477	0.5601857	1.158800743
1417483_at	NKXIFZ	NUCLEAR FACTOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS INHIBITOR, ZETA	0.03226283	0.3261289	0.4695274	0.695427675
1453573_at	HIST1H3D	HISTONE 2, H3C1	0.03230355	0.644705	0.910402	1.31318134
1427635_at	KIF3C	KINESIN FAMILY MEMBER 3C	0.03231055	0.5447145	0.3047797	1.296516796
1433010_at	737047817RJK	RIKEN CDNA 737047817 GENE	0.03234512	0.194186	0.3560396	0.407315166
1474683_x_at	METTL1	METHYLTRANSFERASE-LIKE 1	0.03237271	0.000766769	0.3377759	0.679897336
1439712_at	4921521J11RJK	RIKEN CDNA 4921521J11 GENE	0.03240486	0.7350109	0.2673396	1.432180853
1429305_at	ANKRD10	ANKRYN REPEAT DOMAIN 10	0.03241991	0.061695162	0.120128001	0.6151124
1424905_at	SLC19A11	SOLUTE CARRIER FAMILY 39 (METAL ION TRANSPORTER), MEMBER 11	0.03244235	0.5169909	0.211965	0.859248231
1440336_at	PRMT6	PROTEIN ARGININE N-METHYLTRANSFERASE 6	0.03246264	0.5787422	0.108171	1.304969098
1423853_at	6330427006RJK	RIKEN CDNA 6330427006 GENE	0.03248529	0.4252645	0.6727817471	0.727871471
1448955_at	CDYL	CHROMOSOMAL PROTEIN, Y CHROMOSOME-LIKE	0.0324944	0.5169909	0.121965	1.276155481
1431106_at	953005105RJK	RIKEN CDNA 953005105 GENE	0.03249585	0.0507061	0.0517186	1.36417512
1428342_at	Roes1	REST corepressor 1	0.03250442	0.0455413	0.6743517	0.73108061
1437074_at	SNXS	SORING NEXIN 5	0.03254664	0.0748691	0.3909595	0.77343093
1447244_at	DAK	DHAPYRUVATE KINASE 2 HOMOLOG (YEAST)	0.0325567	0.5574866	0.823766	0.398840269
1445240_at	AI1019796	EXPRESSED SEQUENCE AI1019796	0.03262634	0.3757335	0.1564708	0.64130629
1439499_at	AA415798	EXPRESSED SEQUENCE AA415798	0.0326288	0.8240465	0.431629	0.7424564
1458215_at	SETDB1	ERG-ASSOCIATED PROTEIN	0.03271348	0.6426604	0.8478235	0.64441105
1421224_at	4930506G17RJK	RIKEN CDNA 4930506G17 GENE	0.03272719	0.8427106	0.230363	0.880463476
1449913_at	CFB4	CYTOSOLIC PHOSPHORYLATION ELEMENT BINDING PROTEIN 4	0.03273377	0.0173657	0.431629	0.7424564
1419984_x_at	ZFP644	ZINC FINGER PROTEIN 644	0.0328203	0.003810318	0.7789127	0.848401686
1438750_at	ATRX	ALPHA THALASSEMIA/MENTAL RETARDATION SYNDROME X-LINKED HOMOLOG (HUMAN)	0.03281546	0.2032703	0.5199998	0.769881797
1438746_at	6330107D13RJK	RIKEN CDNA 6330107D13 GENE	0.03282873	0.5104839	0.8349802	0.81974264
1433994_at	9311606P16RJK	RIKEN CDNA 9311606P16 GENE	0.03284657	0.08158164	0.1205159	0.880604546
1429189_at	1110007C02RJK	RIKEN CDNA 1110007C02 GENE	0.0328816	0.6667218	0.2501563	0.826957
1467390_at	Zfp462	zinc finger protein 462	0.03289222	0.4742529	0.4742529	0.785243339
1424515_at	B230354K17RJK	RIKEN CDNA B230354K17 GENE	0.03292239	2.33565E-09	0.0759127	0.835781456
1442726_at	BC014685	CDNA SEQUENCE BC014685	0.03303992	0.5692221	0.0852454	1.15919742
1454136_at	PRUNE	PRUNE HOMOLOG (DROSOPHILA)	0.03306694	0.1776865	0.1801430	0.848140426
1446129_at	---	---	0.03309573	0.4928533	0.61090219	0.774535985
1435339_at	KCTD15	POTASSIUM CHANNEL TETRAMERISATION DOMAIN CONTAINING 15	0.03311747	0.1514147	0.3520005	1.143537359
1421159_at	CENL1	CENL1-LIKE 1	0.03314334	0.6481594	0.107801	0.807814502
1440602_at	GRIK2	GLUTAMATE RECEPTOR, IONOTROPIC, KAINATE 2 (BETA 2)	0.03315276	0.08469167	0.9439325	0.274650593
1442722_at	---	---	0.03316165	0.04535551	0.7301195	0.629393281
1435901_at	ALDOA-PS2	ALDOSE 1,4 ISOMERASE	0.03319721	0.09596367	0.378174197	0.82416184
1428200_x_at	N1AN1	N-TERMINAL ASN AMIDASE	0.03319882	0.9369554	0.922644	0.784110937
1443157_at	---	---	0.03320373	0.02292211	0.0519224	0.76298145
1441854_at	MFAP5	MICROFIBRILLAR ASSOCIATED PROTEIN 5	0.03321246	0.2265815	0.378174197	0.200198233
1444912_at	---	---	0.03323964	0.00668337	0.3306102	0.725942686
1445061_at	---	---	0.03335939	0.2702577	0.910411	0.61501258
1440951_at	NKXBL1					

142757_a	CDA	CYTIDINE DEAMINASE	0.03478602	6.22154E-06	0.308009	1.327959623
144796_a	C78676	EXPRESSED SEQUENCE: C78676	0.03479859	0.5005629	0.1750963	1.700227238
1441623_a	---	---	0.03479689	0.1272333	0.4170674	2.342947664
1436426_a	573059K17R1K	R1KEN CDNA 573059K17 GENE	0.03484504	0.00851909	0.2396349	0.811872278
1420519_a	HAS3	HYALURONAN SYNTHASE 3	0.03487623	0.0181691	0.0231897	1.960690165
1425456_a	BC003965	CDNA SEQUENCE BC003965	0.03490701	0.792418	0.881497	0.836661492
1452244_a	63306015R1K	R1KEN CDNA 63306015 GENE	0.03497887	0.3975873	0.7071891	0.627141481
1436615_a	OTC	ORNITHINE TRANS-CARBAMYLASE	0.03497959	0.3370314	0.5500729	0.483801707
1447281_a	---	---	0.03498865	0.1546845	0.0522284	0.52547544
1422277_a	GLRA1	GLYCINE RECEPTOR, ALPHA 1 SUBUNIT	0.0350244	0.0115665	0.7663103	0.698751056
1409548_a	Elnk2	elphn R2	0.03503687	0.00602742	0.8444251	1.260037629
1444084_a	PRKG4	PROLINE RICH GLA (G-CARBOXYGLUTAMIC ACID) 4 (TRANSMEMBRANE)	0.03504841	0.0581542	0.520314	1.544994771
1445424_a	ADRA1D	ADRENERGIC RECEPTOR, ALPHA 1D	0.03509085	0.05413668	0.960257	1.427562684
1447344_a	---	---	0.03511888	0.0373914	0.3979271	1.214344746
1427571_a	SHH	SONIC HEDGEHOG	0.03515337	0.0168973	0.1843139	0.622686826
1434156_a	RAB11FIP4	RAB11 FAMILY INTERACTING PROTEIN 4 (CLASS II)	0.03515737	0.999138	0.8588399	1.203682177
1442755_a	PANK2	PANTOTHENATE KINASE 2 (HALLERVORDEN-SPATZ SYNDROME)	0.035114545	0.7019035	0.3601418	1.523095438
1424703_a	HBMK1	HBMK METHYLTRANSFERASE FAMILY MEMBER 1	0.03515228	0.08952818	0.998676	1.207931355
1429845_a	1700019L03R1K	R1KEN CDNA 1700019L03 GENE	0.03517118	0.8051304	0.33817	1.586663206
1429113_a	ROR1	RECEPTOR TYROSINE KINASE-LIKE ORPHAN RECEPTOR 1	0.03517229	0.3376804	0.4175476	0.590700849
1422791_a	PAFAR1B2	PLATELET-ACTIVATING FACTOR ACETYLDIHYDROLASE, ISOFORM 1B, ALPHA2 SUBUNIT	0.03515333	0.006429635	0.66078099	1.292428836
1416111_a	CD83	CD83 ANTIGEN	0.03524127	0.6747701	0.5330676	0.715717038
1416173_a	PEST1	PISCADILLO HOMOLOG 1, CONTAINING BRCT DOMAIN (ZEBRAFISH)	0.0353552	0.7024998	0.5929732	0.844964181
1417164_a	DCSP10	DIAL SPECIFICITY PHOSPHATASE 10	0.03536202	0.0791714	0.09004224	0.84280562
1424880_a	TRH1	TRIBBLIS HOMOLOG 1 (DROSOPHILA)	0.03538977	0.8013604	0.0876436	1.93572517
1438265_a	WWC2	DNA SEGMENT, CHR 8, ERATO DOI 594, EXPRESSED	0.03540212	0.7024998	0.1895193	0.879002109
1429234_a	Sept11	0.03546521	0.9630766	0.3400181	1.1972124	0.8400118
1452280_a	FARP1	FERM-HOGEF (ARHGEF) AND PLECKSTRIN DOMAIN PROTEIN 1 (CHONDROCTE-DERIVED)	0.03552745	0.4076252	0.2399914	1.187066722
1419178_a	CD3G	CD3 ANTIGEN, GAMMA POLYPEPTIDE	0.03559366	0.8784198	0.792674	2.176575406
1433125_a	0.03560893	0.00916226	0.0916226	0.0916226	0.0916226	0.0916226
1458051_a	A23084021R1K	R1KEN CDNA A23084021 GENE	0.03561235	0.5886284	0.5556388	1.333665267
1441481_a	MFAP3L	MICROFIBRILLAR-ASSOCIATED PROTEIN 3-LIKE	0.03563561	0.6714651	0.466439	1.147076523
1439544_a	RPS6KA4	RIBOSOMAL PROTEIN S6 KINASE, POLYPEPTIDE 4	0.03564483	0.3174195	0.6218622	1.915407234
1420307_a	PITPNB	PHOSPHATIDYLINOSITOL TRANSFER, BETA	0.03567077	0.04512988	0.490272	1.108568881
1437124_a	A630552C17R1K	R1KEN CDNA A630552C17 GENE	0.03567287	0.7835696	0.500554	0.731295478
1420785_a	GAB2	GROWTH FACTOR RECEPTOR BOUND PROTEIN 2-ASSOCIATED PROTEIN 2	0.03567978	0.03110082	0.06144965	1.13626416
1429200_a	SAAL1	SERUM AMYLASE A-LIKE 1	0.03570179	0.0137923	0.1856729	1.15731451
1424056_a	Zfp608	Zinc finger protein 608	0.03572325	0.02006874	0.8856588	1.265459881
1430905_a	1110012016R1K	R1KEN CDNA 1110012016 GENE	0.03573083	0.8644991	0.111376	1.560767839
1430013_a	TFP	TYROSINE PHOSPHATASE FACTOR	0.03579254	0.0567297	0.6979123	0.869721523
1424138_a	RHBD1F	RHOMBOD FAMILY 1 (DROSOPHILA)	0.03580473	0.0858831	0.3073806	1.130289113
1454229_a	493342409R1K	R1KEN CDNA 493342409 GENE	0.03584223	0.009100787	0.1932982	0.816027124
1421115_a	TLTB1	TLTB-LIKE TYROSINE KINASE 3 LIGAND	0.03587821	0.4549742	0.481396	1.319164586
1447222_a	Hsp12a	heat shock protein 12A	0.03595962	0.0764281	0.566456	1.281660602
1422673_a	PRKCM	PROTEIN KINASE C, MU	0.03602628	0.4704506	0.6252391	0.7547007
1455756_a	730040105R1K	R1KEN CDNA 730040105 GENE	0.03602223	0.05959373	0.11718034	1.11718034
1427782_a	Chrl1	corticotropin releasing hormone receptor 1	0.03603002	0.763944	0.6988662	1.29599052
1429150_a	1700072M12R1K	R1KEN CDNA 1700072M12 GENE	0.03610848	0.9665933	0.6728316	0.45589803
1455262_a	TRSD4	TIROMOSPONDIN, TYPE 1, DOMAIN CONTAINING 4	0.03610791	0.6239469	0.6239469	0.84574421
1425822_a	Rzb1	ras responsive element binding protein 1	0.0362479	0.7603489	0.9385186	0.715456085
1458052_a	---	---	0.03626233	0.4174777	0.7564731	1.581509096
1438338_a	PP2R1B	PROTEIN PHOSPHATASE 2 (FORMERLY 2A), REGULATORY SUBUNIT A (PP 65), BETA ISOFORM	0.03634942	0.299423	0.6239469	0.84574421
1459544_a	---	---	0.03636331	0.678966	0.6784757	1.408818325
1434766_a	PRKAA2	PROTEIN KINASE, AMP-ACTIVATED, ALPHA 2 CATALYTIC SUBUNIT	0.03637836	0.4511977	0.07732672	1.09147061
1453019_a	2310046A06R1K	R1KEN CDNA 2310046A06 GENE	0.03637836	0.4511977	0.07732672	1.09147061
1420666_a	Dcs2b	double C2, beta	0.03642034	0.8584059	0.4609319	0.76038315
1416118_a	H1FOO	H1 HISTONE FAMILY MEMBER 0, OOCYTE-SPECIFIC	0.03643236	0.0784445	0.0880129	0.386056076
1428432_a	2310047A01R1K	R1KEN CDNA 2310047A01 GENE	0.03642416	0.2985287	1.147426107	0.6239469
1424494_a	231014712R1K	R1KEN CDNA 231014712 GENE	0.03644929	0.03903093	0.288433	1.13661596
1450157_a	11MMR	HYALURONAN-MEDIATED MOTILITY RECEPTOR (RHAMM)	0.03646173	0.7022962	0.5970584	0.443347171
1441226_a	Spn1	spn1, (f-spondin) extracellular matrix protein	0.03646614	0.9548653	0.280277	0.79839379
1442071_a	ARCF1	ATP-BINDING CASSETTE, SUB-FAMILY F (OABP), MEMBER 1	0.03646614	0.4797357	0.097106	0.857173212
144821_a	HLRAPP1	INTERLEUKIN 1 RECEPTOR ACCESSORY PROTEIN-LIKE 1	0.03646614	0.9786167	0.7525178	0.391979987
1442923_a	PIK6	PI3K PROTEIN TYROSINE KINASE 6	0.03671299	0.836641	0.6019147	0.2925253
1422643_a	MOND1	MONOPYRROXYGENASE, DIBI-LIKE 1	0.03672313	0.6515107	0.789090002	0.897860002
1460302_a	THBS1	TIROMOSPONDIN	0.03674687	0.4013688	0.4642201	1.901402656
1429666_a	KCTD16	POTASSIUM CHANNEL TETRAMERISATION DOMAIN CONTAINING 16	0.03674742	0.1207784	0.1430754	1.116256474
1439985_a	---	---	0.03675854	0.883746	0.66071072	0.856971072
1460197_a	STEAP1	STEAP FAMILY MEMBER 4	0.03677358	0.06498151	0.27279151	1.753676511
1421941_a	Camk4	calcium/calmodulin-dependent protein kinase IV	0.03677744	0.2216339	0.9284385	1.267500203
1417172_a	CYP4B16	CYTOCHROME P450, FAMILY 4, SUBFAMILY F, POLYPEPTIDE 16	0.03677744	0.5547429	0.9284385	1.31964586
1422894_a	SMBT1	SCM-LIKE WITH FOUR MBT DOMAINS 1	0.03683474	0.5370218	0.3645338	1.22904488
1428721_a	Podag3	Prostaglandin gamma subfamily 3	0.03685041	0.9799793	0.9199757	1.397670722
1422400_a	SEMA7A	SEMAPHORIN 7A, IMMUNOGLOBULIN DOMAIN (IG), AND GPI MEMBRANE ANCHOR, (SEMAPHORIN) 7A	0.03685238	0.03789665	0.8073965	1.185421562
1428914_a	2310014D11R1K	R1KEN CDNA 2310014D11 GENE	0.03685238	0.2878318	0.3379987	0.820183512
1434594_a	ABD0406	EXPRESSED SEQUENCE ABD0406	0.03691911	0.1422711	0.8274741	1.65330385
1425562_a	TRN1	TRNA-NUCLEOTIDYL TRANSFERASE, CCA-ADDING, 1	0.03694246	0.1471864	0.808259787	0.808259787
1446598_a	PRKCA	PROTEIN KINASE C, ALPHA	0.03702378	0.6925257	0.16889369	1.223595619
1422826_a	IGFALS1	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN, ACID LABILE SUBUNIT	0.03703573	0.2188323	0.9495626	1.85779073
1454119_a	0.03704614	0.3820263	0.03704614	0.3820263	0.748198267	1.147584265
1444268_a	BC004004	CDNA SEQUENCE BC004004	0.03706061	0.00974454	0.2425042	1.136044169
1430280_a	1810062017R1K	R1KEN CDNA 1810062017 GENE	0.03709001	0.4466881	0.02523612	1.709871694
1445131_a	C9ORF9	CHROMOSOME 9 OPEN READING FRAME (ORF) 9	0.0371088	0.5651119	0.5651119	0.5651119
1436366_a	PPP1R15B	EXPRESSED SEQUENCE A066441	0.03711112	0.70897466	0.1900014	1.151872829
1419985_a	CDC39	COILED-COIL DOMAIN CONTAINING 69	0.03713158	0.4522742	0.7518328	0.59642924
1431860_a	ZFP179	ZINC FINGER PROTEIN 179	0.03714497	0.01494007	0.911137	0.812957323
1434177_a	CCU1	CYCLOPHILIN CONVERTING ENZYME 1	0.03715499	0.000115403	0.03646625	1.02666625
1440781_a	BS30007D8R1K	R1KEN CDNA BS30007D8 GENE	0.03717799	0.0580138	0.4489302	0.634566506
1434776_a	RRM2B	RIBONUCLEOTIDE REDUCTASE M2 B (TP53 INDUCIBLE)	0.03718333	0.816184	0.271641	0.777109586
1429198_a	1810009007R1K	R1KEN CDNA 1810009007 GENE	0.03719643	0.3801397	0.5513009	0.897860183
1421516_a	NRA1A	NUCLEAR RECEPTOR SUBFAMILY A, GROUP A, MEMBER 1	0.0372129	0.5471959	0.1504084	0.780758105
1441272_a	MATR3	MATRIX 3	0.03730303	0.2373005	0.3588338	0.864510811
1426235_a	473247D19R1K	R1KEN CDNA 473247D19 GENE	0.03731361	0.4974062	0.727418875	0.860711072
1425788_a	ECHDC2	ENOYL COENZYME A HYDRATASE DOMAIN CONTAINING 2	0.03736113	0.0504055	0.2722415	0.786317941
1424455_a	C79845	EXPRESSED SEQUENCE C79845	0.03740399	0.4032599	0.8347304	1.61694247
1428311_a	ZFP15	ZINC FINGER PROTEIN 15	0.03740962	0.7634538	0.54277196	0.845277594
1439713_a	WNT5B	WINGLESS-RELATED MMTV INTEGRATION SITE 5B	0.03747366	0.05166941	0.6470712	1.338324134
1420585_a	NNT2	NUCLEAR RNA EXPORT FACTOR 2	0.03754243	0.1789662	0.7084729	0.682293006
1427242_a	DDNA4	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 4	0.03754455	0.01610979	0.2324368	0.818911522
1446560_a	Pso23	protease, serine, 23	0.03759883	0.5534879	0.82816	1.41914799
1425198_a	FBXJ10	F-BOX AND LEUCINE-RICH REPEAT FAMILY 10	0.03794686	0.2330091	0.6470039	0.863739109
1454421_a	0.03804232R1K	R1KEN CDNA 03804232 GENE	0.03796042	0.3758068	0.185014677	1.850146777
1417289_a	Pknox2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	0.03798002	1.42174E-07	0.2870586	0.851321598
1440360_a	ARL4P5	ADP-RIBOSYLATION FACTOR-LIKE 5 INTERACTING PROTEIN 5	0.03798249	0.4726207	0.5155841	0.810384445
1421817_a	CSR1	CYCLOPHILIN REDUCTASE 1	0.03797289	0.3314454	0.6181377	1.142396066
1434948_a	TTCC9	TETRAHYDROPTERIDE REPEAT DOMAIN 9	0.03797607	0.2251336	0.2689143	1.093151992
1459484_a	Tmem2	Transmembrane protein 2	0.03777495	0.01668189	0.1123311	0.575460268
1420625_a	2310016F19R1K	R1KEN CDNA 2310016F19 GENE	0.03797138	0.1953572	0.0550196	1.123114233

1421034_u_at	HLRA	INTERLEUKIN 4 RECEPTOR, ALPHA	0.03931418	0.1788588	0.07024461	1.516127539
1419968_u_at	SGCB	SARCOGLYCAN, BETA-DYSTRORPHIN-ASSOCIATED GLYCOPROTEIN	0.03933531	0.4466463	0.3949115	0.855701587
1423798_u_at	SHK1	SH3-BINDING KINASE 1	0.03935352	0.114866	0.08920523	1.454840051
1424037_u_at	ITPKA	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE A	0.03933578	0.1924209	0.9349646	1.2366436
1454043_u_at	MAP2K3	MITOGEN ACTIVATED PROTEIN KINASE 3	0.03936924	0.6468772	0.50154	1.732524766
1451714_u_at	MAP2K3	MITOGEN ACTIVATED PROTEIN KINASE 3	0.03941519	0.3251309	0.217997	0.891258977
1434567_u_at	4732396080R1K	RIKEN CDNA 473239608 GENE	0.03949924	0.0796028	0.08136688	1.174073485
1417489_u_at	NPY2R	NEUROPEPTIDE Y RECEPTOR Y2	0.03951948	0.7731262	0.648164398	0.823291348
1460574_u_at	FAT4	HYPOTHETICAL PROTEIN 9430004M15	0.03952528	0.00245924	0.7554875	0.751255622
1447906_u_at	---	---	0.0395263	0.194397	0.1423083	0.734272357
1420462_u_at	HLR1AP2L	INTERLEUKIN 1 RECEPTOR ACCESSORY PROTEIN-LIKE 2	0.0395757	0.1012278	0.2740104	0.580106922
1441455_u_at	Appp19	CAMP-regulated phosphoprotein 19	0.0395827	0.1191993	0.64816	1.652390838
1448432_u_at	Picd1	phospholipase C, delta 1	0.0395263	0.2054446	0.5208841	1.359138575
1448751_u_at	Apo2l2	adipose-related protein complex 3, mr. 2 subunit	0.03966998	0.0462166	0.475463	1.10401497
1429794_u_at	PRK11	PROTEIN KINASE RECEPTOR, PXX, LIGAND-GATED ION CHANNEL, 1	0.0396715	0.1781295	0.31097	0.472264397
1433992_u_at	APXL	APICAL PROTEIN, XENOPUS LAEVIS-LIKE	0.03969003	0.1946388	0.5230953	0.726757697
1417324_u_at	MAST2	MICROTUBULE ASSOCIATED SERINE/THREONINE KINASE 2	0.0397151	0.2968487	0.8987348	1.13701176
1424498_u_at	573099420R1K	RIKEN CDNA 463340233 GENE	0.03974602	0.106677	0.992489	0.698014684
1447894_u_at	VPS52	SAC2 (SUPPRESSOR OF ACTIN MUTATIONS 2, HOMOLOG)-LIKE B, CEREVISIAE	0.03981602	0.4731191	0.7424967	0.785808604
1419507_u_at	KRTAP15	KERATIN ASSOCIATED PROTEIN 15	0.03982942	0.04634807	0.05978838	0.488613138
1423644_u_at	AC01	AC01	0.03984307	0.0318159	0.0518223	0.83131189
1452342_u_at	APBB2	AMYLOID BETA (A4) PRECURSOR PROTEIN-BINDING, FAMILY B, MEMBER 2	0.03984751	0.2654754	0.1613914	1.126597448
1437716_u_at	Klf22	EXPRESSED SEQUENCE AL033113	0.03988169	0.1096493	0.4024961	1.153642121
1458117_u_at	GABR11	GTPASE ACTIVATING RANGAP-DOMAIN-LIKE 1	0.03988635	0.8037641	0.146862	0.855721227
1452199_u_at	2700094910R1K	RIKEN CDNA 2700094101 GENE	0.03988458	0.0176538	0.2671309	0.819719151
1435727_u_at	D15KRTD366E	DNA SEGMENT, CHR 15, ERATO DOI 366, EXPRESSED	0.03991537	0.8888887	0.7920333	0.779962626
1424525_u_at	493042021R1K	RIKEN CDNA 493042021 GENE	0.03996978	0.1991666	0.1599131	1.430238734
1447690_u_at	LSR	LIPOLYSIS STIMULATED LIPOPROTEIN RECEPTOR	0.03996314	0.1701339	0.3768962	3.516295004
142130_u_at	Tc14	tetraoctapeptide repeat domain 14	0.03997319	0.0965609	0.728671	0.821383199
1446623_u_at	---	---	0.03999678	0.1991666	0.1599131	1.430238734
1459931_u_at	2810021G02R1K	RIKEN CDNA 2810021G02 GENE	0.04001911	0.0421297	0.7286052	1.191852111
1445840_u_at	---	---	0.04006027	0.6327497	0.46489	1.959428735
1432544_u_at	ZADH1	ZINC BINDING ALCOHOL DEHYDROGENASE, DOMAIN CONTAINING 1	0.04011303	0.0884987	0.31097	0.472264397
1438982_u_at	2810417J12R1K	RIKEN CDNA 2810417J12 GENE	0.04014717	0.02568177	0.1671187	1.231676117
1429741_u_at	Kcav1	potassium channel, subfamily V, member 1	0.04015715	0.4183579	0.8531571	1.216059089
1419097_u_at	STOM	STOMATIN	0.04015716	0.07114883	0.6884252	0.869459492
1452418_u_at	220010424R1K	RIKEN CDNA 1200014624 GENE	0.04016549	0.04754565	0.491458	1.212918108
1432062_u_at	MDGA1	MAM DOMAIN CONTAINING GLYCOSYLPHOSPHATIDYLINOSITOL ANCHOR 1	0.04016099	0.4616441	0.8121055	0.606368422
1426015_u_at	Aph	aspartate-beta-dehydrogenase	0.04019006	0.08801171	0.3184489	0.828080232
1442166_u_at	CPIP5	CPIP5	0.040204	0.0380763	0.1982189	0.828080232
1437793_u_at	TNKS2	TANKYRASE, TRF1-INTERACTING ANKYRIN-RELATED ADP-RIBOSE POLYMERASE 2	0.04025739	0.1388997	0.6028426	0.889233955
1428952_u_at	PDA2	PROTEIN DISULFIDE ISOMERASE ASSOCIATED 2	0.04026229	0.1635141	0.1627749	1.380799739
1421382_u_at	PRK4	PROLACTIN RECEPTOR RELATED 5	0.04024807	0.5915604	0.1614141	1.911971617
1448923_u_at	PRKRA	PROTEIN KINASE, INTERFERON INDUCIBLE DOUBLE STRANDED RNA DEPENDENT ACTIVATOR	0.04028854	0.1230992	0.400271	0.76732408
1435980_u_at	WNT6	WINGLESS-RELATED MMTV INTEGRATION SITE 6	0.04031214	0.4660805	0.9399472	0.615937145
1456137_u_at	Nesn3	neurosin III	0.04033886	0.06790557	0.1253784	1.253784021
1431040_u_at	LOC638977	RIKEN CDNA 4930578F06 GENE	0.04036721	0.2784062	0.1471355	1.479056006
1450438_u_at	Ncam1	neural cell adhesion molecule 1	0.04039822	0.0995198	0.3040202	1.830343034
1429279_u_at	WRAS2	WRONTOXYANIN, TRICARBYNYLTHIASE 2 (MITOCHONDRIAL)	0.04041123	0.5340465	0.863626799	0.73066195
1454960_u_at	Smao3	MAD homolog 3 (Drosophila)	0.04041919	0.2898554	0.2369999	1.10400382
1423705_u_at	5330428N10R1K	RIKEN CDNA 5330428N10 GENE	0.04041486	0.03809396	0.1810214	1.142922803
1425267_u_at	GCAP3	GRANULE CELL ANTISENSE POSITIVE 8	0.04044179	0.5644831	0.408518086	0.815212354
1454913_u_at	993104106R1K	RIKEN CDNA 993104106 GENE	0.04050819	0.1154806	0.8313809	0.751606015
1457936_u_at	MAPK8	MITOGEN ACTIVATED PROTEIN KINASE 8	0.04054466	0.0430399	0.1616713	1.048749466
1442377_u_at	---	---	0.04057586	0.94316	0.05910881	0.732223654
1446389_u_at	NR1P1	NUCLEAR RECEPTOR INTERACTING PROTEIN 1	0.04057891	0.5232321	0.501798	2.054636526
1458529_u_at	LOC1215714	HYPOTHETICAL PROTEIN A93001009	0.04059732	0.451908	0.1731718	0.622876098
1460527_u_at	933040709R1K	RIKEN CDNA 933040709 GENE	0.04059859	0.06312508	0.99529153	1.524127353
1425646_u_at	BC016495	CDNA SEQUENCE BC016495	0.04064683	0.205058	0.3137412	0.712166534
1425994_u_at	ASAH2	N-ACYL SPHINGOSINE AMIDOHYDROLASE	0.0406955	0.0821988	0.2652325	1.32777286
1450716_u_at	ADAMTS15	A DISINTTEGRIN-LIKE AND METALLOPEPTIDASE (REPROLYSIN TYPE) WITH THROMBOSPONDIN TYPE 1 MOTIF, 1	0.04080299	0.6004644	0.7021431	0.782196531
1434096_u_at	Srsf4	serine-arginine family 4 (non-exchange), member 4	0.0408544	0.7237648	0.904378	0.921184106
1454462_u_at	Adcy2	adenylyl cyclase 2	0.04086269	0.0314885	0.2318252	1.098585642
1437702_u_at	TGM6	TRANSGLUTAMINASE 6	0.04101383	0.8880442	0.0641721	0.675515231
1434966_u_at	SPK3	SPINNING FACTOR, ARGININE/SERINE, MEMBER 3	0.04102276	0.06101382	0.040478	1.043731878
1456809_u_at	---	---	0.04102776	0.0821696	0.8834819	0.753301967
1423968_u_at	UGT3A2	EXPRESSED SEQUENCE A311915	0.04101782	0.851254	0.111538	0.851166759
1455739_u_at	643070406	HYPOTHETICAL PROTEIN 643070406	0.04105071	0.0389716	0.425024	0.921448496
1445029_u_at	A330019N05	RIKEN CDNA A330019N05 GENE	0.0411433	0.2619883	0.9801267	0.745891338
1441184_u_at	TRPC4AP	TRANSIENT RECEPTOR POTENTIAL, CATION CHANNEL, SUBFAMILY C, MEMBER 4 ASSOCIATED PROTEIN	0.04114258	0.7423148	0.9987994	0.446694078
1456126_u_at	IRAK1	INTERLEUKIN 1 RECEPTOR ADAPTIN 1	0.0411667	0.4508757	0.258126	0.82124556
1448400_u_at	SMAL	SWI5NF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY D, MEMBER 2	0.04117877	0.722602	0.8008907	0.748543363
1441654_u_at	GNAL2	GUANINE NUCLEOTIDE BINDING PROTEIN, ALPHA 2	0.04123801	0.0581567	0.0584237	1.248637523
1427522_u_at	ARIHAP20	ARIHAP20	0.04128877	0.04164296	0.1876341	1.09763506
1444704_u_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone A730905.12 product unclassified, full insert sequence	0.04133876	0.0268393	0.4556495	1.297322969
1433071_u_at	6430605C03R1K	RIKEN CDNA 6430605C03 GENE	0.04136794	0.1029711	0.65154	0.471758031
1448050_u_at	MAPK14	mitogen-activated protein kinase kinase kinase kinase 14	0.04139973	0.2139237	0.1461615	1.253292968
1451723_u_at	A530898.17	HYPOTHETICAL PROTEIN A530898.17	0.04139959	0.1489666	0.3495254	0.616080926
1450096_u_at	GNAL12	GUANINE NUCLEOTIDE BINDING PROTEIN, ALPHA 12	0.04144853	0.2423687	0.09866665	0.780896464
1438375_u_at	Fhlb2	Fhlb2	0.04145537	0.1762177	0.07286543	1.770728068
1427950_u_at	ZFP294	ZINC FINGER PROTEIN 294	0.04147355	0.01009917	0.5858136	1.084012291
1421268_u_at	UGCG	UDP-GLUCOSE CERAMIDE GLUCOSYLTRANSFERASE	0.0415474	1.604546-06	0.1019116	1.020211639
1438018_u_at	Hsok1	hook homolog 1 (Drosophila)	0.04155642	0.0953124	0.818151827	0.818151827
1454501_u_at	6130419D04R1K	RIKEN CDNA 6130419D04 GENE	0.04160884	0.0864558	0.3764444	0.770386801
1451727_u_at	UZAF1-RS2	UZ SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR (UZAF1), RELATED SEQUENCE 2	0.04163797	0.00072388	0.6483704	0.909664489
1433590_u_at	HERC3	HECT DOMAIN AND RLD 3	0.04166161	0.000199118	0.156692	0.792673909
1446121_u_at	B2302080R1K	RIKEN CDNA B2302080R8 GENE	0.04167661	0.0495817	0.142999172	0.820999172
1425896_u_at	FBN1	FIBRILLIN 1	0.04171001	0.6627323	0.7223801	0.699771894
1444498_u_at	C7862	EST C7862	0.04171729	0.2977369	0.1682583	2.361266577
1437433_u_at	IRGLAL2	IRGAP1L-BETA1,CGNAC BETA 1,3-GALACTOSYLTRANSFERASE, POLYPEPTIDE 2	0.04171847	0.0120931	0.5391291	0.917312719
1448551_u_at	TRIM2	TRIPARTITE MOTIF PROTEIN 2	0.04174904	2.00516E-11	0.4322264	0.867132157
1454355_u_at	1810021M19R1K	RIKEN CDNA 1810021M19 GENE	0.04174979	0.6289159	0.2434267	1.17601755
1431170_u_at	EPHA3	EPHRIAN A3	0.04175997	0.1981382	0.8571144	0.910798355
1446503_u_at	---	---	0.04181307	0.9471918	0.276065	1.682335674
1455303_u_at	REXAP	REGULATORY FACTOR-ASSOCIATED PROTEIN	0.04181397	0.068821534	0.3389789	0.822039135
1441168_u_at	NYX	NYCTALOPIN	0.04182056	0.7737319	0.6212859	0.681586621
1446344_u_at	NYX	NYCTALOPIN	0.0418372	0.02239268	0.88287422	1.6444147
1439628_u_at	Rab38	Rab38, member of RAS oncogene family	0.04191669	0.000288176	0.95154	1.275517127
1423062_u_at	GRBPL1	GRANULE CELL GROWTH FACTOR-BINDING PROTEIN 3	0.04199732	0.619749	0.261052224	0.827424449
1420701_u_at	KLK1B1	KALLIKREIN 1-RELATED PEPTIDASE B1	0.04204837	0.6353504	0.9293355	0.5300998
1441859_u_at	---	---	0.04209292	0.2575559	0.5232095	1.70881837
1430859_u_at	533042701R1K	RIKEN CDNA 533042701 GENE	0.04209391	0.4549421	1.383484433	0.81834433
1441866_u_at	SRS10	SPLICING FACTOR, ARGININE/SERINE-RICH 10 (TRANSFEROR 2 HOMOLOG, DROSOPHILA)	0.04207264	0.2647683	0.7095547	0.769696745
1440918_u_at	RASGRF2	RAS PROTEIN-SPECIFIC GUANINE NUCLEOTIDE-RELEASING FACTOR 2	0.04212968	0.0443666	0.4667566	0.838757293
1423796_u_at	PAIP1	RIKEN CDNA 9330221R1 GENE	0.04219889	0.6353202	0.580878125	0.79313205
1456852_u_at	PAIP1	POLYADENYLATE BINDING PROTEIN-INTERACTING PROTEIN 1	0.04221872	0.1994976	0.0842033	1.152359626
1457003_u_at	AW490526	EXPRESSED SEQUENCE AW490526	0.04222431	0.1263791	0.662518	

1453340_at	1700571003RIK	RIKEN CDNA 1700571003 GENE	0.00394149	0.3812653	0.2058984	0.414545505
1453533_at	A93025200RIK	RIKEN CDNA A93025200 GENE	0.04396134	0.5252156	0.4906474	0.84043505
1454696_x_at	CEACAM11	CEA-RELATED CELL ADHESION MOLECULE 11	0.04400186	0.4751955	0.33598	0.640467444
1454908_at	PAM	PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE	0.04402677	0.40497639	0.236254	1.139251614
1457375_at	Ssoad22	small nuclear RNA, C/D box 22	0.04404044	0.05633047	0.1061879	0.6426963827
1421718_at	STRM	STRIMIN	0.04404096	0.1360005	0.1360005	1.906304955
1458448_at	AA-08296	EXPRESSED SEQUENCE AA08296	0.04406097	0.0361782	0.2708608	1.611197213
1453400_at	KIA04015	KIA04015 PROTEIN	0.04406097	0.5583838	0.7208608	0.5758398
1416732_at	Top2b	topoisomerase (DNA) II beta	0.04412542	0.00034491	0.00034491	1.131136879
1424754_at	MSA47	MEMBRANE-SPANNING 4-DOMAINS, SUBFAMILY A, MEMBER 7	0.04417628	0.1041287	0.1041287	1.459673852
1424704_at	2110076703RIK	RIKEN CDNA 2110076703 GENE	0.04417796	0.9592994	0.5471479	1.196216333
1444021_at	D1SERTD466E	DNA SEGMENT, CHR 15, ERATO D01 466, EXPRESSED	0.04418241	0.6215904	0.6466675	2.225239777
1422065_at	KLR18D	KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY B MEMBER 18D	0.04420118	0.4678845	0.8043314	0.413676028
1429075_x_at	1700018908RIK	RIKEN CDNA 1700018908 GENE	0.04420128	0.0952888	0.09999106	1.465612447
1454943_at	FXR1P	FXR INTERACTING (WITH TRANSCRIPTION-ACTIVATION DOMAIN) PROTEIN 1	0.04420184	0.7668292	0.2096772	0.828431917
1442340_at	CYR61	CYSTEINE RICH PROTEIN 61	0.04420472	0.5025667	0.0661427	1.593166018
1420403_at	Alp2c2	Alpase, Ca++ transporting, plasma membrane 2	0.04411103	0.000151675	0.4040829	1.159692132
1425256_at	LDR2	LEUCINE-DEPENDENT RECEPTOR 2	0.04434045	0.16627379	0.16627379	1.901229647
1443623_x_at	6430571L13RIK	RIKEN CDNA 6430571L13 GENE	0.04437651	0.4886309	0.3727287	0.461175455
1425718_at	EDDI	EE UBIQUITIN-PROTEIN LIGASE, HECT DOMAIN CONTAINING, 1	0.04440343	0.3397605	0.8536469	0.878616227
1442373_at	EPH3	EPH RECEPTOR A3	0.04441256	0.1228804	0.3714249	0.818481236
1447861_x_at	Mgl1	Myoid oncotic viral integration site-related gene 1	0.04442718	0.04716395	0.9700014	0.742936229
1449789_x_at	L1Y664C	L1Y664C	0.04443495	0.0463636	0.3051579	1.607712353
1434626_at	RPS3D3	RNA POLYMERASE II POLYMERASE SUBUNIT 3	0.04449289	0.7156474	0.8161527	0.844666275
1445483_at	ABL2	V-ABL ONCOGENE, MURINE LEUKEMIA VIRAL ONCOGENE 2 (ARG, ABL2-RELATED GENE)	0.04459949	0.00334498	0.8121848	1.618969934
1445259_at	DM2DH	DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR	0.04460209	0.1223559	0.8094244	0.850708223
1452527_at	AGR2	ANTERIOR GRADIENT 2 (XENOPUS LAEVIS)	0.04461161	0.1902015	0.0599241	0.620379047
1455802_x_at	Gls	Glutaminase	0.04464285	0.58378909	0.28307149	1.862353568
1453708_at	Gls	Glutaminase	0.04472765	0.2746796	0.1833876	1.386378376
1454073_at	MET3	METADIN 3	0.04475449	0.7683758	0.4723861	0.821338229
1416929_at	RBM12	RNA BINDING MOTIF PROTEIN 12	0.04479263	0.1158889	0.8761251	0.793861387
1433331_at	C030404M01RIK	RIKEN CDNA C030404M01 GENE	0.0448101	0.408859	0.4636006	0.509826136
1418946_at	STGAL1	STB BETA-GALACTOSIDASE ALPHA-2,3-SIALYLTRANSFERASE 1	0.04485729	0.6368476	0.0812922	1.221516983
1456786_at	LDR2	LIM domain binding 2	0.04488264	0.2065505	0.3486254	1.389486674
1438144_x_at	ATXN2	ATAXIN 2	0.04488327	0.00265765	0.7850621	1.32641385
1443799_at	PPP1R14C	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14C	0.04491491	0.06017621	0.3315476	0.762256074
1443402_at	SAMD8	STERILE ALPHA MOTIF DOMAIN CONTAINING 8	0.04497363	0.8634647	0.1544643	0.9789066272
1417994_x_at	ACCN1	AMILORIDE-SENSITIVE CATION CHANNEL 1, NEURONAL (DEGENERIN)	0.04501307	0.7698365	0.1251123	0.897859495
1447163_x_at	---	---	0.04502622	0.8648927	0.1533985	0.97914894
1435338_at	0610030E20RIK	RIKEN CDNA 0610030E20 GENE	0.04512489	0.04349704	0.8488425	1.1874809525
1419389_at	Pde10a	phosphodiesterase 10A	0.04518683	0.1758866	0.944667	0.830742622
1444923_at	---	---	0.04521419	0.4820385	0.9738973	0.801185762
1419629_at	Ehnl2	ehpelin B2	0.04527272	0.5883859	0.52421	1.244851349
1426777_x_at	WASL	WISKOTT-ALDRICH SYNDROME-LIKE (HUMAN)	0.04527822	0.1541494	0.5351303	1.199846242
1449254_at	Ecd	ectodysplasin-A	0.04527922	0.2739541	0.902095	0.610287488
1434847_at	CNNM4	CNNM4	0.04531581	0.50035499	0.0969236	0.701229648
1433342_at	5730416F02RIK	RIKEN CDNA 5730416F02 GENE	0.04539249	0.7839371	0.8433734	0.436916786
1443434_at	4932490922RIK	RIKEN CDNA 4932490922 GENE	0.04540766	0.00315226	0.8528676	0.83661357
1449248_at	CLC2	CHLORIDE CHANNEL 2	0.04548468	0.00345307	0.11783036	1.178303628
1452329_at	ADAMTS1	A DISINTEGRIN-LIKE AND METALLOPEPTIDASE (REPROLYSIN TYPE) WITH THROMBOSPONDIN TYPE 1 MOTIF, 7	0.04552291	0.4891138	0.2196926	2.459253156
1451031_at	SFRP4	SECRETED FRIZZLED-RELATED SEQUENCE PROTEIN 4	0.0456234	0.000376555	0.969929	1.31423157
1419332_at	GFY16	GDF-LIKE DOMAIN, MULTIPLE 4	0.04564977	0.0177253	0.6706624	0.782462409
1449541_x_at	170001014RIK	RIKEN CDNA 170001014 GENE	0.04568579	0.7322593	0.6470998	0.557580341
1453512_at	5830407P18RIK	RIKEN CDNA 5830407P18 GENE	0.04570401	0.00126377	0.9441456	1.14675939
1441034_at	---	---	0.04576268	0.6848879	0.0647996	0.655514628
1443033_at	RBM14	RNA BINDING MOTIF PROTEIN 14	0.04578468	0.1172059	0.26988609	0.689114571
1447371_at	LOC236469	SIMILAR TO BLOODHIRSTY	0.04581455	0.00211438	0.937717	1.69501647
1429053_at	1110012H17RIK	RIKEN CDNA 1110012H17 GENE	0.04588337	0.04073824	0.144909819	0.81829199
1428617_at	Hic2c	hist cell factor 2	0.04600307	0.0147336	0.6578053	0.81269129
1422634_at	V502	V-SET AND IMMUNOGLOBULIN DOMAIN CONTAINING 2	0.04601234	0.5800509	0.6840057	2.486208887
1453708_x_at	GS102	GLUTATHIONE S-TRANSFERASE OMIKGA 2	0.04603536	0.8909247	0.1453888	0.661265066
1416613_at	CYP11B1	CYP11B1 (CYTOCHROME P450, FAMILY 1, SUBFAMILY B, POLYPEPTIDE 1)	0.04608691	0.4636559	0.52421	0.720494486
1429354_at	THEM5	THIOESTERASE SUPERFAMILY MEMBER 5	0.0461031	0.4232935	0.4017412	0.584415329
1433101_at	9030419P21RIK	RIKEN CDNA 9030419P21 GENE	0.0461043	0.7815699	0.6057721	0.832756375
1436813_at	KHSRP	KATY TYPE SPLICING REGULATORY PROTEIN	0.04611411	0.0159247	0.720494486	0.720494486
1443881_x_at	KCTD12	EXPRESSED SEQUENCE AW38430	0.04611849	0.2948588	0.602957	0.73380117
1454358_at	2900060N12RIK	RIKEN CDNA 2900060N12 GENE	0.04625799	0.8461043	0.6296492	1.69877042
1446719_at	---	---	0.04630782	0.739934	0.4206645	0.742526265
1455712_at	HIST3H2A	RIKEN CDNA 4930534G0 GENE	0.04631364	0.3376052	0.4206645	0.760406228
1429987_at	9930013L23RIK	RIKEN CDNA 9930013L23RIK GENE	0.04636711	0.4660845	0.6262656	0.851111349
1451238_at	1810049G20RIK	RIKEN CDNA 1810049G20RIK GENE	0.04636782	0.269915	0.3438086	0.732474782
1458878_at	Ypc1	Yamaguchi sarcoma viral (y-yes) oncogene homolog 1	0.04639045	0.11578	0.8717211	0.792759488
1416498_at	PPIC	PEPTIDYL PROLYL ISOMERASE C	0.04639463	0.9701804	0.9741171	0.448498994
1447200_at	DTNA	CRYSTALLIN, ALPHA	0.04641711	0.0412488	0.8375704	0.805292922
1419005_at	CRYBB3	CRYSTALLIN, BETA B3	0.04648035	0.06104097	0.08921371	1.05063191
1451056_at	PSM27	PROTEASOME (PROSOM, MACROPAIN) 26S SUBUNIT, NON-ATPASE, 7	0.04650313	0.54575359	0.6749115	0.854134078
1451423_at	TBC12	TUBULIN-SPECIFIC CLASP PROTEIN C	0.04651124	0.002161425	0.144838	1.074694117
1420497_at	CEBZ	CCAAT-ENHANCER BINDING PROTEIN ZETA	0.04657932	0.4881159	0.3479115	1.24066847
1426885_x_at	CDK2AP1	CDK2 (CYCLIN-DEPENDENT KINASE 2)-ASSOCIATED PROTEIN 1	0.04661122	0.5255605	0.64627209	0.20962797
1459310_at	---	---	0.04661764	0.3492287	0.2010062	0.485948003
1426561_x_at	Npat	nephronectin	0.04663603	0.0326229	0.7304484	1.143951501
1424314_at	9130131B05RIK	RIKEN CDNA 9130131B05 GENE	0.04665068	0.2783339	0.3251697	1.33964723
1453102_at	ZZZ3	Zinc Finger, ZZ Domain Containing 3	0.04665573	0.1003191	0.772762	0.744681138
1447167_at	AL03314	EXPRESSED SEQUENCE AL03314	0.04665802	0.908217	0.1459587	0.907475386
1421036_at	NPAS2	NEURONAL PAS DOMAIN PROTEIN 2	0.04667041	0.6776079	0.9757239	1.287757521
1451339_at	SULF1	SULFATE OXIDASE	0.04670969	0.06507042	0.847835331	0.847835331
1415961_at	ITMC2	INTEGRAL MEMBRANE PROTEIN 2C	0.04670984	0.07905616	0.5419709	0.760042279
1456489_at	PCF11	RIKEN CDNA 250000109 GENE	0.04680997	0.4813906	0.5866207	1.192311714
1450111_at	STAR2M	RIKEN CDNA 6423194 GENE	0.04686869	0.1601602	0.951191	1.564894243
1442918_at	NAV3	NEURON NAVIGATOR 3	0.04689345	0.02243558	0.8423138	1.10051406
1416620_x_at	SCARB1	SCAVENGER RECEPTOR CLASS B, MEMBER 1	0.04689998	0.134222	0.4987985	1.207531578
1433794_at	2104040B12RIK	RIKEN CDNA 2104040B12 GENE	0.04694537	0.07879955	0.8543789	0.8543789
1418314_at	MTF2	METAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 2	0.04696955	0.0093346	0.7490012	1.01930491
1435741_at	PDE8B	PHOSPHODIESTERASE 8B	0.04697406	0.7934646	0.9400881	0.805282769
1429655_at	RUDCD1	NUC DOMAIN CONTAINING 1	0.0469847	0.00019674	0.8383222	0.8383222
1456842_at	---	---	0.04698337	0.0703547	0.685822	0.512122308
1442252_at	KIF13A	KINESIN FAMILY MEMBER 13A	0.04704626	0.1204975	0.4679884	1.2868028
1453334_at	B22018A2N24RIK	RIKEN CDNA B22018A2N24RIK GENE	0.04706235	0.3335182	0.855728278	0.855728278
1440393_at	ODZ2	ODD OZTEN-M HOMOLOG 2 (DROSOPHILA)	0.0470718	0.2569302	0.5454676	2.147812722
1436865_at	SLC26A11	SOLUTE CARRIER FAMILY 26, MEMBER 11	0.04711666	0.2871879	0.1985105	0.864494849
1420066_x_at	G2f40	CD190 antigen	0.04715023	0.9901607	0.4804899	0.4804899
1451863_at	UTS2R	UROFENNSIN 2 RECEPTOR	0.04716319	0.4020848	0.3713586	2.023008255
1448973_at	SUL1D1	SULFOTRANSFERASE FAMILY 1D, MEMBER 1	0.04721128	0.9621293	0.666049	2.13048765
1423153_at	PRKFB	PROTEIN PHOSPHATASE RELATED PROTEIN B	0.04722454	0.04834857	0.0798614	0.843243078
1451264_at	PRMD6	RIKEN CDNA 2601901919 GENE	0.04732376	0.0123229	0.2099362	0.84155069
1439717_at	B2304B2M20RIK	RIKEN CDNA B2304B2M20RIK GENE	0.04737068	0.1855939	0.1109228	1.236562859
1451241_at	LAMB1-1	LAMBIN B1 SUBUNIT 1	0.04737183	0.01096234	0.1608609	0.7235918231
1424792_at	RPP49	RIBONUCLEASE P-40 SUBUNIT (HUMAN)	0.04742137	0.1592933	0.7937312	0.812625892
1427072_at	STAR2	START DOMAIN CONTAINING 8	0.04749449	0.7165273	0.1256604	1.159241743
1423445_at	2110016G11RIK	RIKEN CDNA 2110016G11 GENE	0.04750288	0.4992227	0.6868409	0.517267801
1434033_at	Tscl	transmembrane cell surface type 1 homolog of Drosophila (Egfp)	0.04751332	0.2104977	0.780466292	0.780466292
1460280_at	GRAP2	GRB2-RELATED ADAPTOR PROTEIN 2	0.04752155	0.9872165	0.9675172	0.535986028
1425290_at	AAS1470	EST AAS1470	0.04752478	0.6920191	0.9442278	0.782624645
1449546_at	ZFRP17	ZINC FINGER PROTEIN 617	0.04754155	0.061572041	0.8537309	0.922321291
1434927_at	IFSBP7	HEAT SHOCK PROTEIN FAMILY, MEMBER 7 (CARDIOVASCULAR)	0.04754859	0.6974744	0.0527378	1.550024372
1449703_at	ZFAND2A	ZINC FINGER, AN1-TYPE DOMAIN 2A	0.04760037	0.1613036	0.5358821	1.450077705
1455791_at	---	---	0.04760671	0.3971967	0.6197135	0.53782879
1442287_at	---	---	0.04763797	0.0511998	0.8620464	0.709881818
1436906_at	RNF166	RING FINGER PROTEIN 166				

1420582_at	CD209E	CD209E ANTIGEN	0.0487239	0.5692887	0.4050335	2.637701798
1422347_at	CHEK2	CHK2 CHECKPOINT HOMOLOG (S. POMBE)	0.0487558	0.1684693	0.4513852	0.740625663
1448618_at	MVP	MAJOR VAILT PROTEIN	0.0488269	0.2394245	0.303222	1.225705278
1441936_x_at	--	--	0.04885487	0.2471208	0.8148172	0.795712589
1443164_at	VPS13D	VACUOLAR PROTEIN SORTING 13D (YEAST)	0.04885491	0.7419631	0.4574515	1.559262908
1460399_at	BC018601	CDNA SEQUENCE BC018601	0.04882584	0.00475218	0.6618422	1.190310396
1422169_a_at	Bdnf	brain derived neurotrophic factor	0.04894924	0.9389392	0.236607	1.351794539
1441806_at	CID1L	CHROMOSOMAL HELICASE DNA BINDING PROTEIN L-LIKE	0.04899339	0.7018542	0.4908076	1.647511038
1449752_at	SPSB1	SPLARYANODINE RECEPTOR DOMAIN AND SOCS BOX CONTAINING 1	0.0490082	0.6756749	0.4316653	1.503045893
1440973_at	LOC552874	HYPOTHETICAL LOC552874	0.04902615	0.9342804	0.2780002	1.218307429
1448069_at	TM4SF1	TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1	0.04903619	0.7234735	0.09881945	0.699652631
1445618_at	--	--	0.04909033	3.52451E-05	0.4813784	0.685338676
1432237_at	5730522E02RIK	RIKEN CDNA 5730522E02 GENE	0.04912053	0.3424898	0.3537554	0.816197829
1422125_at	HTR2B	5-HYDROXYTRYPTAMINE (SEROTONIN) RECEPTOR 2B	0.04916555	0.1237356	0.6259502	2.206544508
1446027_at	--	--	0.04922584	0.0670149	0.8714413	0.600198594
1416935_at	TRPV2	TRANSIENT RECEPTOR POTENTIAL CATION CHANNEL, SUBFAMILY V, MEMBER 2	0.04923812	0.4231931	0.8176565	1.245555723
1430107_at	9230116B18RIK	RIKEN CDNA 9230116B18 GENE	0.04928557	0.3699192	0.57312149	0.576635568
1430290_at	--	--	0.04928807	0.09970136	0.05313704	3.994704449
1450472_x_at	Smad3	MAD homolog 3 (Drosophila)	0.04934396	0.07085675	0.4339804	1.230677983
1425149_a_at	PDC1	PHOSDUCIN-LIKE	0.04935565	0.002218962	0.7099298	0.834717191
1430030_at	5330420P16RIK	RIKEN CDNA 5330420P16 GENE	0.04936672	0.8623812	0.3006821	0.866996475
1439379_x_at	PRM1	PROTAMINE 1	0.04939434	0.1345723	0.1793334	2.791033024
1447392_x_at	CPD	CARBOXYPEPTIDASE D	0.04941198	0.01261584	0.4025655	1.154921776
1428057_x_at	AINAK	AINAK NUCLEOPROTEIN (DESMOYOKIN)	0.04944526	0.8237613	0.5122049	0.464858293
1447578_at	1700084J12RIK	RIKEN CDNA 1700084J12 GENE	0.04944993	0.3736071	0.08629759	0.553433262
1451971_at	CUL4A	RIKEN CDNA 2810470J1 GENE	0.04949131	0.01932693	0.9161423	0.866998789
1418164_at	EPIM	EPIMORPHIN	0.04953017	0.2798975	0.3302809	0.865720462
1450867_at	MRPL17	MITOCHONDRIAL RIBOSOMAL PROTEIN L17	0.04953106	0.5281225	0.15347259	0.862239186
1424213_at	UBIAD1	UBI A PRENYLTRANSFERASE DOMAIN CONTAINING 1	0.04955903	0.5533272	0.2124688	0.917210009
1438402_at	9630050M13RIK	RIKEN CDNA 9630050M13 GENE	0.04957938	0.05830923	0.2357729	1.142046082
1441416_at	INPP4B	INOSITOL POLYPHOSPHATE-4-PHOSPHATASE, TYPE II	0.04964201	0.5307435	0.6865671	0.603174976
1430566_at	4733401A01RIK	RIKEN CDNA 4733401A01 GENE	0.04968408	0.09466921	0.1454461	1.226113081
1418758_x_at	PSCD3	PLECKSTRIN HOMOMLOGY SECT AND COILED-COIL DOMAINS 3	0.04970199	0.03614459	0.9154211	0.841691319
1424433_at	TROVE2	TROVE DOMAIN FAMILY MEMBER 2	0.04971025	0.007593724	0.8310785	1.373310808
1443719_x_at	DDX42	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 42	0.04971952	0.004178711	0.9446287	1.361790863
1428727_at	463142C13RIK	RIKEN CDNA 463142C13 GENE	0.04973459	0.8813748	0.7873255	0.822474638
1437782_at	Cttnm2	ctninin associated protein-like 2	0.04974123	0.3792485	0.8218268	0.725474645
1457531_a_at	A930017K11RIK	RIKEN CDNA A930017K11 GENE	0.04986262	0.06084651	0.4808383	0.832359182
1440412_at	ICSF4D	IMMUNOGLOBULIN SUPERFAMILY MEMBER 4	0.04989325	1.1910036	0.7483153	1.545891783
1423158_at	AA409587	EXPRESSED SEQUENCE AA409587	0.04990148	0.00185428	0.06778104	0.895667064
1440969_at	BC030308	CDNA SEQUENCE BC030308	0.04997339	0.4522375	0.3780786	1.150506178
1421243_at	RNF144	RING FINGER PROTEIN 144	0.04999526	0.1644724	0.3477377	1.71022664
1445625_at	--	--	0.0499991	0.4763303	0.3682932	0.552383372

# Table S2

Term	Count	Percentage	P-value
<b>Biological Process</b>			
cellular physiological process	852	42.58%	1.14E-11
development	213	10.64%	1.63E-07
protein modification	166	8.30%	3.14E-07
biopolymer modification	170	8.50%	5.21E-07
intracellular signaling cascade	112	5.60%	9.73E-07
protein amino acid phosphorylation	79	3.95%	1.26E-06
primary metabolism	572	28.59%	1.65E-06
biopolymer metabolism	247	12.34%	3.72E-06
cell adhesion	74	3.70%	4.97E-06
metabolism	630	31.48%	5.56E-06
protein metabolism	280	13.99%	3.23E-05
macromolecule metabolism	360	17.99%	3.45E-05
metal ion transport	52	2.60%	3.55E-05
locomotion	41	2.05%	5.34E-05
cellular morphogenesis	52	2.60%	8.12E-05
localization of cell	40	2.00%	8.33E-05
cell motility	40	2.00%	8.33E-05
cellular metabolism	593	29.59%	1.23E-04
cellular protein metabolism	261	13.04%	1.33E-04
cellular macromolecule metabolism	264	13.19%	1.38E-04
phosphorylation	80	4.00%	1.54E-04
localization	280	13.99%	2.16E-04
ion transport	81	4.05%	2.26E-04
establishment of localization	277	13.84%	2.76E-04
morphogenesis	42	2.10%	2.97E-04
phosphorus metabolism	91	4.55%	3.01E-04
phosphate metabolism	91	4.55%	3.01E-04
behavior	36	1.80%	3.74E-04
vasculature development	26	1.30%	4.62E-04
neuropeptide signaling pathway	18	0.90%	4.65E-04
cellular process	1010	50.47%	5.21E-04
axonogenesis	22	1.10%	6.00E-04
axon guidance	15	0.75%	7.11E-04
second-messenger-mediated signaling	19	0.95%	7.39E-04
cell migration	32	1.60%	8.93E-04
phosphoinositide-mediated signaling	10	0.50%	0.001216148
cation transport	57	2.85%	0.001340741
nervous system development	57	2.85%	0.001840581
system development	61	3.05%	0.001851433
blood vessel development	24	1.20%	0.001858189
positive regulation of lyase activity	6	0.30%	0.001965128
adenylate cyclase activation	6	0.30%	0.001965128
positive regulation of cyclase activity	6	0.30%	0.001965128
regulation of adenylate cyclase activity	6	0.30%	0.001965128
positive regulation of adenylate cyclase activity	6	0.30%	0.001965128
cell differentiation	92	4.60%	0.002102036
locomotor behavior	24	1.20%	0.002582194
regulation of biological process	298	14.89%	0.002813205
blood vessel morphogenesis	21	1.05%	0.003406136
cell ion homeostasis	17	0.85%	0.003609544
potassium ion transport	23	1.15%	0.003718339
positive regulation of biological process	72	3.60%	0.003957223
regulation of cyclase activity	6	0.30%	0.00403197
regulation of lyase activity	6	0.30%	0.00403197
cation homeostasis	16	0.80%	0.004394293
synaptic transmission	22	1.10%	0.004928679
neuron morphogenesis during differentiation	22	1.10%	0.005325219
neurite morphogenesis	22	1.10%	0.005325219
cellular morphogenesis during differentiation	24	1.20%	0.005533013
metal ion homeostasis	15	0.75%	0.005938089
positive regulation of cell differentiation	11	0.55%	0.00613525
G-protein signaling, coupled to IP3 second messenger (phospholipase C activator)	9	0.45%	0.006348302
organ development	93	4.65%	0.00640895
glycoprotein metabolism	17	0.85%	0.007055098
glutamine metabolism	5	0.25%	0.00720438
endothelial cell differentiation	5	0.25%	0.00720438
positive regulation of positive chemotaxis	4	0.20%	0.007439389
induction of positive chemotaxis	4	0.20%	0.007439389
regulation of chemotaxis	4	0.20%	0.007439389
positive regulation of chemotaxis	4	0.20%	0.007439389
regulation of positive chemotaxis	4	0.20%	0.007439389
positive chemotaxis	4	0.20%	0.007439389
transmission of nerve impulse	24	1.20%	0.00836101
cell homeostasis	19	0.95%	0.008425675
ion homeostasis	18	0.90%	0.008616173
cell development	36	1.80%	0.009283267
feeding behavior	7	0.35%	0.009794733
cell-cell signaling	32	1.60%	0.010286953
glycoprotein biosynthesis	15	0.75%	0.010658793
regulation of development	24	1.20%	0.011532122
angiogenesis	17	0.85%	0.011771439
protein amino acid glycosylation	14	0.70%	0.011948245
sensory perception of pain	5	0.25%	0.01380451
transport	239	11.94%	0.01422248
G-protein signaling, adenylate cyclase activating pathway	7	0.35%	0.014370585
positive regulation of enzyme activity	16	0.80%	0.014507494
positive regulation of development	12	0.60%	0.014830012
neuron development	24	1.20%	0.016541785
biopolymer glycosylation	14	0.70%	0.018733563
regulation of cell differentiation	19	0.95%	0.018787525
regulation of enzyme activity	23	1.15%	0.02087568
glutamine family amino acid metabolism	7	0.35%	0.020253167
di-, tri-valent inorganic cation homeostasis	13	0.65%	0.021255789
regulation of cell shape	9	0.45%	0.024536457
monovalent inorganic cation transport	34	1.70%	0.025323587
muscle development	15	0.75%	0.028398115
regulation of cellular process	266	13.29%	0.029469295
L-glutamate transport	3	0.15%	0.031670461
determination of left/right symmetry	6	0.30%	0.032228758
calcium ion homeostasis	9	0.45%	0.034300203
positive regulation of myeloid cell differentiation	4	0.20%	0.035439407
L-amino acid transport	5	0.25%	0.036021384
determination of symmetry	6	0.30%	0.037837265
determination of bilateral symmetry	6	0.30%	0.037837265
muscle contraction	11	0.55%	0.038962737
organ morphogenesis	49	2.45%	0.040427467
homeostasis	24	1.20%	0.042172623
cAMP-mediated signaling	8	0.40%	0.0474288
regulation of physiological process	260	12.99%	0.048956065
cell-cell adhesion	20	1.00%	0.049323667
glycine catabolism	3	0.15%	0.049822082
acidic amino acid transport	3	0.15%	0.049822082
dendritic cell differentiation	3	0.15%	0.049822082
dendritic cell activation	3	0.15%	0.049822082

Term	Count	Percentage	P-value
<b>Cellular component</b>			
intracellular	645	32.23%	5.92E-06
chromatin	24	1.20%	2.03E-04
nucleus	325	16.24%	8.29E-04
membrane fraction	46	2.30%	0.002597032
chromosome	36	1.80%	0.002609631
cell fraction	49	2.45%	0.005004769
intracellular organelle	530	26.49%	0.005196371
organelle	530	26.49%	0.005907698
apicolateral plasma membrane	14	0.70%	0.006193355
apical junction complex	14	0.70%	0.006193355
intracellular membrane-bound organelle	465	23.24%	0.010257364
membrane-bound organelle	465	23.24%	0.011447643
microtubule cytoskeleton	32	1.60%	0.011999726
extracellular matrix	32	1.60%	0.015276231
nuclear envelope-endoplasmic reticulum network	13	0.65%	0.015501046
cytoplasm	290	14.49%	0.021446215
cell junction	22	1.10%	0.028921266
endoplasmic reticulum membrane	12	0.60%	0.02778193
synapse	19	0.95%	0.029746707
intercellular junction	18	0.90%	0.03254508
extracellular matrix (sensu Metazoa)	30	1.50%	0.034195217
endomembrane system	33	1.65%	0.03604724
tight junction	10	0.50%	0.047964206

Term	Count	Percentage	P-value
<b>Molecular function</b>			
metal ion binding	332	16.59%	3.19E-12
ion binding	332	16.59%	3.19E-12
binding	922	46.08%	1.57E-11
protein binding	401	20.04%	1.59E-11
cation binding	307	15.34%	5.50E-11
calcium ion binding	107	5.35%	3.19E-09
nucleotide binding	200	10.00%	5.45E-09
purine nucleotide binding	178	8.90%	2.01E-08
catalytic activity	482	24.09%	3.18E-08
adenyl nucleotide binding	149	7.45%	4.69E-08
protein serine/threonine kinase activity	71	3.55%	6.81E-08
phosphotransferase activity, alcohol group as acceptor	93	4.65%	7.95E-08
ATP binding	144	7.20%	9.01E-08
protein kinase activity	83	4.15%	9.42E-08
transferase activity	193	9.65%	1.71E-07
kinase activity	111	5.55%	5.42E-07
protein-tyrosine kinase activity	50	2.50%	2.14E-06
ion channel activity	51	2.55%	5.88E-06
transferase activity, transferring phosphorus-containing groups	118	5.90%	8.96E-06
GTPase regulator activity	41	2.05%	1.50E-05
MAP kinase activity	8	0.40%	2.22E-05
alpha-type channel activity	51	2.55%	5.91E-05
channel or pore class transporter activity	51	2.55%	2.18E-04
voltage-gated ion channel activity	26	1.30%	2.30E-04
small GTPase regulator activity	27	1.35%	5.06E-04
GTPase activity	21	1.05%	5.69E-04
enzyme activator activity	27	1.35%	7.11E-04
enzyme regulator activity	67	3.35%	8.41E-04
GTPase activator activity	21	1.05%	0.001155503
identical protein binding	23	1.15%	0.001159824
growth factor binding	11	0.55%	0.001166443
transition metal ion binding	190	9.50%	0.001706054
protein dimerization activity	23	1.15%	0.00312798
zinc ion binding	155	7.75%	0.003208255
hydrolase activity	190	9.50%	0.004106437
nucleic acid binding	268	13.39%	0.004154899
guanyl-nucleotide exchange factor activity	18	0.90%	0.004419441
UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity	4	0.20%	0.006391092
calmodulin binding	16	0.80%	0.007081357
ion transporter activity	72	3.60%	0.007135401
alkali metal ion binding	21	1.05%	0.0077174
kinase regulator activity	13	0.65%	0.0080787
cAMP-dependent protein kinase activity	21	1.05%	0.010154351
cyclic nucleotide-dependent protein kinase activity	21	1.05%	0.010154351
beta-1,3-galactosyltransferase activity	4	0.20%	0.010586056
protein kinase CK2 activity	21	1.05%	0.010851123
transcription factor binding	23	1.15%	0.01295359
insulin-like growth factor binding	6	0.30%	0.015050779
protein homodimerization activity	12	0.60%	0.016871587
potassium ion binding	14	0.70%	0.017554617
galactosyltransferase activity	7	0.35%	0.021805542
cytoskeletal protein binding	35	1.75%	0.023601126
transferase activity, transferring glycosyl groups	26	1.30%	0.024534485
transferase activity, transferring one-carbon groups	20	1.00%	0.025078598
neurotransmitter receptor activity	14	0.70%	0.027898329
neurotransmitter binding	14	0.70%	0.027898329
RNA binding	48	2.40%	0.029316354
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydri	49	2.45%	0.030172284
hydrolase activity, acting on acid anhydrides	49	2.45%	0.03338244
DNA binding	160	8.00%	0.034344446
transferase activity, transferring hexosyl groups	18	0.90%	0.036821029
pyrophosphatase activity	19	0.95%	0.03882894
pyrophosphatase activity	48	2.40%	0.039010075
exonuclease activity	9	0.45%	0.039115199
transporter activity	130	6.50%	0.03939801
protein kinase regulator activity	10	0.50%	0.03986377
extracellular matrix structural constituent	10	0.50%	0.03986377
lipid binding	25	1.25%	0.041043297
aminomethyltransferase activity	3	0.15%	0.04511114
peptide YY receptor activity	3	0.15%	0.04511114
UDP-glycosyltransferase activity	12	0.60%	0.045306344
GTP binding	33	1.65%	0.046853032



# Table S3

Donor ID	CNS-related illness	Death Cause	Gender	Age	Cluster
#1	NONE	PNEUMONIA	FEMALE	79	A
#2	NONE	PNEUMONIA	MALE	79	A
#3	NONE	MYOCARDIAL INFARCTION	MALE	90<	A
#4	NONE	CARDIAC ARREST	FEMALE	90<	A
#5	NONE	UNKNOWN	MALE	43	B
#6	NONE	CONGESTIVE CARDIOMYOPATHY	FEMALE	36	A
#7	NONE	CARDIORESPIRATORY FAILURE	FEMALE	90<	B
#8	NONE	CARDIORESPIRATORY FAILURE	FEMALE	90	B
#9	NONE	CARDIORESPIRATORY FAILURE	MALE	75	A
#10	NONE	MYOCARDIAL INFARCTION	FEMALE	85	B
#11	NONE	CARDIAC ARREST	FEMALE	86	A
#12	NONE	ACUTE RESPIRATORY INSUFFICIENCY	FEMALE	90<	A
#13	NONE	CHRONIC RENAL FAILURE	FEMALE	83	B
#14	NONE	CARDIAC ARREST	MALE	53	A
#15	NONE	LUNG CANCER	FEMALE	87	B
#16	NONE	MOTOR VEHICLE ACCIDENT	MALE	28	A
#17	NONE	MYOCARDIAL INFARCTION	MALE	41	A
#18	NONE	MOTOR VEHICLE ACCIDENT	MALE	31	A
#19	NONE	CARDIAC ARREST	MALE	27	A
#20	NONE	CHRONIC OBSTRUCTIVE LUNG DISEASE	FEMALE	87	A
#21	NONE	TRAUMA	MALE	29	A
#22	NONE	GUNSHOT WOUND TO CHEST	MALE	22	A
#23	NONE	MULTIPLE GUNSHOT WOUND	MALE	20	A
#24	NONE	MOTOR VEHICLE ACCIDENT	MALE	70	B
#25	NONE	CARDIAC ARREST	MALE	90<	B
#26	NONE	CARDIAC ARREST	FEMALE	89	B
#27	NONE	CARDIAC ARREST	MALE	66	B
#28	NONE	CARDIAC ARREST	MALE	69	B
#29	NONE	CARDIAC ARREST	MALE	74	B
#30	NONE	CARDIAC ARRHYTHMIA	MALE	39	A
#31	NONE	MULTIPLE GUNSHOT WOUND	MALE	20	A
#32	NONE	MALIGNANT MELANOMA	FEMALE	85	A
#33	NONE	ASTHMA	MALE	34	A
#34	NONE	CARDIAC ARRHYTHMIA	MALE	26	A
#35	NONE	GUNSHOT WOUND	FEMALE	24	A
#36	NONE	MYOCARDIAL INFARCTION	MALE	52	A
#37	NONE	MYOCARDIAL INFARCTION	MALE	41	A
#38	NONE	MYOCARDIAL INFARCTION	MALE	44	A
#39	NONE	CARDIAC ARREST	FEMALE	89	B
#40	NONE	CARDIAC ARREST	FEMALE	90<	A
#41	NONE	ACUTE RESPIRATORY INSUFFICIENCY	MALE	90	A
#42	NONE	MYELODYSPLASTIC SYNDROME	MALE	90	B
#43	NONE	CARDIAC ARREST	FEMALE	85	A
#44	NONE	CARDIAC ARREST	FEMALE	82	A
#45	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	84	B
#46	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	87	B
#47	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	73	B
#48	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	66	B
#49	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	90<	B
#50	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	66	B
#51	Schizophrenia	CARDIAC FAILURE	MALE	82	B
#52	Schizophrenia	CARDIORESPIRATORY FAILURE	FEMALE	74	B
#53	Schizophrenia	SUICIDE BY HANGING	FEMALE	39	A
#54	Schizophrenia	ACUTE RESPIRATORY INSUFFICIENCY	MALE	40	B
#55	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	79	B
#56	Schizophrenia	CORONARY ARTERY DISEASE	FEMALE	65	B
#57	Schizophrenia	CARDIAC ARREST	MALE	57	B
#58	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	82	B
#59	Schizophrenia	CARDIORESPIRATORY FAILURE	FEMALE	90	B
#60	Schizophrenia	SUICIDE	MALE	30	B
#61	Schizophrenia	CARDIORESPIRATORY FAILURE	MALE	73	B
#62	Schizophrenia	SUICIDE BY HANGING	MALE	29	A
#63	Schizoaffective disorder	SUICIDE	MALE	18	B
#64	Bipolar disorder	SUICIDE BY HANGING	MALE	34	B
#65	Bipolar disorder	SUICIDE BY DRUG OVERDOSE	MALE	24	B

# Table S4

Mouse Affimetrix probes	Corresponding mouse genes	Human orthologues	Human Affimetrix probes	% P flag in 166 human hippocampal data in BioExpress	F value for specific 21 psychiatric patients
1454653_at	RIKEN cDNA A730016F12 gene	LOC151835	239139_at	92.17	11.816
1417420_at	cyclin D1	CCND1	208712_at	52.41	7.9104
1441634_at	netrin G1	NTNG1	236088_at	23.49	6.6809
1419093_at	tryptophan 2,3-dioxygenase	TDO2	205943_at	52.41	4.8376
1416266_at	prodynorphin	PDYN	206803_at	40.36	4.1403
1444298_at	RIKEN cDNA A130090K04 gene	PIP3-E	214735_at	75.3	4.0516
1422711_a_at	pregnancy upregulated non-ubiquitously expressed CaM kinase	PNCK	229411_at	28.92	3.7059
1418754_at	adenylate cyclase 8	ADCY8	206811_at	90.96	3.4637
1437865_at	spermatogenesis associated 13	SPATA13	225564_at	96.99	2.9952
1428809_at	RIKEN cDNA 1810010H24 gene	LOC284018	226901_at	87.35	2.7169

# Table S5

A

SNP ID <sup>a</sup>	position <sup>b</sup>	MAF <sup>c</sup> (%)	phenotype <sup>d</sup>	Nnnumber	genotype <sup>e</sup>			P-value		
					M/M	M/m	m/m	genotype	allele	
1 rs1432832	1	17.2	SCZ	376	201	145	30	0.507	0.344	
					115	70	38	7	0.759	0.451
					347	200	120	27		
2 rs873593	4071	0.8	BP	376	123	176	77	<b>0.0263</b>	<b>0.0321</b>	
					111	27	64	20	0.0524	<b>0.0243</b>
					346	126	175	45		
3 rs919740	7693	41.4	SCZ	376	123	176	77	<b>0.0263</b>	<b>0.0321</b>	
					111	27	64	20	0.0524	<b>0.0243</b>
					346	126	175	45		
4 rs1432833	12389	47.7	BP	376	123	176	77	0.789	0.526	
					115	36	60	19	0.445	0.694
					347	114	160	73		
5 rs9686770	15341	44.5	SCZ	377	133	168	76	0.789	0.526	
					115	36	60	19	0.445	0.694
					347	114	160	73		
6 rs3797616	20538	7.0	BP	377	182	156	39	0.233	0.630	
					115	54	49	12	0.609	0.630
					343	151	163	29		
7 rs874084	22712	29.7	SCZ	377	182	156	39	0.233	0.630	
					115	54	49	12	0.609	0.630
					343	151	163	29		
8 rs2304042	28735	28.9	SCZ	376	192	150	34	0.574	0.847	
					115	46	57	12	0.141	0.0556
					347	174	148	25		
9 rs3822606	32387	28.9	BP	376	178	154	46	0.774	0.544	
					115	59	46	10	0.798	0.502
					343	166	141	36		
10 rs4958445	35182	29.7	CON	376	178	154	46	0.774	0.544	
					115	59	46	10	0.798	0.502
					343	166	141	36		
11 rs3776824	36931	30.5	SCZ	378	178	154	46	0.774	0.544	
					115	59	46	10	0.798	0.502
					343	166	141	36		
12 rs10463294	37433	0	BP	376	147	174	55	0.696	0.391	
					115	48	56	11	0.592	0.644
					347	145	157	45		
13 rs10463293	37469	39.8	CON	376	147	174	55	0.696	0.391	
					115	48	56	11	0.592	0.644
					347	145	157	45		
14 rs880100	38185	0	SCZ	378	178	154	46	0.774	0.544	
					115	59	46	10	0.798	0.502
					343	166	141	36		
15 rs2288799	42129	36.7	BP	376	147	174	55	0.696	0.391	
					115	48	56	11	0.592	0.644
					347	145	157	45		
16 rs3756577	44898	22.7	CON	376	147	174	55	0.696	0.391	
					115	48	56	11	0.592	0.644
					347	145	157	45		
17 rs4958454	46790	41.4	SCZ	379	132	173	74	0.415	0.796	
					105	39	44	22	0.297	0.774
					344	109	174	61		
18 rs 869192	47931	35.2	BP	376	149	163	64	0.509	0.277	
					115	43	51	21	0.927	0.776
					347	123	160	64		
19 rs10066581	57861	21	CON	376	149	163	64	0.509	0.277	
					115	43	51	21	0.927	0.776
					347	123	160	64		
20 rs3822607	61749	40.6	SCZ	376	236	117	23	<b>0.0213</b>	0.164	
					115	69	39	7	0.0817	0.155
					347	224	116	7		
21 rs2053053	64149	18.0	BP	376	109	185	82	0.202	0.294	
					115	36	61	18	0.916	0.693
					347	102	187	58		
22 rs7711408	692680	31.2	CON	376	109	185	82	0.202	0.294	
					115	36	61	18	0.916	0.693
					347	102	187	58		
23 rs2241695	70718	32.8	SCZ	376	274	89	13	0.275	0.555	
					115	75	33	7	0.133	0.165
					347	241	98	8		
24 rs2241694	70934	13.3	BP	376	182	156	38	0.204	0.507	
					115	46	52	17	<b>0.0195</b>	<b>0.0210</b>
					347	167	157	23		
25 rs957709	71716	16.4	CON	376	182	156	38	0.204	0.507	
					115	46	52	17	<b>0.0195</b>	<b>0.0210</b>
					347	167	157	23		
26 rs887346	77550	22.7	SCZ	376	178	166	32	0.867	0.734	
					115	43	56	16	0.124	0.0558
					347	158	160	29		
27 rs2241694	70934	13.3	BP	376	264	97	15	<b>0.0358</b>	<b>0.0303</b>	
					115	79	33	3	0.213	0.116
					347	262	81	4		
28 rs887346	77550	22.7	CON	376	178	166	32	0.867	0.734	
					115	43	56	16	0.124	0.0558
					347	158	160	29		
29 rs2241694	70934	13.3	SCZ	376	264	97	15	<b>0.0358</b>	<b>0.0303</b>	
					115	79	33	3	0.213	0.116
					347	262	81	4		
30 rs887346	77550	22.7	BP	376	179	160	37	0.305	0.134	
					115	46	54	15	<b>0.0331</b>	<b>0.00967</b>
					347	181	141	25		

- a. Gray box represents 'haplotype-tagging (ht) SNPs' for association analysis
- b. NT029289.10
- c. MAF=minor allele frequency of 64 controls
- d. SCZ=schizophrenia, BP=bipolar disorder, CON=control
- e. M=major allele, m=minor allele
- f. Bold numbers represent significant P-values

B

Block	Combination of htSNPs	Global P-value <sup>a</sup>	
		SCZ	BP
II	SNP7-8	0.891	0.185
III	SNP11-15	0.791	0.344
IV	SNP17-18	0.287	0.461
V	SNP19-20	0.429	0.102
VI	SNP21-22-23-24	0.252	<b>0.0015</b>

a. Bold numbers represent significant P-values

C

SNPID	phenotype	Number	genotype			P-value		
			M/M	M/m	m/m	genotype	allele	
3 rs919740	BP	382	108	204	55	0.455	0.871	
			149	43	80	26	0.860	0.745
			382	119	196	67		
19 rs10066581	CON	380	224	117	16	0.273	0.293	
			149	95	50	4	0.140	0.117
			380	225	128	27		
21 rs2053053	BP	382	268	95	4	0.211	0.294	
			149	93	54	2	0.0520	0.173
			382	271	100	11		
22 rs7711408	CON	368	197	145	26	0.222	0.0878	
			149	66	69	14	0.631	0.589
			381	184	159	38		
23 rs2241695	BP	367	172	164	31	0.110	0.169	
			149	69	65	15	0.609	0.486
			378	170	158	50		
24 rs2241694	CON	366	282	75	9	0.0922	0.0529	
			149	112	29	8	0.0690	0.651
			382	268	104	10		
26 rs887346	BP	370	176	148	46	0.772	0.946	
			149	69	64	16		
			370	176	148	46		

## Supplementary Table Legends

**Table S1. List of genes that were significantly upregulated or downregulated in the hippocampus of alpha-CaMKII<sup>+/-</sup> mice.**

**Table S2. Gene Ontology annotations of the genes that were significantly upregulated or downregulated in the hippocampus of alpha-CaMKII<sup>+/-</sup> mice.**

**Table S3. Donors offering hippocampi for GeneChip analysis.** Expression data from total 166 hippocampi were used in BioExpress database including additional 98 donors with various CNS-related illness. A, Cluster A in Figure 5 (normal control-enriched cluster); B, Cluster B (schizophrenic psychiatric patient-enriched cluster).

**Table S4. Affymetrix probes used as alpha-CaMKII<sup>+/-</sup> mice-specific hippocampal biomarkers.** F value was calculated to segregate 21 schizophrenic or its related psychiatric patients shown in Additional Table 3 from the rest of 145 donors.

**Table S5. Association analysis of alpha-CaMKII gene with schizophrenia and bipolar disorder.** (A) Summary of haplotype-tagging single nucleotide polymorphisms (htSNPs) and association analysis of alpha-CaMKII in first-set samples. (B) Haplotype-wise analysis of first-set samples. (C) Summary of the second-set confirmation analysis of significant htSNPs in first-set samples.