Experimental Procedures

Cell Culture

Huh 7.5.1 hepatoma cells (a gift from F. Chisari), HEK-293T and HeLa MAGI cells were maintained at 37°C in humidified air containing 5% CO_2 in Dulbecco's modified Eagle's medium (DMEM;Cellgro) supplemented with 15% (vol/vol) fetal bovine serum (FBS;Gibco) and 2 mM L-glutamine (Gibco). Medium was prepared on a weekly basis to maintain maximum L-glutamine activity.

Virus stock and viral infections

Infectious genotype 2a JFH1 strain HCV was obtained from T. Wakita. Large scale viral preparations were prepared through inoculation of Huh 7.5.1 cells with seed strain, followed by cultivation for 3-5 days, then collection and clarification (1500 rpm x 15 minutes) of supernatant. Viral aliquots were stored at -80°C until use.

New Guinea C strain of dengue was prepared in C6/36 cells. Influenza A/ WSN/33 (H1N1) (a kind gift from Peter Palese, Microbiology Department, Mt. Sinai School of Medicine, NY, NY) was propagated and assessed as previously described (PMID:20064371). Rescue assays for dengue and influenza were performed in HeLa MAGI cells.

siRNA screen

siRNAs for screen optimization and follow up (Dharmacon siGENOME) were obtained from Dharmacon with the exception of GFP, which was obtained from Sigma. Control siRNAs for HCV rescue from IFN included IFNAR smartpool (positive) and NT2 and NT3 non-targeting and GFP siRNAs (negative). Throughout the screen, on-plate Z factors were monitored for quality control, and an average value of 0.21 was maintained. The original screen was performed using siRNA pools, composed of 4 siRNA per gene (Dharmacon siGenome pooled siRNA library) as in prior publications (PMID: 19717417). The deconvolution screen was performed using Dharmacon Set of Four siGenome sets. Post screen studies were performed using Dharmacon SiGENOME Set-of-Four-Upgrade sets for individual genes, and

Dharmacon NT2, NT3 and Sigma GFP negative controls. Conditions were established for optimal cell count, transfection reagent concentration, IFN dose, and JFH1 titer to achieve maximal dynamic range between cells transfected with IFNAR siRNA versus non-targeting siRNA. Transfections were performed using Oligofectamine (Invitrogen) in reverse transfection format. For 384 well assays, liquid dispensing machines (Matrix WellMate) were employed to deliver all reagents. Transfections were performed in 384 well format in triplicate for the screen, then 384, 96, 24 or 6-well format for follow up assays, depending on assay. Oligofectamine was diluted 140μl/10,000μl (0.014) in reduced serum medium (Opti-mem®, Gibco) and dispensed to individual wells, followed by robotic addition of 1um siRNA (Velocity11 Bravo), and then cells (1100 cells/ well) for a final siRNA concentration of 1.5 μM and final lipid concentration of 0.4 percent of total volume. Throughout transfection experiments, cells were maintained in DMEM supplemented with 15% FBS. Medium was prepared fresh weekly to minimize L-glutamine degradation. 24 hours following transfection, 5μl of medium was added to wells on the plate periphery to decrease edge-effect. 48 hours following transfection, medium was aspirated from all wells and replaced with fresh medium containing 100 IU/ml of IFN alpha (PBL). 24 hours following IFN treatment, medium was removed and replaced with medium containing JFH1 (MOI of 1). Cells were then incubated for 48 hours, followed by immunofluorescence. Deconvolution screening was performed in an identical manner except that for each gene 4 individual siRNAs were used, instead of a pool, and positive values were determined based on 2 fold rescue above the mean of on-plate negative controls.

Immunofluorescence

HCV anti-core antibody was prepared through culture of hybridoma containing cells obtained from TJ Liang. For immunofluorescence experiments, cells were fixed in 4% PFA (Sigma), then permeabilized in 0.2% Triton, then overnight incubation with anti-core antibody at 4°C. Cells were then stained with goat anti mouse Alexa 488 secondary antibody (Invitrogen) for 1 hour, followed by incubation in Hoechst. Cells were imaged using FITC and DAPI and images captured using an IXM2 automated microscope at the Harvard Longwood ICCB, and analyzed using either a custom script (Tiao Xie, Harvard ICCB-L) during screen and for 384 well plate experiments or MetaXpress cell scoring software, for 96 well plate experiments where debris less significantly influenced results. For dengue virus and influenza virus immunofluorescence, identical conditions were used except that anti-dengue envelope and anti-HA 29 primary antibodies were used for dengue and influenza, respectively.

Image Analysis / Scoring

Images were scored for percent infected cells. Total number of cells was determined by number of nuclei labeled with Hoechst, and the number of infected cells was determined by number of green cells corresponding to individual nuclei. To increase accuracy of cell scoring, a custom script was designed using the following algorithm (**Fig. S2**). Algorithm: The algorithm first segments the DAPI channel to pick up all the individual nuclei. A rough thresholding is performed for the entire DAPI image. The nuclear segmentation then gets refined by adjusting the threshold on a per-object basis and dividing clustered nuclei. To score all the cells in the FITC channel, the FITC image is smoothed and the image background is calculated using the smoothed image. Thresholding is performed for the FITC image using scaled image background. To score positive cells, the algorithm matches nuclear segmentation with FITC segmentation to find FITC positive nuclei. In order to remove the large circular debris in the FITC channel, the size and shape of all the objects identified are measured, and the objects with area and roundness above a given threshold are removed.

Percent infection was then calculated for each well, and the median absolute deviation (MAD) was determined for each plate. Wells were considered positive if they 1) scored >= 3 x MAD (which is roughly equal to 2 x the corrected MAD) and 3) revealed an image consistent with score on visual inspection. Wells eliminated during visual inspection are summarized in **Table S2**.

Data were analyzed using IPA (Ingenuity Systems).

Total RNA isolation and quantitative RT PCR (qRT-PCR)

Intracellular total cellular and viral RNA was isolated using QIAshredder^{TM} (Qiagen) , followed by removal of genomic DNA and RNA isolation using RNEasy plus kits (Qiagen), all according to manufacterer's protocols. RNA was stored at -80°C, then reverse transcribed by random priming using the High capacity cDNA reverse transcription kit (Applied Biosciences)and quantified by real-time PCR using the DyNAmo

HS SYBR green qPCR kit (Finnzyme;Espoo,Finland). qRT-PCR results were interpreted using delta / delta CT (PMID 11328886), using GAPDH as an internal control.

Gene specific primers are provided in **Table S8**. Efficiency curves were performed on all primers to rule out concentration dependent amplification characteristics prior to testing of candidate gene knockdown.

Western Blot

Whole cell protein extraction and Western Blot analysis

Cells were collected, washed with PBS and resuspended in lysis buffer (50 mM Tris, pH 7.4, 150 mM NaCl, 5 mM EDTA, 1% NP-40, 0.5% sodiumdeoxycholate, 0.1% SDS) supplemented with a protease inhibitor cocktail (Roche). The cells were sonicated and lysates were clarified by centrifugation for 20 min at 14,000 x g. The supernatant was collected as the whole-cell extract.

Protein concentrations were determined with the Bio-Rad DC^{TM} Protein Assay kit (Bio-Rad). Samples containing equal amounts of protein were subjected to sodium dodecyl sulfate-polyacrilamide gel electrophoresis (4 to 12% Bis-Tris or 3 to 8% Tris Acetate gels; Novex). The proteins were transferred to nitrocellulose membranes using the iBlot® gel transfer system (Invitrogen). Nonspecific sites were blocked by incubation for 15 min at room temperature with 5% nonfat milk and 0.1% Tween 20 in PBS (PBST; pH 7.4), and the membranes were incubated for 2h at room temperature with the primary antibody. Membranes then were washed in PBST; pH 7.4 and treated with the appropriate Horseradish peroxidase (HRP)-conjugated secondary antibody for 2h at room temperature. The immunoblots were washed in PBST, and proteins were detected with an enhanced chemioluminescence detection kit (Amersham Biosciences) and autoradiography. Anti-Actin antibody was used to check for equal protein loading. The intensity of the bands was determined by densitometry.

Primary antibodies used in this paper were mouse anti-Actin (Sigma-Aldrich; A2228), goat anti-ALG10 (Santa-Cruz; sc-109491), rabbit anti-BCHE (Abcam; ab82307), rabbit anti-DPP4 (Sigma-Aldrich; D1445), and rabbit anti-GUCY1B3 (Sigma-Aldrich; HPA020870), mouse anti-MYST1 (Santa-Cruz; sc-130651), mouse anti-PPP3CB (Abcam; ab58161), rabbit anti-PRIC285 (Abcam; ab129781) and rabbit anti-SLC27A2 (Sigma-Aldrich; SAB2102193). Secondary antibodies were HRP-conjugated anti-mouse

(Amersham Bioscience; NA9310), HRP-conjugated anti-rabbit (Amersham Bioscience NA9340) and HRP-conjugated anti-goat (Santa-Cruz; sc-2020).

Lifecycle Assays

Lifecycle Assay Scoring System

To simplify interpretation of these results (fold-rescue values for 4 siRNA duplexes per gene for nine genes), a scoring system was established (**Table S10, Supplemental Methods**). For each lifecycle assay, the fold-rescue values for all siRNA duplexes for a given gene that demonstrated a statistically significant rescue effect were summed (**Table S10**). In this way, strength (fold-rescue) and validity (number of siRNAs that rescued infection) are represented as a single value to aid in interpretation and comparison. Lifecycle rescue scores greater than or equal to four were scored positive, because this represents an average of 2-fold or greater rescue for 2 or more siRNA, the criteria used during the validation round screening.

Entry pseudoparticles

HCV pseudoparticles were generated by cotransfection of plasmids expressing 1) the JFH1 envelope or VSV envelope (a gift from F Cosset), 2) HIV gag – pol (a gift from J Luban), and 3) a ZS green-containing reporter genome (a gift from J Luban) into HEK-293T cells using Lipofectamine 2000 (Invitrogen). Pseudoparticles were harvested from the supernatant 48 and 72 hours after transfection, clarified then aliquotted and stored at -80°C. Pseudoparticles were titered for infectivity prior to use. Entry assays were performed using identical conditions to the screening assay described above, except JFH1 pseudoparticles replaced infectious JFH1.

Replication

HCV replication was assessed using the OR6 HCV GT1b full genome replicon, a gift from N. Kato. OR6 cells were grown in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS) and 500 ug/ml G418 and cultured at 37°C, 5% CO2. Transfections were performed in identical conditions to siRNA screen. 48h post transfection, cells were treated with IFN-α 6IU/ml for 24H. Cells were then lysed and renilla (OR6) and ATP (Cell Titer Glo) signal assessed.

HCV RNA production assay

JFH1 RNA production was assessed at 48h postinfection by performing HCV IEG siRNA transfection identical to those described for the screen assay, but in 24 well plates, followed by isolation of total intracellular RNA and quantification of JFH1 RNA genome by qRT-PCR as described above.

Egress and production of fully infectious particles assay

Egress and production of fully infectious virus were assessed by replicate plating of supernatant from cells transfected as described above for screening assay. At 48 hours post JFH1 infection, the viral supernatant from the transfected cells in the source plate was transferred in a well-by-well manner to a destination plate containing fresh untransfected Huh7.5.1 cells that had been plated 24h prior, and cells were incubated for 48h, then stained using HCV core antibody and Hoechst as described above.

shRNA knockdown cells

Lentiviral pseudoparticles were generated by co-transfection of plasmids expressing distinct PDIP1 shRNAs and a puromycin resistance cassette, HIV-gag pol, and VSV-G envelope into HEK-293T cells. Lentiviral pseudoparticles were transduced into Huh7.5.1 cells followed by puromycin selection. Selected cells were assessed for target gene knockdown using qRT-PCR and western blot and for IFN-α-rescue phenotype using core staining and qRT-PCR.

Overexpression

Plasmids containing long and short isoform PDIP1 and full and truncated BCHE were kindly provided by T. Satoh and J.K. Reddy and R. Chilukuri, respectively. Huh 7.5.1 cells were plated in 6 well dishes then transfected with IEG containing plasmid or vector control using Fugene according to manufacturer's instructions. After 24h, medium was replaced with fresh 15% DMEM containing JFH1 to yield an MOI of 1. Cells were then incubated for 48h followed by RNA isolation, cDNA preparation, and qRT-PCR.

Statistical analysis

Data are expressed as means ± standard error of the mean for at least three independent experiments. Student's *t* test was used to compare experimental conditions and controls. A *P* value <0.05 was considered significant (*).

Supplementary Tables

Table S1: Complete screen data: excel file
Table S2: Potential False Negatives eliminated due to cytotoxicity: excel file
Table S3: IFN-enhancement scores for Dependency Factor K/Ds: excel file
Table S4: Top 120, annotated: excel file
Table S5: IPA analysis results Top 120: included here
Table S6: Are IEGs ISGs?: excel file
Table S7: Comparison to other IEG screens: excel file
Table S8: Primers: included here
Table S9: Phenotype Knockdown Comparison: excel file
Table S10: Lifecycle Rescue Scores: excel file
Table S11: Non-HCV Viral Rescue Scores: excel file

Table S1. Complete Screen Dataset

50001.00	A02	M-003879-00	cyclin-dependent kin	1033.00	CDKN3
50001.00	A04	M-003247-02	cyclin-dependent kin	1032.00	CDKN2D
50001.00	A05	M-005300-00	AP2 associated kinas	22848.00	AAK1
50001.00	A06	M-003246-01	cyclin-dependent kin	1031.00	CDKN2C
50001.00	A07	M-005301-01	apoptosis-associated	9625.00	AATK
50001.00	A08	M-003245-02	cyclin-dependent kin	1030.00	CDKN2B
50001.00	A09	M-004061-00	ceramide kinase	64781.00	CERK
50001.00	A10	M-003244-03	cyclin-dependent kin	1028.00	CDKN1C
50001.00	A11	M-009511-00	Rap guanine nucleoti	11069.00	RAPGEF4
50001.00	A12	M-003472-00	cyclin-dependent kin	1027.00	CDKN1B
50001.00	A13	M-003255-02	CHK1 checkpoint hor	1111.00	CHEK1
50001.00	A14	M-003471-00	cyclin-dependent kin	1026.00	CDKN1A
50001.00	A15	M-003256-05	CHK2 checkpoint hor	11200.00	CHEK2
50001.00	A16	M-004799-02	cyclin-dependent kin	6792.00	CDKL5
50001.00	A17	M-006704-00	choline kinase alpha	1119.00	CHKA
50001.00	A18	M-004798-00	cyclin-dependent kin	51265.00	CDKL3
50001.00	A19	M-006705-00	choline kinase beta	1120.00	CHKB
50001.00	A20	M-004797-00	cyclin-dependent kin	8999.00	CDKL2
50001.00	A21	M-005462-01	cholinergic receptor,	1128.00	CHRM1
50001.00	A23	M-003473-01	conserved helix-loop	1147.00	CHUK
50001.00	B02	M-011927-00	integrin beta 1 bindi	9270.00	ITGB1BP1
50001.00	B04	M-004214-01	hormonally upregula	30811.00	HUNK
50001.00	B05	M-003257-02	polo-like kinase 3 (D	1263.00	PLK3
50001.00	B06	M-007691-01	CDC42 binding prote	55561.00	CDC42BPG
50001.00	B07	M-012217-00	connector enhancer	10256.00	CNKSR1
50001.00	B08	M-004618-00	serine/threonine kin	55351.00	STK32B
50001.00	B09	M-012101-00	collagen, type IV, alp	10087.00	COL4A3BP
50001.00	B10	M-005007-00	eukaryotic translatio	27102.00	EIF2AK1
50001.00	B11	M-019847-01	coatomer protein co	9276.00	COPB2
50001.00	B12	M-006736-00	hexokinase 3 (white	3101.00	HK3
50001.00	B13	M-004031-02	Cdc2-related kinase,	51755.00	CRKRS
50001.00	B14	M-006735-01	hexokinase 2	3099.00	HK2
50001.00	B15	M-012023-01	v-crk sarcoma virus	1399.00	CRKL
50001.00	B16	M-006820-01	hexokinase 1	3098.00	HK1
50001.00	B17	M-003109-02	colony stimulating fa	1436.00	CSF1R
50001.00	B18	M-004808-02	homeodomain inter	147746.00	HIPK4
50001.00	B19	M-003110-02	c-src tyrosine kinase	1445.00	CSK
50001.00	B20	M-004810-00	homeodomain inter	10114.00	HIPK3
50001.00	B21	M-003957-03	casein kinase 1, alph	1452.00	CSNK1A1
50001.00	B23	M-003478-00	casein kinase 1, delt	1453.00	CSNK1D
50001.00	C02	M-004323-01	cyclin-dependent kin	8814.00	CDKL1
50001.00	C04	M-003243-02	cyclin-dependent kin	1025.00	CDK9
50001.00	C05	M-013591-01	cyclin-dependent kin	51550.00	CINP
50001.00	C06	M-003242-02	cyclin-dependent kin	1024.00	CDK8

50001.00	C07	M-004613-00	citron (rho-interactir	11113.00	CIT
50001.00	C08	M-003241-01	cyclin-dependent kin	1022.00	CDK7
50001.00	C09	M-006706-01	creatine kinase, brair	1152.00	CKB
50001.00	C10	M-003240-02	cyclin-dependent kin	1021.00	CDK6
50001.00	C11	M-006707-00	creatine kinase, mus	1158.00	CKM
50001.00	C12	M-012957-00	CDK5 regulatory sub	80279.00	CDK5RAP3
50001.00	C13	M-006708-00	creatine kinase, mito	1159.00	CKMT1B
50001.00	C14	M-013297-01	CDK5 regulatory sub	51654.00	CDK5RAP1
50001.00	C15	M-006709-00	creatine kinase, mito	1160.00	CKMT2
50001.00	C16	M-008885-00	cyclin-dependent kin	8941.00	CDK5R2
50001.00	C17	M-004586-01	CDC28 protein kinase	1163.00	CKS1B
50001.00	C18	M-008988-00	cyclin-dependent kin	8851.00	CDK5R1
50001.00	C19	M-007678-00	CDC28 protein kinase	1164.00	CKS2
50001.00	C20	M-003239-01	cyclin-dependent kin	1020.00	CDK5
50001.00	C21	M-004800-00	CDC-like kinase 1	1195.00	CLK1
50001.00	C23	M-004801-01	CDC-like kinase 2	1196.00	CLK2
50001.00	D02	M-003266-03	homeodomain intera	28996.00	HIPK2
50001.00	D04	M-004809-02	homeodomain intera	204851.00	HIPK1
50001.00	D05	M-003479-01	casein kinase 1, epsil	1454.00	CSNK1E
50001.00	D06	M-003141-02	hemopoietic cell kina	3055.00	HCK
50001.00	D07	M-004666-01	casein kinase 1, gam	53944.00	CSNK1G1
50001.00	D08	M-005330-02	alpha-kinase 2	115701.00	ALPK2
50001.00	D09	M-004678-00	casein kinase 1, gam	1455.00	CSNK1G2
50001.00	D10	M-005006-00	heat shock 22kDa pr	26353.00	HSPB8
50001.00	D11	M-004679-02	casein kinase 1, gam	1456.00	CSNK1G3
50001.00	D12	M-006734-01	guanylate kinase 1	2987.00	GUK1
50001.00	D13	M-003475-00	casein kinase 2, alph	1457.00	CSNK2A1
50001.00	D14	M-004515-01	guanylate cyclase 2F,	2986.00	GUCY2F
50001.00	D15	M-004752-00	casein kinase 2, alph	1459.00	CSNK2A2
50001.00	D16	M-005329-01	guanylate cyclase 2D	3000.00	GUCY2D
50001.00	D17	M-007679-00	casein kinase 2, beta	1460.00	CSNK2B
50001.00	D18	M-005328-00	guanylate cyclase 2C	2984.00	GUCY2C
50001.00	D19	M-007871-00	chemokine (C-X-C m	3627.00	CXCL10
50001.00	D20	M-010924-00	general transcription	2965.00	GTF2H1
50001.00	D21	M-004417-02	death-associated prc	1612.00	DAPK1
50001.00	D23	M-004418-02	death-associated prc	23604.00	DAPK2
50001.00	E02	M-003238-02	cyclin-dependent kin	1019.00	CDK4
50001.00	E04	M-003237-01	cyclin-dependent kin	1018.00	CDK3
50001.00	E05	M-004802-01	CDC-like kinase 3	1198.00	CLK3
50001.00	E06	M-003236-04	cyclin-dependent kin	1017.00	CDK2
50001.00	E07	M-004803-00	CDC-like kinase 4	57396.00	CLK4
50001.00	E08	M-004689-00	cell division cycle 2-li	23097.00	CDC2L6
50001.00	E09	M-003100-01	c-abl oncogene 1, re	25.00	ABL1
50001.00	E10	M-003235-04	cyclin-dependent kin	8558.00	CDK10
50001.00	E11	M-003101-01	v-abl Abelson murine	27.00	ABL2
50001.00	E12	M-003234-02	cell division cycle 7 h	8317.00	CDC7
50001.00	E13	M-003102-02	tyrosine kinase, non-	10188.00	TNK2

50001.00	E14	M-004075-01	CDC42 binding prote	9578.00	CDC42BPB
50001.00	E15	M-004924-01	activin A receptor, ty	90.00	ACVR1
50001.00	E16	M-003814-02	CDC42 binding prote	8476.00	CDC42BPA
50001.00	E17	M-004925-01	activin A receptor, ty	91.00	ACVR1B
50001.00	E18	M-004688-00	cell division cycle 2-li	8621.00	CDC2L5
50001.00	E19	M-004926-01	activin A receptor, ty	92.00	ACVR2A
50001.00	E20	M-004026-01	cell division cycle 2-li	985.00	CDC2L2
50001.00	E21	M-004927-00	activin A receptor, ty	93.00	ACVR2B
50001.00	E23	M-005302-02	activin A receptor ty	94.00	ACVRL1
50001.00	F02	M-003010-03	glycogen synthase ki	2932.00	GSK3B
50001.00	F04	M-003009-01	glycogen synthase ki	2931.00	GSK3A
50001.00	F05	M-004947-00	death-associated pro	1613.00	DAPK3
50001.00	F06	M-005327-00	germ cell associated	83903.00	GSG2
50001.00	F07	M-004884-01	doublecortin-like kin	9201.00	DCLK1
50001.00	F08	M-004628-00	G protein-coupled re	131890.00	GRK7
50001.00	F09	M-006710-00	deoxycytidine kinase	1633.00	DCK
50001.00	F10	M-004627-01	G protein-coupled re	2870.00	GRK6
50001.00	F11	M-003111-03	discoidin domain rec	780.00	DDR1
50001.00	F12	M-004626-00	G protein-coupled re	2869.00	GRK5
50001.00	F13	M-003112-03	discoidin domain rec	4921.00	DDR2
50001.00	F14	M-004625-00	G protein-coupled re	2868.00	GRK4
50001.00	F15	M-006711-02	diacylglycerol kinase,	1606.00	DGKA
50001.00	F16	M-006729-00	glucosamine (UDP-N	10020.00	GNE
50001.00	F17	M-006712-01	diacylglycerol kinase,	1607.00	DGKB
50001.00	F18	M-019878-01	glia maturation facto	9535.00	GMFG
50001.00	F19	M-006713-03	diacylglycerol kinase,	8527.00	DGKD
50001.00	F20	M-019100-00	glia maturation facto	2764.00	GMFB
50001.00	F21	M-011493-00	diacylglycerol kinase,	8526.00	DGKE
50001.00	F23	M-006715-00	diacylglycerol kinase,	1608.00	DGKG
50001.00	G02	M-004687-01	cell division cycle 2-li	984.00	CDC2L1
50001.00	G04	M-003224-03	cell division cycle 2,	983.00	CDC2
50001.00	G05	M-004504-02	ADAM metallopeptid	8754.00	ADAM9
50001.00	G06	M-007732-00	cytidine and dCMP d	81602.00	CDADC1
50001.00	G07	M-005303-02	aarF domain contain	57143.00	ADCK1
50001.00	G08	M-013630-02	CD7 molecule	924.00	CD7
50001.00	G09	M-005304-01	aarF domain contain	90956.00	ADCK2
50001.00	G10	M-005234-01	CD4 molecule	920.00	CD4
50001.00	G11	M-005305-01	aarF domain contain	79934.00	ADCK4
50001.00	G12	M-003775-01	CD3e molecule, epsil	916.00	CD3E
50001.00	G13	M-018919-00	aarF domain contain	203054.00	ADCK5
50001.00	G14	M-004686-01	cell cycle related kin	23552.00	CCRK
50001.00	G15	M-004733-02	adenosine kinase	132.00	ADK
50001.00	G16	M-007843-01	chemokine (C-C moti	6351.00	CCL4
50001.00	G17	M-005419-00	adrenergic, alpha-1A	148.00	ADRA1A
50001.00	G18	M-007831-00	chemokine (C-C moti	6347.00	CCL2
50001.00	G19	M-005420-01	adrenergic, alpha-1B	147.00	ADRA1B
50001.00	G20	M-005311-01	calcium/calmodulin-	8573.00	CASK

50001.00	G21	M-005426-01	adrenergic, beta-2-,	154.00	ADRB2
50001.00	G23	M-004325-01	adrenergic, beta, rec	156.00	ADRBK1
50001.00	H02	M-015091-01	glycerol kinase 2	2712.00	GK2
50001.00	H04	M-006727-00	glycerol kinase	2710.00	GK
50001.00	H05	M-006717-01	diacylglycerol kinase	9162.00	DGKI
50001.00	H06	M-007914-00	GDNF family recepto	2675.00	GFRA2
50001.00	H07	M-005079-02	diacylglycerol kinase	1609.00	DGKQ
50001.00	H08	M-010819-01	glucokinase (hexokin	2645.00	GCK
50001.00	H09	M-006718-00	diacylglycerol kinase	8525.00	DGKZ
50001.00	H10	M-011663-00	growth associated pr	2596.00	GAP43
50001.00	H11	M-006719-02	deoxyguanosine kina	1716.00	DGUOK
50001.00	H12	M-006725-00	galactokinase 2	2585.00	GALK2
50001.00	H13	M-004949-00	unc-51-like kinase 3	25989.00	ULK3
50001.00	H14	M-007728-01	galactokinase 1	2584.00	GALK1
50001.00	H15	M-005313-01	EPH receptor A6	285220.00	EPHA6
50001.00	H16	M-005005-01	cyclin G associated k	2580.00	GAK
50001.00	H17	M-006808-00	dihydroxyacetone ki	26007.00	DAK
50001.00	H18	M-003140-03	FYN oncogene relate	2534.00	FYN
50001.00	H19	M-025870-00	homolog of rat pragr	157285.00	PRAGMIN
50001.00	H20	M-020174-01	FYN binding protein	2533.00	FYB
50001.00	H21	M-003113-01	serine/threonine/tyr	55359.00	STYK1
50001.00	H23	M-009415-00	discs, large homolog	1739.00	DLG1
50001.00	I02	M-006815-00	carbohydrate kinase-	23729.00	CARKL
50001.00	I04	M-005013-01	TNNI3 interacting kir	51086.00	TNNI3K
50001.00	I05	M-004326-00	adrenergic, beta, rec	157.00	ADRBK2
50001.00	I06	M-004397-00	caspase recruitment	79092.00	CARD14
50001.00	I07	M-005429-01	angiotensin II recept	186.00	AGTR2
50001.00	I08	M-004395-00	caspase recruitment	29775.00	CARD10
50001.00	I09	M-006811-02	adenylate kinase 1	203.00	AK1
50001.00	I10	M-004842-01	calcium/calmodulin-	10645.00	CAMKK2
50001.00	I11	M-006812-00	adenylate kinase 2	204.00	AK2
50001.00	I12	M-004912-00	calcium/calmodulin-	84254.00	CAMKK1
50001.00	I13	M-006700-01	adenylate kinase 3-li	205.00	AK3L1
50001.00	I14	M-004944-01	calcium/calmodulin-	814.00	CAMK4
50001.00	I15	M-006701-00	adenylate kinase 3	50808.00	AK3
50001.00	I16	M-004536-01	calcium/calmodulin-	818.00	CAMK2G
50001.00	I17	M-004897-02	adenylate kinase 5	26289.00	AK5
50001.00	I18	M-004042-02	calcium/calmodulin-	817.00	CAMK2D
50001.00	I19	M-007257-00	adenylate kinase 7	122481.00	AK7
50001.00	I20	M-004943-03	calcium/calmodulin-	816.00	CAMK2B
50001.00	I21	M-011426-01	A kinase (PRKA) anch	8165.00	AKAP1
50001.00	I23	M-009277-01	A kinase (PRKA) anch	11215.00	AKAP11
50001.00	J02	M-007255-00	fucokinase	197258.00	FUK
50001.00	J04	M-003139-01	fyn-related kinase	2444.00	FRK
50001.00	J05	M-011252-01	discs, large homolog	1740.00	DLG2
50001.00	J06	M-006691-00	frataxin	2395.00	FXN
50001.00	J07	M-009462-01	discs, large homolog	1741.00	DLG3

50001.00	J08	M-003008-01	FK506 binding protei	2475.00	FRAP1
50001.00	J09	M-007882-01	discs, large homolog	1742.00	DLG4
50001.00	J10	M-006817-00	fructosamine-3-kinas	79672.00	FN3KRP
50001.00	J11	M-004637-00	dystrophia myotonic	1760.00	DMPK
50001.00	J12	M-006724-00	fructosamine 3 kinas	64122.00	FN3K
50001.00	J13	M-012251-00	DnaJ (Hsp40) homol	5611.00	DNAJC3
50001.00	J14	M-003138-01	fms-related tyrosine	2324.00	FLT4
50001.00	J15	M-011254-00	docking protein 1, 62	1796.00	DOK1
50001.00	J16	M-003137-01	fms-related tyrosine	2322.00	FLT3
50001.00	J17	M-006720-00	deoxythymidylate ki	1841.00	DTYMK
50001.00	J18	M-003136-02	fms-related tyrosine	2321.00	FLT1
50001.00	J19	M-003484-02	dual specificity phos	1843.00	DUSP1
50001.00	J20	M-007727-00	tetra-peptide repeat	348825.00	TPRXL
50001.00	J21	M-003965-01	dual specificity phos	11221.00	DUSP10
50001.00	J23	M-003565-01	dual specificity phos	1844.00	DUSP2
50001.00	K02	M-004942-00	calcium/calmodulin-	815.00	CAMK2A
50001.00	K04	M-004941-01	calcium/calmodulin-	57172.00	CAMK1G
50001.00	K05	M-008868-01	A kinase (PRKA) anch	11214.00	AKAP13
50001.00	K06	M-004946-00	calcium/calmodulin-	57118.00	CAMK1D
50001.00	K07	M-009765-01	A kinase (PRKA) anch	10566.00	AKAP3
50001.00	K08	M-004940-00	calcium/calmodulin-	8536.00	CAMK1
50001.00	K09	M-008442-00	A kinase (PRKA) anch	8852.00	AKAP4
50001.00	K10	M-019939-01	calmodulin 3 (phosp	808.00	CALM3
50001.00	K11	M-011954-00	A kinase (PRKA) anch	9495.00	AKAP5
50001.00	K12	M-006703-02	inositol 1,3,4,5,6-per	64768.00	IPPK
50001.00	K13	M-008497-01	A kinase (PRKA) anch	9472.00	AKAP6
50001.00	K14	M-003633-01	tribbles homolog 1 (	10221.00	TRIB1
50001.00	K15	M-013371-00	A kinase (PRKA) anch	9465.00	AKAP7
50001.00	K16	M-018324-01	chromosome 7 open	10842.00	C7orf16
50001.00	K17	M-009656-01	A kinase (PRKA) anch	10270.00	AKAP8
50001.00	K18	M-007254-01	chromosome 6 open	221264.00	C6orf199
50001.00	K19	M-003000-01	v-akt murine thymo	207.00	AKT1
50001.00	K20	M-003754-01	tribbles homolog 3 (	57761.00	TRIB3
50001.00	K21	M-003001-01	v-akt murine thymo	208.00	AKT2
50001.00	K23	M-003002-01	v-akt murine thymo	10000.00	AKT3
50001.00	L02	M-005326-00	mixed lineage kinase	197259.00	MLKL
50001.00	L04	M-006803-00	chromosome 9 open	158067.00	C9orf98
50001.00	L05	M-004517-00	dual specificity phos	56940.00	DUSP22
50001.00	L06	M-004052-02	NIMA (never in mito	152110.00	NEK10
50001.00	L07	M-003963-02	dual specificity phos	1846.00	DUSP4
50001.00	L08	M-004624-00	hypothetical protein	124923.00	FLJ25006
50001.00	L09	M-003566-01	dual specificity phos	1847.00	DUSP5
50001.00	L10	M-005321-00	hypothetical protein	84197.00	FLJ23356
50001.00	L11	M-003964-01	dual specificity phos	1848.00	DUSP6
50001.00	L12	M-005320-01	leucine-rich repeat k	79705.00	LRRK1
50001.00	L13	M-003567-00	dual specificity phos	1849.00	DUSP7
50001.00	L14	M-004843-00	yeast Sps1/Ste20-rel	80122.00	YSK4

50001.00	L15	M-003568-00	dual specificity phos	1850.00	DUSP8
50001.00	L16	M-007253-00	threonine synthase-l	79896.00	THNSL1
50001.00	L17	M-004805-00	dual-specificity tyros	1859.00	DYRK1A
50001.00	L18	M-005319-01	unc-51-like kinase 4	54986.00	ULK4
50001.00	L19	M-004806-01	dual-specificity tyros	9149.00	DYRK1B
50001.00	L20	M-004020-03	microtubule associat	84930.00	MASTL
50001.00	L21	M-004730-02	dual-specificity tyros	8445.00	DYRK2
50001.00	L23	M-004731-00	dual-specificity tyros	8444.00	DYRK3
50001.00	M02	M-003108-01	TP53 regulating kina	112858.00	TP53RK
50001.00	M04	M-005310-00	testis-specific serine	283629.00	TSSK4
50001.00	M05	M-003103-02	anaplastic lymphoma	238.00	ALK
50001.00	M06	M-004101-00	BUB1 budding uninhi	701.00	BUB1B
50001.00	M07	M-004929-01	activin A receptor, ty	130399.00	ACVR1C
50001.00	M08	M-004102-00	BUB1 budding uninhi	699.00	BUB1
50001.00	M09	M-005306-01	amyotrophic lateral	55437.00	ALS2CR2
50001.00	M10	M-003107-01	Bruton agammaglob	695.00	BTK
50001.00	M11	M-004685-01	PFTAIRE protein kina	65061.00	PFTK2
50001.00	M12	M-004938-01	bromodomain, testis	676.00	BRDT
50001.00	M13	M-005307-01	anti-Mullerian horm	269.00	AMHR2
50001.00	M14	M-004935-01	bromodomain conta	6046.00	BRD2
50001.00	M15	M-007803-00	angiopoietin 4	51378.00	ANGPT4
50001.00	M16	M-003460-01	v-raf murine sarcom	673.00	BRAF
50001.00	M17	M-004930-01	ankyrin repeat and k	255239.00	ANKK1
50001.00	M18	M-003106-02	BMX non-receptor ty	660.00	BMX
50001.00	M19	M-005308-02	receptor-interacting	54101.00	RIPK4
50001.00	M20	M-005309-02	bone morphogenetic	659.00	BMPR2
50001.00	M21	M-007687-01	SPEG complex locus	10290.00	SPEG
50001.00	M23	M-005138-00	adaptor protein, pho	26060.00	APPL1
50001.00	N02	M-006318-00	NAD kinase	65220.00	NADK
50001.00	N04	M-007726-00	IQ motif containing	64799.00	IQCH
50001.00	N05	M-004732-01	dual-specificity tyros	8798.00	DYRK4
50001.00	N06	M-007260-00	riboflavin kinase	55312.00	RFK
50001.00	N07	M-017723-01	endothelin 2	1907.00	EDN2
50001.00	N08	M-007256-00	acylglycerol kinase	55750.00	AGK
50001.00	N09	M-004950-00	eukaryotic elongatio	29904.00	EEF2K
50001.00	N10	M-005078-00	ethanolamine kinase	55224.00	ETNK2
50001.00	N11	M-003114-01	epidermal growth fa	1956.00	EGFR
50001.00	N12	M-005318-00	SCY1-like 2 (S. cerevi	55681.00	SCYL2
50001.00	N13	M-004883-01	eukaryotic translatio	9451.00	EIF2AK3
50001.00	N14	M-003135-02	Gardner-Rasheed fel	2268.00	FGR
50001.00	N15	M-005314-00	eukaryotic translatio	27104.00	EIF2AK4
50001.00	N16	M-003134-01	fibroblast growth fac	2264.00	FGFR4
50001.00	N17	M-006721-01	ethanolamine kinase	55500.00	ETNK1
50001.00	N18	M-003133-01	fibroblast growth fac	2261.00	FGFR3
50001.00	N19	M-007676-00	Rap guanine nucleoti	10411.00	RAPGEF3
50001.00	N20	M-003132-01	fibroblast growth fac	2263.00	FGFR2
50001.00	N21	M-003115-02	EPH receptor A1	2041.00	EPHA1

50001.00	N23	M-003116-01	EPH receptor A2	1969.00	EPHA2
50001.00	O02	M-004934-01	bone morphogenetic	658.00	BMPR1B
50001.00	O04	M-004933-03	bone morphogenetic	657.00	BMPR1A
50001.00	O05	M-003563-02	v-raf murine sarcoma	369.00	ARAF
50001.00	O06	M-005071-00	BMP2 inducible kinas	55589.00	BMP2K
50001.00	O07	M-004931-00	NUAK family, SNF1-li	9891.00	NUAK1
50001.00	O08	M-020353-01	B-cell linker	29760.00	BLNK
50001.00	O09	M-004165-01	DBF4 homolog (S. ce	10926.00	DBF4
50001.00	O10	M-003105-03	B lymphoid tyrosine	640.00	BLK
50001.00	O11	M-013023-00	ropporin 1-like	83853.00	ROPN1L
50001.00	O12	M-005436-00	bradykinin receptor I	624.00	BDKRB2
50001.00	O13	M-003201-02	ataxia telangiectasia	472.00	ATM
50001.00	O14	M-003875-04	breakpoint cluster re	613.00	BCR
50001.00	O15	M-003202-04	ataxia telangiectasia	545.00	ATR
50001.00	O16	M-004932-00	branched chain keto	10295.00	BCKDK
50001.00	O17	M-003326-02	aurora kinase B	9212.00	AURKB
50001.00	O18	M-008914-00	azurocidin 1 (cationic	566.00	AZU1
50001.00	O19	M-019573-01	aurora kinase C	6795.00	AURKC
50001.00	O20	M-003104-02	AXL receptor tyrosin	558.00	AXL
50001.00	O21	M-003631-01	arginine vasopressin	552.00	AVPR1A
50001.00	O23	M-005431-00	arginine vasopressin	553.00	AVPR1B
50001.00	P02	M-003131-02	fibroblast growth fac	2260.00	FGFR1
50001.00	P04	M-003130-01	feline sarcoma oncog	2242.00	FES
50001.00	P05	M-003117-02	EPH receptor A3	2042.00	EPHA3
50001.00	P06	M-003129-01	fer (fps/fes related) t	2241.00	FER
50001.00	P07	M-003118-01	EPH receptor A4	2043.00	EPHA4
50001.00	P08	M-005317-02	Fas-activated serine/	10922.00	FASTK
50001.00	P09	M-005315-02	EPH receptor A5	2044.00	EPHA5
50001.00	P10	M-006530-01	ecotropic viral integr	2122.00	EVI1
50001.00	P11	M-003119-01	EPH receptor A7	2045.00	EPHA7
50001.00	P12	M-004951-01	endoplasmic reticulu	2081.00	ERN1
50001.00	P13	M-003120-02	EPH receptor A8	2046.00	EPHA8
50001.00	P14	M-004807-01	mitogen-activated pr	225689.00	MAPK15
50001.00	P15	M-003121-01	EPH receptor B1	2047.00	EPHB1
50001.00	P16	M-003128-02	v-erb-a erythroblasti	2066.00	ERBB4
50001.00	P17	M-003122-01	EPH receptor B2	2048.00	EPHB2
50001.00	P18	M-003127-02	v-erb-b2 erythroblas	2065.00	ERBB3
50001.00	P19	M-003123-02	EPH receptor B3	2049.00	EPHB3
50001.00	P20	M-003126-01	v-erb-b2 erythroblas	2064.00	ERBB2
50001.00	P21	M-003124-01	EPH receptor B4	2050.00	EPHB4
50001.00	P23	M-003125-01	EPH receptor B6	2051.00	EPHB6
					mdmdMAD
					3MAD
					MADc
50001.00	C22				
50001.00	D22				
50001.00	E22				

50001.00 F22

mn

sd

50001.00 G22

50001.00 H22

50001.00 I22

50001.00 J22

mn

sd

3psSD

3ngSD

SumSD

MeanDf

SumovrMn

1minus

% inf	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**
9.15	1.88	0.49	19.88	11.71	2.61	10.57	0.60	-0.12
10.52	3.25	0.84	10.68	2.51	0.56	7.50	3.67	-0.75
9.99	2.72	0.71	3.89	4.28	-0.95	8.68	2.49	-0.51
3.81	3.46	-0.90	13.69	5.52	1.23	4.94	6.23	-1.28
7.05	0.22	-0.06	12.15	3.98	0.89	12.54	1.37	0.28
11.10	3.83	0.99	18.94	10.77	2.40	10.22	0.95	-0.20
10.70	3.43	0.89	15.74	7.57	1.69	9.50	1.67	-0.34
7.18	0.09	-0.02	11.51	3.34	0.74	11.34	0.17	0.04
4.97	2.30	-0.60	7.68	0.49	-0.11	17.23	6.06	1.24
5.52	1.75	-0.46	12.06	3.89	0.87	8.63	2.54	-0.52
22.31	**15.04**	3.91	19.60	11.43	2.54	66.93	55.76	11.46
7.57	0.30	0.08	11.27	3.10	0.69	5.72	5.45	-1.12
8.38	1.11	0.29	13.84	5.67	1.26	10.02	1.15	-0.24
7.57	0.30	0.08	16.34	8.17	1.82	13.37	2.20	0.45
8.39	1.12	0.29	12.88	4.71	1.05	21.71	10.54	2.16
5.06	2.21	-0.58	10.86	2.69	0.60	8.87	2.30	-0.47
8.57	1.30	0.34	8.79	0.62	0.14	6.50	4.67	-0.96
3.83	3.44	-0.90	14.04	5.87	1.31	15.80	4.63	0.95
4.80	2.47	-0.64	13.41	5.24	1.17	9.86	1.31	-0.27
5.04	2.23	-0.58	9.09	0.92	0.21	6.10	5.07	-1.04
9.72	2.45	0.64	7.05	1.12	-0.25	8.21	2.96	-0.61
7.00	0.27	-0.07	4.87	3.30	-0.73	5.15	6.02	-1.24
10.22	2.95	0.77	8.44	0.27	0.06	9.60	1.57	-0.32
9.85	2.58	0.67	5.99	2.18	-0.49	9.47	1.70	-0.35
10.82	3.55	0.92	5.28	2.89	-0.64	4.93	6.24	-1.28
13.16	5.89	1.53	9.32	1.15	0.26	12.30	1.13	0.23
25.49	**18.22**	4.74	13.16	4.99	1.11	23.43	12.26	2.52
14.49	7.22	1.88	11.56	3.39	0.75	19.77	8.60	1.77
29.52	**22.25**	5.78	20.61	12.44	2.77	31.51	20.34	4.18
8.11	0.84	0.22	9.37	1.20	0.27	9.54	1.63	-0.33
1.73	5.54	-1.44	4.71	3.46	-0.77	3.94	7.23	-1.49
8.86	1.59	0.41	9.15	0.98	0.22	10.07	1.10	-0.23
18.21	**10.94**	2.84	10.40	2.23	0.50	9.22	1.95	-0.40
7.64	0.37	0.09	3.05	5.12	-1.14	9.39	1.78	-0.37
6.40	0.87	-0.23	3.64	4.53	-1.01	5.54	5.63	-1.16
3.08	4.19	-1.09	5.88	2.29	-0.51	7.40	3.77	-0.77
4.48	2.79	-0.73	6.32	1.85	-0.41	11.36	0.19	0.04
4.77	2.50	-0.65	7.04	1.13	-0.25	11.45	0.28	0.06
4.05	3.22	-0.84	3.24	4.93	-1.10	9.17	2.00	-0.41
8.84	1.57	0.41	9.30	1.13	0.25	9.81	1.36	-0.28
12.48	5.21	1.35	2.99	5.18	-1.15	12.69	1.52	0.31
8.90	1.63	0.42	2.69	5.48	-1.22	19.62	8.45	1.74
6.50	0.77	-0.20	3.34	4.83	-1.07	17.56	6.39	1.31
2.69	4.58	-1.19	0.89	7.28	-1.62	5.10	6.07	-1.25

9.05	1.78	0.46	4.24	3.93	-0.88	11.48	0.31	0.06
4.96	2.31	-0.60	1.88	6.29	-1.40	8.90	2.27	-0.47
9.34	2.07	0.54	4.55	3.62	-0.81	12.27	1.10	0.23
13.13	5.86	1.52	4.79	3.38	-0.75	25.05	13.88	2.85
17.74	**10.47**	2.72	4.36	3.81	-0.85	19.37	8.20	1.68
12.82	5.55	1.44	5.01	3.16	-0.70	17.96	6.79	1.39
19.69	**12.42**	3.23	5.95	2.22	-0.49	24.97	13.80	2.83
7.30	0.03	0.01	5.18	2.99	-0.67	17.36	6.19	1.27
6.47	0.80	-0.21	2.44	5.73	-1.27	9.14	2.03	-0.42
31.77	**24.50**	6.37	16.21	8.04	1.79	42.62	31.45	6.46
12.01	4.74	1.23	5.17	3.00	-0.67	14.66	3.49	0.72
8.37	1.10	0.29	2.29	5.88	-1.31	10.21	0.96	-0.20
9.69	2.42	0.63	4.34	3.83	-0.85	17.77	6.60	1.36
4.87	2.40	-0.62	3.80	4.37	-0.97	7.58	3.59	-0.74
14.60	7.33	1.90	6.08	2.09	-0.46	11.06	0.11	-0.02
4.47	2.80	-0.73	3.92	4.25	-0.95	16.77	5.60	1.15
6.57	0.70	-0.18	1.58	6.59	-1.47	2.94	8.23	-1.69
7.51	0.24	0.06	10.77	2.60	0.58	10.91	0.26	-0.05
11.86	4.59	1.19	12.62	4.45	0.99	15.75	4.58	0.94
7.30	0.03	0.01	10.30	2.13	0.47	11.30	0.13	0.03
13.15	5.88	1.53	13.28	5.11	1.14	18.26	7.09	1.46
6.63	0.64	-0.17	5.31	2.86	-0.64	13.77	2.60	0.53
5.80	1.47	-0.38	5.11	3.06	-0.68	7.92	3.25	-0.67
8.38	1.11	0.29	12.19	4.02	0.89	8.77	2.40	-0.49
8.73	1.46	0.38	5.50	2.67	-0.59	12.67	1.50	0.31
3.21	4.06	-1.06	6.41	1.76	-0.39	6.04	5.13	-1.05
7.00	0.27	-0.07	4.75	3.42	-0.76	11.57	0.40	0.08
13.67	6.40	1.66	12.47	4.30	0.96	17.66	6.49	1.33
5.53	1.74	-0.45	6.14	2.03	-0.45	6.68	4.49	-0.92
7.80	0.53	0.14	4.22	3.95	-0.88	11.86	0.69	0.14
4.50	2.77	-0.72	5.59	2.58	-0.57	13.12	1.95	0.40
6.31	0.96	-0.25	13.49	5.32	1.18	10.44	0.73	-0.15
7.31	0.04	0.01	11.10	2.93	0.65	11.04	0.13	-0.03
11.01	3.74	0.97	9.93	1.76	0.39	15.79	4.62	0.95
4.81	2.46	-0.64	3.87	4.30	-0.96	8.25	2.92	-0.60
2.86	4.41	-1.15	10.62	2.45	0.54	12.36	1.19	0.24
12.90	5.63	1.46	10.34	2.17	0.48	7.49	3.68	-0.76
11.14	3.87	1.00	5.83	2.34	-0.52	16.70	5.53	1.14
14.41	7.14	1.86	7.71	0.46	-0.10	4.74	6.43	-1.32
10.52	3.25	0.84	6.59	1.58	-0.35	15.30	4.13	0.85
11.98	4.71	1.22	4.54	3.63	-0.81	4.35	6.82	-1.40
14.12	6.85	1.78	7.07	1.10	-0.24	11.53	0.36	0.07
14.80	7.53	1.96	6.78	1.39	-0.31	8.40	2.77	-0.57
17.77	**10.50**	2.73	14.87	6.70	1.49	20.47	9.30	1.91
7.92	0.65	0.17	2.42	5.75	-1.28	5.20	5.97	-1.23
11.32	4.05	1.05	7.50	0.67	-0.15	11.95	0.78	0.16
12.02	4.75	1.23	6.97	1.20	-0.27	8.73	2.44	-0.50

10.18	2.91	0.76	8.98	0.81	0.18	8.08	3.09	-0.64
6.42	0.85	-0.22	6.17	2.00	-0.45	9.56	1.61	-0.33
13.17	5.90	1.53	4.81	3.36	-0.75	7.36	3.81	-0.78
8.62	1.35	0.35	8.67	0.50	0.11	6.24	4.93	-1.01
7.87	0.60	0.16	5.41	2.76	-0.61	5.57	5.60	-1.15
7.94	0.67	0.17	4.39	3.78	-0.84	16.88	5.71	1.17
8.14	0.87	0.23	6.90	1.27	-0.28	19.47	8.30	1.70
9.40	2.13	0.55	9.85	1.68	0.37	18.88	7.71	1.58
8.37	1.10	0.28	9.16	0.99	0.22	18.53	7.36	1.51
4.85	2.42	-0.63	0.85	7.32	-1.63	2.09	9.09	-1.87
19.18	**11.91**	3.10	4.23	3.94	-0.88	6.20	4.97	-1.02
9.10	1.83	0.47	1.28	6.89	-1.53	3.18	7.99	-1.64
9.86	2.59	0.67	4.92	3.25	-0.72	4.46	6.71	-1.38
6.08	1.19	-0.31	4.32	3.85	-0.86	4.23	6.94	-1.43
7.93	0.66	0.17	5.79	2.38	-0.53	4.49	6.68	-1.37
21.50	**14.23**	3.70	6.62	1.55	-0.34	12.65	1.48	0.30
9.01	1.74	0.45	2.62	5.55	-1.24	4.17	7.00	-1.44
16.02	**8.75**	2.27	5.22	2.95	-0.66	8.13	3.04	-0.62
9.98	2.71	0.70	4.24	3.93	-0.88	3.98	7.19	-1.48
4.20	3.07	-0.80	3.69	4.48	-1.00	3.33	7.84	-1.61
14.36	7.09	1.84	7.94	0.23	-0.05	14.15	2.98	0.61
6.52	0.75	-0.19	6.47	1.70	-0.38	4.83	6.34	-1.30
10.23	2.96	0.77	3.53	4.64	-1.03	8.36	2.81	-0.58
17.64	**10.37**	2.69	10.73	2.56	0.57	7.81	3.36	-0.69
6.63	0.64	-0.17	4.98	3.19	-0.71	4.74	6.43	-1.32
13.55	6.28	1.63	13.98	5.81	1.29	12.00	0.83	0.17
12.56	5.29	1.37	10.00	1.83	0.41	18.69	7.52	1.55
10.65	3.38	0.88	9.20	1.03	0.23	6.13	5.04	-1.04
6.16	1.11	-0.29	6.40	1.77	-0.39	5.90	5.27	-1.08
2.02	5.25	-1.37	5.66	2.51	-0.56	9.12	2.05	-0.42
5.65	1.62	-0.42	11.38	3.21	0.71	16.42	5.25	1.08
3.32	3.95	-1.03	3.16	5.01	-1.11	7.21	3.96	-0.82
3.33	3.94	-1.03	4.41	3.76	-0.84	9.87	1.30	-0.27
6.98	0.29	-0.08	4.35	3.82	-0.85	8.48	2.69	-0.55
4.92	2.35	-0.61	3.12	5.05	-1.12	5.59	5.58	-1.15
3.00	4.27	-1.11	2.80	5.37	-1.20	9.48	1.69	-0.35
4.35	2.92	-0.76	4.69	3.48	-0.77	10.09	1.08	-0.22
2.48	4.79	-1.25	2.46	5.71	-1.27	4.87	6.30	-1.29
2.47	4.80	-1.25	8.38	0.21	0.05	3.73	7.44	-1.53
2.89	4.38	-1.14	3.48	4.69	-1.04	23.70	12.53	2.57
12.83	5.56	1.45	14.79	6.62	1.47	30.96	19.79	4.07
4.83	2.44	-0.64	9.84	1.67	0.37	18.01	6.84	1.41
3.90	3.37	-0.88	3.57	4.60	-1.02	10.04	1.13	-0.23
3.30	3.97	-1.03	2.15	6.02	-1.34	15.38	4.21	0.86
4.79	2.48	-0.65	10.09	1.92	0.43	19.40	8.23	1.69
6.19	1.08	-0.28	12.46	4.29	0.96	14.82	3.65	0.75
5.22	2.05	-0.53	8.62	0.45	0.10	14.78	3.61	0.74

13.38	6.11	1.59	7.07	1.10	-0.24	39.70	28.53	5.86
3.79	3.48	-0.91	12.97	4.80	1.07	13.11	1.94	0.40
3.84	3.43	-0.89	14.41	6.24	1.39	6.29	4.88	-1.00
6.40	0.87	-0.23	5.75	2.42	-0.54	5.93	5.24	-1.08
6.57	0.70	-0.18	18.42	10.25	2.28	21.40	10.23	2.10
2.60	4.67	-1.21	9.97	1.80	0.40	2.63	8.54	-1.75
6.80	0.47	-0.12	10.69	2.52	0.56	11.57	0.40	0.08
2.80	4.47	-1.16	16.33	8.16	1.82	10.87	0.30	-0.06
2.01	5.26	-1.37	8.42	0.25	0.06	3.50	7.67	-1.58
4.32	2.95	-0.77	12.85	4.68	1.04	11.50	0.33	0.07
7.26	0.01	0.00	12.41	4.24	0.94	14.11	2.94	0.60
5.77	1.50	-0.39	11.71	3.54	0.79	13.50	2.33	0.48
3.49	3.78	-0.98	12.62	4.45	0.99	7.71	3.46	-0.71
2.10	5.17	-1.35	12.88	4.71	1.05	15.44	4.27	0.88
2.58	4.69	-1.22	13.45	5.28	1.17	9.71	1.46	-0.30
1.70	5.57	-1.45	8.63	0.46	0.10	9.79	1.38	-0.28
3.70	3.57	-0.93	14.15	5.98	1.33	16.51	5.34	1.10
4.14	3.13	-0.82	18.47	10.30	2.29	12.02	0.85	0.17
1.79	5.48	-1.43	9.08	0.90	0.20	13.18	2.01	0.41
2.68	4.59	-1.19	15.10	6.93	1.54	10.94	0.23	-0.05
2.20	5.07	-1.32	11.79	3.62	0.81	11.34	0.17	0.03
4.05	3.22	-0.84	13.45	5.28	1.17	13.68	2.51	0.51
12.02	4.75	1.23	6.71	1.46	-0.32	10.25	0.93	-0.19
15.12	**7.85**	2.04	8.12	0.05	-0.01	12.28	1.11	0.23
12.44	5.17	1.34	9.17	1.00	0.22	10.96	0.21	-0.04
6.99	0.28	-0.07	16.16	7.99	1.78	18.86	7.69	1.58
8.60	1.33	0.35	9.39	1.22	0.27	11.24	0.07	0.01
4.96	2.31	-0.60	8.80	0.63	0.14	12.96	1.79	0.37
3.19	4.08	-1.06	4.83	3.34	-0.74	3.71	7.46	-1.53
4.54	2.73	-0.71	4.58	3.59	-0.80	8.66	2.51	-0.52
5.15	2.12	-0.55	12.74	4.57	1.02	11.14	0.03	-0.01
9.01	1.74	0.45	11.64	3.47	0.77	15.46	4.29	0.88
4.02	3.25	-0.84	11.02	2.85	0.63	11.07	0.10	-0.02
10.24	2.97	0.77	9.73	1.56	0.35	11.77	0.60	0.12
13.07	5.80	1.51	9.75	1.58	0.35	14.34	3.17	0.65
9.30	2.03	0.53	8.28	0.11	0.02	16.40	5.23	1.07
6.25	1.02	-0.27	7.37	0.81	-0.18	18.39	7.22	1.48
12.80	5.53	1.44	8.66	0.49	0.11	20.71	9.54	1.96
15.95	**8.68**	2.26	9.07	0.90	0.20	12.61	1.44	0.30
9.20	1.93	0.50	4.97	3.20	-0.71	13.99	2.82	0.58
15.37	**8.10**	2.11	5.36	2.81	-0.62	23.69	12.52	2.57
14.44	7.17	1.86	10.93	2.76	0.61	25.33	14.16	2.91
2.95	4.32	-1.12	8.87	0.70	0.16	9.20	1.97	-0.40
6.46	0.81	-0.21	11.28	3.11	0.69	14.44	3.27	0.67
5.96	1.31	-0.34	7.81	0.36	-0.08	12.95	1.78	0.37
9.54	2.27	0.59	10.07	1.90	0.42	15.37	4.20	0.86
7.76	0.49	0.13	12.21	4.04	0.90	17.26	6.09	1.25

7.76	0.49	0.13	15.01	6.84	1.52	21.28	10.11	2.08
11.30	4.03	1.05	6.10	2.07	-0.46	10.04	1.13	-0.23
6.85	0.42	-0.11	6.73	1.44	-0.32	10.80	0.37	-0.08
9.67	2.40	0.62	8.85	0.68	0.15	21.71	10.54	2.16
8.78	1.51	0.39	5.59	2.58	-0.57	11.64	0.47	0.10
7.03	0.24	-0.06	7.66	0.51	-0.11	9.74	1.43	-0.30
8.37	1.10	0.29	5.77	2.40	-0.53	20.83	9.66	1.98
13.69	6.42	1.67	14.69	6.52	1.45	26.03	14.86	3.05
3.55	3.72	-0.97	5.86	2.31	-0.51	11.96	0.79	0.16
3.60	3.67	-0.95	5.87	2.30	-0.51	9.83	1.34	-0.28
6.98	0.29	-0.08	7.77	0.40	-0.09	17.24	6.07	1.25
3.17	4.10	-1.07	3.79	4.38	-0.98	16.75	5.58	1.14
2.50	4.77	-1.24	5.82	2.35	-0.52	10.90	0.27	-0.06
5.19	2.08	-0.54	3.33	4.84	-1.08	12.46	1.29	0.26
10.07	2.80	0.73	7.89	0.28	-0.06	13.02	1.85	0.38
10.60	3.33	0.87	4.89	3.28	-0.73	15.29	4.12	0.85
12.34	5.07	1.32	13.91	5.74	1.28	24.11	12.94	2.66
3.98	3.29	-0.86	8.69	0.52	0.12	14.06	2.89	0.59
11.25	3.98	1.03	7.44	0.73	-0.16	14.24	3.07	0.63
7.23	0.04	-0.01	8.30	0.13	0.03	14.29	3.12	0.64
6.58	0.69	-0.18	10.32	2.15	0.48	12.30	1.13	0.23
5.06	2.21	-0.58	5.63	2.54	-0.56	5.75	5.42	-1.11
8.41	1.14	0.29	6.54	1.63	-0.36	11.62	0.45	0.09
7.46	0.19	0.05	11.45	3.28	0.73	8.78	2.39	-0.49
10.68	3.41	0.88	11.42	3.25	0.72	11.60	0.43	0.09
4.94	2.33	-0.61	17.20	9.03	2.01	18.47	7.30	1.50
5.07	2.20	-0.57	17.30	9.13	2.03	14.82	3.65	0.75
5.06	2.21	-0.58	10.77	2.60	0.58	8.70	2.47	-0.51
6.43	0.84	-0.22	10.02	1.85	0.41	11.71	0.54	0.11
9.63	2.36	0.61	18.45	10.28	2.29	8.20	2.97	-0.61
5.50	1.77	-0.46	10.85	2.68	0.60	10.27	0.90	-0.18
15.20	**7.93**	2.06	18.40	10.23	2.28	11.20	0.03	0.01
4.30	2.97	-0.77	10.25	2.08	0.46	7.35	3.82	-0.79
6.74	0.53	-0.14	34.18	26.01	5.79	7.17	4.00	-0.82
3.20	4.07	-1.06	8.03	0.14	-0.03	2.85	8.32	-1.71
12.41	5.14	1.33	4.67	3.50	-0.78	13.57	2.40	0.49
6.56	0.71	-0.18	5.45	2.72	-0.61	9.80	1.37	-0.28
7.33	0.06	0.01	8.58	0.41	0.09	17.32	6.15	1.26
8.37	1.10	0.28	9.38	1.21	0.27	16.55	5.38	1.10
9.88	2.61	0.68	10.33	2.16	0.48	20.35	9.18	1.89
6.90	0.37	-0.10	6.22	1.95	-0.43	20.00	8.83	1.81
9.03	1.76	0.46	7.03	1.14	-0.25	11.73	0.56	0.11
3.71	3.56	-0.93	2.38	5.79	-1.29	11.80	0.63	0.13
6.40	0.87	-0.23	8.23	0.06	0.01	18.77	7.60	1.56
7.61	0.34	0.09	8.73	0.56	0.12	17.81	6.64	1.36
4.41	2.86	-0.75	8.75	0.58	0.13	15.83	4.66	0.96
4.42	2.85	-0.74	8.72	0.55	0.12	17.91	6.74	1.38

2.61	4.67	-1.21	5.25	2.92	-0.65	8.92	2.25	-0.46
11.03	3.76	0.98	18.99	10.82	2.41	28.39	17.22	3.54
2.47	4.80	-1.25	9.41	1.24	0.28	7.57	3.60	-0.74
2.16	5.11	-1.33	10.14	1.97	0.44	18.01	6.84	1.40
5.38	1.89	-0.49	11.10	2.93	0.65	15.02	3.85	0.79
4.29	2.98	-0.78	8.48	0.31	0.07	20.48	9.31	1.91
6.38	0.89	-0.23	17.31	9.14	2.03	19.64	8.47	1.74
4.11	3.16	-0.82	6.09	2.08	-0.46	12.03	0.86	0.18
5.08	2.19	-0.57	7.41	0.76	-0.17	8.50	2.67	-0.55
1.95	5.32	-1.38	9.26	1.09	0.24	9.01	2.16	-0.44
3.06	4.21	-1.10	6.10	2.07	-0.46	6.13	5.04	-1.04
6.50	0.77	-0.20	13.22	5.05	1.12	12.08	0.91	0.19
4.97	2.30	-0.60	6.82	1.35	-0.30	13.00	1.83	0.38
6.23	1.04	-0.27	3.68	4.49	-1.00	5.60	5.57	-1.15
2.61	4.66	-1.21	6.75	1.42	-0.32	7.02	4.15	-0.85
2.53	4.74	-1.23	20.43	12.26	2.73	13.48	2.31	0.47
3.52	3.75	-0.98	6.90	1.27	-0.28	5.80	5.37	-1.10
6.68	0.59	-0.16	17.38	9.21	2.05	13.89	2.72	0.56
5.56	1.71	-0.45	9.25	1.08	0.24	7.25	3.92	-0.81
2.66	4.61	-1.20	9.66	1.49	0.33	8.99	2.18	-0.45
4.78	2.49	-0.65	26.40	18.23	4.06	12.35	1.18	0.24
5.84	1.43	-0.37	5.96	2.21	-0.49	10.03	1.14	-0.23
3.42	3.85	-1.00	7.07	1.10	-0.24	7.86	3.31	-0.68
4.83	2.44	-0.63	3.81	4.36	-0.97	6.28	4.89	-1.01
4.35	2.92	-0.76	11.62	3.45	0.77	16.66	5.49	1.13
5.26	2.01	-0.52	6.98	1.19	-0.26	10.86	0.31	-0.07
6.55	0.72	-0.19	8.89	0.72	0.16	13.78	2.61	0.54
7.52	0.25	0.07	5.64	2.53	-0.56	12.99	1.82	0.37
8.70	1.43	0.37	1.07	7.10	-1.58	7.24	3.93	-0.81
4.03	3.24	-0.84	3.79	4.38	-0.97	6.84	4.33	-0.89
7.68	0.41	0.11	6.03	2.14	-0.48	7.76	3.41	-0.70
3.60	3.67	-0.96	2.01	6.16	-1.37	9.41	1.76	-0.36
7.81	0.54	0.14	1.49	6.68	-1.49	7.69	3.48	-0.72
7.98	0.71	0.18	3.96	4.21	-0.94	11.90	0.73	0.15
7.28	0.01	0.00	3.79	4.38	-0.98	10.01	1.16	-0.24
13.03	5.76	1.50	16.94	8.77	1.95	17.30	6.13	1.26
13.21	5.94	1.54	5.88	2.29	-0.51	17.63	6.46	1.33
8.91	1.64	0.43	5.48	2.69	-0.60	14.28	3.11	0.64
13.23	5.96	1.55	12.18	4.01	0.89	17.73	6.56	1.35
6.23	1.04	-0.27	3.61	4.56	-1.01	8.48	2.69	-0.55
3.51	3.76	-0.98	3.11	5.06	-1.13	6.89	4.28	-0.88
14.74	7.47	1.94	12.81	4.64	1.03	20.05	8.88	1.82
8.73	1.46	0.38	6.50	1.67	-0.37	8.36	2.81	-0.58
10.07	2.80	0.73	4.56	3.61	-0.80	12.95	1.78	0.37
8.56	1.29	0.33	6.50	1.67	-0.37	11.20	0.03	0.01
9.94	2.67	0.69	7.09	1.08	-0.24	11.82	0.65	0.13
6.72	0.55	-0.14	3.94	4.23	-0.94	10.96	0.21	-0.04

7.39	0.12	0.03	7.95	0.22	-0.05	10.96	0.21	-0.04
71.23	**63.96**	16.63	6.89	1.28	-0.29	4.26	6.91	-1.42
13.11	5.84	1.52	8.68	0.51	0.11	10.55	0.62	-0.13
39.99	**32.72**	8.51	30.78	22.61	5.03	27.61	16.44	3.38
10.32	3.05	0.79	5.79	2.38	-0.53	13.49	2.32	0.48
5.24	2.03	-0.53	7.79	0.38	-0.08	9.76	1.41	-0.29
3.74	3.53	-0.92	8.22	0.05	0.01	13.49	2.32	0.48
13.01	5.74	1.49	13.47	5.30	1.18	8.59	2.58	-0.53
9.86	2.59	0.67	10.29	2.12	0.47	8.15	3.02	-0.62
6.42	0.85	-0.22	3.25	4.92	-1.10	5.94	5.23	-1.08
9.64	2.37	0.62	14.29	6.12	1.36	15.26	4.09	0.84
15.68	**8.41**	2.19	10.48	2.31	0.51	19.03	7.86	1.62
8.76	1.49	0.39	12.91	4.74	1.06	10.71	0.46	-0.09
4.79	2.48	-0.64	2.40	5.77	-1.28	3.28	7.89	-1.62
7.33	0.06	0.02	4.52	3.65	-0.81	13.48	2.31	0.47
6.96	0.31	-0.08	6.08	2.09	-0.47	9.60	1.57	-0.32
9.96	2.69	0.70	4.49	3.68	-0.82	12.60	1.43	0.29
8.57	1.30	0.34	3.53	4.64	-1.03	16.10	4.93	1.01
4.91	2.36	-0.61	7.23	0.94	-0.21	9.61	1.56	-0.32
6.93	0.34	-0.09	5.67	2.50	-0.56	14.21	3.04	0.62
7.97	0.70	0.18	4.20	3.97	-0.88	9.06	2.11	-0.43
15.90	**8.63**	2.24	8.71	0.54	0.12	12.34	1.17	0.24
11.43	4.16	1.08	12.86	4.69	1.04	11.46	0.29	0.06
8.69	1.42	0.37	12.39	4.22	0.94	14.17	3.00	0.62
10.69	3.42	0.89	11.18	3.01	0.67	8.10	3.07	-0.63
4.42	2.85	-0.74	7.56	0.61	-0.14	4.40	6.77	-1.39
9.62	2.35	0.61	10.79	2.62	0.58	9.59	1.58	-0.33
5.26	2.01	-0.52	16.91	8.74	1.95	6.77	4.40	-0.90
14.22	6.95	1.80	26.19	18.02	4.01	12.59	1.42	0.29
8.43	1.16	0.30	20.88	12.71	2.83	3.84	7.33	-1.51
18.38	**11.11**	2.89	14.31	6.14	1.37	2.53	8.64	-1.77
8.34	1.07	0.28	8.78	0.61	0.14	4.70	6.47	-1.33
6.65	0.62	-0.16	13.54	5.37	1.19	5.32	5.85	-1.20
6.70	0.57	-0.15	13.85	5.68	1.26	5.91	5.26	-1.08
5.11	2.16	-0.56	11.80	3.63	0.81	3.77	7.40	-1.52
10.45	3.18	0.83	13.32	5.15	1.15	10.46	0.71	-0.15
3.48	3.79	-0.99	8.48	0.31	0.07	6.07	5.10	-1.05
7.88	0.61	0.16	15.30	7.13	1.59	10.82	0.35	-0.07
5.52	1.75	-0.45	14.81	6.64	1.48	14.16	2.99	0.61
4.04	3.23	-0.84	5.40	2.77	-0.62	7.11	4.06	-0.83
3.55	3.72	-0.97	6.83	1.34	-0.30	2.30	8.87	-1.82
7.27	2.60		8.17	3.04		11.17	3.29	
	7.80			9.11			9.87	
	3.85			4.49			4.87	
35.47		29.41		64.23				
30.44		54.02		57.27				
50.43		51.16		50.11				

32.79	48.63	42.30
37.28	45.80	53.48
9.01	11.15	9.42
7.19	7.37	17.57
1.99	9.54	9.31
7.23	5.19	17.19
2.73	4.34	16.54
4.78	6.61	15.15
2.82	2.33	3.92
27.02	33.44	28.26
8.45	7.00	11.76
35.47	40.44	40.02
32.50	39.19	38.33
1.09	1.03	1.04
-0.09	-0.03	-0.04

x toxic a,b,c

y

x toxic a,b,c

x toxic a,b,c

y

y

x toxic a,b

x	toxic a,b,c

y

y

					% inf	abs dev	robust Z
50002.00	A02	M-004866- NIMA (nev	284086.00	NEK8	8.88	0.54	-0.12
50002.00	A04	M-003795- NIMA (nev	140609.00	NEK7	15.54	6.12	1.33
50002.00	A05	M-004811- intestinal c	22858.00	ICK	10.40	0.98	0.21
50002.00	A06	M-004166- NIMA (nev	10783.00	NEK6	9.27	0.15	-0.03
50002.00	A07	M-003012- insulin-like	3480.00	IGF1R	9.70	0.28	0.06
50002.00	A08	M-003519- NIMA (nev	6787.00	NEK4	8.88	0.54	-0.12
50002.00	A09	M-006737- inositol he	9807.00	IHPK1	10.81	1.39	0.30
50002.00	A10	M-004867- NIMA (nev	4752.00	NEK3	9.53	0.11	0.02
50002.00	A11	M-006738- inositol he	51447.00	IHPK2	6.69	2.73	-0.59
50002.00	A12	M-004090- NIMA (nev	4751.00	NEK2	11.60	2.18	0.47
50002.00	A13	M-006739- inositol he	117283.00	IHPK3	12.91	3.49	0.76
50002.00	A14	M-004865- NIMA (nev	79858.00	NEK11	15.86	6.44	1.40
50002.00	A15	M-009371- inhibitor of	8518.00	IKBKAP	12.31	2.89	0.63
50002.00	A16	M-004864- NIMA (nev	4750.00	NEK1	8.99	0.43	-0.09
50002.00	A17	M-003503- inhibitor of	3551.00	IKBKB	13.71	4.29	0.93
50002.00	A18	M-006751- Coenzyme	80347.00	COASY	15.52	6.10	1.32
50002.00	A19	M-003723- inhibitor of	9641.00	IKBKE	17.45	8.03	1.74
50002.00	A20	M-015419- neurobeac	26960.00	NBEA	23.28	13.86	3.01
50002.00	A21	M-007967- interleukin	3558.00	IL2	12.90	3.48	0.76
50002.00	A23	M-004499- integrin-lin	3611.00	ILK	9.10	0.32	-0.07
50002.00	B02	M-024516- Ras protei	5924.00	RASGRF2	2.33	7.09	-1.54
50002.00	B04	M-004838- renal tumo	5891.00	RAGE	7.41	2.01	-0.44
50002.00	B05	M-004869- NIMA (nev	91754.00	NEK9	7.66	1.76	-0.38
50002.00	B06	M-003601- v-raf-1 mu	5894.00	RAF1	9.68	0.26	0.06
50002.00	B07	M-004763- nemo-like	51701.00	NLK	7.24	2.18	-0.47
50002.00	B08	M-003560- ras-related	5879.00	RAC1	4.94	4.48	-0.97
50002.00	B09	M-006821- non-metas	4830.00	NME1	12.55	3.13	0.68
50002.00	B10	M-006785- aldehyde d	5832.00	ALDH18A1	9.98	0.56	0.12
50002.00	B11	M-005102- non-metas	4831.00	NME2	13.81	4.39	0.95
50002.00	B12	M-005367- PX domain	54899.00	PXK	9.84	0.42	0.09
50002.00	B13	M-006753- non-metas	4832.00	NME3	10.19	0.77	0.17
50002.00	B14	M-008072- protein tyr	11122.00	PTPRT	6.41	3.01	-0.65
50002.00	B15	M-006494- non-metas	4833.00	NME4	11.14	1.72	0.37
50002.00	B16	M-004017- protein tyr	5801.00	PTPRR	15.38	5.96	1.29
50002.00	B17	M-006754- non-metas	8382.00	NME5	12.42	3.00	0.65
50002.00	B18	M-008476- protein tyr	5795.00	PTPRJ	19.11	9.69	2.10
50002.00	B19	M-006755- non-metas	10201.00	NME6	9.44	0.02	0.00
50002.00	B20	M-008069- protein tyr	5793.00	PTPRG	13.35	3.93	0.85
50002.00	B21	M-006756- non-metas	29922.00	NME7	13.77	4.35	0.95
50002.00	B23	M-005354- natriuretic	4881.00	NPR1	6.47	2.95	-0.64
50002.00	C02	M-006750- N-acetylglu	55577.00	NAGK	6.62	2.80	-0.61
50002.00	C04	M-004863- myosin IIIB	140469.00	MYO3B	11.24	1.82	0.39
50002.00	C05	M-010260- integrin-lin	80895.00	ILKAP	11.13	1.71	0.37
50002.00	C06	M-004862- myosin IIIA	53904.00	MYO3A	6.91	2.51	-0.55
50002.00	C07	M-006740- inositol pol	253430.00	IPMK	5.07	4.35	-0.95
50002.00	C08	M-005352- myosin ligh	85366.00	MYLK2	8.53	0.89	-0.19

50002.00	C09	M-003014- insulin rece	3643.00	INSR	4.26	5.16	-1.12
50002.00	C10	M-005351- myosin, ligl	4638.00	MYLK	12.07	2.65	0.58
50002.00	C11	M-005332- insulin rece	3645.00	INSRR	10.04	0.62	0.13
50002.00	C12	M-006749- mevalonat	4598.00	MVK	10.37	0.95	0.21
50002.00	C13	M-004760- interleukin	3654.00	IRAK1	10.49	1.07	0.23
50002.00	C14	M-006748- mevalonat	4597.00	MVD	6.84	2.58	-0.56
50002.00	C15	M-004761- interleukin	3656.00	IRAK2	19.66	10.24	2.22
50002.00	C16	M-003158- muscle, ske	4593.00	MUSK	13.73	4.31	0.94
50002.00	C17	M-004762- interleukin	11213.00	IRAK3	9.95	0.53	0.12
50002.00	C18	M-003753- serine/thre	51765.00	RP6-213H1	13.75	4.33	0.94
50002.00	C19	M-003015- insulin rece	3667.00	IRS1	6.87	2.55	-0.56
50002.00	C20	M-003157- macrophag	4486.00	MST1R	15.01	5.59	1.21
50002.00	C21	M-003144- IL2-inducib	3702.00	ITK	12.91	3.49	0.76
50002.00	C23	M-006741- inositol 1,3	3705.00	ITPK1	12.50	3.08	0.67
50002.00	D02	M-003600- protein tyr	84867.00	PTPN5	1.99	7.43	-1.61
50002.00	D04	M-003169- twinfilin, a	11344.00	TWF2	5.91	3.51	-0.76
50002.00	D05	M-005355- natriuretic	4882.00	NPR2	7.56	1.86	-0.40
50002.00	D06	M-003168- twinfilin, a	5756.00	TWF1	9.42	0.00	0.00
50002.00	D07	M-005356- nuclear rec	29959.00	NRBP1	6.90	2.52	-0.55
50002.00	D08	M-003167- PTK7 prote	5754.00	PTK7	8.99	0.43	-0.09
50002.00	D09	M-026286- neuregulin	10718.00	NRG3	10.52	1.10	0.24
50002.00	D10	M-003166- PTK6 prote	5753.00	PTK6	18.81	9.39	2.04
50002.00	D11	M-003159- neurotropl	4914.00	NTRK1	15.59	6.17	1.34
50002.00	D12	M-003165- PTK2B prot	2185.00	PTK2B	6.13	3.29	-0.71
50002.00	D13	M-003160- neurotropl	4915.00	NTRK2	10.07	0.65	0.14
50002.00	D14	M-003164- PTK2 prote	5747.00	PTK2	10.22	0.80	0.17
50002.00	D15	M-003161- neurotropl	4916.00	NTRK3	21.93	12.51	2.72
50002.00	D16	M-005366- protein ser	85481.00	PSKH2	9.49	0.07	0.02
50002.00	D17	M-007733- tumor prot	89882.00	TPD52L3	20.61	11.19	2.43
50002.00	D18	M-005365- protein ser	5681.00	PSKH1	13.97	4.55	0.99
50002.00	D19	M-004870- oxidative-s	9943.00	OXSR1	23.13	13.71	2.98
50002.00	D20	M-004171- TAO kinase	9344.00	TAOK2	11.70	2.28	0.50
50002.00	D21	M-007734- hypothetic	55197.00	P15RS	15.32	5.90	1.28
50002.00	D23	M-005357- SCY1-like 3	57147.00	SCYL3	14.02	4.60	1.00
50002.00	E02	M-020064- mannose r	9902.00	MRC2	3.04	6.38	-1.39
50002.00	E04	M-015738- myelin pro	9019.00	MPZL1	3.67	5.75	-1.25
50002.00	E05	M-006742- inositol 1,4	3706.00	ITPKA	5.02	4.40	-0.96
50002.00	E06	M-010612- membrane	4356.00	MPP3	5.08	4.34	-0.94
50002.00	E07	M-006743- inositol 1,4	3707.00	ITPKB	3.23	6.19	-1.35
50002.00	E08	M-009729- membrane	4355.00	MPP2	3.38	6.04	-1.31
50002.00	E09	M-006744- inositol 1,4	80271.00	ITPKC	5.35	4.07	-0.88
50002.00	E10	M-010252- membrane	4354.00	MPP1	11.91	2.49	0.54
50002.00	E11	M-003145- Janus kinas	3716.00	JAK1	22.12	12.70	2.76
50002.00	E12	M-003859- v-mos Mol	4342.00	MOS	8.77	0.65	-0.14
50002.00	E13	M-003146- Janus kinas	3717.00	JAK2	4.92	4.50	-0.98
50002.00	E14	M-004908- MAP kinas	2872.00	MKNK2	5.09	4.33	-0.94
50002.00	E15	M-003147- Janus kinas	3718.00	JAK3	12.89	3.47	0.75

50002.00	E16	M-004879- MAP kinase	8569.00	MKNK1	7.90	1.52	-0.33
50002.00	E17	M-004844- TAO kinase	51347.00	TAOK3	7.69	1.73	-0.38
50002.00	E18	M-004861- misshapen-	50488.00	MINK1	7.29	2.13	-0.46
50002.00	E19	M-003148- kinase inse	3791.00	KDR	6.48	2.94	-0.64
50002.00	E20	M-005350- alpha-kinas	57538.00	ALPK3	12.66	3.24	0.70
50002.00	E21	M-006745- ketohexoki	3795.00	KHK	10.91	1.49	0.32
50002.00	E23	M-004542- TRAF2 and	23043.00	TNIK	7.25	2.17	-0.47
50002.00	F02	M-006795- phosphorib	5636.00	PRPSAP2	4.05	5.37	-1.17
50002.00	F04	M-006794- phosphorib	5635.00	PRPSAP1	2.25	7.17	-1.56
50002.00	F05	M-007735- protein kin	29993.00	PACSIN1	14.36	4.94	1.07
50002.00	F06	M-004877- phosphorib	5634.00	PRPS2	1.09	8.33	-1.81
50002.00	F07	M-012956- phosphopr	55824.00	PAG1	4.18	5.24	-1.14
50002.00	F08	M-006784- phosphorib	5631.00	PRPS1	1.70	7.72	-1.68
50002.00	F09	M-003521- p21/Cdc42,	5058.00	PAK1	2.81	6.61	-1.44
50002.00	F10	M-004074- PRP4 pre-m	8899.00	PRPF4B	7.27	2.15	-0.47
50002.00	F11	M-003597- p21 (CDKN	5062.00	PAK2	15.11	5.69	1.24
50002.00	F12	M-004661- protein kin	5616.00	PRKY	3.70	5.72	-1.24
50002.00	F13	M-003614- p21 (CDKN	5063.00	PAK3	10.88	1.46	0.32
50002.00	F14	M-004660- protein kin	5613.00	PRKX	3.41	6.01	-1.31
50002.00	F15	M-003615- p21(CDKN1	10298.00	PAK4	2.16	7.26	-1.58
50002.00	F16	M-005031- WNK lysine	65266.00	WNK4	2.15	7.27	-1.58
50002.00	F17	M-004338- p21(CDKN1	56924.00	PAK6	5.48	3.94	-0.86
50002.00	F18	M-005364- WNK lysine	65267.00	WNK3	9.48	0.06	0.01
50002.00	F19	M-003973- p21(CDKN1	57144.00	PAK7	7.02	2.40	-0.52
50002.00	F20	M-005363- WNK lysine	65268.00	WNK2	3.57	5.85	-1.27
50002.00	F21	M-004057- pantothena	53354.00	PANK1	16.82	7.40	1.61
50002.00	F23	M-006758- pantothena	79646.00	PANK3	5.51	3.91	-0.85
50002.00	G02	M-005349- CaM kinase	79012.00	CAMKV	6.25	3.17	-0.69
50002.00	G04	M-007684- acyl-Coenzy	80724.00	ACAD10	7.89	1.53	-0.33
50002.00	G05	M-004046- microtubul	23031.00	MAST3	3.37	6.05	-1.32
50002.00	G06	M-005348- serine/thre	83931.00	STK40	15.55	6.13	1.33
50002.00	G07	M-004779- KIAA0999 p	23387.00	KIAA0999	5.66	3.76	-0.82
50002.00	G08	M-008770- phosphatid	138429.00	PIP5KL1	3.31	6.11	-1.33
50002.00	G09	M-004846- TAO kinase	57551.00	TAOK1	6.84	2.58	-0.56
50002.00	G10	M-005017- doublecort	166614.00	DCLK2	2.78	6.64	-1.44
50002.00	G11	M-023172- membrane	57574.00	MARCH4	6.82	2.60	-0.57
50002.00	G12	M-005347- chromosom	169436.00	C9orf96	8.83	0.59	-0.13
50002.00	G13	M-005336- KIAA1639 p	57729.00	KIAA1639	8.76	0.66	-0.14
50002.00	G14	M-005016- hypothetica	167359.00	MGC42105	20.01	10.59	2.30
50002.00	G15	M-005337- doublecort	85443.00	DCLK3	13.86	4.44	0.96
50002.00	G16	M-004681- casein kina	122011.00	CSNK1A1L	7.09	2.33	-0.51
50002.00	G17	M-004063- mixed linea	84451.00	KIAA1804	9.55	0.13	0.03
50002.00	G18	M-004783- PIP5K1A ps	206426.00	MGC26597	14.02	4.60	1.00
50002.00	G19	M-004619- BR serine/t	84446.00	BRSK1	11.96	2.54	0.55
50002.00	G20	M-004634- serine/thre	202374.00	STK32A	26.60	17.18	3.73
50002.00	G21	M-005338- lemur tyros	114783.00	LMTK3	11.70	2.28	0.49
50002.00	G23	M-004963- kinesin fam	23303.00	KIF13B	7.60	1.82	-0.40

50002.00	H02	M-005362- WNK lysin	65125.00	WNK1	6.17	3.25	-0.71
50002.00	H04	M-006426- protein kin	8575.00	PRKRA	3.83	5.59	-1.22
50002.00	H05	M-006759- pantothen	55229.00	PANK4	6.40	3.02	-0.66
50002.00	H06	M-003527- eukaryotic	5610.00	EIF2AK2	6.54	2.88	-0.63
50002.00	H07	M-007736- 3'-phospho	9061.00	PAPSS1	2.94	6.48	-1.41
50002.00	H08	M-004659- protein kin	5593.00	PRKG2	3.59	5.83	-1.27
50002.00	H09	M-006760- 3'-phospho	9060.00	PAPSS2	3.42	6.00	-1.30
50002.00	H10	M-004658- protein kin	5592.00	PRKG1	12.90	3.48	0.76
50002.00	H11	M-005018- PAS domai	23178.00	PASK	9.03	0.39	-0.09
50002.00	H12	M-005030- protein kin	5591.00	PRKDC	9.75	0.33	0.07
50002.00	H13	M-006796- phosphoen	5105.00	PCK1	7.39	2.03	-0.44
50002.00	H14	M-004197- protein kin	25865.00	PRKD2	6.55	2.87	-0.62
50002.00	H15	M-006797- phosphoen	5106.00	PCK2	3.93	5.49	-1.19
50002.00	H16	M-003526- protein kin	5590.00	PRKCZ	8.84	0.58	-0.13
50002.00	H17	M-004313- PCTAIRE pr	5127.00	PCTK1	9.30	0.12	-0.03
50002.00	H18	M-010618- protein kin	5589.00	PRKCSH	12.68	3.26	0.71
50002.00	H19	M-004835- PCTAIRE pr	5128.00	PCTK2	11.76	2.34	0.51
50002.00	H20	M-003525- protein kin	5588.00	PRKCQ	8.38	1.04	-0.23
50002.00	H21	M-004836- PCTAIRE pr	5129.00	PCTK3	15.81	6.39	1.39
50002.00	H23	M-003162- platelet-de	5156.00	PDGFRA	7.85	1.57	-0.34
50002.00	I02	M-005346- hypothetic	93627.00	MGC16169	6.62	2.80	-0.61
50002.00	I04	M-003156- met proto-	4233.00	MET	9.56	0.14	0.03
50002.00	I05	M-003981- U2AF hom	127933.00	UHMK1	22.50	13.08	2.84
50002.00	I06	M-003155- c-mer prot	10461.00	MERTK	14.13	4.71	1.02
50002.00	I07	M-003150- v-kit Hardy	3815.00	KIT	5.62	3.80	-0.83
50002.00	I08	M-004029- maternal e	9833.00	MELK	10.05	0.63	0.14
50002.00	I09	M-003149- lemur tyro	22853.00	LMTK2	6.68	2.74	-0.60
50002.00	I10	M-021396- MAP3K12	51562.00	MBIP	7.57	1.85	-0.40
50002.00	I11	M-005322- kinase sup	283455.00	KSR2	5.58	3.84	-0.83
50002.00	I12	M-003154- megakaryo	4145.00	MATK	14.32	4.90	1.06
50002.00	I13	M-005009- alpha-kina	80216.00	ALPK1	6.48	2.94	-0.64
50002.00	I14	M-004633- microtubul	23139.00	MAST2	5.95	3.47	-0.75
50002.00	I15	M-004632- LATS, large	9113.00	LATS1	8.32	1.10	-0.24
50002.00	I16	M-005345- MAP/micr	57787.00	MARK4	6.60	2.82	-0.61
50002.00	I17	M-003865- LATS, large	26524.00	LATS2	9.76	0.34	0.07
50002.00	I18	M-003517- MAP/micr	4140.00	MARK3	13.33	3.91	0.85
50002.00	I19	M-003151- lymphocyt	3932.00	LCK	18.42	9.00	1.95
50002.00	I20	M-004260- MAP/micr	2011.00	MARK2	7.70	1.72	-0.37
50002.00	I21	M-012120- lymphocyt	3937.00	LCP2	16.44	7.02	1.52
50002.00	I23	M-006930- PDZ and LI	10611.00	PDLIM5	16.50	7.08	1.54
50002.00	J02	M-005029- protein kin	23683.00	PRKD3	3.12	6.30	-1.37
50002.00	J04	M-005028- protein kin	5587.00	PRKD1	4.87	4.55	-0.99
50002.00	J05	M-003163- platelet-de	5159.00	PDGFRB	5.83	3.59	-0.78
50002.00	J06	M-004612- protein kin	5586.00	PKN2	8.86	0.56	-0.12
50002.00	J07	M-005019- pyruvate d	5163.00	PDK1	12.93	3.51	0.76
50002.00	J08	M-004175- protein kin	5585.00	PKN1	7.69	1.73	-0.38
50002.00	J09	M-005020- pyruvate d	5164.00	PDK2	14.00	4.58	0.99

50002.00	J10	M-004656- protein kin	5584.00	PRKCI	8.94	0.48	-0.11
50002.00	J11	M-005021- pyruvate d	5165.00	PDK3	5.78	3.64	-0.79
50002.00	J12	M-004655- protein kin	5583.00	PRKCH	7.41	2.01	-0.44
50002.00	J13	M-019425- pyruvate d	5166.00	PDK4	7.47	1.95	-0.42
50002.00	J14	M-004654- protein kin	5582.00	PRKCG	16.13	6.71	1.46
50002.00	J15	M-003017- 3-phosphoi	5170.00	PDPK1	10.70	1.28	0.28
50002.00	J16	M-004653- protein kin	5581.00	PRKCE	9.63	0.21	0.04
50002.00	J17	M-005070- pyridoxal (	8566.00	PDXK	12.68	3.26	0.71
50002.00	J18	M-003524- protein kin	5580.00	PRKCD	11.59	2.17	0.47
50002.00	J19	M-006761- 6-phospho	5207.00	PFKFB1	17.40	7.98	1.73
50002.00	J20	M-003758- protein kin	5579.00	PRKCB1	19.13	9.71	2.11
50002.00	J21	M-006762- 6-phospho	5208.00	PFKFB2	16.62	7.20	1.56
50002.00	J23	M-006763- 6-phospho	5209.00	PFKFB3	13.03	3.61	0.78
50002.00	K02	M-004259- MAP/micro	4139.00	MARK1	7.26	2.16	-0.47
50002.00	K04	M-005015- mitogen-ac	8550.00	MAPKAPK5	5.77	3.65	-0.79
50002.00	K05	M-007730- LIM domain	3984.00	LIMK1	7.75	1.67	-0.36
50002.00	K06	M-005014- mitogen-ac	7867.00	MAPKAPK3	5.28	4.14	-0.90
50002.00	K07	M-003311- LIM domain	3985.00	LIMK2	9.35	0.07	-0.02
50002.00	K08	M-003516- mitogen-ac	9261.00	MAPKAPK2	15.45	6.03	1.31
50002.00	K09	M-015901- ecotropic v	115704.00	EVI5L	5.70	3.72	-0.81
50002.00	K10	M-003505- mitogen-ac	5601.00	MAPK9	9.26	0.16	-0.03
50002.00	K11	M-005011- PDLIM1 int	149420.00	PDIK1L	13.50	4.08	0.88
50002.00	K12	M-003596- mitogen-ac	23162.00	MAPK8IP3	13.78	4.36	0.95
50002.00	K13	M-006804- phosphorib	221823.00	PRPS1L1	12.16	2.74	0.59
50002.00	K14	M-012462- mitogen-ac	23542.00	MAPK8IP2	12.25	2.83	0.61
50002.00	K15	M-005340- nuclear rec	340371.00	NRBP2	8.53	0.89	-0.19
50002.00	K16	M-003595- mitogen-ac	9479.00	MAPK8IP1	6.35	3.07	-0.67
50002.00	K17	M-005342- MLCK prote	91807.00	MLCK	16.51	7.09	1.54
50002.00	K18	M-003514- mitogen-ac	5599.00	MAPK8	6.91	2.51	-0.55
50002.00	K19	M-003152- leukocyte t	4058.00	LTK	8.93	0.49	-0.11
50002.00	K20	M-003513- mitogen-ac	5598.00	MAPK7	7.57	1.85	-0.40
50002.00	K21	M-005343- protein kin	92335.00	LYK5	16.56	7.14	1.55
50002.00	K23	M-003153- v-yes-1 Yar	4067.00	LYN	10.86	1.44	0.31
50002.00	L02	M-020124- protein inte	9463.00	PICK1	2.66	6.76	-1.47
50002.00	L04	M-003523- protein kin	5578.00	PRKCA	5.91	3.51	-0.76
50002.00	L05	M-006764- 6-phospho	5210.00	PFKFB4	10.44	1.02	0.22
50002.00	L06	M-007673- protein kin	5577.00	PRKAR2B	5.85	3.57	-0.78
50002.00	L07	M-006822- phosphofru	5211.00	PFKL	7.90	1.52	-0.33
50002.00	L08	M-007671- protein kin	5576.00	PRKAR2A	4.83	4.59	-1.00
50002.00	L09	M-006765- phosphofru	5213.00	PFKM	8.67	0.75	-0.16
50002.00	L10	M-007670- protein kin	5573.00	PRKAR1A	11.20	1.78	0.39
50002.00	L11	M-010253- phosphofru	5214.00	PFKP	7.54	1.88	-0.41
50002.00	L12	M-009859- protein kin	53632.00	PRKAG3	28.44	19.02	4.13
50002.00	L13	M-004837- PFTAIRE pr	5218.00	PFTK1	5.57	3.85	-0.84
50002.00	L14	M-009056- protein kin	5571.00	PRKAG1	12.94	3.52	0.77
50002.00	L15	M-006767- phosphogly	5230.00	PGK1	11.69	2.27	0.49
50002.00	L16	M-004651- protein kin	5568.00	PRKACG	15.30	5.88	1.28

50002.00	L17	M-006768- phosphogly	5232.00	PGK2	12.53	3.11	0.67
50002.00	L18	M-004650- protein kin	5567.00	PRKACB	13.77	4.35	0.94
50002.00	L19	M-019682- phosphoryl	5255.00	PHKA1	10.81	1.39	0.30
50002.00	L20	M-004649- protein kin	5566.00	PRKACA	16.75	7.33	1.59
50002.00	L21	M-007669- phosphoryl	5256.00	PHKA2	16.52	7.10	1.54
50002.00	L23	M-005023- phosphoryl	5260.00	PHKG1	5.69	3.73	-0.81
50002.00	M02	M-003594- mitogen-ac	5597.00	MAPK6	7.63	1.79	-0.39
50002.00	M04	M-003593- mitogen-ac	5596.00	MAPK4	12.53	3.11	0.68
50002.00	M05	M-020068- SMAD fami	4092.00	SMAD7	12.74	3.32	0.72
50002.00	M06	M-003592- mitogen-ac	5595.00	MAPK3	20.18	10.76	2.34
50002.00	M07	M-009453- membrane	260425.00	MAGI3	8.43	0.99	-0.22
50002.00	M08	M-003512- mitogen-ac	1432.00	MAPK14	4.91	4.51	-0.98
50002.00	M09	M-004813- male germ	4117.00	MAK	22.61	13.19	2.87
50002.00	M10	M-003591- mitogen-ac	5603.00	MAPK13	14.63	5.21	1.13
50002.00	M11	M-005936- mucosa as	10892.00	MALT1	22.06	12.64	2.74
50002.00	M12	M-003590- mitogen-ac	6300.00	MAPK12	10.47	1.05	0.23
50002.00	M13	M-003571- mitogen-ac	5604.00	MAP2K1	11.09	1.67	0.36
50002.00	M14	M-003972- mitogen-ac	5600.00	MAPK11	13.11	3.69	0.80
50002.00	M15	M-003572- mitogen-ac	8649.00	MAP2K1IP	16.55	7.13	1.55
50002.00	M16	M-004324- mitogen-ac	5602.00	MAPK10	10.00	0.58	0.13
50002.00	M17	M-003573- mitogen-ac	5605.00	MAP2K2	11.75	2.33	0.50
50002.00	M18	M-003555- mitogen-ac	5594.00	MAPK1	15.80	6.38	1.38
50002.00	M19	M-003509- mitogen-ac	5606.00	MAP2K3	15.82	6.40	1.39
50002.00	M20	M-003589- mitogen-ac	11183.00	MAP4K5	12.04	2.62	0.57
50002.00	M21	M-003574- mitogen-ac	6416.00	MAP2K4	26.92	17.50	3.80
50002.00	M23	M-003966- mitogen-ac	5607.00	MAP2K5	19.07	9.65	2.10
50002.00	N02	M-005361- protein kin	5563.00	PRKAA2	1.77	7.65	-1.66
50002.00	N04	M-005027- protein kin	5562.00	PRKAA1	7.87	1.55	-0.34
50002.00	N05	M-004881- phosphoryl	5261.00	PHKG2	7.36	2.06	-0.45
50002.00	N06	M-008486- protein ph	5531.00	PPP4C	6.65	2.77	-0.60
50002.00	N07	M-006769- phosphatid	55300.00	PI4K2B	7.74	1.69	-0.37
50002.00	N08	M-003599- protein ph	5516.00	PPP2CB	1.06	8.36	-1.82
50002.00	N09	M-006770- phosphatid	55361.00	PI4K2A	15.78	6.36	1.38
50002.00	N10	M-003598- protein ph	5515.00	PPP2CA	7.64	1.78	-0.39
50002.00	N11	M-006771- phosphoin	5286.00	PIK3C2A	8.16	1.26	-0.27
50002.00	N12	M-012745- protein ph	84152.00	PPP1R1B	7.33	2.09	-0.46
50002.00	N13	M-006772- phosphoin	5287.00	PIK3C2B	10.73	1.31	0.28
50002.00	N14	M-006783- polynucleo	11284.00	PNKP	8.91	0.51	-0.11
50002.00	N15	M-006773- phosphoin	5288.00	PIK3C2G	17.24	7.82	1.70
50002.00	N16	M-006782- phosphom	10654.00	PMVK	6.80	2.62	-0.57
50002.00	N17	M-003018- phosphoin	5290.00	PIK3CA	8.52	0.90	-0.20
50002.00	N18	M-010904- exosome c	5394.00	EXOSC10	17.56	8.14	1.77
50002.00	N19	M-003019- phosphoin	5291.00	PIK3CB	6.34	3.08	-0.67
50002.00	N21	M-005274- phosphoin	5294.00	PIK3CG	10.59	1.17	0.25
50002.00	N23	M-003020- phosphoin	5295.00	PIK3R1	3.42	6.00	-1.30
50002.00	O02	M-003971- mitogen-ac	9448.00	MAP4K4	8.04	1.38	-0.30
50002.00	O04	M-003588- mitogen-ac	8491.00	MAP4K3	15.22	5.80	1.26

50002.00	O05	M-003967- mitogen-ac	5608.00	MAP2K6	9.86	0.44	0.10
50002.00	O06	M-003587- mitogen-ac	5871.00	MAP4K2	9.41	0.01	0.00
50002.00	O07	M-004016- mitogen-ac	5609.00	MAP2K7	10.30	0.88	0.19
50002.00	O08	M-003586- mitogen-ac	11184.00	MAP4K1	5.38	4.04	-0.88
50002.00	O09	M-003575- mitogen-ac	4214.00	MAP3K1	11.22	1.80	0.39
50002.00	O10	M-003585- mitogen-ac	4293.00	MAP3K9	14.59	5.17	1.12
50002.00	O11	M-003576- mitogen-ac	4294.00	MAP3K10	10.72	1.30	0.28
50002.00	O12	M-003511- mitogen-ac	1326.00	MAP3K8	10.92	1.50	0.32
50002.00	O13	M-003577- mitogen-ac	4296.00	MAP3K11	8.96	0.46	-0.10
50002.00	O14	M-003790- mitogen-ac	6885.00	MAP3K7	24.13	14.71	3.20
50002.00	O15	M-003312- mitogen-ac	7786.00	MAP3K12	8.13	1.29	-0.28
50002.00	O16	M-003969- mitogen-ac	9064.00	MAP3K6	3.75	5.67	-1.23
50002.00	O17	M-003579- mitogen-ac	9175.00	MAP3K13	9.16	0.26	-0.06
50002.00	O18	M-003584- mitogen-ac	4217.00	MAP3K5	7.18	2.24	-0.49
50002.00	O19	M-003580- mitogen-ac	9020.00	MAP3K14	6.21	3.21	-0.70
50002.00	O20	M-003789- mitogen-ac	4216.00	MAP3K4	12.74	3.32	0.72
50002.00	O21	M-003582- mitogen-ac	10746.00	MAP3K2	16.78	7.36	1.60
50002.00	O23	M-003301- mitogen-ac	4215.00	MAP3K3	8.00	1.42	-0.31
50002.00	P02	M-004647- protein kin	29941.00	PKN3	32.26	22.84	4.96
50002.00	P04	M-005026- protein kin	9088.00	PKMYT1	13.49	4.07	0.88
50002.00	P05	M-003021- phosphoin	5296.00	PIK3R2	8.15	1.27	-0.28
50002.00	P06	M-006781- pyruvate ki	5315.00	PKM2	13.96	4.54	0.99
50002.00	P07	M-019546- phosphoin	8503.00	PIK3R3	17.00	7.58	1.65
50002.00	P08	M-006780- pyruvate ki	5313.00	PKLR	11.29	1.87	0.41
50002.00	P09	M-005025- phosphoin	30849.00	PIK3R4	8.96	0.46	-0.10
50002.00	P10	M-008224- protein kin	5570.00	PKIB	19.40	9.98	2.17
50002.00	P11	M-006776- phosphatid	5297.00	PI4KA	6.50	2.92	-0.64
50002.00	P12	M-012321- protein kin	5569.00	PKIA	6.14	3.28	-0.71
50002.00	P13	M-006777- phosphatid	5298.00	PI4KB	4.57	4.85	-1.06
50002.00	P14	M-004615- serine/thre	282974.00	STK32C	8.51	0.91	-0.20
50002.00	P15	M-003923- pim-1 oncc	5292.00	PIM1	18.48	9.06	1.97
50002.00	P16	M-014699- PITPNM fa	83394.00	PITPNM3	12.00	2.58	0.56
50002.00	P17	M-005359- pim-2 oncc	11040.00	PIM2	12.99	3.57	0.78
50002.00	P18	M-004535- phosphatid	79837.00	PIP4K2C	11.26	1.84	0.40
50002.00	P19	M-004030- PTEN induc	65018.00	PINK1	7.09	2.33	-0.51
50002.00	P20	M-006779- phosphatid	8396.00	PIP4K2B	6.24	3.18	-0.69
50002.00	P21	M-004780- phosphatid	8394.00	PIP5K1A	10.45	1.03	0.22
50002.00	P23	M-006778- phosphatid	5305.00	PIP4K2A	9.02	0.40	-0.09
				mdmdMAD	9.42	3.11	
				3*MAD		9.33	
				MADc		4.60	
50002.00	C22				59.88		45.31
50002.00	D22				56.50		53.04
50002.00	E22				52.34		50.56
50002.00	F22				45.47		52.86
				mn	53.55		50.44
				sd	6.21		3.61

50002.00	G22		12.43	11.21
50002.00	H22		5.62	4.06
50002.00	I22		11.51	8.86
50002.00	J22		8.89	7.09
		mn	9.61	7.81
		sd	3.05	3.01
		3psSD	18.62	10.82
		3ngSD	9.16	9.03
		SumSD	27.79	19.85
		MeanDf	43.94	42.64
		SumovrMn	0.63	0.47
		1minus	0.37	0.53

% inf	abs dev	robust Z	% inf	abs dev	robust Z		
8.14	0.96	-0.23	14.83	5.30	0.96		
10.18	1.08	0.25	9.58	0.05	0.01		
8.22	0.88	-0.21	6.50	3.03	-0.55		
9.11	0.01	0.00	7.45	2.08	-0.38		
5.76	3.34	-0.78	6.69	2.84	-0.52		
3.82	5.28	-1.24	2.90	6.63	-1.21		
9.06	0.04	-0.01	8.05	1.48	-0.27		
10.36	1.26	0.30	2.38	7.15	-1.30		
9.34	0.24	0.06	6.85	2.68	-0.49		
5.37	3.73	-0.88	5.22	4.31	-0.79		
16.84	7.74	1.81	8.88	0.65	-0.12		
7.96	1.14	-0.27	8.32	1.21	-0.22		
11.87	2.77	0.65	4.30	5.23	-0.95		
5.98	3.12	-0.73	5.59	3.94	-0.72		
11.02	1.92	0.45	3.73	5.80	-1.06		
12.21	3.11	0.73	9.10	0.43	-0.08		
14.68	5.58	1.31	6.09	3.44	-0.63		
20.10	11.00	2.58	12.99	3.46	0.63	y	
13.72	4.62	1.08	12.24	2.71	0.49		
16.85	7.75	1.82	7.57	1.96	-0.36		
10.10	1.00	0.23	3.05	6.48	-1.18		
12.09	2.99	0.70	3.62	5.91	-1.08		
17.12	8.02	1.88	3.48	6.05	-1.10		
16.69	7.59	1.78	5.50	4.03	-0.73		
11.17	2.07	0.49	2.35	7.18	-1.31		
10.28	1.18	0.28	0.51	9.02	-1.65		
17.00	7.90	1.85	5.01	4.52	-0.82		
6.29	2.81	-0.66	0.68	8.85	-1.61		
12.54	3.44	0.81	3.79	5.74	-1.05		
9.28	0.18	0.04	1.24	8.29	-1.51		
15.38	6.28	1.47	1.95	7.58	-1.38		
11.59	2.49	0.58	3.48	6.05	-1.10		
13.22	4.12	0.97	3.59	5.94	-1.08		
11.57	2.47	0.58	1.61	7.92	-1.44		
6.52	2.58	-0.60	1.91	7.62	-1.39		
27.22	18.12	4.25	4.72	4.81	-0.88	x	debris a,c
6.81	2.29	-0.54	3.81	5.72	-1.04		
13.96	4.86	1.14	11.57	2.04	0.37		
10.09	0.99	0.23	8.16	1.37	-0.25		
6.66	2.44	-0.57	3.61	5.92	-1.08		
2.86	6.24	-1.46	4.53	5.00	-0.91		
7.30	1.80	-0.42	6.68	2.85	-0.52		
13.04	3.94	0.92	19.92	10.39	1.89		
4.39	4.71	-1.11	5.73	3.80	-0.69		
8.74	0.36	-0.09	5.70	3.83	-0.70		
8.45	0.65	-0.15	10.49	0.96	0.17		

4.40	4.70	-1.10	7.59	1.94	-0.35	
8.58	0.52	-0.12	15.33	5.80	1.06	
7.83	1.27	-0.30	7.01	2.52	-0.46	
10.78	1.68	0.39	15.00	5.47	1.00	
9.80	0.70	0.16	9.40	0.13	-0.02	
9.63	0.53	0.12	7.57	1.96	-0.36	
16.76	7.66	1.80	25.27	15.74	2.87	y
19.26	10.16	2.38	11.59	2.06	0.38	
9.94	0.84	0.20	9.18	0.35	-0.07	
6.74	2.36	-0.55	15.14	5.61	1.02	
15.98	6.88	1.61	15.05	5.52	1.01	
7.61	1.49	-0.35	16.37	6.84	1.25	
6.67	2.43	-0.57	17.87	8.34	1.52	
13.94	4.84	1.14	24.05	14.52	2.65	
1.88	7.22	-1.69	7.58	1.95	-0.36	
7.03	2.07	-0.49	11.14	1.61	0.29	
6.59	2.51	-0.59	10.16	0.63	0.11	
3.79	5.31	-1.25	5.82	3.71	-0.68	
3.93	5.17	-1.21	6.70	2.83	-0.52	
5.45	3.65	-0.86	7.97	1.56	-0.29	
6.56	2.54	-0.59	11.01	1.48	0.27	
7.19	1.91	-0.45	12.40	2.87	0.52	
6.09	3.01	-0.71	7.77	1.76	-0.32	
6.92	2.18	-0.51	11.09	1.56	0.28	
10.38	1.28	0.30	8.20	1.33	-0.24	
10.99	1.89	0.44	13.21	3.68	0.67	
15.86	6.76	1.58	12.36	2.83	0.52	
13.01	3.91	0.92	3.15	6.38	-1.16	
17.12	8.02	1.88	9.16	0.37	-0.07	
10.51	1.41	0.33	8.74	0.79	-0.14	
13.00	3.90	0.92	13.62	4.09	0.74	
3.65	5.45	-1.28	6.67	2.86	-0.52	
12.82	3.72	0.87	11.63	2.10	0.38	
9.95	0.85	0.20	5.78	3.75	-0.69	
0.74	8.36	-1.96	10.85	1.32	0.24	
4.14	4.96	-1.16	8.80	0.73	-0.13	
3.13	5.98	-1.40	5.45	4.08	-0.74	
5.91	3.19	-0.75	8.76	0.77	-0.14	
2.51	6.59	-1.55	3.21	6.32	-1.15	
0.51	8.59	-2.01	4.02	5.51	-1.01	
2.68	6.42	-1.51	4.32	5.21	-0.95	
2.30	6.80	-1.60	3.68	5.85	-1.07	
22.32	13.22	3.10	34.18	24.65	4.49	y
3.49	5.61	-1.32	6.22	3.31	-0.60	
5.69	3.41	-0.80	7.25	2.28	-0.42	
0.86	8.24	-1.93	6.51	3.02	-0.55	
4.15	4.95	-1.16	8.86	0.67	-0.12	

2.75	6.35	-1.49	7.30	2.23	-0.41	
6.22	2.88	-0.68	7.29	2.24	-0.41	
2.26	6.84	-1.61	3.15	6.38	-1.16	
7.17	1.93	-0.45	9.73	0.20	0.04	
4.30	4.80	-1.13	6.62	2.91	-0.53	
12.98	3.88	0.91	12.04	2.51	0.46	
14.11	5.01	1.18	17.21	7.68	1.40	
7.49	1.61	-0.38	3.62	5.91	-1.08	
7.56	1.54	-0.36	7.16	2.37	-0.43	
13.87	4.77	1.12	13.70	4.17	0.76	
15.09	5.99	1.40	6.52	3.01	-0.55	
14.08	4.98	1.17	13.81	4.28	0.78	
8.56	0.54	-0.13	3.24	6.29	-1.15	
4.31	4.79	-1.12	4.38	5.15	-0.94	
11.65	2.55	0.60	10.73	1.20	0.22	
23.80	14.70	3.45	15.02	5.49	1.00	
7.79	1.31	-0.31	3.62	5.91	-1.08	
21.07	11.97	2.81	12.10	2.57	0.47	
11.70	2.60	0.61	4.56	4.97	-0.91	
11.13	2.03	0.48	3.91	5.62	-1.02	
7.39	1.71	-0.40	2.99	6.54	-1.19	
13.76	4.66	1.09	8.74	0.79	-0.14	
13.64	4.54	1.06	9.84	0.31	0.06	
12.95	3.85	0.90	6.24	3.29	-0.60	
12.69	3.59	0.84	8.76	0.77	-0.14	
16.02	6.92	1.62	16.85	7.32	1.33	
11.01	1.91	0.45	14.77	5.24	0.95	
5.52	3.58	-0.84	16.35	6.82	1.24	
28.62	19.52	4.58	16.18	6.65	1.21	
5.80	3.30	-0.77	7.87	1.66	-0.30	
16.28	7.18	1.68	17.16	7.63	1.39	
11.33	2.23	0.52	7.59	1.94	-0.35	
5.35	3.75	-0.88	3.58	5.96	-1.09	
9.26	0.16	0.04	5.33	4.20	-0.77	
7.20	1.90	-0.45	9.34	0.19	-0.04	
6.41	2.69	-0.63	9.94	0.41	0.07	
13.01	3.91	0.92	11.48	1.95	0.36	
11.28	2.18	0.51	9.35	0.18	-0.03	
18.25	9.15	2.15	18.54	9.01	1.64	y
17.49	8.39	1.97	12.24	2.71	0.49	
7.77	1.33	-0.31	8.98	0.55	-0.10	
8.45	0.65	-0.15	10.88	1.35	0.25	
13.84	4.74	1.11	19.09	9.56	1.74	
10.57	1.47	0.35	25.01	15.48	2.82	
11.39	2.29	0.54	14.32	4.79	0.87	
9.34	0.24	0.06	11.35	1.82	0.33	
4.77	4.33	-1.02	5.42	4.11	-0.75	

14.84	5.74	1.35	13.44	3.91	0.71	
4.13	4.97	-1.17	9.13	0.40	-0.07	
5.90	3.20	-0.75	10.08	0.55	0.10	
16.16	7.06	1.66	24.57	15.04	2.74	
4.45	4.65	-1.09	7.53	2.00	-0.37	
9.71	0.61	0.14	8.63	0.90	-0.16	
5.86	3.24	-0.76	5.27	4.26	-0.78	
8.04	1.06	-0.25	13.21	3.68	0.67	
10.48	1.38	0.32	16.07	6.54	1.19	
4.69	4.41	-1.03	8.46	1.07	-0.20	
10.07	0.97	0.23	9.91	0.38	0.07	
7.58	1.52	-0.36	11.46	1.93	0.35	
3.67	5.43	-1.27	5.12	4.41	-0.80	
5.16	3.94	-0.92	10.60	1.07	0.19	
6.38	2.72	-0.64	5.10	4.43	-0.81	
19.64	10.54	2.47	18.34	8.81	1.61	
8.40	0.70	-0.16	11.83	2.30	0.42	
5.93	3.17	-0.74	7.21	2.32	-0.42	
11.46	2.36	0.55	12.81	3.28	0.60	
7.21	1.89	-0.44	5.81	3.72	-0.68	
6.62	2.48	-0.58	11.76	2.23	0.41	
7.19	1.91	-0.45	11.05	1.52	0.28	
8.40	0.70	-0.16	26.79	17.26	3.15	y
8.76	0.34	-0.08	21.08	11.55	2.11	
8.27	0.83	-0.19	11.42	1.89	0.34	
9.13	0.03	0.01	14.64	5.11	0.93	
10.14	1.04	0.24	15.16	5.63	1.03	
10.62	1.52	0.36	17.63	8.10	1.48	
10.50	1.40	0.33	8.88	0.65	-0.12	
11.80	2.70	0.63	20.12	10.59	1.93	
6.77	2.33	-0.55	12.68	3.15	0.57	
11.40	2.30	0.54	19.84	10.31	1.88	
4.18	4.92	-1.15	9.16	0.37	-0.07	
8.89	0.21	-0.05	11.97	2.44	0.44	
12.77	3.67	0.86	16.14	6.61	1.20	
14.38	5.28	1.24	8.31	1.22	-0.22	
11.86	2.76	0.65	20.63	11.10	2.02	
4.99	4.11	-0.96	15.42	5.89	1.07	
18.61	9.51	2.23	18.67	9.14	1.67	
13.76	4.66	1.09	25.43	15.90	2.90	
14.59	5.49	1.29	18.12	8.59	1.56	
14.19	5.09	1.19	13.35	3.82	0.70	
6.86	2.24	-0.53	7.63	1.90	-0.35	
10.93	1.83	0.43	10.32	0.79	0.14	
15.41	6.31	1.48	15.43	5.90	1.07	
11.10	2.00	0.47	6.02	3.51	-0.64	
15.78	6.68	1.57	21.45	11.92	2.17	

13.18	4.08	0.96	14.50	4.97	0.91	
13.84	4.74	1.11	14.09	4.56	0.83	
16.38	7.28	1.71	9.64	0.11	0.02	
7.39	1.71	-0.40	9.53	0.00	0.00	
10.64	1.54	0.36	11.82	2.29	0.42	
16.13	7.03	1.65	9.70	0.17	0.03	
9.14	0.04	0.01	12.40	2.87	0.52	
16.09	6.99	1.64	9.38	0.15	-0.03	
10.93	1.83	0.43	12.67	3.14	0.57	
8.56	0.54	-0.13	8.64	0.89	-0.16	
12.75	3.65	0.86	10.65	1.12	0.20	
17.82	8.72	2.04	16.99	7.46	1.36	
9.75	0.65	0.15	12.37	2.84	0.52	
7.18	1.92	-0.45	5.23	4.30	-0.79	
5.97	3.13	-0.73	2.77	6.76	-1.23	
4.42	4.68	-1.10	4.13	5.40	-0.99	
5.08	4.02	-0.94	3.93	5.60	-1.02	
7.18	1.92	-0.45	4.92	4.61	-0.84	
9.26	0.16	0.04	6.36	3.17	-0.58	
7.54	1.56	-0.37	3.92	5.61	-1.02	
12.77	3.67	0.86	6.58	2.95	-0.54	
11.15	2.05	0.48	9.88	0.35	0.06	
9.13	0.03	0.01	5.52	4.01	-0.73	
15.73	6.63	1.55	23.45	13.92	2.54	
8.08	1.02	-0.24	6.82	2.71	-0.49	
12.08	2.98	0.70	5.27	4.26	-0.78	
6.69	2.41	-0.57	5.08	4.45	-0.81	
12.55	3.45	0.81	9.81	0.28	0.05	
5.42	3.68	-0.86	7.23	2.30	-0.42	
6.26	2.84	-0.67	6.73	2.80	-0.51	
26.55	17.45	4.09	7.27	2.26	-0.41	
16.49	7.39	1.73	14.57	5.04	0.92	
6.90	2.20	-0.52	5.59	3.94	-0.72	
7.00	2.10	-0.49	8.83	0.70	-0.13	
5.99	3.11	-0.73	15.93	6.40	1.17	
6.22	2.88	-0.67	58.49	48.96	8.93	
4.55	4.55	-1.07	7.30	2.23	-0.41	
8.55	0.55	-0.13	13.94	4.41	0.80	
4.84	4.26	-1.00	12.94	3.41	0.62	
9.19	0.09	0.02	14.21	4.68	0.85	
9.66	0.56	0.13	14.53	5.00	0.91	
5.88	3.22	-0.76	7.63	1.90	-0.35	
31.77	22.67	5.32	23.51	13.98	2.55	y
7.47	1.63	-0.38	7.18	2.35	-0.43	
11.05	1.95	0.46	13.22	3.69	0.67	
10.29	1.19	0.28	8.94	0.59	-0.11	
11.34	2.24	0.52	12.03	2.50	0.45	

8.24	0.86	-0.20	15.31	5.78	1.05		
9.22	0.12	0.03	16.21	6.68	1.22		
7.63	1.47	-0.34	5.01	4.52	-0.82		
9.85	0.75	0.17	11.07	1.54	0.28		
12.05	2.95	0.69	16.41	6.88	1.25		
9.83	0.73	0.17	3.33	6.20	-1.13		
2.44	6.66	-1.56	4.79	4.74	-0.86		
5.94	3.16	-0.74	11.67	2.14	0.39		
6.96	2.14	-0.50	9.17	0.36	-0.07		
13.59	4.49	1.05	23.30	13.77	2.51	y	
12.91	3.81	0.89	10.03	0.50	0.09		
5.18	3.92	-0.92	3.40	6.13	-1.12		
14.32	5.22	1.22	20.63	11.10	2.02	x	art b,c
7.23	1.87	-0.44	14.90	5.37	0.98		
10.07	0.97	0.23	17.44	7.91	1.44		
6.86	2.24	-0.53	11.38	1.85	0.34		
4.25	4.85	-1.14	9.29	0.24	-0.04		
4.39	4.71	-1.11	4.24	5.29	-0.96		
6.07	3.03	-0.71	12.03	2.50	0.46		
6.23	2.87	-0.67	12.59	3.06	0.56		
6.62	2.48	-0.58	9.90	0.37	0.07		
5.53	3.57	-0.84	11.92	2.39	0.43		
4.64	4.46	-1.05	14.29	4.76	0.87		
7.02	2.08	-0.49	17.82	8.29	1.51		
16.84	7.74	1.81	24.87	15.34	2.80	y	
20.36	11.26	2.64	21.66	12.13	2.21	y	
7.59	1.51	-0.35	9.80	0.27	0.05		
8.57	0.53	-0.12	14.26	4.73	0.86		
4.71	4.39	-1.03	13.90	4.37	0.80		
6.36	2.74	-0.64	8.90	0.63	-0.12		
6.63	2.47	-0.58	7.80	1.73	-0.32		
3.81	5.29	-1.24	5.91	3.62	-0.66		
13.02	3.92	0.92	23.82	14.29	2.60		
4.36	4.74	-1.11	10.99	1.46	0.27		
3.61	5.49	-1.29	6.88	2.65	-0.48		
9.12	0.02	0.00	16.90	7.37	1.34		
9.55	0.45	0.11	17.07	7.54	1.37		
6.31	2.79	-0.65	19.47	9.94	1.81		
12.93	3.83	0.90	16.82	7.29	1.33		
15.14	6.04	1.42	10.20	0.67	0.12		
5.08	4.02	-0.94	16.23	6.70	1.22		
10.71	1.61	0.38	24.28	14.75	2.69		
8.55	0.55	-0.13	7.75	1.78	-0.32		
9.45	0.35	0.08	14.18	4.65	0.85		
3.06	6.04	-1.42	7.62	1.91	-0.35		
6.02	3.08	-0.72	13.66	4.13	0.75		
8.81	0.29	-0.07	12.21	2.68	0.49		

8.53	0.57	-0.13	12.53	3.00	0.55		
5.00	4.10	-0.96	11.93	2.40	0.44		
10.31	1.21	0.28	13.54	4.01	0.73		
6.13	2.97	-0.70	12.13	2.60	0.47		
8.31	0.79	-0.18	17.92	8.39	1.53		
7.95	1.15	-0.27	13.96	4.43	0.81		
6.27	2.83	-0.67	14.03	4.50	0.82		
4.46	4.64	-1.09	12.02	2.49	0.45		
9.02	0.08	-0.02	13.77	4.24	0.77		
11.43	2.33	0.55	16.57	7.04	1.28		
4.97	4.13	-0.97	9.19	0.34	-0.06		
5.17	3.93	-0.92	9.14	0.39	-0.07		
11.27	2.17	0.51	11.83	2.30	0.42		
9.59	0.49	0.12	12.52	2.99	0.54		
10.65	1.55	0.36	11.13	1.60	0.29		
7.40	1.70	-0.40	20.47	10.94	1.99		
10.06	0.96	0.22	9.30	0.23	-0.04		
12.07	2.97	0.70	4.97	4.56	-0.83		
37.50	28.40	6.66	5.68	3.85	-0.70	x	toxic a,b,c
11.45	2.35	0.55	4.82	4.71	-0.86		
10.65	1.55	0.36	6.14	3.39	-0.62		
15.53	6.43	1.51	10.90	1.37	0.25		
9.10	0.00	0.00	6.96	2.58	-0.47		
8.49	0.61	-0.14	14.25	4.72	0.86		
5.89	3.21	-0.75	6.22	3.31	-0.60		
13.16	4.06	0.95	4.72	4.81	-0.88		
9.28	0.18	0.04	4.20	5.34	-0.97		
7.54	1.56	-0.37	4.53	5.00	-0.91		
6.38	2.72	-0.64	8.97	0.56	-0.10		
4.15	4.95	-1.16	4.91	4.62	-0.84		
7.11	1.99	-0.47	8.19	1.34	-0.25		
7.44	1.66	-0.39	6.94	2.59	-0.47		
10.41	1.31	0.31	11.04	1.51	0.27		
12.78	3.68	0.86	14.13	4.60	0.84		
5.81	3.29	-0.77	7.91	1.62	-0.30		
14.08	4.98	1.17	6.64	2.89	-0.53		
3.49	5.61	-1.32	5.17	4.36	-0.80		
9.16	0.06	0.02	11.02	1.49	0.27		
9.10	2.88		9.53	3.71			
	8.64			11.12			
	4.26			5.49			
	59.02						
	45.98						
	54.62						
	56.38						
	54.00						
	5.64						

6.37
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					% inf	abs dev	robust Z
50003.00	A05	M-006786- ribokinase	64080.00	RBKS	11.82	0.15	0.03
50003.00	A07	M-003170- ret proto-o	5979.00	RET	10.87	0.80	-0.15
50003.00	A09	M-006552- tripartite m	5987.00	TRIM27	8.13	3.54	-0.66
50003.00	A11	M-004662- G protein-c	6011.00	GRK1	18.28	6.61	1.23
50003.00	A13	M-005368- RIO kinase	83732.00	RIOK1	8.02	3.65	-0.68
50003.00	A15	M-005040- RIO kinase	8780.00	RIOK3	21.94	10.27	1.92
50003.00	A17	M-004445- receptor (T	8737.00	RIPK1	6.93	4.74	-0.89
50003.00	A19	M-003602- receptor-in	8767.00	RIPK2	12.51	0.84	0.16
50003.00	A21	M-003534- receptor-in	11035.00	RIPK3	12.02	0.35	0.06
50003.00	A23	M-005032- ribonucleas	6041.00	RNASEL	12.35	0.68	0.13
50003.00	C05	M-003536- Rho-associ	6093.00	ROCK1	27.79	**16.12**	3.01
50003.00	C07	M-004610- Rho-associ	9475.00	ROCK2	5.05	6.62	-1.24
50003.00	C09	M-003171- receptor ty	4919.00	ROR1	5.07	6.60	-1.23
50003.00	C11	M-003172- receptor ty	4920.00	ROR2	7.16	4.51	-0.84
50003.00	C13	M-003173- v-ros UR2 s	6098.00	ROS1	5.88	5.79	-1.08
50003.00	C15	M-012350- retinitis pig	6102.00	RP2	10.79	0.88	-0.16
50003.00	C17	M-003025- ribosomal p	6195.00	RPS6KA1	7.05	4.62	-0.86
50003.00	C19	M-004663- ribosomal p	6196.00	RPS6KA2	18.99	7.32	1.36
50003.00	C21	M-003026- ribosomal p	6197.00	RPS6KA3	22.11	10.44	1.95
50003.00	C23	M-004664- ribosomal p	8986.00	RPS6KA4	16.54	4.87	0.91
50003.00	E04	M-005398- zeta-chain	7535.00	ZAP70	9.64	2.03	-0.38
50003.00	E05	M-004665- ribosomal p	9252.00	RPS6KA5	12.47	0.80	0.15
50003.00	E06	M-005068- sterile alph	51776.00	ZAK	13.75	2.08	0.39
50003.00	E07	M-004670- ribosomal p	27330.00	RPS6KA6	7.51	4.16	-0.78
50003.00	E08	M-012329- tyrosine 3-m	10971.00	YWHAQ	3.49	8.18	-1.53
50003.00	E09	M-003616- ribosomal p	6198.00	RPS6KB1	9.64	2.03	-0.38
50003.00	E10	M-010626- tyrosine 3-m	7533.00	YWHAH	12.68	1.01	0.19
50003.00	E11	M-004671- ribosomal p	6199.00	RPS6KB2	11.58	0.09	-0.02
50003.00	E12	M-003184- v-yes-1 Yar	7525.00	YES1	9.69	1.98	-0.37
50003.00	E13	M-005371- ribosomal p	26750.00	RPS6KC1	17.29	5.62	1.05
50003.00	E14	M-006793- xylulokinas	9942.00	XYLB	13.99	2.32	0.43
50003.00	E15	M-005372- ribosomal p	83694.00	RPS6KL1	9.09	2.58	-0.48
50003.00	E16	M-012386- WNT inhibi	11197.00	WIF1	11.16	0.51	-0.10
50003.00	E17	M-003174- RYK recept	6259.00	RYK	11.22	0.45	-0.08
50003.00	E18	M-005050- WEE1 hom	7465.00	WEE1	14.89	3.22	0.60
50003.00	E19	M-004672- microtubul	22983.00	MAST1	22.01	10.34	1.93
50003.00	E20	M-005397- vaccinia rel	51231.00	VRK3	13.32	1.65	0.31
50003.00	E21	M-011505- src kinase a	8631.00	SKAP1	17.80	6.13	1.14
50003.00	E23	M-005373- SCY1-like 1	57410.00	SCYL1	7.67	4.00	-0.75
50003.00	G02	M-004684- vaccinia rel	7444.00	VRK2	4.59	7.08	-1.32
50003.00	G04	M-004683- vaccinia rel	7443.00	VRK1	16.48	4.81	0.90
50003.00	G05	M-007737- selenophos	22929.00	SEPHS1	11.37	0.30	-0.06
50003.00	G06	M-006792- uridine-cyt	54963.00	UCKL1	8.47	3.20	-0.60
50003.00	G07	M-003027- serum/gluc	6446.00	SGK1	16.21	4.54	0.85
50003.00	G08	M-005077- uridine-cyt	7371.00	UCK2	25.67	**14.00**	2.61
50003.00	G09	M-004673- serum/gluc	10110.00	SGK2	16.50	4.83	0.90

50003.00	G10	M-004059- cytidylate k	51727.00	CMPK	20.28	8.61	1.61
50003.00	G11	M-004162- serum/gluc	23678.00	SGK3	18.37	6.70	1.25
50003.00	G12	M-005396- unc-51-like	9706.00	ULK2	17.22	5.55	1.03
50003.00	G13	M-018841- SHC (Src hc	6464.00	SHC1	17.20	5.53	1.03
50003.00	G14	M-005049- unc-51-like	8408.00	ULK1	23.08	**11.41**	2.13
50003.00	G15	M-004778- SNF1-like k	23235.00	SNF1LK2	11.34	0.33	-0.06
50003.00	G16	M-007739- UDP-glucos	7360.00	UGP2	23.63	**11.96**	2.23
50003.00	G17	M-003850- STE20-like	9748.00	SLK	13.05	1.38	0.26
50003.00	G18	M-004062- uridine-cyt	83549.00	UCK1	16.90	5.23	0.97
50003.00	G19	M-005033- PI-3-kinase	23049.00	SMG1	14.56	2.89	0.54
50003.00	G20	M-003183- TYRO3 prot	7301.00	TYRO3	25.97	**14.30**	2.67
50003.00	G21	M-005374- NUAK fami	81788.00	NUAK2	9.43	2.24	-0.42
50003.00	G23	M-003959- SNF1-like k	150094.00	SNF1LK	15.72	4.05	0.75
50003.00	I02	M-003182- tyrosine kir	7297.00	TYK2	26.84	**15.17**	2.83
50003.00	I04	M-006791- thioredoxir	51314.00	TXNDC3	8.41	3.26	-0.61
50003.00	I05	M-003325- polo-like ki	10769.00	PLK2	5.22	6.45	-1.20
50003.00	I06	M-003181- TXK tyrosin	7294.00	TXK	6.11	5.56	-1.04
50003.00	I07	M-004322- SNF relatec	54861.00	SNRK	10.48	1.19	-0.22
50003.00	I08	M-005395- titin	7273.00	TTN	11.67	0.00	0.00
50003.00	I09	M-011511- suppressor	8651.00	SOCS1	7.95	3.72	-0.70
50003.00	I10	M-004105- TTK proteir	7272.00	TTK	11.83	0.16	0.03
50003.00	I11	M-017374- suppressor	9655.00	SOCS5	5.19	6.48	-1.21
50003.00	I12	M-004682- tau tubulin	146057.00	TTBK2	8.61	3.06	-0.57
50003.00	I13	M-007677- sperm autc	53340.00	SPA17	10.40	1.27	-0.24
50003.00	I14	M-004680- tau tubulin	84630.00	TTBK1	27.32	**15.65**	2.92
50003.00	I15	M-020826- CDC42 sma	56990.00	CDC42SE2	13.82	2.15	0.40
50003.00	I16	M-013077- testis-speci	60385.00	TSKS	2.66	9.01	-1.68
50003.00	I17	M-004172- sphingosin	8877.00	SPHK1	8.81	2.86	-0.53
50003.00	I18	M-005393- transient re	54822.00	TRPM7	17.82	6.15	1.15
50003.00	I19	M-004831- sphingosin	56848.00	SPHK2	15.76	4.09	0.76
50003.00	I20	M-005048- transient re	140803.00	TRPM6	8.28	3.39	-0.63
50003.00	I21	M-007738- selenophos	22928.00	SEPHS2	25.83	**14.16**	2.64
50003.00	I23	M-010230- sequestosc	8878.00	SQSTM1	14.62	2.95	0.55
50003.00	K02	M-005047- triple funct	7204.00	TRIO	6.90	4.77	-0.89
50003.00	K04	M-020821- T cell recep	50852.00	TRAT1	8.98	2.69	-0.50
50003.00	K05	M-003175- v-src sarcoi	6714.00	SRC	8.05	3.62	-0.68
50003.00	K06	M-005391- tribbles hoi	28951.00	TRIB2	7.96	3.71	-0.69
50003.00	K07	M-005376- src-related	6725.00	SRMS	14.61	2.94	0.55
50003.00	K08	M-005045- serine/thre	11139.00	TRAD	3.61	8.06	-1.50
50003.00	K09	M-003982- SFRS protei	6732.00	SRPK1	6.80	4.87	-0.91
50003.00	K10	M-006789- thiamin pyi	27010.00	TPK1	8.49	3.18	-0.59
50003.00	K11	M-004839- SFRS protei	6733.00	SRPK2	9.87	1.80	-0.34
50003.00	K12	M-005390- PDZ binding	55872.00	PBK	14.96	3.29	0.61
50003.00	K13	M-007290- abl-interac	10006.00	ABI1	13.56	1.89	0.35
50003.00	K14	M-003180- tyrosine kir	8711.00	TNK1	11.56	0.11	-0.02
50003.00	K15	M-005034- testis-speci	83983.00	TSSK6	9.19	2.48	-0.46
50003.00	K16	M-008090- tumor necr	8797.00	TNFRSF10A	4.59	7.08	-1.32

50003.00	K17	M-004168- serine/thre	6793.00	STK10	12.34	0.67	0.12
50003.00	K18	M-005156- toll-like rec	10333.00	TLR6	20.24	8.57	1.60
50003.00	K19	M-005035- serine/thre	6794.00	STK11	8.63	3.04	-0.57
50003.00	K20	M-008088- toll-like rec	7099.00	TLR4	11.81	0.14	0.03
50003.00	K21	M-004054- serine/thre	8576.00	STK16	9.49	2.18	-0.41
50003.00	K23	M-005377- serine/thre	9263.00	STK17A	8.52	3.15	-0.59
50003.00	M02	M-007745- toll-like rec	7098.00	TLR3	7.67	4.00	-0.75
50003.00	M04	M-008086- toll-like rec	7096.00	TLR1	16.23	4.56	0.85
50003.00	M05	M-004051- serine/thre	9262.00	STK17B	12.24	0.57	0.11
50003.00	M06	M-005389- tousled-lik	11011.00	TLK2	5.96	5.71	-1.07
50003.00	M07	M-005036- polo-like ki	10733.00	PLK4	9.50	2.17	-0.41
50003.00	M08	M-004174- tousled-lik	9874.00	TLK1	12.82	1.15	0.21
50003.00	M09	M-005378- serine/thre	8859.00	STK19	11.52	0.15	-0.03
50003.00	M10	M-006788- thymidine	7084.00	TK2	19.74	8.07	1.50
50003.00	M11	M-005379- testis-speci	23617.00	TSSK2	9.07	2.60	-0.49
50003.00	M12	M-006787- thymidine	7083.00	TK1	14.09	2.42	0.45
50003.00	M13	M-004050- testis-speci	81629.00	TSSK3	28.12	**16.45**	3.07
50003.00	M14	M-009932- tight juncti	9414.00	TJP2	16.67	5.00	0.93
50003.00	M15	M-005038- testis-speci	83942.00	TSSK1B	5.71	5.96	-1.11
50003.00	M16	M-003179- tyrosine ki	7075.00	TIE1	14.54	2.87	0.53
50003.00	M17	M-004840- SFRS prote	26576.00	SRPK3	25.87	**14.20**	2.65
50003.00	M18	M-003930- transformi	7048.00	TGFBR2	12.58	0.91	0.17
50003.00	M19	M-004872- serine/thre	8428.00	STK24	12.62	0.95	0.18
50003.00	M20	M-003929- transformi	7046.00	TGFBR1	38.38	**26.71**	4.98
50003.00	M21	M-004873- serine/thre	10494.00	STK25	12.78	1.11	0.21
50003.00	M23	M-005381- BR serine/t	9024.00	BRSK2	16.03	4.36	0.81
50003.00	O02	M-005386- testis expre	56155.00	TEX14	3.73	7.94	-1.48
50003.00	O04	M-005044- testis-speci	10420.00	TESK2	14.23	2.56	0.48
50003.00	O05	M-004874- serine/thre	6788.00	STK3	10.98	0.69	-0.13
50003.00	O06	M-005043- testis-speci	7016.00	TESK1	4.65	7.02	-1.31
50003.00	O07	M-005382- serine/thre	56164.00	STK31	9.45	2.22	-0.42
50003.00	O08	M-003178- TEK tyrosin	7010.00	TEK	18.75	7.08	1.32
50003.00	O09	M-005383- serine/thre	65975.00	STK33	10.93	0.74	-0.14
50003.00	O10	M-003177- tec protein	7006.00	TEC	19.98	8.31	1.55
50003.00	O11	M-005384- serine/thre	140901.00	STK35	22.30	10.63	1.98
50003.00	O12	M-003788- TANK-bindi	29110.00	TBK1	16.18	4.51	0.84
50003.00	O13	M-005039- serine/thre	27148.00	STK36	15.30	3.63	0.68
50003.00	O14	M-004171- TAO kinase	9344.00	TAOK2	5.24	6.43	-1.20
50003.00	O15	M-004674- serine/thre	11329.00	STK38	7.55	4.12	-0.77
50003.00	O16	M-005385- TAF1 RNA	138474.00	TAF1L	9.66	2.01	-0.38
50003.00	O17	M-003313- serine/thre	23012.00	STK38L	11.61	0.06	-0.01
50003.00	O18	M-005041- TAF1 RNA	6872.00	TAF1	8.98	2.69	-0.50
50003.00	O19	M-004875- serine thre	27347.00	STK39	11.54	0.13	-0.02
50003.00	O20	M-003176- spleen tyro	6850.00	SYK	12.14	0.47	0.09
50003.00	O21	M-004157- serine/thre	6789.00	STK4	6.33	5.34	-1.00
50003.00	O23	M-003545- aurora kin	6790.00	AURKA	9.78	1.89	-0.35
					11.67	3.62	

				3MAD		10.87	
				MADc		5.36	
50003.00	C22				61.59		44.54
50003.00	D22				48.51		51.06
50003.00	E22				63.62		48.21
50003.00	F22				52.96		53.30
				mn	56.67		49.28
				sd	7.14		3.78
50003.00	G22				11.92		9.90
50003.00	H22				5.87		9.67
50003.00	I22				7.83		8.15
50003.00	J22				6.12		9.68
				mn	7.94		9.35
				sd	2.80		0.81
				3psSD	21.42		11.34
				3ngSD	8.39		2.42
				SumSD	29.81		13.77
				MeanDf	48.74		39.93
				SumovrMn	0.61		0.34
				1minus	0.39		0.66
50003.00	G03	M-003290-	polo-like kinase 1 (Dros	PLK1 SMAR	24.40		27.25
50003.00	H03	M-003290-	polo-like kinase 1 (Dros	PLK1 SMAR	20.55		25.17
50003.00	I03	D-001206-	siControl non-targeting		12.78		13.11
50003.00	J03	D-001206-	siControl non-targeting		10.88		10.45

% inf	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**	
11.01	2.23	0.48	3.87	4.42	-1.00	
8.56	0.22	-0.05	4.99	3.30	-0.74	
9.96	1.18	0.26	5.14	3.15	-0.71	
8.18	0.60	-0.13	10.94	2.65	0.60	
8.37	0.41	-0.09	5.13	3.16	-0.71	
13.34	4.56	0.99	17.18	8.89	2.00	
5.20	3.58	-0.78	5.07	3.23	-0.73	
7.60	1.18	-0.26	5.14	3.15	-0.71	
8.78	0.00	0.00	7.40	0.89	-0.20	
5.08	3.70	-0.80	10.23	1.94	0.44	
23.35	**14.57**	3.17	28.20	**19.91**	4.49	y
6.51	2.27	-0.49	6.62	1.67	-0.38	
7.64	1.14	-0.25	5.22	3.07	-0.69	
9.82	1.04	0.23	4.10	4.19	-0.94	
4.50	4.28	-0.93	5.97	2.32	-0.52	
9.06	0.28	0.06	8.32	0.03	0.01	
4.92	3.86	-0.84	4.65	3.64	-0.82	
10.22	1.44	0.31	15.76	7.47	1.68	
15.62	6.84	1.49	23.14	**14.85**	3.35	
16.77	7.99	1.74	9.17	0.88	0.20	
11.62	2.84	0.62	7.82	0.47	-0.11	
8.32	0.46	-0.10	8.09	0.20	-0.04	
14.55	5.77	1.25	8.43	0.14	0.03	
6.02	2.76	-0.60	5.48	2.81	-0.63	
5.67	3.11	-0.68	1.71	6.58	-1.48	
10.08	1.30	0.28	4.57	3.72	-0.84	
9.31	0.53	0.11	6.60	1.69	-0.38	
5.14	3.64	-0.79	7.31	0.98	-0.22	
6.54	2.24	-0.49	12.80	4.51	1.02	
7.59	1.19	-0.26	10.67	2.38	0.54	
6.85	1.93	-0.42	5.24	3.05	-0.69	
7.51	1.27	-0.28	4.93	3.36	-0.76	
3.45	5.33	-1.16	4.84	3.45	-0.78	
5.67	3.11	-0.68	7.04	1.25	-0.28	
20.60	**11.82**	2.57	7.24	1.05	-0.24	
6.64	2.14	-0.47	10.09	1.80	0.41	
4.33	4.45	-0.97	5.05	3.24	-0.73	
5.59	3.19	-0.69	13.16	4.87	1.10	
4.77	4.01	-0.87	8.46	0.17	0.04	
11.41	2.63	0.57	5.15	3.14	-0.71	
7.84	0.94	-0.20	7.86	0.43	-0.10	
11.89	3.11	0.68	8.52	0.23	0.05	
10.79	2.01	0.44	7.12	1.17	-0.26	
15.05	6.27	1.37	7.49	0.80	-0.18	
19.26	**10.48**	2.28	8.49	0.20	0.05	y
12.28	3.50	0.76	6.99	1.30	-0.29	

19.36	**10.58**	2.30	16.65	8.36	1.88	
11.33	2.55	0.56	9.66	1.37	0.31	
14.55	5.77	1.26	7.63	0.66	-0.15	
13.25	4.47	0.97	5.53	2.76	-0.62	
21.07	**12.29**	2.68	19.63	**11.34**	2.56	y
8.67	0.11	-0.02	4.98	3.31	-0.75	
15.66	6.88	1.50	11.95	3.66	0.83	
10.03	1.25	0.27	5.52	2.78	-0.63	
11.13	2.35	0.51	17.41	**9.12**	2.06	
9.74	0.96	0.21	9.39	1.10	0.25	
13.71	4.93	1.07	14.72	6.43	1.45	
6.13	2.65	-0.58	8.29	0.00	0.00	
12.38	3.60	0.78	5.18	3.11	-0.70	
20.56	**11.78**	2.56	30.12	**21.83**	4.92	y
7.26	1.52	-0.33	14.03	5.74	1.30	
11.89	3.11	0.68	9.70	1.41	0.32	
14.45	5.67	1.23	12.35	4.06	0.91	
7.85	0.93	-0.20	15.37	7.08	1.60	
11.08	2.30	0.50	13.94	5.65	1.28	
6.97	1.81	-0.39	13.34	5.05	1.14	
15.37	6.59	1.43	11.79	3.50	0.79	
11.98	3.20	0.70	9.70	1.41	0.32	
6.58	2.20	-0.48	8.01	0.28	-0.06	
9.79	1.01	0.22	9.07	0.78	0.18	
19.49	**10.71**	2.33	24.96	**16.67**	3.76	y
5.77	3.01	-0.65	11.93	3.64	0.82	
5.67	3.11	-0.68	6.81	1.48	-0.33	
10.71	1.93	0.42	6.23	2.06	-0.46	
22.51	**13.73**	2.99	23.04	**14.75**	3.33	y
14.91	6.13	1.33	17.95	**9.66**	2.18	
5.58	3.20	-0.70	8.87	0.58	0.13	
17.42	8.64	1.88	25.56	**17.27**	3.89	y
8.07	0.71	-0.16	11.21	2.92	0.66	
2.01	6.77	-1.47	7.44	0.85	-0.19	
14.10	5.32	1.16	25.52	**17.23**	3.88	
2.04	6.74	-1.47	4.77	3.52	-0.79	
5.82	2.96	-0.64	7.25	1.04	-0.23	
5.53	3.25	-0.71	4.57	3.73	-0.84	
5.64	3.14	-0.68	5.89	2.40	-0.54	
3.83	4.95	-1.08	12.47	4.18	0.94	
2.66	6.12	-1.33	12.20	3.91	0.88	
6.08	2.70	-0.59	7.96	0.33	-0.07	
10.43	1.65	0.36	6.27	2.02	-0.45	
3.40	5.38	-1.17	5.70	2.59	-0.58	
12.09	3.31	0.72	14.25	5.96	1.34	
6.56	2.22	-0.48	9.65	1.36	0.31	
2.93	5.85	-1.27	9.91	1.62	0.37	

6.85	1.93	-0.42	12.20	3.91	0.88	
11.93	3.15	0.68	15.11	6.82	1.54	
8.97	0.19	0.04	10.32	2.03	0.46	
8.31	0.47	-0.10	11.24	2.95	0.67	
8.79	0.01	0.00	12.31	4.02	0.91	
13.51	4.73	1.03	15.86	7.57	1.71	
1.56	7.22	-1.57	1.42	6.87	-1.55	
6.39	2.39	-0.52	10.25	1.96	0.44	
2.96	5.82	-1.27	4.96	3.33	-0.75	
2.49	6.29	-1.37	5.29	3.00	-0.68	
2.25	6.53	-1.42	6.53	1.77	-0.40	
5.79	2.99	-0.65	7.52	0.77	-0.17	
3.28	5.50	-1.20	2.56	5.73	-1.29	
6.28	2.50	-0.54	5.23	3.06	-0.69	
2.87	5.91	-1.29	2.23	6.06	-1.37	
3.12	5.66	-1.23	3.13	5.16	-1.16	
11.92	3.14	0.68	7.94	0.35	-0.08	
4.60	4.18	-0.91	9.75	1.46	0.33	
5.51	3.27	-0.71	5.99	2.30	-0.52	
3.00	5.78	-1.26	7.68	0.61	-0.14	
11.09	2.31	0.50	11.94	3.65	0.82	
5.67	3.11	-0.68	6.65	1.64	-0.37	
6.43	2.35	-0.51	5.26	3.03	-0.68	
7.98	0.80	-0.17	25.09	**16.80**	3.79	y
12.25	3.47	0.76	17.33	**9.04**	2.04	
9.92	1.14	0.25	9.16	0.87	0.20	
5.78	3.00	-0.65	0.82	7.47	-1.68	
5.85	2.93	-0.64	3.06	5.23	-1.18	
9.76	0.98	0.21	9.60	1.31	0.30	
7.52	1.26	-0.28	8.34	0.05	0.01	
9.04	0.26	0.06	4.14	4.15	-0.94	
14.75	5.97	1.30	9.14	0.85	0.19	
13.03	4.25	0.92	7.51	0.78	-0.18	
7.72	1.06	-0.23	9.38	1.09	0.25	
13.42	4.64	1.01	6.76	1.53	-0.35	
17.27	8.49	1.85	10.83	2.54	0.57	
16.56	7.78	1.69	8.96	0.67	0.15	
8.54	0.24	-0.05	7.12	1.17	-0.26	
10.64	1.86	0.41	4.96	3.33	-0.75	
8.80	0.02	0.01	7.02	1.27	-0.29	
9.35	0.57	0.12	11.27	2.98	0.67	
9.57	0.79	0.17	13.29	5.00	1.13	
11.25	2.47	0.54	11.29	3.00	0.68	
19.20	**10.42**	2.27	12.78	4.49	1.01	
9.32	0.54	0.12	7.94	0.35	-0.08	
10.83	2.05	0.45	17.69	**9.40**	2.12	
8.78	3.11		8.29	3.00		

26.34	9.32	24.87	8.99
	4.60		4.43
	57.99		
	47.81		
	52.50		
	53.82		
	53.03		
	4.19		
	3.92		
	6.01		
	3.48		
	11.42		
	6.21		
	3.65		
	12.58		
	10.94		
	23.51		
	46.82		
	0.50		
	0.50		
	26.54		
	22.73		
	13.69		
	13.89		

					% inf	abs dev
50004.00	A02	M-016036- guanine nucleotide binding p	2791.00	GNG11	3.81	6.13
50004.00	A04	M-017238- guanine nucleotide binding p	59345.00	GNB4	3.37	6.57
50004.00	A05	M-005413- adenylate cyclase activating	117.00	ADCYAP1R	8.36	1.58
50004.00	A06	M-011671- guanine nucleotide binding p	2784.00	GNB3	6.42	3.52
50004.00	A07	M-005414- adrenomedullin receptor	11318.00	ADMR	4.92	5.02
50004.00	A08	M-017242- guanine nucleotide binding p	2782.00	GNB1	17.74	7.80
50004.00	A09	M-005415- adenosine A1 receptor	134.00	ADORA1	9.12	0.82
50004.00	A10	M-010405- guanine nucleotide binding p	2781.00	GNAZ	21.99	**12.05**
50004.00	A11	M-005416- adenosine A2a receptor	135.00	ADORA2A	10.49	0.55
50004.00	A12	M-010408- guanine nucleotide binding p	2780.00	GNAT2	8.13	1.81
50004.00	A13	M-005417- adenosine A2b receptor	136.00	ADORA2B	13.99	4.05
50004.00	A14	M-009827- guanine nucleotide binding p	2779.00	GNAT1	11.11	1.17
50004.00	A15	M-005418- adenosine A3 receptor	140.00	ADORA3	6.33	3.61
50004.00	A16	M-010825- GNAS complex locus	2778.00	GNAS	4.18	5.76
50004.00	A17	M-005419- adrenergic, alpha-1A-, recept	148.00	ADRA1A	12.69	2.75
50004.00	A18	M-008562- guanine nucleotide binding p	2776.00	GNAQ	7.68	2.26
50004.00	A19	M-005420- adrenergic, alpha-1B-, recept	147.00	ADRA1B	10.51	0.57
50004.00	A20	M-009486- guanine nucleotide binding p	2775.00	GNAO1	3.69	6.25
50004.00	A21	M-005421- adrenergic, alpha-1D-, recept	146.00	ADRA1D	2.95	6.99
50004.00	A23	M-005422- adrenergic, alpha-2A-, recept	150.00	ADRA2A	5.53	4.41
50004.00	B02	M-005650- latrophilin 1	22859.00	LPHN1	0.77	9.17
50004.00	B04	M-008400- similar to POSSIBLE GUSTAT	115131.00	LOC115131	0.53	9.41
50004.00	B05	M-020575- guanine nucleotide binding p	55970.00	GNG12	1.47	8.47
50004.00	B06	M-003681- luteinizing hormone/choriog	3973.00	LHCGR	2.50	7.44
50004.00	B07	M-012804- guanine nucleotide binding p	2785.00	GNG3	1.28	8.66
50004.00	B08	M-005649- relaxin/insulin-like family pe	59350.00	RXFP1	3.02	6.92
50004.00	B09	M-017066- guanine nucleotide binding p	2786.00	GNG4	5.15	4.80
50004.00	B10	M-004092- G-protein signalling modulat	29899.00	GPSM2	7.61	2.33
50004.00	B11	M-012699- guanine nucleotide binding p	2787.00	GNG5	3.56	6.38
50004.00	B12	M-012166- LanC lantibiotic synthetase c	10314.00	LANCL1	2.34	7.60
50004.00	B13	M-019807- guanine nucleotide binding p	2788.00	GNG7	4.53	5.41
50004.00	B14	M-006253- potassium inwardly-rectifyin	3765.00	KCNJ9	5.78	4.16
50004.00	B15	M-005517- gonadotropin-releasing horm	2798.00	GNRHR	3.18	6.76
50004.00	B16	M-006251- potassium inwardly-rectifyin	3763.00	KCNJ6	16.22	6.28
50004.00	B17	M-005518- gonadotropin-releasing horm	114814.00	GNRHR2	11.43	1.49
50004.00	B18	M-006250- potassium inwardly-rectifyin	3762.00	KCNJ5	2.32	7.62
50004.00	B19	M-005519- G protein-coupled bile acid r	151306.00	GPBAR1	10.41	0.47
50004.00	B20	M-006248- potassium inwardly-rectifyin	3760.00	KCNJ3	1.63	8.31
50004.00	B21	M-005521- G protein-coupled receptor 1	139760.00	GPR119	6.00	3.94
50004.00	B23	M-005522- G protein-coupled receptor 1	11245.00	GPR176	12.82	2.88
50004.00	C02	M-005184- guanine nucleotide binding p	2773.00	GNAI3	0.95	8.99
50004.00	C04	M-010404- guanine nucleotide binding p	2770.00	GNAI1	6.96	2.98
50004.00	C05	M-005423- adrenergic, alpha-2B-, recept	151.00	ADRA2B	3.72	6.22
50004.00	C06	M-009327- guanine nucleotide binding p	2769.00	GNA15	4.00	5.94
50004.00	C07	M-005424- adrenergic, alpha-2C-, recept	152.00	ADRA2C	11.24	1.30
50004.00	C08	M-008561- guanine nucleotide binding p	9630.00	GNA14	6.82	3.12

50004.00	C09	M-005425-	adrenergic, beta-1-, receptor	153.00	ADRB1	9.92	0.02
50004.00	C10	M-009948-	guanine nucleotide binding p	10672.00	GNA13	8.95	0.99
50004.00	C11	M-005426-	adrenergic, beta-2-, receptor	154.00	ADRB2	12.70	2.76
50004.00	C12	M-005516-	glucagon-like peptide 2 recep	9340.00	GLP2R	8.62	1.32
50004.00	C13	M-005427-	adrenergic, beta-3-, receptor	155.00	ADRB3	0.87	9.07
50004.00	C14	M-005515-	glucagon-like peptide 1 recep	2740.00	GLP1R	8.71	1.23
50004.00	C15	M-004325-	adrenergic, beta, receptor ki	156.00	ADRBK1	6.11	3.83
50004.00	C16	M-012860-	G protein-coupled receptor k	9815.00	GIT2	12.95	3.01
50004.00	C17	M-004326-	adrenergic, beta, receptor ki	157.00	ADRBK2	10.80	0.86
50004.00	C18	M-020565-	G protein-coupled receptor k	28964.00	GIT1	10.88	0.94
50004.00	C19	M-005428-	angiotensin II receptor, type	185.00	AGTR1	16.42	6.48
50004.00	C20	M-005514-	gastric inhibitory polypeptide	2696.00	GIPR	12.43	2.49
50004.00	C21	M-005429-	angiotensin II receptor, type	186.00	AGTR2	9.23	0.71
50004.00	C23	M-005430-	angiotensin II receptor-like 1	187.00	AGTRL1	27.37	**17.43**
50004.00	D02	M-008750-	olfactory receptor, family 10,	144124.00	OR10A5	3.41	6.54
50004.00	D04	M-009073-	olfactory receptor, family 5,	120065.00	OR5P2	5.82	4.12
50004.00	D05	M-005523-	G protein-coupled receptor 1	2825.00	GPR1	10.05	0.11
50004.00	D06	M-009061-	olfactory receptor, family 5,	120066.00	OR5P3	7.19	2.75
50004.00	D07	M-005524-	prolactin releasing hormone	2834.00	PRLHR	7.99	1.95
50004.00	D08	M-005647-	interleukin 8 receptor, beta	3579.00	IL8RB	8.25	1.69
50004.00	D09	M-005525-	relaxin/insulin-like family pep	339403.00	RXFP4	6.02	3.92
50004.00	D10	M-005646-	interleukin 8 receptor, alpha	3577.00	IL8RA	4.68	5.26
50004.00	D11	M-005526-	G protein-coupled receptor 1	83550.00	GPR101	3.02	6.92
50004.00	D12	M-004756-	interleukin 8	3576.00	IL8	7.19	2.75
50004.00	D13	M-005527-	trace amine associated recep	83551.00	TAAR8	6.83	3.11
50004.00	D14	M-005644-	5-hydroxytryptamine (seroto	3363.00	HTR7	9.95	0.01
50004.00	D15	M-005528-	purinergic receptor P2Y, G-p	9934.00	P2RY14	4.46	5.48
50004.00	D16	M-005643-	5-hydroxytryptamine (seroto	3362.00	HTR6	6.82	3.12
50004.00	D17	M-005531-	G protein-coupled receptor 1	266977.00	GPR110	3.49	6.45
50004.00	D18	M-005642-	5-hydroxytryptamine (seroto	3361.00	HTR5A	4.72	5.22
50004.00	D19	M-005532-	G protein-coupled receptor 1	222611.00	GPR111	6.45	3.49
50004.00	D20	M-005641-	5-hydroxytryptamine (seroto	3360.00	HTR4	9.33	0.61
50004.00	D21	M-005533-	G protein-coupled receptor 1	139378.00	GPR112	6.08	3.87
50004.00	D23	M-005534-	G protein-coupled receptor 1	165082.00	GPR113	11.86	1.92
50004.00	E02	M-005513-	growth hormone secretagog	2693.00	GHSR	3.29	6.65
50004.00	E04	M-005512-	growth hormone releasing h	2692.00	GHRHR	14.52	4.58
50004.00	E05	M-003000-	v-akt murine thymoma viral	207.00	AKT1	15.53	5.59
50004.00	E06	M-005511-	glucagon receptor	2642.00	GCGR	5.21	4.73
50004.00	E07	M-011813-	ADP-ribosylation factor-like	403.00	ARL3	11.14	1.20
50004.00	E08	M-017201-	glucagon	2641.00	GCG	9.73	0.21
50004.00	E09	M-011971-	arrestin, beta 1	408.00	ARRB1	8.03	1.91
50004.00	E10	M-004140-	galanin receptor 2	8811.00	GALR2	9.64	0.30
50004.00	E11	M-003631-	arginine vasopressin recepto	552.00	AVPR1A	8.47	1.47
50004.00	E12	M-005509-	gamma-aminobutyric acid (G	2550.00	GABBR1	18.41	8.47
50004.00	E13	M-005431-	arginine vasopressin recepto	553.00	AVPR1B	3.50	6.44
50004.00	E14	M-005506-	frizzled homolog 9 (Drosophi	8326.00	FZD9	7.83	2.11
50004.00	E15	M-005432-	arginine vasopressin recepto	554.00	AVPR2	2.83	7.11

50004.00	E16	M-003962- frizzled homolog 8 (Drosophi	8325.00	FZD8	14.08	4.14
50004.00	E17	M-005433- brain-specific angiogenesis ir	575.00	BAI1	10.23	0.29
50004.00	E18	M-003671- frizzled homolog 7 (Drosophi	8324.00	FZD7	4.72	5.22
50004.00	E19	M-003632- brain-specific angiogenesis ir	576.00	BAI2	11.56	1.62
50004.00	E20	M-005505- frizzled homolog 6 (Drosophi	8323.00	FZD6	10.56	0.62
50004.00	E21	M-005434- brain-specific angiogenesis ir	577.00	BAI3	11.74	1.80
50004.00	E23	M-005435- bradykinin receptor B1	623.00	BDKRB1	13.07	3.13
50004.00	F02	M-006205- 5-hydroxytryptamine (seroto	9177.00	HTR3B	0.91	9.03
50004.00	F04	M-006204- 5-hydroxytryptamine (seroto	3359.00	HTR3A	2.59	7.35
50004.00	F05	M-005536- G protein-coupled receptor 1	221393.00	GPR115	3.97	5.97
50004.00	F06	M-005640- 5-hydroxytryptamine (seroto	3358.00	HTR2C	4.14	5.80
50004.00	F07	M-005537- G protein-coupled receptor 1	221395.00	GPR116	1.04	8.90
50004.00	F08	M-005638- 5-hydroxytryptamine (seroto	3356.00	HTR2A	3.27	6.67
50004.00	F09	M-005521- G protein-coupled receptor 1	139760.00	GPR119	3.99	5.95
50004.00	F10	M-005637- 5-hydroxytryptamine (seroto	3355.00	HTR1F	2.84	7.10
50004.00	F11	M-005538- G protein-coupled receptor 1	2835.00	GPR12	7.29	2.65
50004.00	F12	M-005636- 5-hydroxytryptamine (seroto	3354.00	HTR1E	9.06	0.88
50004.00	F13	M-005539- G protein-coupled receptor 1	84435.00	GPR123	6.85	3.09
50004.00	F14	M-005635- 5-hydroxytryptamine (seroto	3352.00	HTR1D	6.47	3.47
50004.00	F15	M-005540- G protein-coupled receptor 1	25960.00	GPR124	5.17	4.77
50004.00	F16	M-005634- 5-hydroxytryptamine (seroto	3351.00	HTR1B	7.75	2.19
50004.00	F17	M-005541- G protein-coupled receptor 1	57211.00	GPR126	9.18	0.76
50004.00	F18	M-005633- 5-hydroxytryptamine (seroto	3350.00	HTR1A	5.05	4.89
50004.00	F19	M-005543- G protein-coupled receptor 1	84873.00	GPR128	14.55	4.61
50004.00	F20	M-005632- histamine receptor H4	59340.00	HRH4	21.62	**11.68**
50004.00	F21	M-005507- G protein-coupled receptor 1	29933.00	GPR132	16.95	7.01
50004.00	F23	M-025110- opsin 5	221391.00	OPN5	17.89	7.95
50004.00	G02	M-005504- frizzled homolog 5 (Drosophi	7855.00	FZD5	18.01	8.07
50004.00	G04	M-005503- frizzled homolog 4 (Drosophi	8322.00	FZD4	21.56	**11.62**
50004.00	G05	M-005436- bradykinin receptor B2	624.00	BDKRB2	22.72	**12.78**
50004.00	G06	M-005502- frizzled homolog 3 (Drosophi	7976.00	FZD3	21.94	**12.00**
50004.00	G07	M-005437- Burkitt lymphoma receptor 1	643.00	BLR1	6.31	3.63
50004.00	G08	M-005501- frizzled homolog 2 (Drosophi	2535.00	FZD2	6.18	3.76
50004.00	G09	M-005438- bombesin-like receptor 3	680.00	BRS3	14.31	4.37
50004.00	G10	M-005500- frizzled homolog 10 (Drosopl	11211.00	FZD10	9.96	0.02
50004.00	G11	M-005440- transmembrane protein 11	8834.00	TMEM11	9.97	0.03
50004.00	G12	M-005499- frizzled homolog 1 (Drosophi	8321.00	FZD1	16.91	6.97
50004.00	G13	M-011001- complement component 3	718.00	C3	18.73	8.79
50004.00	G14	M-005498- Duffy blood group, chemokir	2532.00	DARC	6.20	3.74
50004.00	G15	M-005441- complement component 3a	719.00	C3AR1	22.20	**12.26**
50004.00	G16	M-005497- follicle stimulating hormone	2492.00	FSHR	25.86	**15.92**
50004.00	G17	M-007819- complement component 5	727.00	C5	13.69	3.75
50004.00	G18	M-005141- formyl peptide receptor-like	2359.00	FPRL2	15.14	5.20
50004.00	G19	M-005442- complement component 5a	728.00	C5AR1	17.38	7.44
50004.00	G20	M-005140- formyl peptide receptor-like	2358.00	FPRL1	14.66	4.72
50004.00	G21	M-017985- neuropeptide VF precursor	64111.00	NPVF	15.30	5.36
50004.00	G23	M-021447- calcitonin/calcitonin-related	796.00	CALCA	12.35	2.41

50004.00	H02	M-005631- histamine receptor H3	11255.00	HRH3	6.99	2.95
50004.00	H04	M-005630- histamine receptor H2	3274.00	HRH2	12.20	2.26
50004.00	H05	M-005544- urotensin 2 receptor	2837.00	UTS2R	4.57	5.37
50004.00	H06	M-004340- histamine receptor H1	3269.00	HRH1	13.80	3.86
50004.00	H07	M-005545- G protein-coupled receptor 1	353345.00	GPR141	18.96	9.02
50004.00	H08	M-006688- G protein-coupled receptor 1	338442.00	GPR109A	10.09	0.15
50004.00	H09	M-005677- G protein-coupled receptor 1	4935.00	GPR143	13.46	3.52
50004.00	H10	M-005628- G protein-coupled receptor 1	8843.00	GPR109B	14.70	4.76
50004.00	H11	M-005548- melanin-concentrating horm	84539.00	MCHR2	10.52	0.58
50004.00	H12	M-005625- G protein-coupled receptor 1	29909.00	GPR171	12.26	2.32
50004.00	H13	M-005549- G protein-coupled receptor 1	115330.00	GPR146	10.30	0.36
50004.00	H14	M-005624- gastrin-releasing peptide rec	2925.00	GRPR	26.19	**16.25**
50004.00	H15	M-005550- G protein-coupled receptor 1	2838.00	GPR15	11.82	1.88
50004.00	H16	M-005623- glutamate receptor, metabot	2918.00	GRM8	10.96	1.02
50004.00	H17	M-005508- G protein-coupled receptor 1	165829.00	GPR156	7.09	2.85
50004.00	H18	M-005622- glutamate receptor, metabot	2917.00	GRM7	10.47	0.53
50004.00	H19	M-016136- G protein-coupled receptor 1	80045.00	GPR157	24.84	**14.90**
50004.00	H20	M-005621- glutamate receptor, metabot	2916.00	GRM6	22.48	**12.54**
50004.00	H21	M-005520- G protein-coupled receptor 1	26996.00	GPR160	19.19	9.25
50004.00	H23	M-005720- G protein-coupled receptor 1	23432.00	GPR161	10.94	1.00
50004.00	I02	M-003667- formyl peptide receptor 1	2357.00	FPR1	14.37	4.43
50004.00	I04	M-005494- G protein-coupled receptor 1	151556.00	GPR155	9.81	0.13
50004.00	I05	M-003635- calcitonin receptor	799.00	CALCR	10.90	0.96
50004.00	I06	M-009071- olfactory receptor, family 7,	219445.00	OR7E5P	11.00	1.06
50004.00	I07	M-004350- calcitonin receptor-like	10203.00	CALCRL	24.66	**14.72**
50004.00	I08	M-016964- tRNA-histidine guanylyltrans	54974.00	THG1L	12.28	2.34
50004.00	I09	M-017646- calmodulin 1 (phosphorylase	801.00	CALM1	7.83	2.11
50004.00	I10	M-010743- G protein-coupled receptor 1	79581.00	GPR172A	21.53	**11.59**
50004.00	I11	M-005444- calcium-sensing receptor (hy	846.00	CASR	17.48	7.54
50004.00	I12	M-015863- notchless homolog 1 (Drosop	54475.00	NLE1	11.00	1.06
50004.00	I13	M-005445- chemokine binding protein 2	1238.00	CCBP2	11.62	1.68
50004.00	I14	M-010712- G protein-coupled receptor 1	55065.00	GPR172B	19.92	9.98
50004.00	I15	M-007828- chemokine (C-C motif) ligand	6361.00	CCL17	6.12	3.82
50004.00	I16	M-014769- FKSG83	83954.00	FKSG83	19.09	9.15
50004.00	I17	M-007831- chemokine (C-C motif) ligand	6347.00	CCL2	8.64	1.30
50004.00	I18	M-005493- G protein-coupled receptor 1	84636.00	GPR174	11.89	1.95
50004.00	I19	M-007835- chemokine (C-C motif) ligand	6368.00	CCL23	5.22	4.72
50004.00	I20	M-005492- coagulation factor II (thromb	9002.00	F2RL3	6.51	3.43
50004.00	I21	M-007837- chemokine (C-C motif) ligand	6370.00	CCL25	11.33	1.39
50004.00	I23	M-007841- chemokine (C-C motif) ligand	6348.00	CCL3	3.87	6.07
50004.00	J02	M-005620- glutamate receptor, metabot	2915.00	GRM5	10.15	0.21
50004.00	J04	M-005619- glutamate receptor, metabot	2914.00	GRM4	6.68	3.26
50004.00	J05	M-005551- G protein-coupled receptor 1	2840.00	GPR17	13.76	3.82
50004.00	J06	M-005618- glutamate receptor, metabot	2913.00	GRM3	7.39	2.55
50004.00	J07	M-005552- G protein-coupled receptor 1	2841.00	GPR18	11.71	1.77
50004.00	J08	M-005617- glutamate receptor, metabot	2912.00	GRM2	11.30	1.36
50004.00	J09	M-005553- G protein-coupled receptor 1	2842.00	GPR19	10.86	0.92

50004.00	J10	M-005616- glutamate receptor, metabot	2911.00	GRM1	17.77	7.83
50004.00	J11	M-005554- chemokine (C-C motif) recep	2826.00	CCR10	8.65	1.29
50004.00	J12	M-005615- relaxin/insulin-like family pep	122042.00	RXFP2	16.03	6.09
50004.00	J13	M-005555- G protein-coupled receptor 2	2843.00	GPR20	7.07	2.87
50004.00	J14	M-005614- G protein-coupled receptor 1	27239.00	GPR162	20.31	10.37
50004.00	J15	M-005556- G protein-coupled receptor 2	2844.00	GPR21	24.62	**14.68**
50004.00	J16	M-004628- G protein-coupled receptor k	131890.00	GRK7	14.12	4.18
50004.00	J17	M-005557- G protein-coupled receptor 2	2845.00	GPR22	7.99	1.96
50004.00	J18	M-004627- G protein-coupled receptor k	2870.00	GRK6	7.44	2.50
50004.00	J19	M-005558- G protein-coupled receptor 2	2846.00	GPR23	3.84	6.10
50004.00	J20	M-004626- G protein-coupled receptor k	2869.00	GRK5	5.47	4.47
50004.00	J21	M-005559- melanin-concentrating horm	2847.00	MCHR1	12.57	2.63
50004.00	J23	M-005560- G protein-coupled receptor 2	2848.00	GPR25	8.06	1.88
50004.00	K02	M-005491- coagulation factor II (thromb	2151.00	F2RL2	4.72	5.22
50004.00	K04	M-005095- coagulation factor II (thromb	2150.00	F2RL1	4.78	5.16
50004.00	K05	M-005448- chemokine (C-C motif) recep	1230.00	CCR1	7.48	2.46
50004.00	K06	M-005094- coagulation factor II (thromb	2149.00	F2R	10.32	0.38
50004.00	K07	M-005449- chemokine (C-C motif) recep	1231.00	CCR2	7.50	2.44
50004.00	K08	M-005490- G protein-coupled receptor 3	9283.00	GPR37L1	7.52	2.42
50004.00	K09	M-005450- chemokine (C-C motif) recep	1232.00	CCR3	7.50	2.44
50004.00	K10	M-004601- ectonucleotide pyrophospha	5168.00	ENPP2	6.09	3.85
50004.00	K11	M-005451- chemokine (C-C motif) recep	1233.00	CCR4	16.89	6.95
50004.00	K12	M-005489- egf-like module containing, n	84658.00	EMR3	14.51	4.57
50004.00	K13	M-004855- chemokine (C-C motif) recep	1234.00	CCR5	15.51	5.57
50004.00	K14	M-005487- egf-like module containing, n	2015.00	EMR1	18.82	8.88
50004.00	K15	M-005453- chemokine (C-C motif) recep	1235.00	CCR6	12.46	2.52
50004.00	K16	M-021612- EGF, latrophilin and seven tra	64123.00	ELTD1	9.93	0.01
50004.00	K17	M-005454- chemokine (C-C motif) recep	1236.00	CCR7	11.91	1.97
50004.00	K18	M-010269- elongation of very long chain	6785.00	ELOVL4	15.18	5.24
50004.00	K19	M-005455- chemokine (C-C motif) recep	1237.00	CCR8	10.78	0.84
50004.00	K20	M-003657- endothelin receptor type B	1910.00	EDNRB	23.12	**13.18**
50004.00	K21	M-005456- chemokine (C-C motif) recep	10803.00	CCR9	10.09	0.15
50004.00	K23	M-005457- chemokine (C-C motif) recep	51554.00	CCRL1	26.57	**16.63**
50004.00	L02	M-004625- G protein-coupled receptor k	2868.00	GRK4	5.46	4.48
50004.00	L04	M-005613- G protein-coupled receptor,	222545.00	GPRC6A	6.60	3.34
50004.00	L05	M-005561- G protein-coupled receptor 2	2849.00	GPR26	4.22	5.72
50004.00	L06	M-005612- G protein-coupled receptor,	55507.00	GPRC5D	2.82	7.12
50004.00	L07	M-005562- G protein-coupled receptor 2	2850.00	GPR27	6.91	3.04
50004.00	L08	M-005611- G protein-coupled receptor,	55890.00	GPRC5C	6.77	3.17
50004.00	L09	M-003951- G protein-coupled receptor 3	2827.00	GPR3	5.12	4.82
50004.00	L10	M-005610- G protein-coupled receptor,	51704.00	GPRC5B	8.78	1.16
50004.00	L11	M-005563- G protein-coupled receptor 3	2852.00	GPR30	8.10	1.84
50004.00	L12	M-005609- G protein-coupled receptor 9	222487.00	GPR97	6.31	3.63
50004.00	L13	M-005564- G protein-coupled receptor 3	2853.00	GPR31	6.15	3.79
50004.00	L14	M-004604- G protein-coupled receptor 9	57121.00	GPR92	10.45	0.51
50004.00	L15	M-005565- G protein-coupled receptor 3	2854.00	GPR32	13.92	3.98
50004.00	L16	M-004541- succinate receptor 1	56670.00	SUCNR1	14.44	4.50

50004.00	L17	M-005566- G protein-coupled receptor	2857.00	GPR34	9.53	0.41
50004.00	L18	M-005608- G protein-coupled receptor	54112.00	GPR88	9.47	0.47
50004.00	L19	M-005567- G protein-coupled receptor	2859.00	GPR35	7.41	2.53
50004.00	L20	M-005607- G protein-coupled receptor	53836.00	GPR87	13.65	3.71
50004.00	L21	M-003604- G protein-coupled receptor	2861.00	GPR37	16.89	6.95
50004.00	L23	M-005568- motilin receptor	2862.00	MLNR	7.17	2.77
50004.00	M02	M-005485- endothelin receptor type A	1909.00	EDNRA	5.56	4.38
50004.00	M04	M-004791- endothelial differentiation, s	53637.00	EDG8	10.61	0.67
50004.00	M05	M-005458- chemokine (C-C motif) recep	9034.00	CCRL2	9.60	0.34
50004.00	M06	M-004895- endothelial differentiation, l	23566.00	EDG7	4.31	5.63
50004.00	M07	M-003775- CD3e molecule, epsilon (CD3	916.00	CD3E	4.77	5.17
50004.00	M08	M-005484- endothelial differentiation, l	8698.00	EDG6	14.49	4.55
50004.00	M09	M-003638- CD97 molecule	976.00	CD97	8.91	1.03
50004.00	M10	M-003952- endothelial differentiation, s	9294.00	EDG5	16.75	6.81
50004.00	M11	M-005459- cadherin, EGF LAG seven-pas	9620.00	CELSR1	12.50	2.56
50004.00	M12	M-004602- endothelial differentiation, l	9170.00	EDG4	18.13	8.19
50004.00	M13	M-005460- cadherin, EGF LAG seven-pas	1952.00	CELSR2	9.11	0.83
50004.00	M14	M-005208- endothelial differentiation, s	1903.00	EDG3	18.35	8.41
50004.00	M15	M-005461- cadherin, EGF LAG seven-pas	1951.00	CELSR3	19.17	9.23
50004.00	M16	M-003656- endothelial differentiation, l	1902.00	EDG2	15.48	5.54
50004.00	M17	M-019937- chromatin assembly factor 1,	8208.00	CHAF1B	14.37	4.43
50004.00	M18	M-003655- endothelial differentiation, s	1901.00	EDG1	19.00	9.06
50004.00	M19	M-005463- cholinergic receptor, muscar	1129.00	CHRM2	5.09	4.85
50004.00	M20	M-005858- endothelin converting enzym	9718.00	ECE2	24.88	**14.94**
50004.00	M21	M-005464- cholinergic receptor, muscar	1131.00	CHRM3	16.78	6.84
50004.00	M23	M-005467- chemokine-like receptor 1	1240.00	CMKLR1	16.53	6.59
50004.00	N02	M-005606- purinergic receptor P2Y, G-p	53829.00	P2RY13	3.41	6.53
50004.00	N04	M-005605- G protein-coupled receptor	54329.00	GPR85	10.51	0.57
50004.00	N05	M-005569- G protein-coupled receptor	2863.00	GPR39	6.99	2.95
50004.00	N06	M-005604- G protein-coupled receptor	53831.00	GPR84	15.13	5.19
50004.00	N07	M-005570- G protein-coupled receptor	2828.00	GPR4	7.46	2.48
50004.00	N08	M-005602- G protein-coupled receptor	27197.00	GPR82	6.56	3.38
50004.00	N09	M-005571- free fatty acid receptor 1	2864.00	FFAR1	8.41	1.53
50004.00	N10	M-005601- G protein-coupled receptor	27198.00	GPR81	8.71	1.23
50004.00	N11	M-005572- free fatty acid receptor 3	2865.00	FFAR3	11.58	1.64
50004.00	N12	M-005600- oxoglutarate (alpha-ketoglut	27199.00	OXGR1	19.20	9.26
50004.00	N13	M-005573- G protein-coupled receptor	2866.00	GPR42	10.27	0.33
50004.00	N14	M-005599- neuropeptides B/W receptor	2832.00	NPBWR2	17.75	7.81
50004.00	N15	M-005574- free fatty acid receptor 2	2867.00	FFAR2	22.70	**12.76**
50004.00	N16	M-005598- G protein-coupled receptor	27201.00	GPR78	9.62	0.32
50004.00	N17	M-005575- G protein-coupled receptor	11251.00	GPR44	7.86	2.08
50004.00	N18	M-005597- G protein-coupled receptor	27202.00	GPR77	12.01	2.07
50004.00	N19	M-005576- G protein-coupled receptor	11250.00	GPR45	13.42	3.48
50004.00	N20	M-005596- G protein-coupled receptor	10936.00	GPR75	16.42	6.48
50004.00	N21	M-003673- leucine-rich repeat-containin	55366.00	LGR4	19.36	9.42
50004.00	N23	M-005577- leucine-rich repeat-containin	8549.00	LGR5	16.09	6.15
50004.00	O02	M-005482- Epstein-Barr virus induced ge	1880.00	EBI2	8.64	1.30

50004.00	O04	M-005481- dopamine receptor D5	1816.00	DRD5	7.84	2.10
50004.00	O05	M-004711- cannabinoid receptor 1 (brai	1268.00	CNR1	12.90	2.96
50004.00	O06	M-005477- dopamine receptor D1	1812.00	DRD1	31.39	**21.45**
50004.00	O07	M-005469- cannabinoid receptor 2 (mac	1269.00	CNR2	9.64	0.30
50004.00	O08	M-012997- defensin, beta 4	1673.00	DEFB4	11.69	1.75
50004.00	O09	M-003647- corticotropin releasing horm	1394.00	CRHR1	8.59	1.35
50004.00	O10	M-005476- cysteinyl leukotriene recepto	57105.00	CYSLTR2	15.11	5.17
50004.00	O11	M-005470- corticotropin releasing horm	1395.00	CRHR2	12.51	2.57
50004.00	O12	M-005475- cysteinyl leukotriene recepto	10800.00	CYSLTR1	10.16	0.22
50004.00	O13	M-015421- cryptochrome 1 (photolyase-	1407.00	CRY1	21.94	**12.00**
50004.00	O14	M-005474- chemokine (C-X-C motif) rece	10663.00	CXCR6	27.49	**17.55**
50004.00	O15	M-005471- chemokine (C-X3-C motif) re	1524.00	CX3CR1	10.02	0.08
50004.00	O16	M-005139- chemokine (C-X-C motif) rece	7852.00	CXCR4	16.95	7.01
50004.00	O17	M-003898- chemokine (C-X-C motif) liga	2919.00	CXCL1	8.34	1.60
50004.00	O18	M-005472- chemokine (C-X-C motif) rece	2833.00	CXCR3	14.91	4.97
50004.00	O19	M-007873- chemokine (C-X-C motif) liga	6387.00	CXCL12	17.68	7.74
50004.00	O20	M-007881- chemokine (C-X-C motif) liga	4283.00	CXCL9	5.79	4.15
50004.00	O21	M-007877- chemokine (C-X-C motif) liga	2920.00	CXCL2	13.56	3.62
50004.00	O23	M-007878- chemokine (C-X-C motif) liga	2921.00	CXCL3	7.72	2.22
50004.00	P02	M-005595- neuropeptide FF receptor 2	10886.00	NPFFR2	4.85	5.09
50004.00	P04	M-005594- prokineticin receptor 2	128674.00	PROKR2	11.16	1.22
50004.00	P05	M-005578- G protein-coupled receptor 5	9248.00	GPR50	11.54	1.60
50004.00	P06	M-005593- prokineticin receptor 1	10887.00	PROKR1	11.86	1.92
50004.00	P07	M-005579- gamma-aminobutyric acid (G	9568.00	GABBR2	12.48	2.54
50004.00	P08	M-005603- G protein-coupled receptor 8	10888.00	GPR83	5.12	4.82
50004.00	P09	M-005580- G protein-coupled receptor 5	9293.00	GPR52	4.11	5.83
50004.00	P10	M-005592- neuropeptides B/W receptor	2831.00	NPBWR1	6.34	3.60
50004.00	P11	M-004901- KISS1 receptor	84634.00	KISS1R	12.28	2.34
50004.00	P12	M-005591- G protein-coupled receptor 6	8111.00	GPR68	7.89	2.05
50004.00	P13	M-005581- G protein-coupled receptor 5	9290.00	GPR55	9.35	0.59
50004.00	P14	M-005590- neuromedin U receptor 1	10316.00	NMUR1	20.62	10.68
50004.00	P15	M-004552- G protein-coupled receptor 5	9289.00	GPR56	12.66	2.72
50004.00	P16	M-005589- G protein-coupled receptor 6	8477.00	GPR65	10.51	0.57
50004.00	P17	M-005583- trace amine associated recep	9287.00	TAAR2	9.56	0.38
50004.00	P18	M-003812- G protein-coupled receptor 6	10149.00	GPR64	19.62	9.68
50004.00	P19	M-005584- G protein-coupled receptor 6	2830.00	GPR6	12.05	2.11
50004.00	P20	M-005587- G protein-coupled receptor 6	81491.00	GPR63	5.38	4.56
50004.00	P21	M-005585- G protein-coupled receptor 6	83873.00	GPR61	16.94	7.00
50004.00	P23	M-005586- G protein-coupled receptor 6	118442.00	GPR62	6.64	3.30
				MAD	9.94	3.76
		0.05		3MAD		11.27
				MADc		5.56
50004.00	C22				53.16	
50004.00	D22				45.35	
50004.00	E22				37.29	
50004.00	F22				53.85	
				mn	47.41	

				sd	7.77
50004.00	G22				4.89
50004.00	H22				10.50
50004.00	I22				3.61
50004.00	J22				5.02
				mn	6.01
				sd	3.07
				3psSD	23.32
				3ngSD	9.20
				SumSD	32.52
				MeanDf	41.41
				SumovrMn	0.79
				1minus	0.21

50004.00	G03	M-003290-	polo-like kinase 1 (Drosophila)	PLK1 SMA	18.33
50004.00	H03	M-003290-	polo-like kinase 1 (Drosophila)	PLK1 SMA	7.36
50004.00	I03	D-001206-	siControl non-targeting siRNA #2		11.82
50004.00	J03	D-001206-	siControl non-targeting siRNA #2		25.05

robust Z	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**	
-1.10	2.67	4.82	-1.07	2.64	7.01	-1.37	
-1.18	4.24	3.25	-0.72	5.26	4.39	-0.86	
-0.28	4.56	2.93	-0.65	6.19	3.46	-0.68	
-0.63	5.28	2.21	-0.49	6.65	3.00	-0.59	
-0.90	3.72	3.77	-0.84	5.02	4.64	-0.90	
1.40	10.53	3.04	0.68	17.34	7.69	1.50	
-0.15	5.25	2.24	-0.50	5.92	3.73	-0.73	
2.17	14.94	7.45	1.66	21.60	**11.95**	2.34	y
0.10	7.17	0.32	-0.07	10.72	1.07	0.21	
-0.33	5.03	2.46	-0.55	6.13	3.52	-0.69	
0.73	10.24	2.75	0.61	7.86	1.79	-0.35	
0.21	13.32	5.83	1.30	6.92	2.73	-0.53	
-0.65	7.49	0.00	0.00	6.68	2.97	-0.58	
-1.04	7.97	0.48	0.11	7.88	1.77	-0.35	
0.49	8.04	0.55	0.12	4.14	5.51	-1.07	
-0.41	9.13	1.64	0.36	9.88	0.23	0.05	
0.10	11.72	4.23	0.94	14.53	4.88	0.96	
-1.12	6.97	0.52	-0.12	11.54	1.89	0.37	
-1.26	4.98	2.51	-0.56	6.61	3.04	-0.59	
-0.79	6.79	0.70	-0.16	8.92	0.73	-0.14	
-1.65	1.59	5.90	-1.31	3.16	6.49	-1.27	
-1.69	0.28	7.21	-1.60	3.91	5.74	-1.12	
-1.52	0.70	6.79	-1.51	4.64	5.01	-0.98	
-1.34	1.80	5.69	-1.27	5.95	3.71	-0.72	
-1.56	1.45	6.04	-1.34	2.40	7.25	-1.42	
-1.25	3.08	4.41	-0.98	9.50	0.15	-0.03	
-0.86	4.04	3.45	-0.77	11.87	2.22	0.43	
-0.42	3.40	4.09	-0.91	11.39	1.74	0.34	
-1.15	2.96	4.53	-1.01	9.06	0.59	-0.11	
-1.37	1.84	5.65	-1.26	4.33	5.32	-1.04	
-0.97	4.44	3.05	-0.68	5.08	4.57	-0.89	
-0.75	2.36	5.13	-1.14	6.49	3.16	-0.62	
-1.22	3.63	3.86	-0.86	7.36	2.29	-0.45	
1.13	10.72	3.23	0.72	17.07	7.42	1.45	
0.27	8.17	0.68	0.15	12.66	3.01	0.59	
-1.37	4.02	3.47	-0.77	8.77	0.88	-0.17	
0.08	13.41	5.92	1.32	15.18	5.53	1.08	
-1.49	2.83	4.66	-1.04	5.30	4.35	-0.85	
-0.71	9.63	2.14	0.48	8.92	0.73	-0.14	
0.52	13.44	5.95	1.32	19.44	9.79	1.91	
-1.62	4.74	2.75	-0.61	7.23	2.42	-0.47	
-0.54	18.54	**11.05**	2.46	22.60	**12.95**	2.53	y
-1.12	5.71	1.78	-0.40	6.33	3.32	-0.65	
-1.07	7.15	0.34	-0.08	11.82	2.17	0.42	
0.23	14.35	6.86	1.53	20.44	**10.79**	2.11	
-0.56	12.76	5.27	1.17	12.21	2.56	0.50	

0.00	13.41	5.92	1.32	17.95	8.30	1.62	
-0.18	9.12	1.63	0.36	12.59	2.94	0.58	
0.50	19.19	**11.70**	2.60	18.91	9.26	1.81	
-0.24	12.57	5.08	1.13	16.35	6.70	1.31	
-1.63	10.34	2.85	0.63	7.05	2.60	-0.51	
-0.22	17.86	**10.37**	2.31	16.04	6.39	1.25	
-0.69	8.07	0.58	0.13	9.65	0.00	0.00	
0.54	9.78	2.29	0.51	12.81	3.16	0.62	
0.15	14.14	6.65	1.48	11.32	1.67	0.33	
0.17	20.86	**13.37**	2.97	14.64	4.99	0.98	
1.17	17.13	**9.64**	2.14	15.96	6.31	1.23	
0.45	18.64	**11.15**	2.48	16.47	6.82	1.33	
-0.13	12.49	5.00	1.11	7.82	1.84	-0.36	
3.13	25.95	**18.46**	4.11	24.97	**15.32**	3.00	y
-1.18	3.69	3.80	-0.84	8.32	1.33	-0.26	
-0.74	5.73	1.76	-0.39	9.41	0.24	-0.05	
0.02	10.82	3.33	0.74	10.18	0.53	0.10	
-0.49	15.69	8.20	1.82	8.85	0.80	-0.16	
-0.35	4.96	2.53	-0.56	5.58	4.07	-0.79	
-0.30	9.77	2.28	0.51	13.66	4.01	0.78	
-0.71	6.42	1.07	-0.24	13.37	3.72	0.73	
-0.95	7.89	0.40	0.09	9.64	0.01	0.00	
-1.25	4.40	3.09	-0.69	8.76	0.89	-0.17	
-0.49	8.24	0.75	0.17	12.93	3.28	0.64	
-0.56	9.06	1.57	0.35	7.38	2.27	-0.44	
0.00	11.07	3.58	0.80	21.31	**11.66**	2.28	
-0.99	6.22	1.27	-0.28	10.87	1.22	0.24	
-0.56	9.14	1.65	0.37	13.85	4.20	0.82	
-1.16	6.28	1.21	-0.27	8.43	1.22	-0.24	
-0.94	13.39	5.90	1.31	14.07	4.42	0.86	
-0.63	9.09	1.60	0.35	12.51	2.86	0.56	
-0.11	11.10	3.61	0.80	7.95	1.70	-0.33	
-0.70	8.28	0.79	0.18	14.36	4.71	0.92	
0.34	8.37	0.88	0.20	10.93	1.28	0.25	
-1.20	1.40	6.09	-1.36	10.34	0.69	0.14	
0.82	4.20	3.29	-0.73	16.73	7.08	1.38	
1.00	7.73	0.24	0.05	26.70	**17.05**	3.33	
-0.85	2.34	5.15	-1.15	8.74	0.91	-0.18	
0.22	3.80	3.69	-0.82	14.03	4.38	0.86	
-0.04	4.51	2.98	-0.66	19.43	9.78	1.91	
-0.34	0.75	6.74	-1.50	11.43	1.78	0.35	
-0.05	8.98	1.49	0.33	16.95	7.30	1.43	
-0.26	3.15	4.34	-0.97	5.94	3.71	-0.72	
1.52	12.49	5.00	1.11	18.87	9.22	1.80	
-1.16	4.82	2.67	-0.60	7.70	1.95	-0.38	
-0.38	2.69	4.80	-1.07	10.70	1.05	0.21	
-1.28	6.10	1.39	-0.31	9.56	0.09	-0.02	

0.74	8.17	0.68	0.15	17.12	7.47	1.46	
0.05	10.16	2.67	0.59	10.00	0.35	0.07	
-0.94	9.87	2.38	0.53	16.03	6.38	1.25	
0.29	17.68	**10.19**	2.27	24.87	**15.22**	2.98	y
0.11	19.46	**11.97**	2.66	16.03	6.38	1.25	
0.32	23.37	**15.88**	3.53	16.24	6.59	1.29	
0.56	10.48	2.99	0.67	14.66	5.01	0.98	
-1.62	3.46	4.03	-0.90	4.16	5.49	-1.07	
-1.32	3.98	3.51	-0.78	7.31	2.34	-0.46	
-1.07	5.19	2.30	-0.51	9.29	0.36	-0.07	
-1.04	7.02	0.47	-0.10	8.26	1.39	-0.27	
-1.60	2.90	4.59	-1.02	3.71	5.94	-1.16	
-1.20	3.47	4.02	-0.89	8.69	0.96	-0.19	
-1.07	6.17	1.32	-0.29	9.57	0.08	-0.01	
-1.28	11.04	3.55	0.79	7.47	2.18	-0.42	
-0.48	5.69	1.80	-0.40	9.86	0.21	0.04	
-0.16	4.37	3.12	-0.69	6.64	3.01	-0.59	
-0.56	7.68	0.19	0.04	3.05	6.60	-1.29	
-0.63	5.57	1.92	-0.43	7.24	2.41	-0.47	
-0.86	7.57	0.08	0.02	6.55	3.10	-0.61	
-0.39	5.31	2.18	-0.49	5.50	4.15	-0.81	
-0.14	6.87	0.62	-0.14	4.77	4.88	-0.95	
-0.88	4.08	3.41	-0.76	7.35	2.30	-0.45	
0.83	9.96	2.47	0.55	9.77	0.12	0.02	
2.10	23.08	**15.59**	3.47	14.80	5.15	1.01	y
1.26	5.02	2.47	-0.55	7.60	2.05	-0.40	
1.43	12.74	5.25	1.17	7.07	2.58	-0.50	
1.45	3.22	4.27	-0.95	13.29	3.64	0.71	
2.09	6.79	0.70	-0.16	15.02	5.37	1.05	
2.30	5.65	1.84	-0.41	19.48	9.83	1.92	
2.16	4.53	2.96	-0.66	18.49	8.84	1.73	
-0.65	1.18	6.31	-1.40	4.86	4.79	-0.94	
-0.68	0.72	6.77	-1.51	6.93	2.72	-0.53	
0.78	4.90	2.59	-0.58	8.59	1.06	-0.21	
0.00	4.86	2.63	-0.58	9.54	0.11	-0.02	
0.00	2.52	4.97	-1.11	11.68	2.03	0.40	
1.25	9.25	1.76	0.39	9.82	0.17	0.03	
1.58	7.14	0.35	-0.08	10.03	0.38	0.07	
-0.67	4.58	2.91	-0.65	6.43	3.22	-0.63	
2.21	7.77	0.28	0.06	10.89	1.24	0.24	
2.86	10.67	3.18	0.71	14.50	4.85	0.95	
0.67	7.42	0.07	-0.02	6.64	3.01	-0.59	
0.93	14.99	7.50	1.67	21.38	**11.73**	2.29	
1.34	9.79	2.30	0.51	10.31	0.65	0.13	
0.85	13.35	5.86	1.30	12.65	3.00	0.59	
0.96	15.56	8.07	1.79	15.44	5.79	1.13	
0.43	14.55	7.06	1.57	13.12	3.47	0.68	

-0.53	2.47	5.02	-1.12	2.14	7.51	-1.47	
0.41	7.20	0.29	-0.06	6.86	2.79	-0.54	
-0.97	3.62	3.87	-0.86	1.14	8.51	-1.66	
0.69	3.33	4.16	-0.93	5.06	4.59	-0.90	
1.62	6.70	0.79	-0.18	8.99	0.66	-0.13	
0.03	3.13	4.36	-0.97	3.53	6.12	-1.19	
0.63	4.75	2.74	-0.61	3.16	6.49	-1.27	
0.86	6.35	1.14	-0.25	7.20	2.45	-0.48	
0.10	4.77	2.72	-0.61	7.13	2.52	-0.49	
0.42	5.21	2.28	-0.51	7.76	1.89	-0.37	
0.06	2.98	4.51	-1.00	2.61	7.04	-1.38	
2.92	12.59	5.10	1.13	10.99	1.34	0.26	
0.34	8.04	0.55	0.12	3.19	6.46	-1.26	
0.18	5.52	1.97	-0.44	6.63	3.02	-0.59	
-0.51	5.43	2.06	-0.46	2.96	6.69	-1.31	
0.10	12.58	5.09	1.13	6.23	3.42	-0.67	
2.68	17.31	**9.82**	2.19	12.53	2.88	0.56	y
2.25	18.51	**11.02**	2.45	13.30	3.65	0.71	y
1.66	23.75	**16.26**	3.62	11.09	1.44	0.28	
0.18	7.71	0.22	0.05	7.51	2.14	-0.42	
0.80	1.65	5.84	-1.30	9.85	0.20	0.04	
-0.02	1.35	6.14	-1.37	5.22	4.43	-0.86	
0.17	3.05	4.45	-0.99	12.86	3.21	0.63	
0.19	5.19	2.30	-0.51	6.87	2.78	-0.54	
2.65	8.52	1.03	0.23	19.88	10.23	2.00	
0.42	2.95	4.54	-1.01	10.48	0.83	0.16	
-0.38	4.76	2.73	-0.61	4.22	5.43	-1.06	
2.08	6.66	0.83	-0.19	12.71	3.06	0.60	
1.36	4.30	3.19	-0.71	9.56	0.09	-0.02	
0.19	5.17	2.32	-0.52	10.53	0.88	0.17	
0.30	6.28	1.21	-0.27	8.48	1.17	-0.23	
1.80	8.14	0.65	0.15	12.93	3.28	0.64	
-0.69	3.09	4.40	-0.98	9.44	0.21	-0.04	
1.65	10.82	3.33	0.74	16.32	6.67	1.31	
-0.23	8.54	1.05	0.23	14.59	4.94	0.97	
0.35	11.66	4.17	0.93	11.26	1.61	0.32	
-0.85	4.67	2.82	-0.63	20.03	**10.38**	2.03	
-0.62	4.47	3.02	-0.67	13.47	3.82	0.75	
0.25	10.30	2.81	0.62	9.94	0.29	0.06	
-1.09	3.86	3.63	-0.81	11.05	1.40	0.27	
0.04	4.16	3.33	-0.74	6.80	2.85	-0.56	
-0.59	7.01	0.48	-0.11	8.20	1.46	-0.28	
0.69	9.62	2.13	0.47	6.95	2.70	-0.53	
-0.46	8.28	0.79	0.18	3.45	6.20	-1.21	
0.32	4.47	3.02	-0.67	7.96	1.69	-0.33	
0.24	2.79	4.70	-1.05	8.82	0.83	-0.16	
0.17	3.99	3.50	-0.78	3.14	6.51	-1.27	

1.41	13.82	6.33	1.41	15.58	5.93	1.16	
-0.23	4.46	3.03	-0.68	9.41	0.24	-0.05	
1.09	10.19	2.70	0.60	13.76	4.11	0.80	
-0.52	3.48	4.01	-0.89	4.91	4.74	-0.93	
1.86	16.33	8.84	1.97	13.62	3.97	0.78	
2.64	20.67	**13.18**	2.93	25.00	**15.35**	3.00	y
0.75	13.46	5.97	1.33	7.06	2.59	-0.50	
-0.35	12.10	4.61	1.02	19.20	9.55	1.87	
-0.45	3.44	4.05	-0.90	10.13	0.48	0.09	
-1.10	6.42	1.07	-0.24	6.90	2.75	-0.54	
-0.80	6.89	0.60	-0.13	8.62	1.03	-0.20	
0.47	11.63	4.14	0.92	12.05	2.40	0.47	
-0.34	8.36	0.87	0.19	11.22	1.57	0.31	
-0.94	10.67	3.18	0.71	13.10	3.45	0.68	
-0.93	6.34	1.15	-0.26	15.59	5.94	1.16	
-0.44	8.63	1.14	0.25	21.32	**11.67**	2.28	
0.07	6.34	1.15	-0.26	19.55	9.90	1.94	
-0.44	6.83	0.66	-0.15	11.96	2.31	0.45	
-0.44	4.56	2.93	-0.65	11.89	2.24	0.44	
-0.44	10.33	2.84	0.63	12.09	2.44	0.48	
-0.69	10.82	3.33	0.74	10.06	0.40	0.08	
1.25	13.77	6.28	1.40	18.26	8.61	1.68	
0.82	16.06	8.57	1.91	16.44	6.79	1.33	
1.00	13.94	6.45	1.44	14.56	4.91	0.96	
1.60	11.47	3.98	0.88	13.14	3.49	0.68	
0.45	10.49	3.00	0.67	15.67	6.02	1.18	
0.00	10.51	3.02	0.67	18.54	8.89	1.74	
0.35	9.92	2.43	0.54	11.43	1.78	0.35	
0.94	15.53	8.04	1.79	18.32	8.67	1.69	
0.15	8.94	1.45	0.32	11.64	1.99	0.39	
2.37	23.75	**16.26**	3.62	15.77	6.12	1.20	y
0.03	9.06	1.57	0.35	7.92	1.73	-0.34	
2.99	17.77	**10.28**	2.29	22.78	**13.13**	2.57	y
-0.81	8.67	1.18	0.26	7.40	2.25	-0.44	
-0.60	9.03	1.54	0.34	3.44	6.21	-1.21	
-1.03	11.34	3.85	0.86	5.48	4.17	-0.81	
-1.28	8.70	1.21	0.27	4.56	5.09	-0.99	
-0.55	8.94	1.45	0.32	6.48	3.17	-0.62	
-0.57	10.23	2.74	0.61	8.44	1.21	-0.24	
-0.87	9.26	1.77	0.39	5.20	4.45	-0.87	
-0.21	12.74	5.25	1.17	5.49	4.16	-0.81	
-0.33	12.06	4.57	1.02	3.60	6.05	-1.18	
-0.65	10.33	2.84	0.63	5.52	4.13	-0.81	
-0.68	5.41	2.08	-0.46	3.81	5.84	-1.14	
0.09	15.66	8.17	1.82	8.84	0.81	-0.16	
0.71	8.11	0.62	0.14	5.80	3.85	-0.75	
0.81	17.34	**9.85**	2.19	6.98	2.67	-0.52	

-0.07	5.88	1.61	-0.36	6.78	2.87	-0.56	
-0.08	10.69	3.20	0.71	7.52	2.13	-0.42	
-0.46	6.32	1.17	-0.26	4.99	4.66	-0.91	
0.67	13.53	6.04	1.34	4.98	4.67	-0.91	
1.25	12.89	5.40	1.20	6.51	3.14	-0.61	
-0.50	2.40	5.09	-1.13	3.30	6.35	-1.24	
-0.79	3.44	4.05	-0.90	1.99	7.66	-1.50	
0.12	8.24	0.75	0.17	2.42	7.23	-1.41	
-0.06	5.60	1.89	-0.42	2.17	7.48	-1.46	
-1.01	1.86	5.63	-1.25	3.55	6.10	-1.19	
-0.93	1.79	5.70	-1.27	2.05	7.60	-1.48	
0.82	6.62	0.87	-0.19	5.77	3.88	-0.76	
-0.19	5.47	2.02	-0.45	7.57	2.08	-0.41	
1.22	7.07	0.42	-0.09	3.64	6.01	-1.17	
0.46	7.09	0.40	-0.09	2.65	7.00	-1.37	
1.47	6.76	0.73	-0.16	3.79	5.86	-1.14	
-0.15	5.20	2.29	-0.51	4.56	5.09	-0.99	
1.51	6.63	0.86	-0.19	4.83	4.82	-0.94	
1.66	11.49	4.00	0.89	11.16	1.51	0.30	
1.00	8.13	0.64	0.14	5.05	4.60	-0.90	
0.80	3.58	3.91	-0.87	4.40	5.25	-1.02	
1.63	2.69	4.80	-1.07	4.95	4.70	-0.92	
-0.87	5.69	1.80	-0.40	6.77	2.88	-0.56	
2.69	15.06	7.57	1.68	12.86	3.21	0.63	
1.23	9.13	1.64	0.36	11.25	1.60	0.31	
1.18	8.25	0.76	0.17	5.81	3.84	-0.75	
-1.17	2.04	5.45	-1.21	5.25	4.40	-0.86	
0.10	8.59	1.10	0.24	19.33	9.68	1.89	
-0.53	2.23	5.26	-1.17	7.55	2.10	-0.41	
0.93	6.72	0.77	-0.17	6.75	2.90	-0.57	
-0.45	1.64	5.85	-1.30	5.12	4.53	-0.88	
-0.61	1.78	5.71	-1.27	8.26	1.39	-0.27	
-0.28	5.51	1.98	-0.44	8.64	1.01	-0.20	
-0.22	6.24	1.25	-0.28	5.00	4.65	-0.91	
0.29	5.19	2.30	-0.51	5.84	3.81	-0.74	
1.67	4.88	2.61	-0.58	8.11	1.54	-0.30	
0.06	3.74	3.75	-0.83	9.72	0.07	0.02	
1.41	17.22	**9.73**	2.16	12.66	3.01	0.59	
2.30	17.34	**9.85**	2.19	10.21	0.56	0.11	y
-0.06	6.34	1.15	-0.26	15.17	5.52	1.08	
-0.37	5.17	2.32	-0.52	8.36	1.29	-0.25	
0.37	7.18	0.31	-0.07	6.34	3.31	-0.65	
0.63	7.99	0.50	0.11	8.99	0.66	-0.13	
1.17	13.45	5.96	1.33	15.26	5.61	1.10	
1.69	9.13	1.64	0.36	17.74	8.09	1.58	
1.11	3.61	3.88	-0.86	6.25	3.40	-0.66	
-0.23	3.45	4.04	-0.90	5.54	4.11	-0.80	

-0.38	1.77	5.72	-1.27	9.05	0.60	-0.12	
0.53	4.09	3.40	-0.76	8.29	1.36	-0.26	
3.86	15.54	8.05	1.79	20.78	**11.13**	2.18	y
-0.06	5.27	2.22	-0.49	14.35	4.70	0.92	
0.31	3.99	3.50	-0.78	12.60	2.95	0.58	
-0.24	3.56	3.93	-0.87	12.45	2.80	0.55	
0.93	6.71	0.78	-0.17	15.96	6.31	1.23	
0.46	3.76	3.73	-0.83	16.25	6.60	1.29	
0.04	11.98	4.49	1.00	13.91	4.26	0.83	
2.16	8.65	1.16	0.26	22.02	**12.37**	2.42	y
3.16	14.79	7.30	1.62	30.48	**20.83**	4.07	y
0.01	6.48	1.01	-0.23	15.31	5.66	1.11	
1.26	12.36	4.87	1.08	27.29	**17.64**	3.45	
-0.29	4.19	3.30	-0.74	10.01	0.36	0.07	
0.89	11.83	4.34	0.97	23.75	**14.10**	2.76	
1.39	15.90	8.41	1.87	31.90	**22.25**	4.35	
-0.75	10.51	3.02	0.67	12.63	2.98	0.58	
0.65	21.18	**13.69**	3.05	23.85	**14.20**	2.78	y
-0.40	12.79	5.30	1.18	15.98	6.33	1.24	
-0.92	6.14	1.35	-0.30	7.02	2.63	-0.51	
0.22	14.26	6.77	1.51	9.15	0.50	-0.10	
0.29	10.05	2.56	0.57	11.92	2.27	0.45	
0.34	7.90	0.41	0.09	12.21	2.56	0.50	
0.46	14.71	7.22	1.61	19.30	9.65	1.89	
-0.87	5.72	1.77	-0.39	7.56	2.09	-0.41	
-1.05	7.49	0.00	0.00	11.31	1.66	0.32	
-0.65	10.00	2.51	0.56	11.67	2.02	0.40	
0.42	9.68	2.19	0.49	14.15	4.50	0.88	
-0.37	8.95	1.46	0.32	14.14	4.49	0.88	
-0.11	8.18	0.69	0.15	14.24	4.59	0.90	
1.92	14.14	6.65	1.48	22.92	**13.27**	2.59	
0.49	14.14	6.65	1.48	17.21	7.56	1.48	
0.10	9.28	1.79	0.40	9.64	0.01	0.00	
-0.07	5.56	1.93	-0.43	10.95	1.30	0.25	
1.74	11.63	4.14	0.92	24.53	**14.88**	2.91	
0.38	9.00	1.51	0.34	11.42	1.77	0.35	
-0.82	11.62	4.13	0.92	15.12	5.47	1.07	
1.26	10.87	3.38	0.75	15.14	5.49	1.07	
-0.59	6.27	1.22	-0.27	10.28	0.63	0.12	
	7.49	3.04		9.65	3.46		
		9.11			10.37		
		4.49			5.12		
54.78		49.41					
53.47		48.23					
52.04		39.98					
46.22		29.80					
51.63		41.85					

3.78	9.07
6.66	11.02
6.94	3.40
7.97	9.37
9.42	8.01
7.75	7.95
1.25	3.27
11.33	27.21
3.75	9.81
15.08	37.02
43.88	33.90
0.34	1.09
0.66	-0.09

4.83	28.03
18.25	9.68
3.00	6.22
11.02	14.06

					% inf	**abs dev**	**robust Z**
50005.00	A02	M-026243- olfactory re	26740.00	OR1J2	9.05	1.83	0.45
50005.00	A04	M-005738- taste recep	80835.00	TAS1R1	13.28	6.06	1.49
50005.00	A05	M-005651- latrophilin	23266.00	LPHN2	3.52	3.70	-0.91
50005.00	A06	M-005737- trace amin	134860.00	TAAR9	3.40	3.82	-0.94
50005.00	A07	M-005652- latrophilin	23284.00	LPHN3	4.72	2.50	-0.62
50005.00	A08	M-005736- trace amin	134864.00	TAAR1	6.23	0.99	-0.24
50005.00	A09	M-005653- leukotriene	1241.00	LTB4R	2.75	4.47	-1.10
50005.00	A10	M-005735- tachykinin	6870.00	TACR3	4.65	2.57	-0.64
50005.00	A11	M-005654- leukotriene	56413.00	LTB4R2	6.70	0.52	-0.13
50005.00	A12	M-005734- tachykinin	6865.00	TACR2	3.24	3.98	-0.98
50005.00	A13	M-003684- MAS1 oncc	4142.00	MAS1	4.66	2.56	-0.63
50005.00	A14	M-005733- tachykinin	6869.00	TACR1	6.57	0.65	-0.16
50005.00	A15	M-005655- MAS1 oncc	116511.00	MAS1L	4.74	2.48	-0.61
50005.00	A16	M-005732- trace amin	319100.00	TAAR6	6.22	1.00	-0.25
50005.00	A17	M-005656- G protein-c	84059.00	GPR98	3.66	3.56	-0.88
50005.00	A18	M-005731- somatostat	6755.00	SSTR5	4.29	2.93	-0.72
50005.00	A19	M-010652- family with	23344.00	FAM62A	3.15	4.07	-1.01
50005.00	A20	M-005730- somatostat	6754.00	SSTR4	9.77	2.55	0.63
50005.00	A21	M-005657- melanocor	4157.00	MC1R	6.65	0.57	-0.14
50005.00	A23	M-005658- melanocor	4158.00	MC2R	5.15	2.07	-0.51
50005.00	B05	M-005739- taste recep	80834.00	TAS1R2	5.10	2.12	-0.52
50005.00	B07	M-013246- taste recep	50834.00	TAS2R1	2.92	4.30	-1.06
50005.00	B09	M-012883- taste recep	50839.00	TAS2R10	11.01	3.79	0.94
50005.00	B11	M-012882- taste recep	50838.00	TAS2R13	5.59	1.63	-0.40
50005.00	B13	M-010016- taste recep	50840.00	TAS2R14	4.58	2.64	-0.65
50005.00	B15	M-013103- taste recep	50833.00	TAS2R16	7.58	0.36	0.09
50005.00	B17	M-010109- taste recep	50831.00	TAS2R3	15.14	7.92	1.95
50005.00	B19	M-017680- taste recep	259285.00	TAS2R39	11.06	3.84	0.95
50005.00	B21	M-013102- taste recep	50832.00	TAS2R4	14.38	7.16	1.77
50005.00	B23	M-017662- taste recep	259286.00	TAS2R40	17.52	**10.30**	2.54
50005.00	C02	M-005729- somatostat	6753.00	SSTR3	2.25	4.97	-1.23
50005.00	C04	M-005728- somatostat	6752.00	SSTR2	9.72	2.50	0.62
50005.00	C05	M-005659- melanocor	4159.00	MC3R	2.63	4.59	-1.13
50005.00	C06	M-003711- somatostat	6751.00	SSTR1	5.04	2.18	-0.54
50005.00	C07	M-005660- melanocor	4160.00	MC4R	8.53	1.31	0.32
50005.00	C08	M-020198- somatostat	6750.00	SST	15.26	8.04	1.98
50005.00	C09	M-005661- melanocor	4161.00	MC5R	7.26	0.04	0.01
50005.00	C10	M-005727- G protein-c	54328.00	GPR173	15.67	**8.45**	2.08
50005.00	C11	M-003978- olfactory re	143503.00	OR51E1	16.23	**9.01**	2.22
50005.00	C12	M-010620- sortilin 1	6272.00	SORT1	5.25	1.97	-0.49
50005.00	C13	M-016259- GLI pathog	256710.00	GLIPR1L1	3.81	3.41	-0.84
50005.00	C14	M-005726- smoothene	6608.00	SMO	7.37	0.15	0.04
50005.00	C15	M-008997- olfactory re	284521.00	OR2L13	7.53	0.31	0.08
50005.00	C16	M-005724- secretin re	6344.00	SCTR	3.23	3.99	-0.98
50005.00	C17	M-012641- motilin	4295.00	MLN	6.11	1.11	-0.27
50005.00	C18	M-004774- relaxin/insu	51289.00	RXFP3	10.66	3.44	0.85

50005.00	C19	M-005662- MAS-relate	219928.00	MRGPRF	9.44	2.22	0.55
50005.00	C20	M-005723- retinal pig	10692.00	RRH	14.41	7.19	1.77
50005.00	C21	M-005665- MAS-relate	259249.00	MRGPRX1	9.17	1.95	0.48
50005.00	C23	M-005666- MAS-relate	117194.00	MRGPRX2	10.77	3.55	0.87
50005.00	D05	M-017775- taste recep	259287.00	TAS2R41	4.10	3.12	-0.77
50005.00	D07	M-017828- taste recep	259292.00	TAS2R46	3.23	3.99	-0.99
50005.00	D09	M-017830- taste recep	259294.00	TAS2R48	6.68	0.54	-0.13
50005.00	D11	M-013385- taste recep	54429.00	TAS2R5	14.29	7.07	1.74
50005.00	D13	M-018268- taste recep	338398.00	TAS2R60	10.83	3.61	0.89
50005.00	D15	M-010015- taste recep	50837.00	TAS2R7	17.96	**10.74**	2.65
50005.00	D17	M-010014- taste recep	50836.00	TAS2R8	8.13	0.91	0.23
50005.00	D19	M-010018- taste recep	50835.00	TAS2R9	7.84	0.62	0.15
50005.00	D21	M-017431- transducin	10607.00	TBL3	5.01	2.21	-0.55
50005.00	D23	M-005740- thromboxa	6915.00	TBXA2R	5.87	1.35	-0.33
50005.00	E02	M-017459- retinal oute	6094.00	ROM1	4.05	3.17	-0.78
50005.00	E04	M-004662- G protein-c	6011.00	GRK1	9.36	2.14	0.53
50005.00	E05	M-005667- MAS-relate	117195.00	MRGPRX3	6.63	0.59	-0.15
50005.00	E06	M-005722- rhodopsin (	6010.00	RHO	2.84	4.38	-1.08
50005.00	E07	M-005668- MAS-relate	117196.00	MRGPRX4	7.64	0.42	0.10
50005.00	E08	M-009711- regulator o	8787.00	RGS9	12.48	5.26	1.30
50005.00	E09	M-011035- membrane	2206.00	MS4A2	4.29	2.93	-0.72
50005.00	E10	M-015720- regulator o	6000.00	RGS7	9.13	1.91	0.47
50005.00	E11	M-005669- melatonin	4543.00	MTNR1A	4.93	2.29	-0.57
50005.00	E12	M-019082- regulator o	9628.00	RGS6	10.66	3.44	0.85
50005.00	E13	M-005670- melatonin	4544.00	MTNR1B	8.31	1.09	0.27
50005.00	E14	M-008384- regulator o	8490.00	RGS5	7.31	0.09	0.02
50005.00	E15	M-003687- neuromedi	4829.00	NMBR	5.21	2.02	-0.50
50005.00	E16	M-009900- regulator o	5999.00	RGS4	13.11	5.89	1.45
50005.00	E17	M-005671- neuromedi	56923.00	NMUR2	6.96	0.26	-0.06
50005.00	E18	M-008302- regulator o	5998.00	RGS3	10.27	3.05	0.75
50005.00	E19	M-005354- natriuretic	4881.00	NPR1	6.90	0.32	-0.08
50005.00	E20	M-008452- regulator o	8601.00	RGS20	5.73	1.49	-0.37
50005.00	E21	M-005355- natriuretic	4882.00	NPR2	12.43	5.21	1.29
50005.00	E23	M-008049- natriuretic	4883.00	NPR3	10.95	3.73	0.92
50005.00	F05	M-005741- oxoeicosan	165140.00	OXER1	2.70	4.52	-1.12
50005.00	F07	M-004055- thyrotropi	29953.00	TRHDE	3.82	3.40	-0.84
50005.00	F09	M-005747- thyrotropi	7201.00	TRHR	3.92	3.30	-0.81
50005.00	F11	M-012553- thyroid sti	7252.00	TSHB	6.28	0.94	-0.23
50005.00	F13	M-005748- thyroid sti	7253.00	TSHR	6.87	0.35	-0.09
50005.00	F15	M-021383- vasoactive	7432.00	VIP	4.82	2.40	-0.59
50005.00	F17	M-005749- vasoactive	7433.00	VIPR1	4.00	3.22	-0.80
50005.00	F19	M-005750- vasoactive	7434.00	VIPR2	12.66	5.44	1.34
50005.00	F21	M-013177- vomeronas	57191.00	VN1R1	11.66	4.44	1.09
50005.00	F23	M-008957- vomeronas	317701.00	VN1R2	9.42	2.20	0.54
50005.00	G02	M-009887- regulator o	5997.00	RGS2	0.37	6.85	-1.69
50005.00	G04	M-019997- GIPC PDZ d	10755.00	GIPC1	2.59	4.63	-1.14
50005.00	G05	M-017695- neuropepti	4852.00	NPY	5.04	2.18	-0.54

50005.00	G06	M-008896- regulator o	10287.00	RGS19	5.68	1.54	-0.38
50005.00	G07	M-005672- neuropepti	4886.00	NPY1R	5.87	1.35	-0.33
50005.00	G08	M-008386- regulator o	6004.00	RGS16	4.83	2.39	-0.59
50005.00	G09	M-005673- neuropepti	4887.00	NPY2R	3.22	4.00	-0.99
50005.00	G10	M-008826- regulator o	10636.00	RGS14	4.62	2.60	-0.64
50005.00	G11	M-005674- neuropepti	4889.00	NPY5R	9.39	2.17	0.53
50005.00	G12	M-008610- regulator o	6002.00	RGS12	9.77	2.55	0.63
50005.00	G13	M-005675- neurotensi	4923.00	NTSR1	8.60	1.38	0.34
50005.00	G14	M-009419- regulator o	8786.00	RGS11	4.92	2.30	-0.57
50005.00	G15	M-005676- neurotensi	23620.00	NTSR2	13.91	6.69	1.65
50005.00	G16	M-009501- regulator o	5996.00	RGS1	19.05	**11.83**	2.92
50005.00	G17	M-005678- opsin 1 (co	5956.00	OPN1LW	3.58	3.64	-0.90
50005.00	G18	M-005721- retinal G pr	5995.00	RGR	13.40	6.18	1.52
50005.00	G19	M-005679- opsin 1 (co	2652.00	OPN1MW	5.20	2.02	-0.50
50005.00	G20	M-011102- peripherin	5961.00	PRPH2	10.78	3.56	0.88
50005.00	G21	M-005680- opsin 1 (co	611.00	OPN1SW	10.55	3.33	0.82
50005.00	G23	M-005681- opsin 3 (en	23596.00	OPN3	10.74	3.52	0.87
50005.00	H05	M-017659- vomeronas	317702.00	VN1R3	1.01	6.21	-1.53
50005.00	H07	M-017651- vomeronas	317703.00	VN1R4	2.84	4.38	-1.08
50005.00	H09	M-017642- vomeronas	317705.00	VN1R5	4.49	2.73	-0.67
50005.00	H11	M-013375- WD repeat	54554.00	WDR5B	2.51	4.71	-1.16
50005.00	H13	M-005751- chemokine	2829.00	XCR1	2.83	4.39	-1.08
50005.00	H15	M-005752- xenotropic	9213.00	XPR1	6.67	0.55	-0.14
50005.00	I02	M-009719- RAS, dexan	51655.00	RASD1	3.82	3.40	-0.84
50005.00	I04	M-003700- receptor (G	10267.00	RAMP1	8.82	1.60	0.40
50005.00	I05	M-005682- opsin 4 (m	94233.00	OPN4	4.76	2.46	-0.61
50005.00	I06	M-009778- protein tyr	5777.00	PTPN6	5.02	2.20	-0.54
50005.00	I07	M-005683- opioid rece	4985.00	OPRD1	9.55	2.33	0.58
50005.00	I08	M-005718- parathyroi	5746.00	PTHR2	10.22	3.00	0.74
50005.00	I09	M-005684- opioid rece	4986.00	OPRK1	7.65	0.43	0.11
50005.00	I10	M-005717- parathyroi	5745.00	PTHR1	10.61	3.39	0.84
50005.00	I11	M-005685- opiate rece	4987.00	OPRL1	10.38	3.16	0.78
50005.00	I12	M-012547- parathyroi	5741.00	PTH	19.00	**11.78**	2.91
50005.00	I13	M-005686- opioid rece	4988.00	OPRM1	9.67	2.45	0.60
50005.00	I14	M-005716- prostaglan	5739.00	PTGIR	6.28	0.94	-0.23
50005.00	I15	M-020479- olfactory re	26539.00	OR10H1	5.37	1.85	-0.46
50005.00	I16	M-005715- prostaglan	5737.00	PTGFR	9.12	1.90	0.47
50005.00	I17	M-008904- olfactory re	26538.00	OR10H2	5.76	1.46	-0.36
50005.00	I18	M-005714- prostaglan	5734.00	PTGER4	10.02	2.80	0.69
50005.00	I19	M-008901- olfactory re	26476.00	OR10J1	6.18	1.04	-0.26
50005.00	I20	M-005713- prostaglan	5733.00	PTGER3	11.71	4.49	1.11
50005.00	I21	M-008813- olfactory re	26531.00	OR11A1	11.41	4.19	1.03
50005.00	I23	M-008814- olfactory re	26529.00	OR12D2	6.80	0.42	-0.10
50005.00	K02	M-005712- prostaglan	5732.00	PTGER2	3.65	3.57	-0.88
50005.00	K04	M-005711- prostaglan	5731.00	PTGER1	3.96	3.26	-0.81
50005.00	K05	M-009796- olfactory re	81797.00	OR12D3	11.54	4.32	1.07
50005.00	K06	M-005710- prostaglan	5729.00	PTGDR	5.14	2.08	-0.51

50005.00	K07	M-008911- olfactory re	8383.00	OR1A1	5.58	1.64	-0.41
50005.00	K08	M-005709- platelet-act	5724.00	PTAFR	3.25	3.97	-0.98
50005.00	K09	M-008912- olfactory re	26189.00	OR1A2	7.94	0.72	0.18
50005.00	K10	M-021325- proline-rich	5545.00	PRB4	15.21	7.99	1.97
50005.00	K11	M-021656- olfactory re	26188.00	OR1C1	6.52	0.70	-0.17
50005.00	K12	M-005708- pancreatic	5540.00	PPYR1	6.81	0.41	-0.10
50005.00	K13	M-009079- olfactory re	4991.00	OR1D2	11.16	3.94	0.97
50005.00	K14	M-005707- trace amin	9038.00	TAAR5	8.79	1.57	0.39
50005.00	K15	M-009066- olfactory re	8385.00	OR1D4	4.95	2.27	-0.56
50005.00	K16	M-005274- phosphoin	5294.00	PIK3CG	7.08	0.14	-0.04
50005.00	K17	M-020461- olfactory re	8386.00	OR1D5	14.43	7.21	1.78
50005.00	K18	M-003019- phosphoin	5291.00	PIK3CB	16.31	**9.09**	2.24
50005.00	K19	M-009038- olfactory re	8387.00	OR1E1	21.73	**14.51**	3.58
50005.00	K20	M-013394- phosducin-	5082.00	PDCL	26.75	**19.53**	4.82
50005.00	K21	M-012609- olfactory re	8388.00	OR1E2	17.43	**10.21**	2.52
50005.00	K23	M-008798- olfactory re	4992.00	OR1F1	20.97	**13.75**	3.39
50005.00	M02	M-013000- phosducin	5132.00	PDC	3.85	3.37	-0.83
50005.00	M04	M-005695- purinergic r	286530.00	P2RY8	6.92	0.30	-0.07
50005.00	M05	M-009068- olfactory re	8390.00	OR1G1	17.28	**10.06**	2.48
50005.00	M06	M-004579- pyrimidine	5031.00	P2RY6	6.04	1.18	-0.29
50005.00	M07	M-009046- olfactory re	79541.00	OR2A4	11.84	4.62	1.14
50005.00	M08	M-004603- purinergic r	10161.00	P2RY5	8.86	1.64	0.41
50005.00	M09	M-008800- olfactory re	81697.00	OR2B2	9.95	2.73	0.67
50005.00	M10	M-005693- pyrimidine	5030.00	P2RY4	7.95	0.73	0.18
50005.00	M11	M-008801- olfactory re	4993.00	OR2C1	3.93	3.29	-0.81
50005.00	M12	M-003688- purinergic r	5029.00	P2RY2	9.56	2.34	0.58
50005.00	M13	M-021427- olfactory re	81472.00	OR2C3	8.09	0.87	0.21
50005.00	M14	M-005692- purinergic r	64805.00	P2RY12	10.35	3.13	0.77
50005.00	M15	M-020188- olfactory re	26211.00	OR2F1	14.22	7.00	1.73
50005.00	M16	M-005691- purinergic r	5032.00	P2RY11	8.22	1.00	0.25
50005.00	M17	M-018165- olfactory re	26716.00	OR2H1	16.66	**9.44**	2.33
50005.00	M18	M-005690- purinergic r	27334.00	P2RY10	12.31	5.09	1.26
50005.00	M19	M-008264- olfactory re	7932.00	OR2H2	3.02	4.20	-1.04
50005.00	M20	M-005689- purinergic r	5028.00	P2RY1	13.31	6.09	1.50
50005.00	M21	M-014667- olfactory re	26707.00	OR2J2	13.97	6.75	1.67
50005.00	M23	M-020799- olfactory re	56656.00	OR2S2	5.79	1.43	-0.35
50005.00	O02	M-005688- oxytocin re	5021.00	OXTR	14.32	7.10	1.75
50005.00	O04	M-005687- neuropepti	64106.00	NPFFR1	9.44	2.22	0.55
50005.00	O05	M-021670- olfactory re	26696.00	OR2T1	5.71	1.51	-0.37
50005.00	O06	M-009107- olfactory re	26493.00	OR8B8	6.00	1.22	-0.30
50005.00	O07	M-014666- olfactory re	26692.00	OR2W1	6.80	0.42	-0.10
50005.00	O08	M-012818- olfactory re	26658.00	OR7C2	12.75	5.53	1.36
50005.00	O09	M-009039- olfactory re	4994.00	OR3A1	7.18	0.04	-0.01
50005.00	O10	M-013817- olfactory re	26659.00	OR7A5	8.01	0.79	0.20
50005.00	O11	M-009040- olfactory re	4995.00	OR3A2	6.44	0.78	-0.19
50005.00	O12	M-009112- olfactory re	26333.00	OR7A17	14.30	7.08	1.75
50005.00	O13	M-008612- olfactory re	8392.00	OR3A3	4.42	2.80	-0.69

50005.00	O14	M-009100-	olfactory re	8590.00	OR6A2	6.44	0.78	-0.19
50005.00	O15	M-023248-	olfactory re	26689.00	OR4D1	13.57	6.35	1.57
50005.00	O16	M-009795-	olfactory re	81696.00	OR5V1	7.17	0.05	-0.01
50005.00	O17	M-009098-	olfactory re	79345.00	OR51B2	9.62	2.40	0.59
50005.00	O18	M-008791-	olfactory re	10798.00	OR5I1	6.51	0.71	-0.18
50005.00	O19	M-009072-	olfactory re	79339.00	OR51B4	9.97	2.75	0.68
50005.00	O20	M-026622-	olfactory re	338674.00	OR5F1	17.82	**10.60**	2.62
50005.00	O21	M-008774-	olfactory re	81285.00	OR51E2	20.19	**12.97**	3.20
50005.00	O23	M-009058-	olfactory re	23538.00	OR52A1	10.95	3.73	0.92
					mdn	7.22	2.74	
					3xMAD		8.21	
					MADc		4.05	
50005.00	C22					41.18		51.89
50005.00	D22					47.36		50.38
50005.00	E22					47.90		49.97
50005.00	F22					50.47		42.26
					mn	46.73		48.62
					sd	3.94		4.32
50005.00	G22					11.85		5.82
50005.00	H22					6.14		14.43
50005.00	I22					8.10		3.35
50005.00	J22					7.45		3.16
					mn	8.38		6.69
					sd	2.45		5.30
					3psSD	11.81		12.97
					3ngSD	7.36		15.90
					SumSD	19.17		28.87
					MeanDf	38.35		41.93
					SumovrMn	0.50		0.69
					1minus	0.50		0.31
50005.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	4.90		8.04
50005.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	4.49		31.25
50005.00	I03	D-001206-:	siControl non-targeting			8.67		9.52
50005.00	J03	D-001206-:	siControl non-targeting			8.17		15.46
50005.00	L03	D-001600-(	siGLO RISC-free siRNA			11.81		24.22

% inf	abs dev	robust Z	% inf	abs dev	robust Z
7.81	0.39	-0.08	12.64	2.17	0.40
12.97	4.77	1.01	6.19	4.28	-0.78
4.67	3.53	-0.75	6.62	3.85	-0.70
3.43	4.77	-1.02	3.46	7.01	-1.27
9.88	1.68	0.36	7.33	3.14	-0.57
12.47	4.27	0.91	9.80	0.67	-0.12
3.05	5.15	-1.10	7.78	2.69	-0.49
5.58	2.62	-0.56	8.26	2.21	-0.40
4.22	3.98	-0.85	5.63	4.84	-0.88
5.25	2.95	-0.63	4.54	5.93	-1.08
6.06	2.14	-0.46	11.64	1.17	0.21
7.77	0.43	-0.09	6.59	3.88	-0.71
9.55	1.35	0.29	10.13	0.34	-0.06
3.46	4.74	-1.01	5.51	4.96	-0.90
8.88	0.68	0.15	10.36	0.12	-0.02
6.09	2.11	-0.45	7.44	3.03	-0.55
17.38	9.18	1.95	6.78	3.69	-0.67
16.74	8.54	1.82	39.35	**28.88**	5.26
8.66	0.46	0.10	18.12	7.65	1.39
5.87	2.33	-0.50	20.08	9.61	1.75
12.81	4.61	0.98	4.15	6.32	-1.15
5.19	3.01	-0.64	2.11	8.36	-1.52
12.29	4.09	0.87	9.55	0.92	-0.17
8.36	0.16	0.03	5.78	4.69	-0.85
6.42	1.78	-0.38	8.22	2.25	-0.41
8.01	0.19	-0.04	4.90	5.57	-1.01
13.73	5.53	1.18	12.31	1.84	0.34
8.74	0.54	0.12	12.80	2.33	0.43
10.44	2.24	0.48	10.12	0.35	-0.06
15.26	7.06	1.50	17.92	7.45	1.36
2.58	5.62	-1.20	4.00	6.47	-1.18
4.53	3.67	-0.78	13.72	3.25	0.59
1.65	6.55	-1.39	5.14	5.33	-0.97
1.94	6.26	-1.33	8.41	2.06	-0.37
4.34	3.86	-0.82	9.14	1.33	-0.24
7.42	0.78	-0.17	17.38	6.91	1.26
2.00	6.20	-1.32	3.72	6.75	-1.23
7.38	0.82	-0.18	11.64	1.17	0.21
10.87	2.67	0.57	14.26	3.79	0.69
7.75	0.45	-0.10	7.77	2.70	-0.49
10.48	2.28	0.48	9.56	0.91	-0.17
8.33	0.13	0.03	8.49	1.98	-0.36
6.44	1.76	-0.37	10.74	0.27	0.05
5.52	2.68	-0.57	2.89	7.58	-1.38
4.65	3.55	-0.76	4.17	6.30	-1.15
4.71	3.49	-0.74	15.37	4.90	0.89

9.16	0.96	0.21	15.93	5.46	0.99	
15.50	7.30	1.55	22.10	**11.63**	2.12	
13.75	5.55	1.18	8.89	1.58	-0.29	
13.63	5.43	1.16	14.30	3.83	0.70	
3.91	4.29	-0.91	4.14	6.33	-1.15	
6.54	1.66	-0.35	5.08	5.39	-0.98	
6.37	1.83	-0.39	11.16	0.69	0.13	
20.31	**12.11**	2.58	23.90	**13.43**	2.45	y
16.32	8.12	1.73	15.69	5.22	0.95	
20.76	**12.56**	2.67	16.66	6.19	1.13	y
18.63	**10.43**	2.22	7.59	2.88	-0.52	
18.27	**10.07**	2.14	10.34	0.13	-0.02	
9.14	0.94	0.20	5.74	4.73	-0.86	
6.69	1.51	-0.32	8.97	1.50	-0.27	
3.87	4.33	-0.92	2.49	7.98	-1.45	
5.09	3.11	-0.66	15.86	5.39	0.98	
7.13	1.07	-0.23	12.06	1.59	0.29	
2.97	5.23	-1.11	4.14	6.33	-1.15	
5.61	2.59	-0.55	6.66	3.81	-0.69	
5.91	2.29	-0.49	24.79	**14.32**	2.61	
4.35	3.85	-0.82	6.76	3.71	-0.68	
14.69	6.49	1.38	20.69	10.22	1.86	
3.50	4.70	-1.00	9.65	0.82	-0.15	
6.11	2.09	-0.44	12.17	1.70	0.31	
3.72	4.48	-0.95	9.21	1.26	-0.23	
1.94	6.26	-1.33	11.37	0.90	0.16	
5.57	2.63	-0.56	9.55	0.92	-0.17	
9.49	1.29	0.27	20.76	10.29	1.87	
10.66	2.46	0.52	18.25	7.78	1.42	
8.84	0.64	0.14	12.44	1.97	0.36	
9.13	0.93	0.20	11.79	1.32	0.24	
9.56	1.36	0.29	11.32	0.85	0.16	
14.14	5.94	1.26	23.37	**12.90**	2.35	
5.52	2.68	-0.57	10.58	0.11	0.02	
10.38	2.18	0.46	7.62	2.85	-0.52	
5.80	2.40	-0.51	9.51	0.96	-0.17	
15.17	6.97	1.48	20.78	10.31	1.88	
16.25	8.05	1.71	14.50	4.03	0.73	
8.11	0.09	-0.02	10.17	0.30	-0.05	
3.74	4.46	-0.95	8.63	1.84	-0.33	
4.37	3.83	-0.82	8.42	2.05	-0.37	
15.05	6.85	1.46	24.66	**14.19**	2.58	
4.54	3.66	-0.78	14.25	3.78	0.69	
2.56	5.64	-1.20	15.05	4.58	0.83	
3.52	4.68	-1.00	4.82	5.65	-1.03	
6.17	2.03	-0.43	5.05	5.42	-0.99	
3.22	4.98	-1.06	3.71	6.76	-1.23	

11.38	3.18	0.68	11.73	1.26	0.23
3.15	5.05	-1.07	14.39	3.92	0.71
3.17	5.03	-1.07	13.62	3.15	0.57
4.37	3.83	-0.82	5.12	5.35	-0.97
4.70	3.50	-0.74	8.12	2.35	-0.43
3.84	4.36	-0.93	10.69	0.22	0.04
7.01	1.19	-0.25	10.14	0.33	-0.06
11.95	3.75	0.80	17.27	6.80	1.24
6.01	2.19	-0.47	12.87	2.40	0.44
10.52	2.32	0.49	11.53	1.06	0.19
7.82	0.38	-0.08	9.64	0.83	-0.15
2.17	6.03	-1.28	6.41	4.06	-0.74
7.09	1.11	-0.24	14.82	4.35	0.79
4.95	3.25	-0.69	6.46	4.01	-0.73
7.11	1.09	-0.23	11.06	0.59	0.11
5.67	2.53	-0.54	4.49	5.98	-1.09
4.18	4.02	-0.86	9.96	0.51	-0.09
9.04	0.84	0.18	9.82	0.65	-0.12
10.78	2.58	0.55	9.14	1.33	-0.24
16.01	7.81	1.66	7.04	3.43	-0.62
13.05	4.85	1.03	9.13	1.34	-0.24
7.88	0.32	-0.07	7.70	2.77	-0.50
18.11	**9.91**	2.11	15.24	4.77	0.87
4.12	4.08	-0.87	6.66	3.81	-0.69
12.20	4.00	0.85	8.10	2.37	-0.43
11.69	3.49	0.74	6.26	4.21	-0.77
7.28	0.92	-0.20	7.74	2.73	-0.50
6.15	2.05	-0.44	6.57	3.90	-0.71
12.58	4.38	0.93	7.63	2.84	-0.52
7.53	0.67	-0.14	8.43	2.04	-0.37
12.95	4.75	1.01	13.96	3.49	0.64
15.55	7.35	1.57	11.62	1.15	0.21
16.15	7.95	1.69	19.83	9.36	1.71
10.34	2.14	0.46	8.85	1.62	-0.29
7.42	0.78	-0.17	12.69	2.22	0.40
4.60	3.60	-0.77	8.60	1.87	-0.34
8.36	0.16	0.03	13.28	2.81	0.51
2.09	6.11	-1.30	7.78	2.69	-0.49
2.83	5.37	-1.14	9.69	0.78	-0.14
3.14	5.06	-1.08	6.93	3.54	-0.64
6.10	2.10	-0.45	15.07	4.60	0.84
9.49	1.29	0.27	19.80	9.33	1.70
4.92	3.28	-0.70	11.39	0.92	0.17
3.14	5.06	-1.08	2.86	7.61	-1.38
5.34	2.86	-0.61	4.77	5.70	-1.04
17.20	9.00	1.92	9.84	0.63	-0.11
4.74	3.46	-0.74	7.83	2.64	-0.48

8.30	0.10	0.02	7.21	3.26	-0.59		
6.56	1.64	-0.35	5.97	4.50	-0.82		
7.21	0.99	-0.21	8.55	1.92	-0.35		
15.55	7.35	1.57	12.88	2.41	0.44		
11.64	3.44	0.73	8.75	1.72	-0.31		
8.95	0.75	0.16	5.56	4.91	-0.89		
14.86	6.66	1.42	12.67	2.20	0.40		
11.13	2.93	0.62	12.87	2.40	0.44		
6.16	2.04	-0.44	5.39	5.08	-0.92		
8.26	0.06	0.01	12.59	2.12	0.39		
10.33	2.13	0.45	11.60	1.13	0.21		
13.52	5.32	1.13	16.72	6.25	1.14		
14.73	6.53	1.39	18.13	7.66	1.39		
20.92	**12.72**	2.71	20.01	9.54	1.74	y	
11.06	2.86	0.61	17.45	6.98	1.27		
15.53	7.33	1.56	18.66	8.19	1.49		
9.61	1.41	0.30	9.51	0.96	-0.17		
16.52	8.32	1.77	13.88	3.41	0.62		
7.34	0.86	-0.18	19.41	8.94	1.63		
11.04	2.84	0.60	11.95	1.48	0.27		
19.92	**11.72**	2.49	16.93	6.46	1.18		
9.57	1.37	0.29	14.71	4.24	0.77		
14.82	6.62	1.41	22.15	**11.68**	2.13		
14.35	6.15	1.31	19.92	9.45	1.72		
9.42	1.22	0.26	13.00	2.53	0.46		
16.57	8.37	1.78	19.57	9.10	1.66		
10.16	1.96	0.42	14.69	4.22	0.77		
10.86	2.66	0.57	9.83	0.64	-0.11		
18.35	**10.15**	2.16	40.56	**30.09**	5.48	x	toxic a,b,c
11.37	3.17	0.67	18.47	8.00	1.46		
24.99	**16.79**	3.57	28.94	**18.47**	3.36	y	
12.92	4.72	1.00	14.92	4.45	0.81		
8.90	0.70	0.15	8.97	1.50	-0.27		
8.14	0.06	-0.01	21.43	10.96	2.00		
13.59	5.39	1.15	8.14	2.33	-0.42		
7.00	1.20	-0.26	6.76	3.71	-0.67		
11.37	3.17	0.68	13.25	2.78	0.51		
8.97	0.77	0.16	9.08	1.39	-0.25		
8.83	0.63	0.13	5.82	4.65	-0.85		
5.85	2.35	-0.50	12.83	2.36	0.43		
5.93	2.27	-0.48	7.07	3.40	-0.62		
12.62	4.42	0.94	18.06	7.59	1.38		
6.77	1.43	-0.30	11.97	1.50	0.27		
8.76	0.56	0.12	18.36	7.89	1.44		
6.96	1.24	-0.26	15.28	4.81	0.88		
18.12	**9.92**	2.11	19.92	9.45	1.72		
7.02	1.18	-0.25	9.95	0.52	-0.09		

14.27	6.07	1.29	15.59	5.12	0.93	
15.67	7.47	1.59	22.10	**11.63**	2.12	
7.05	1.15	-0.24	14.68	4.21	0.77	
2.79	5.41	-1.15	11.29	0.82	0.15	
7.46	0.74	-0.16	17.40	6.93	1.26	
6.88	1.32	-0.28	20.35	9.88	1.80	
25.33	**17.13**	3.65	28.56	**18.09**	3.29	y
22.20	**14.00**	2.98	29.18	**18.71**	3.41	y
10.66	2.46	0.52	13.65	3.18	0.58	
8.20	3.17		10.47	3.71		
	9.52			11.13		
	4.70			5.49		
	47.65					
	54.91					
	58.41					
	58.16					
	54.78					
	5.02					
	5.94					
	9.52					
	15.26					
	9.41					
	10.03					
	3.86					
	15.06					
	11.59					
	26.64					
	44.75					
	0.60					
	0.40					
	22.69					
	24.24					
	11.18					
	9.12					
	14.34					

Human3 Pc	M-013302-	delta-like 1 (Drosophila)	28514.00	DLL1	A02
Human3 Pc	M-015911-	delta-like 1 homolog (Drosophila)	8788.00	DLK1	A04
Human3 Pc	M-020249-	septin 11	55752.00	SEPT11	A05
Human3 Pc	M-008984-	DIRAS family, GTP-binding RAS-like 1	148252.00	DIRAS1	A06
Human3 Pc	M-011192-	angio-associated, migratory cell protein	14.00	AAMP	A07
Human3 Pc	M-004421-	death effector domain containing	9191.00	DEDD	A08
Human3 Pc	M-007302-	ATP-binding cassette, sub-family B (MDR/TAP),	5244.00	ABCB4	A09
Human3 Pc	M-011022-	damage-specific DNA binding protein 2, 48kDa	1643.00	DDB2	A10
Human3 Pc	M-007309-	ATP-binding cassette, sub-family C (CFTR/MRP)	89845.00	ABCC10	A11
Human3 Pc	M-011840-	deleted in azoospermia 1	1617.00	DAZ1	A12
Human3 Pc	M-009909-	ATP-binding cassette, sub-family D (ALD), mem	5825.00	ABCD3	A13
Human3 Pc	M-004420-	death-associated protein 6	1616.00	DAXX	A14
Human3 Pc	M-008284-	ATP-binding cassette, sub-family G (WHITE), m	64240.00	ABCG5	A15
Human3 Pc	M-004419-	death inducer-obliterator 1	11083.00	DIDO1	A16
Human3 Pc	M-008397-	ATP-binding cassette, sub-family G (WHITE), m	64241.00	ABCG8	A17
Human3 Pc	M-015200-	dachshund homolog 2 (Drosophila)	117154.00	DACH2	A18
Human3 Pc	M-013586-	ankyrin repeat and BTB (POZ) domain containi	80325.00	ABTB1	A19
Human3 Pc	M-013222-	dachshund homolog 1 (Drosophila)	1602.00	DACH1	A20
Human3 Pc	M-008864-	acylphosphatase 2, muscle type	98.00	ACYP2	A21
Human3 Pc	M-009410-	adducin 2 (beta)	119.00	ADD2	A23
Human3 Pc	M-019830-	lin-7 homolog A (C. elegans)	8825.00	LIN7A	B02
Human3 Pc	M-031935-	LIM domains containing 1	8994.00	LIMD1	B04
Human3 Pc	M-012618-	dynein, axonemal, heavy chain 11	8701.00	DNAH11	B05
Human3 Pc	M-020010-	lipoma HMGIC fusion partner	10186.00	LHFP	B06
Human3 Pc	M-009296-	dynein, axonemal, heavy chain 5	1767.00	DNAH5	B07
Human3 Pc	M-010607-	lectin, galactoside-binding, soluble, 8 (galectin	3964.00	LGALS8	B08
Human3 Pc	M-010586-	dynein, light chain, roadblock-type 1	83658.00	DYNLRB1	B09
Human3 Pc	M-012232-	lectin, galactoside-binding, soluble, 4 (galectin	3960.00	LGALS4	B10
Human3 Pc	M-015304-	dynein, light chain, roadblock-type 2	83657.00	DYNLRB2	B11
Human3 Pc	M-020134-	lectin, galactoside-binding, soluble, 2	3957.00	LGALS2	B12
Human3 Pc	M-020110-	dynein, cytoplasmic 1, light intermediate chain	1783.00	DYNC1LI2	B13
Human3 Pc	M-010683-	lectin, galactoside-binding, soluble, 12 (galecti	85329.00	LGALS12	B14
Human3 Pc	M-019818-	developmentally regulated GTP binding protei	4733.00	DRG1	B15
Human3 Pc	M-015396-	lymphoid enhancer-binding factor 1	51176.00	LEF1	B16
Human3 Pc	M-011257-	developmentally regulated GTP binding protei	1819.00	DRG2	B17
Human3 Pc	M-010128-	lipopolysaccharide binding protein	3929.00	LBP	B18
Human3 Pc	M-012219-	AT rich interactive domain 3B (BRIGHT-like)	10620.00	ARID3B	B19
Human3 Pc	M-006472-	lymphocyte-activation gene 3	3902.00	LAG3	B20
Human3 Pc	M-011643-	atrophin 1	1822.00	ATN1	B21
Human3 Pc	M-011995-	desmocollin 1	1823.00	DSC1	B23
Human3 Pc	M-014010-	dishevelled associated activator of morphogen	23500.00	DAAM2	C02
Human3 Pc	M-015834-	cold shock domain containing E1, RNA-binding	7812.00	CSDE1	C04
Human3 Pc	M-021376-	NCK interacting protein with SH3 domain	51517.00	NCKIPSD	C05
Human3 Pc	M-004263-	cysteine-rich, angiogenic inducer, 61	3491.00	CYR61	C06
Human3 Pc	M-011203-	aggrecan	176.00	ACAN	C07
Human3 Pc	M-011020-	cytochrome b-245, alpha polypeptide	1535.00	CYBA	C08

Human3 Pc	M-011952-	allograft inflammatory factor 1	199.00	AIF1	C09
Human3 Pc	M-012741-	CUG triplet repeat, RNA binding protein 2	10659.00	CUGBP2	C10
Human3 Pc	M-011951-	absent in melanoma 2	9447.00	AIM2	C11
Human3 Pc	M-020881-	catenin, beta interacting protein 1	56998.00	CTNNBIP1	C12
Human3 Pc	M-017351-	A kinase (PRKA) anchor protein 2	11217.00	AKAP2	C13
Human3 Pc	M-012633-	connective tissue growth factor	1490.00	CTGF	C14
Human3 Pc	M-020229-	PDZ and LIM domain 3	27295.00	PDLIM3	C15
Human3 Pc	M-011247-	cleavage stimulation factor, 3' pre-RNA, subuni	1479.00	CSTF3	C16
Human3 Pc	M-017697-	par-3 partitioning defective 3 homolog B (C. ele	117583.00	PARD3B	C17
Human3 Pc	M-016071-	versican	1462.00	VCAN	C18
Human3 Pc	M-012515-	ankyrin repeat domain 1 (cardiac muscle)	27063.00	ANKRD1	C19
Human3 Pc	M-008423-	corticotropin releasing hormone binding protei	1393.00	CRHBP	C20
Human3 Pc	M-016466-	ankyrin repeat domain 5	63926.00	ANKRD5	C21
Human3 Pc	M-012363-	annexin A10	11199.00	ANXA10	C23
Human3 Pc	M-011317-	AF4/FMR2 family, member 3	3899.00	AFF3	D02
Human3 Pc	M-011069-	L1 cell adhesion molecule	3897.00	L1CAM	D04
Human3 Pc	M-011996-	desmocollin 2	1824.00	DSC2	D05
Human3 Pc	M-019756-	kaptin (actin binding protein)	11133.00	KPTN	D06
Human3 Pc	M-003651-	desmocollin 3	1825.00	DSC3	D07
Human3 Pc	M-007083-	Kruppel-like factor 16	83855.00	KLF16	D08
Human3 Pc	M-011644-	desmoglein 1	1828.00	DSG1	D09
Human3 Pc	M-006975-	Kruppel-like factor 15	28999.00	KLF15	D10
Human3 Pc	M-011645-	desmoglein 2	1829.00	DSG2	D11
Human3 Pc	M-007132-	Kruppel-like factor 14	136259.00	KLF14	D12
Human3 Pc	M-011646-	desmoglein 3 (pemphigus vulgaris antigen)	1830.00	DSG3	D13
Human3 Pc	M-012901-	calcium and integrin binding family member 3	117286.00	CIB3	D14
Human3 Pc	M-011258-	dystrobrevin, alpha	1837.00	DTNA	D15
Human3 Pc	M-012230-	calcium and integrin binding family member 2	10518.00	CIB2	D16
Human3 Pc	M-004132-	heterogeneous nuclear ribonucleoprotein U-lik	11100.00	HNRPUL1	D17
Human3 Pc	M-012460-	KIN, antigenic determinant of recA protein hon	22944.00	KIN	D18
Human3 Pc	M-011855-	EGF-containing fibulin-like extracellular matrix	2202.00	EFEMP1	D19
Human3 Pc	M-008786-	kinesin family member C2	90990.00	KIFC2	D20
Human3 Pc	M-012094-	embryonal Fyn-associated substrate	10278.00	EFS	D21
Human3 Pc	M-006527-	early growth response 2 (Krox-20 homolog, Drc	1959.00	EGR2	D23
Human3 Pc	M-008805-	cAMP responsive element binding protein-like	1388.00	CREBL1	E02
Human3 Pc	M-004412-	CASP2 and RIPK1 domain containing adaptor w	8738.00	CRADD	E04
Human3 Pc	M-011212-	annexin A11	311.00	ANXA11	E05
Human3 Pc	M-012721-	coronin, actin binding protein, 2B	10391.00	CORO2B	E06
Human3 Pc	M-011811-	annexin A13	312.00	ANXA13	E07
Human3 Pc	M-011420-	coronin, actin binding protein, 2A	7464.00	CORO2A	E08
Human3 Pc	M-011213-	amyloid beta (A4) precursor protein-binding, fa	322.00	APBB1	E09
Human3 Pc	M-017331-	coronin, actin binding protein, 1C	23603.00	CORO1C	E10
Human3 Pc	M-017611-	amyloid beta (A4) precursor protein-binding, fa	10307.00	APBB3	E11
Human3 Pc	M-012010-	contactin 2 (axonal)	6900.00	CNTN2	E12
Human3 Pc	M-003869-	adenomatosis polyposis coli	324.00	APC	E13
Human3 Pc	M-011613-	contactin 1	1272.00	CNTN1	E14
Human3 Pc	M-009847-	adenomatosis polyposis coli 2	10297.00	APC2	E15

Human3 Pc	M-004003-	clathrin, light chain (Lcb)	1212.00	CLTB	E16
Human3 Pc	M-011571-	amyloid P component, serum	325.00	APCS	E17
Human3 Pc	M-004002-	clathrin, light chain (Lca)	1211.00	CLTA	E18
Human3 Pc	M-017633-	heat shock 70kDa protein 4-like	22824.00	HSPA4L	E19
Human3 Pc	M-020504-	calsyntenin 3	9746.00	CLSTN3	E20
Human3 Pc	M-004178-	amyloid beta (A4) precursor-like protein 1	333.00	APLP1	E21
Human3 Pc	M-017310-	apolipoprotein L, 4	80832.00	APOL4	E23
Human3 Pc	M-012933-	kinesin-associated protein 3	22920.00	KIFAP3	F02
Human3 Pc	M-015105-	TSPY-like 5	85453.00	TSPYL5	F04
Human3 Pc	M-003005-	eukaryotic translation initiation factor 4E bindi	1978.00	EIF4EBP1	F05
Human3 Pc	M-014057-	leucine rich repeat containing 7	57554.00	LRRC7	F06
Human3 Pc	M-018671-	eukaryotic translation initiation factor 4E bindi	1979.00	EIF4EBP2	F07
Human3 Pc	M-024048-	TBC1 domain family, member 9 (with GRAM dc	23158.00	TBC1D9	F08
Human3 Pc	M-003773-	ELAV (embryonic lethal, abnormal vision, Drosc	1994.00	ELAVL1	F09
Human3 Pc	M-021238-	zinc finger CCCH-type containing 11A	9877.00	ZC3H11A	F10
Human3 Pc	M-019801-	ELAV (embryonic lethal, abnormal vision, Drosc	1993.00	ELAVL2	F11
Human3 Pc	M-021049-	KIAA0494	9813.00	KIAA0494	F12
Human3 Pc	M-011264-	ELAV (embryonic lethal, abnormal vision, Drosc	1995.00	ELAVL3	F13
Human3 Pc	M-009490-	KH-type splicing regulatory protein (FUSE bindi	8570.00	KHSRP	F14
Human3 Pc	M-012851-	engulfment and cell motility 1	9844.00	ELMO1	F15
Human3 Pc	M-020019-	KH domain containing, RNA binding, signal tran	10657.00	KHDRBS1	F16
Human3 Pc	M-008893-	ectodermal-neural cortex (with BTB-like domai	8507.00	ENC1	F17
Human3 Pc	M-009244-	jumonji, AT rich interactive domain 2	3720.00	JARID2	F18
Human3 Pc	M-011026-	endoglin (Osler-Rendu-Weber syndrome 1)	2022.00	ENG	F19
Human3 Pc	M-006957-	suppressor of zeste 12 homolog (Drosophila)	23512.00	SUZ12	F20
Human3 Pc	M-004005-	epidermal growth factor receptor pathway sub	2060.00	EPS15	F21
Human3 Pc	M-020729-	erythroid associated factor	51327.00	ERAF	F23
Human3 Pc	M-013883-	calsyntenin 2	64084.00	CLSTN2	G02
Human3 Pc	M-005288-	claspin homolog (Xenopus laevis)	63967.00	CLSPN	G04
Human3 Pc	M-010362-	androgen-induced proliferation inhibitor	23047.00	APRIN	G05
Human3 Pc	M-011830-	calmegin	1047.00	CLGN	G06
Human3 Pc	M-012820-	ADP-ribosylation factor interacting protein 2 (a	23647.00	ARFIP2	G07
Human3 Pc	M-006831-	cytoplasmic linker associated protein 1	23332.00	CLASP1	G08
Human3 Pc	M-009751-	Rho guanine nucleotide exchange factor (GEF)	9828.00	ARHGEF17	G09
Human3 Pc	M-012801-	CDKN1A interacting zinc finger protein 1	25792.00	CIZ1	G10
Human3 Pc	M-005093-	Rho guanine nucleotide exchange factor (GEF)	7984.00	ARHGEF5	G11
Human3 Pc	M-020189-	cold inducible RNA binding protein	1153.00	CIRBP	G12
Human3 Pc	M-009882-	ras homolog gene family, member U	58480.00	RHOU	G13
Human3 Pc	M-004410-	cell death-inducing DFFA-like effector b	27141.00	CIDEB	G14
Human3 Pc	M-019289-	activating transcription factor 7 interacting pro	55729.00	ATF7IP	G15
Human3 Pc	M-004409-	cell death-inducing DFFA-like effector a	1149.00	CIDEA	G16
Human3 Pc	M-021098-	apoptosis, caspase activation inhibitor	57099.00	AVEN	G17
Human3 Pc	M-011240-	chromogranin A (parathyroid secretory protein	1113.00	CHGA	G18
Human3 Pc	M-009787-	BTB and CNC homology 1, basic leucine zipper	60468.00	BACH2	G19
Human3 Pc	M-019938-	chromatin assembly factor 1, subunit A (p150)	10036.00	CHAF1A	G20
Human3 Pc	M-003870-	BCL2-antagonist of cell death	572.00	BAD	G21
Human3 Pc	M-011961-	BCL2-associated athanogene 2	9532.00	BAG2	G23

Human3 Pc	M-016604-	influenza virus NS1A binding protein	10625.00	IVNS1ABP	H02
Human3 Pc	M-021394-	integrin beta 1 binding protein (melusin) 2	26548.00	ITGB1BP2	H04
Human3 Pc	M-012709-	Era G-protein-like 1 (E. coli)	26284.00	ERAL1	H05
Human3 Pc	M-004565-	integrin, alpha V (vitronectin receptor, alpha pc	3685.00	ITGAV	H06
Human3 Pc	M-020877-	Enah/Vasp-like	51466.00	EVL	H07
Human3 Pc	M-022258-	DENN/MADD domain containing 4A	10260.00	DENND4A	H08
Human3 Pc	M-005119-	Ewing sarcoma breakpoint region 1	2130.00	EWSR1	H09
Human3 Pc	M-019175-	insulinoma-associated 2	84684.00	INSM2	H10
Human3 Pc	M-007897-	coagulation factor V (proaccelerin, labile factor	2153.00	F5	H11
Human3 Pc	M-006535-	insulinoma-associated 1	3642.00	INSM1	H12
Human3 Pc	M-011032-	coagulation factor VIII, procoagulant componer	2157.00	F8	H13
Human3 Pc	M-006983-	inhibitor of growth family, member 4	51147.00	ING4	H14
Human3 Pc	M-004025-	bromodomain PHD finger transcription factor	2186.00	BPTF	H15
Human3 Pc	M-007000-	inhibitor of growth family, member 3	54556.00	ING3	H16
Human3 Pc	M-011899-	Fanconi anemia, complementation group G	2189.00	FANCG	H17
Human3 Pc	M-006534-	inhibitor of growth family, member 2	3622.00	ING2	H18
Human3 Pc	M-007899-	ficolin (collagen/fibrinogen domain containing l	2220.00	FCN2	H19
Human3 Pc	M-006533-	inhibitor of growth family, member 1	3621.00	ING1	H20
Human3 Pc	M-011916-	fibroblast growth factor (acidic) intracellular bi	9158.00	FIBP	H21
Human3 Pc	M-015808-	armadillo repeat containing 1	55156.00	ARMC1	H23
Human3 Pc	M-019430-	cell growth regulator with EF-hand domain 1	10669.00	CGREF1	I02
Human3 Pc	M-015703-	CGG triplet repeat binding protein 1	8545.00	CGGBP1	I04
Human3 Pc	M-011957-	BCL2-associated athanogene 3	9531.00	BAG3	I05
Human3 Pc	M-012707-	cofilin 1 (non-muscle)	1072.00	CFL1	I06
Human3 Pc	M-011960-	BCL2-associated athanogene 5	9529.00	BAG5	I07
Human3 Pc	M-011832-	centrin, EF-hand protein, 3 (CDC31 homolog, ye	1070.00	CETN3	I08
Human3 Pc	M-011922-	membrane associated guanylate kinase, WW ai	9223.00	MAGI1	I09
Human3 Pc	M-011831-	centrin, EF-hand protein, 1	1068.00	CETN1	I10
Human3 Pc	M-013664-	BAI1-associated protein 3	8938.00	BAIAP3	I11
Human3 Pc	M-012364-	centrosomal protein 250kDa	11190.00	CEP250	I12
Human3 Pc	M-012708-	breast carcinoma amplified sequence 2	10286.00	BCAS2	I13
Human3 Pc	M-003251-	centromere protein C 1	1060.00	CENPC1	I14
Human3 Pc	M-006996-	B-cell CLL/lymphoma 11A (zinc finger protein)	53335.00	BCL11A	I15
Human3 Pc	M-003250-	centromere protein B, 80kDa	1059.00	CENPB	I16
Human3 Pc	M-003307-	B-cell CLL/lymphoma 2	596.00	BCL2	I17
Human3 Pc	M-003249-	centromere protein A	1058.00	CENPA	I18
Human3 Pc	M-018874-	B-cell CLL/lymphoma 6, member B (zinc finger		255877.00	BCL6B	I19
Human3 Pc	M-011608-	CCAAT/enhancer binding protein (C/EBP), gami	1054.00	CEBPG	I20
Human3 Pc	M-013141-	B-cell CLL/lymphoma 7A	605.00	BCL7A	I21
Human3 Pc	M-017228-	B-cell CLL/lymphoma 7B	9275.00	BCL7B	I23
Human3 Pc	M-017705-	insulin-like growth factor 2 mRNA binding prote	10644.00	IGF2BP2	J02
Human3 Pc	M-003977-	insulin-like growth factor 2 mRNA binding prote	10642.00	IGF2BP1	J04
Human3 Pc	M-016536-	pleckstrin homology domain containing, family	79990.00	PLEKHH3	J05
Human3 Pc	M-008675-	insulin-like growth factor binding protein 7	3490.00	IGFBP7	J06
Human3 Pc	M-018212-	zinc finger protein 547	284306.00	ZNF547	J07
Human3 Pc	M-006625-	insulin-like growth factor binding protein 6	3489.00	IGFBP6	J08
Human3 Pc	M-020175-	filamin B, beta (actin binding protein 278)	2317.00	FLNB	J09

Human3 Pc	M-010897-	insulin-like growth factor binding protein 5	3488.00	IGFBP5	J10
Human3 Pc	M-011661-	fibromodulin	2331.00	FMOD	J11
Human3 Pc	M-012583-	insulin-like growth factor binding protein 4	3487.00	IGFBP4	J12
Human3 Pc	M-019631-	fragile X mental retardation 1	2332.00	FMR1	J13
Human3 Pc	M-010896-	insulin-like growth factor binding protein 2, 36	3485.00	IGFBP2	J14
Human3 Pc	M-010086-	FBJ murine osteosarcoma viral oncogene hom	2354.00	FOSB	J15
Human3 Pc	M-012559-	insulin-like growth factor binding protein 1	3484.00	IGFBP1	J16
Human3 Pc	M-020108-	fascin homolog 2, actin-bundling protein, retin	25794.00	FSCN2	J17
Human3 Pc	M-010929-	insulin-like growth factor binding protein, acid	3483.00	IGFALS	J18
Human3 Pc	M-020889-	fascin homolog 3, actin-bundling protein, testic	29999.00	FSCN3	J19
Human3 Pc	M-004203-	interferon-induced protein 35	3430.00	IFI35	J20
Human3 Pc	M-013615-	follistatin-like 1	11167.00	FSTL1	J21
Human3 Pc	M-019634-	ferritin, heavy polypeptide 1	2495.00	FTH1	J23
Human3 Pc	M-010346-	chromodomain protein, Y-linked, 2A	9426.00	CDY2A	K02
Human3 Pc	M-008916-	chromodomain protein, Y-linked, 1	9085.00	CDY1	K04
Human3 Pc	M-009404-	BCS1-like (yeast)	617.00	BCS1L	K05
Human3 Pc	M-019154-	CDK5 regulatory subunit associated protein 2	55755.00	CDK5RAP2	K06
Human3 Pc	M-020228-	B double prime 1, subunit of RNA polymerase I	55814.00	BDP1	K07
Human3 Pc	M-013169-	cadherin 9, type 2 (T1-cadherin)	1007.00	CDH9	K08
Human3 Pc	M-004391-	baculoviral IAP repeat-containing 7 (livin)	79444.00	BIRC7	K09
Human3 Pc	M-013523-	cadherin 8, type 2	1006.00	CDH8	K10
Human3 Pc	M-004636-	BCL2/adenovirus E1B 19kDa interacting protei	664.00	BNIP3	K11
Human3 Pc	M-011826-	cadherin 7, type 2	1005.00	CDH7	K12
Human3 Pc	M-011900-	bromodomain and PHD finger containing, 1	7862.00	BRPF1	K13
Human3 Pc	M-011991-	cadherin 6, type 2, K-cadherin (fetal kidney)	1004.00	CDH6	K14
Human3 Pc	M-015153-	BTB (POZ) domain containing 14B	112939.00	BTBD14B	K15
Human3 Pc	M-003641-	cadherin 5, type 2, VE-cadherin (vascular epithe	1003.00	CDH5	K16
Human3 Pc	M-013474-	calcium binding protein 1	9478.00	CABP1	K17
Human3 Pc	M-003640-	cadherin 4, type 1, R-cadherin (retinal)	1002.00	CDH4	K18
Human3 Pc	M-016674-	calmodulin 2 (phosphorylase kinase, delta)	805.00	CALM2	K19
Human3 Pc	M-013051-	cadherin-like 23	64072.00	CDH23	K20
Human3 Pc	M-013401-	calmodulin-like 5	51806.00	CALML5	K21
Human3 Pc	M-003636-	calnexin	821.00	CANX	K23
Human3 Pc	M-013035-	intercellular adhesion molecule 5, telencephali	7087.00	ICAM5	L02
Human3 Pc	M-012014-	integrin-binding sialoprotein (bone sialoprotei	3381.00	IBSP	L04
Human3 Pc	M-011548-	far upstream element (FUSE) binding protein 1	8880.00	FUBP1	L05
Human3 Pc	M-003678-	hypoxia up-regulated 1	10525.00	HYOU1	L06
Human3 Pc	M-012914-	FUS interacting protein (serine/arginine-rich) 1	10772.00	FUSIP1	L07
Human3 Pc	M-004357-	XIAP associated factor-1	54739.00	XAF1	L08
Human3 Pc	M-012011-	fragile X mental retardation, autosomal homol	8087.00	FXR1	L09
Human3 Pc	M-021115-	angiogenic factor with G patch and FHA domai	55109.00	AGGF1	L10
Human3 Pc	M-011955-	fragile X mental retardation, autosomal homol	9513.00	FXR2	L11
Human3 Pc	M-020432-	replication protein A4, 34kDa	29935.00	RPA4	L12
Human3 Pc	M-012455-	GRB2-associated binding protein 2	9846.00	GAB2	L13
Human3 Pc	M-004972-	heat shock 105kDa/110kDa protein 1	10808.00	HSPH1	L14
Human3 Pc	M-013083-	GA binding protein transcription factor, beta su	2553.00	GABPB2	L15
Human3 Pc	M-010600-	heat shock 60kDa protein 1 (chaperonin)	3329.00	HSPD1	L16

Human3 Pc	M-013057-	giant axonal neuropathy (gigaxonin)	8139.00	GAN	L17
Human3 Pc	M-008952-	heat shock 27kDa protein family, member 7 (ca	27129.00	HSPB7	L18
Human3 Pc	M-019844-	glial cells missing homolog 2 (Drosophila)	9247.00	GCM2	L19
Human3 Pc	M-004750-	heat shock 70kDa protein 9 (mortalin)	3313.00	HSPA9	L20
Human3 Pc	M-008717-	GTP binding protein overexpressed in skeletal r	2669.00	GEM	L21
Human3 Pc	M-018999-	GIPC PDZ domain containing family, member 2	54810.00	GIPC2	L23
Human3 Pc	M-013506-	cadherin 20, type 2	28316.00	CDH20	M02
Human3 Pc	M-011605-	cadherin 2, type 1, N-cadherin (neuronal)	1000.00	CDH2	M04
Human3 Pc	M-019498-	capping protein (actin filament), gelsolin-like	822.00	CAPG	M05
Human3 Pc	M-013105-	cadherin 19, type 2	28513.00	CDH19	M06
Human3 Pc	M-011823-	calcyphosine	828.00	CAPS	M07
Human3 Pc	M-011992-	cadherin 18, type 2	1016.00	CDH18	M08
Human3 Pc	M-012212-	capping protein (actin filament) muscle Z-line, a	829.00	CAPZA1	M09
Human3 Pc	M-011828-	cadherin 16, KSP-cadherin	1014.00	CDH16	M10
Human3 Pc	M-004396-	NLR family, CARD domain containing 4	58484.00	NLRC4	M11
Human3 Pc	M-003639-	cadherin 15, M-cadherin (myotubule)	1013.00	CDH15	M12
Human3 Pc	M-003464-	nucleotide-binding oligomerization domain cor	64127.00	NOD2	M13
Human3 Pc	M-003878-	cadherin 13, H-cadherin (heart)	1012.00	CDH13	M14
Human3 Pc	M-004399-	caspase recruitment domain family, member 6	84674.00	CARD6	M15
Human3 Pc	M-011827-	cadherin 12, type 2 (N-cadherin 2)	1010.00	CDH12	M16
Human3 Pc	M-011227-	calsequestrin 1 (fast-twitch, skeletal muscle)	844.00	CASQ1	M17
Human3 Pc	M-013493-	cadherin 11, type 2, OB-cadherin (osteoblast)	1009.00	CDH11	M18
Human3 Pc	M-011228-	calsequestrin 2 (cardiac muscle)	845.00	CASQ2	M19
Human3 Pc	M-013520-	cadherin 10, type 2 (T2-cadherin)	1008.00	CDH10	M20
Human3 Pc	M-010033-	chromobox homolog 3 (HP1 gamma homolog,	11335.00	CBX3	M21
Human3 Pc	M-004296-	chromobox homolog 5 (HP1 alpha homolog, Dr	23468.00	CBX5	M23
Human3 Pc	M-019455-	heat shock 70kDa protein 6 (HSP70B')	3310.00	HSPA6	N02
Human3 Pc	M-008198-	heat shock 70kDa protein 5 (glucose-regulated	3309.00	HSPA5	N04
Human3 Pc	M-015484-	GLI-Kruppel family member GLI4	2738.00	GLI4	N05
Human3 Pc	M-012636-	heat shock 70kDa protein 4	3308.00	HSPA4	N06
Human3 Pc	M-014924-	GLIS family zinc finger 2	84662.00	GLIS2	N07
Human3 Pc	M-010599-	heat shock 70kDa protein 2	3306.00	HSPA2	N08
Human3 Pc	M-012671-	glycoprotein V (platelet)	2814.00	GP5	N09
Human3 Pc	M-012110-	heat shock 70kDa protein 1-like	3305.00	HSPA1L	N10
Human3 Pc	M-012540-	glycoprotein IX (platelet)	2815.00	GP9	N11
Human3 Pc	M-003501-	heat shock 70kDa protein 1B	3304.00	HSPA1B	N12
Human3 Pc	M-018892-	GRP1 (general receptor for phosphoinositides 1	160622.00	GRASP	N13
Human3 Pc	M-018281-	KRR1, small subunit (SSU) processome compon	11103.00	KRR1	N14
Human3 Pc	M-011677-	G-rich RNA sequence binding factor 1	2926.00	GRSF1	N15
Human3 Pc	M-017353-	Hermansky-Pudlak syndrome 4	89781.00	HPS4	N16
Human3 Pc	M-007775-	gelsolin (amyloidosis, Finnish type)	2934.00	GSN	N17
Human3 Pc	M-019860-	WD repeat domain 57 (U5 snRNP specific)	9410.00	WDR57	N18
Human3 Pc	M-013081-	PDZ and LIM domain 7 (enigma)	9260.00	PDLIM7	N19
Human3 Pc	M-017424-	hippocalcin-like 1	3241.00	HPCAL1	N20
Human3 Pc	M-018239-	GTF2I repeat domain containing 2	84163.00	GTF2IRD2	N21
Human3 Pc	M-012581-	general transcription factor IIIC, polypeptide 1,	2975.00	GTF3C1	N23
Human3 Pc	M-003877-	cadherin 1, type 1, E-cadherin (epithelial)	999.00	CDH1	O02

Human3 Pc	M-003233- cell division cycle 6 homolog (S. cerevisiae)	990.00	CDC6	O04
Human3 Pc	M-009555- chromobox homolog 6	23466.00	CBX6	O05
Human3 Pc	M-011237- CDC5 cell division cycle 5-like (S. pombe)	988.00	CDC5L	O06
Human3 Pc	M-008355- chromobox homolog 8 (Pc class homolog, Dros	57332.00	CBX8	O07
Human3 Pc	M-017358- CDC42 effector protein (Rho GTPase binding) 3	10602.00	CDC42EP3	O08
Human3 Pc	M-020107- chaperonin containing TCP1, subunit 2 (beta)	10576.00	CCT2	O09
Human3 Pc	M-003231- cell division cycle 37 homolog (S. cerevisiae)	11140.00	CDC37	O10
Human3 Pc	M-018339- chaperonin containing TCP1, subunit 3 (gamma	7203.00	CCT3	O11
Human3 Pc	M-017252- CD9 molecule	928.00	CD9	O12
Human3 Pc	M-012797- chaperonin containing TCP1, subunit 5 (epsilon	22948.00	CCT5	O13
Human3 Pc	M-017257- CD81 molecule	975.00	CD81	O14
Human3 Pc	M-016559- chaperonin containing TCP1, subunit 6A (zeta 1	908.00	CCT6A	O15
Human3 Pc	M-004538- CD58 molecule	965.00	CD58	O16
Human3 Pc	M-020115- chaperonin containing TCP1, subunit 7 (eta)	10574.00	CCT7	O17
Human3 Pc	M-015970- CD48 molecule	962.00	CD48	O18
Human3 Pc	M-003637- CD151 molecule (Raph blood group)	977.00	CD151	O19
Human3 Pc	M-019505- CD47 molecule	961.00	CD47	O20
Human3 Pc	M-019501- CD22 molecule	933.00	CD22	O21
Human3 Pc	M-019503- CD34 molecule	947.00	CD34	O23
Human3 Pc	M-020884- neurotrimin	50863.00	HNT	P02
Human3 Pc	M-004079- heterogeneous nuclear ribonucleoprotein D (A	3184.00	HNRPD	P04
Human3 Pc	M-017209- H1 histone family, member 0	3005.00	H1F0	P05
Human3 Pc	M-010409- hyaluronan-mediated motility receptor (RHAM	3161.00	HMMR	P06
Human3 Pc	M-006483- H2A histone family, member J	55766.00	H2AFJ	P07
Human3 Pc	M-012710- high-mobility group nucleosomal binding doma	3151.00	HMGN2	P08
Human3 Pc	M-011683- H2A histone family, member Z	3015.00	H2AFZ	P09
Human3 Pc	M-013495- high mobility group AT-hook 2	8091.00	HMGA2	P10
Human3 Pc	M-012051- H3 histone, family 3B (H3.3B)	3021.00	H3F3B	P11
Human3 Pc	M-018122- high-mobility group protein 2-like 1	10042.00	HMG2L1	P12
Human3 Pc	M-019910- fibroblast growth factor binding protein 1	9982.00	FGFBP1	P13
Human3 Pc	M-015324- human immunodeficiency virus type I enhance	3097.00	HIVEP2	P14
Human3 Pc	M-007770- hairy and enhancer of split 1, (Drosophila)	3280.00	HES1	P15
Human3 Pc	M-011448- histone cluster 2, H2be	8349.00	HIST2H2BE	P16
Human3 Pc	M-016117- hairy and enhancer of split 4 (Drosophila)	57801.00	HES4	P17
Human3 Pc	M-006630- histone cluster 1, H1c	3006.00	HIST1H1C	P18
Human3 Pc	M-009020- hairy and enhancer of split 7 (Drosophila)	84667.00	HES7	P19
Human3 Pc	M-016867- drebrin-like	28988.00	DBNL	P20
Human3 Pc	M-020242- HIG1 domain family, member 1A	25994.00	HIGD1A	P21
Human3 Pc	M-016867- drebrin-like	28988.00	DBNL	P23
			mdn	
			3xMAD	
			MADc	
Human3 Pools: Remaining Druggable Genome			IFNAR	C22
Human3 Pools: Remaining Druggable Genome				D22
Human3 Pools: Remaining Druggable Genome				E22
Human3 Pools: Remaining Druggable Genome				F22
				m

					sd
Human3 Pools: Remaining Druggable Genome					G22
Human3 Pools: Remaining Druggable Genome					H22
Human3 Pools: Remaining Druggable Genome					I22
Human3 Pools: Remaining Druggable Genome					J22
					m
					sd
Human3 Po	D-001206-	siControl non-targeting siRNA #2			I03
Human3 Po	D-001206-	siControl non-targeting siRNA #2			J03
					m
					sd
					3psSD
					3ngSD
					SM SD
					Mn Diff
			Z6		SMovrMn
					1-SMovrM

Human3 Po	**D-001600-**	**siGLO RISC-free siRNA**			**K03**
Human3 Po	M-003290-	polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMAR	H03
Human3 Po	M-003290-	polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMAR	G03
Human3 Po	D-001206-	siControl non-targeting siRNA #2			I03
Human3 Po	D-001206-	siControl non-targeting siRNA #2			J03
Human3 Po	**D-001600-**	**siGLO RISC-free siRNA**			**L03**

% inf	abs dev	robust Z	% inf	abs dev	robust Z	% inf	abs dev	robust Z
7.34	0.78	0.16	8.48	5.26	2.18	2.41	2.37	-0.71
7.24	0.68	0.14	3.19	0.03	-0.01	5.55	0.77	0.23
2.81	3.75	-0.79	2.17	1.05	-0.44	1.08	3.70	-1.11
2.89	3.67	-0.78	4.64	1.42	0.59	3.32	1.46	-0.44
4.58	1.98	-0.42	4.02	0.80	0.33	4.07	0.71	-0.21
7.24	0.68	0.14	7.79	4.57	1.89	3.70	1.08	-0.32
5.16	1.40	-0.30	8.43	5.21	2.16	4.52	0.26	-0.08
1.79	4.77	-1.01	2.67	0.55	-0.23	2.69	2.09	-0.63
3.35	3.21	-0.68	3.51	0.29	0.12	7.71	2.93	0.88
3.74	2.82	-0.60	6.05	2.83	1.17	2.44	2.34	-0.70
1.83	4.73	-1.00	5.04	1.82	0.75	2.06	2.72	-0.81
4.15	2.41	-0.51	5.25	2.03	0.84	3.25	1.53	-0.46
8.07	1.51	0.32	8.28	5.06	2.09	8.26	3.48	1.04
11.53	4.97	1.05	11.52	8.30	3.44	6.88	2.10	0.63
1.42	5.14	-1.09	1.32	1.90	-0.79	0.79	3.99	-1.20
9.12	2.56	0.54	8.94	5.72	2.37	5.39	0.61	0.18
7.91	1.35	0.28	4.04	0.82	0.34	3.18	1.60	-0.48
4.50	2.06	-0.44	4.78	1.56	0.65	2.69	2.09	-0.63
12.11	5.55	1.17	9.98	6.76	2.80	4.54	0.24	-0.07
7.72	1.16	0.24	4.00	0.78	0.32	1.48	3.30	-0.99
1.18	5.38	-1.14	1.34	1.88	-0.78	5.22	0.44	0.13
7.33	0.77	0.16	9.21	5.99	2.48	9.74	4.96	1.49
1.15	5.41	-1.14	1.02	2.20	-0.91	6.46	1.68	0.50
1.51	5.05	-1.07	1.45	1.77	-0.73	6.01	1.23	0.37
9.47	2.91	0.61	2.04	1.18	-0.49	2.94	1.84	-0.55
7.95	1.39	0.29	5.01	1.79	0.74	8.34	3.56	1.07
4.77	1.79	-0.38	2.76	0.46	-0.19	4.64	0.14	-0.04
3.08	3.48	-0.74	2.44	0.78	-0.32	6.31	1.53	0.46
3.05	3.51	-0.74	2.11	1.11	-0.46	5.94	1.16	0.35
7.75	1.19	0.25	4.16	0.94	0.39	7.88	3.10	0.93
4.68	1.88	-0.40	1.11	2.12	-0.88	3.13	1.65	-0.49
1.27	5.29	-1.12	0.55	2.67	-1.10	5.74	0.96	0.29
6.58	0.02	0.00	3.76	0.54	0.22	3.88	0.90	-0.27
6.84	0.28	0.06	5.12	1.90	0.79	4.27	0.51	-0.15
3.34	3.22	-0.68	0.60	2.62	-1.08	0.91	3.87	-1.16
2.56	4.00	-0.84	1.09	2.13	-0.88	0.81	3.97	-1.19
2.40	4.16	-0.88	0.17	3.05	-1.26	2.63	2.15	-0.65
6.44	0.12	-0.03	1.56	1.66	-0.69	5.53	0.75	0.22
3.03	3.53	-0.75	1.26	1.96	-0.81	0.11	4.67	-1.40
3.49	3.07	-0.65	0.97	2.25	-0.93	1.29	3.49	-1.05
10.87	4.31	0.91	3.89	0.67	0.28	15.72	10.94	3.28
7.81	1.25	0.26	3.94	0.72	0.30	4.77	0.01	0.00
8.88	2.32	0.49	6.74	3.52	1.46	14.62	9.84	2.95
1.16	5.40	-1.14	0.85	2.37	-0.98	3.27	1.51	-0.45
13.42	6.86	1.45	3.11	0.11	-0.04	6.70	1.92	0.58
2.61	3.95	-0.84	1.22	2.00	-0.83	3.56	1.22	-0.36

14.19	7.63	1.61	10.51	**7.29**	3.02	8.63	3.85	1.16
2.92	3.64	-0.77	2.30	0.92	-0.38	4.48	0.30	-0.09
5.56	1.00	-0.21	3.38	0.16	0.06	7.97	3.19	0.96
3.43	3.13	-0.66	3.67	0.45	0.19	3.05	1.73	-0.52
5.70	0.86	-0.18	2.70	0.52	-0.22	3.00	1.78	-0.53
11.70	5.14	1.09	5.75	2.53	1.05	10.61	5.83	1.75
3.64	2.92	-0.62	1.73	1.49	-0.62	10.27	5.49	1.65
8.79	2.23	0.47	3.96	0.74	0.30	6.61	1.83	0.55
2.61	3.95	-0.84	0.56	2.66	-1.10	2.66	2.12	-0.63
7.07	0.51	0.11	5.34	2.12	0.88	5.78	1.00	0.30
3.89	2.67	-0.56	4.25	1.03	0.43	4.98	0.20	0.06
2.45	4.11	-0.87	0.60	2.62	-1.08	2.30	2.48	-0.74
0.83	5.73	-1.21	0.78	2.44	-1.01	1.49	3.29	-0.99
3.86	2.70	-0.57	0.69	2.53	-1.05	1.35	3.43	-1.03
2.17	4.39	-0.93	2.50	0.72	-0.30	1.72	3.06	-0.92
1.21	5.35	-1.13	2.22	1.00	-0.42	5.09	0.31	0.09
12.98	6.42	1.35	18.12	**14.90**	6.17	14.19	**9.41**	2.82
2.12	4.44	-0.94	1.21	2.01	-0.83	4.51	0.27	-0.08
5.42	1.14	-0.24	4.80	1.58	0.65	2.81	1.97	-0.59
1.15	5.41	-1.14	1.92	1.30	-0.54	1.75	3.03	-0.91
7.33	0.77	0.16	7.68	4.46	1.84	7.94	3.16	0.95
14.14	7.58	1.60	9.86	**6.64**	2.75	6.69	1.91	0.57
1.71	4.85	-1.02	2.92	0.30	-0.13	3.74	1.04	-0.31
3.98	2.58	-0.55	2.23	0.99	-0.41	2.87	1.91	-0.57
8.66	2.10	0.44	2.65	0.57	-0.24	5.74	0.96	0.29
11.13	4.57	0.96	3.18	0.04	-0.02	4.60	0.18	-0.05
2.01	4.55	-0.96	2.51	0.71	-0.29	1.83	2.95	-0.88
3.96	2.60	-0.55	6.81	3.59	1.48	2.74	2.04	-0.61
2.53	4.03	-0.85	2.67	0.55	-0.23	2.48	2.30	-0.69
4.76	1.80	-0.38	5.55	2.33	0.97	4.61	0.17	-0.05
4.25	2.31	-0.49	5.57	2.35	0.97	3.60	1.18	-0.35
5.03	1.53	-0.32	1.37	1.85	-0.77	2.91	1.87	-0.56
2.30	4.26	-0.90	2.59	0.63	-0.26	0.99	3.79	-1.14
15.79	9.23	1.95	9.35	**6.13**	2.54	4.75	0.03	-0.01
13.93	7.37	1.56	2.90	0.32	-0.13	5.18	0.40	0.12
2.91	3.65	-0.77	0.73	2.49	-1.03	2.14	2.64	-0.79
12.20	5.64	1.19	4.03	0.81	0.33	3.98	0.80	-0.24
16.99	**10.43**	2.20	4.78	1.56	0.64	5.08	0.30	0.09
24.93	**18.37**	3.88	5.84	2.62	1.08	10.08	5.30	1.59
9.09	2.53	0.53	1.27	1.95	-0.81	4.37	0.41	-0.12
10.68	4.12	0.87	4.03	0.81	0.34	5.38	0.60	0.18
7.78	1.22	0.26	0.66	2.56	-1.06	5.17	0.39	0.12
5.99	0.57	-0.12	2.14	1.08	-0.45	0.88	3.90	-1.17
4.44	2.12	-0.45	3.09	0.13	-0.06	5.08	0.30	0.09
6.47	0.09	-0.02	0.88	2.34	-0.97	8.83	4.05	1.22
17.36	**10.80**	2.28	2.24	0.98	-0.41	3.63	1.15	-0.34
36.09	**29.53**	6.23	24.62	**21.40**	8.86	18.62	**13.84**	4.15

6.46	0.10	-0.02	3.84	0.62	0.25	3.46	1.32	-0.40
5.71	0.86	-0.18	2.19	1.03	-0.43	4.52	0.26	-0.08
6.98	0.42	0.09	2.30	0.93	-0.38	2.36	2.42	-0.72
21.31	**14.75**	3.11	3.17	0.05	-0.02	5.80	1.02	0.31
3.23	3.33	-0.70	0.23	2.99	-1.24	3.34	1.44	-0.43
14.92	8.36	1.76	6.18	2.96	1.22	6.29	1.51	0.45
14.07	7.51	1.58	1.82	1.40	-0.58	2.16	2.62	-0.78
13.98	7.42	1.57	11.32	**8.10**	3.35	12.12	**7.34**	2.20
2.94	3.62	-0.76	3.21	0.01	-0.01	7.87	3.09	0.93
10.28	3.72	0.78	3.62	0.40	0.17	6.42	1.64	0.49
8.82	2.26	0.48	5.50	2.28	0.94	2.55	2.23	-0.67
11.82	5.26	1.11	5.56	2.34	0.97	4.18	0.60	-0.18
0.86	5.70	-1.21	3.23	0.01	0.00	0.96	3.82	-1.15
16.77	**10.21**	2.16	8.07	4.85	2.01	5.52	0.74	0.22
5.22	1.34	-0.28	1.76	1.46	-0.60	1.45	3.33	-1.00
11.62	5.06	1.07	3.34	0.12	0.05	1.22	3.56	-1.07
6.74	0.18	0.04	2.43	0.79	-0.33	1.39	3.39	-1.02
6.41	0.15	-0.03	1.82	1.40	-0.58	1.74	3.04	-0.91
6.43	0.13	-0.03	0.37	2.85	-1.18	0.86	3.92	-1.18
8.63	2.07	0.44	2.04	1.18	-0.49	2.38	2.40	-0.72
6.17	0.39	-0.08	2.17	1.05	-0.44	1.95	2.83	-0.85
2.47	4.09	-0.87	0.36	2.86	-1.18	0.14	4.64	-1.39
14.79	8.23	1.74	1.84	1.38	-0.57	2.06	2.72	-0.82
24.35	**17.79**	3.76	4.57	1.35	0.56	8.96	4.18	1.25
4.70	1.86	-0.39	2.57	0.65	-0.27	1.19	3.59	-1.08
2.52	4.04	-0.85	0.70	2.52	-1.04	0.59	4.19	-1.26
3.86	2.70	-0.57	1.28	1.94	-0.80	2.57	2.21	-0.66
6.10	0.46	-0.10	3.07	0.15	-0.06	4.50	0.28	-0.08
3.42	3.14	-0.66	1.89	1.33	-0.55	4.49	0.29	-0.09
3.61	2.95	-0.62	3.81	0.59	0.25	8.43	3.65	1.10
0.84	5.72	-1.21	0.26	2.96	-1.23	1.91	2.87	-0.86
6.55	0.01	0.00	3.36	0.14	0.06	10.27	5.49	1.65
9.82	3.26	0.69	4.33	1.11	0.46	9.40	4.62	1.39
8.91	2.35	0.50	2.78	0.44	-0.18	8.94	4.16	1.25
6.00	0.56	-0.12	1.41	1.81	-0.75	2.32	2.46	-0.74
23.19	**16.63**	3.51	11.37	**8.15**	3.38	8.93	4.15	1.24
8.06	1.50	0.32	2.36	0.86	-0.36	4.88	0.10	0.03
7.17	0.61	0.13	7.57	4.35	1.80	4.34	0.44	-0.13
3.48	3.08	-0.65	1.61	1.61	-0.67	4.32	0.46	-0.14
3.78	2.78	-0.59	4.84	1.62	0.67	2.08	2.70	-0.81
2.22	4.34	-0.92	1.79	1.43	-0.59	2.19	2.59	-0.78
5.46	1.10	-0.23	3.40	0.18	0.07	3.60	1.18	-0.35
13.80	7.24	1.53	4.29	1.07	0.44	3.83	0.95	-0.28
4.55	2.01	-0.43	3.37	0.15	0.06	1.93	2.85	-0.85
3.66	2.90	-0.61	1.81	1.41	-0.58	3.74	1.04	-0.31
11.80	5.24	1.10	7.71	4.49	1.86	6.81	2.03	0.61
6.92	0.36	0.07	4.61	1.39	0.57	2.35	2.43	-0.73

3.23	3.33	-0.70	1.14	2.08	-0.86	2.72	2.06	-0.62
3.76	2.80	-0.59	2.01	1.21	-0.50	1.93	2.85	-0.85
5.30	1.26	-0.27	3.22	0.00	0.00	1.99	2.79	-0.83
21.43	**14.87**	3.14	6.19	2.97	1.23	13.92	**9.14**	2.74
12.66	6.10	1.29	3.02	0.20	-0.08	3.90	0.88	-0.26
6.32	0.24	-0.05	2.51	0.71	-0.30	2.05	2.73	-0.82
3.53	3.03	-0.64	4.11	0.89	0.37	2.06	2.72	-0.81
8.97	2.41	0.51	3.13	0.09	-0.04	3.71	1.07	-0.32
13.42	6.86	1.45	3.22	0.00	0.00	2.72	2.06	-0.62
15.60	9.04	1.91	7.81	4.59	1.90	8.73	3.95	1.19
6.25	0.31	-0.07	0.90	2.32	-0.96	1.58	3.20	-0.96
16.92	**10.36**	2.19	8.61	**5.39**	2.23	7.01	2.23	0.67
8.17	1.61	0.34	2.85	0.37	-0.15	3.37	1.41	-0.42
2.67	3.89	-0.82	3.37	0.15	0.06	1.52	3.26	-0.98
27.21	**20.65**	4.36	10.28	**7.06**	2.92	10.96	6.18	1.85
3.10	3.46	-0.73	1.92	1.30	-0.54	1.76	3.02	-0.91
16.37	**9.81**	2.07	4.20	0.98	0.41	9.51	4.73	1.42
17.56	**11.00**	2.32	5.50	2.28	0.94	9.66	4.88	1.46
18.00	**11.44**	2.41	5.14	1.92	0.79	5.35	0.57	0.17
11.37	4.81	1.01	10.99	**7.77**	3.22	6.13	1.35	0.40
2.83	3.73	-0.79	1.43	1.79	-0.74	2.44	2.34	-0.70
5.04	1.52	-0.32	1.75	1.47	-0.61	6.11	1.33	0.40
7.81	1.25	0.26	2.75	0.47	-0.19	4.67	0.11	-0.03
1.80	4.76	-1.01	2.52	0.70	-0.29	1.46	3.32	-1.00
15.94	9.38	1.98	7.07	3.85	1.59	7.45	2.67	0.80
1.24	5.32	-1.13	0.74	2.48	-1.03	1.78	3.00	-0.90
4.24	2.32	-0.49	2.14	1.08	-0.45	2.20	2.58	-0.77
19.30	**12.74**	2.69	4.51	1.29	0.53	4.26	0.52	-0.16
5.21	1.35	-0.29	2.21	1.01	-0.42	1.61	3.17	-0.95
2.82	3.74	-0.79	2.40	0.82	-0.34	3.50	1.28	-0.38
4.66	1.90	-0.40	2.15	1.07	-0.45	4.02	0.76	-0.23
25.84	**19.28**	4.07	5.49	2.27	0.94	8.56	3.78	1.13
13.07	6.51	1.37	1.46	1.76	-0.73	5.65	0.87	0.26
3.65	2.91	-0.62	0.46	2.76	-1.14	1.59	3.19	-0.96
5.74	0.82	-0.18	1.26	1.96	-0.81	2.47	2.31	-0.69
17.86	**11.30**	2.38	3.29	0.07	0.03	6.92	2.14	0.64
5.91	0.65	-0.14	1.13	2.09	-0.87	2.18	2.60	-0.78
24.40	**17.84**	3.77	7.96	4.74	1.96	12.05	**7.27**	2.18
10.73	4.17	0.88	0.40	2.82	-1.17	4.10	0.68	-0.20
2.13	4.43	-0.94	0.78	2.44	-1.01	1.22	3.56	-1.07
2.67	3.89	-0.82	4.09	0.87	0.36	3.40	1.38	-0.41
22.37	**15.81**	3.34	18.26	**15.04**	6.23	23.72	**18.94**	5.68
4.04	2.52	-0.53	2.07	1.15	-0.48	2.81	1.97	-0.59
21.74	**15.18**	3.20	5.85	2.63	1.09	12.47	**7.69**	2.31
23.50	**16.94**	3.58	10.56	**7.34**	3.04	10.58	5.80	1.74
23.34	**16.78**	3.54	13.98	**10.76**	4.46	15.10	**10.32**	3.09
15.78	9.22	1.95	11.12	**7.90**	3.27	15.97	**11.19**	3.36

9.78	3.22	0.68	3.44	0.22	0.09	8.39	3.61	1.08
9.57	3.01	0.63	7.46	4.24	1.76	6.36	1.58	0.47
6.59	0.03	0.00	1.08	2.14	-0.89	5.56	0.78	0.23
4.69	1.87	-0.40	0.95	2.27	-0.94	8.20	3.42	1.03
8.98	2.42	0.51	4.35	1.13	0.47	17.36	12.58	3.77
4.39	2.17	-0.46	0.90	2.32	-0.96	1.79	2.99	-0.90
4.58	1.99	-0.42	3.95	0.73	0.30	6.43	1.65	0.50
2.16	4.40	-0.93	1.34	1.88	-0.78	1.69	3.09	-0.93
7.59	1.03	0.22	2.14	1.08	-0.45	7.75	2.97	0.89
2.21	4.35	-0.92	1.26	1.96	-0.81	2.19	2.59	-0.78
6.18	0.38	-0.08	2.92	0.30	-0.13	6.18	1.40	0.42
4.25	2.31	-0.49	2.18	1.04	-0.43	2.48	2.30	-0.69
2.47	4.09	-0.86	0.64	2.58	-1.07	1.30	3.48	-1.04
15.97	9.41	1.99	16.06	12.84	5.32	22.10	17.32	5.20
18.18	11.62	2.45	14.43	11.21	4.64	12.10	7.32	2.19
14.40	7.84	1.66	8.04	4.82	2.00	9.21	4.43	1.33
4.45	2.11	-0.45	4.86	1.64	0.68	4.48	0.30	-0.09
5.25	1.31	-0.28	2.63	0.59	-0.25	3.12	1.66	-0.50
4.68	1.88	-0.40	5.06	1.84	0.76	5.21	0.43	0.13
17.49	10.93	2.31	11.44	8.22	3.40	18.27	13.49	4.04
12.90	6.34	1.34	5.42	2.20	0.91	5.43	0.65	0.20
5.66	0.90	-0.19	12.75	9.53	3.95	6.37	1.59	0.48
7.80	1.24	0.26	5.75	2.53	1.05	5.42	0.64	0.19
4.51	2.05	-0.43	2.01	1.21	-0.50	2.54	2.24	-0.67
7.21	0.65	0.14	3.96	0.74	0.31	4.45	0.33	-0.10
15.38	8.82	1.86	8.56	5.34	2.21	8.49	3.71	1.11
5.90	0.66	-0.14	2.16	1.06	-0.44	3.03	1.75	-0.52
34.33	27.77	5.86	18.17	14.95	6.19	22.89	18.11	5.43
3.02	3.54	-0.75	1.20	2.02	-0.84	2.96	1.82	-0.55
1.27	5.29	-1.12	0.73	2.49	-1.03	1.75	3.03	-0.91
6.18	0.38	-0.08	3.86	0.64	0.27	3.96	0.82	-0.24
3.76	2.80	-0.59	0.30	2.92	-1.21	1.68	3.10	-0.93
7.38	0.82	0.17	1.94	1.28	-0.53	3.16	1.62	-0.49
3.49	3.07	-0.65	2.95	0.27	-0.11	7.25	2.47	0.74
1.76	4.80	-1.02	3.36	0.14	0.06	3.20	1.58	-0.47
2.07	4.49	-0.95	2.10	1.12	-0.46	3.49	1.29	-0.39
4.07	2.49	-0.53	2.43	0.79	-0.33	5.62	0.84	0.25
17.16	10.60	2.24	9.60	6.38	2.64	11.42	6.64	1.99
13.70	7.14	1.51	9.38	6.16	2.55	15.71	10.93	3.28
16.93	10.37	2.19	5.27	2.05	0.85	7.17	2.39	0.72
12.05	5.49	1.16	8.44	5.22	2.16	18.85	14.07	4.22
9.34	2.78	0.59	5.64	2.42	1.00	8.85	4.07	1.22
7.63	1.07	0.23	6.18	2.96	1.23	9.73	4.95	1.48
10.06	3.50	0.74	4.61	1.39	0.58	9.07	4.29	1.29
7.93	1.37	0.29	6.87	3.65	1.51	10.19	5.41	1.62
7.70	1.14	0.24	4.66	1.44	0.59	6.98	2.20	0.66
7.10	0.54	0.11	2.77	0.45	-0.19	4.84	0.06	0.02

9.30	2.74	0.58	6.29	3.07	1.27	8.17	3.39	1.02
1.79	4.77	-1.01	1.22	2.00	-0.83	3.26	1.52	-0.46
18.93	12.37	2.61	16.68	13.46	5.57	22.28	17.50	5.25
1.96	4.60	-0.97	2.13	1.09	-0.45	4.01	0.77	-0.23
1.33	5.23	-1.10	1.18	2.04	-0.85	2.99	1.79	-0.54
3.89	2.67	-0.56	3.21	0.01	-0.01	5.82	1.04	0.31
17.08	10.52	2.22	3.92	0.70	0.29	11.34	6.56	1.97
21.33	14.77	3.12	9.92	6.70	2.77	8.30	3.52	1.06
11.16	4.60	0.97	4.32	1.10	0.45	5.48	0.70	0.21
16.48	9.92	2.09	6.60	3.38	1.40	9.92	5.14	1.54
10.45	3.89	0.82	6.73	3.51	1.45	9.09	4.31	1.29
12.09	5.53	1.17	2.92	0.30	-0.12	15.41	10.63	3.19
17.97	11.41	2.41	6.32	3.10	1.28	15.28	10.50	3.15
17.40	10.84	2.29	5.84	2.62	1.08	12.66	7.88	2.36
5.52	1.04	-0.22	1.87	1.35	-0.56	5.90	1.12	0.34
6.16	0.40	-0.09	2.05	1.17	-0.48	5.34	0.56	0.17
4.48	2.08	-0.44	0.55	2.67	-1.11	2.49	2.29	-0.69
15.19	8.63	1.82	4.85	1.63	0.67	8.97	4.19	1.26
7.82	1.26	0.27	1.66	1.56	-0.65	4.05	0.73	-0.22
5.55	1.01	-0.21	2.40	0.82	-0.34	3.27	1.51	-0.45
7.67	1.11	0.23	1.67	1.55	-0.64	8.10	3.32	1.00
17.79	11.23	2.37	3.70	0.48	0.20	8.44	3.66	1.10
4.59	1.97	-0.42	1.34	1.88	-0.78	5.98	1.20	0.36
9.71	3.15	0.66	0.90	2.32	-0.96	7.58	2.80	0.84
6.92	0.36	0.07	1.62	1.60	-0.66	6.09	1.31	0.39
4.02	2.54	-0.54	0.86	2.36	-0.98	10.01	5.23	1.57
9.04	2.48	0.52	2.65	0.57	-0.24	2.85	1.93	-0.58
3.18	3.38	-0.72	6.29	3.07	1.27	4.79	0.01	0.00
1.88	4.68	-0.99	2.77	0.45	-0.19	3.79	0.99	-0.30
7.42	0.86	0.18	5.12	1.90	0.79	2.06	2.72	-0.81
17.96	11.40	2.41	14.33	11.11	4.60	13.08	8.30	2.49
7.51	0.95	0.20	6.63	3.41	1.41	8.17	3.39	1.02
4.47	2.09	-0.44	4.56	1.34	0.55	3.68	1.10	-0.33
9.32	2.76	0.58	5.08	1.86	0.77	6.91	2.13	0.64
15.27	8.71	1.84	6.20	2.98	1.23	6.63	1.85	0.56
13.11	6.55	1.38	4.34	1.12	0.46	5.25	0.47	0.14
6.45	0.11	-0.02	2.85	0.37	-0.16	2.97	1.81	-0.54
4.66	1.90	-0.40	1.52	1.70	-0.70	4.10	0.68	-0.20
4.06	2.50	-0.53	0.72	2.50	-1.04	3.22	1.56	-0.47
3.13	3.43	-0.73	0.63	2.59	-1.07	4.61	0.17	-0.05
12.48	5.92	1.25	2.59	0.63	-0.26	10.19	5.41	1.62
9.84	3.28	0.69	1.77	1.45	-0.60	6.83	2.05	0.61
4.03	2.53	-0.54	1.57	1.65	-0.68	0.99	3.79	-1.14
6.90	0.34	0.07	2.48	0.74	-0.31	4.40	0.38	-0.11
11.95	5.39	1.14	1.78	1.44	-0.60	2.75	2.03	-0.61
21.52	14.96	3.16	1.59	1.63	-0.67	5.34	0.56	0.17
6.49	0.07	-0.02	4.98	1.76	0.73	7.83	3.05	0.92

4.48	2.08	-0.44	2.38	0.84	-0.35	5.80	1.02	0.31
12.02	5.46	1.15	8.12	**4.90**	2.03	11.25	6.47	1.94
13.63	7.07	1.49	4.70	1.48	0.61	9.41	4.63	1.39
7.94	1.38	0.29	2.19	1.03	-0.43	8.31	3.53	1.06
8.33	1.77	0.37	3.32	0.10	0.04	6.89	2.11	0.63
8.48	1.92	0.40	3.61	0.39	0.16	5.07	0.29	0.09
9.92	3.36	0.71	6.00	2.78	1.15	3.49	1.29	-0.39
9.21	2.65	0.56	3.33	0.11	0.04	2.90	1.88	-0.56
49.29	**42.73**	9.02	20.01	**16.79**	6.95	20.65	**15.87**	4.76
8.01	1.45	0.31	1.30	1.92	-0.79	6.29	1.51	0.45
2.26	4.30	-0.91	0.21	3.01	-1.25	4.66	0.12	-0.04
11.41	4.85	1.02	1.59	1.63	-0.68	7.33	2.55	0.77
9.64	3.08	0.65	4.38	1.16	0.48	6.53	1.75	0.53
4.50	2.06	-0.44	0.75	2.47	-1.02	2.05	2.73	-0.82
17.26	**10.70**	2.26	2.63	0.59	-0.25	10.33	5.55	1.66
20.76	**14.20**	3.00	2.35	0.87	-0.36	9.19	4.41	1.32
20.48	**13.92**	2.94	2.17	1.05	-0.44	7.99	3.21	0.96
7.33	0.77	0.16	1.15	2.07	-0.86	6.28	1.50	0.45
1.98	4.58	-0.97	0.32	2.90	-1.20	4.73	0.05	-0.01
3.96	2.60	-0.55	2.86	0.36	-0.15	5.33	0.55	0.17
5.48	1.08	-0.23	5.95	2.73	1.13	10.97	6.19	1.86
3.37	3.19	-0.67	4.44	1.22	0.50	4.04	0.75	-0.22
1.68	4.88	-1.03	3.25	0.03	0.01	5.63	0.85	0.25
5.03	1.53	-0.32	3.18	0.04	-0.02	8.50	3.72	1.11
7.73	1.17	0.25	7.83	4.61	1.91	8.49	3.71	1.11
8.93	2.37	0.50	6.61	3.39	1.40	7.05	2.27	0.68
9.56	3.00	0.63	7.96	4.74	1.96	7.96	3.18	0.95
3.68	2.88	-0.61	3.52	0.30	0.12	6.24	1.46	0.44
3.86	2.70	-0.57	4.79	1.57	0.65	4.48	0.30	-0.09
3.12	3.44	-0.73	4.63	1.41	0.58	10.98	6.20	1.86
4.94	1.62	-0.34	4.76	1.54	0.63	12.28	**7.50**	2.25
13.53	6.97	1.47	4.17	0.95	0.39	10.20	5.42	1.63
3.93	2.63	-0.56	6.40	3.18	1.32	8.17	3.39	1.02
3.82	2.74	-0.58	9.68	**6.46**	2.68	5.39	0.61	0.18
2.00	4.56	-0.96	3.69	0.47	0.19	4.42	0.36	-0.11
8.49	1.93	0.41	11.30	**8.08**	3.34	16.62	**11.84**	3.55
4.59	1.97	-0.42	6.95	3.73	1.54	3.25	1.53	-0.46
19.59	**13.03**	2.75	13.92	**10.70**	4.43	23.00	**18.22**	5.46
10.58	4.02	0.85	3.58	0.36	0.15	4.69	0.09	-0.03
6.56	3.20		3.22	1.63		4.78	2.25	
	9.60			4.89			6.76	
	4.74			2.41			3.33	
38.94		27.14		53.57				
55.40		51.06		43.98				
58.95		31.40		43.07				
67.16		30.81		27.84				
55.11		**35.10**		**42.12**				

11.85	10.81	10.63	
22.07	14.13	16.03	
29.61	17.90	15.94	
38.18	6.20	14.42	
35.63	9.83	17.75	
31.37	12.02	16.04	
7.17	5.09	1.36	
8.16	1.00	2.69	
10.62	6.71	2.87	
9.39	3.85	2.78	
1.74	4.04	0.13	0.00
35.56	32.42	31.90	
5.22	12.11	0.38	
40.78	44.53	32.28	
45.72	31.25	39.34	
0.89	1.42	0.82	
0.11	-0.42	0.18	
34.79	**28.02**	**28.79**	
13.93	6.67	18.90	
2.06	3.07	6.04	
8.16	1.00	2.69	
10.62	6.71	2.87	
30.63	**35.30**	**36.73**	

y

y

y

x debris b

y

x toxic a,b,c

x debris b,c

y

y

y

y
y
y
y

y
y

y

y

y
y

y

y

y

y
y

y

y

x b artifact

y

					% inf	abs dev
50007.00	A02	M-018338- metallothionein 2A	4502.00	MT2A	1.10	3.64
50007.00	A04	M-012724- metallothionein 1A	4489.00	MT1A	2.71	2.03
50007.00	A05	M-012122- lectin, mannose-binding, 1	3998.00	LMAN1	1.52	3.22
50007.00	A06	M-009842- Ras-associated protein Rap1	51277.00	RBJ	1.09	3.65
50007.00	A07	M-012416- leiomodin 1 (smooth muscl	25802.00	LMOD1	2.10	2.64
50007.00	A08	M-018981- high-mobility group box 1	3146.00	HMGB1	3.64	1.10
50007.00	A09	M-018773- leucine-rich PPR-motif conta	10128.00	LRPPRC	5.26	0.52
50007.00	A10	M-007666- polycystic kidney disease 1 (	5310.00	PKD1	3.90	0.84
50007.00	A11	M-011078- latent transforming growth	4053.00	LTBP2	1.26	3.49
50007.00	A12	M-017166- RAD51 associated protein 1	10635.00	RAD51AP1	7.27	2.53
50007.00	A13	M-010522- neighbor of BRCA1 gene 1	4077.00	NBR1	0.49	4.25
50007.00	A14	M-018972- PIN2-interacting protein 1	54984.00	PINX1	4.33	0.41
50007.00	A15	M-012796- metal response element bin	22823.00	MTF2	1.56	3.18
50007.00	A16	M-004004- phosphatidylinositol binding	8301.00	PICALM	10.78	6.04
50007.00	A17	M-013618- microtubule-actin crosslinki	23499.00	MACF1	0.77	3.97
50007.00	A18	M-014862- PHD finger protein 6	84295.00	PHF6	0.46	4.28
50007.00	A19	M-017491- mucosal vascular addressin	8174.00	MADCAM1	3.13	1.61
50007.00	A20	M-012912- PHD finger protein 2	5253.00	PHF2	4.57	0.17
50007.00	A21	M-003561- SMAD family member 2	4087.00	SMAD2	8.76	4.02
50007.00	A23	M-009018- v-maf musculoaponeurotic	9935.00	MAFB	1.50	3.24
50007.00	B02	M-019749- C-type lectin domain family	7123.00	CLEC3B	10.85	6.11
50007.00	B04	M-013948- TCDD-inducible poly(ADP-ri	25976.00	TIPARP	2.14	2.60
50007.00	B05	M-006546- pleiomorphic adenoma gen	5325.00	PLAGL1	3.75	0.99
50007.00	B06	M-019488- timeless homolog (Drosophi	8914.00	TIMELESS	2.86	1.88
50007.00	B07	M-018037- pleckstrin homology domai	59338.00	PLEKHA1	20.33	15.59
50007.00	B08	M-013042- TIA1 cytotoxic granule-asso	7072.00	TIA1	6.25	1.51
50007.00	B09	M-009585- phospholipid transfer protei	5360.00	PLTP	1.07	3.67
50007.00	B10	M-011189- transferrin	7018.00	TF	8.62	3.88
50007.00	B11	M-009344- PMS1 postmeiotic segregati	5378.00	PMS1	8.09	3.35
50007.00	B12	M-021219- telomeric repeat binding fac	54386.00	TERF2IP	0.76	3.98
50007.00	B13	M-010032- PMS2 postmeiotic segregati	5395.00	PMS2	0.65	4.09
50007.00	B14	M-003546- telomeric repeat binding fac	7014.00	TERF2	3.81	0.93
50007.00	B15	M-019926- proline-rich nuclear recepto	10957.00	PNRC1	10.89	6.15
50007.00	B16	M-010542- telomeric repeat binding fac	7013.00	TERF1	7.72	2.98
50007.00	B17	M-004205- POT1 protection of telomer	25913.00	POT1	3.68	1.06
50007.00	B18	M-012749- t-complex 1	6950.00	TCP1	5.81	1.07
50007.00	B19	M-011358- protein phosphatase 1, regu	5514.00	PPP1R10	5.82	1.08
50007.00	B20	M-009590- transcription factor-like 5 (b	10732.00	TCFL5	14.83	10.09
50007.00	B21	M-004065- protein phosphatase 1, regu	26051.00	PPP1R16B	0.50	4.24
50007.00	B23	M-025402- protein phosphatase 1, regu	55607.00	PPP1R9A	1.20	3.54
50007.00	C02	M-021410- polyhomeotic homolog 2 (D	1912.00	PHC2	7.26	2.52
50007.00	C04	M-011850- polyhomeotic homolog 1 (D	1911.00	PHC1	10.69	5.95
50007.00	C05	M-003903- v-maf musculoaponeurotic	23764.00	MAFF	10.52	5.78
50007.00	C06	M-011750- profilin 2	5217.00	PFN2	3.28	1.46
50007.00	C07	M-006824- microtubule-associated prot	22919.00	MAPRE1	7.88	3.14
50007.00	C08	M-013012- prefoldin subunit 4	5203.00	PFDN4	5.65	0.91

50007.00	C09	M-012501- microtubule-associated prot	10982.00	MAPRE2	5.36	0.62
50007.00	C10	M-015385- pleckstrin homology domair	54477.00	PLEKHA5	5.62	0.88
50007.00	C11	M-012588- MYC-associated zinc finger p	4150.00	MAZ	3.81	0.93
50007.00	C12	M-017029- platelet/endothelial cell adh	5175.00	PECAM1	7.80	3.06
50007.00	C13	M-013616- methyl-CpG binding domain	53615.00	MBD3	4.74	0.00
50007.00	C14	M-016116- PDZ and LIM domain 1 (elfin	9124.00	PDLIM1	1.60	3.14
50007.00	C15	M-011080- mannose-binding lectin (pro	4153.00	MBL2	3.39	1.35
50007.00	C16	M-004440- programmed cell death 6	10016.00	PDCD6	12.23	7.49
50007.00	C17	M-003686- melanoma cell adhesion mo	4162.00	MCAM	8.86	4.12
50007.00	C18	M-004437- programmed cell death 2	5134.00	PDCD2	6.15	1.41
50007.00	C19	M-017379- minichromosome maintenai	8888.00	MCM3AP	0.67	4.07
50007.00	C20	M-011747- procollagen C-endopeptidas	5118.00	PCOLCE	3.33	1.41
50007.00	C21	M-011081- Mediterranean fever	4210.00	MEFV	5.49	0.75
50007.00	C23	M-011082- multiple endocrine neoplasi	4221.00	MEN1	1.89	2.85
50007.00	D02	M-003816- transcription factor 7-like 2 (	6934.00	TCF7L2	5.99	1.25
50007.00	D04	M-019641- transcription factor 19 (SC1)	6941.00	TCF19	9.71	4.97
50007.00	D05	M-013810- PR domain containing 12	59335.00	PRDM12	3.12	1.62
50007.00	D06	M-012376- transcription elongation fact	6923.00	TCEB2	9.36	4.62
50007.00	D07	M-014346- PR domain containing 14	63978.00	PRDM14	12.18	7.44
50007.00	D08	M-016892- Tax1 (human T-cell leukemia	8887.00	TAX1BP1	2.80	1.94
50007.00	D09	M-020332- PR domain containing 5	11107.00	PRDM5	14.19	**9.45**
50007.00	D10	M-017430- Tar (HIV-1) RNA binding prot	6895.00	TARBP2	0.52	4.22
50007.00	D11	M-015181- PR domain containing 7	11105.00	PRDM7	2.34	2.40
50007.00	D12	M-005255- TRAF family member-associa	10010.00	TANK	6.58	1.84
50007.00	D13	M-020688- PR domain containing 9	56979.00	PRDM9	5.31	0.57
50007.00	D14	M-019979- T-cell acute lymphocytic leul	6887.00	TAL2	3.95	0.79
50007.00	D15	M-017655- prolactin regulatory elemen	10113.00	PREB	1.52	3.22
50007.00	D16	M-003928- T-cell acute lymphocytic leul	6886.00	TAL1	1.43	3.31
50007.00	D17	M-019902- perforin 1 (pore forming pro	5551.00	PRF1	11.08	6.34
50007.00	D18	M-017217- TAF9B RNA polymerase II, TA	51616.00	TAF9B	2.93	1.81
50007.00	D19	M-020069- proteoglycan 3	10394.00	PRG3	1.31	3.43
50007.00	D20	M-020953- zinc finger protein 589	51385.00	ZNF589	1.34	3.40
50007.00	D21	M-015402- protein-kinase, interferon-in	5612.00	PRKRIR	3.95	0.79
50007.00	D23	M-011497- PRP18 pre-mRNA processing	8559.00	PRPF18	2.62	2.12
50007.00	E02	M-013556- protocadherin gamma subfa	5098.00	PCDHGC3	3.13	1.61
50007.00	E04	M-011508- protocadherin gamma subfa	8641.00	PCDHGB4	5.91	1.17
50007.00	E05	M-021466- milk fat globule-EGF factor 8	4240.00	MFGE8	5.55	0.81
50007.00	E06	M-013540- protocadherin gamma subfa	9708.00	PCDHGA8	4.25	0.49
50007.00	E07	M-007731- malignant fibrous histiocyto	9258.00	MFHAS1	17.63	**12.89**
50007.00	E08	M-011507- protocadherin gamma subfa	26025.00	PCDHGA12	10.99	6.25
50007.00	E09	M-014259- RAS-like, family 11, member	65997.00	RASL11B	5.24	0.50
50007.00	E10	M-013525- protocadherin beta 6	56130.00	PCDHB6	11.24	6.50
50007.00	E11	M-011084- MHC class I polypeptide-rela	4276.00	MICA	3.59	1.15
50007.00	E12	M-013524- protocadherin beta 5	26167.00	PCDHB5	3.48	1.26
50007.00	E13	M-012178- MHC class I polypeptide-rela	4277.00	MICB	7.70	2.96
50007.00	E14	M-013281- protocadherin beta 4	56131.00	PCDHB4	11.25	6.51
50007.00	E15	M-014201- mesoderm induction early re	57708.00	MIER1	8.10	3.36

50007.00	E16	M-013282- protocadherin beta 3	56132.00	PCDHB3	9.00	4.26
50007.00	E17	M-009428- protein inhibitor of activatec	9063.00	PIAS2	11.31	6.57
50007.00	E18	M-013283- protocadherin beta 2	56133.00	PCDHB2	6.64	1.90
50007.00	E19	M-013942- MBD2-interacting zinc finge	25988.00	MIZF	1.34	3.40
50007.00	E20	M-013531- protocadherin beta 15	56121.00	PCDHB15	2.37	2.37
50007.00	E21	M-003280- antigen identified by monoc	4288.00	MKI67	4.31	0.43
50007.00	E23	M-016687- MKI67 (FHA domain) interac	84365.00	MKI67IP	1.69	3.05
50007.00	F02	M-016218- synaptotagmin binding, cytc	10492.00	SYNCRIP	1.83	2.91
50007.00	F04	M-019864- symplekin	8189.00	SYMPK	2.82	1.92
50007.00	F05	M-015638- PRP4 pre-mRNA processing	9128.00	PRPF4	5.81	1.07
50007.00	F06	M-011398- supervillin	6840.00	SVIL	4.51	0.23
50007.00	F07	M-012252- PRP8 pre-mRNA processing	10594.00	PRPF8	1.88	2.86
50007.00	F08	M-015679- stress 70 protein chaperone	6782.00	STCH	1.32	3.42
50007.00	F09	M-031718- periaxin	57716.00	PRX	0.61	4.13
50007.00	F10	M-017232- synovial sarcoma, X breakpc	6759.00	SSX4	1.41	3.33
50007.00	F11	M-004998- presenilin 1 (Alzheimer dise	5663.00	PSEN1	4.14	0.60
50007.00	F12	M-011783- structure specific recognitio	6749.00	SSRP1	10.91	6.17
50007.00	F13	M-017212- proteasome (prosome, mac	5708.00	PSMD2	0.64	4.10
50007.00	F14	M-012264- signal sequence receptor, de	6748.00	SSR4	9.44	4.70
50007.00	F15	M-005163- paxillin	5829.00	PXN	0.20	4.54
50007.00	F16	M-012374- signal sequence receptor, ga	6747.00	SSR3	7.67	2.93
50007.00	F17	M-008793- RAB26, member RAS oncoge	25837.00	RAB26	7.50	2.76
50007.00	F18	M-010627- sushi-repeat-containing prot	8406.00	SRPX	3.56	1.18
50007.00	F19	M-009920- RAB32, member RAS oncoge	10981.00	RAB32	15.28	10.54
50007.00	F20	M-014070- spastin	6683.00	SPAST	15.33	10.59
50007.00	F21	M-008924- RAB40A, member RAS oncog	142684.00	RAB40A	3.08	1.66
50007.00	F23	M-008353- RAB40B, member RAS oncog	10966.00	RAB40B	5.21	0.47
50007.00	G02	M-013530- protocadherin beta 14	56122.00	PCDHB14	14.22	9.48
50007.00	G04	M-013528- protocadherin beta 12	56124.00	PCDHB12	42.12	37.38
50007.00	G05	M-013300- McKusick-Kaufman syndrom	8195.00	MKKS	4.01	0.73
50007.00	G06	M-013527- protocadherin beta 11	56125.00	PCDHB11	5.83	1.09
50007.00	G07	M-015434- megakaryoblastic leukemia	57591.00	MKL1	4.77	0.03
50007.00	G08	M-013278- protocadherin beta 10	56126.00	PCDHB10	6.82	2.08
50007.00	G09	M-019478- myeloid leukemia factor 1	4291.00	MLF1	11.24	6.50
50007.00	G10	M-013658- protocadherin beta 1	29930.00	PCDHB1	4.67	0.07
50007.00	G11	M-003906- mutL homolog 1, colon canc	4292.00	MLH1	4.54	0.20
50007.00	G12	M-013248- protocadherin alpha subfam	56134.00	PCDHAC2	6.92	2.18
50007.00	G13	M-009939- mutL homolog 3 (E. coli)	27030.00	MLH3	9.78	5.04
50007.00	G14	M-013249- protocadherin alpha subfam	56135.00	PCDHAC1	3.37	1.37
50007.00	G15	M-010580- myeloid/lymphoid or mixed-	55904.00	MLL5	22.47	17.73
50007.00	G16	M-013440- protocadherin alpha 9	9752.00	PCDHA9	3.47	1.27
50007.00	G17	M-020075- myeloid/lymphoid or mixed-	4301.00	MLLT4	2.99	1.75
50007.00	G18	M-013254- protocadherin alpha 8	56140.00	PCDHA8	3.92	0.82
50007.00	G19	M-010524- myeloid/lymphoid or mixed-	4302.00	MLLT6	1.88	2.86
50007.00	G20	M-013255- protocadherin alpha 7	56141.00	PCDHA7	5.86	1.12
50007.00	G21	M-019001- ligand dependent nuclear re	254251.00	LCORL	4.80	0.06
50007.00	G23	M-016320- methylmalonic aciduria (cob	166785.00	MMAA	0.95	3.79

50007.00	H02	M-016676- SPARC-like 1 (mast9, hevin)	8404.00	SPARCL1	3.21	1.53
50007.00	H04	M-003710- secreted protein, acidic, cyst	6678.00	SPARC	1.51	3.23
50007.00	H05	M-010368- RAB40C, member RAS oncog	57799.00	RAB40C	10.62	5.88
50007.00	H06	M-015429- Sp7 transcription factor	121340.00	SP7	2.89	1.85
50007.00	H07	M-008780- RAB4B, member RAS oncoge	53916.00	RAB4B	32.47	**27.73**
50007.00	H08	M-011875- SP110 nuclear body protein	3431.00	SP110	7.34	2.60
50007.00	H09	M-008541- RAB guanine nucleotide excl	27342.00	RABGEF1	11.93	7.19
50007.00	H10	M-015307- SP100 nuclear antigen	6672.00	SP100	7.70	2.96
50007.00	H11	M-003294- RAD17 homolog (S. pombe)	5884.00	RAD17	3.22	1.52
50007.00	H12	M-020142- sorbin and SH3 domain cont	10580.00	SORBS1	9.45	4.71
50007.00	H13	M-006832- RAD21 homolog (S. pombe)	5885.00	RAD21	1.42	3.32
50007.00	H14	M-012983- SON DNA binding protein	6651.00	SON	9.57	4.83
50007.00	H15	M-005231- RAD23 homolog A (S. cerevi:	5886.00	RAD23A	0.88	3.86
50007.00	H16	M-027197- suppressor of cytokine signa	30837.00	SOCS7	16.56	**11.82**
50007.00	H17	M-011759- RAD23 homolog B (S. cerevi:	5887.00	RAD23B	11.21	6.47
50007.00	H18	M-011776- small nuclear ribonucleopro	6638.00	SNRPN	13.43	**8.69**
50007.00	H19	M-012295- retinoic acid induced 1	10743.00	RAI1	1.33	3.41
50007.00	H20	M-012601- small nuclear RNA activating	6619.00	SNAPC3	5.62	0.88
50007.00	H21	M-009235- v-ral simian leukemia viral o	5898.00	RALA	18.48	**13.74**
50007.00	H23	M-008403- v-ral simian leukemia viral o	5899.00	RALB	2.66	2.08
50007.00	I02	M-013256- protocadherin alpha 6	56142.00	PCDHA6	3.35	1.39
50007.00	I04	M-013257- protocadherin alpha 5	56143.00	PCDHA5	5.34	0.60
50007.00	I05	M-010525- myeloid cell nuclear differer	4332.00	MNDA	6.75	2.01
50007.00	I06	M-013258- protocadherin alpha 4	56144.00	PCDHA4	4.93	0.19
50007.00	I07	M-026427- AT rich interactive domain 5	84159.00	ARID5B	4.90	0.16
50007.00	I08	M-013259- protocadherin alpha 3	56145.00	PCDHA3	4.36	0.38
50007.00	I09	M-019279- MKL/myocardin-like 2	57496.00	MKL2	5.93	1.19
50007.00	I10	M-013260- protocadherin alpha 2	56146.00	PCDHA2	4.51	0.23
50007.00	I11	M-006373- septin 9	10801.00	SEPT9	7.23	2.49
50007.00	I12	M-013250- protocadherin alpha 13	56136.00	PCDHA13	9.84	5.10
50007.00	I13	M-003909- mutS homolog 2, colon canc	4436.00	MSH2	10.77	6.03
50007.00	I14	M-013251- protocadherin alpha 12	56137.00	PCDHA12	1.48	3.26
50007.00	I15	M-019116- mutS homolog 4 (E. coli)	4438.00	MSH4	4.11	0.63
50007.00	I16	M-013252- protocadherin alpha 11	56138.00	PCDHA11	3.75	0.99
50007.00	I17	M-011337- mutS homolog 5 (E. coli)	4439.00	MSH5	2.46	2.28
50007.00	I18	M-013253- protocadherin alpha 10	56139.00	PCDHA10	3.84	0.90
50007.00	I19	M-019287- mutS homolog 6 (E. coli)	2956.00	MSH6	9.39	4.65
50007.00	I20	M-013261- protocadherin alpha 1	56147.00	PCDHA1	4.40	0.34
50007.00	I21	M-006346- mesothelin	10232.00	MSLN	1.48	3.26
50007.00	I23	M-007370- mitochondrial carrier homol	23787.00	MTCH1	2.97	1.77
50007.00	J02	M-017386- snail homolog 2 (Drosophila	6591.00	SNAI2	7.97	3.23
50007.00	J04	M-010847- snail homolog 1 (Drosophila	6615.00	SNAI1	1.75	2.99
50007.00	J05	M-012007- RANBP2-like and GRIP doma	84220.00	RGPD5	18.62	**13.88**
50007.00	J06	M-006837- structural maintenance of cl	10051.00	SMC4	10.92	6.18
50007.00	J07	M-011484- RAN binding protein 3	8498.00	RANBP3	1.45	3.29
50007.00	J08	M-008312- SWI/SNF related, matrix ass	6601.00	SMARCC2	1.62	3.12
50007.00	J09	M-017219- Ras association (RalGDS/AF-	11186.00	RASSF1	2.83	1.91

50007.00	J10	M-006660- solute carrier family 9 (sodiu	9351.00	SLC9A3R2	4.12	0.62
50007.00	J11	M-010585- Ras association (RalGDS/AF-	83593.00	RASSF5	7.41	2.67
50007.00	J12	M-012286- stem-loop (histone) binding	7884.00	SLBP	1.75	2.99
50007.00	J13	M-003299- retinoblastoma-like 2 (p130)	5934.00	RBL2	10.04	5.30
50007.00	J14	M-019545- survival of motor neuron pro	8487.00	SIP1	1.52	3.22
50007.00	J15	M-015436- RNA binding motif protein 1	54033.00	RBM11	6.63	1.89
50007.00	J16	M-012990- SIN3 homolog A, transcriptic	25942.00	SIN3A	5.80	1.06
50007.00	J17	M-010854- RNA binding motif protein 1	64783.00	RBM15	3.38	1.36
50007.00	J18	M-013430- sialic acid binding Ig-like lect	89858.00	SIGLEC12	5.55	0.81
50007.00	J19	M-009220- RNA binding motif protein 5	10181.00	RBM5	5.72	0.98
50007.00	J20	M-015154- sialic acid binding Ig-like lect	114132.00	SIGLEC11	0.55	4.19
50007.00	J21	M-020032- RNA binding motif protein 6	10180.00	RBM6	7.33	2.59
50007.00	J23	M-011377- RNA binding motif, single str	5937.00	RBMS1	0.75	3.99
50007.00	K02	M-011349- protocadherin 8	5100.00	PCDH8	5.26	0.52
50007.00	K04	M-008837- protocadherin 7	5099.00	PCDH7	3.96	0.78
50007.00	K05	M-015905- myocardin	93649.00	MYOCD	19.10	**14.36**
50007.00	K06	M-011509- dachsous 1 (Drosophila)	8642.00	DCHS1	11.45	6.71
50007.00	K07	M-013486- myosin, heavy chain 1, skele	4619.00	MYH1	9.72	4.98
50007.00	K08	M-013654- protocadherin 15	65217.00	PCDH15	1.87	2.87
50007.00	K09	M-011737- myosin, heavy chain 11, smo	4629.00	MYH11	16.26	**11.52**
50007.00	K10	M-013621- protocadherin 12	51294.00	PCDH12	4.91	0.17
50007.00	K11	M-012621- myosin, heavy chain 13, skel	8735.00	MYH13	2.40	2.34
50007.00	K12	M-013624- protocadherin 11 Y-linked	83259.00	PCDH11Y	5.47	0.73
50007.00	K13	M-021252- myosin, heavy chain 2, skele	4620.00	MYH2	6.99	2.25
50007.00	K14	M-013619- protocadherin 11 X-linked	27328.00	PCDH11X	1.96	2.78
50007.00	K15	M-012645- myosin, heavy chain 6, cardi	4624.00	MYH6	1.29	3.45
50007.00	K16	M-010487- protocadherin 1	5097.00	PCDH1	7.01	2.27
50007.00	K17	M-007668- myosin, heavy chain 9, non-i	4627.00	MYH9	7.57	2.83
50007.00	K18	M-013201- poly(rC) binding protein 4	57060.00	PCBP4	1.74	3.00
50007.00	K19	M-019044- myosin, light chain 9, regula	10398.00	MYL9	2.01	2.73
50007.00	K20	M-012002- poly(rC) binding protein 2	5094.00	PCBP2	3.01	1.73
50007.00	K21	M-007217- myosin X	4651.00	MYO10	2.25	2.49
50007.00	K23	M-013964- myosin VIIA and Rab interac	25924.00	MYRIP	4.74	0.00
50007.00	L02	M-014191- sex hormone-binding globul	6462.00	SHBG	10.03	5.29
50007.00	L04	M-013625- spen homolog, transcription	23013.00	SPEN	2.77	1.97
50007.00	L05	M-011378- RNA binding motif, single str	5939.00	RBMS2	3.97	0.77
50007.00	L06	M-012626- sarcoglycan, epsilon	8910.00	SGCE	3.46	1.28
50007.00	L07	M-012967- AT rich interactive domain 4	51742.00	ARID4B	9.63	4.89
50007.00	L08	M-015980- surfactant, pulmonary-assoc	6441.00	SFTPD	12.48	7.74
50007.00	L09	M-009491- RAS (RAD and GEM)-like GTI	28954.00	REM1	25.25	**20.51**
50007.00	L10	M-011893- splicing factor, arginine/seri	6433.00	SFRS8	9.30	4.56
50007.00	L11	M-019839- RALBP1 associated Eps dom	9185.00	REPS2	3.60	1.14
50007.00	L12	M-015909- splicing factor, arginine/seri	6432.00	SFRS7	19.43	**14.69**
50007.00	L13	M-019061- replication factor C (activato	5982.00	RFC2	13.83	**9.09**
50007.00	L14	M-030081- splicing factor, arginine/seri	6428.00	SFRS3	5.19	0.45
50007.00	L15	M-008691- replication factor C (activato	5984.00	RFC4	2.23	2.51
50007.00	L16	M-019711- splicing factor, arginine/seri	6427.00	SFRS2	4.49	0.25

50007.00	L17	M-013577- regulatory factor X, 4 (influe	5992.00	RFX4	2.87	1.87
50007.00	L18	M-011929- splicing factor, arginine/seri	9295.00	SFRS11	15.66	**10.92**
50007.00	L19	M-009389- Rho-related BTB domain cor	9886.00	RHOBTB1	4.18	0.56
50007.00	L20	M-006455- splicing factor proline/glutar	6421.00	SFPQ	0.60	4.14
50007.00	L21	M-009252- Rho-related BTB domain cor	23221.00	RHOBTB2	2.91	1.83
50007.00	L23	M-015388- PDZ and LIM domain 4	8572.00	PDLIM4	0.95	3.79
50007.00	M02	M-020387- zinc finger protein 395	55893.00	ZNF395	1.67	3.07
50007.00	M04	M-012242- paired box gene 9	5083.00	PAX9	1.74	3.00
50007.00	M05	M-009258- A kinase (PRKA) anchor prot	26993.00	AKAP8L	22.44	**17.70**
50007.00	M06	M-012241- paired box gene 5 (B-cell line	5079.00	PAX5	16.38	**11.64**
50007.00	M07	M-019113- NLR family, pyrin domain co	338322.00	NLRP10	22.35	**17.61**
50007.00	M08	M-020120- paired box gene 1	5075.00	PAX1	7.24	2.50
50007.00	M09	M-018073- NLR family, pyrin domain co	126204.00	NLRP13	6.39	1.65
50007.00	M10	M-005287- parvin, alpha	55742.00	PARVA	1.92	2.82
50007.00	M11	M-019075- NLR family, pyrin domain co	338323.00	NLRP14	19.90	**15.16**
50007.00	M12	M-015602- par-3 partitioning defective	56288.00	PARD3	5.51	0.77
50007.00	M13	M-020253- NLR family, pyrin domain co	55655.00	NLRP2	7.30	2.56
50007.00	M14	M-011744- regenerating islet-derived 3	5068.00	REG3A	1.61	3.13
50007.00	M15	M-009641- nibrin	4683.00	NBN	9.03	4.29
50007.00	M16	M-015343- protein kinase C and casein I	29763.00	PACSIN3	7.68	2.94
50007.00	M17	M-012561- neural cell adhesion molecu	4684.00	NCAM1	7.05	2.31
50007.00	M18	M-016608- osteoclast stimulating factor	26578.00	OSTF1	5.19	0.45
50007.00	M19	M-010613- neural cell adhesion molecu	4685.00	NCAM2	15.94	**11.20**
50007.00	M20	M-020118- periostin, osteoblast specific	10631.00	POSTN	11.15	6.41
50007.00	M21	M-019672- nuclear cap binding protein	4686.00	NCBP1	9.36	4.62
50007.00	M23	M-013101- necdin homolog (mouse)	4692.00	NDN	5.77	1.03
50007.00	N02	M-019808- splicing factor 3a, subunit 3,	10946.00	SF3A3	3.94	0.80
50007.00	N04	M-016051- splicing factor 3a, subunit 1,	10291.00	SF3A1	2.39	2.35
50007.00	N05	M-008390- Ras-like without CAAX 1	6016.00	RIT1	5.25	0.51
50007.00	N06	M-019260- septin 6	23157.00	SEPT6	9.78	5.04
50007.00	N07	M-012298- RNA binding protein S1, seri	10921.00	RNPS1	3.69	1.05
50007.00	N08	M-017317- septin 3	55964.00	SEPT3	1.50	3.24
50007.00	N09	M-013329- snurportin 1	10073.00	SNUPN	2.41	2.33
50007.00	N10	M-013443- septin 1	1731.00	SEPT1	4.80	0.06
50007.00	N11	M-008199- retinal pigment epithelium-s	6121.00	RPE65	5.84	1.10
50007.00	N12	M-013850- selenoprotein N, 1	57190.00	SEPN1	2.82	1.92
50007.00	N13	M-019356- retinitis pigmentosa GTPase	6103.00	RPGR	9.75	5.01
50007.00	N14	M-008079- selectin P (granule membrar	6403.00	SELP	10.67	5.93
50007.00	N15	M-016070- Ras-related GTP binding A	10670.00	RRAGA	3.55	1.19
50007.00	N16	M-013468- selenium binding protein 1	8991.00	SELENBP1	16.42	**11.68**
50007.00	N17	M-019359- retinoschisis (X-linked, juver	6247.00	RS1	7.36	2.62
50007.00	N18	M-008077- selectin E (endothelial adhe	6401.00	SELE	9.40	4.66
50007.00	N19	M-005294- CAP-GLY domain containing	6249.00	CLIP1	4.63	0.11
50007.00	N20	M-011963- SEC22 vesicle trafficking pro	9554.00	SEC22B	15.27	**10.53**
50007.00	N21	M-012666- runt-related transcription fa	864.00	RUNX3	6.88	2.14
50007.00	N23	M-012258- S100 calcium binding protei	6271.00	S100A1	3.04	1.70
50007.00	O02	M-008350- oxysterol binding protein-lik	114876.00	OSBPL1A	8.27	3.53

50007.00	O04	M-009747- oxysterol binding protein	5007.00	OSBP	2.13	2.61
50007.00	O05	M-009358- neogenin homolog 1 (chicke	4756.00	NEO1	1.60	3.14
50007.00	O06	M-003288- origin recognition complex,	23594.00	ORC6L	9.86	5.12
50007.00	O07	M-004765- nuclear factor of kappa light	4792.00	NFKBIA	2.03	2.71
50007.00	O08	M-009113- oligodendrocyte lineage trar	10215.00	OLIG2	1.16	3.58
50007.00	O09	M-015321- nescient helix loop helix 1	4807.00	NHLH1	1.67	3.07
50007.00	O10	M-010857- nucleobindin 2	4925.00	NUCB2	4.74	0.00
50007.00	O11	M-019241- nidogen 2 (osteonidogen)	22795.00	NID2	6.58	1.84
50007.00	O12	M-015822- nucleobindin 1	4924.00	NUCB1	5.42	0.68
50007.00	O13	M-017671- ninjurin 1	4814.00	NINJ1	2.50	2.24
50007.00	O14	M-004705- nucleotide binding protein 2	10101.00	NUBP2	5.99	1.25
50007.00	O15	M-004432- nucleolar protein 3 (apoptos	8996.00	NOL3	3.35	1.39
50007.00	O16	M-019603- nucleotide binding protein 1	4682.00	NUBP1	0.66	4.08
50007.00	O17	M-019843- nucleolar and coiled-body pl	9221.00	NOLC1	3.47	1.27
50007.00	O18	M-012186- neurogranin (protein kinase	4900.00	NRGN	15.61	**10.87**
50007.00	O19	M-011342- neuro-oncological ventral ar	4857.00	NOVA1	4.26	0.48
50007.00	O20	M-019920- neuronal cell adhesion mole	4897.00	NRCAM	5.17	0.43
50007.00	O21	M-012590- neuro-oncological ventral ar	4858.00	NOVA2	2.28	2.46
50007.00	O23	M-008644- nephrosis 1, congenital, Finr	4868.00	NPHS1	7.99	3.25
50007.00	P02	M-015910- serum deprivation response	8436.00	SDPR	2.71	2.03
50007.00	P04	M-003706- syndecan 4	6385.00	SDC4	1.15	3.59
50007.00	P05	M-012138- S100 calcium binding protei	6282.00	S100A11	5.16	0.42
50007.00	P06	M-003642- signal peptide, CUB domain,	57758.00	SCUBE2	3.95	0.79
50007.00	P07	M-027738- S100 calcium binding protei	6284.00	S100A13	2.57	2.17
50007.00	P08	M-009876- sterol carrier protein 2	6342.00	SCP2	8.40	3.66
50007.00	P09	M-010723- S100 calcium binding protei	57402.00	S100A14	0.11	4.63
50007.00	P10	M-011987- SCO cytochrome oxidase de	9997.00	SCO2	2.65	2.09
50007.00	P11	M-012191- S100 calcium binding protei	6273.00	S100A2	14.83	**10.09**
50007.00	P12	M-003705- secretoglobin, family 2A, me	4250.00	SCGB2A2	7.08	2.34
50007.00	P13	M-011767- S100 calcium binding protei	6274.00	S100A3	9.22	4.48
50007.00	P14	M-011422- secretogranin II (chromogra	7857.00	SCG2	10.53	5.79
50007.00	P15	M-004792- S100 calcium binding protei	6275.00	S100A4	1.40	3.34
50007.00	P16	M-011106- ataxin 7	6314.00	ATXN7	0.61	4.13
50007.00	P17	M-011770- S100 calcium binding protei	6279.00	S100A8	20.80	**16.06**
50007.00	P18	M-004510- ataxin 1	6310.00	ATXN1	4.68	0.06
50007.00	P19	M-004295- S100 calcium binding protei	6286.00	S100P	4.94	0.20
50007.00	P20	M-007033- sal-like 4 (Drosophila)	57167.00	SALL4	8.47	3.73
50007.00	P21	M-006560- sal-like 1 (Drosophila)	6299.00	SALL1	1.05	3.69
50007.00	P23	M-006973- sal-like 3 (Drosophila)	27164.00	SALL3	3.37	1.37
				mdn	4.74	2.75
				3MAD		8.24
				MADc		4.07
50007.00	C22				56.72	
50007.00	D22				52.77	
50007.00	E22				54.97	
50007.00	F22				55.33	
				m	**54.95**	

					sd	1.64
50007.00	G22					20.97
50007.00	H22					26.20
50007.00	I22					29.20
50007.00	J22					19.22
50007.00	K22					14.35
					m	22.24
					sd	6.72
					3psSD	4.91
					3ngSD	20.16
					SM SD	25.07
					Mn Diff	32.70
					SMovrMn	0.77
					1-SMovrMn	0.23
50007.00	G03	M-003290-	polo-like kinase 1 (Drosophil	5347.00	PLK1 SMARTpo	8.11
50007.00	H03	M-003290-	polo-like kinase 1 (Drosophil	5347.00	PLK1 SMARTpo	3.36
50007.00	I03	D-001206-	siControl non-targeting siRNA #2			1.71
50007.00	J03	D-001206-	siControl non-targeting siRNA #2			2.41
50007.00	K03	D-001600-	siGLO RISC-free siRNA			20.14
50007.00	L03	D-001600-	siGLO RISC-free siRNA			29.10

robust Z	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**	
0.89	1.94	2.01	0.62	1.41	2.38	0.80	
0.50	0.99	2.96	0.91	2.67	1.12	0.38	
0.79	3.98	0.03	0.01	4.04	0.25	0.08	
0.90	2.71	1.24	0.38	5.78	1.99	0.67	
0.65	2.72	1.23	0.38	24.79	**21.00**	7.05	
0.27	4.10	0.15	0.04	5.86	2.07	0.70	
0.13	2.38	1.57	0.48	5.78	1.99	0.67	
0.21	4.47	0.52	0.16	3.65	0.14	0.05	
0.86	1.46	2.49	0.76	1.98	1.81	0.61	
0.62	7.91	3.96	1.22	8.96	5.17	1.74	
1.04	2.73	1.22	0.37	2.46	1.33	0.44	
0.10	3.70	0.25	0.08	1.98	1.81	0.61	
0.78	0.66	3.29	1.01	1.77	2.02	0.68	
1.48	9.04	5.09	1.56	11.39	**7.60**	2.55	
0.98	1.04	2.91	0.90	1.96	1.83	0.61	
1.05	0.92	3.03	0.93	0.54	3.25	1.09	
0.40	2.41	1.54	0.47	4.78	0.99	0.33	
0.04	2.54	1.41	0.43	2.72	1.07	0.36	
0.99	5.57	1.62	0.50	4.66	0.87	0.29	
0.80	3.54	0.41	0.13	1.23	2.56	0.86	
1.50	5.74	1.79	0.55	3.09	0.70	0.24	
0.64	1.72	2.23	0.69	0.60	3.19	1.07	
0.24	0.31	3.64	1.12	0.89	2.90	0.97	
0.46	2.12	1.83	0.56	2.28	1.51	0.51	
3.83	15.47	**11.52**	3.55	16.80	**13.01**	4.36	y
0.37	2.27	1.68	0.52	2.23	1.56	0.52	
0.90	3.54	0.41	0.13	1.15	2.64	0.89	
0.95	9.12	5.17	1.59	8.52	4.73	1.59	
0.82	2.76	1.19	0.37	7.91	4.12	1.38	
0.98	3.88	0.07	0.02	0.13	3.66	1.23	
1.00	0.71	3.24	1.00	0.15	3.64	1.22	
0.23	2.01	1.94	0.60	2.36	1.43	0.48	
1.51	3.53	0.42	0.13	8.51	4.72	1.58	
0.73	6.96	3.01	0.93	5.05	1.26	0.42	
0.26	1.42	2.53	0.78	1.75	2.04	0.68	
0.26	3.12	0.83	0.26	3.09	0.70	0.23	
0.27	1.79	2.16	0.66	4.03	0.24	0.08	
2.48	8.87	4.92	1.51	14.26	**10.47**	3.51	y
1.04	0.59	3.36	1.03	1.03	2.76	0.93	
0.87	0.48	3.47	1.07	3.79	0.00	0.00	
0.62	6.12	2.17	0.67	3.04	0.75	0.25	
1.46	14.62	**10.67**	3.28	6.74	2.95	0.99	
1.42	7.01	3.06	0.94	13.76	**9.97**	3.35	
0.36	5.19	1.24	0.38	2.49	1.30	0.43	
0.77	6.07	2.12	0.65	4.82	1.03	0.34	
0.22	4.74	0.79	0.24	7.12	3.33	1.12	

0.15	6.68	2.73	0.84	5.81	2.02	0.68	
0.22	6.52	2.57	0.79	6.02	2.23	0.75	
0.23	6.41	2.46	0.76	4.12	0.33	0.11	
0.75	2.72	1.23	0.38	2.86	0.93	0.31	
0.00	0.76	3.19	0.98	2.17	1.62	0.54	
0.77	2.95	1.00	0.31	1.66	2.13	0.71	
0.33	3.54	0.41	0.12	3.55	0.24	0.08	
1.84	5.82	1.87	0.58	5.76	1.97	0.66	
1.01	2.32	1.64	0.50	3.70	0.09	0.03	
0.35	3.60	0.35	0.11	4.65	0.86	0.29	
1.00	1.83	2.12	0.65	0.65	3.14	1.05	
0.35	1.43	2.52	0.78	0.63	3.16	1.06	
0.18	6.24	2.29	0.71	3.80	0.01	0.00	
0.70	0.90	3.05	0.94	0.98	2.81	0.94	
0.31	10.33	6.38	1.96	6.57	2.78	0.93	
1.22	11.20	**7.25**	2.23	14.75	**10.96**	3.68	y
0.40	5.64	1.69	0.52	4.75	0.96	0.32	
1.13	2.30	1.65	0.51	3.52	0.27	0.09	
1.83	8.80	4.85	1.49	11.24	**7.45**	2.50	
0.48	3.75	0.20	0.06	1.79	2.00	0.67	
2.32	17.38	**13.43**	4.13	27.39	**23.60**	7.92	y
1.04	2.82	1.13	0.35	0.62	3.17	1.06	
0.59	1.86	2.09	0.64	3.29	0.50	0.17	
0.45	8.21	4.26	1.31	8.28	4.49	1.51	
0.14	7.43	3.48	1.07	9.27	5.48	1.84	
0.19	3.68	0.27	0.08	1.42	2.37	0.80	
0.79	5.92	1.97	0.60	1.98	1.81	0.61	
0.81	2.17	1.78	0.55	3.08	0.71	0.24	
1.56	20.25	**16.30**	5.02	17.61	**13.82**	4.64	y
0.45	3.96	0.01	0.00	3.75	0.04	0.01	
0.84	3.89	0.06	0.02	1.54	2.25	0.75	
0.84	5.87	1.92	0.59	2.05	1.74	0.59	
0.19	10.86	**6.91**	2.12	6.67	2.88	0.97	
0.52	3.24	0.71	0.22	3.44	0.35	0.12	
0.39	2.79	1.16	0.36	3.19	0.60	0.20	
0.29	12.29	**8.34**	2.57	5.94	2.15	0.72	
0.20	9.27	5.32	1.64	4.36	0.57	0.19	
0.12	6.62	2.67	0.82	5.34	1.55	0.52	
3.17	10.74	**6.79**	2.09	9.36	5.57	1.87	y
1.54	20.72	**16.77**	5.16	24.96	**21.17**	7.10	y
0.12	7.49	3.54	1.09	6.64	2.85	0.96	
1.60	15.81	**11.86**	3.65	7.95	4.16	1.40	
0.28	8.46	4.51	1.39	5.99	2.20	0.74	
0.31	3.62	0.33	0.10	3.47	0.32	0.11	
0.73	15.93	**11.98**	3.68	19.38	**15.59**	5.23	y
1.60	28.99	**25.04**	7.70	22.60	**18.81**	6.31	y
0.83	10.74	**6.79**	2.09	10.92	**7.13**	2.39	y

1.05	14.93	**10.98**	3.38	10.11	**6.32**	2.12	y
1.61	10.00	6.05	1.86	16.19	**12.40**	4.16	
0.47	9.64	5.69	1.75	6.39	2.60	0.87	
0.84	2.64	1.31	0.40	2.14	1.65	0.55	
0.58	5.03	1.08	0.33	3.99	0.20	0.07	
0.11	2.57	1.38	0.43	5.54	1.75	0.59	
0.75	2.01	1.94	0.60	3.63	0.16	0.05	
0.72	2.91	1.04	0.32	3.96	0.17	0.06	
0.47	2.72	1.23	0.38	1.40	2.39	0.80	
0.26	4.31	0.36	0.11	8.10	4.31	1.44	
0.06	4.76	0.81	0.25	7.27	3.48	1.17	
0.70	6.87	2.92	0.90	5.26	1.47	0.49	
0.84	1.28	2.67	0.82	2.70	1.09	0.37	
1.01	3.99	0.04	0.01	1.41	2.38	0.80	
0.82	2.82	1.13	0.35	2.68	1.11	0.37	
0.15	3.66	0.29	0.09	1.54	2.25	0.75	
1.52	15.62	**11.67**	3.59	12.62	**8.83**	2.96	y
1.01	2.92	1.03	0.32	1.95	1.84	0.62	
1.16	6.64	2.69	0.83	2.74	1.05	0.35	
1.11	1.43	2.52	0.78	0.57	3.22	1.08	
0.72	2.51	1.44	0.44	7.40	3.61	1.21	
0.68	7.05	3.10	0.96	7.36	3.57	1.20	
0.29	6.76	2.81	0.86	4.34	0.55	0.19	
2.59	9.60	5.65	1.74	11.47	**7.68**	2.58	y
2.60	9.08	5.13	1.58	8.67	4.88	1.64	
0.41	1.25	2.70	0.83	1.44	2.35	0.79	
0.12	5.36	1.41	0.43	4.64	0.85	0.28	
2.33	8.02	4.07	1.25	16.77	**12.98**	4.36	y
9.19	43.83	**39.88**	12.27	41.67	**37.88**	12.71	y
0.18	1.57	2.38	0.73	1.78	2.01	0.67	
0.27	3.08	0.87	0.27	4.64	0.85	0.29	
0.01	6.14	2.19	0.67	6.59	2.80	0.94	
0.51	5.37	1.42	0.44	5.98	2.19	0.73	
1.60	9.22	5.27	1.62	15.87	**12.08**	4.05	
0.02	1.20	2.75	0.85	4.09	0.30	0.10	
0.05	3.21	0.74	0.23	5.30	1.51	0.51	
0.54	2.91	1.04	0.32	2.13	1.66	0.56	
1.24	7.93	3.98	1.22	6.39	2.60	0.87	
0.34	4.39	0.44	0.14	9.35	5.56	1.87	
4.36	8.46	4.51	1.39	26.31	**22.52**	7.56	y
0.31	3.47	0.48	0.15	3.46	0.33	0.11	
0.43	1.94	2.01	0.62	1.78	2.01	0.67	
0.20	1.40	2.55	0.79	1.73	2.06	0.69	
0.70	0.99	2.96	0.91	2.88	0.91	0.30	
0.27	3.87	0.08	0.02	6.55	2.76	0.93	
0.01	2.39	1.56	0.48	7.59	3.80	1.28	
0.93	0.98	2.97	0.91	4.55	0.76	0.25	

0.38	6.14	2.19	0.67	5.54	1.75	0.59	
0.79	2.25	1.70	0.52	3.09	0.70	0.24	
1.45	4.61	0.66	0.20	13.50	**9.71**	3.26	
0.45	0.84	3.11	0.96	1.98	1.81	0.61	
6.81	34.02	**30.07**	9.25	27.30	**23.51**	7.89	y
0.64	7.91	3.96	1.22	5.05	1.26	0.42	
1.77	10.53	**6.58**	2.03	15.15	**11.36**	3.81	y
0.73	2.22	1.73	0.53	4.76	0.97	0.33	
0.37	2.70	1.25	0.38	3.44	0.35	0.12	
1.16	10.95	**7.00**	2.15	10.31	**6.52**	2.19	y
0.82	1.10	2.85	0.88	3.67	0.12	0.04	
1.19	8.56	4.61	1.42	6.65	2.86	0.96	
0.95	2.62	1.33	0.41	2.07	1.72	0.58	
2.90	13.92	**9.97**	3.07	12.12	**8.33**	2.80	y
1.59	6.59	2.64	0.81	5.92	2.13	0.72	
2.13	10.07	6.12	1.88	7.66	3.87	1.30	
0.84	0.66	3.29	1.01	1.81	1.98	0.66	
0.22	4.88	0.93	0.28	3.90	0.11	0.04	
3.38	13.81	**9.86**	3.03	28.75	**24.96**	8.38	y
0.51	0.71	3.24	1.00	2.25	1.54	0.52	
0.34	2.48	1.47	0.45	5.16	1.37	0.46	
0.15	4.70	0.75	0.23	5.25	1.46	0.49	
0.50	3.62	0.33	0.10	7.21	3.42	1.15	
0.05	3.80	0.15	0.05	3.05	0.74	0.25	
0.04	2.78	1.17	0.36	2.77	1.02	0.34	
0.09	0.67	3.28	1.01	1.60	2.19	0.74	
0.29	3.42	0.53	0.16	3.82	0.03	0.01	
0.06	0.75	3.20	0.99	3.92	0.13	0.04	
0.61	0.93	3.02	0.93	3.05	0.74	0.25	
1.25	4.66	0.71	0.22	5.20	1.41	0.47	
1.48	5.25	1.30	0.40	6.45	2.66	0.89	
0.80	0.43	3.52	1.08	2.65	1.14	0.38	
0.15	4.09	0.14	0.04	3.39	0.40	0.14	
0.24	1.15	2.80	0.86	0.90	2.89	0.97	
0.56	1.32	2.63	0.81	2.17	1.62	0.54	
0.22	0.32	3.63	1.12	1.26	2.53	0.85	
1.14	0.97	2.98	0.92	3.56	0.23	0.08	
0.08	1.71	2.24	0.69	3.78	0.01	0.00	
0.80	0.32	3.63	1.12	0.95	2.84	0.95	
0.43	0.44	3.51	1.08	0.84	2.95	0.99	
0.79	5.64	1.69	0.52	4.80	1.01	0.34	
0.74	4.07	0.12	0.04	1.59	2.20	0.74	
3.41	16.88	**12.93**	3.98	17.49	**13.70**	4.60	y
1.52	9.58	5.63	1.73	8.49	4.70	1.58	
0.81	2.15	1.80	0.55	2.13	1.66	0.56	
0.77	2.87	1.08	0.33	3.13	0.66	0.22	
0.47	1.96	1.99	0.61	1.53	2.26	0.76	

0.15	3.31	0.64	0.20	3.85	0.06	0.02	
0.66	4.72	0.77	0.24	4.24	0.45	0.15	
0.73	7.98	4.03	1.24	5.40	1.61	0.54	
1.30	8.01	4.06	1.25	4.57	0.78	0.26	
0.79	1.45	2.50	0.77	2.00	1.79	0.60	
0.47	6.44	2.49	0.77	7.21	3.42	1.15	
0.26	7.39	3.44	1.06	7.19	3.40	1.14	
0.34	6.46	2.51	0.77	3.64	0.15	0.05	
0.20	2.94	1.01	0.31	3.51	0.28	0.09	
0.24	5.72	1.77	0.54	5.00	1.21	0.41	
1.03	0.81	3.14	0.97	0.44	3.35	1.12	
0.64	5.01	1.06	0.33	5.73	1.94	0.65	
0.98	1.42	2.53	0.78	3.77	0.02	0.01	
0.13	5.72	1.77	0.55	12.09	**8.30**	2.79	
0.19	5.22	1.27	0.39	4.58	0.79	0.27	
3.53	14.91	**10.96**	3.37	18.54	**14.75**	4.95	y
1.65	9.13	5.18	1.59	7.29	3.50	1.17	
1.22	5.86	1.91	0.59	9.71	5.92	1.99	
0.70	3.95	0.00	0.00	1.37	2.42	0.81	
2.83	13.36	**9.41**	2.89	9.77	5.98	2.01	y
0.04	6.12	2.17	0.67	6.76	2.97	1.00	
0.58	2.84	1.11	0.34	2.29	1.50	0.50	
0.18	9.49	5.54	1.70	2.27	1.52	0.51	
0.55	5.52	1.57	0.48	3.15	0.64	0.21	
0.68	5.25	1.30	0.40	5.32	1.53	0.51	
0.85	2.00	1.95	0.60	5.11	1.32	0.44	
0.56	6.20	2.25	0.69	11.56	**7.77**	2.61	
0.70	7.53	3.58	1.10	9.00	5.21	1.75	
0.74	1.40	2.55	0.78	0.99	2.80	0.94	
0.67	1.77	2.18	0.67	2.65	1.14	0.38	
0.43	3.17	0.78	0.24	4.13	0.34	0.11	
0.61	2.02	1.93	0.59	4.35	0.56	0.19	
0.00	4.09	0.14	0.04	5.28	1.49	0.50	
1.30	19.05	**15.10**	4.64	14.05	**10.26**	3.44	y
0.48	6.86	2.91	0.89	4.66	0.87	0.29	
0.19	4.86	0.91	0.28	2.19	1.60	0.54	
0.31	5.28	1.33	0.41	1.78	2.01	0.67	
1.20	11.25	**7.30**	2.25	6.57	2.78	0.93	
1.90	11.19	**7.24**	2.23	4.20	0.41	0.14	
5.04	25.36	**21.41**	6.59	14.75	**10.96**	3.68	y
1.12	17.36	**13.41**	4.13	10.33	**6.54**	2.19	y
0.28	1.86	2.09	0.64	1.65	2.14	0.72	
3.61	22.50	**18.55**	5.71	8.77	4.98	1.67	y
2.23	16.38	**12.43**	3.82	10.77	**6.98**	2.34	y
0.11	5.45	1.50	0.46	1.12	2.67	0.90	
0.62	4.36	0.41	0.13	1.05	2.74	0.92	
0.06	7.94	3.99	1.23	2.05	1.74	0.58	

0.46	6.66	2.71	0.83	1.81	1.98	0.67	
2.68	15.11	**11.16**	3.43	11.08	**7.29**	2.45	y
0.14	5.20	1.25	0.38	1.51	2.28	0.76	
1.02	1.15	2.80	0.86	0.34	3.45	1.16	
0.45	2.72	1.23	0.38	0.49	3.30	1.11	
0.93	2.98	0.97	0.30	1.65	2.14	0.72	
0.75	0.89	3.06	0.94	1.72	2.07	0.69	
0.74	0.81	3.14	0.97	3.45	0.34	0.11	
4.35	20.90	**16.95**	5.22	19.56	**15.77**	5.29	y
2.86	14.54	**10.59**	3.26	10.25	**6.46**	2.17	y
4.33	16.84	**12.89**	3.97	10.65	**6.86**	2.30	y
0.61	9.88	5.93	1.83	6.79	3.00	1.01	
0.41	3.32	0.63	0.19	4.65	0.86	0.29	
0.69	0.91	3.04	0.94	0.44	3.35	1.13	
3.72	16.53	**12.58**	3.87	13.51	**9.72**	3.26	y
0.19	2.08	1.87	0.57	2.15	1.64	0.55	
0.63	1.75	2.20	0.68	1.89	1.90	0.64	
0.77	0.98	2.97	0.91	1.22	2.57	0.86	
1.05	5.52	1.57	0.48	9.56	5.77	1.94	
0.72	3.09	0.86	0.26	2.39	1.40	0.47	
0.57	2.23	1.72	0.53	2.77	1.02	0.34	
0.11	3.01	0.94	0.29	2.47	1.32	0.44	
2.75	10.52	6.57	2.02	11.33	**7.54**	2.53	y
1.57	6.20	2.25	0.69	5.79	2.00	0.67	
1.14	2.50	1.45	0.45	2.96	0.83	0.28	
0.25	0.83	3.12	0.96	1.41	2.38	0.80	
0.20	1.53	2.42	0.74	1.80	1.99	0.67	
0.58	1.56	2.39	0.73	3.59	0.20	0.07	
0.13	4.32	0.37	0.11	3.99	0.20	0.07	
1.24	2.78	1.17	0.36	2.79	1.00	0.34	
0.26	8.45	4.50	1.38	1.83	1.96	0.66	
0.80	1.17	2.78	0.85	2.76	1.03	0.35	
0.57	2.97	0.98	0.30	1.31	2.48	0.83	
0.01	3.45	0.50	0.16	2.29	1.50	0.50	
0.27	4.93	0.98	0.30	8.32	4.53	1.52	
0.47	1.60	2.35	0.72	1.57	2.22	0.75	
1.23	4.26	0.31	0.09	2.72	1.07	0.36	
1.46	7.00	3.05	0.94	10.65	**6.86**	2.30	
0.29	2.15	1.80	0.55	6.48	2.69	0.90	
2.87	8.45	4.50	1.38	5.75	1.96	0.66	
0.64	2.03	1.92	0.59	3.44	0.35	0.12	
1.15	7.92	3.97	1.22	7.94	4.15	1.39	
0.03	1.23	2.72	0.84	1.37	2.42	0.81	
2.59	5.06	1.11	0.34	12.32	**8.53**	2.86	y
0.52	1.38	2.57	0.79	1.76	2.03	0.68	
0.42	1.24	2.71	0.83	0.91	2.88	0.97	
0.87	4.60	0.65	0.20	2.93	0.86	0.29	

0.64	1.51	2.44	0.75	0.56	3.23	1.08	
0.77	3.12	0.83	0.25	1.78	2.01	0.68	
1.26	8.89	4.94	1.52	12.05	**8.26**	2.77	
0.67	2.29	1.66	0.51	1.78	2.01	0.67	
0.88	2.14	1.81	0.56	1.38	2.41	0.81	
0.75	2.20	1.75	0.54	2.98	0.81	0.27	
0.00	5.06	1.11	0.34	4.38	0.59	0.20	
0.45	4.53	0.58	0.18	3.59	0.20	0.07	
0.17	3.92	0.03	0.01	1.60	2.19	0.74	
0.55	2.10	1.85	0.57	2.79	1.00	0.34	
0.31	3.41	0.54	0.17	3.31	0.48	0.16	
0.34	3.59	0.36	0.11	3.14	0.65	0.22	
1.00	3.70	0.25	0.08	2.78	1.01	0.34	
0.31	3.53	0.42	0.13	6.18	2.39	0.80	
2.67	16.19	**12.24**	3.77	5.61	1.82	0.61	y
0.12	4.84	0.89	0.27	4.04	0.25	0.08	
0.11	8.56	4.61	1.42	6.34	2.55	0.85	
0.60	4.17	0.22	0.07	1.51	2.28	0.77	
0.80	12.77	**8.82**	2.71	7.14	3.35	1.12	
0.50	3.94	0.01	0.00	2.23	1.56	0.52	
0.88	1.90	2.05	0.63	0.80	2.99	1.00	
0.10	3.34	0.61	0.19	2.10	1.69	0.57	
0.19	5.24	1.29	0.40	0.60	3.19	1.07	
0.53	6.50	2.55	0.79	1.78	2.01	0.67	
0.90	3.69	0.26	0.08	3.58	0.21	0.07	
1.14	2.57	1.38	0.43	2.08	1.71	0.57	
0.51	1.00	2.95	0.91	1.02	2.77	0.93	
2.48	12.58	**8.63**	2.65	3.92	0.13	0.04	y
0.58	10.30	6.35	1.95	4.21	0.42	0.14	
1.10	12.73	**8.78**	2.70	8.36	4.57	1.53	
1.42	12.36	**8.41**	2.59	5.04	1.25	0.42	
0.82	1.89	2.06	0.63	1.96	1.83	0.62	
1.01	1.30	2.65	0.82	3.40	0.39	0.13	
3.95	26.27	**22.32**	6.87	15.33	**11.54**	3.87	y
0.01	6.31	2.36	0.73	2.15	1.64	0.55	
0.05	4.61	0.66	0.20	3.48	0.31	0.10	
0.92	7.29	3.34	1.03	7.71	3.92	1.32	
0.91	2.82	1.13	0.35	1.17	2.62	0.88	
0.34	3.38	0.57	0.17	1.60	2.19	0.74	
	3.95	2.19		3.79	2.01		
		6.58			6.04		
		3.25			2.98		
		55.32		3411.00	42.83		
62.18		64.44					
68.48		63.57					
63.79		57.35					
64.81		**60.17**					

3.28	4.52
20.20	21.77
16.69	36.07
6.43	15.76
23.16	25.21
15.65	27.99
16.43	25.36
6.89	8.38
9.83	13.57
20.67	25.14
30.49	38.70
48.39	34.81
0.63	1.11
0.37	-0.11
5.63	3.87
6.02	4.35
1.37	1.35
3.15	2.01
24.29	37.21
34.93	25.94

					% inf	**abs dev**
50008.00	A02	M-011223- Kruppel-lik	687.00	KLF9	1.45	6.63
50008.00	A04	M-017422- BRF1 homo	2972.00	BRF1	1.22	6.86
50008.00	A05	M-009298- tenascin C	3371.00	TNC	1.88	6.20
50008.00	A06	M-006377- bromodom	10902.00	BRD8	3.07	5.01
50008.00	A07	M-012379- tumor necr	7130.00	TNFAIP6	1.80	6.28
50008.00	A08	M-003462- breast canc	675.00	BRCA2	2.89	5.19
50008.00	A09	M-016358- TNFAIP3 in	10318.00	TNIP1	1.13	6.95
50008.00	A10	M-011595- basonuclin	646.00	BNC1	3.06	5.02
50008.00	A11	M-012656- troponin C	7134.00	TNNC1	1.22	6.86
50008.00	A12	M-010318- basic helix-	8553.00	BHLHB2	1.68	6.40
50008.00	A13	M-015960- troponin I t	7135.00	TNNI1	9.75	1.67
50008.00	A14	M-011591- B-cell CLL/l	604.00	BCL6	4.54	3.54
50008.00	A15	M-008106- tenascin XB	7148.00	TNXB	4.54	3.54
50008.00	A16	M-006901- bromodom	9031.00	BAZ1B	6.68	1.40
50008.00	A17	M-006417- heat shock	7184.00	HSP90B1	3.51	4.57
50008.00	A18	M-008563- basic leucin	10538.00	BATF	4.15	3.93
50008.00	A19	M-012685- thyroid hor	9322.00	TRIP10	2.05	6.03
50008.00	A20	M-013087- BarH-like h	56033.00	BARX1	3.05	5.03
50008.00	A21	M-019053- trophinin	7216.00	TRO	2.49	5.59
50008.00	A23	M-019980- trophinin a	10024.00	TROAP	5.19	2.89
50008.00	B02	M-017537- homeobox	3213.00	HOXB3	3.52	4.56
50008.00	B04	M-011695- homeobox	3212.00	HOXB2	8.75	0.67
50008.00	B05	M-020734- BCL2-assoc	9774.00	BCLAF1	10.63	2.55
50008.00	B06	M-012226- homeobox	10481.00	HOXB13	3.90	4.18
50008.00	B07	M-011224- basic trans	690.00	BTF3L1	11.12	3.04
50008.00	B08	M-011694- homeobox	3211.00	HOXB1	8.79	0.71
50008.00	B09	M-011598- B-cell trans	694.00	BTG1	5.64	2.44
50008.00	B10	M-006337- homeobox	3205.00	HOXA9	4.15	3.93
50008.00	B11	M-012308- BTG family,	7832.00	BTG2	7.67	0.41
50008.00	B12	M-017573- homeobox	3204.00	HOXA7	7.73	0.35
50008.00	B13	M-008197- calreticulin	811.00	CALR	5.85	2.23
50008.00	B14	M-017574- homeobox	3202.00	HOXA5	5.79	2.29
50008.00	B15	M-012333- cartilage pa	8092.00	CART1	4.32	3.76
50008.00	B16	M-011693- homeobox	3201.00	HOXA4	13.15	5.07
50008.00	B17	M-011824- runt-relate	862.00	RUNX1T1	7.21	0.87
50008.00	B18	M-021416- homeobox	3199.00	HOXA2	3.76	4.32
50008.00	B19	M-010557- core-bindin	9139.00	CBFA2T2	10.02	1.94
50008.00	B20	M-011052- homeobox	3209.00	HOXA13	5.41	2.67
50008.00	B21	M-017195- core-bindin	863.00	CBFA2T3	8.90	0.82
50008.00	B23	M-011602- core-bindin	865.00	CBFB	2.96	5.12
50008.00	C02	M-011216- bagpipe ho	579.00	BAPX1	9.57	1.49
50008.00	C04	M-007750- BTB and CN	**571.00**	**BACH1**	**33.42**	**25.34**
50008.00	C05	M-020028- Usher synd	10083.00	USH1C	9.92	1.84
50008.00	C06	M-008865- activating t	11016.00	ATF7	1.45	6.63
50008.00	C07	M-013351- vascular ce	7412.00	VCAM1	9.12	1.04
50008.00	C08	M-009917- activating t	22926.00	ATF6	8.31	0.23

50008.00	C09	M-012383- villin 1	7429.00	VIL1	23.12	15.04
50008.00	C10	M-008822- activating t	22809.00	ATF5	8.55	0.47
50008.00	C11	M-017370- ezrin	7430.00	EZR	9.39	1.31
50008.00	C12	M-005125- activating t	468.00	ATF4	3.49	4.59
50008.00	C13	M-012384- pre-B lymp	7441.00	VPREB1	5.08	3.00
50008.00	C14	M-008663- activating t	467.00	ATF3	24.15	16.07
50008.00	C15	M-013409- vitronectin	7448.00	VTN	5.27	2.81
50008.00	C16	M-010045- activating t	466.00	ATF1	13.68	5.60
50008.00	C17	M-009754- von Willeb	7450.00	VWF	14.08	6.00
50008.00	C18	M-015412- AT-binding	463.00	ATBF1	6.51	1.57
50008.00	C19	M-011557- WAS prote	8936.00	WASF1	8.69	0.61
50008.00	C20	M-020460- ash1 (abse	55870.00	ASH1L	7.74	0.34
50008.00	C21	M-012301- WAS prote	10810.00	WASF3	5.86	2.22
50008.00	C23	M-010975- WAS/WAS	7456.00	WIPF1	1.87	6.21
50008.00	D02	M-012108- homeobox	3207.00	HOXA11	9.08	1.00
50008.00	D04	M-006336- homeobox	3206.00	HOXA10	18.56	10.48
50008.00	D05	M-008356- chromobo	8535.00	CBX4	10.40	2.32
50008.00	D06	M-017464- homeobox	3198.00	HOXA1	2.65	5.43
50008.00	D07	M-012631- caudal typ	1044.00	CDX1	2.28	5.80
50008.00	D08	M-020146- high-mobili	10362.00	HMG20B	12.80	4.72
50008.00	**D09**	**M-015636- caudal typ**	**1045.00**	**CDX2**	**30.40**	**22.32**
50008.00	D10	M-015454- high-mobili	10363.00	HMG20A	14.24	6.16
50008.00	**D11**	**M-010141- caudal typ**	**1046.00**	**CDX4**	**18.12**	**10.04**
50008.00	D12	M-010960- motor neu	3110.00	MNX1	14.55	6.47
50008.00	D13	M-006422- CCAAT/enh	1050.00	CEBPA	0.99	7.09
50008.00	D14	M-017163- H2.0-like h	3142.00	HLX1	9.39	1.31
50008.00	D15	M-006423- CCAAT/enh	1051.00	CEBPB	5.33	2.75
50008.00	D16	M-008953- zinc finger	3104.00	ZBTB48	10.97	2.89
50008.00	D17	M-009310- checkpoint	1112.00	CHES1	9.88	1.80
50008.00	D18	M-014345- human imr	59269.00	HIVEP3	2.04	6.04
50008.00	D19	M-016022- Cbp/p300-i	4435.00	CITED1	3.39	4.69
50008.00	D20	M-013610- HIR histone	7290.00	HIRA	4.72	3.36
50008.00	D21	M-015358- Cbp/p300-i	10370.00	CITED2	3.07	5.01
50008.00	D23	M-011008- excision re	1161.00	ERCC8	3.45	4.63
50008.00	**E02**	**M-008307- achaete-sc**	**429.00**	**ASCL1**	**23.20**	**15.12**
50008.00	E04	M-017255- aristaless r	170302.00	ARX	11.34	3.26
50008.00	E05	M-009253- MLX intera	51085.00	MLXIPL	3.34	4.74
50008.00	E06	M-013992- aristaless-li	60529.00	ALX4	8.58	0.50
50008.00	E07	M-017558- zinc finger,	64393.00	ZMAT3	13.53	5.45
50008.00	E08	M-020156- aristaless-li	257.00	ALX3	2.02	6.06
50008.00	E09	M-010555- WNT1 indu	8840.00	WISP1	6.50	1.58
50008.00	**E10**	**M-012305- TFIIA-alph**	**11036.00**	**ALF**	**24.80**	**16.72**
50008.00	E11	M-010554- WNT1 indu	8839.00	WISP2	4.06	4.02
50008.00	E12	M-020276- AF4/FMR2	27125.00	AFF4	10.10	2.02
50008.00	E13	M-005067- xeroderma	7507.00	XPA	5.38	2.70
50008.00	E14	M-013683- activator o	29777.00	ABT1	2.79	5.29
50008.00	E15	M-009394- X-ray repai	7515.00	XRCC1	6.02	2.06

50008.00	E16	M-004373- apoptosis a	26574.00	AATF	1.98	6.10
50008.00	E17	M-012200- Yes-associa	10413.00	YAP1	8.24	0.16
50008.00	E18	M-006914- zinc finger	9839.00	ZEB2	10.18	2.10
50008.00	E19	M-017302- tyrosine 3-	7531.00	YWHAE	6.52	1.56
50008.00	E20	M-003935- vav 1 onco	7409.00	VAV1	1.39	6.69
50008.00	E21	M-003332- tyrosine 3-	7534.00	YWHAZ	5.03	3.05
50008.00	E23	M-011797- zonadhesin	7455.00	ZAN	12.60	4.52
50008.00	F02	M-006532- hypermeth	3090.00	HIC1	9.02	0.94
50008.00	F04	M-011756- hematopoi	3087.00	HHEX	5.22	2.86
50008.00	F05	M-020319- CCR4-NOT	4849.00	CNOT3	11.28	3.20
50008.00	F06	M-008690- hairy/enha	26508.00	HEYL	18.59	10.51
50008.00	F07	M-018791- CCR4-NOT	9337.00	CNOT8	12.42	4.34
50008.00	**F08**	**M-008223- hairy/enha**	**23493.00**	**HEY2**	**28.13**	**20.05**
50008.00	F09	M-021441- Kruppel-lik	1316.00	KLF6	11.92	3.84
50008.00	F10	M-008709- hairy/enha	23462.00	HEY1	5.28	2.80
50008.00	F11	M-003619- cAMP resp	1385.00	CREB1	1.90	6.18
50008.00	F12	M-019521- HESX home	8820.00	HESX1	15.22	7.14
50008.00	F13	M-008436- cAMP resp	9586.00	CREB5	7.95	0.13
50008.00	F14	M-019953- host cell fa	3054.00	HCFC1	3.78	4.30
50008.00	F15	M-011242- cAMP resp	1389.00	CREBL2	6.87	1.21
50008.00	F16	M-020415- host cell fa	29915.00	HCFC2	4.86	3.22
50008.00	F17	M-011534- cellular rep	8804.00	CREG1	5.08	3.00
50008.00	F18	M-009812- heart and r	9421.00	HAND1	9.87	1.79
50008.00	F19	M-009528- cAMP resp	1390.00	CREM	7.28	0.80
50008.00	F20	M-020036- general tra	9330.00	GTF3C3	9.33	1.25
50008.00	F21	M-011112- cone-rod h	1406.00	CRX	14.01	5.93
50008.00	F23	M-015793- cold shock	8531.00	CSDA	2.20	5.88
50008.00	G02	M-006434- twist homo	7291.00	TWIST1	5.72	2.36
50008.00	G03	M-003290- polo-like ki	5347.00	PLK1 SMARTpool	9.94	1.86
50008.00	G04	M-004308- pituitary tu	9232.00	PTTG1	10.61	2.53
50008.00	G05	M-013938- CREB/ATF b	58487.00	CREBZF	4.81	3.27
50008.00	G06	M-004158- glucocortic	2909.00	GRLF1	6.30	1.78
50008.00	G07	M-015308- zinc finger	7541.00	ZFP161	7.90	0.18
50008.00	G08	M-020653- eukaryotic	8892.00	EIF2B2	5.64	2.44
50008.00	G09	M-007017- zinc finger	55734.00	ZFP64	5.09	2.99
50008.00	G10	M-006444- Wiskott-Al	8976.00	WASL	10.53	2.45
50008.00	G11	M-012405- zinc finger	23414.00	ZFPM2	3.44	4.64
50008.00	G12	M-005199- vav 2 onco	7410.00	VAV2	8.96	0.88
50008.00	G13	M-017505- Zic family n	7546.00	ZIC2	12.37	4.29
50008.00	G14	M-003029- tuberous sc	7249.00	TSC2	8.64	0.56
50008.00	G15	M-011799- Zic family n	7547.00	ZIC3	4.04	4.04
50008.00	G16	M-013804- CDC42 sma	56882.00	CDC42SE1	10.49	2.41
50008.00	G17	M-006574- zinc finger	7556.00	ZNF10	14.81	6.73
50008.00	G18	M-005194- son of seve	6654.00	SOS1	2.36	5.72
50008.00	G19	M-019770- zinc finger	7678.00	ZNF124	10.89	2.81
50008.00	G20	M-017524- signal-indu	6494.00	SIPA1	8.97	0.89
50008.00	G21	M-019625- zinc finger	7705.00	ZNF146	15.95	7.87

50008.00	G23	M-012659- zinc finger	7709.00	ZBTB17	14.98	6.90
50008.00	H02	M-012635- general tra	2971.00	GTF3A	8.80	0.72
50008.00	H03	M-003290- polo-like ki	5347.00	PLK1 SMARTpool	24.35	16.27
50008.00	H04	M-013262- GTF2I repe	9569.00	GTF2IRD1	4.82	3.26
50008.00	H05	M-017332- **Kv channel**	**30818.00**	**KCNIP3**	**21.16**	**13.08**
50008.00	H06	M-013638- general tra	2969.00	GTF2I	11.02	2.94
50008.00	H07	M-020165- CCCTC-binc	10664.00	CTCF	6.96	1.12
50008.00	H08	M-010922- general tra	2958.00	GTF2A2	13.18	5.10
50008.00	H09	M-011635- cut-like 1, (	1523.00	CUTL1	15.16	7.08
50008.00	H10	M-010910- general tra	2957.00	GTF2A1	3.15	4.93
50008.00	H11	M-017689- **D site of al**	**1628.00**	**DBP**	**22.42**	**14.34**
50008.00	H12	M-012044- goosecoid-	2928.00	GSCL	2.22	5.86
50008.00	H13	M-004819- DNA-dama	1649.00	DDIT3	8.36	0.28
50008.00	H14	M-012284- glucocortic	10691.00	GMEB1	4.14	3.94
50008.00	H15	M-003881- DEK oncog	7913.00	DEK	8.60	0.52
50008.00	H16	M-011043- GLI-Kruppe	2737.00	GLI3	4.10	3.98
50008.00	H17	M-011846- distal-less l	1746.00	DLX2	4.96	3.12
50008.00	H18	M-006468- GLI-Kruppe	2736.00	GLI2	16.50	8.42
50008.00	H19	M-012030- distal-less l	1747.00	DLX3	7.59	0.49
50008.00	H20	**M-003896- glioma-ass**	**2735.00**	**GLI1**	**26.76**	**18.68**
50008.00	H21	**M-011640- distal-less l**	**1748.00**	**DLX4**	**21.45**	**13.37**
50008.00	H23	M-012031- distal-less l	1749.00	DLX5	8.81	0.73
50008.00	I02	**M-019714- secretogra**	**6447.00**	**SCG5**	**35.89**	**27.81**
50008.00	I04	M-005180- stratifin	2810.00	SFN	8.51	0.43
50008.00	I05	M-013706- zinc finger	90338.00	ZNF160	18.31	10.23
50008.00	I06	M-019586- SET translo	6418.00	SET	6.39	1.69
50008.00	I07	**M-021348- zinc finger,**	**7750.00**	**ZMYM2**	**31.17**	**23.09**
50008.00	I08	M-011230- serpin pept	871.00	SERPINH1	17.50	9.42
50008.00	I09	**M-021469- zinc finger**	**7752.00**	**ZNF200**	**37.98**	**29.90**
50008.00	I10	M-012564- serpin pept	5345.00	SERPINF2	4.99	3.09
50008.00	I11	M-012774- zinc finger	7570.00	ZNF22	13.16	5.08
50008.00	I12	M-012737- serpin pept	5270.00	SERPINE2	13.00	4.92
50008.00	I13	**M-015360- zinc finger**	**10472.00**	**ZNF238**	**26.62**	**18.54**
50008.00	I14	M-009540- serpin pept	3053.00	SERPIND1	11.84	3.76
50008.00	I15	M-013539- POZ (BTB) a	23598.00	PATZ1	15.39	7.31
50008.00	I16	M-012535- serpin pept	462.00	SERPINC1	21.04	12.96
50008.00	I17	M-020972- zinc finger	51711.00	ZNF325~withdrawn	17.69	9.61
50008.00	I18	M-015400- serpin pept	5272.00	SERPINB9	10.13	2.05
50008.00	I19	M-014928- zinc finger	84671.00	ZNF347	13.70	5.62
50008.00	I20	M-017707- serpin pept	5269.00	SERPINB6	11.36	3.28
50008.00	I21	**M-017515- zinc finger**	**########**	**ZNF384**	**22.04**	**13.96**
50008.00	I23	M-019775- zinc finger	7594.00	ZNF43	16.78	8.70
50008.00	J02	M-019828- growth fact	8328.00	GFI1B	7.59	0.49
50008.00	J04	M-019947- growth fact	2672.00	GFI1	6.02	2.06
50008.00	J05	M-028911- distal-less l	1750.00	DLX6	12.75	4.67
50008.00	J06	**M-011491- glial cells n**	**8521.00**	**GCM1**	**19.97**	**11.89**
50008.00	J07	**M-012668- doublesex**	**1761.00**	**DMRT1**	**21.97**	**13.89**

50008.00	J08	M-020172- gastrulatio	2637.00	GBX2	19.56	11.48
50008.00	J09	M-015339- doublesex	10655.00	DMRT2	16.64	8.56
50008.00	J10	M-010324- GATA bindi	140628.00	GATA5	10.76	2.68
50008.00	J11	M-031988- doublesex	58524.00	DMRT3	1.81	6.27
50008.00	J12	M-008244- GATA bindi	2626.00	GATA4	4.97	3.11
50008.00	J13	M-003866- cyclin D bir	9988.00	DMTF1	3.43	4.65
50008.00	J14	M-003781- GATA bindi	2625.00	GATA3	9.23	1.15
50008.00	J15	**M-009908- down-regu**	**1810.00**	**DR1**	**27.12**	**19.04**
50008.00	J16	M-009024- GATA bindi	2624.00	GATA2	5.32	2.76
50008.00	J17	M-012032- AT rich inte	1820.00	ARID3A	11.56	3.48
50008.00	J18	M-009610- GATA bindi	2623.00	GATA1	12.25	4.17
50008.00	J19	M-019955- double hor	26584.00	DUX1	4.56	3.52
50008.00	J20	M-011662- GA binding	2551.00	GABPA	5.85	2.23
50008.00	J21	M-019945- double hor	26583.00	DUX2	2.82	5.26
50008.00	J23	M-019906- double hor	26582.00	DUX3	1.28	6.80
50008.00	K02	M-012549- serpin pept	6906.00	SERPINA7	5.08	3.00
50008.00	K04	M-011603- serpin pept	866.00	SERPINA6	6.95	1.13
50008.00	K05	M-020998- zinc finger	51710.00	ZNF44	15.67	7.59
50008.00	K06	M-008847- serpin pept	5265.00	SERPINA1	5.36	2.72
50008.00	K07	**M-018540- zinc finger**	**10773.00**	**ZBTB6**	**29.43**	**21.35**
50008.00	K08	M-011105- S-antigen;	6295.00	SAG	15.04	6.96
50008.00	K09	M-031884- zinc finger	199692.00	ZNF627	17.38	9.30
50008.00	K10	M-012259- S100 calciu	6285.00	S100B	10.43	2.35
50008.00	K11	M-006579- zinc finger	7625.00	ZNF74	16.48	8.40
50008.00	K12	M-019891- Ras and Ra	9610.00	RIN1	4.60	3.48
50008.00	K13	M-015952- zinc finger	7629.00	ZNF76	13.87	5.79
50008.00	K14	M-009290- replication	5981.00	RFC1	12.46	4.38
50008.00	K15	M-019777- zinc finger	7637.00	ZNF84	14.83	6.75
50008.00	K16	M-013425- RAS guanyl	115727.00	RASGRP4	2.54	5.54
50008.00	K17	M-019982- zinc finger	10009.00	ZBTB33	5.15	2.93
50008.00	K18	M-009365- RAS guanyl	10235.00	RASGRP2	6.25	1.83
50008.00	K19	**M-019092- IKAROS far**	**10320.00**	**IKZF1**	**23.32**	**15.24**
50008.00	K20	M-008928- RAS guanyl	10125.00	RASGRP1	4.07	4.01
50008.00	K21	M-006946- IKAROS fan	22807.00	IKZF2	1.90	6.18
50008.00	K23	M-003948- ZW10, kine	9183.00	ZW10	3.58	4.50
50008.00	L02	M-009307- forkhead b	50943.00	FOXP3	11.82	3.74
50008.00	L04	M-010359- forkhead b	93986.00	FOXP2	7.42	0.66
50008.00	L05	M-003259- E2F transcr	1869.00	E2F1	2.83	5.25
50008.00	L06	M-004256- forkhead b	27086.00	FOXP1	16.70	8.62
50008.00	L07	M-011847- E4F transcr	1877.00	E4F1	2.33	5.75
50008.00	L08	M-003007- forkhead b	2309.00	FOXO3A	10.62	2.54
50008.00	L09	M-009697- endothelial	8721.00	EDF1	2.54	5.54
50008.00	L10	**M-003006- forkhead b**	**2308.00**	**FOXO1A**	**24.67**	**16.59**
50008.00	L11	M-006526- early growt	1958.00	EGR1	11.71	3.63
50008.00	L12	M-009733- forkhead b	8456.00	FOXN1	11.19	3.11
50008.00	L13	M-006528- early growt	1960.00	EGR3	5.04	3.04
50008.00	L14	M-009762- forkhead b	2305.00	FOXM1	7.64	0.44

50008.00	L15	M-006529- early growt	1961.00	EGR4	4.99	3.09
50008.00	L16	M-009075- forkhead b	668.00	FOXL2	18.77	10.69
50008.00	L17	**M-012421- ets homolc**	**26298.00**	**EHF**	**20.75**	**12.67**
50008.00	L18	M-008986- forkhead b	2300.00	FOXL1	5.83	2.25
50008.00	L19	M-012669- E74-like fac	1997.00	ELF1	4.41	3.67
50008.00	L20	M-010314- forkhead b	2302.00	FOXJ1	7.04	1.04
50008.00	L21	M-012754- E74-like fac	1998.00	ELF2	6.83	1.25
50008.00	L23	M-016080- E74-like fac	1999.00	ELF3	5.61	2.47
50008.00	M02	M-009771- RAS proteir	8437.00	RASAL1	10.96	2.88
50008.00	M04	M-003694- prosaposin	5660.00	PSAP	13.58	5.50
50008.00	M05	M-016734- zyxin	7791.00	ZYX	5.80	2.28
50008.00	M06	M-030847- protein kin	5575.00	PRKAR1B	9.71	1.63
50008.00	M07	M-010742- annexin A4	307.00	ANXA4	8.42	0.34
50008.00	M08	M-017376- protein phc	5523.00	PPP2R3A	9.29	1.21
50008.00	M09	M-011209- annexin A5	308.00	ANXA5	14.51	6.43
50008.00	M10	M-014932- protein phc	84687.00	PPP1R9B	9.11	1.03
50008.00	M11	M-003456- apoptotic p	317.00	APAF1	16.15	8.07
50008.00	M12	M-008593- Rap guanin	51735.00	RAPGEF6	6.78	1.30
50008.00	M13	M-004179- amyloid be	334.00	APLP2	5.84	2.24
50008.00	M14	M-015092- NLR family,	91662.00	NLRP12	13.00	4.92
50008.00	M15	M-003731- amyloid be	351.00	APP	9.67	1.59
50008.00	M16	M-020202- kininogen 1	3827.00	KNG1	6.81	1.27
50008.00	M17	M-016253- Rho GDP di	396.00	ARHGDIA	5.01	3.07
50008.00	M18	**M-008365- intersectin**	**6453.00**	**ITSN1**	**30.54**	**22.46**
50008.00	M19	M-009883- rho/rac gua	9181.00	ARHGEF2	6.32	1.76
50008.00	M20	**M-006457- IQ motif cc**	**10788.00**	**IQGAP2**	**16.18**	8.10
50008.00	M21	M-008804- ras homolc	399.00	RHOH	9.09	1.01
50008.00	M23	M-011585- ADP-ribosy	402.00	ARL2	2.80	5.28
50008.00	N02	**M-008802- forkhead b**	**2299.00**	**FOXI1**	**23.15**	**15.07**
50008.00	N04	M-008636- forkhead b	8928.00	FOXH1	3.97	4.11
50008.00	N05	**M-020177- E74-like fac**	**2000.00**	**ELF4**	**48.93**	**40.85**
50008.00	N06	M-019124- forkhead b	2290.00	FOXG1B	11.99	3.91
50008.00	N07	M-011265- E74-like fac	2001.00	ELF5	19.17	11.09
50008.00	N08	M-008261- forkhead b	2295.00	FOXF2	4.17	3.91
50008.00	N09	M-003885- ELK1, mem	2002.00	ELK1	3.89	4.19
50008.00	N10	M-009628- forkhead b	2294.00	FOXF1	4.16	3.92
50008.00	N11	M-010320- ELK3, ETS-c	2004.00	ELK3	11.04	2.96
50008.00	N12	M-009139- forkhead b	2301.00	FOXE3	4.75	3.33
50008.00	N13	M-010315- ELK4, ETS-c	2005.00	ELK4	1.26	6.82
50008.00	N14	M-011863- forkhead b	2304.00	FOXE1	8.43	0.35
50008.00	N15	M-022717- empty spira	2016.00	EMX1	4.43	3.65
50008.00	N16	M-026142- forkhead b	2298.00	FOXD4	8.84	0.76
50008.00	N17	M-017904- empty spira	2018.00	EMX2	7.51	0.57
50008.00	N18	M-009152- forkhead b	27022.00	FOXD3	1.97	6.11
50008.00	N19	M-011266- engrailed h	2019.00	EN1	2.94	5.14
50008.00	N20	M-009133- forkhead b	2306.00	FOXD2	2.86	5.22
50008.00	N21	M-011267- engrailed h	2020.00	EN2	3.16	4.92

50008.00	N23	M-017483- eomesoder	8320.00	EOMES	6.48	1.60
50008.00	O02	M-004694- IQ motif co	8826.00	IQGAP1	7.13	0.95
50008.00	O04	M-004777- insulin-like	3486.00	IGFBP3	16.92	8.84
50008.00	O05	M-004378- PYD and CA	29108.00	PYCARD	9.58	1.50
50008.00	**O06**	**M-005187- heat shock**	**3326.00**	**HSP90AB1**	**35.91**	**27.83**
50008.00	**O07**	**M-003459- baculoviral**	**332.00**	**BIRC5**	**29.28**	**21.20**
50008.00	**O08**	**M-005186- heat shock**	**3320.00**	**HSP90AA1**	**32.52**	**24.44**
50008.00	O09	M-016223- regulator o	1104.00	RCC1	12.32	4.24
50008.00	O10	M-008852- heat shock	3316.00	HSPB2	5.81	2.27
50008.00	O11	M-004133- regulator o	1102.00	RCBTB2	16.74	8.66
50008.00	O12	M-013420- histidine-ri	3273.00	HRG	8.08	0.00
50008.00	O13	M-011544- developme	8853.00	DDEF2	12.71	4.63
50008.00	O14	M-015131- guanylate c	2979.00	GUCA1B	6.35	1.73
50008.00	O15	M-008713- deleted in l	10395.00	DLC1	14.20	6.12
50008.00	**O16**	**M-006840- Rap guanir**	**2889.00**	**RAPGEF1**	**27.87**	**19.79**
50008.00	O17	M-008519- FERM, Rho	10160.00	FARP1	8.11	0.03
50008.00	O18	M-008239- Rap guanin	9771.00	RAPGEF5	11.51	3.43
50008.00	O19	M-009612- FYVE, RhoG	2245.00	FGD1	6.58	1.50
50008.00	**O20**	**M-011283- glucokinas**	**2646.00**	**GCKR**	**24.45**	**16.37**
50008.00	O21	M-012803- RAB GTPas	23637.00	RABGAP1	6.49	1.59
50008.00	O23	M-011108- survival of	6606.00	SMN1	3.19	4.89
50008.00	P02	M-011862- forkhead b	2297.00	FOXD1	4.14	3.94
50008.00	P04	M-008987- forkhead b	2303.00	FOXC2	2.00	6.08
50008.00	P05	M-009674- Ets2 repres	2077.00	ERF	6.36	1.72
50008.00	P06	M-009318- forkhead b	2296.00	FOXC1	8.49	0.41
50008.00	P07	M-003887- v-ets erythr	2113.00	ETS1	7.10	0.98
50008.00	P08	M-008906- forkhead b	27023.00	FOXB1	2.86	5.22
50008.00	P09	M-003888- v-ets erythr	2114.00	ETS2	6.58	1.50
50008.00	P10	M-008863- forkhead b	3171.00	FOXA3	3.48	4.60
50008.00	**P11**	**M-010509- ets variant**	**2117.00**	**ETV3**	**28.66**	**20.58**
50008.00	P12	M-010089- forkhead b	3170.00	FOXA2	5.02	3.06
50008.00	P13	M-004207- ets variant	2118.00	ETV4	4.57	3.51
50008.00	P14	M-010319- forkhead b	3169.00	FOXA1	8.58	0.50
50008.00	P15	M-010510- ets variant	2120.00	ETV6	10.78	2.70
50008.00	P16	M-004110- FOS-like an	2355.00	FOSL2	4.96	3.12
50008.00	P17	M-017938- ets variant	51513.00	ETV7	10.99	2.91
50008.00	P18	M-004341- FOS-like an	8061.00	FOSL1	13.09	5.01
50008.00	P19	M-011652- even-skipp	2128.00	EVX1	4.06	4.02
50008.00	P20	M-003265- v-fos FBJ m	2353.00	FOS	3.52	4.56
50008.00	P21	M-009350- forkhead b	55810.00	FOXJ2	4.67	3.41
50008.00	P23	M-009029- forkhead-li	2307.00	FKHL18	4.87	3.21
						mdn
						3MAD
						MADc
50008.00	C22				41.03	
50008.00	D22				52.91	

50008.00	E22			55.64
50008.00	F22			46.12
				48.93
				5.73
50008.00	I03	D-001206-	siControl non-targetin	10.67
50008.00	J03	D-001206-	siControl non-targeting siRNA #2	7.46
				9.06
				2.27

50008	G22	Human3 P	RNAi
50008	H22	Human3 P	RNAi
50008	I22	Human3 P	RNAi
50008	J22	Human3 P	RNAi

50008	K03	Human3 P	RNAi	D-001600-	siGLO RISC-free siRNA
50008	L03	Human3 P	RNAi	D-001600-	siGLO RISC-free siRNA

robust Z	% inf	abs dev	robust Z	% inf	abs dev	robust Z	
-1.143232	4.79	0.60	0.17559	2.43	3.83	-0.83	
-1.182096	1.62	2.57	-0.763308	6.51	0.25	0.05	
-1.069075	1.18	3.01	-0.89252	4.99	1.27	-0.28	
-0.863423	4.44	0.25	0.072084	5.04	1.22	-0.27	
-1.082961	1.49	2.70	-0.80086	3.69	2.57	-0.56	
-0.894679	6.33	2.14	0.633651	5.87	0.39	-0.08	
-1.198156	4.91	0.72	0.212431	7.32	1.06	0.23	
-0.865596	1.89	2.30	-0.68148	9.32	3.06	0.66	
-1.183459	0.57	3.62	-1.074039	2.48	3.78	-0.82	
-1.10354	1.78	2.41	-0.715331	3.85	2.41	-0.52	
0.287917	6.93	2.74	0.811403	7.35	1.09	0.24	
-0.61092	3.57	0.62	-0.183793	6.26	0.00	0.00	
-0.610144	2.82	1.37	-0.408071	4.71	1.55	-0.34	
-0.240635	2.05	2.14	-0.634599	7.01	0.75	0.16	
-0.787248	1.17	3.02	-0.89714	2.09	4.17	-0.91	
-0.677125	1.95	2.24	-0.663563	3.06	3.20	-0.70	
-1.039544	0.83	3.36	-0.99679	3.27	2.99	-0.65	
-0.867683	1.18	3.01	-0.892372	3.03	3.23	-0.70	
-0.964352	1.41	2.78	-0.824641	4.06	2.20	-0.48	
-0.498002	1.67	2.52	-0.748204	4.62	1.64	-0.36	
-0.78535	6.25	2.06	0.607768	3.31	2.95	-0.64	
0.115332	6.02	1.83	0.539119	3.13	3.13	-0.68	
0.440768	5.92	1.73	0.511014	5.53	0.73	-0.16	
-0.721163	1.29	2.90	-0.859972	2.42	3.84	-0.83	
0.525119	11.12	6.93	2.051223	8.69	2.43	0.53	
0.123233	8.38	4.19	1.239612	4.22	2.04	-0.44	
-0.42062	2.48	1.71	-0.506957	1.20	5.06	-1.10	
-0.67678	1.75	2.44	-0.723949	3.12	3.14	-0.68	
-0.069431	2.94	1.25	-0.370963	3.82	2.44	-0.53	
-0.060581	2.88	1.31	-0.388258	6.51	0.25	0.05	
-0.383584	2.60	1.59	-0.473728	4.95	1.31	-0.29	
-0.394555	2.30	1.89	-0.561686	5.36	0.90	-0.20	
-0.648697	1.87	2.32	-0.688085	4.83	1.44	-0.31	
0.875118	10.23	6.04	1.788534	10.96	4.70	1.02	
-0.148935	2.27	1.92	-0.569504	5.35	0.91	-0.20	
-0.744019	1.42	2.77	-0.822065	3.61	2.65	-0.58	
0.335026	1.57	2.62	-0.776042	7.94	1.68	0.36	
-0.460174	3.90	0.29	-0.087958	3.33	2.93	-0.64	
0.141742	3.98	0.21	-0.062637	9.86	3.60	0.78	
-0.883105	0.83	3.36	-0.995102	2.62	3.64	-0.79	
0.256798	3.76	0.43	-0.129834	2.77	3.49	-0.76	
4.372003	**16.52**	12.33	3.651047	14.29	8.03	1.74	y
0.318294	4.54	0.35	0.102677	2.29	3.97	-0.86	
-1.14337	1.39	2.80	-0.831186	2.41	3.85	-0.84	
0.180537	7.49	3.30	0.975058	6.20	0.06	-0.01	
0.03945	3.83	0.36	-0.107711	3.75	2.51	-0.55	

2.594753	9.21	5.02	1.485835	9.85	3.59	0.78	
0.080971	1.30	2.89	-0.858669	3.67	2.59	-0.56	
0.22668	4.21	0.02	0.003465	10.10	3.84	0.83	
-0.790473	1.26	2.93	-0.86865	4.11	2.15	-0.47	
-0.51746	2.47	1.72	-0.511429	4.01	2.25	-0.49	
2.772082	10.08	5.89	1.742334	12.83	6.57	1.43	
-0.48384	2.77	1.42	-0.422553	3.11	3.15	-0.69	
0.96568	3.61	0.58	-0.173546	9.38	3.12	0.68	
1.034852	3.20	0.99	-0.293963	7.17	0.91	0.20	
-0.271047	2.51	1.68	-0.499257	4.63	1.63	-0.36	
0.106259	3.04	1.15	-0.341229	2.78	3.48	-0.76	
-0.058753	2.24	1.95	-0.579218	6.74	0.48	0.10	
-0.381877	1.64	2.55	-0.755252	3.02	3.24	-0.70	
-1.070748	0.96	3.23	-0.95677	1.55	4.71	-1.03	
0.17355	5.65	1.46	0.431023	3.16	3.10	-0.67	
1.808334	16.74	**12.55**	3.715609	11.27	5.01	1.09	
0.400403	8.09	3.90	1.152662	9.22	2.96	0.64	
-0.93689	3.22	0.97	-0.287329	3.29	2.97	-0.65	
-1.000266	1.89	2.30	-0.681569	1.52	4.74	-1.03	
0.814054	13.86	**9.67**	2.862389	10.48	4.22	0.92	
3.850196	**19.22**	**15.03**	4.448887	**25.68**	**19.42**	4.22	y
1.062796	6.39	2.20	0.651006	10.30	4.04	0.88	
1.73209	**13.68**	**9.49**	2.808489	**18.42**	**12.16**	2.64	y
1.116616	6.00	1.81	0.535565	11.03	4.77	1.04	
-1.223118	1.91	2.28	-0.677097	2.76	3.50	-0.76	
0.226576	2.79	1.40	-0.416955	10.56	4.30	0.93	
-0.473784	3.25	0.94	-0.279955	4.09	2.17	-0.47	
0.499072	1.84	2.35	-0.696436	6.37	0.11	0.02	
0.310773	5.07	0.88	0.260083	12.40	6.14	1.33	
-1.041493	2.92	1.27	-0.378307	6.00	0.26	-0.06	
-0.809017	1.50	2.69	-0.797513	8.56	2.30	0.50	
-0.579749	2.10	2.09	-0.620058	7.05	0.79	0.17	
-0.864303	1.06	3.13	-0.928147	3.02	3.24	-0.70	
-0.797373	1.44	2.75	-0.817149	5.33	0.93	-0.20	
2.608036	**15.12**	**10.93**	3.235543	9.22	2.96	0.64	y
0.563414	6.42	2.23	0.660098	5.18	1.08	-0.23	
-0.817417	3.16	1.03	-0.307793	2.70	3.56	-0.77	
0.086887	8.31	4.12	1.217934	3.13	3.13	-0.68	
0.941012	4.67	0.48	0.140436	5.45	0.81	-0.18	
-1.045374	1.37	2.82	-0.836132	2.18	4.08	-0.89	
-0.271926	5.23	1.04	0.306875	6.23	0.03	-0.01	
2.885068	**12.04**	**7.85**	2.3225	11.56	5.30	1.15	y
-0.692443	1.21	2.98	-0.884701	1.57	4.69	-1.02	
0.348481	6.35	2.16	0.638893	7.21	0.95	0.21	
-0.465883	3.69	0.50	-0.148196	4.65	1.61	-0.35	
-0.911791	2.68	1.51	-0.447815	4.29	1.97	-0.43	
-0.354501	1.55	2.64	-0.781965	5.01	1.25	-0.27	

-1.051998	0.42	3.77	-1.119167	1.98	4.28	-0.93	
0.028773	5.29	1.10	0.324022	7.26	1.00	0.22	
0.362626	6.78	2.59	0.764788	15.55	9.29	2.02	
-0.267752	2.84	1.35	-0.40197	5.36	0.90	-0.20	
-1.15322	0.60	3.59	-1.066025	2.43	3.83	-0.83	
-0.525878	2.38	1.81	-0.53829	4.62	1.64	-0.36	
0.780589	2.81	1.38	-0.410173	9.30	3.04	0.66	
0.163408	3.98	0.21	-0.063851	4.85	1.41	-0.31	
-0.492207	2.17	2.02	-0.599001	5.33	0.93	-0.20	
0.552719	3.20	0.99	-0.295828	4.86	1.40	-0.31	
1.813854	5.13	0.94	0.278	5.68	0.58	-0.13	
0.748677	7.16	2.97	0.879341	4.33	1.93	-0.42	
3.458797	**25.11**	**20.92**	6.194419	**27.77**	**21.51**	4.67	y
0.663635	9.48	5.29	1.564671	11.21	4.95	1.08	
-0.482443	5.46	1.27	0.374931	4.94	1.32	-0.29	
-1.065004	3.86	0.33	-0.098471	2.09	4.17	-0.91	
1.2315	8.44	4.25	1.256819	12.62	6.36	1.38	
-0.022304	2.67	1.52	-0.450835	7.63	1.37	0.30	
-0.741156	1.70	2.49	-0.73926	1.13	5.13	-1.11	
-0.207619	4.33	0.14	0.038678	5.45	0.81	-0.18	
-0.555186	1.99	2.20	-0.654234	9.20	2.94	0.64	
-0.516494	3.62	0.57	-0.169963	6.34	0.08	0.02	
0.309082	11.20	**7.01**	2.074915	14.15	7.89	1.71	
-0.137809	2.23	1.96	-0.580729	9.83	3.57	0.78	
0.216434	3.30	0.89	-0.264703	8.95	2.69	0.58	
1.024157	4.04	0.15	-0.046348	14.37	8.11	1.76	
-1.013565	0.77	3.42	-1.013848	2.84	3.42	-0.74	
-0.406923	3.17	1.02	-0.30415	2.34	3.92	-0.85	
0.322227	15.33	**11.14**	3.297143	3.78	2.48	-0.54	
0.437145	5.66	1.47	0.434636	2.32	3.94	-0.86	
-0.563914	3.95	0.24	-0.071817	4.24	2.02	-0.44	
-0.307081	6.55	2.36	0.698598	3.14	3.12	-0.68	
-0.030774	9.91	5.72	1.693735	5.28	0.98	-0.21	
-0.420741	4.39	0.20	0.05775	2.43	3.83	-0.83	
-0.515201	5.94	1.75	0.517766	10.17	3.91	0.85	
0.42231	8.42	4.23	1.250718	7.70	1.44	0.31	
-0.799926	2.54	1.65	-0.491231	3.65	2.61	-0.57	
0.151781	5.50	1.31	0.3866	13.34	7.08	1.54	
0.740397	9.15	4.96	1.467355	6.56	0.30	0.06	
0.096789	4.62	0.43	0.127317	10.16	3.90	0.85	
-0.695961	5.44	1.25	0.367942	6.03	0.23	-0.05	
0.416445	5.79	1.60	0.471803	12.35	6.09	1.32	
1.161638	6.49	2.30	0.680918	16.39	**10.13**	2.20	
-0.986897	2.17	2.02	-0.598735	7.99	1.73	0.38	
0.48441	3.70	0.49	-0.147544	11.95	5.69	1.24	
0.153213	3.01	1.18	-0.350943	21.94	**15.68**	3.41	
1.358458	7.97	3.78	1.118041	25.08	**18.82**	4.09	

1.190272	4.72	0.52	0.154059	18.01	**11.75**	2.55	
0.125475	11.18	**6.99**	2.069584	3.04	3.22	-0.70	
2.806754	8.82	4.63	1.370809	6.34	0.08	0.02	
-0.562534	4.00	0.19	-0.056329	2.41	3.85	-0.84	
2.257347	**13.27**	**9.08**	2.686177	17.51	**11.25**	2.44	y
0.508042	4.39	0.20	0.056536	4.15	2.11	-0.46	
-0.193284	1.62	2.57	-0.762567	1.17	5.09	-1.11	
0.879603	8.49	4.30	1.270709	10.23	3.97	0.86	
1.222012	5.35	1.16	0.34268	12.12	5.86	1.27	
-0.849606	2.05	2.14	-0.635488	4.02	2.24	-0.49	
2.473487	**13.45**	**9.26**	2.739781	15.75	**9.49**	2.06	y
-1.010857	5.19	1.00	0.294821	6.27	0.01	0.00	
0.048041	3.72	0.47	-0.139666	6.85	0.59	0.13	
-0.679729	2.23	1.96	-0.580906	3.60	2.66	-0.58	
0.089527	3.71	0.48	-0.143901	6.45	0.19	0.04	
-0.685681	2.39	1.80	-0.535743	1.90	4.36	-0.95	
-0.53747	2.50	1.69	-0.501922	4.48	1.78	-0.39	
1.45316	3.01	1.18	-0.349995	11.65	5.39	1.17	
-0.083265	4.23	0.04	0.00921	7.29	1.03	0.22	
3.222302	10.33	6.14	1.817261	**38.90**	**32.64**	7.10	y
2.307371	3.79	0.40	-0.119143	**25.22**	**18.96**	4.12	y
0.127217	2.02	2.17	-0.644579	21.27	**15.01**	3.26	
4.797556	**32.41**	**28.22**	8.355752	**19.15**	**12.89**	2.80	y
0.074329	6.75	2.56	0.75617	4.79	1.47	-0.32	
1.764864	18.07	**13.88**	4.10979	6.79	0.53	0.11	
-0.290953	4.27	0.08	0.021205	4.54	1.72	-0.37	
3.983537	**19.99**	**15.80**	4.676925	**27.37**	**21.11**	4.59	y
1.624623	7.09	2.90	0.8571	11.31	5.05	1.10	
5.157387	**22.94**	**18.75**	5.551765	13.80	7.54	1.64	y
-0.533089	3.74	0.45	-0.135283	4.87	1.39	-0.30	
0.876843	3.28	0.91	-0.270803	7.04	0.78	0.17	
0.848553	6.94	2.75	0.812203	9.99	3.73	0.81	
3.198325	8.98	4.79	1.415735	**22.69**	**16.43**	3.57	y
0.649145	8.37	4.18	1.235762	20.78	**14.52**	3.16	
1.260652	4.52	0.33	0.094888	12.51	6.25	1.36	
2.236819	8.76	4.57	1.351796	15.51	9.25	2.01	y
1.658605	8.52	4.33	1.282318	22.82	**16.56**	3.60	
0.354518	11.43	**7.24**	2.143327	13.59	7.33	1.59	
0.969992	4.69	0.50	0.145204	16.17	**9.91**	2.15	
0.565656	6.19	2.00	0.592101	9.71	3.45	0.75	
2.408455	7.70	3.51	1.037309	**25.67**	**19.41**	4.22	y
1.501977	5.99	1.80	0.531508	25.99	**19.73**	4.29	
-0.083317	2.23	1.96	-0.583187	4.64	1.62	-0.35	
-0.354725	4.10	0.09	-0.026891	4.02	2.24	-0.49	
0.806119	5.26	1.07	0.315552	4.68	1.58	-0.34	
2.050694	**12.32**	**8.13**	2.405423	**17.25**	**10.99**	2.39	y
2.397243	**15.69**	**11.50**	3.404055	**17.22**	**10.96**	2.38	y

1.980659	**12.48**	**8.29**	2.454585	**16.42**	**10.16**	2.21	y
1.47731	10.18	5.99	1.771061	13.17	6.91	1.50	
0.462157	1.45	2.74	-0.813417	3.15	3.11	-0.68	
-1.08165	0.90	3.29	-0.976399	1.38	4.88	-1.06	
-0.5354	1.08	3.11	-0.922816	6.95	0.69	0.15	
-0.801323	1.16	3.03	-0.898917	8.66	2.40	0.52	
0.199373	10.09	5.90	1.744703	7.42	1.16	0.25	
3.285091	**15.70**	**11.51**	3.406128	**24.56**	**18.30**	3.98	y
-0.475578	2.53	1.66	-0.492415	8.33	2.07	0.45	
0.600501	4.19	0.00	0	9.64	3.38	0.74	
0.71987	7.02	2.83	0.835954	11.95	5.69	1.24	
-0.607056	2.50	1.69	-0.500945	4.01	2.25	-0.49	
-0.383429	5.81	1.62	0.478259	11.46	5.20	1.13	
-0.906737	1.39	2.80	-0.831394	8.54	2.28	0.49	
-1.173023	2.78	1.41	-0.41891	3.70	2.56	-0.56	
-0.516581	1.63	2.56	-0.759843	0.88	5.38	-1.17	
-0.193854	2.21	1.98	-0.588725	2.12	4.14	-0.90	
1.310331	8.38	4.19	1.238635	4.83	1.43	-0.31	
-0.468505	0.89	3.30	-0.977267	2.07	4.19	-0.91	
3.6827	**23.24**	**19.05**	5.641203	**20.54**	**14.28**	3.10	y
1.201657	9.58	5.39	1.594524	12.14	5.88	1.28	
1.605476	8.20	4.01	1.186216	10.99	4.73	1.03	
0.406268	5.17	0.98	0.290172	7.10	0.84	0.18	
1.448847	13.13	**8.94**	2.645308	10.60	4.34	0.94	
-0.599828	4.23	0.04	0.010632	1.95	4.31	-0.94	
1.000007	10.16	5.97	1.766323	11.98	5.72	1.24	
0.755922	1.88	2.31	-0.685982	5.95	0.31	-0.07	
1.164053	7.19	3.00	0.885679	13.39	7.13	1.55	
-0.955071	0.38	3.81	-1.130127	0.69	5.57	-1.21	
-0.504074	2.95	1.24	-0.368179	5.12	1.14	-0.25	
-0.31512	3.54	0.65	-0.194988	2.21	4.05	-0.88	
2.628563	8.95	4.76	1.408479	**22.45**	**16.19**	3.52	y
-0.690424	1.42	2.77	-0.821857	2.48	3.78	-0.82	
-1.066091	1.12	3.07	-0.910022	5.44	0.82	-0.18	
-0.775949	1.12	3.07	-0.909312	3.44	2.82	-0.61	
0.645523	7.97	3.78	1.116679	2.96	3.30	-0.72	
-0.112624	5.73	1.54	0.454804	4.26	2.00	-0.44	
-0.90584	0.85	3.34	-0.991663	2.69	3.57	-0.78	
1.487659	13.70	**9.51**	2.814116	13.75	7.49	1.63	
-0.990468	1.75	2.44	-0.723297	1.36	4.90	-1.07	
0.438353	8.04	3.85	1.137795	9.12	2.86	0.62	
-0.955278	0.65	3.54	-1.048403	0.72	5.54	-1.21	
2.862471	**14.27**	**10.08**	2.98322	13.90	7.64	1.66	y
0.626893	3.37	0.82	-0.244327	6.23	0.03	-0.01	
0.536332	3.76	0.43	-0.127524	7.47	1.21	0.26	
-0.523894	1.29	2.90	-0.85938	7.78	1.52	0.33	
-0.075934	2.24	1.95	-0.579633	7.34	1.08	0.23	

-0.533089	0.68	3.51	-1.040117	1.71	4.55	-0.99	
1.844731	8.42	4.23	1.250837	15.15	8.89	1.93	
2.185587	2.95	1.24	-0.368653	**16.67**	**10.41**	2.26	y
-0.38719	2.18	2.01	-0.596188	4.60	1.66	-0.36	
-0.632568	1.01	3.18	-0.942481	6.12	0.14	-0.03	
-0.179674	1.48	2.71	-0.803644	8.26	2.00	0.44	
-0.215606	1.52	2.67	-0.790791	7.34	1.08	0.23	
-0.42557	1.13	3.06	-0.907298	4.33	1.93	-0.42	
0.497864	8.39	4.20	1.241419	2.81	3.45	-0.75	
0.948947	10.80	6.61	1.955269	5.10	1.16	-0.25	
-0.393124	5.74	1.55	0.457677	4.27	1.99	-0.43	
0.281396	5.67	1.48	0.436709	8.81	2.55	0.55	
0.058874	5.52	1.33	0.391753	5.96	0.30	-0.07	
0.209344	5.80	1.61	0.475475	16.32	**10.06**	2.19	
1.109716	23.18	**18.99**	5.622546	14.20	7.94	1.72	
0.17826	4.90	0.71	0.208404	8.08	1.82	0.40	
1.392785	11.30	**7.11**	2.105419	12.38	6.12	1.33	
-0.224386	5.25	1.06	0.313953	5.20	1.06	-0.23	
-0.38524	7.47	3.28	0.970616	9.06	2.80	0.61	
0.848381	8.78	4.59	1.357482	11.86	5.60	1.22	
0.274807	8.74	4.55	1.347264	6.99	0.73	0.16	
-0.218987	4.67	0.48	0.139755	5.44	0.82	-0.18	
-0.528655	3.30	0.89	-0.265354	4.34	1.92	-0.42	
3.875208	**26.07**	**21.88**	6.478135	**34.16**	**27.90**	6.06	y
-0.303235	2.03	2.16	-0.641766	10.30	4.04	0.88	
1.398478	**13.96**	**9.77**	2.893189	**17.86**	**11.60**	2.52	y
0.175534	12.11	**7.92**	2.344119	9.33	3.07	0.67	
-0.909859	1.96	2.23	-0.661608	6.53	0.27	0.06	
2.599928	**14.13**	**9.94**	2.941758	9.84	3.58	0.78	y
-0.708882	1.67	2.52	-0.746664	1.84	4.42	-0.96	
7.047106	**18.84**	**14.65**	4.335756	**18.84**	**12.58**	2.73	y
0.675365	2.76	1.43	-0.42504	3.64	2.62	-0.57	
1.914075	5.74	1.55	0.456255	7.65	1.39	0.30	
-0.674296	2.20	1.99	-0.589998	4.16	2.10	-0.46	
-0.722578	2.14	2.05	-0.609011	1.91	4.35	-0.95	
-0.675124	3.15	1.04	-0.309185	1.13	5.13	-1.12	
0.511664	4.24	0.05	0.014067	12.90	6.64	1.44	
-0.574626	2.42	1.77	-0.525999	3.13	3.13	-0.68	
-1.175351	1.56	2.63	-0.779389	1.64	4.62	-1.01	
0.060944	2.52	1.67	-0.494814	7.31	1.05	0.23	
-0.628549	3.43	0.76	-0.225107	1.88	4.38	-0.95	
0.132375	1.70	2.49	-0.738638	7.37	1.11	0.24	
-0.098031	2.32	1.87	-0.554608	5.32	0.94	-0.21	
-1.053205	0.57	3.62	-1.073736	1.08	5.18	-1.13	
-0.886934	0.93	3.26	-0.96564	1.72	4.55	-0.99	
-0.899285	1.83	2.36	-0.69919	3.63	2.63	-0.57	
-0.847967	3.27	0.92	-0.274091	5.39	0.87	-0.19	

-0.275014	1.94	2.25	-0.668035	6.31	0.05	0.01		
-0.163408	11.74	**7.55**	2.235727	3.84	2.43	-0.53		
1.526127	11.78	**7.59**	2.246685	7.72	1.46	0.32		
0.259782	4.81	0.62	0.180772	3.85	2.41	-0.52		
4.800316	**19.43**	**15.24**	4.512264	11.79	5.53	1.20	y	
3.657515	**21.47**	**17.28**	5.11553	**19.58**	**13.32**	2.90	y	
4.217099	**23.53**	**19.34**	5.726792	**23.09**	**16.83**	3.66	y	
0.731255	9.88	5.69	1.682452	10.03	3.77	0.82		
-0.390329	4.67	0.48	0.140525	4.50	1.76	-0.38		
1.494732	7.74	3.55	1.049866	11.41	5.15	1.12		
0	5.63	1.44	0.424744	6.60	0.34	0.07		
0.799909	5.45	1.26	0.371999	13.49	7.23	1.57		
-0.297749	3.89	0.30	-0.090712	5.59	0.67	-0.15		
1.056586	6.51	2.32	0.685182	14.93	8.67	1.88		
3.413948	**12.91**	**8.72**	2.581043	**29.55**	**23.29**	5.06	y	
0.006175	1.83	2.36	-0.69999	7.29	1.03	0.22		
0.592221	5.93	1.74	0.514597	19.82	**13.56**	2.95		
-0.258609	0.97	3.22	-0.95417	7.65	1.39	0.30		
2.824521	11.31	**7.12**	2.107788	**23.02**	**16.76**	3.64	y	
-0.273116	2.42	1.77	-0.525496	11.99	5.73	1.25		
-0.843413	1.09	3.10	-0.920802	3.16	3.10	-0.67		
-0.678746	3.69	0.50	-0.149587	5.50	0.77	-0.17		
-1.048117	4.79	0.60	0.176004	3.38	2.88	-0.63		
-0.295645	3.84	0.35	-0.103624	5.87	0.39	-0.08		
0.07088	3.70	0.49	-0.146833	3.65	2.61	-0.57		
-0.168341	8.40	4.21	1.244469	10.04	3.78	0.82		
-0.899734	0.72	3.47	-1.028221	2.73	3.53	-0.77		
-0.258109	4.33	0.14	0.041284	6.10	0.16	-0.04		
-0.793026	5.95	1.76	0.521024	4.81	1.45	-0.32		
3.550049	**23.71**	**19.52**	5.780692	**32.40**	**26.14**	5.68	y	
-0.52712	4.67	0.48	0.141947	3.81	2.45	-0.53		
-0.604969	3.08	1.11	-0.329827	8.63	2.37	0.52		
0.086111	4.49	0.30	0.087721	6.19	0.07	-0.02		
0.465607	13.62	**9.43**	2.7922	9.45	3.19	0.69		
-0.538057	3.39	0.80	-0.238789	6.83	0.57	0.12		
0.502522	4.74	0.55	0.161374	8.96	2.70	0.59		
0.864768	5.66	1.47	0.43357	18.05	**11.79**	2.56		
-0.692287	5.48	1.29	0.380025	5.19	1.07	-0.23		
-0.785678	6.17	1.98	0.585674	5.39	0.87	-0.19		
-0.587978	7.68	3.49	1.03112	2.96	3.30	-0.72		
-0.553012	5.17	0.98	0.287832	6.14	0.12	-0.03		
8.08	3.92		4.19	2.28		6.26		3.11
	11.75			6.84				9.32
	5.80			3.38				4.60
						Z 8		
40.39		51.92			**A**	**B**	**C**	
29.96		56.23		3psSD	17.18	17.52		13.64

35.01	43.66	3ngSD	6.80	5.02	1.82
45.57	49.37	SumSD	23.98	22.54	15.46
37.73	50.29	DiffMn	39.86	33.71	46.49
5.84	4.55	SmovrDiff	0.60	0.67	0.33
5.21	4.23	1minus	0.40	0.33	0.67
2.84	3.38				
4.02	3.80				
1.67	0.61				

15.4	5.133	30.092
14.664	5.8148	28.564
31.962	13.182	30.188
19.997	25.137	27.591

46.795	22.34	20.981
35.378	30.174	22.107

					% inf
50009.00	A02	M-011353- PHD finger protein 1	5252.00	PHF1	14.20
50009.00	A04	M-011352- prefoldin subunit 5	5204.00	PFDN5	1.17
50009.00	A05	M-017532- homeobox B5	3215.00	HOXB5	2.29
50009.00	A06	M-011351- prefoldin subunit 1	5201.00	PFDN1	3.37
50009.00	A07	M-017336- homeobox B6	3216.00	HOXB6	2.82
50009.00	A08	M-009815- SUB1 homolog (S. cerevisiae)	10923.00	SUB1	3.96
50009.00	A09	M-010515- homeobox B7	3217.00	HOXB7	4.05
50009.00	A10	M-015428- pre-B-cell leukemia homeobox interacting	57326.00	PBXIP1	3.19
50009.00	A11	M-017601- homeobox C10	3226.00	HOXC10	3.33
50009.00	A12	M-011745- paired box gene 7	5081.00	PAX7	3.59
50009.00	A13	M-017602- homeobox C11	3227.00	HOXC11	2.92
50009.00	A14	M-012240- paired box gene 4	5078.00	PAX4	2.65
50009.00	A15	M-017600- homeobox C13	3229.00	HOXC13	10.03
50009.00	A16	M-012399- paired box gene 3 (Waardenburg syndrom	5077.00	PAX3	3.44
50009.00	A17	M-013462- homeobox C4	3221.00	HOXC4	3.11
50009.00	A18	M-004434- PRKC, apoptosis, WT1, regulator	5074.00	PAWR	3.00
50009.00	A19	M-013381- homeobox C5	3222.00	HOXC5	2.98
50009.00	A20	M-013892- GATA zinc finger domain containing 2B	57459.00	GATAD2B	5.77
50009.00	A21	M-011871- homeobox C6	3223.00	HOXC6	3.39
50009.00	A23	M-012341- homeobox C9	3225.00	HOXC9	12.95
50009.00	B02	M-003331- tumor protein p73	7161.00	TP73	13.60
50009.00	B04	M-003548- tumor protein p53 binding protein, 1	7158.00	TP53BP1	7.83
50009.00	B05	M-012017- paired-like (aristaless) homeobox 2a	401.00	PHOX2A	2.65
50009.00	B06	M-005059- TATA element modulatory factor 1	7110.00	TMF1	7.74
50009.00	B07	M-011553- paired-like homeobox 2b	8929.00	PHOX2B	2.35
50009.00	B08	M-017174- T-cell leukemia homeobox 2	3196.00	TLX2	1.93
50009.00	B09	M-020049- putative homeodomain transcription fact	10745.00	PHTF1	7.69
50009.00	B10	M-003933- T-cell leukemia homeobox 1	3195.00	TLX1	8.58
50009.00	B11	M-004164- protein inhibitor of activated STAT, 3	10401.00	PIAS3	1.91
50009.00	B12	M-019105- thyroid transcription factor 1	7080.00	TITF1	2.56
50009.00	B13	M-006445- protein inhibitor of activated STAT, 4	51588.00	PIAS4	3.32
50009.00	B14	M-006598- Kruppel-like factor 11	8462.00	KLF11	1.15
50009.00	B15	M-012613- pirin (iron-binding nuclear protein)	8544.00	PIR	0.85
50009.00	B16	M-006566- Kruppel-like factor 10	7071.00	KLF10	1.32
50009.00	B17	M-017246- paired-like homeodomain transcription fa	5307.00	PITX1	3.32
50009.00	B18	M-011405- TIA1 cytotoxic granule-associated RNA bir	7073.00	TIAL1	1.07
50009.00	B19	M-017315- paired-like homeodomain transcription fa	5308.00	PITX2	8.90
50009.00	B20	M-017279- TGFB-induced factor homeobox 2-like, Y-l	90655.00	TGIF2LY	1.88
50009.00	B21	M-017325- paired-like homeodomain transcription fa	5309.00	PITX3	1.46
50009.00	B23	M-021413- PBX/knotted 1 homeobox 1	5316.00	PKNOX1	11.29
50009.00	C02	M-009857- orthodenticle homeobox 1	5013.00	OTX1	0.88
50009.00	C04	M-019872- one cut domain, family member 2	9480.00	ONECUT2	0.96
50009.00	C05	M-011696- homeobox D10	3236.00	HOXD10	2.41
50009.00	C06	M-012672- one cut homeobox 1	3175.00	ONECUT1	7.94
50009.00	C07	M-013095- homeobox D11	3237.00	HOXD11	8.26
50009.00	C08	M-010213- Y box binding protein 1	4904.00	YBX1	4.39

50009.00	C09	M-013096- homeobox D12	3238.00	HOXD12	6.28
50009.00	C10	M-010322- neural retina leucine zipper	4901.00	NRL	5.52
50009.00	C11	M-011053- homeobox D13	3239.00	HOXD13	2.14
50009.00	C12	M-006686- nuclear receptor interacting protein 1	8204.00	NRIP1	3.24
50009.00	C13	M-017579- homeobox D4	3233.00	HOXD4	2.70
50009.00	C14	M-017924- nuclear respiratory factor 1	4899.00	NRF1	5.62
50009.00	C15	M-013244- homeobox D8	3234.00	HOXD8	3.85
50009.00	C16	M-004202- N-myc (and STAT) interactor	9111.00	NMI	2.76
50009.00	C17	M-012494- homeobox D9	3235.00	HOXD9	2.09
50009.00	C18	M-018223- NK6 transcription factor related, locus 2 (	84504.00	NKX6-2	3.49
50009.00	C19	M-011872- hairless homolog (mouse)	55806.00	HR	3.23
50009.00	C20	M-020083- NK6 transcription factor related, locus 1 (	4825.00	NKX6-1	2.50
50009.00	C21	M-011294- heat shock factor binding protein 1	3281.00	HSBP1	4.24
50009.00	C23	M-012109- heat shock transcription factor 1	3297.00	HSF1	4.46
50009.00	D02	M-019164- TGFB-induced factor homeobox 2-like, X-l	90316.00	TGIF2LX	4.24
50009.00	D04	M-017124- TGFB-induced factor homeobox 2	60436.00	TGIF2	3.44
50009.00	D05	M-011354- pleiomorphic adenoma gene 1	5324.00	PLAG1	1.66
50009.00	D06	M-011404- TGFB-induced factor homeobox 1	7050.00	TGIF1	0.95
50009.00	D07	M-010531- pleiomorphic adenoma gene-like 2	5326.00	PLAGL2	4.18
50009.00	D08	M-009680- transcription factor EC	22797.00	TFEC	7.09
50009.00	D09	M-009899- jumonji, AT rich interactive domain 1B	10765.00	JARID1B	4.77
50009.00	D10	M-009798- transcription factor EB	7942.00	TFEB	2.08
50009.00	D11	M-012546- POU domain, class 1, transcription factor	5449.00	POU1F1	0.53
50009.00	D12	M-009363- transcription factor binding to IGHM enha	7030.00	TFE3	3.62
50009.00	D13	M-020133- POU domain, class 2, associating factor 1	5450.00	POU2AF1	1.88
50009.00	D14	M-003328- transcription factor Dp-2 (E2F dimerizatio	7029.00	TFDP2	2.22
50009.00	D15	M-019689- POU domain, class 2, transcription factor	5451.00	POU2F1	3.45
50009.00	D16	M-003327- transcription factor Dp-1	7027.00	TFDP1	5.79
50009.00	D17	M-019690- POU domain, class 2, transcription factor	5452.00	POU2F2	3.49
50009.00	D18	M-016232- transcription factor CP2	7024.00	TFCP2	2.28
50009.00	D19	M-020587- POU domain, class 2, transcription factor	25833.00	POU2F3	5.45
50009.00	D20	M-009504- transcription factor AP-4 (activating enha	7023.00	TFAP4	10.35
50009.00	D21	M-017709- POU domain, class 3, transcription factor	5453.00	POU3F1	10.71
50009.00	D23	M-020029- POU domain, class 3, transcription factor	5454.00	POU3F2	7.30
50009.00	E02	M-015422- NK3 transcription factor related, locus 1 (	4824.00	NKX3-1	5.82
50009.00	E04	M-008241- NK2 transcription factor related, locus 8 (	26257.00	NKX2-8	1.88
50009.00	E05	M-011874- heat shock transcription factor 2	3298.00	HSF2	4.12
50009.00	E06	M-019795- NK2 transcription factor related, locus 5 (	1482.00	NKX2-5	11.04
50009.00	E07	M-011295- heat shock transcription factor 4	3299.00	HSF4	10.79
50009.00	E08	M-016090- NK2 transcription factor related, locus 3 (	159296.00	NKX2-3	6.98
50009.00	E09	M-015065- heat shock transcription factor, Y-linked 1	86614.00	HSFY1	16.44
50009.00	E10	M-011341- NK2 transcription factor related, locus 2 (	4821.00	NKX2-2	4.03
50009.00	E11	M-019678- ecdysoneless homolog (Drosophila)	11319.00	ECD	6.91
50009.00	E12	M-009353- nuclear transcription factor Y, gamma	4802.00	NFYC	9.32
50009.00	E13	M-016068- HIV-1 Tat interactive protein 2, 30kDa	10553.00	HTATIP2	9.33
50009.00	E14	M-010002- nuclear transcription factor Y, beta	4801.00	NFYB	2.72
50009.00	E15	M-011699- interferon regulatory factor 8	3394.00	IRF8	8.71

50009.00	E16	M-009213- nuclear transcription factor Y, alpha	4800.00	NFYA	0.87
50009.00	E17	M-009905- inhibitor of DNA binding 3, dominant nega	3399.00	ID3	2.18
50009.00	E18	M-013665- nuclear factor of kappa light polypeptide	4796.00	NFKBIL2	5.47
50009.00	E19	M-008913- inhibitor of DNA binding 4, dominant nega	3400.00	ID4	6.08
50009.00	E20	M-003918- nuclear factor of kappa light polypeptide	4791.00	NFKB2	4.20
50009.00	E21	M-020004- interferon, gamma-inducible protein 16	3428.00	IFI16	4.92
50009.00	E23	M-008354- forkhead box K2	3607.00	FOXK2	1.00
50009.00	F02	M-005238- transcription factor AP-2 gamma (activati	7022.00	TFAP2C	3.55
50009.00	F04	M-015663- transcription factor AP-2 delta (activating	83741.00	TFAP2D	0.90
50009.00	F05	M-020135- POU domain, class 3, transcription factor	5455.00	POU3F3	2.74
50009.00	F06	M-017730- transcription factor AP-2 beta (activating	7021.00	TFAP2B	3.33
50009.00	F07	M-019344- POU domain, class 3, transcription factor	5456.00	POU3F4	2.95
50009.00	F08	M-006348- transcription factor AP-2 alpha (activating	7020.00	TFAP2A	1.54
50009.00	F09	M-016061- POU domain, class 4, transcription factor	5457.00	POU4F1	1.97
50009.00	F10	M-019734- transcription factor A, mitochondrial	7019.00	TFAM	1.71
50009.00	F11	M-012593- POU domain, class 4, transcription factor	5459.00	POU4F3	4.44
50009.00	F12	M-012604- TEA domain family member 3	7005.00	TEAD3	7.34
50009.00	F13	M-005111- peroxisome proliferator-activated recepto	10891.00	PPARGC1A	3.46
50009.00	F14	M-012603- TEA domain family member 1 (SV40 trans	7003.00	TEAD1	0.91
50009.00	F15	M-009322- PR domain containing 1, with ZNF domain	639.00	PRDM1	5.95
50009.00	F16	M-009724- MAX-like protein X	6945.00	MLX	3.92
50009.00	F17	M-007043- PR domain containing 16	63976.00	PRDM16	2.75
50009.00	F18	M-020097- vacuolar protein sorting 72 homolog (S. ce	6944.00	VPS72	4.47
50009.00	F19	M-010550- PR domain containing 2, with ZNF domain	7799.00	PRDM2	8.02
50009.00	F20	M-006564- zinc finger E-box binding homeobox 1	6935.00	ZEB1	4.83
50009.00	F21	M-006940- PR domain containing 4	11108.00	PRDM4	7.34
50009.00	F23	M-020137- prophet of Pit1, paired-like homeodomain	5626.00	PROP1	2.14
50009.00	G02	M-003520- nuclear factor of kappa light polypeptide	4790.00	NFKB1	5.67
50009.00	G03	M-003290- polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMAF	6.40
50009.00	G04	M-009250- nuclear factor I/X (CCAAT-binding transcri	4784.00	NFIX	3.97
50009.00	G05	M-012442- interleukin enhancer binding factor 3, 90k	3609.00	ILF3	6.26
50009.00	G06	M-012704- nuclear factor, interleukin 3 regulated	4783.00	NFIL3	6.34
50009.00	G07	M-011059- pancreatic and duodenal homeobox 1	3651.00	PDX1	15.67
50009.00	G08	M-008362- nuclear factor I/C (CCAAT-binding transcri	4782.00	NFIC	4.42
50009.00	G09	M-011704- interferon regulatory factor 1	3659.00	IRF1	9.61
50009.00	G10	M-008456- nuclear factor I/B	4781.00	NFIB	3.33
50009.00	G11	M-011705- interferon regulatory factor 2	3660.00	IRF2	7.36
50009.00	G12	M-008661- nuclear factor I/A	4774.00	NFIA	8.14
50009.00	G13	M-006875- interferon regulatory factor 3	3661.00	IRF3	4.73
50009.00	G14	M-009308- nuclear factor (erythroid-derived 2)-like 3	9603.00	NFE2L3	3.79
50009.00	G15	M-019668- interferon regulatory factor 4	3662.00	IRF4	3.90
50009.00	G16	M-003755- nuclear factor (erythroid-derived 2)-like 2	4780.00	NFE2L2	5.27
50009.00	G17	M-011706- interferon regulatory factor 5	3663.00	IRF5	7.01
50009.00	G18	M-019733- nuclear factor (erythroid-derived 2)-like 1	4779.00	NFE2L1	3.70
50009.00	G19	M-012227- interferon regulatory factor 6	3664.00	IRF6	5.66
50009.00	G20	M-010049- nuclear factor (erythroid-derived 2), 45kD	4778.00	NFE2	5.37
50009.00	G21	M-011810- interferon regulatory factor 7	3665.00	IRF7	15.56

50009.00	G23	M-020865-	iroquois homeobox protein 4	50805.00	IRX4	4.70
50009.00	H02	M-014703-	transcription factor 7-like 1 (T-cell specific	83439.00	TCF7L1	3.32
50009.00	H03	M-003290-	polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMA	6.71
50009.00	H04	M-019735-	transcription factor 7 (T-cell specific, HM	6932.00	TCF7	8.70
50009.00	H05	M-012402-	paired related homeobox 1	5396.00	PRRX1	3.27
50009.00	H06	M-004594-	transcription factor 4	6925.00	TCF4	8.37
50009.00	H07	M-013242-	paired related homeobox 2	51450.00	PRRX2	3.46
50009.00	H08	M-009384-	transcription factor 3 (E2A immunoglobuli	6929.00	TCF3	6.69
50009.00	H09	M-012136-	purine-rich element binding protein A	5813.00	PURA	8.60
50009.00	H10	M-009923-	transcription factor 21	6943.00	TCF21	2.11
50009.00	H11	M-003296-	retinoblastoma 1 (including osteosarcom	5925.00	RB1	11.77
50009.00	H12	M-012154-	transcription factor 20 (AR1)	6942.00	TCF20	14.72
50009.00	H13	M-013107-	RB-associated KRAB zinc finger	57786.00	RBAK	6.37
50009.00	H14	M-009721-	transcription factor 2, hepatic; LF-B3; vari	6928.00	TCF2	4.80
50009.00	H15	M-003949-	AT rich interactive domain 4A (RBP1-like)	5926.00	ARID4A	11.26
50009.00	H16	M-010091-	transcription factor 15 (basic helix-loop-h	6939.00	TCF15	5.43
50009.00	H17	M-003297-	jumonji, AT rich interactive domain 1A	5927.00	JARID1A	4.16
50009.00	H18	M-006356-	transcription factor 12 (HTF4, helix-loop-h	6938.00	TCF12	4.65
50009.00	H19	M-004767-	v-rel reticuloendotheliosis viral oncogene	5971.00	RELB	12.13
50009.00	H20	M-008215-	transcription factor 1, hepatic; LF-B1, hep	6927.00	TCF1	4.26
50009.00	H21	M-008367-	arginine-glutamic acid dipeptide (RE) repe	473.00	RERE	8.38
50009.00	H23	M-006466-	RE1-silencing transcription factor	5978.00	REST	4.53
50009.00	I02	M-009584-	nuclear factor of activated T-cells, cytopla	4776.00	NFATC4	6.58
50009.00	I03	D-001206-	siControl non-targeting siRNA #2			3.52
50009.00	I04	M-009391-	nuclear factor of activated T-cells, cytopla	4775.00	NFATC3	3.88
50009.00	I05	M-020858-	interferon-stimulated transcription factor	10379.00	ISGF3G	9.82
50009.00	I06	M-003606-	nuclear factor of activated T-cells, cytopla	4773.00	NFATC2	6.27
50009.00	I07	M-016725-	ISL2 transcription factor, LIM/homeodom	64843.00	ISL2	3.65
50009.00	I08	M-003605-	nuclear factor of activated T-cells, cytopla	4772.00	NFATC1	8.66
50009.00	I09	M-003268-	jun oncogene	3725.00	JUN	4.89
50009.00	I10	M-009618-	nuclear factor of activated T-cells 5, tonici	10725.00	NFAT5	4.94
50009.00	I11	M-003269-	jun B proto-oncogene	3726.00	JUNB	2.87
50009.00	I12	M-008667-	neurogenic differentiation 1	4760.00	NEUROD1	4.94
50009.00	I13	M-003900-	jun D proto-oncogene	3727.00	JUND	3.18
50009.00	I14	M-020145-	nuclear receptor co-repressor 2	9612.00	NCOR2	4.15
50009.00	I15	M-020168-	Kruppel-like factor 1 (erythroid)	10661.00	KLF1	7.97
50009.00	I16	M-003518-	nuclear receptor co-repressor 1	9611.00	NCOR1	6.03
50009.00	I17	M-013353-	Kruppel-like factor 12	11278.00	KLF12	4.79
50009.00	I18	M-010321-	nuclear receptor coactivator 4	8031.00	NCOA4	4.21
50009.00	I19	M-006994-	Kruppel-like factor 13	51621.00	KLF13	6.25
50009.00	I20	M-014489-	Nanog homeobox	79923.00	NANOG	5.10
50009.00	I21	M-006928-	Kruppel-like factor 2 (lung)	10365.00	KLF2	11.33
50009.00	I23	M-006987-	Kruppel-like factor 3 (basic)	51274.00	KLF3	8.22
50009.00	J02	M-012278-	transcription elongation regulator 1	10915.00	TCERG1	7.18
50009.00	J04	M-005143-	transcription elongation factor B (SIII), pol	6924.00	TCEB3	3.86
50009.00	J05	M-010147-	regulatory factor X, 1 (influences HLA clas	5989.00	RFX1	3.74
50009.00	J06	M-022071-	transcription elongation factor A (SII), 3	6920.00	TCEA3	2.00

50009.00	J07	M-011129- regulatory factor X, 2 (influences HLA clas	5990.00	RFX2	4.99
50009.00	J08	M-016235- transcription elongation factor A (SII), 2	6919.00	TCEA2	0.83
50009.00	J09	M-011764- regulatory factor X, 3 (influences HLA clas	5991.00	RFX3	3.12
50009.00	J10	M-010496- transcription elongation factor A (SII), 1	6917.00	TCEA1	4.35
50009.00	J11	M-011103- regulatory factor X, 5 (influences HLA clas	5993.00	RFX5	5.78
50009.00	J12	M-011896- T-box 6	6911.00	TBX6	4.16
50009.00	J13	M-011503- regulatory factor X-associated ankyrin-cor	8625.00	RFXANK	2.78
50009.00	J14	M-013410- T-box 5	6910.00	TBX5	2.33
50009.00	J15	M-011104- regulatory factor X-associated protein	5994.00	RFXAP	0.84
50009.00	J16	M-013376- T-box 4	9496.00	TBX4	2.58
50009.00	J17	M-006555- rearranged L-myc fusion	6018.00	RLF	2.33
50009.00	J18	M-012197- T-box 3 (ulnar mammary syndrome)	6926.00	TBX3	3.78
50009.00	J19	M-019150- ras responsive element binding protein 1	6239.00	RREB1	4.56
50009.00	J20	M-013116- T-box 22	50945.00	TBX22	7.65
50009.00	J21	M-003926- runt-related transcription factor 1 (acute	861.00	RUNX1	5.28
50009.00	J23	M-012665- runt-related transcription factor 2	860.00	RUNX2	9.84
50009.00	K02	M-020080- NGFI-A binding protein 2 (EGR1 binding pr	4665.00	NAB2	4.68
50009.00	K04	M-022771- myelin transcription factor 1-like	23040.00	MYT1L	3.98
50009.00	K05	M-005089- Kruppel-like factor 4 (gut)	9314.00	KLF4	4.02
50009.00	K06	M-005271- myelin transcription factor 1	4661.00	MYT1	2.08
50009.00	K07	M-013571- Kruppel-like factor 5 (intestinal)	688.00	KLF5	5.67
50009.00	K08	M-010029- myogenin (myogenic factor 4)	4656.00	MYOG	2.45
50009.00	K09	M-019540- Kruppel-like factor 7 (ubiquitous)	8609.00	KLF7	2.66
50009.00	K10	M-010316- myogenic differentiation 1	4654.00	MYOD1	1.09
50009.00	K11	M-012289- ladybird homeobox 1	10660.00	LBX1	1.85
50009.00	K12	M-009758- myogenic factor 6 (herculin)	4618.00	MYF6	3.21
50009.00	K13	M-016010- LIM domain binding 1	8861.00	LDB1	0.79
50009.00	K14	M-009759- myogenic factor 5	4617.00	MYF5	2.18
50009.00	K15	M-012570- LIM domain binding 2	9079.00	LDB2	1.82
50009.00	K16	M-003913- v-myc myelocytomatosis viral related onc	4613.00	MYCN	1.53
50009.00	K17	M-013588- LIM homeobox 3	8022.00	LHX3	2.20
50009.00	K18	M-010591- v-myc myelocytomatosis viral oncogene h	4611.00	MYCL2	2.14
50009.00	K19	M-010590- LIM homeobox 4	89884.00	LHX4	5.46
50009.00	K20	M-003912- v-myc myelocytomatosis viral oncogene h	4610.00	MYCL1	1.74
50009.00	K21	M-013034- LIM homeobox 5	64211.00	LHX5	1.24
50009.00	K23	M-012840- LIM homeobox 6	26468.00	LHX6	1.08
50009.00	L02	M-005217- T-box 21	30009.00	TBX21	1.46
50009.00	L04	M-012196- T-box 2	6909.00	TBX2	8.66
50009.00	L05	M-012140- Sin3A-associated protein, 18kDa	10284.00	SAP18	2.47
50009.00	L06	M-011910- T-box 19	9095.00	TBX19	1.95
50009.00	L07	M-011538- Sin3A-associated protein, 30kDa	8819.00	SAP30	13.82
50009.00	L08	M-012300- T-box, brain, 1	10716.00	TBR1	1.73
50009.00	L09	M-017666- sex comb on midleg-like 1 (Drosophila)	6322.00	SCML1	5.71
50009.00	L10	M-017254- TBP-like 1	9519.00	TBPL1	7.41
50009.00	L11	M-011107- short stature homeobox	6473.00	SHOX	9.03
50009.00	L12	M-011790- TATA box binding protein	6908.00	TBP	4.21
50009.00	L13	M-011390- short stature homeobox 2	6474.00	SHOX2	7.28

50009.00	L14	M-012394- TAR DNA binding protein	23435.00	TARDBP	3.54
50009.00	L15	M-020093- sine oculis homeobox homolog 1 (Drosop	6495.00	SIX1	2.09
50009.00	L16	M-011400- TAF9 RNA polymerase II, TATA box bindin	6880.00	TAF9	1.77
50009.00	L17	M-017024- sine oculis homeobox homolog 2 (Drosop	10736.00	SIX2	3.60
50009.00	L18	M-012939- TAF7-like RNA polymerase II, TATA box bi	54457.00	TAF7L	2.71
50009.00	L19	M-019974- sine oculis homeobox homolog 3 (Drosop	6496.00	SIX3	4.00
50009.00	L20	M-013669- TAF7 RNA polymerase II, TATA box bindin	6879.00	TAF7	4.76
50009.00	L21	M-020267- sine oculis homeobox homolog 4 (Drosop	51804.00	SIX4	5.39
50009.00	L23	M-019526- sine oculis homeobox homolog 6 (Drosop	4990.00	SIX6	12.40
50009.00	M02	M-003282- v-myc myelocytomatosis viral oncogene h	4609.00	MYC	4.72
50009.00	M04	M-010444- v-myb myeloblastosis viral oncogene hom	4605.00	MYBL2	4.78
50009.00	M05	M-018211- LIM homeobox transcription factor 1, alp	4009.00	LMX1A	4.08
50009.00	M06	M-010526- v-myb myeloblastosis viral oncogene hom	4603.00	MYBL1	7.75
50009.00	M07	M-012586- LIM homeobox transcription factor 1, bet	4010.00	LMX1B	6.13
50009.00	M08	M-003910- v-myb myeloblastosis viral oncogene hom	4602.00	MYB	7.48
50009.00	M09	M-020814- leucine zipper, putative tumor suppressor	11178.00	LZTS1	8.90
50009.00	M10	M-009947- MAX interactor 1	4601.00	MXI1	6.17
50009.00	M11	M-009325- MAX dimerization protein 1	4084.00	MXD1	6.10
50009.00	M12	M-010060- MAX dimerization protein 4	10608.00	MXD4	7.85
50009.00	M13	M-020067- SMAD family member 3	4088.00	SMAD3	15.75
50009.00	M14	M-020078- metal-regulatory transcription factor 1	4520.00	MTF1	5.76
50009.00	M15	M-003902- SMAD family member 4	4089.00	SMAD4	9.81
50009.00	M16	M-012346- mitochondrial transcription termination f	7978.00	MTERF	5.30
50009.00	M17	M-003746- v-maf musculoaponeurotic fibrosarcoma	4094.00	MAF	5.14
50009.00	M18	M-008482- metastasis associated 1 family, member 2	9219.00	MTA2	5.77
50009.00	M19	M-009109- v-maf musculoaponeurotic fibrosarcoma	4097.00	MAFG	5.84
50009.00	M20	M-011734- msh homeobox 2	4488.00	MSX2	2.81
50009.00	M21	M-008580- v-maf musculoaponeurotic fibrosarcoma	7975.00	MAFK	9.92
50009.00	M23	M-008359- methyl-CpG binding domain protein 1	4152.00	MBD1	5.91
50009.00	N02	M-012239- TAF6-like RNA polymerase II, p300/CBP-a	10629.00	TAF6L	5.19
50009.00	N04	M-012147- TAF6 RNA polymerase II, TATA box bindin	6878.00	TAF6	3.40
50009.00	N05	M-007576- solute carrier family 40 (iron-regulated tr	30061.00	SLC40A1	15.19
50009.00	N06	M-012520- TAF5-like RNA polymerase II, p300/CBP-a	27097.00	TAF5L	12.47
50009.00	N07	M-011393- SWI/SNF related, matrix associated, actin	6603.00	SMARCD2	7.59
50009.00	N08	M-012357- TAF5 RNA polymerase II, TATA box bindin	6877.00	TAF5	5.77
50009.00	N09	M-009459- SWI/SNF related, matrix associated, actin	6604.00	SMARCD3	6.55
50009.00	N10	M-023415- TAF4b RNA polymerase II, TATA box bindi	6875.00	TAF4B	5.31
50009.00	N11	M-017522- SWI/SNF related, matrix associated, actin	6605.00	SMARCE1	2.88
50009.00	N12	M-012145- TATA box binding protein (TBP)-associate	9014.00	TAF1B	6.92
50009.00	N13	M-017263- AT rich interactive domain 1A (SWI-like)	8289.00	ARID1A	13.58
50009.00	N14	M-012149- TAF12 RNA polymerase II, TATA box bindi	6883.00	TAF12	5.97
50009.00	N15	M-019579- small nuclear RNA activating complex, pol	6618.00	SNAPC2	6.13
50009.00	N16	M-012148- TAF11 RNA polymerase II, TATA box bindi	6882.00	TAF11	6.68
50009.00	N17	M-010056- Jun dimerization protein p21SNFT	55509.00	SNFT	7.22
50009.00	N18	M-012265- TAF10 RNA polymerase II, TATA box bindi	6881.00	TAF10	1.73
50009.00	N19	M-012446- SNW domain containing 1	22938.00	SNW1	9.96
50009.00	N20	M-017508- transcriptional adaptor 3 (NGG1 homolog	10474.00	TADA3L	7.34

50009.00	N21	M-017192- SRY (sex determining region Y)-box 10	6663.00	SOX10	11.28
50009.00	N23	M-012354- SRY (sex determining region Y)-box 15	6665.00	SOX15	8.50
50009.00	O02	M-011733- msh homeobox 1	4487.00	MSX1	7.61
50009.00	O04	M-006335- musculin (activated B-cell factor-1)	9242.00	MSC	4.83
50009.00	O05	M-011555- methyl-CpG binding domain protein 2	8932.00	MBD2	1.63
50009.00	O06	M-019852- mortality factor 4	10934.00	MORF4	4.01
50009.00	O07	M-019917- myelodysplasia syndrome 1	4197.00	MDS1	5.31
50009.00	O08	M-009373- MAX binding protein	4335.00	MNT	5.51
50009.00	O09	M-013094- methyl CpG binding protein 2 (Rett syndro	4204.00	MECP2	6.63
50009.00	O10	M-003016- myeloid/lymphoid or mixed-lineage leuke	4303.00	MLLT7	4.42
50009.00	O11	M-009362- MADS box transcription enhancer factor 2	4205.00	MEF2A	9.71
50009.00	O12	M-019827- myeloid/lymphoid or mixed-lineage leuke	8028.00	MLLT10	7.83
50009.00	O13	M-009342- MADS box transcription enhancer factor 2	4207.00	MEF2B	7.13
50009.00	O14	M-009670- myeloid/lymphoid or mixed-lineage leuke	9757.00	MLL4	6.02
50009.00	O15	M-009455- MADS box transcription enhancer factor 2	4208.00	MEF2C	10.00
50009.00	O16	M-009914- myeloid/lymphoid or mixed-lineage leuke	4297.00	MLL	16.12
50009.00	O17	M-009884- MADS box transcription enhancer factor 2	4209.00	MEF2D	11.97
50009.00	O18	M-014759- Mix1 homeobox-like 1 (Xenopus laevis)	83881.00	MIXL1	6.21
50009.00	O19	M-011330- Meis homeobox 2	4212.00	MEIS2	2.53
50009.00	O20	M-008674- microphthalmia-associated transcription f	4286.00	MITF	3.44
50009.00	O21	M-011878- mesenchyme homeobox 1	4222.00	MEOX1	1.97
50009.00	O23	M-012176- mesenchyme homeobox 2	4223.00	MEOX2	15.35
50009.00	P02	M-017516- transcriptional adaptor 2 (ADA2 homolog,	6871.00	TADA2L	15.97
50009.00	P04	M-011399- T, brachyury homolog (mouse)	6862.00	T	4.20
50009.00	P05	M-019035- SRY (sex determining region Y)-box 18	54345.00	SOX18	7.28
50009.00	P06	M-012602- suppressor of Ty 4 homolog 1 (S. cerevisia	6827.00	SUPT4H1	4.36
50009.00	P07	M-011778- SRY (sex determining region Y)-box 2	6657.00	SOX2	8.05
50009.00	P08	M-015382- suppressor of fused homolog (Drosophila)	51684.00	SUFU	7.25
50009.00	P09	M-011779- SRY (sex determining region Y)-box 4	6659.00	SOX4	7.58
50009.00	P10	M-019194- synovial sarcoma, X breakpoint 1	6756.00	SSX1	7.41
50009.00	P11	M-019032- SRY (sex determining region Y)-box 8	30812.00	SOX8	5.21
50009.00	P12	M-011780- sex determining region Y	6736.00	SRY	9.30
50009.00	P13	M-021507- SRY (sex determining region Y)-box 9 (can	6662.00	SOX9	13.12
50009.00	P14	M-009800- serum response factor (c-fos serum respo	6722.00	SRF	11.35
50009.00	P15	M-026959- Sp1 transcription factor	6667.00	SP1	6.59
50009.00	P16	M-006891- sterol regulatory element binding transcri	6720.00	SREBF1	18.97
50009.00	P17	M-016508- SP140 nuclear body protein	11262.00	SP140	11.93
50009.00	P18	M-019722- Spi-B transcription factor (Spi-1/PU.1 relat	6689.00	SPIB	10.94
50009.00	P19	M-023096- Sp3 transcription factor	6670.00	SP3	5.80
50009.00	P20	M-010537- spleen focus forming virus (SFFV) proviral	6688.00	SPI1	8.76
50009.00	P21	M-006562- Sp4 transcription factor	6671.00	SP4	9.23
50009.00	P23	M-020199- SAM pointed domain containing ets trans	25803.00	SPDEF	28.18
				mdmdMAD	4.77
				3xMAD	
				MADc	
50009.00	C22				21.10

50009.00	D22				24.85
50009.00	E22				29.36
50009.00	F22				34.40
				mn	27.43
				sd	5.74
50009.00	G22				6.14
50009.00	H22				3.99
50009.00	I22				7.85
50009.00	J22				2.14
					5.03
					2.49
50009.00	K03	D-001600-(	siGLO RISC-free siRNA		8.35
50009.00	L03	D-001600-(	siGLO RISC-free siRNA		20.79
50009.00	J03	D-001206-:	siControl non-targeting siRNA #2		3.49

abs dev	**robust Z**	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**
9.44	3.03	0.80	3.75	-1.18	10.00	5.13	1.34
3.59	-1.15	0.83	3.72	-1.17	0.98	3.89	-1.02
2.47	-0.79	1.55	3.00	-0.95	2.84	2.03	-0.53
1.39	-0.45	0.77	3.78	-1.19	3.92	0.95	-0.25
1.94	-0.62	1.17	3.38	-1.07	0.67	4.20	-1.10
0.80	-0.26	0.54	4.01	-1.26	1.37	3.50	-0.92
0.71	-0.23	2.49	2.06	-0.64	2.36	2.51	-0.66
1.57	-0.51	0.90	3.65	-1.15	1.77	3.10	-0.81
1.43	-0.46	2.50	2.05	-0.64	1.84	3.03	-0.79
1.17	-0.38	0.23	4.32	-1.36	1.70	3.17	-0.83
1.84	-0.59	0.72	3.83	-1.21	1.85	3.02	-0.79
2.11	-0.68	1.36	3.19	-1.00	3.59	1.28	-0.34
5.27	1.69	8.19	3.64	1.18	4.12	0.75	-0.20
1.32	-0.43	1.64	2.91	-0.91	2.95	1.92	-0.50
1.65	-0.53	1.79	2.76	-0.87	0.94	3.93	-1.03
1.76	-0.57	1.07	3.48	-1.10	0.75	4.12	-1.08
1.78	-0.57	2.07	2.48	-0.78	2.92	1.95	-0.51
1.01	0.32	6.94	2.39	0.78	2.68	2.19	-0.57
1.37	-0.44	5.57	1.02	0.34	2.80	2.07	-0.54
8.19	2.62	6.67	2.12	0.69	0.00	4.87	-1.27
8.84	2.83	0.90	3.65	-1.15	3.79	1.08	-0.28
3.07	0.98	2.96	1.59	-0.49	5.75	0.88	0.23
2.11	-0.68	7.73	3.18	1.03	9.99	5.12	1.33
2.98	0.95	4.61	0.06	0.03	4.88	0.01	0.00
2.41	-0.77	2.02	2.53	-0.79	3.12	1.75	-0.46
2.83	-0.91	3.70	0.85	-0.26	1.27	3.60	-0.94
2.93	0.94	3.26	1.29	-0.40	3.03	1.84	-0.48
3.82	1.22	4.18	0.37	-0.11	5.27	0.40	0.10
2.85	-0.91	2.25	2.30	-0.72	0.57	4.30	-1.13
2.20	-0.71	6.94	2.39	0.78	2.84	2.03	-0.53
1.44	-0.46	3.49	1.06	-0.32	3.75	1.12	-0.29
3.61	-1.16	1.25	3.30	-1.04	0.79	4.08	-1.07
3.91	-1.26	0.56	3.99	-1.26	0.93	3.94	-1.03
3.44	-1.11	2.78	1.77	-0.55	1.58	3.29	-0.86
1.44	-0.47	2.64	1.91	-0.60	1.07	3.80	-0.99
3.69	-1.19	0.66	3.89	-1.23	2.99	1.88	-0.49
4.14	1.33	6.78	2.23	0.73	3.28	1.59	-0.42
2.88	-0.92	1.69	2.86	-0.90	0.11	4.76	-1.24
3.30	-1.06	3.64	0.91	-0.28	0.83	4.04	-1.06
6.53	2.09	4.06	0.49	-0.14	0.94	3.93	-1.03
3.88	-1.25	6.09	1.54	0.51	2.51	2.36	-0.62
3.80	-1.22	2.18	2.37	-0.74	5.16	0.29	0.07
2.35	-0.76	5.12	0.57	0.20	2.68	2.19	-0.57
3.18	1.02	13.63	9.08	2.91	7.47	2.60	0.68
3.50	1.12	3.18	1.37	-0.42	1.41	3.46	-0.91
0.37	-0.12	3.97	0.58	-0.17	1.77	3.10	-0.81

1.52	0.49	7.23	2.68	0.87	3.22	1.65	-0.43	
0.76	0.24	6.37	1.82	0.59	1.65	3.22	-0.84	
2.62	-0.84	5.04	0.49	0.17	2.03	2.84	-0.74	
1.52	-0.49	2.07	2.48	-0.78	3.03	1.84	-0.48	
2.06	-0.66	6.76	2.21	0.72	3.24	1.63	-0.43	
0.86	0.27	3.49	1.06	-0.32	3.49	1.38	-0.36	
0.91	-0.29	3.60	0.95	-0.29	3.13	1.75	-0.46	
2.00	-0.64	1.88	2.67	-0.84	2.07	2.80	-0.73	
2.67	-0.86	3.67	0.88	-0.27	2.39	2.48	-0.65	
1.27	-0.41	2.86	1.69	-0.52	1.63	3.24	-0.85	
1.53	-0.49	2.92	1.63	-0.51	2.37	2.50	-0.65	
2.26	-0.73	2.67	1.88	-0.59	2.72	2.15	-0.56	
0.52	-0.17	4.11	0.44	-0.13	4.85	0.02	-0.01	
0.30	-0.10	5.00	0.45	0.16	2.81	2.06	-0.54	
0.52	-0.17	0.78	3.77	-1.19	2.74	2.13	-0.56	
1.32	-0.42	6.41	1.86	0.61	5.21	0.34	0.09	
3.10	-1.00	3.14	1.41	-0.44	2.84	2.03	-0.53	
3.81	-1.22	3.50	1.05	-0.32	1.38	3.49	-0.91	
0.58	-0.19	3.91	0.64	-0.19	3.68	1.19	-0.31	
2.33	0.74	4.83	0.28	0.10	4.63	0.24	-0.07	
0.01	0.00	5.42	0.87	0.29	4.72	0.15	-0.04	
2.68	-0.86	2.42	2.13	-0.67	2.97	1.90	-0.50	
4.23	-1.36	1.56	3.00	-0.94	2.43	2.44	-0.64	
1.14	-0.37	4.78	0.23	0.09	9.41	4.54	1.18	
2.88	-0.92	1.90	2.65	-0.83	7.42	2.55	0.66	
2.54	-0.82	3.52	1.03	-0.31	1.84	3.03	-0.79	
1.31	-0.42	1.46	3.09	-0.97	2.23	2.64	-0.69	
1.03	0.33	5.26	0.71	0.24	6.21	1.34	0.35	
1.27	-0.41	1.89	2.66	-0.84	2.65	2.22	-0.58	
2.48	-0.80	3.58	0.97	-0.30	2.41	2.46	-0.64	
0.69	0.22	3.81	0.74	-0.22	5.23	0.36	0.09	
5.59	1.79	8.63	4.08	1.32	12.79	**7.92**	2.06	
5.95	1.91	11.46	**6.91**	2.22	15.97	**11.10**	2.89	y
2.54	0.81	4.85	0.30	0.11	3.54	1.33	-0.35	
1.06	0.34	23.78	**19.23**	6.15	4.46	0.41	-0.11	
2.88	-0.92	1.94	2.61	-0.82	3.80	1.07	-0.28	
0.64	-0.21	4.97	0.42	0.15	9.64	4.77	1.24	
6.28	2.01	12.39	**7.84**	2.52	14.01	**9.14**	2.38	y
6.03	1.93	6.24	1.69	0.55	12.03	7.16	1.86	
2.22	0.71	5.19	0.64	0.22	6.04	1.17	0.30	
11.68	3.75	12.72	**8.17**	2.62	8.80	3.93	1.02	y
0.73	-0.24	6.36	1.81	0.59	12.46	7.59	1.98	
2.15	0.69	7.79	3.24	1.05	12.94	**8.07**	2.10	
4.56	1.46	10.55	6.00	1.93	23.80	**18.93**	4.94	
4.57	1.47	8.78	4.23	1.36	15.98	**11.11**	2.90	
2.04	-0.66	1.88	2.67	-0.84	6.33	1.46	0.38	
3.95	1.27	4.40	0.15	-0.03	3.68	1.19	-0.31	

3.89	-1.25	2.75	1.80	-0.56	4.49	0.38	-0.10	
2.58	-0.83	1.15	3.40	-1.07	3.41	1.46	-0.38	
0.71	0.23	1.34	3.21	-1.01	6.41	1.54	0.40	
1.32	0.42	4.60	0.05	0.03	3.92	0.95	-0.25	
0.56	-0.18	4.95	0.40	0.14	5.44	0.57	0.15	
0.16	0.05	6.01	1.46	0.48	9.64	4.77	1.24	
3.76	-1.21	3.54	1.01	-0.31	2.81	2.06	-0.54	
1.21	-0.39	0.75	3.80	-1.20	3.00	1.87	-0.49	
3.86	-1.24	1.55	3.00	-0.94	4.71	0.16	-0.04	
2.02	-0.65	4.36	0.19	-0.05	11.71	6.84	1.78	
1.43	-0.46	6.82	2.27	0.74	9.11	4.24	1.10	
1.81	-0.58	3.38	1.17	-0.36	7.82	2.95	0.77	
3.22	-1.03	4.34	0.21	-0.05	3.31	1.56	-0.41	
2.79	-0.90	4.86	0.31	0.11	1.87	3.00	-0.79	
3.05	-0.98	1.56	2.99	-0.94	5.16	0.29	0.07	
0.32	-0.11	14.83	**10.28**	3.29	8.65	3.78	0.98	
2.58	0.83	15.01	**10.46**	3.35	15.66	**10.79**	2.81	y
1.30	-0.42	4.99	0.44	0.16	5.38	0.51	0.13	
3.85	-1.24	0.77	3.78	-1.19	1.47	3.40	-0.89	
1.19	0.38	1.11	3.44	-1.08	2.35	2.52	-0.66	
0.84	-0.27	2.09	2.46	-0.77	5.59	0.72	0.19	
2.01	-0.65	1.78	2.77	-0.87	2.65	2.22	-0.58	
0.29	-0.09	6.41	1.86	0.61	1.80	3.07	-0.80	
3.26	1.04	7.18	2.63	0.85	8.47	3.60	0.94	
0.07	0.02	1.31	3.24	-1.02	1.83	3.04	-0.80	
2.58	0.83	6.75	2.20	0.72	6.53	1.66	0.43	
2.62	-0.84	3.18	1.37	-0.42	2.28	2.59	-0.68	
0.91	0.29	4.41	0.14	-0.03	3.48	1.39	-0.37	
1.64	0.53	8.17	3.62	1.17	7.37	2.50	0.65	
0.79	-0.26	10.72	6.17	1.98	9.48	4.61	1.20	
1.50	0.48	6.81	2.26	0.73	12.32	7.45	1.94	
1.58	0.51	3.52	1.03	-0.31	3.25	1.62	-0.43	
10.91	3.50	37.24	**32.69**	10.45	26.73	**21.86**	5.70	y
0.34	-0.11	6.76	2.21	0.72	5.10	0.23	0.06	
4.85	1.55	9.66	5.11	1.64	12.85	**7.98**	2.08	
1.43	-0.46	4.92	0.37	0.13	4.59	0.28	-0.08	
2.60	0.83	6.11	1.56	0.51	16.16	**11.29**	2.94	
3.38	1.08	7.01	2.46	0.80	12.36	7.49	1.95	
0.03	-0.01	10.43	5.88	1.89	4.68	0.19	-0.05	
0.97	-0.31	2.21	2.34	-0.73	2.91	1.96	-0.51	
0.86	-0.28	3.95	0.60	-0.18	2.76	2.11	-0.55	
0.51	0.16	6.64	2.09	0.68	3.70	1.17	-0.31	
2.25	0.72	3.86	0.69	-0.21	5.69	0.82	0.21	
1.06	-0.34	2.91	1.64	-0.51	2.92	1.95	-0.51	
0.90	0.29	4.66	0.11	0.05	7.78	2.91	0.76	
0.61	0.19	6.48	1.93	0.63	5.84	0.97	0.25	
10.80	3.46	12.45	**7.90**	2.54	6.15	1.28	0.33	y

0.06	-0.02	7.25	2.70	0.87	1.29	3.58	-0.94	
1.44	-0.46	0.94	3.61	-1.14	1.82	3.05	-0.80	
1.95	0.62	2.62	1.93	-0.60	2.86	2.01	-0.53	
3.94	1.26	7.46	2.91	0.94	5.75	0.88	0.23	
1.49	-0.48	3.63	0.92	-0.28	3.70	1.17	-0.31	
3.61	1.16	11.83	**7.28**	2.34	10.91	6.04	1.57	
1.30	-0.42	7.56	3.01	0.98	3.95	0.92	-0.24	
1.93	0.62	12.34	**7.79**	2.50	8.80	3.93	1.02	
3.84	1.23	4.02	0.53	-0.16	1.99	2.88	-0.75	
2.65	-0.85	1.51	3.04	-0.96	0.38	4.49	-1.17	
7.01	2.25	12.30	**7.75**	2.49	7.49	2.62	0.68	y
9.96	3.19	9.01	4.46	1.44	10.38	5.51	1.44	
1.61	0.51	7.42	2.87	0.93	9.97	5.10	1.33	
0.04	0.01	5.44	0.89	0.30	1.53	3.34	-0.87	
6.50	2.08	3.06	1.49	-0.46	3.35	1.52	-0.40	
0.67	0.21	3.66	0.89	-0.27	2.50	2.37	-0.62	
0.60	-0.19	3.19	1.36	-0.42	3.34	1.53	-0.40	
0.11	-0.04	2.29	2.26	-0.71	1.40	3.47	-0.91	
7.37	2.36	16.69	**12.14**	3.89	10.01	5.14	1.34	y
0.50	-0.16	1.59	2.96	-0.93	2.42	2.45	-0.64	
3.62	1.16	11.99	**7.44**	2.39	7.32	2.45	0.64	
0.23	-0.08	3.62	0.93	-0.28	0.71	4.16	-1.09	
1.82	0.58	8.41	3.86	1.25	1.21	3.66	-0.96	
1.24	-0.40	11.07	**6.52**	2.09	9.09	4.22	1.10	
0.88	-0.28	5.47	0.92	0.31	8.50	3.63	0.95	
5.06	1.62	35.79	**31.24**	9.99	35.76	**30.89**	8.06	y
1.51	0.48	15.76	**11.21**	3.59	17.34	**12.47**	3.25	y
1.11	-0.36	2.70	1.85	-0.58	8.85	3.98	1.04	
3.90	1.25	5.59	1.04	0.34	11.37	6.50	1.69	
0.13	0.04	9.00	4.45	1.43	11.27	6.40	1.67	
0.18	0.06	5.26	0.71	0.24	14.85	**9.98**	2.60	
1.89	-0.61	7.44	2.89	0.94	8.64	3.77	0.98	
0.18	0.06	4.45	0.10	-0.02	6.86	1.99	0.52	
1.58	-0.51	2.07	2.48	-0.78	3.39	1.48	-0.39	
0.61	-0.20	2.48	2.07	-0.65	3.36	1.51	-0.40	
3.21	1.03	6.18	1.63	0.53	5.02	0.15	0.04	
1.27	0.40	4.47	0.08	-0.01	3.94	0.93	-0.25	
0.03	0.01	3.47	1.08	-0.33	1.39	3.48	-0.91	
0.55	-0.18	4.50	0.05	0.00	2.02	2.85	-0.75	
1.49	0.48	6.07	1.52	0.50	11.96	7.09	1.85	
0.34	0.11	2.95	1.60	-0.50	3.87	1.00	-0.26	
6.57	2.11	4.05	0.50	-0.14	7.89	3.02	0.79	
3.46	1.11	12.93	**8.38**	2.69	2.97	1.90	-0.50	
2.42	0.77	0.00	4.55	-1.44	2.76	2.11	-0.55	
0.90	-0.29	3.08	1.47	-0.45	6.13	1.26	0.33	
1.02	-0.33	7.75	3.20	1.04	5.23	0.36	0.09	
2.76	-0.89	3.22	1.33	-0.41	2.67	2.20	-0.58	

0.23	0.07	4.84	0.29	0.11	6.19	1.32	0.34	
3.93	-1.26	4.15	0.40	-0.11	1.26	3.61	-0.94	
1.64	-0.53	6.07	1.52	0.50	7.68	2.81	0.73	
0.41	-0.13	18.44	**13.89**	4.45	14.97	**10.10**	2.63	y
1.02	0.32	3.17	1.38	-0.43	6.17	1.30	0.34	
0.60	-0.19	6.05	1.50	0.49	11.77	6.90	1.80	
1.98	-0.64	6.77	2.22	0.72	10.33	5.46	1.42	
2.43	-0.78	1.70	2.85	-0.90	3.25	1.62	-0.42	
3.92	-1.26	5.06	0.51	0.18	2.98	1.89	-0.50	
2.18	-0.70	2.92	1.63	-0.51	2.92	1.95	-0.51	
2.43	-0.78	2.41	2.14	-0.67	4.52	0.35	-0.09	
0.98	-0.32	5.36	0.81	0.27	1.50	3.37	-0.88	
0.20	-0.07	5.12	0.57	0.20	4.37	0.50	-0.13	
2.89	0.92	5.72	1.17	0.39	10.44	5.57	1.45	
0.52	0.16	8.50	3.95	1.27	8.28	3.41	0.89	
5.08	1.63	5.16	0.61	0.21	0.00	4.87	-1.27	
0.08	-0.03	7.49	2.94	0.95	4.95	0.08	0.02	
0.78	-0.25	4.40	0.15	-0.03	10.06	5.19	1.35	
0.74	-0.24	9.78	5.23	1.68	12.32	7.45	1.94	
2.68	-0.86	8.67	4.12	1.33	11.80	6.93	1.81	
0.91	0.29	12.35	**7.80**	2.50	16.26	**11.39**	2.97	y
2.31	-0.74	6.10	1.55	0.51	11.26	6.39	1.66	
2.10	-0.68	5.67	1.12	0.37	10.90	6.03	1.57	
3.67	-1.18	5.21	0.66	0.22	8.60	3.73	0.97	
2.91	-0.93	3.01	1.54	-0.48	7.56	2.69	0.70	
1.55	-0.50	2.53	2.02	-0.63	7.17	2.30	0.60	
3.97	-1.27	2.20	2.35	-0.74	5.98	1.11	0.29	
2.58	-0.83	2.65	1.90	-0.59	1.29	3.58	-0.94	
2.94	-0.94	3.60	0.95	-0.29	2.44	2.43	-0.64	
3.23	-1.04	4.59	0.04	0.03	3.31	1.56	-0.41	
2.56	-0.82	3.41	1.14	-0.35	2.20	2.67	-0.70	
2.62	-0.84	7.00	2.45	0.80	6.64	1.77	0.46	
0.70	0.22	8.59	4.04	1.30	12.28	7.41	1.93	
3.02	-0.97	3.84	0.71	-0.21	4.57	0.30	-0.08	
3.52	-1.13	2.30	2.25	-0.70	1.29	3.58	-0.94	
3.68	-1.18	6.64	2.09	0.68	0.57	4.30	-1.12	
3.30	-1.06	4.05	0.50	-0.15	4.38	0.49	-0.13	
3.90	1.25	11.02	**6.47**	2.08	11.18	6.31	1.64	
2.29	-0.74	3.64	0.91	-0.28	8.28	3.41	0.89	
2.81	-0.90	4.64	0.09	0.04	6.92	2.05	0.53	
9.06	2.90	15.01	**10.46**	3.35	21.39	**16.52**	4.31	y
3.03	-0.97	1.47	3.08	-0.97	2.84	2.03	-0.53	
0.95	0.30	3.31	1.24	-0.38	7.12	2.25	0.59	
2.65	0.85	7.29	2.74	0.89	12.17	7.30	1.90	
4.27	1.37	8.02	3.47	1.12	15.73	**10.86**	2.83	
0.55	-0.18	7.07	2.52	0.82	6.69	1.82	0.47	
2.52	0.81	4.72	0.17	0.07	3.81	1.06	-0.28	

1.22	-0.39	4.41	0.14	-0.03	4.92	0.05	0.01	
2.67	-0.86	1.78	2.77	-0.87	1.53	3.34	-0.87	
2.99	-0.96	5.14	0.59	0.20	2.87	2.00	-0.52	
1.16	-0.37	2.97	1.59	-0.49	2.30	2.57	-0.67	
2.05	-0.66	4.13	0.42	-0.12	5.54	0.67	0.17	
0.76	-0.25	2.35	2.20	-0.69	3.62	1.25	-0.33	
0.00	0.00	1.63	2.92	-0.92	3.96	0.91	-0.24	
0.63	0.20	4.01	0.54	-0.16	6.87	2.00	0.52	
7.64	2.45	10.16	5.61	1.81	0.75	4.12	-1.08	
0.04	-0.01	5.34	0.79	0.27	8.47	3.60	0.94	
0.02	0.00	3.23	1.32	-0.41	6.16	1.29	0.33	
0.68	-0.22	6.80	2.25	0.73	13.15	**8.28**	2.16	
2.99	0.96	11.17	**6.62**	2.13	25.36	**20.49**	5.34	y
1.37	0.44	4.35	0.20	-0.05	9.15	4.28	1.11	
2.72	0.87	4.98	0.43	0.15	17.82	**12.95**	3.38	
4.14	1.33	5.13	0.58	0.20	9.84	4.97	1.29	
1.41	0.45	5.16	0.61	0.21	15.27	**10.40**	2.71	
1.34	0.43	8.24	3.69	1.19	16.70	**11.83**	3.08	
3.09	0.99	6.18	1.63	0.53	8.59	3.72	0.97	
10.99	3.52	29.81	**25.26**	8.08	26.78	**21.91**	5.71	y
1.00	0.32	5.56	1.01	0.33	7.45	2.58	0.67	
5.05	1.62	3.88	0.67	-0.20	4.96	0.09	0.02	
0.54	0.17	4.21	0.34	-0.09	5.93	1.06	0.27	
0.38	0.12	5.45	0.90	0.30	7.26	2.39	0.62	
1.01	0.32	4.32	0.23	-0.06	1.83	3.04	-0.80	
1.08	0.34	3.29	1.26	-0.39	11.47	6.60	1.72	
1.95	-0.63	2.00	2.55	-0.80	2.03	2.84	-0.74	
5.16	1.65	4.36	0.19	-0.05	5.50	0.63	0.16	
1.15	0.37	18.31	**13.76**	4.41	3.53	1.34	-0.35	
0.43	0.14	4.96	0.41	0.14	0.85	4.02	-1.05	
1.36	-0.44	6.81	2.26	0.73	6.19	1.32	0.34	
10.43	3.34	15.94	**11.39**	3.65	25.88	**21.01**	5.48	y
7.71	2.47	7.92	3.37	1.09	11.63	6.76	1.76	
2.83	0.91	9.69	5.14	1.65	10.55	5.68	1.48	
1.01	0.32	4.99	0.44	0.15	3.82	1.05	-0.28	
1.79	0.57	2.35	2.20	-0.69	6.48	1.61	0.42	
0.55	0.18	6.02	1.47	0.48	6.90	2.03	0.53	
1.88	-0.60	5.21	0.66	0.22	1.43	3.44	-0.90	
2.16	0.69	2.41	2.14	-0.67	8.75	3.88	1.01	
8.82	2.83	3.97	0.58	-0.17	8.50	3.63	0.95	
1.21	0.39	1.98	2.57	-0.81	4.71	0.16	-0.04	
1.37	0.44	3.63	0.92	-0.28	2.31	2.56	-0.67	
1.92	0.62	5.63	1.08	0.36	5.16	0.29	0.07	
2.46	0.79	4.14	0.41	-0.12	6.23	1.36	0.35	
3.03	-0.98	2.34	2.21	-0.69	2.11	2.76	-0.72	
5.20	1.67	12.28	**7.73**	2.48	1.75	3.12	-0.82	
2.58	0.83	3.12	1.43	-0.44	8.15	3.28	0.85	

6.52	2.09	6.49	1.94	0.63	8.01	3.14	0.82	
3.74	1.20	7.79	3.24	1.05	0.00	4.87	-1.27	
2.85	0.91	14.14	9.59	3.08	8.11	3.24	0.84	
0.07	0.02	5.80	1.25	0.41	5.95	1.08	0.28	
3.13	-1.00	6.91	2.36	0.77	11.47	6.60	1.72	
0.75	-0.24	6.96	2.41	0.78	22.03	17.16	4.47	
0.55	0.18	2.13	2.42	-0.76	7.70	2.83	0.74	
0.75	0.24	1.97	2.58	-0.81	5.91	1.04	0.27	
1.87	0.60	10.67	6.12	1.97	10.94	6.07	1.58	
0.34	-0.11	7.45	2.90	0.94	6.47	1.60	0.41	
4.95	1.59	8.22	3.67	1.19	9.65	4.78	1.24	
3.07	0.98	5.06	0.51	0.18	9.67	4.80	1.25	
2.37	0.76	4.13	0.42	-0.12	6.16	1.29	0.34	
1.26	0.40	8.92	4.37	1.41	3.68	1.19	-0.31	
5.24	1.68	6.40	1.85	0.60	8.14	3.27	0.85	
11.36	3.64	8.47	3.92	1.27	4.16	0.71	-0.19	
7.21	2.31	10.65	6.10	1.96	4.39	0.48	-0.13	
1.45	0.46	10.57	6.02	1.93	1.77	3.10	-0.81	
2.23	-0.72	0.92	3.63	-1.14	4.90	0.03	0.01	
1.32	-0.42	3.58	0.97	-0.30	6.52	1.65	0.43	
2.79	-0.90	2.78	1.77	-0.55	5.35	0.48	0.12	
10.59	3.39	15.83	11.28	3.61	2.00	2.87	-0.75	x
11.21	3.59	5.81	1.26	0.42	5.56	0.69	0.18	
0.56	-0.18	0.95	3.60	-1.14	1.69	3.18	-0.83	
2.52	0.81	4.51	0.04	0.00	7.93	3.06	0.79	
0.40	-0.13	3.36	1.19	-0.36	13.92	9.05	2.36	
3.29	1.05	1.18	3.37	-1.06	8.53	3.66	0.95	
2.49	0.80	3.07	1.48	-0.46	5.26	0.39	0.10	
2.82	0.90	2.17	2.38	-0.75	7.05	2.18	0.57	
2.65	0.85	2.12	2.43	-0.76	5.55	0.68	0.17	
0.45	0.14	1.31	3.24	-1.02	3.00	1.87	-0.49	
4.54	1.45	4.91	0.36	0.13	7.03	2.16	0.56	
8.36	2.68	5.73	1.18	0.39	17.98	13.11	3.42	y
6.59	2.11	6.88	2.33	0.76	11.37	6.50	1.69	
1.83	0.59	9.35	4.80	1.55	4.15	0.72	-0.19	
14.21	4.56	9.58	5.03	1.62	2.16	2.71	-0.71	
7.17	2.30	11.24	6.69	2.15	11.15	6.28	1.64	x
6.18	1.98	9.56	5.01	1.61	2.30	2.57	-0.67	
1.04	0.33	3.68	0.87	-0.26	7.71	2.84	0.74	
4.00	1.28	5.00	0.45	0.16	11.85	6.98	1.82	
4.47	1.43	3.24	1.31	-0.40	4.85	0.02	-0.01	
23.42	7.51	0.00	4.55	-1.44	7.25	2.38	0.62	
2.11		4.51	2.12		4.88	2.59		
6.32			6.35			7.77		
3.12			3.13			3.83		
					Z 9 new analyses			
	29.88		25.48			**A**	**B**	**C**

	20.29		32.48		3psSD	17.23	17.63	8.64
	33.06		28.26		3ngSD	7.46	5.29	5.17
	32.24		28.89		SumSD	24.70	22.92	13.82
	28.87		28.78		DiffMn	22.40	25.39	26.25
	5.88		2.88		SmovrDiff	1.10	0.90	0.53
					1minus	-0.10	0.10	0.47
	3.06		0.56					
	3.69		1.76					
	1.45		4.50					
	5.71		3.29					
	3.48		2.53					
	1.76		1.72					
	20.49		21.49					
	18.68		20.39					
1.27	4.92	0.37	4.24	0.63				

toxic a,b,c

toxic a,b,c

					% inf	**abs dev**	**robust Z**
50010.00	A02	M-009464- branched chain ket	594.00	BCKDHB	1.43	1.38	-0.69
50010.00	A04	M-012563- branched chain ket	593.00	BCKDHA	0.13	2.68	-1.33
50010.00	A05	M-003330- tumor protein p73	8626.00	TP73L	1.05	1.76	-0.87
50010.00	A06	M-020191- branched chain am	587.00	BCAT2	0.61	2.20	-1.09
50010.00	A07	M-013313- transcriptional reg	55809.00	TRERF1	0.41	2.40	-1.19
50010.00	A08	M-012084- branched chain am	586.00	BCAT1	1.07	1.74	-0.86
50010.00	A09	M-012684- thyroid hormone r	9321.00	TRIP11	1.69	1.12	-0.55
50010.00	A10	M-008251- bile acid Coenzyme	570.00	BAAT	0.43	2.38	-1.18
50010.00	A11	M-009644- trichorhinophalang	7227.00	TRPS1	1.57	1.24	-0.62
50010.00	A12	M-012387- xylosylprotein beta	11285.00	B4GALT7	0.78	2.03	-1.01
50010.00	A13	M-018340- TSC22 domain fam	8848.00	TSC22D1	1.46	1.35	-0.67
50010.00	A14	M-012965- UDP-Gal:betaGlcN	2683.00	B4GALT1	1.10	1.71	-0.85
50010.00	A15	M-012378- transcription termi	7270.00	TTF1	1.82	0.99	-0.49
50010.00	A16	M-009034- UDP-GlcNAc:betaG	10331.00	B3GNT3	1.35	1.46	-0.72
50010.00	A17	M-012862- twist homolog 2 (	117581.00	TWIST2	1.29	1.52	-0.76
50010.00	A18	M-013932- autism susceptibili	26053.00	AUTS2	1.92	0.89	-0.44
50010.00	A19	M-020551- zinc finger and BTB	27033.00	ZBTB32	3.01	0.20	0.10
50010.00	A20	M-011930- ATPase, H+ transp	9296.00	ATP6V1F	1.23	1.58	-0.78
50010.00	A21	M-020670- upstream binding t	7343.00	UBTF	5.41	2.60	1.29
50010.00	A23	M-003617- upstream transcrip	7391.00	USF1	8.14	5.33	2.64
50010.00	B02	M-004253- glyceraldehyde-3-p	2597.00	GAPDH	4.46	1.65	0.82
50010.00	B04	M-017204- guanidinoacetate	2593.00	GAMT	3.18	0.37	0.18
50010.00	B05	M-008643- 3-hydroxybutyrate	622.00	BDH1	2.27	0.54	-0.27
50010.00	B06	M-010327- galactose-1-phospl	2592.00	GALT	5.81	3.00	1.49
50010.00	B07	M-005792- complement facto	629.00	CFB	2.82	0.01	0.00
50010.00	B08	M-008341- galactosamine (N-	2588.00	GALNS	1.40	1.41	-0.70
50010.00	B09	M-008422- betaine-homocyste	635.00	BHMT	1.93	0.88	-0.44
50010.00	B10	M-011279- beta-1,4-N-acetyl-	2583.00	B4GALNT1	3.77	0.96	0.48
50010.00	B11	M-003862- biliverdin reductas	644.00	BLVRA	4.26	1.45	0.72
50010.00	B12	M-009904- UDP-galactose-4-e	2582.00	GALE	3.39	0.58	0.29
50010.00	B13	M-008262- biphenyl hydrolase	670.00	BPHL	0.90	1.91	-0.95
50010.00	B14	M-011038- galactosylceramida	2581.00	GALC	7.44	4.63	2.30
50010.00	B15	M-010210- brain and reproduc	9577.00	BRE	0.81	2.00	-0.99
50010.00	B16	M-010121- glutamate decarbo	2571.00	GAD1	1.89	0.92	-0.46
50010.00	B17	M-005797- complement comp	717.00	C2	1.40	1.41	-0.70
50010.00	B18	M-008181- glucose-6-phospha	2539.00	G6PD	2.84	0.03	0.02
50010.00	B19	M-018195- haloacid dehaloge	81932.00	HDHD3	3.37	0.56	0.28
50010.00	B20	M-011037- glucose-6-phospha	2538.00	G6PC	3.36	0.55	0.27
50010.00	B21	M-008926- acyl-CoA thioester	134526.00	ACOT12	6.45	3.64	1.81
50010.00	B23	M-017896- calcium/calmoduli	55450.00	CAMK2N1	5.32	2.51	1.25
50010.00	C02	M-013221- ATPase, H+ transp	51382.00	ATP6V1D	1.27	1.54	-0.77
50010.00	C04	M-017536- ATP synthase, H+ t	522.00	ATP5J	7.08	4.27	2.12
50010.00	C05	M-003618- upstream transcrip	7392.00	USF2	3.87	1.06	0.52
50010.00	C06	M-008292- 5-aminoimidazole-	471.00	ATIC	8.59	5.78	2.87
50010.00	C07	M-019550- undifferentiated e	8433.00	UTF1	2.14	0.67	-0.33
50010.00	C08	M-009713- aspartoacylase (Ca	443.00	ASPA	10.38	7.57	3.76

50010.00	C09	M-012486-	ventral anterior ho	25806.00	VAX2	1.63	1.18	-0.59
50010.00	C10	M-009377-	asparagine synthet	440.00	ASNS	1.88	0.93	-0.46
50010.00	C11	M-012531-	VENT homeobox h	27287.00	VENTX	1.74	1.07	-0.53
50010.00	C12	M-005228-	N-acylsphingosine	427.00	ASAH1	2.66	0.15	-0.08
50010.00	C13	M-016654-	visual system hom	30813.00	VSX1	2.74	0.07	-0.04
50010.00	C14	M-008564-	ADP-ribosyltransfe	419.00	ART3	3.80	0.99	0.49
50010.00	C15	M-009101-	Wilms tumor 1	7490.00	WT1	3.40	0.59	0.29
50010.00	C16	M-010387-	ADP-ribosyltransfe	417.00	ART1	3.11	0.30	0.15
50010.00	C17	M-011796-	YY1 transcription f	7528.00	YY1	4.33	1.52	0.76
50010.00	C18	M-008240-	acyloxyacyl hydrol	313.00	AOAH	2.47	0.34	-0.17
50010.00	C19	M-011816-	zinc finger protein	677.00	ZFP36L1	2.73	0.08	-0.04
50010.00	C20	M-012534-	aminomethyltrans	275.00	AMT	4.82	2.01	1.00
50010.00	C21	M-019768-	zinc finger protein	7539.00	ZFP37	1.94	0.87	-0.43
50010.00	C23	M-020934-	zinc finger and BTB	51043.00	ZBTB7B	2.51	0.30	-0.15
50010.00	D02	M-017391-	FXYD domain cont	486.00	FXYD2	2.07	0.74	-0.37
50010.00	D04	M-009936-	follicular lymphom	2531.00	FVT1	3.27	0.46	0.23
50010.00	D05	M-005800-	calpain 10	11132.00	CAPN10	2.76	0.05	-0.02
50010.00	D06	M-003668-	fucosyltransferase	2530.00	FUT8	1.32	1.49	-0.74
50010.00	D07	M-004403-	caspase 14, apopt	23581.00	CASP14	8.22	5.41	2.69
50010.00	D08	M-008171-	fucosyltransferase	2528.00	FUT6	1.59	1.22	-0.60
50010.00	D09	M-004307-	caspase 3, apoptos	836.00	CASP3	2.86	0.05	0.03
50010.00	D10	M-008992-	fucosyltransferase	2524.00	FUT2	1.84	0.97	-0.48
50010.00	D11	M-004406-	caspase 6, apoptos	839.00	CASP6	3.73	0.92	0.46
50010.00	D12	M-008960-	fucosyltransferase	2523.00	FUT1	1.05	1.76	-0.88
50010.00	D13	M-004407-	caspase 7, apoptos	840.00	CASP7	2.30	0.51	-0.25
50010.00	D14	M-005882-	furin (paired basic	5045.00	FURIN	1.55	1.26	-0.62
50010.00	D15	M-008617-	cystathionine-beta	875.00	CBS	1.18	1.63	-0.81
50010.00	D16	M-009023-	fucosidase, alpha-L	2517.00	FUCA1	0.78	2.03	-1.01
50010.00	D17	M-009222-	CD38 molecule	952.00	CD38	0.63	2.18	-1.08
50010.00	D18	M-012451-	FtsJ homolog 1 (E.	24140.00	FTSJ1	0.78	2.03	-1.01
50010.00	D19	M-009523-	cell division cycle 2	8697.00	CDC23	6.69	3.88	1.93
50010.00	D20	M-008768-	AKT interacting pr	64400.00	AKTIP	1.78	1.03	-0.51
50010.00	D21	M-009051-	carboxylesterase 1	1066.00	CES1	4.57	1.76	0.87
50010.00	D23	M-009617-	carboxylesterase 4	51716.00	CES4	2.30	0.51	-0.25
50010.00	E02	M-010174-	adenosine monoph	272.00	AMPD3	2.64	0.17	-0.08
50010.00	E04	M-004443-	apoptosis-inducing	84883.00	AIFM2	3.89	1.08	0.54
50010.00	E05	M-013583-	zinc finger with KR	23660.00	ZKSCAN5	4.06	1.25	0.62
50010.00	E06	M-009460-	alpha-methylacyl-C	23600.00	AMACR	4.25	1.44	0.72
50010.00	E07	M-006572-	zinc finger protein,	7543.00	ZFX	3.88	1.07	0.53
50010.00	E08	M-027144-	asparagine-linked g	10195.00	ALG3	3.22	0.41	0.21
50010.00	E09	M-006573-	zinc finger protein,	7544.00	ZFY	6.49	3.68	1.83
50010.00	E10	M-019473-	myo-inositol oxyge	55586.00	MIOX	0.81	2.00	-0.99
50010.00	E11	M-018011-	zinc fingers and ho	11244.00	ZHX1	3.43	0.62	0.31
50010.00	E12	M-010376-	aldolase A, fructos	226.00	ALDOA	3.13	0.32	0.16
50010.00	E13	M-017676-	zinc fingers and ho	22882.00	ZHX2	2.11	0.70	-0.35
50010.00	E14	M-008715-	aldehyde dehydrog	501.00	ALDH7A1	4.14	1.33	0.66
50010.00	E15	M-011798-	Zic family member	7545.00	ZIC1	6.44	3.63	1.80

50010.00	E16	M-004044- aldehyde dehydro	4329.00	ALDH6A1	3.93	1.12	0.56
50010.00	E17	M-006583- zinc finger protein	7695.00	ZNF136	1.00	1.81	-0.90
50010.00	E18	M-009793- aldehyde dehydro	7915.00	ALDH5A1	1.14	1.67	-0.83
50010.00	E19	M-013965- zinc finger protein	7702.00	ZNF143	4.13	1.32	0.66
50010.00	E20	M-008120- aldehyde dehydro	8659.00	ALDH4A1	4.75	1.94	0.96
50010.00	E21	M-018719- zinc finger and BTB	7704.00	ZBTB16	1.23	1.58	-0.78
50010.00	E23	M-012658- zinc finger protein	7707.00	ZNF148	2.67	0.14	-0.07
50010.00	F02	M-005881- folate hydrolase (p	2346.00	FOLH1	1.73	1.08	-0.53
50010.00	F04	M-010093- farnesyltransferase	2342.00	FNTB	3.75	0.94	0.47
50010.00	F05	M-031939- fumarylacetoaceta	51011.00	FAHD2A	1.92	0.89	-0.44
50010.00	F06	M-008807- farnesyltransferase	2339.00	FNTA	1.33	1.48	-0.73
50010.00	F07	M-008651- amidohydrolase d	51005.00	AMDHD2	7.59	4.78	2.37
50010.00	F08	M-008136- flavin containing m	2330.00	FMO5	2.65	0.16	-0.08
50010.00	F09	M-009378- choline acetyltrans	1103.00	CHAT	5.32	2.51	1.25
50010.00	F10	M-009418- flavin containing m	2329.00	FMO4	7.30	4.49	2.23
50010.00	F11	M-012632- chitinase 3-like 2	1117.00	CHI3L2	7.12	4.31	2.14
50010.00	F12	M-009255- flavin containing m	2326.00	FMO1	4.51	1.70	0.85
50010.00	F13	M-009070- carbohydrate (N-a	4166.00	CHST6	7.34	4.53	2.25
50010.00	F14	M-013743- endo-beta-N-acety	64772.00	FLJ21865	2.80	0.01	0.00
50010.00	F15	M-005810- tripeptidyl peptida	1200.00	TPP1	4.54	1.73	0.86
50010.00	F16	M-020804- inositol monophos	54928.00	IMPAD1	2.85	0.04	0.02
50010.00	F17	M-005811- ClpP caseinolytic p	8192.00	CLPP	3.67	0.86	0.43
50010.00	F18	M-005873- chromosome 9 ope	84909.00	C9orf3	1.21	1.60	-0.79
50010.00	F19	M-013022- COX10 homolog, c	1352.00	COX10	3.96	1.15	0.57
50010.00	F20	M-008596- ubiquitin-conjugati	65264.00	UBE2Z	0.40	2.41	-1.20
50010.00	F21	M-021442- COX15 homolog, c	1355.00	COX15	1.69	1.12	-0.55
50010.00	F23	M-005815- carboxypeptidase	1357.00	CPA1	2.63	0.18	-0.09
50010.00	G02	M-008119- aldehyde dehydro	222.00	ALDH3B2	5.49	2.68	1.33
50010.00	G04	M-009236- aldehyde dehydro	221.00	ALDH3B1	2.94	0.13	0.07
50010.00	G05	M-019623- vascular endotheli	7716.00	VEZF1	5.16	2.35	1.17
50010.00	G06	M-004038- aldehyde dehydro	218.00	ALDH3A1	0.87	1.94	-0.96
50010.00	G07	M-019558- zinc finger protein	7727.00	ZNF174	11.16	8.35	4.14
50010.00	G08	M-009766- aldehyde dehydro	217.00	ALDH2	6.25	3.44	1.71
50010.00	G09	M-012361- zinc finger protein	10168.00	ZNF197	4.69	1.88	0.93
50010.00	G10	M-008254- aldehyde dehydro	219.00	ALDH1B1	8.54	5.73	2.84
50010.00	G11	M-019702- zinc finger protein	7572.00	ZNF24	7.56	4.75	2.36
50010.00	G12	M-009082- aldehyde dehydro	220.00	ALDH1A3	3.81	1.00	0.50
50010.00	G13	M-006958- zinc finger protein	23528.00	ZNF281	2.76	0.05	-0.03
50010.00	G14	M-008118- aldehyde dehydro	8854.00	ALDH1A2	2.52	0.29	-0.14
50010.00	G15	M-012776- zinc finger protein	7581.00	ZNF33A	2.36	0.45	-0.22
50010.00	G16	M-008589- aminolevulinate, d	212.00	ALAS2	2.95	0.14	0.07
50010.00	G17	M-006577- zinc finger protein	7584.00	ZNF35	2.69	0.12	-0.06
50010.00	G18	M-008655- aldo-keto reductas	22977.00	AKR7A3	4.40	1.59	0.79
50010.00	G19	M-007685- zinc finger protein	6940.00	ZNF354A	2.04	0.77	-0.38
50010.00	G20	M-008117- aldo-keto reductas	8574.00	AKR7A2	5.73	2.92	1.45
50010.00	G21	M-013163- zinc finger protein	57541.00	ZNF398	3.16	0.35	0.18
50010.00	G23	M-006578- myeloid zinc finger	7593.00	MZF1	1.03	1.78	-0.88

50010.00	H02	M-004796- oleoyl-ACP hydrola	55301.00	OLAH	1.25	1.56	-0.78
50010.00	H04	M-019121- fukutin related pro	79147.00	FKRP	4.71	1.90	0.94
50010.00	H05	M-005816- carboxypeptidase	1358.00	CPA2	4.00	1.19	0.59
50010.00	H06	M-008200- FK506 binding prot	51303.00	FKBP11	7.97	**5.16**	2.56
50010.00	H07	M-005819- carboxypeptidase	93979.00	CPA5	5.82	3.01	1.49
50010.00	H08	M-004952- fragile histidine tri	2272.00	FHIT	5.89	3.08	1.53
50010.00	H09	M-005820- carboxypeptidase	57094.00	CPA6	21.62	**18.81**	9.34
50010.00	H10	M-013064- fibroblast growth f	53834.00	FGFRL1	4.86	2.05	1.02
50010.00	H11	M-005821- carboxypeptidase	1360.00	CPB1	1.83	0.98	-0.49
50010.00	H12	M-008128- ferredoxin reducta	2232.00	FDXR	3.74	0.93	0.46
50010.00	H13	M-005822- carboxypeptidase	1361.00	CPB2	4.70	1.89	0.94
50010.00	H14	M-012313- Fukuyama type co	2218.00	FCMD	5.02	2.21	1.10
50010.00	H15	M-005827- carboxypeptidase	130749.00	CPO	2.46	0.35	-0.18
50010.00	H16	M-010139- fructose-1,6-bisph	8789.00	FBP2	5.91	3.10	1.54
50010.00	H17	M-009749- carnitine palmitoyl	1374.00	CPT1A	3.27	0.46	0.23
50010.00	H18	M-009635- fumarylacetoaceta	2184.00	FAH	7.83	**5.02**	2.49
50010.00	H19	M-008574- carnitine palmitoyl	1376.00	CPT2	8.58	**5.77**	2.86
50010.00	H20	M-007748- acyl-CoA synthetas	23305.00	ACSL6	10.94	**8.13**	4.04
50010.00	H21	M-009524- carnitine acetyltra	1384.00	CRAT	11.44	**8.63**	4.28
50010.00	H23	M-009230- carnitine O-octano	54677.00	CROT	3.88	1.07	0.53
50010.00	I02	M-010038- aldo-keto reductas	6718.00	AKR1D1	0.94	1.87	-0.93
50010.00	I04	M-004041- aldo-keto reductas	1109.00	AKR1C4	1.94	0.87	-0.43
50010.00	I05	M-017732- zinc finger protein	7596.00	ZNF45	6.08	3.27	1.63
50010.00	I06	M-008116- aldo-keto reductas	8644.00	AKR1C3	1.13	1.68	-0.83
50010.00	I07	M-015554- zinc finger protein	55769.00	ZNF83	2.97	0.16	0.08
50010.00	I08	M-009691- aldo-keto reductas	57016.00	AKR1B10	3.64	0.83	0.41
50010.00	I09	M-019562- zinc finger protein	7639.00	ZNF85	1.30	1.51	-0.75
50010.00	I10	M-010232- A kinase (PRKA) an	9590.00	AKAP12	1.67	1.14	-0.57
50010.00	I11	M-019778- CCHC-type zinc fin	7555.00	CNBP	1.46	1.35	-0.67
50010.00	I12	M-008810- S-adenosylhomocy	10768.00	AHCYL1	1.19	1.62	-0.80
50010.00	I13	M-006945- IKAROS family zinc	22806.00	IKZF3	3.28	0.47	0.23
50010.00	I14	M-009599- S-adenosylhomocy	191.00	AHCY	5.59	2.78	1.38
50010.00	I15	M-010993- autoimmune regul	326.00	AIRE	1.23	1.58	-0.79
50010.00	I16	M-008925- alanine-glyoxylate	189.00	AGXT	0.78	2.03	-1.01
50010.00	I17	M-017471- cAMP responsive e	10488.00	CREB3	0.54	2.27	-1.13
50010.00	I18	M-009267- alkylglycerone pho	8540.00	AGPS	1.53	1.28	-0.64
50010.00	I19	M-016645- HIV-1 Tat specific f	27336.00	HTATSF1	2.64	0.17	-0.08
50010.00	I20	M-003811- 1-acylglycerol-3-ph	10555.00	AGPAT2	1.22	1.59	-0.79
50010.00	I21	M-016947- RRN3 RNA polyme	54700.00	RRN3	1.00	1.81	-0.90
50010.00	I23	M-019850- transcription elong	9338.00	TCEAL1	1.20	1.61	-0.80
50010.00	J02	M-005869- coagulation factor	2161.00	F12	1.72	1.09	-0.54
50010.00	J04	M-005868- coagulation factor	2160.00	F11	0.53	2.28	-1.13
50010.00	J05	M-011631- crystallin, mu	1428.00	CRYM	6.93	**4.12**	2.04
50010.00	J06	M-012578- exostoses (multipl	2137.00	EXTL3	1.33	1.48	-0.74
50010.00	J07	M-008314- cysteine sulfinic ac	51380.00	CSAD	6.52	3.71	1.84
50010.00	J08	M-012577- exostoses (multipl	2135.00	EXTL2	1.86	0.95	-0.47
50010.00	J09	M-011956- galactose-3-O-sulf	9514.00	GAL3ST1	4.83	2.02	1.00

50010.00	J10	M-019803- exostoses (multipl	2134.00	EXTL1	0.68	2.13	-1.06
50010.00	J11	M-008962- C-terminal binding	1488.00	CTBP2	1.21	1.60	-0.80
50010.00	J12	M-011031- exostoses (multipl	2132.00	EXT2	7.29	**4.48**	2.23
50010.00	J13	M-003481- cystathionase (cyst	1491.00	CTH	5.95	3.14	1.56
50010.00	J14	M-011030- exostoses (multipl	2131.00	EXT1	1.47	1.34	-0.66
50010.00	J15	M-006644- CTP synthase	1503.00	CTPS	1.83	0.98	-0.48
50010.00	J16	M-008127- electron-transferri	2110.00	ETFDH	1.28	1.53	-0.76
50010.00	J17	M-006645- CTP synthase II	56474.00	CTPS2	1.95	0.86	-0.43
50010.00	J18	M-008315- esterase D/formylg	2098.00	ESD	2.09	0.72	-0.36
50010.00	J19	M-005834- chymotrypsin-like	1506.00	CTRL	1.81	1.00	-0.49
50010.00	J20	M-019249- protein disulfide is	9601.00	PDIA4	0.77	2.04	-1.01
50010.00	J21	M-004266- cathepsin B	1508.00	CTSB	3.40	0.59	0.29
50010.00	J23	M-005835- cathepsin C	1075.00	CTSC	4.79	1.98	0.99
50010.00	K02	M-003810- 1-acylglycerol-3-ph	10554.00	AGPAT1	0.82	1.99	-0.99
50010.00	K04	M-004037- aspartylglucosami	175.00	AGA	6.60	3.79	1.88
50010.00	K05	M-013340- BRF2, subunit of R	55290.00	BRF2	6.05	3.24	1.61
50010.00	K06	M-031750- aflatoxin B1 aldehy	246181.00	AFAR3	3.94	1.13	0.56
50010.00	K07	M-020166- CUG triplet repeat,	10658.00	CUGBP1	6.61	3.80	1.89
50010.00	K08	M-010986- adenylosuccinate l	158.00	ADSL	2.93	0.12	0.06
50010.00	K09	M-012614- density-regulated	8562.00	DENR	2.81	0.00	0.00
50010.00	K10	M-009297- poly (ADP-ribose)	10039.00	PARP3	3.72	0.91	0.45
50010.00	K11	M-003882- eukaryotic translat	1917.00	EEF1A2	3.80	0.99	0.49
50010.00	K12	M-007244- poly (ADP-ribose)	143.00	PARP4	3.40	0.59	0.30
50010.00	K13	M-011647- eukaryotic translat	1933.00	EEF1B2	2.48	0.33	-0.16
50010.00	K14	M-020822- ADP-ribosylhydrol	54936.00	ADPRHL2	3.22	0.41	0.20
50010.00	K15	M-011908- eukaryotic translat	9086.00	EIF1AY	1.58	1.23	-0.61
50010.00	K16	M-008526- ADP-ribosylhydrol	113622.00	ADPRHL1	2.45	0.36	-0.18
50010.00	K17	M-016686- eukaryotic translat	8890.00	EIF2B4	1.65	1.16	-0.58
50010.00	K18	M-005771- ADAM metallopep	9509.00	ADAMTS2	3.10	0.29	0.15
50010.00	K19	M-012625- eukaryotic translat	8893.00	EIF2B5	4.18	1.37	0.68
50010.00	K20	M-005765- ADAM metallopep	140766.00	ADAMTS14	4.95	2.14	1.06
50010.00	K21	M-019532- eukaryotic translat	8669.00	EIF3S1	3.98	1.17	0.58
50010.00	K23	M-019531- eukaryotic translat	8668.00	EIF3S2	3.85	1.04	0.51
50010.00	L02	M-008393- epoxide hydrolase	2052.00	EPHX1	1.22	1.59	-0.79
50010.00	L04	M-009805- ectonucleotide pyr	59084.00	ENPP5	8.44	**5.63**	2.79
50010.00	L05	M-003649- cathepsin D	1509.00	CTSD	9.48	**6.67**	3.31
50010.00	L06	M-009214- ectonucleotide pyr	22875.00	ENPP4	1.35	1.46	-0.72
50010.00	L07	M-005836- cathepsin E	1510.00	CTSE	4.45	1.64	0.81
50010.00	L08	M-015640- elaC homolog 2 (E.	60528.00	ELAC2	4.86	2.05	1.02
50010.00	L09	M-005837- cathepsin F	8722.00	CTSF	1.29	1.52	-0.75
50010.00	L10	M-005861- elastase 2, neutrop	1991.00	ELA2	4.77	1.96	0.97
50010.00	L11	M-005838- cathepsin G	1511.00	CTSG	2.12	0.69	-0.34
50010.00	L12	M-004276- egl nine homolog 1	54583.00	EGLN1	3.63	0.82	0.41
50010.00	L13	M-005839- cathepsin H	1512.00	CTSH	3.32	0.51	0.25
50010.00	L14	M-011261- ephrin-B3	1949.00	EFNB3	3.04	0.23	0.11
50010.00	L15	M-005841- cathepsin L1	1514.00	CTSL1	1.91	0.90	-0.45
50010.00	L16	M-006858- ephrin-A4	1945.00	EFNA4	0.86	1.95	-0.97

50010.00	L17	M-005842- cathepsin L2	1515.00	CTSL2	2.97	0.16	0.08
50010.00	L18	M-019190- ephrin-A3	1944.00	EFNA3	1.78	1.03	-0.51
50010.00	L19	M-005843- cathepsin O	1519.00	CTSO	7.57	**4.76**	2.36
50010.00	L20	M-010343- enoyl Coenzyme A	1892.00	ECHS1	0.88	1.93	-0.96
50010.00	L21	M-005844- cathepsin S	1520.00	CTSS	6.51	3.70	1.83
50010.00	L23	M-005845- cathepsin W	1521.00	CTSW	1.24	1.57	-0.78
50010.00	M02	M-010756- ADAM metallopep	203102.00	ADAM32	3.46	0.65	0.32
50010.00	M04	M-008808- ADAM metallopep	11086.00	ADAM29	2.61	0.20	-0.10
50010.00	M05	M-003883- eukaryotic translat	8667.00	EIF3S3	22.89	**20.08**	9.97
50010.00	M06	M-010701- ADAM metallopep	8749.00	ADAM18	12.88	**10.07**	5.00
50010.00	M07	M-019533- eukaryotic translat	8666.00	EIF3S4	0.77	2.04	-1.01
50010.00	M08	M-009588- adenosine deamin	100.00	ADA	2.01	0.80	-0.40
50010.00	M09	M-019535- eukaryotic translat	8665.00	EIF3S5	3.96	1.15	0.57
50010.00	M10	M-009832- aminoacylase 1	95.00	ACY1	2.08	0.73	-0.36
50010.00	M11	M-010518- eukaryotic translat	3646.00	EIF3S6	2.99	0.18	0.09
50010.00	M12	M-005756- acrosin	49.00	ACR	3.47	0.66	0.33
50010.00	M13	M-017556- eukaryotic translat	8664.00	EIF3S7	1.93	0.88	-0.44
50010.00	M14	M-008366- acid phosphatase,	93650.00	ACPT	3.56	0.75	0.37
50010.00	M15	M-009036- eukaryotic translat	8663.00	EIF3S8	0.00	2.81	-1.39
50010.00	M16	M-008665- acid phosphatase 6	51205.00	ACP6	1.92	0.89	-0.44
50010.00	M17	M-019196- eukaryotic translat	8662.00	EIF3S9	4.91	2.10	1.04
50010.00	M18	M-008205- acid phosphatase 2	53.00	ACP2	1.68	1.13	-0.56
50010.00	M19	M-020179- eukaryotic translat	1975.00	EIF4B	8.85	**6.04**	3.00
50010.00	M20	M-005074- acyl-Coenzyme A o	51.00	ACOX1	11.33	**8.52**	4.23
50010.00	M21	M-003884- eukaryotic translat	1977.00	EIF4E	21.80	**18.99**	9.42
50010.00	M23	M-010517- immature colon ca	3396.00	ICT1	2.36	0.45	-0.22
50010.00	N02	M-004035- enoyl Coenzyme A	1891.00	ECH1	3.37	0.56	0.28
50010.00	N04	M-008979- ubiquitin-conjugati	63893.00	UBE2O	2.72	0.09	-0.04
50010.00	N05	M-005846- cathepsin Z	1522.00	CTSZ	0.91	1.90	-0.94
50010.00	N06	M-008455- dihydropyrimidina	1807.00	DPYS	43.56	**40.75**	20.23
50010.00	N07	M-017667- cytochrome b-561	11068.00	CYB561D2	3.61	0.80	0.40
50010.00	N08	M-004181- dipeptidyl-peptida	1803.00	DPP4	9.83	**7.02**	3.49
50010.00	N09	M-008600- cytochrome b5 red	51706.00	CYB5R1	9.46	**6.65**	3.30
50010.00	N10	M-005853- dipeptidyl-peptida	10072.00	DPP3	1.42	1.39	-0.69
50010.00	N11	M-008752- cytochrome b5 red	51700.00	CYB5R2	2.95	0.14	0.07
50010.00	N12	M-011535- dolichyl-phosphate	8813.00	DPM1	1.27	1.54	-0.76
50010.00	N13	M-008635- cytochrome P450,	1584.00	CYP11B1	2.94	0.13	0.07
50010.00	N14	M-008343- dipeptidase 3	64180.00	DPEP3	1.01	1.80	-0.89
50010.00	N15	M-008806- cytochrome P450,	1589.00	CYP21A2	1.41	1.40	-0.69
50010.00	N16	M-005931- dipeptidase 2	64174.00	DPEP2	3.63	0.82	0.41
50010.00	N17	M-008233- cytochrome P450,	1593.00	CYP27A1	1.85	0.96	-0.48
50010.00	N18	M-005852- dipeptidase 1 (rena	1800.00	DPEP1	0.96	1.85	-0.92
50010.00	N19	M-008286- cytochrome P450,	1558.00	CYP2C8	7.29	**4.48**	2.22
50010.00	N20	M-009769- ADP-ribosyltransfe	420.00	ART4	1.59	1.22	-0.60
50010.00	N21	M-008285- cytochrome P450,	1559.00	CYP2C9	3.84	1.03	0.51
50010.00	N23	M-008934- cytochrome P450,	9420.00	CYP7B1	1.16	1.65	-0.82
50010.00	O02	M-005755- angiotensin I conve	59272.00	ACE2	5.49	2.68	1.33

50010.00	O04	M-009408- acetyl-Coenzyme A	38.00	ACAT1	8.28	5.47	2.71
50010.00	O05	M-015386- mitochondrial tran	54516.00	MTRF1L	2.61	0.20	-0.10
50010.00	O06	M-009392- acyl-Coenzyme A d	37.00	ACADVL	2.68	0.13	-0.06
50010.00	O07	M-013054- eukaryotic translat	7458.00	EIF4H	2.91	0.10	0.05
50010.00	O08	M-003855- acyl-Coenzyme A d	36.00	ACADSB	1.31	1.50	-0.75
50010.00	O09	M-016315- alpha 1,4-galactosy	53947.00	A4GALT	3.06	0.25	0.13
50010.00	O10	M-010041- acyl-Coenzyme A d	35.00	ACADS	5.16	2.35	1.17
50010.00	O11	M-009247- aminoadipate-sem	10157.00	AASS	2.27	0.54	-0.27
50010.00	O12	M-008111- acyl-Coenzyme A d	34.00	ACADM	5.59	2.78	1.38
50010.00	O13	M-004060- 4-aminobutyrate a	18.00	ABAT	3.27	0.46	0.23
50010.00	O14	M-009851- acyl-Coenzyme A d	33.00	ACADL	5.81	3.00	1.49
50010.00	O15	M-008331- abhydrolase doma	11057.00	ABHD2	2.35	0.46	-0.23
50010.00	O16	M-009329- acetyl-Coenzyme A	30.00	ACAA1	1.23	1.58	-0.78
50010.00	O17	M-008587- abhydrolase doma	171586.00	ABHD3	0.97	1.84	-0.91
50010.00	O18	M-009657- abhydrolase doma	79852.00	ABHD9	3.45	0.64	0.32
50010.00	O19	M-009567- abhydrolase doma	63874.00	ABHD4	4.44	1.63	0.81
50010.00	O20	M-008028- abhydrolase doma	79575.00	ABHD8	2.49	0.32	-0.16
50010.00	O21	M-009257- abhydrolase doma	51099.00	ABHD5	5.69	2.88	1.43
50010.00	O23	M-008683- abhydrolase doma	57406.00	ABHD6	2.91	0.10	0.05
50010.00	P02	M-008125- dimethylglycine de	29958.00	DMGDH	31.37	28.56	14.18
50010.00	P04	M-009941- dihydrolipoamide S	1743.00	DLST	1.23	1.58	-0.78
50010.00	P05	M-009756- D-amino-acid oxida	1610.00	DAO	2.50	0.31	-0.15
50010.00	P06	M-009554- cytochrome b5 red	1727.00	CYB5R3	1.50	1.31	-0.65
50010.00	P07	M-008290- debranching enzym	51163.00	DBR1	2.48	0.33	-0.16
50010.00	P08	M-008859- hydroxysteroid (17	51170.00	HSD17B11	2.24	0.57	-0.28
50010.00	P09	M-008794- dodecenoyl-Coenz	1632.00	DCI	1.94	0.87	-0.43
50010.00	P10	M-009481- hydroxysteroid (17	51171.00	HSD17B14	2.68	0.13	-0.07
50010.00	P11	M-008835- dicarbonyl/L-xylulo	51181.00	DCXR	1.32	1.49	-0.74
50010.00	P12	M-009619- dihydroorotate deh	1723.00	DHODH	2.58	0.23	-0.12
50010.00	P13	M-010156- dopa decarboxylas	1644.00	DDC	2.12	0.69	-0.34
50010.00	P14	M-005849- desert hedgehog h	50846.00	DHH	2.13	0.68	-0.34
50010.00	P15	M-009642- 2,4-dienoyl CoA re	1666.00	DECR1	1.88	0.93	-0.46
50010.00	P16	M-008799- dihydrofolate redu	1719.00	DHFR	3.94	1.13	0.56
50010.00	P17	M-009627- 2,4-dienoyl CoA re	26063.00	DECR2	0.42	2.39	-1.19
50010.00	P18	M-020182- 7-dehydrocholeste	1717.00	DHCR7	0.79	2.02	-1.00
50010.00	P19	M-006675- degenerative sperm	8560.00	DEGS1	4.04	1.23	0.61
50010.00	P20	M-010222- 24-dehydrocholest	1718.00	DHCR24	2.48	0.33	-0.16
50010.00	P21	M-003922- diacylglycerol O-ac	8694.00	DGAT1	1.92	0.89	-0.44
50010.00	P23	M-006716- diacylglycerol kinas	160851.00	DGKH	28.17	25.36	12.59
				mdn	2.81	1.36	
				3xMAD		4.08	
				MADc		2.01	
50010.00	C22				23.96		11.88
50010.00	D22				15.15		15.88
50010.00	E22				11.25		11.89
50010.00	F22				19.64		18.44

					mn	17.50	14.52
					sd	4.77	2.79
50010.00	G22						
50010.00	H22					2.08	2.50
50010.00	I22					1.52	0.45
50010.00	J22					1.27	4.42
						0.55	1.82
					mn	1.36	2.30
					sd	0.63	1.65
50010.00	G03	M-003290-	polo-like kinase 1 (	5347.00	PLK1 SMA	4.76	7.98
50010.00	H03	M-003290-	polo-like kinase 1 (	5347.00	PLK1 SMA	12.60	2.55
50010.00	I03	D-001206-	siControl non-targeting siRNA			2.38	3.38
50010.00	J03	D-001206-	siControl non-targeting siRNA			0.85	1.75
50010.00	K03	D-001600-	siGLO RISC-free siRNA			13.85	13.31
50010.00	L03	D-001600-	siGLO RISC-free siRNA			12.56	7.90

% inf	abs dev	robust Z	% inf	abs dev	robust Z	
3.18	1.01	0.59	3.42	0.74	0.40	
2.48	0.31	0.18	0.77	1.91	-1.02	
1.60	0.57	-0.33	1.50	1.18	-0.63	
2.92	0.75	0.44	4.21	1.53	0.82	
1.30	0.87	-0.51	0.92	1.76	-0.94	
2.97	0.80	0.47	2.28	0.40	-0.22	
1.29	0.88	-0.51	1.36	1.32	-0.71	
1.89	0.28	-0.16	1.07	1.61	-0.86	
3.86	1.69	0.98	0.42	2.26	-1.21	
2.26	0.09	0.05	4.47	1.79	0.95	
1.55	0.62	-0.36	1.84	0.84	-0.45	
2.09	0.08	-0.05	3.98	1.30	0.69	
0.24	1.93	-1.12	0.88	1.80	-0.96	
1.73	0.44	-0.26	4.00	1.32	0.70	
2.21	0.04	0.03	2.88	0.20	0.10	
2.25	0.08	0.05	1.37	1.31	-0.70	
2.95	0.78	0.46	0.95	1.73	-0.93	
0.58	1.59	-0.93	2.14	0.54	-0.29	
4.07	1.90	1.11	10.72	8.04	4.29	
1.67	0.50	-0.29	2.05	0.63	-0.34	
3.45	1.28	0.75	3.94	1.26	0.67	
4.18	2.01	1.17	1.74	0.94	-0.50	
2.38	0.21	0.12	1.87	0.81	-0.44	
9.24	7.07	4.12	3.36	0.68	0.36	
3.27	1.10	0.64	1.37	1.31	-0.70	
1.32	0.85	-0.50	0.93	1.75	-0.93	
2.09	0.08	-0.05	1.25	1.43	-0.76	
1.82	0.35	-0.20	3.13	0.45	0.24	
3.21	1.04	0.60	1.10	1.58	-0.84	
2.11	0.06	-0.04	4.49	1.81	0.97	
3.96	1.79	1.04	2.34	0.34	-0.18	
4.51	2.34	1.36	4.49	1.81	0.97	
0.15	2.02	-1.18	1.83	0.85	-0.45	
1.93	0.24	-0.14	3.68	1.00	0.53	
0.85	1.32	-0.77	1.77	0.91	-0.49	
0.63	1.54	-0.90	1.63	1.05	-0.56	
9.79	7.62	4.44	4.28	1.60	0.85	
0.43	1.74	-1.02	1.50	1.18	-0.63	
1.99	0.18	-0.10	1.27	1.41	-0.75	
0.65	1.52	-0.89	0.58	2.10	-1.12	
0.13	2.04	-1.19	1.31	1.37	-0.73	
4.14	1.97	1.15	2.69	0.01	0.01	
5.42	3.25	1.89	2.30	0.38	-0.20	
14.35	12.18	7.10	11.56	8.88	4.74	y
1.59	0.58	-0.34	2.64	0.04	-0.02	
8.34	6.17	3.60	7.66	4.98	2.66	y

1.60	0.57	-0.33	4.52	1.84	0.98	
0.52	1.65	-0.96	1.65	1.03	-0.55	
2.00	0.17	-0.10	1.68	1.00	-0.53	
1.31	0.86	-0.50	2.83	0.15	0.08	
0.31	1.86	-1.08	3.11	0.43	0.23	
0.81	1.36	-0.79	5.00	2.32	1.24	
1.57	0.60	-0.35	1.92	0.76	-0.41	
0.31	1.86	-1.08	1.55	1.13	-0.61	
0.79	1.38	-0.80	2.49	0.19	-0.10	
1.94	0.23	-0.14	1.31	1.37	-0.73	
3.02	0.85	0.50	5.51	2.83	1.51	
2.04	0.13	-0.07	6.27	3.59	1.92	
1.45	0.72	-0.42	1.47	1.21	-0.65	
1.85	0.32	-0.19	5.25	2.57	1.37	
0.32	1.85	-1.08	3.21	0.53	0.29	
1.62	0.55	-0.32	2.67	0.01	-0.01	
0.81	1.36	-0.79	3.65	0.97	0.52	
1.47	0.70	-0.41	0.79	1.89	-1.01	
6.89	**4.72**	2.75	4.31	1.63	0.87	y
2.22	0.05	0.03	2.22	0.46	-0.24	
3.30	1.13	0.66	1.00	1.68	-0.90	
0.65	1.52	-0.89	2.45	0.23	-0.12	
0.93	1.24	-0.72	2.31	0.37	-0.20	
2.86	0.69	0.40	3.57	0.89	0.48	
6.21	**4.04**	2.36	3.70	1.02	0.54	
3.85	1.68	0.98	4.11	1.43	0.77	
2.20	0.03	0.01	3.24	0.56	0.30	
6.17	**4.00**	2.33	3.31	0.63	0.34	
4.54	2.37	1.38	3.66	0.98	0.53	
3.17	1.00	0.58	3.05	0.37	0.20	
5.88	**3.71**	2.16	2.55	0.13	-0.07	
1.66	0.51	-0.30	1.50	1.18	-0.63	
5.21	3.04	1.77	6.30	3.62	1.93	
1.23	0.94	-0.54	3.00	0.32	0.17	
1.80	0.37	-0.21	1.33	1.35	-0.72	
0.65	1.52	-0.88	0.72	1.96	-1.05	
0.68	1.49	-0.87	1.53	1.15	-0.61	
1.66	0.51	-0.29	5.02	2.34	1.25	
0.09	2.08	-1.21	1.56	1.12	-0.60	
1.25	0.92	-0.54	3.30	0.62	0.33	
1.78	0.39	-0.23	6.37	3.69	1.97	
0.37	1.80	-1.05	1.47	1.21	-0.65	
1.61	0.56	-0.33	5.50	2.82	1.50	
5.86	**3.69**	2.15	1.58	1.10	-0.59	
0.37	1.80	-1.05	3.65	0.97	0.52	
0.14	2.03	-1.19	3.68	1.00	0.53	
0.69	1.48	-0.86	1.08	1.60	-0.85	

4.99	2.82	1.64	10.19	**7.51**	4.01		
3.85	1.68	0.98	5.59	2.91	1.55		
3.63	1.46	0.85	4.02	1.34	0.71		
3.21	1.04	0.61	10.96	**8.28**	4.42		
1.53	0.64	-0.38	5.46	2.78	1.49		
0.13	2.04	-1.19	2.52	0.16	-0.08		
1.59	0.58	-0.34	0.60	2.08	-1.11		
2.24	0.07	0.04	0.73	1.95	-1.04		
1.88	0.29	-0.17	0.99	1.69	-0.90		
0.99	1.18	-0.69	1.31	1.37	-0.73		
0.89	1.28	-0.74	0.56	2.12	-1.13		
7.22	**5.05**	2.94	3.99	1.31	0.70	x	toxic a,c
2.90	0.73	0.43	0.39	2.29	-1.22		
8.36	**6.19**	3.61	1.68	1.00	-0.53		
11.66	**9.49**	5.53	4.62	1.94	1.03	y	
5.07	2.90	1.69	0.35	2.33	-1.25		
3.11	0.94	0.55	1.75	0.93	-0.50		
5.82	**3.65**	2.13	3.95	1.27	0.68	y	
2.58	0.41	0.24	0.33	2.35	-1.25		
3.26	1.09	0.64	2.50	0.18	-0.10		
2.37	0.20	0.12	4.23	1.55	0.83		
4.44	2.27	1.32	1.33	1.35	-0.72		
0.78	1.39	-0.81	0.41	2.27	-1.21		
10.15	**7.98**	4.65	3.43	0.75	0.40		
1.43	0.74	-0.43	1.69	0.99	-0.53		
1.82	0.35	-0.21	0.57	2.11	-1.13		
4.07	1.90	1.11	0.24	2.44	-1.30		
3.30	1.13	0.66	3.67	0.99	0.53		
1.97	0.20	-0.11	7.21	**4.53**	2.42		
2.43	0.26	0.15	4.30	1.62	0.87		
2.45	0.28	0.16	2.98	0.30	0.16		
15.55	**13.38**	7.80	9.92	**7.24**	3.86	y	
4.25	2.08	1.21	1.65	1.03	-0.55		
6.19	**4.02**	2.34	2.64	0.04	-0.02		
8.23	**6.06**	3.53	5.65	2.97	1.59	y	
6.26	**4.09**	2.38	5.93	3.25	1.73	y	
4.74	2.57	1.50	1.65	1.03	-0.55		
2.44	0.27	0.16	0.58	2.10	-1.12		
4.53	2.36	1.37	7.59	**4.91**	2.62		
6.29	**4.12**	2.40	4.57	1.89	1.01		
3.35	1.18	0.69	3.46	0.78	0.42		
2.01	0.16	-0.09	5.35	2.67	1.43		
0.82	1.35	-0.79	2.18	0.50	-0.27		
4.09	1.92	1.12	2.28	0.40	-0.22		
3.52	1.35	0.78	8.03	**5.35**	2.86		
2.71	0.54	0.32	1.32	1.36	-0.73		
1.04	1.13	-0.66	0.38	2.30	-1.23		

0.66	1.51	-0.88	0.68	2.00	-1.07		
1.78	0.39	-0.23	0.55	2.13	-1.14		
1.35	0.82	-0.48	0.45	2.23	-1.19		
6.01	**3.84**	2.24	2.01	0.67	-0.36	y	
4.15	1.98	1.16	4.04	1.36	0.73		
2.93	0.76	0.45	3.31	0.63	0.33		
10.70	**8.53**	4.97	9.68	**7.00**	3.74	y	
2.50	0.33	0.19	0.56	2.12	-1.13		
1.41	0.76	-0.44	0.80	1.88	-1.01		
1.06	1.11	-0.65	1.47	1.21	-0.64		
1.42	0.75	-0.44	0.35	2.33	-1.24		
3.65	1.48	0.86	2.38	0.30	-0.16		
1.61	0.56	-0.32	1.80	0.88	-0.47		
10.97	**8.80**	5.13	6.29	3.61	1.92		
3.77	1.60	0.93	4.64	1.96	1.04		
6.31	**4.14**	2.41	6.21	3.53	1.88	y	
2.20	0.03	0.02	6.98	**4.30**	2.30	y	
8.06	**5.89**	3.43	8.62	**5.94**	3.17	y	
12.25	**10.08**	5.88	8.81	**6.13**	3.27	y	
3.02	0.85	0.49	5.76	3.08	1.64		
4.09	1.92	1.12	2.01	0.67	-0.36		
2.80	0.63	0.37	2.65	0.03	-0.02		
6.02	**3.85**	2.24	12.12	**9.44**	5.04	y	
2.12	0.05	-0.03	1.24	1.44	-0.77		
1.39	0.78	-0.46	1.72	0.96	-0.51		
3.65	1.48	0.86	2.69	0.01	0.01		
0.94	1.23	-0.72	4.62	1.94	1.03		
2.56	0.39	0.23	0.94	1.74	-0.93		
1.16	1.01	-0.59	1.65	1.03	-0.55		
2.70	0.53	0.31	2.10	0.58	-0.31		
23.71	**21.54**	12.56	0.71	1.97	-1.05		
9.70	**7.53**	4.39	10.87	**8.19**	4.37	x	toxic a, artifact b
0.99	1.18	-0.69	1.42	1.26	-0.67		
1.36	0.81	-0.47	1.90	0.78	-0.42		
2.00	0.17	-0.10	1.48	1.20	-0.64		
3.87	1.70	0.99	2.04	0.64	-0.34		
1.14	1.03	-0.60	2.53	0.15	-0.08		
2.54	0.37	0.22	2.03	0.65	-0.35		
2.90	0.73	0.43	1.75	0.93	-0.50		
1.83	0.34	-0.20	0.35	2.33	-1.24		
1.05	1.12	-0.65	1.04	1.64	-0.88		
0.47	1.70	-0.99	1.65	1.03	-0.55		
5.55	3.38	1.97	8.97	**6.29**	3.36	y	
0.65	1.52	-0.89	1.09	1.59	-0.85		
4.93	2.76	1.61	7.66	**4.98**	2.66		
2.13	0.04	-0.02	3.66	0.98	0.52		
6.56	**4.39**	2.56	18.03	**15.35**	8.19	y	

2.99	0.82	0.48	4.09	1.41	0.75		
2.70	0.53	0.31	2.19	0.49	-0.26		
3.55	1.38	0.80	3.17	0.49	0.26		
3.17	1.00	0.58	7.72	**5.04**	2.69		
3.99	1.82	1.06	11.48	**8.80**	4.70		
1.54	0.63	-0.37	1.75	0.93	-0.49		
0.63	1.54	-0.90	0.43	2.25	-1.20		
4.50	2.33	1.36	3.05	0.37	0.20		
2.65	0.48	0.28	2.23	0.45	-0.24		
4.21	2.04	1.19	5.58	2.90	1.55		
6.56	**4.39**	2.56	3.73	1.05	0.56		
10.28	**8.11**	4.73	7.30	**4.62**	2.47	y	
6.72	**4.55**	2.65	2.27	0.41	-0.22		
3.29	1.12	0.65	3.11	0.43	0.23		
6.96	**4.79**	2.79	4.23	1.55	0.83		
7.64	**5.47**	3.19	3.85	1.17	0.63		
2.80	0.63	0.37	2.87	0.19	0.10		
4.54	2.37	1.38	3.14	0.46	0.25		
2.41	0.24	0.14	6.47	3.79	2.02		
1.32	0.85	-0.49	1.75	0.93	-0.50		
4.72	2.55	1.48	6.03	3.35	1.79		
1.70	0.47	-0.27	2.32	0.36	-0.19		
1.92	0.25	-0.15	3.19	0.51	0.27		
0.20	1.97	-1.15	1.44	1.24	-0.66		
2.20	0.03	0.02	0.99	1.69	-0.90		
0.58	1.59	-0.92	2.54	0.14	-0.07		
1.03	1.14	-0.66	4.23	1.55	0.82		
1.04	1.13	-0.66	0.86	1.82	-0.97		
1.98	0.19	-0.11	3.32	0.64	0.34		
1.02	1.15	-0.67	3.78	1.10	0.59		
1.05	1.12	-0.65	3.03	0.35	0.19		
0.87	1.30	-0.76	6.01	3.33	1.78		
1.15	1.02	-0.59	2.14	0.54	-0.29		
1.36	0.81	-0.47	2.31	0.37	-0.20		
5.53	3.36	1.96	9.81	**7.13**	3.81	x	artifact a
2.10	0.07	-0.04	6.37	3.69	1.97		
1.01	1.16	-0.68	2.97	0.29	0.15		
2.61	0.44	0.26	2.59	0.09	-0.05		
0.45	1.72	-1.00	3.73	1.05	0.56		
0.96	1.21	-0.70	1.90	0.78	-0.41		
4.28	2.11	1.23	9.39	**6.71**	3.58		
0.74	1.43	-0.83	2.06	0.62	-0.33		
1.55	0.62	-0.36	4.68	2.00	1.06		
1.52	0.65	-0.38	4.84	2.16	1.15		
2.14	0.03	-0.01	3.00	0.32	0.17		
0.91	1.26	-0.73	2.20	0.48	-0.26		
0.93	1.24	-0.72	2.81	0.13	0.07		

0.57	1.60	-0.93	2.69	0.01	0.01	
1.32	0.85	-0.49	4.74	2.06	1.10	
1.68	0.49	-0.28	10.80	**8.12**	4.33	y
0.43	1.74	-1.01	2.24	0.44	-0.24	
5.17	3.00	1.75	5.36	2.68	1.43	
0.97	1.20	-0.70	2.73	0.05	0.03	
2.96	0.79	0.46	2.10	0.58	-0.31	
4.16	1.99	1.16	3.78	1.10	0.59	
17.77	**15.60**	9.09	15.63	**12.95**	6.91	y
7.98	**5.81**	3.39	9.49	**6.81**	3.63	y
0.89	1.28	-0.75	1.08	1.60	-0.86	
3.07	0.90	0.52	2.87	0.19	0.10	
4.20	2.03	1.18	4.67	1.99	1.06	
0.92	1.25	-0.73	1.79	0.89	-0.47	
1.82	0.35	-0.20	1.40	1.28	-0.69	
2.02	0.15	-0.08	1.62	1.06	-0.57	
2.32	0.15	0.09	2.00	0.68	-0.36	
2.39	0.22	0.13	2.87	0.19	0.10	
1.86	0.31	-0.18	1.63	1.05	-0.56	
43.24	**41.07**	23.94	6.43	3.75	2.00	
2.90	0.73	0.43	3.50	0.82	0.44	
1.28	0.89	-0.52	4.51	1.83	0.98	
1.66	0.51	-0.30	11.01	**8.33**	4.45	y
4.43	2.26	1.32	6.28	3.60	1.92	
38.18	**36.01**	20.99	21.29	**18.61**	9.93	
14.77	**12.60**	7.34	3.68	1.00	0.53	
0.48	1.69	-0.99	0.47	2.21	-1.18	
0.78	1.39	-0.81	1.90	0.78	-0.42	
1.81	0.36	-0.21	3.36	0.68	0.36	
3.27	1.10	0.64	0.89	1.79	-0.96	
0.74	1.43	-0.83	1.36	1.32	-0.71	
4.54	2.37	1.38	7.67	**4.99**	2.66	y
5.27	3.10	1.81	10.27	**7.59**	4.05	y
0.72	1.45	-0.84	1.49	1.19	-0.63	
0.88	1.29	-0.75	0.99	1.69	-0.90	
3.41	1.24	0.72	1.56	1.12	-0.60	
1.08	1.09	-0.63	0.56	2.12	-1.13	
0.72	1.45	-0.85	1.18	1.50	-0.80	
1.90	0.27	-0.16	3.13	0.45	0.24	
1.04	1.13	-0.66	3.73	1.05	0.56	
0.87	1.30	-0.76	2.34	0.34	-0.18	
1.01	1.16	-0.67	2.91	0.23	0.12	
2.22	0.05	0.03	8.18	**5.50**	2.94	y
2.45	0.28	0.16	3.95	1.27	0.68	
2.58	0.41	0.24	2.90	0.22	0.12	
1.09	1.08	-0.63	3.38	0.70	0.37	
8.33	**6.16**	3.59	2.10	0.58	-0.31	

2.45	0.28	0.16	7.66	4.98	2.66	y	
2.96	0.79	0.46	6.37	3.69	1.97		
1.26	0.91	-0.53	3.58	0.90	0.48		
1.38	0.79	-0.46	4.30	1.62	0.86		
3.27	1.10	0.64	0.61	2.07	-1.10		
1.18	0.99	-0.57	1.80	0.88	-0.47		
0.85	1.32	-0.77	3.76	1.08	0.57		
0.58	1.59	-0.93	1.77	0.91	-0.49		
3.01	0.84	0.49	7.18	4.50	2.40		
0.81	1.36	-0.79	4.69	2.01	1.08		
2.02	0.15	-0.09	4.48	1.80	0.96		
0.37	1.80	-1.05	1.94	0.74	-0.40		
1.10	1.07	-0.62	2.48	0.20	-0.11		
4.83	2.66	1.55	2.63	0.05	-0.03		
5.06	2.89	1.68	4.05	1.37	0.73		
0.97	1.20	-0.70	2.83	0.15	0.08		
1.92	0.25	-0.14	1.81	0.87	-0.46		
0.56	1.61	-0.94	4.68	2.00	1.07		
1.06	1.11	-0.64	5.36	2.68	1.43		
12.90	10.73	6.26	1.35	1.33	-0.71	x	toxic a,b,c
1.66	0.51	-0.30	0.92	1.76	-0.94		
1.12	1.05	-0.61	1.72	0.96	-0.51		
7.62	5.45	3.18	2.04	0.64	-0.34		
3.51	1.34	0.78	3.00	0.32	0.17		
1.46	0.71	-0.41	2.83	0.15	0.08		
1.41	0.76	-0.45	5.30	2.62	1.40		
3.85	1.68	0.98	1.57	1.11	-0.59		
2.47	0.30	0.18	7.93	5.25	2.80		
2.78	0.61	0.36	3.89	1.21	0.65		
4.72	2.55	1.49	0.89	1.79	-0.95		
2.56	0.39	0.23	2.38	0.30	-0.16		
3.50	1.33	0.77	2.12	0.56	-0.30		
1.76	0.41	-0.24	5.76	3.08	1.65		
3.64	1.47	0.86	1.60	1.08	-0.58		
1.86	0.31	-0.18	1.24	1.44	-0.77		
4.33	2.16	1.26	3.82	1.14	0.61		
0.73	1.44	-0.84	1.75	0.93	-0.49		
2.05	0.12	-0.07	3.52	0.84	0.45		
3.75	1.58	0.92	2.50	0.18	-0.10		
2.17	1.16		2.68	1.27			
	3.48			3.80			
	1.72			1.87			

		A	B	C
22.53	3psSD	14.30	8.37	3.77
20.06	3ngSD	1.90	4.95	2.76
22.89	SumSD	16.20	13.32	6.53
	DiffMn	16.14	12.22	20.50

21.83	SmovrDiff	1.00	1.09	0.32
1.26	1minus	0.00	-0.09	0.68
0.96				
1.29				
0.44				
2.60				
1.32				
0.92				
4.25				
1.41				
3.80				
1.74				
9.72				
13.69				

					% inf	abs dev	robust Z
50011.00	A02	M-016603- nudix (nucleosi	11163.00	NUDT4	1.48	1.15	-0.51
50011.00	A04	M-005218- nudix (nucleosi	4521.00	NUDT1	1.23	1.40	-0.62
50011.00	A05	M-008594- phosphoribosyl	2618.00	GART	2.31	0.32	-0.14
50011.00	A06	M-008217- 5'-nucleotidase	4907.00	NT5E	4.61	1.98	0.87
50011.00	A07	M-008900- glycine amidinc	2628.00	GATM	7.86	5.23	2.30
50011.00	A08	M-032020- 5'-nucleotidase	51251.00	NT5C3	3.54	0.91	0.40
50011.00	A09	M-006366- glucosidase, be	2629.00	GBA	0.39	2.24	-0.98
50011.00	A10	M-019484- neuropilin 1	8829.00	NRP1	5.81	3.18	1.40
50011.00	A11	M-004039- glutaryl-Coenzy	2639.00	GCDH	1.12	1.51	-0.67
50011.00	A12	M-005133- NAD(P)H dehyd	1728.00	NQO1	3.09	0.46	0.20
50011.00	A13	M-010328- GTP cyclohydro	2643.00	GCH1	1.42	1.21	-0.53
50011.00	A14	M-009579- nucleoside pho	4860.00	NP	2.28	0.35	-0.16
50011.00	A15	M-017411- glucosaminyl (N	2651.00	GCNT2	2.03	0.60	-0.27
50011.00	A16	M-009809- nicotinamide nu	23530.00	NNT	3.72	1.09	0.48
50011.00	A17	M-017907- glycine cleavag	2653.00	GCSH	1.21	1.42	-0.62
50011.00	A18	M-010351- nicotinamide N	4837.00	NNMT	1.48	1.15	-0.51
50011.00	A19	M-009856- gamma-glutam	2677.00	GGCX	0.89	1.74	-0.76
50011.00	A20	M-017902- nitrilase family,	56954.00	NIT2	1.13	1.50	-0.66
50011.00	A21	M-005883- gamma-glutam	8836.00	GGH	3.57	0.94	0.41
50011.00	A23	M-016477- geranylgeranyl	9453.00	GGPS1	3.90	1.27	0.56
50011.00	B02	M-009134- ubiquitin-conju	7328.00	UBE2H	3.42	0.79	0.34
50011.00	B04	M-009095- ubiquitin-conju	7327.00	UBE2G2	1.28	1.35	-0.59
50011.00	B05	M-011096- ornithine aminc	4942.00	OAT	3.22	0.59	0.26
50011.00	B06	M-008845- ubiquitin-conju	10477.00	UBE2E3	3.59	0.96	0.42
50011.00	B07	M-006668- ornithine decar	4953.00	ODC1	2.92	0.29	0.13
50011.00	B08	M-008850- ubiquitin-conju	7324.00	UBE2E1	1.70	0.93	-0.41
50011.00	B09	M-009679- oxoglutarate (a	4967.00	OGDH	0.85	1.78	-0.78
50011.00	B10	M-008478- ubiquitin-conju	7323.00	UBE2D3	0.62	2.01	-0.88
50011.00	B11	M-004045- 3-oxoacid CoA t	5019.00	OXCT1	1.44	1.19	-0.52
50011.00	B12	M-010383- ubiquitin-conju	7322.00	UBE2D2	1.48	1.15	-0.50
50011.00	B13	M-012187- 26 serine prote	8909.00	P11	1.72	0.91	-0.40
50011.00	B14	M-004693- ubiquitin-conju	11065.00	UBE2C	0.56	2.07	-0.91
50011.00	B15	M-004275- procollagen-prc	5033.00	P4HA1	0.86	1.77	-0.78
50011.00	B16	M-009930- ubiquitin-conju	7320.00	UBE2B	1.46	1.17	-0.51
50011.00	B17	M-003690- procollagen-prc	5034.00	P4HB	0.39	2.24	-0.98
50011.00	B18	M-009424- ubiquitin-conju	7319.00	UBE2A	4.80	2.17	0.95
50011.00	B19	M-016646- pyrroline-5-carl	29920.00	PYCR2	0.78	1.85	-0.81
50011.00	B20	M-005249- ubiquitin-activa	9039.00	UBE1C	0.12	2.51	-1.10
50011.00	B21	M-008860- proliferation-as	5036.00	PA2G4	0.78	1.85	-0.82
50011.00	B23	M-005983- proprotein conv	5046.00	PCSK6	0.65	1.98	-0.87
50011.00	C02	M-011092- sialidase 1 (lyso	4758.00	NEU1	1.97	0.66	-0.29
50011.00	C04	M-012589- NADH dehydrog	4729.00	NDUFV2	3.26	0.63	0.28
50011.00	C05	M-012538- galactosidase, a	2717.00	GLA	1.11	1.52	-0.67
50011.00	C06	M-031021- NADH dehydrog	374291.00	NDUFS7	1.61	1.02	-0.45
50011.00	C07	M-012539- galactosidase, b	2720.00	GLB1	0.65	1.98	-0.87
50011.00	C08	M-019602- NADH dehydrog	4724.00	NDUFS4	2.15	0.48	-0.21

50011.00	C09	M-009305- glycine dehydrc	2731.00	GLDC	0.77	1.86	-0.82
50011.00	C10	M-015770- NADH dehydro	4720.00	NDUFS2	1.22	1.41	-0.62
50011.00	C11	M-021332- glutaredoxin 2	51022.00	GLRX2	0.92	1.71	-0.75
50011.00	C12	M-008296- N-deacetylase/	64579.00	NDST4	0.51	2.12	-0.93
50011.00	C13	M-008430- glutamate-amn	51557.00	GLULD1	0.40	2.23	-0.98
50011.00	C14	M-017151- trimethylguano	96764.00	TGS1	0.62	2.01	-0.88
50011.00	C15	M-008258- guanosine mon	2766.00	GMPR	0.60	2.03	-0.89
50011.00	C16	M-009347- cytochrome b5	51167.00	CYB5R4	0.43	2.20	-0.97
50011.00	C17	M-009583- guanosine mon	51292.00	GMPR2	0.47	2.16	-0.95
50011.00	C18	M-008399- N-acetyltransfe	9027.00	NAT8	1.65	0.98	-0.43
50011.00	C19	M-016084- guanine nucleo	2790.00	**GNG10**	**2.89**	0.26	0.11
50011.00	C20	M-008560- N-acetyltransfe	10.00	NAT2	0.84	1.79	-0.79
50011.00	C21	M-009894- glyceronephosp	8443.00	GNPAT	1.03	1.60	-0.70
50011.00	C23	M-004995- glucosamine-6-	10007.00	GNPDA1	0.27	2.36	-1.04
50011.00	D02	M-004509- ubiquitin-activa	7317.00	UBE1	0.73	1.90	-0.83
50011.00	D04	M-008616- ubiquitin associ	53347.00	UBASH3A	11.08	**8.45**	3.71
50011.00	D05	M-008797- platelet-activat	5049.00	PAFAH1B2	6.96	4.33	1.90
50011.00	D06	M-012556- tyrosinase-relat	7306.00	TYRP1	3.10	0.47	0.21
50011.00	D07	M-009443- platelet-activat	5050.00	PAFAH1B3	0.72	1.91	-0.84
50011.00	D08	M-012555- tyrosinase (ocu	7299.00	**TYR**	**11.99**	**9.36**	4.11
50011.00	D09	M-009824- propionyl Coen	5096.00	PCCB	0.76	1.87	-0.82
50011.00	D10	M-010676- thioredoxin dor	81567.00	TXNDC5	3.68	1.05	0.46
50011.00	D11	M-005985- proprotein con	5122.00	PCSK1	0.73	1.90	-0.84
50011.00	D12	M-005394- transformation	8295.00	TRRAP	1.07	1.56	-0.69
50011.00	D13	M-005988- proprotein con	9159.00	PCSK7	1.10	1.53	-0.67
50011.00	D14	M-010895- thiopurine S-me	7172.00	TPMT	6.65	4.02	1.76
50011.00	D15	M-011912- apoptosis-induc	9131.00	AIFM1	2.52	0.11	-0.05
50011.00	D16	M-009776- triosephosphat	7167.00	TPI1	3.23	0.60	0.26
50011.00	D17	M-007644- phosphodiester	5138.00	PDE2A	1.52	1.11	-0.49
50011.00	D18	M-006049- transmembrane	64699.00	TMPRSS3	0.55	2.08	-0.92
50011.00	D19	M-007645- phosphodiester	5139.00	PDE3A	2.84	0.21	0.09
50011.00	D20	M-005744- transmembrane	7108.00	TM7SF2	1.05	1.58	-0.69
50011.00	D21	M-007646- phosphodiester	5140.00	PDE3B	1.42	1.21	-0.53
50011.00	D23	M-007647- phosphodiester	5141.00	PDE4A	0.68	1.95	-0.86
50011.00	E02	M-012543- N-acetylglucosa	4669.00	NAGLU	2.32	0.31	-0.14
50011.00	E04	M-010066- 5-methyltetrah	4552.00	MTRR	8.87	**6.24**	2.74
50011.00	E05	M-008226- glucosamine (N	2799.00	GNS	8.95	**6.32**	2.78
50011.00	E06	M-010349- 5,10-methylene	4524.00	MTHFR	5.64	3.01	1.32
50011.00	E07	M-015811- gephyrin	10243.00	GPHN	4.26	1.63	0.72
50011.00	E08	M-009539- methylthioader	4507.00	MTAP	1.74	0.89	-0.39
50011.00	E09	M-008253- glyoxylate redu	9380.00	GRHPR	4.51	1.88	0.83
50011.00	E10	M-012464- methionine sulf	4482.00	MSRA	5.97	3.34	1.47
50011.00	E11	M-003674- protein disulfid	2923.00	PDIA3	9.53	**6.90**	3.03
50011.00	E12	M-013207- mitochondrial r	10884.00	MRPS30	3.15	0.52	0.23
50011.00	E13	M-020112- ATG7 autophag	10533.00	ATG7	8.92	**6.29**	2.76
50011.00	E14	M-019115- molybdenum co	4338.00	MOCS2	2.93	0.30	0.13
50011.00	E15	M-011176- glutathione S-tr	2938.00	GSTA1	2.00	0.63	-0.28

50011.00	E16	M-012180- molybdenum c	4337.00	MOCS1	6.91	4.28	1.88
50011.00	E17	M-011118- glutathione S-tr	2944.00	GSTM1	0.82	1.81	-0.79
50011.00	E18	M-005966- matrix metallop	64066.00	MMP27	2.04	0.59	-0.26
50011.00	E19	M-017472- glutathione S-tr	2947.00	GSTM3	2.09	0.54	-0.24
50011.00	E20	M-005961- matrix metallop	118856.00	MMP21	3.22	0.59	0.26
50011.00	E21	M-011950- glutathione S-tr	9446.00	GSTO1	6.50	3.87	1.70
50011.00	E23	M-006730- guanylate cycla	2977.00	GUCY1A2	1.29	1.34	-0.59
50011.00	F02	M-008653- acyl-CoA thioes	26027.00	ACOT11	0.26	2.37	-1.04
50011.00	F04	M-003941- transferrin rece	7037.00	TFRC	2.79	0.16	0.07
50011.00	F05	M-007648- phosphodiester	5142.00	PDE4B	6.07	3.44	1.51
50011.00	F06	M-009686- transferrin rece	7036.00	TFR2	4.77	2.14	0.94
50011.00	F07	M-007649- phosphodiester	5143.00	PDE4C	1.75	0.88	-0.39
50011.00	F08	M-014046- transcription fa	64216.00	**TFB2M**	**13.21**	**10.58**	4.65
50011.00	F09	M-004757- phosphodiester	5144.00	PDE4D	2.38	0.25	-0.11
50011.00	F10	M-021007- transcription fa	51106.00	TFB1M	8.47	**5.84**	2.57
50011.00	F11	M-004310- phosphodiester	5147.00	PDE6D	1.75	0.88	-0.39
50011.00	F12	M-016112- tyrosyl-DNA ph	55775.00	TDP1	0.84	1.79	-0.79
50011.00	F13	M-003818- phosphodiester	5150.00	PDE7A	1.87	0.76	-0.34
50011.00	F14	M-009324- thromboxane A	6916.00	TBXAS1	1.90	0.73	-0.32
50011.00	F15	M-007659- phosphodiester	27115.00	PDE7B	5.14	2.51	1.10
50011.00	F16	M-009608- tafazzin (cardio	6901.00	TAZ	1.53	1.10	-0.48
50011.00	F17	M-010529- platelet-derive	5157.00	PDGFRL	0.77	1.86	-0.82
50011.00	F18	M-008996- transaldolase 1	6888.00	TALDO1	3.02	0.39	0.17
50011.00	F19	M-010329- pyruvate dehy	5160.00	PDHA1	3.98	1.35	0.59
50011.00	F20	M-012624- synaptojanin 2	8871.00	SYNJ2	1.45	1.19	-0.52
50011.00	F21	M-023925- pyruvate dehy	5161.00	PDHA2	3.23	0.60	0.26
50011.00	F23	M-008803- pyruvate dehy	5162.00	PDHB	0.06	2.57	-1.13
50011.00	G02	M-009626- malonyl-CoA de	23417.00	MLYCD	7.65	**5.02**	2.20
50011.00	G04	M-009248- microsomal glu	4257.00	**MGST1**	**12.21**	**9.58**	4.21
50011.00	G05	M-006731- guanylate cycla	2982.00	GUCY1A3	6.39	3.76	1.65
50011.00	G06	M-012805- meningioma ex	10724.00	MGEA5	3.89	1.26	0.55
50011.00	G07	M-006733- guanylate cycla	2983.00	**GUCY1B3**	**13.62**	**10.99**	4.83
50011.00	G08	M-010187- short-chain de	79154.00	MGC4172	2.87	0.24	0.10
50011.00	G09	M-012541- glucuronidase,	2990.00	GUSB	1.75	0.88	-0.39
50011.00	G10	M-016736- beta-1,3-N-acet	148789.00	B3GALNT2	7.16	4.53	1.99
50011.00	G11	M-017726- glycogen synth	2997.00	GYS1	3.61	0.98	0.43
50011.00	G12	M-015781- chitinase doma	66005.00	CHID1	5.72	3.09	1.36
50011.00	G13	M-012702- glycogen synth	2998.00	GYS2	1.34	1.29	-0.57
50011.00	G14	M-012441- mannosyl (alph	11320.00	MGAT4A	3.53	0.90	0.39
50011.00	G15	M-005888- granzyme A (gr	3001.00	**GZMA**	**10.99**	**8.36**	3.67
50011.00	G16	M-008751- monoacylglycer	80168.00	MOGAT2	2.60	0.03	-0.02
50011.00	G17	M-005889- granzyme B (gr	3002.00	GZMB	5.28	2.65	1.16
50011.00	G18	M-008693- methionyl ami	23173.00	METAP1	3.89	1.26	0.55
50011.00	G19	M-008448- NAD(P) depend	50814.00	NSDHL	9.03	**6.40**	2.81
50011.00	G20	M-009690- mesoderm spe	4232.00	MEST	6.36	3.73	1.64
50011.00	G21	M-011964- H2A histone fa	9555.00	H2AFY	8.91	**6.28**	2.76
50011.00	G23	M-009470- hydroxyacyl-Co	3030.00	HADHA	2.80	0.17	0.07

50011.00	H02	M-011786-	surfeit 1	6834.00	SURF1	8.27	5.64	2.48
50011.00	H04	M-008990-	sulfotransferas	6817.00	SULT1A1	1.75	0.88	-0.39
50011.00	H05	M-019829-	protein disulfid	64714.00	**PDIA2**	**11.32**	8.69	3.82
50011.00	H06	M-006642-	sulfatase 2	55959.00	SULF2	6.60	3.97	1.74
50011.00	H07	M-019826-	protein disulfid	10954.00	PDIA5	6.31	3.68	1.61
50011.00	H08	M-010538-	suppression of	6764.00	**ST5**	**15.69**	13.06	5.74
50011.00	H09	M-009505-	pyruvate dehy	55066.00	PDPR	5.80	3.17	1.39
50011.00	H10	M-003712-	suppression of	6768.00	ST14	12.28	9.65	4.24
50011.00	H11	M-009855-	peroxisomal tra	55825.00	PECR	2.62	0.01	-0.01
50011.00	H12	M-006669-	spermidine syn	6723.00	SRM	7.34	4.71	2.07
50011.00	H13	M-017815-	progressive ext	56652.00	PEO1	6.46	3.83	1.68
50011.00	H14	M-004210-	steroid-5-alpha	6716.00	SRD5A2	4.75	2.12	0.93
50011.00	H15	M-008883-	phosphoglycera	5223.00	PGAM1	2.23	0.40	-0.18
50011.00	H16	M-004211-	steroid-5-alpha	6715.00	SRD5A1	2.14	0.49	-0.22
50011.00	H17	M-008703-	protein geranyl	5229.00	PGGT1B	4.12	1.49	0.66
50011.00	H18	M-009646-	squalene epoxi	6713.00	SQLE	4.61	1.98	0.87
50011.00	H19	M-007674-	phosphorylase	5257.00	PHKB	8.94	6.31	2.77
50011.00	H20	M-006673-	serine palmitoy	10558.00	SPTLC1	6.23	3.60	1.58
50011.00	H21	M-018421-	phosphatase, o	162466.00	PHOSPHO1	4.67	2.04	0.89
50011.00	H23	M-016904-	phosphohistidi	29085.00	PHPT1	3.71	1.08	0.47
50011.00	I02	M-009348-	malic enzyme 1	4199.00	ME1	6.74	4.11	1.81
50011.00	I04	M-004905-	methylcrotono	64087.00	MCCC2	1.56	1.07	-0.47
50011.00	I05	M-008298-	hydroxyacyl-Co	3033.00	HADH	12.07	9.44	4.15
50011.00	I06	M-005939-	membrane-bou	8720.00	MBTPS1	7.67	5.04	2.21
50011.00	I07	M-012052-	hydroxyacylglu	3029.00	HAGH	6.41	3.78	1.66
50011.00	I08	M-013779-	enolase-phosp	58478.00	ENOPH1	6.82	4.19	1.84
50011.00	I09	M-011685-	histidine ammo	3034.00	HAL	4.98	2.35	1.03
50011.00	I10	M-004771-	mitogen-activa	23118.00	MAP3K7IP	4.29	1.66	0.73
50011.00	I11	M-005894-	transmembran	9407.00	TMPRSS11	2.63	0.00	0.00
50011.00	I12	M-009369-	monoamine oxi	4128.00	MAOA	1.85	0.78	-0.34
50011.00	I13	M-011049-	hexosaminidas	3073.00	HEXA	2.39	0.24	-0.10
50011.00	I14	M-012175-	mannosidase,	4126.00	MANBA	5.37	2.74	1.20
50011.00	I15	M-011050-	hexosaminidas	3074.00	HEXB	7.52	4.89	2.15
50011.00	I16	M-009650-	mannosidase, a	4125.00	MAN2B1	5.00	2.37	1.04
50011.00	I17	M-009823-	homogentisate	3081.00	HGD	9.63	7.00	3.08
50011.00	I18	M-009806-	mannosidase, a	4124.00	MAN2A1	1.71	0.92	-0.41
50011.00	I19	M-005895-	HGF activator	3083.00	HGFAC	1.42	1.21	-0.53
50011.00	I20	M-009622-	lysophospholip	23659.00	LYPLA3	4.87	2.24	0.98
50011.00	I21	M-004073-	hypoxia-induci	55662.00	HIF1AN	3.61	0.98	0.43
50011.00	I23	M-006479-	holocarboxylas	3141.00	HLCS	1.73	0.90	-0.40
50011.00	J02	M-009873-	sepiapterin red	6697.00	SPR	4.32	1.69	0.74
50011.00	J04	M-008790-	sterol O-acyltra	8435.00	SOAT2	1.15	1.48	-0.65
50011.00	J05	M-011752-	phosphatidylin	5277.00	PIGA	7.03	4.40	1.93
50011.00	J06	M-006678-	sphingomyelin	55512.00	SMPD3	1.64	0.99	-0.43
50011.00	J07	M-005250-	phosphoinositi	5289.00	PIK3C3	2.47	0.16	-0.07
50011.00	J08	M-006676-	sphingomyelin	6609.00	SMPD1	2.80	0.17	0.08
50011.00	J09	M-006775-	phosphoinositi	5293.00	PIK3CD	2.85	0.22	0.09

50011.00	J10	M-027285- SMA4	11039.00	SMA4	0.83	1.80	-0.79
50011.00	J11	M-004058- phosphatidylin	8395.00	PIP5K1B	3.46	0.83	0.37
50011.00	J12	M-007575- solute carrier fa	6519.00	SLC3A1	0.47	2.16	-0.95
50011.00	J13	M-004782- phosphatidylin	23396.00	PIP5K1C	7.04	4.41	1.94
50011.00	J14	M-007498- solute carrier fa	11001.00	**SLC27A2**	**13.02**	**10.39**	4.57
50011.00	J15	M-005058- phosphatidylin	200576.00	PIP5K3	1.94	0.69	-0.30
50011.00	J16	M-015817- protein arginine	10419.00	**PRMT5**	**12.37**	**9.74**	4.28
50011.00	J17	M-009886- phospholipase	5321.00	PLA2G4A	3.60	0.97	0.43
50011.00	J18	M-011546- ST3 beta-galact	8869.00	ST3GAL5	4.70	2.07	0.91
50011.00	J19	M-005999- plasminogen ac	5327.00	PLAT	2.13	0.50	-0.22
50011.00	J20	M-019206- ST3 beta-galact	6482.00	**ST3GAL1**	**7.94**	**5.31**	2.33
50011.00	J21	M-006000- plasminogen ac	5328.00	PLAU	4.39	1.76	0.77
50011.00	J23	M-008485- phospholipase	5331.00	PLCB3	1.93	0.70	-0.31
50011.00	K02	M-009256- lysophospholip	11313.00	LYPLA2	4.82	2.19	0.96
50011.00	K04	M-010007- lysophospholip	10434.00	LYPLA1	3.57	0.94	0.41
50011.00	K05	M-016220- hydroxymethyl	3145.00	HMBS	5.06	2.43	1.07
50011.00	K06	M-008624- lanosterol synt	4047.00	LSS	3.57	0.94	0.41
50011.00	K07	M-019290- 3-hydroxymeth	3155.00	HMGCL	5.40	2.77	1.22
50011.00	K08	M-010272- lecithin retinol	9227.00	LRAT	5.94	3.31	1.46
50011.00	K09	M-009811- 3-hydroxy-3-me	3156.00	HMGCR	9.02	**6.39**	2.81
50011.00	K10	M-005930- X-prolyl aminop	63929.00	XPNPEP3	0.40	2.23	-0.98
50011.00	K11	M-009808- 3-hydroxy-3-me	3157.00	HMGCS1	7.29	**4.66**	2.05
50011.00	K12	M-009435- ubiquitin-conju	51619.00	UBE2D4	4.93	2.30	1.01
50011.00	K13	M-010179- 3-hydroxy-3-me	3158.00	HMGCS2	2.20	0.43	-0.19
50011.00	K14	M-018979- carboxymethyl	134147.00	CMBL	8.38	**5.75**	2.53
50011.00	K15	M-006372- heme oxygenas	3162.00	HMOX1	6.27	3.64	1.60
50011.00	K16	M-005925- leishmanolysin-	89782.00	LMLN	6.84	4.21	1.85
50011.00	K17	M-009630- heme oxygenas	3163.00	HMOX2	2.76	0.13	0.06
50011.00	K18	M-004043- lipase A, lysoso	3988.00	LIPA	12.57	**9.94**	4.37
50011.00	K19	M-008488- histamine N-me	3176.00	HNMT	2.79	0.16	0.07
50011.00	K20	M-018950- phospholysine	64077.00	LHPP	4.87	2.24	0.99
50011.00	K21	M-004033- protein arginine	3275.00	PRMT2	0.68	1.95	-0.86
50011.00	K23	M-010102- protein arginine	3276.00	PRMT1	3.42	0.79	0.35
50011.00	L02	M-010486- ST6 beta-galact	6480.00	ST6GAL1	0.22	2.41	-1.06
50011.00	L04	M-004906- serine hydroxy	6472.00	SHMT2	4.29	1.66	0.73
50011.00	L05	M-009594- phospholipase	5332.00	PLCB4	4.25	1.62	0.71
50011.00	L06	M-004617- serine hydroxy	6470.00	SHMT1	1.02	1.61	-0.71
50011.00	L07	M-009413- phospholipase	5337.00	PLD1	1.76	0.87	-0.38
50011.00	L08	M-006036- sonic hedgehog	6469.00	SHH	13.23	**10.60**	4.66
50011.00	L09	M-004284- procollagen-lys	5351.00	PLOD1	3.28	0.65	0.28
50011.00	L10	M-020350- SH3-domain bi	23677.00	**SH3BP4**	**9.23**	**6.60**	2.90
50011.00	L11	M-011099- phosphomann	5373.00	PMM2	1.09	1.54	-0.68
50011.00	L12	M-009053- N-sulfoglucosa	6448.00	**SGSH**	**8.42**	**5.79**	2.54
50011.00	L13	M-008973- pancreatic lipas	5406.00	PNLIP	1.57	1.06	-0.47
50011.00	L14	M-014653- sphingosine-1-p	81537.00	SGPP1	1.79	0.84	-0.37
50011.00	L15	M-009145- pancreatic lipas	5407.00	PNLIPRP1	1.51	1.12	-0.49
50011.00	L16	M-031917- SET domain co	387893.00	SETD8	4.89	2.26	0.99

50011.00	L17	M-017678- phenylethanola	5409.00	PNMT	2.54	0.09	-0.04
50011.00	L18	M-014643- SET domain cor	80854.00	SETD7	5.33	2.70	1.19
50011.00	L19	M-011943- polymerase (RN	5433.00	POLR2D	2.06	0.57	-0.25
50011.00	L20	M-006357- SUMO1/sentrir	29843.00	SENP1	0.35	2.28	-1.00
50011.00	L21	M-016499- protein-O-manı	10585.00	POMT1	1.10	1.53	-0.67
50011.00	L23	M-009229- paraoxonase 1	5444.00	PON1	1.49	1.14	-0.50
50011.00	M02	M-005924- legumain	5641.00	LGMN	5.81	3.18	1.40
50011.00	M04	M-014291- tRNA splicing er	79042.00	**TSEN34**	**10.63**	**8.00**	3.51
50011.00	M05	M-009910- hydroxysteroid	3290.00	HSD11B1	3.76	1.13	0.50
50011.00	M06	M-011717- lactase	3938.00	LCT	3.12	0.49	0.21
50011.00	M07	M-008983- hydroxysteroid	3291.00	HSD11B2	2.04	0.59	-0.26
50011.00	M08	M-008373- tubulointerstiti	64129.00	TINAGL1	1.61	1.02	-0.45
50011.00	M09	M-009723- hydroxysteroid	3292.00	HSD17B1	1.81	0.82	-0.36
50011.00	M10	M-009425- leucine carboxy	51451.00	LCMT1	0.70	1.93	-0.85
50011.00	M11	M-008474- hydroxysteroid	51144.00	HSD17B12	4.70	2.07	0.91
50011.00	M12	M-011920- like-glycosyltraı	9215.00	LARGE	1.62	1.01	-0.45
50011.00	M13	M-009478- hydroxysteroid	3294.00	HSD17B2	2.22	0.41	-0.18
50011.00	M14	M-009867- kynureninase (L	8942.00	KYNU	2.55	0.08	-0.04
50011.00	M15	M-008138- hydroxysteroid	3293.00	HSD17B3	5.70	3.07	1.35
50011.00	M16	M-005921- kallikrein B, pla	3818.00	KLKB1	2.05	0.58	-0.25
50011.00	M17	M-008140- hydroxysteroid	51478.00	HSD17B7	1.69	0.94	-0.41
50011.00	M18	M-005914- kallikrein-relate	354.00	KLK3	2.55	0.08	-0.04
50011.00	M19	M-004898- ubiquitin-conju	29089.00	UBE2T	0.51	2.12	-0.93
50011.00	M20	M-005913- kallikrein-relate	3817.00	KLK2	1.60	1.03	-0.45
50011.00	M21	M-010516- hyaluronogluco	3373.00	HYAL1	1.28	1.35	-0.59
50011.00	M23	M-009254- iduronate 2-sul	3423.00	IDS	0.54	2.09	-0.92
50011.00	N02	M-008308- serine dehydrat	113675.00	SDSL	0.84	1.79	-0.79
50011.00	N04	M-011385- succinate dehy	6391.00	SDHC	7.44	**4.81**	2.11
50011.00	N05	M-009676- paraoxonase 2	5445.00	PON2	4.63	2.00	0.88
50011.00	N06	M-009309- sterol-C4-meth	6307.00	**SC4MOL**	**14.71**	**12.08**	5.31
50011.00	N07	M-009675- paraoxonase 3	5446.00	PON3	1.68	0.95	-0.42
50011.00	N08	M-010382- spermidine/spe	6303.00	SAT1	9.28	**6.65**	2.92
50011.00	N09	M-010114- P450 (cytochro	5447.00	POR	3.23	0.60	0.26
50011.00	N10	M-010051- sarcosine dehy	1757.00	SARDH	4.48	1.85	0.81
50011.00	N11	M-012348- pyrophosphata	27068.00	PPA2	2.62	0.01	-0.01
50011.00	N12	M-020035- acyl-CoA synthe	6296.00	ACSM3	1.21	1.42	-0.62
50011.00	N13	M-019098- phosphatidic ac	8611.00	PPAP2A	1.10	1.53	-0.67
50011.00	N14	M-006353- testicular solub	55811.00	SAC	4.01	1.38	0.61
50011.00	N15	M-008256- peptidylprolyl i	51645.00	PPIL1	0.77	1.86	-0.82
50011.00	N16	M-010575- ribonucleotide	50484.00	**RRM2B**	**3.56**	0.93	0.41
50011.00	N17	M-008383- protoporphyrin	5498.00	PPOX	0.11	2.52	-1.11
50011.00	N18	M-010379- ribonucleotide	6241.00	RRM2	2.87	0.24	0.11
50011.00	N19	M-007718- palmitoyl-prote	5538.00	PPT1	1.02	1.61	-0.71
50011.00	N20	M-004270- ribonucleotide	6240.00	RRM1	0.29	2.34	-1.03
50011.00	N21	M-006005- prolylcarboxype	5547.00	PRCP	1.09	1.54	-0.68
50011.00	N23	M-020200- primase, polype	5557.00	PRIM1	0.10	2.53	-1.11
50011.00	O02	M-005245- arylacetamide c	57552.00	AADACL1	1.09	1.54	-0.68

50011.00	O04	M-024152-	mannosidase, a	23324.00	MAN2B2	0.20	2.43	-1.07
50011.00	O05	M-011056-	iduronidase, alp	3425.00	IDUA	3.11	0.48	0.21
50011.00	O06	M-008588-	adenosylhomoc	23382.00	KIAA0828	3.94	1.31	0.57
50011.00	O07	M-005900-	complement fa	3426.00	CFI	3.89	1.26	0.55
50011.00	O08	M-009223-	amine oxidase (	23028.00	AOF2	3.68	1.05	0.46
50011.00	O09	M-019065-	interferon, gam	10437.00	IFI30	2.25	0.38	-0.17
50011.00	O10	M-004785-	histidine acid pl	23262.00	HISPPD1	2.29	0.34	-0.15
50011.00	O11	M-004330-	IMP (inosine m	3615.00	IMPDH2	1.30	1.33	-0.59
50011.00	O12	M-010181-	isovaleryl Coen	3712.00	IVD	2.09	0.54	-0.24
50011.00	O13	M-011539-	inositol polypho	8821.00	INPP4B	7.38	**4.75**	2.09
50011.00	O14	M-013681-	inosine triphosp	3704.00	ITPA	1.21	1.42	-0.63
50011.00	O15	M-020005-	inositol polypho	3632.00	INPP5A	1.26	1.37	-0.60
50011.00	O16	M-015994-	interferon stim	3669.00	ISG20	2.95	0.32	0.14
50011.00	O17	M-021811-	inositol polypho	3633.00	INPP5B	0.32	2.31	-1.02
50011.00	O18	M-020852-	inositol polypho	56623.00	INPP5E	2.07	0.56	-0.24
50011.00	O19	M-007285-	N-acetylneuram	140838.00	NANP	5.16	2.53	1.11
50011.00	O20	M-003013-	inositol polypho	3635.00	INPP5D	1.47	1.16	-0.51
50011.00	O21	M-005884-	gamma-glutam	2678.00	GGT1	2.53	0.10	-0.05
50011.00	O23	M-005885-	gamma-glutam	2679.00	GGT3	3.09	0.46	0.20
50011.00	P02	M-020033-	processing of p	10248.00	POP7	2.94	0.31	0.14
50011.00	P04	M-006026-	renin	5972.00	REN	1.38	1.25	-0.55
50011.00	P05	M-009543-	proline dehydro	5625.00	PRODH	3.46	0.83	0.36
50011.00	P06	M-009451-	retinol dehydro	50700.00	RDH8	3.46	0.83	0.36
50011.00	P07	M-013098-	proline dehydro	58510.00	PRODH2	1.62	1.01	-0.45
50011.00	P08	M-008220-	retinol dehydro	5959.00	RDH5	1.12	1.51	-0.67
50011.00	P09	M-006011-	protease, serin	10279.00	PRSS16	1.15	1.48	-0.65
50011.00	P10	M-006025-	RCE1 homolog,	9986.00	RCE1	1.63	1.00	-0.44
50011.00	P11	M-006016-	protease, serin	5651.00	PRSS7	3.49	0.86	0.38
50011.00	P12	M-007262-	Rab geranylgera	5876.00	RABGGTB	2.63	0.00	0.00
50011.00	P13	M-008207-	growth-inhibitin	219595.00	PSMAL	4.50	1.87	0.82
50011.00	P14	M-005097-	Rab geranylgera	5875.00	RABGGTA	2.98	0.35	0.15
50011.00	P15	M-006019-	proteasome (pr	5699.00	PSMB10	0.40	2.23	-0.98
50011.00	P16	M-008502-	quinoid dihydro	5860.00	QDPR	5.49	2.86	1.26
50011.00	P17	M-011362-	proteasome (pr	5692.00	PSMB4	2.19	0.44	-0.20
50011.00	P18	M-014246-	pyrroline-5-carl	65263.00	PYCRL	1.32	1.31	-0.58
50011.00	P19	M-006020-	proteasome (pr	5694.00	PSMB6	7.23	4.60	2.02
50011.00	P20	M-004691-	prostaglandin I	5740.00	PTGIS	2.23	0.40	-0.17
50011.00	P21	M-006023-	proteasome (pr	5698.00	PSMB9	0.23	2.40	-1.06
50011.00	P23	M-008568-	phosphatidylse	9791.00	PTDSS1	0.00	2.63	-1.16
					mdn	2.63	1.54	
					3MAD		4.61	
		%hits	5.00		MADc		2.28	
					Plate 11 Z scores			

50011.00	C22							21.60
50011.00	D22					13.52		17.66
50011.00	E22					12.68		19.93

50011.00	F22					15.51	23.25
					mn	13.90	20.61
					sd	1.45	2.39
50011.00	G22					0.93	5.58
50011.00	H22						0.91
50011.00	I22					0.00	1.61
50011.00	J22					1.35	2.00
						0.76	2.53
						0.69	2.08
50011.00	G03	M-003290-	polo-like kinase	5347.00	PLK1 SMAR	5.44	3.66
50011.00	H03	M-003290-	polo-like kinase	5347.00	PLK1 SMAR	1.99	3.79
50011.00	I03	D-001206-	siControl non-targeting siR			7.00	4.60
50011.00	J03	D-001206-	siControl non-targeting siR			5.75	3.36
50011.00	K03	D-001600-	siGLO RISC-free siRNA			12.62	10.52
50011.00	L03	D-001600-	siGLO RISC-free siRNA			15.76	10.19

% inf	abs dev	robust Z	% inf	abs dev	robust Z		
1.83	0.80	-0.39	4.48	0.89	0.35		
0.48	2.15	-1.04	0.68	2.91	-1.13		
1.68	0.95	-0.46	1.77	1.82	-0.71		
4.80	2.17	1.06	5.15	1.56	0.61		
8.93	6.30	3.06	8.07	4.48	1.74	x	toxic b,c
3.22	0.59	0.29	4.01	0.42	0.16		
1.45	1.18	-0.58	0.71	2.88	-1.12		
2.72	0.09	0.04	2.18	1.41	-0.55		
1.93	0.70	-0.34	0.39	3.20	-1.24		
2.11	0.52	-0.25	0.46	3.13	-1.22		
2.19	0.44	-0.21	2.66	0.93	-0.36		
3.93	1.30	0.63	1.58	2.01	-0.78		
5.26	2.63	1.28	1.06	2.53	-0.98		
1.61	1.02	-0.50	2.46	1.13	-0.44		
0.79	1.84	-0.89	3.56	0.03	-0.01		
1.51	1.12	-0.55	3.62	0.03	0.01		
1.62	1.01	-0.49	0.50	3.09	-1.20		
0.95	1.68	-0.82	0.83	2.76	-1.07		
2.12	0.51	-0.25	2.13	1.46	-0.57		
1.84	0.79	-0.38	1.56	2.03	-0.79		
1.47	1.16	-0.57	5.87	2.28	0.88		
0.46	2.17	-1.06	0.95	2.64	-1.03		
2.44	0.19	-0.09	1.97	1.62	-0.63		
4.05	1.42	0.69	3.52	0.07	-0.03		
3.55	0.92	0.45	1.66	1.93	-0.75		
3.73	1.10	0.53	4.14	0.55	0.21		
2.17	0.46	-0.22	2.80	0.79	-0.31		
0.39	2.24	-1.09	0.06	3.53	-1.37		
4.61	1.98	0.96	2.89	0.70	-0.27		
2.47	0.16	-0.08	1.49	2.10	-0.82		
2.18	0.45	-0.22	2.36	1.23	-0.48		
3.20	0.57	0.28	2.06	1.53	-0.59		
2.67	0.04	0.02	3.28	0.31	-0.12		
3.29	0.66	0.32	1.32	2.27	-0.88		
2.77	0.14	0.07	1.57	2.02	-0.78		
5.89	3.26	1.58	6.63	3.04	1.18		
1.75	0.88	-0.43	1.27	2.32	-0.90		
1.81	0.82	-0.40	2.67	0.92	-0.36		
0.70	1.93	-0.94	1.39	2.20	-0.85		
6.39	3.76	1.83	3.09	0.50	-0.19		
1.00	1.63	-0.79	1.52	2.07	-0.80		
4.07	1.44	0.70	1.11	2.48	-0.96		
2.00	0.63	-0.31	5.95	2.36	0.92		
0.85	1.78	-0.86	1.89	1.70	-0.66		
0.45	2.18	-1.06	0.86	2.73	-1.06		
0.63	2.00	-0.97	0.96	2.63	-1.02		

1.32	1.31	-0.63	3.51	0.08	-0.03		
1.54	1.09	-0.53	3.10	0.49	-0.19		
0.94	1.69	-0.82	2.40	1.19	-0.46		
4.41	1.78	0.87	3.53	0.06	-0.02		
1.42	1.21	-0.59	3.57	0.02	-0.01		
3.90	1.27	0.62	4.14	0.55	0.21		
2.73	0.10	0.05	3.66	0.07	0.03		
1.36	1.27	-0.62	1.65	1.94	-0.75		
2.37	0.26	-0.13	3.41	0.18	-0.07		
9.23	6.60	3.21	5.00	1.41	0.55		
14.16	11.53	5.60	**13.38**	9.79	3.80	y	
5.87	3.24	1.57	2.85	0.74	-0.29		
3.55	0.92	0.45	3.97	0.38	0.15		
3.53	0.90	0.44	3.54	0.05	-0.02		
0.81	1.82	-0.89	2.96	0.63	-0.24		
6.41	3.78	1.84	7.18	3.59	1.39		
2.95	0.32	0.16	8.75	5.16	2.00		
0.97	1.66	-0.81	3.16	0.43	-0.16		
1.88	0.75	-0.36	3.44	0.15	-0.06		
9.38	6.75	3.28	**23.25**	19.66	7.63	y	
2.41	0.22	-0.11	0.99	2.60	-1.01		
2.63	0.00	0.00	14.61	11.02	4.28		
2.90	0.27	0.13	0.70	2.89	-1.12		
0.63	2.00	-0.97	5.91	2.32	0.90		
0.73	1.90	-0.93	5.31	1.72	0.67		
6.07	3.44	1.67	12.78	9.19	3.57		
3.81	1.18	0.57	2.94	0.65	-0.25		
0.76	1.87	-0.91	5.97	2.38	0.92		
0.62	2.01	-0.98	5.51	1.92	0.75		
0.28	2.35	-1.14	2.69	0.90	-0.35		
2.11	0.52	-0.25	6.25	2.66	1.03		
0.12	2.51	-1.22	1.40	2.19	-0.85		
1.44	1.19	-0.58	3.04	0.55	-0.21		
1.16	1.47	-0.72	4.31	0.72	0.28		
0.93	1.70	-0.83	6.64	3.05	1.18		
4.87	2.24	1.09	5.07	1.48	0.58		
5.22	2.59	1.26	8.84	5.25	2.04	x	art a,b,c
6.70	4.07	1.98	4.20	0.61	0.24		
0.74	1.89	-0.92	1.22	2.37	-0.92		
0.68	1.95	-0.95	1.44	2.15	-0.83		
1.51	1.12	-0.55	2.50	1.09	-0.42		
2.43	0.20	-0.10	6.95	3.36	1.30		
6.16	3.53	1.71	4.34	0.75	0.29		
6.74	4.11	2.00	2.95	0.64	-0.25		
6.34	3.71	1.80	5.52	1.93	0.75		
0.73	1.90	-0.92	2.48	1.11	-0.43		
2.32	0.31	-0.15	2.18	1.41	-0.55		

3.41	0.78	0.38	0.88	2.71	-1.05		
1.46	1.17	-0.57	2.52	1.07	-0.42		
4.17	1.54	0.75	2.34	1.25	-0.49		
1.28	1.35	-0.65	0.99	2.60	-1.01		
5.74	3.11	1.51	2.78	0.81	-0.31		
4.42	1.79	0.87	6.69	3.10	1.20		
5.52	2.89	1.40	1.26	2.33	-0.90		
0.21	2.42	-1.18	1.67	1.92	-0.74		
0.55	2.08	-1.01	2.92	0.67	-0.26		
2.17	0.46	-0.22	6.15	2.56	0.99		
1.23	1.40	-0.68	2.73	0.86	-0.33		
0.65	1.98	-0.96	1.73	1.86	-0.72		
7.26	**4.63**	2.25	**17.62**	**14.03**	5.44	y	
3.81	1.18	0.58	2.41	1.18	-0.46		
1.76	0.87	-0.42	5.54	1.95	0.76		
2.20	0.43	-0.21	3.52	0.07	-0.03		
0.75	1.88	-0.92	0.65	2.94	-1.14		
2.63	0.00	0.00	7.92	4.33	1.68		
2.32	0.31	-0.15	3.74	0.15	0.06		
3.73	1.10	0.54	9.49	**5.90**	2.29		
1.71	0.92	-0.45	8.18	4.59	1.78		
0.65	1.98	-0.96	4.64	1.05	0.41		
1.36	1.27	-0.62	3.60	0.01	0.00		
5.46	2.83	1.38	5.46	1.87	0.72		
5.34	2.71	1.32	11.51	**7.92**	3.07		
3.21	0.58	0.28	8.49	4.90	1.90		
1.71	0.92	-0.45	2.72	0.87	-0.34		
3.46	0.83	0.40	4.59	1.00	0.39		
9.06	**6.43**	3.13	**9.44**	**5.85**	2.27	y	
3.38	0.75	0.37	3.39	0.20	-0.08		
1.57	1.06	-0.51	2.70	0.89	-0.35		
9.85	**7.22**	3.51	**18.25**	**14.66**	5.69	y	
0.84	1.79	-0.87	1.87	1.72	-0.67		
3.42	0.79	0.38	1.69	1.90	-0.74		
10.21	**7.58**	3.68	7.25	3.66	1.42		
2.94	0.31	0.15	4.37	0.78	0.30		
7.72	**5.09**	2.47	8.27	4.68	1.82		
9.19	**6.56**	3.19	7.05	3.46	1.34		
3.78	1.15	0.56	2.92	0.67	-0.26		
9.27	**6.64**	3.23	**12.75**	**9.16**	3.56	y	
4.58	1.95	0.95	6.91	3.32	1.29		
4.82	2.19	1.06	3.69	0.10	0.04		
1.10	1.53	-0.75	2.74	0.85	-0.33		
7.36	**4.73**	2.30	6.48	2.89	1.12	y	
11.17	**8.54**	4.15	7.17	3.58	1.39		
8.59	**5.96**	2.90	3.05	0.54	-0.21	x	art. b,c
3.88	1.25	0.61	3.11	0.48	-0.19		

4.09	1.46	0.71	7.98	4.39	1.70		
0.75	1.88	-0.92	1.54	2.05	-0.80		
7.74	**5.11**	2.49	**19.84**	**16.25**	6.31	y	
2.92	0.29	0.14	4.02	0.43	0.17		
6.74	4.11	2.00	5.86	2.27	0.88		
14.08	**11.45**	5.56	**19.42**	**15.83**	6.14	y	
3.69	1.06	0.52	4.72	1.13	0.44		
7.54	**4.91**	2.39	6.00	2.41	0.93	y	
1.78	0.85	-0.41	2.96	0.63	-0.25		
4.37	1.74	0.84	8.77	5.18	2.01		
8.51	**5.88**	2.86	12.47	**8.88**	3.45	y	
2.66	0.03	0.01	3.59	0.00	0.00		
1.93	0.70	-0.34	1.86	1.73	-0.67		
2.91	0.28	0.14	2.07	1.52	-0.59		
4.67	2.04	0.99	8.11	4.52	1.76		
5.54	2.91	1.42	11.56	**7.97**	3.09		
5.67	3.04	1.48	9.80	**6.21**	2.41	y	
6.60	3.97	1.93	11.02	**7.43**	2.88		
5.12	2.49	1.21	10.16	**6.57**	2.55		
1.82	0.81	-0.39	3.55	0.04	-0.02		
1.01	1.62	-0.79	2.75	0.84	-0.33		
3.34	0.71	0.34	3.41	0.18	-0.07		
7.94	**5.31**	2.58	10.63	**7.04**	2.73	y	
5.47	2.84	1.38	6.45	2.86	1.11		
0.75	1.88	-0.91	2.49	1.10	-0.43		
2.03	0.60	-0.29	1.87	1.72	-0.67		
4.92	2.29	1.11	0.97	2.62	-1.01		
1.95	0.68	-0.33	3.74	0.15	0.06		
4.37	1.74	0.85	2.38	1.21	-0.47		
0.35	2.28	-1.11	2.71	0.88	-0.34		
2.39	0.24	-0.12	2.78	0.81	-0.32		
3.93	1.30	0.63	3.75	0.16	0.06		
3.09	0.46	0.22	4.49	0.90	0.35		
4.09	1.46	0.71	6.69	3.10	1.20		
5.95	3.32	1.61	9.21	**5.62**	2.18	x	toxic b,c
2.63	0.00	0.00	2.48	1.11	-0.43		
1.21	1.42	-0.69	0.24	3.35	-1.30		
2.61	0.02	-0.01	2.96	0.63	-0.24		
1.61	1.02	-0.50	1.76	1.83	-0.71		
0.70	1.93	-0.94	3.17	0.42	-0.16		
3.87	1.24	0.60	0.63	2.96	-1.15		
2.44	0.19	-0.09	0.59	3.00	-1.17		
5.19	2.56	1.25	5.18	1.59	0.62		
0.88	1.75	-0.85	1.88	1.71	-0.67		
5.93	3.30	1.60	4.64	1.05	0.41		
3.35	0.72	0.35	4.47	0.88	0.34		
2.41	0.22	-0.11	2.80	0.79	-0.31		

1.25	1.38	-0.67	0.47	3.12	-1.21	
6.76	4.13	2.01	5.67	2.08	0.81	
3.25	0.62	0.30	0.49	3.10	-1.20	
9.03	**6.40**	3.11	1.87	1.72	-0.67	
14.89	**12.26**	5.96	**18.89**	**15.30**	5.94	y
9.36	**6.73**	3.27	4.74	1.15	0.45	
20.18	**17.55**	8.53	**17.30**	**13.71**	5.32	y
6.90	**4.27**	2.08	5.82	2.23	0.87	
4.91	2.28	1.11	2.32	1.27	-0.49	
3.78	1.15	0.56	1.68	1.91	-0.74	
19.02	**16.39**	7.97	**15.43**	**11.84**	4.60	y
4.14	1.51	0.74	6.90	3.31	1.28	
2.17	0.46	-0.22	1.06	2.53	-0.98	
4.60	1.97	0.96	5.92	2.33	0.90	
2.64	0.01	0.01	5.34	1.75	0.68	
1.14	1.49	-0.73	3.94	0.35	0.14	
1.69	0.94	-0.46	4.60	1.01	0.39	
3.38	0.75	0.36	5.08	1.49	0.58	
4.25	1.62	0.79	4.96	1.37	0.53	
3.57	0.94	0.46	10.81	**7.22**	2.80	y
0.67	1.96	-0.95	1.67	1.92	-0.74	
2.27	0.36	-0.18	5.42	1.83	0.71	
2.96	0.33	0.16	2.42	1.17	-0.45	
1.18	1.45	-0.71	1.51	2.08	-0.81	
3.54	0.91	0.44	8.79	5.20	2.02	
3.49	0.86	0.42	9.67	**6.08**	2.36	
5.36	2.73	1.32	4.99	1.40	0.54	
2.22	0.41	-0.20	3.76	0.17	0.07	
5.49	2.86	1.39	4.75	1.16	0.45	
0.92	1.71	-0.83	1.92	1.67	-0.65	
3.81	1.18	0.57	4.04	0.45	0.17	
0.56	2.07	-1.01	2.82	0.77	-0.30	
1.96	0.67	-0.33	3.95	0.36	0.14	
1.77	0.86	-0.42	1.34	2.25	-0.87	
2.56	0.07	-0.03	4.47	0.88	0.34	
3.10	0.47	0.23	11.08	**7.49**	2.91	
1.33	1.30	-0.63	3.59	0.00	0.00	
2.77	0.14	0.07	6.37	2.78	1.08	
5.70	3.07	1.49	11.77	**8.18**	3.18	y
2.27	0.36	-0.18	3.83	0.24	0.09	
12.22	**9.59**	4.66	**21.42**	**17.83**	6.92	y
0.85	1.78	-0.87	2.35	1.24	-0.48	
13.48	**10.85**	5.27	**13.28**	**9.69**	3.76	y
2.15	0.48	-0.23	3.16	0.43	-0.17	
3.77	1.14	0.55	6.52	2.93	1.14	
1.26	1.37	-0.67	4.94	1.35	0.52	
2.39	0.24	-0.12	4.88	1.29	0.50	

2.74	0.11	0.05	6.02	2.43	0.94	
7.71	**5.08**	2.47	9.09	**5.50**	2.13	y
0.91	1.72	-0.84	0.92	2.67	-1.03	
2.63	0.00	0.00	4.16	0.57	0.22	
3.08	0.45	0.22	4.37	0.78	0.30	
4.28	1.65	0.80	6.33	2.74	1.06	
5.00	2.37	1.15	4.64	1.05	0.41	
7.11	**4.48**	2.18	**12.50**	**8.91**	3.46	y
3.92	1.29	0.63	7.93	4.34	1.69	
7.12	**4.49**	2.18	4.52	0.93	0.36	
5.17	2.54	1.24	2.93	0.66	-0.26	
1.61	1.02	-0.49	1.94	1.65	-0.64	
0.87	1.76	-0.86	2.97	0.62	-0.24	
0.55	2.08	-1.01	1.27	2.32	-0.90	
5.09	2.46	1.20	7.53	3.94	1.53	
2.77	0.14	0.07	3.62	0.03	0.01	
0.96	1.67	-0.81	2.54	1.05	-0.41	
0.69	1.94	-0.94	4.10	0.51	0.20	
4.50	1.87	0.91	5.17	1.58	0.61	
1.00	1.63	-0.79	1.70	1.89	-0.73	
1.95	0.68	-0.33	1.88	1.71	-0.66	
3.36	0.73	0.36	3.31	0.28	-0.11	
0.27	2.36	-1.15	1.48	2.11	-0.82	
2.67	0.04	0.02	2.28	1.31	-0.51	
0.00	2.63	-1.28	0.00	3.59	-1.39	
1.60	1.03	-0.50	0.99	2.60	-1.01	
1.79	0.84	-0.41	1.43	2.16	-0.84	
4.57	1.94	0.94	7.93	4.34	1.69	
3.79	1.16	0.57	11.99	**8.40**	3.26	
12.47	**9.84**	4.78	**18.35**	**14.76**	5.73	y
2.12	0.51	-0.25	2.73	0.86	-0.33	
6.02	3.39	1.65	11.26	**7.67**	2.98	y
4.54	1.91	0.93	7.71	4.12	1.60	
5.65	3.02	1.47	6.89	3.30	1.28	
3.40	0.77	0.38	6.53	2.94	1.14	
0.63	2.00	-0.97	1.08	2.51	-0.97	
0.16	2.47	-1.20	3.96	0.37	0.14	
3.48	0.85	0.41	12.75	**9.16**	3.56	
0.31	2.32	-1.13	0.59	3.00	-1.16	
8.63	**6.00**	2.91	**17.19**	**13.60**	5.28	y
1.80	0.83	-0.41	3.87	0.28	0.11	
0.68	1.95	-0.95	0.95	2.64	-1.03	
3.51	0.88	0.43	7.16	3.57	1.39	
2.95	0.32	0.15	1.57	2.02	-0.78	
1.17	1.46	-0.71	4.06	0.47	0.18	
0.28	2.35	-1.14	0.37	3.22	-1.25	
7.10	**4.47**	2.17	1.67	1.92	-0.74	

1.34	1.29	-0.63	4.17	0.58	0.23	
1.88	0.75	-0.37	1.63	1.96	-0.76	
2.91	0.28	0.14	2.43	1.16	-0.45	
3.36	0.73	0.35	3.43	0.16	-0.06	
3.20	0.57	0.28	7.82	4.23	1.64	
2.57	0.06	-0.03	2.00	1.59	-0.62	
1.58	1.05	-0.51	4.23	0.64	0.25	
3.49	0.86	0.42	2.77	0.82	-0.32	
1.50	1.13	-0.55	1.92	1.67	-0.65	
7.17	**4.54**	2.21	14.52	**10.93**	4.24	y
2.44	0.19	-0.09	8.29	4.70	1.83	
0.69	1.94	-0.94	0.34	3.25	-1.26	
2.19	0.44	-0.21	3.61	0.02	0.01	
0.24	2.39	-1.16	2.50	1.09	-0.42	
0.66	1.97	-0.96	4.18	0.59	0.23	
1.43	1.20	-0.58	6.15	2.56	1.00	
3.49	0.86	0.42	9.76	**6.17**	2.39	
2.03	0.60	-0.29	1.68	1.91	-0.74	
0.62	2.01	-0.98	2.21	1.38	-0.54	
1.43	1.20	-0.58	5.43	1.84	0.71	
1.66	0.97	-0.47	2.47	1.12	-0.44	
1.42	1.21	-0.59	4.17	0.58	0.23	
0.44	2.19	-1.07	2.18	1.41	-0.55	
1.03	1.60	-0.78	3.24	0.35	-0.14	
1.84	0.79	-0.39	3.41	0.18	-0.07	
1.89	0.74	-0.36	2.09	1.50	-0.58	
1.40	1.23	-0.60	2.39	1.20	-0.46	
1.48	1.15	-0.56	3.44	0.15	-0.06	
4.52	1.89	0.92	5.21	1.62	0.63	
7.42	**4.79**	2.33	4.54	0.95	0.37	
2.74	0.11	0.05	4.04	0.45	0.18	
3.06	0.43	0.21	3.87	0.28	0.11	
2.53	0.10	-0.05	8.09	4.50	1.75	
1.73	0.90	-0.44	5.04	1.45	0.56	
1.58	1.05	-0.51	2.08	1.51	-0.59	
0.69	1.94	-0.95	3.13	0.47	-0.18	
3.75	1.12	0.54	4.23	0.64	0.25	
2.39	0.24	-0.12	8.18	4.59	1.78	
0.79	1.84	-0.90	6.54	2.95	1.15	
2.63	1.39		3.59	1.74		
	4.17			5.22		
	2.06			2.58		

29.69		**A**	**B**	**C**
26.28	3psSD	4.36	7.17	14.28
20.77	3ngSD	2.07	6.25	2.49

19.54	SumSD	6.44	13.42	16.77
24.07	DiffMn	13.14	18.08	22.94
4.76	SmovrDiff	0.49	0.74	0.73
	1minus	0.51	0.26	0.27
1.10				
2.28				
0.84				
0.32				
1.13				
0.83				
3.10				
3.38				
4.97				
5.55				
12.67				
27.67				

					% inf	abs dev	robust Z
50012.00	A02	M-012267- tumor necrosis	7127.00	TNFAIP2	1.00	3.84	-0.98
50012.00	A04	M-017794- thymosin, beta	9168.00	TMSB10	0.84	4.00	-1.02
50012.00	A05	M-004910- ubiquitin-conjug	7329.00	UBE2I	2.30	2.54	-0.65
50012.00	A06	M-020635- transmembrane	10329.00	TMEM5	0.82	4.02	-1.03
50012.00	A07	M-007266- ubiquitin-conjug	51465.00	UBE2J1	3.17	1.67	-0.43
50012.00	A08	M-017046- transmembrane	10330.00	TMEM4	0.72	4.12	-1.05
50012.00	A09	M-008614- ubiquitin-conjug	118424.00	UBE2J2	2.28	2.56	-0.65
50012.00	A10	M-017206- transmembrane	117531.00	TMC1	0.07	4.77	-1.22
50012.00	A11	M-008631- ubiquitin-conjug	55585.00	UBE2Q1	0.27	4.57	-1.17
50012.00	A12	M-011973- transmembrane	7104.00	TM4SF4	2.15	2.69	-0.69
50012.00	A13	M-009700- ubiquitin-conjug	54926.00	UBE2R2	1.40	3.44	-0.88
50012.00	A14	M-021321- tetraspanin 7	7102.00	TSPAN7	3.01	1.83	-0.47
50012.00	A15	M-008823- ubiquitin-conjug	7336.00	UBE2V2	2.02	2.82	-0.72
50012.00	A16	M-010610- transmembrane	4071.00	TM4SF1	0.87	3.97	-1.01
50012.00	A17	M-020658- ubiquitin-like 4	8266.00	UBL4A	1.91	2.93	-0.75
50012.00	A18	M-019336- transducin-like	7091.00	TLE4	1.12	3.72	-0.95
50012.00	A19	M-008494- UEV and lactate	55293.00	UEVLD	2.60	2.24	-0.57
50012.00	A20	M-019929- transducin-like	7090.00	TLE3	2.35	2.49	-0.64
50012.00	A21	M-017918- ubiquitin fusion	7353.00	UFD1L	0.54	4.30	-1.10
50012.00	A23	M-006441- UDP-glucose ce	7357.00	UGCG	0.85	3.99	-1.02
50012.00	B02	M-009683- FK506 binding p	55033.00	FKBP14	7.03	2.19	0.56
50012.00	B04	M-010344- flap structure-s	2237.00	FEN1	3.38	1.46	-0.37
50012.00	B05	M-019750- troponin C type	7125.00	TNNC2	3.41	1.43	-0.36
50012.00	B06	M-011036- ferrochelatase (	2235.00	FECH	1.23	3.61	-0.92
50012.00	B07	M-019751- troponin I type	7136.00	TNNI2	1.53	3.31	-0.84
50012.00	B08	M-009442- farnesyl-diphos	2222.00	FDFT1	9.41	4.57	1.16
50012.00	B09	M-020917- troponin I type	7137.00	TNNI3	14.10	9.26	2.36
50012.00	B10	M-003490- F-box and WD r	23291.00	FBXW11	3.30	1.54	-0.39
50012.00	B11	M-023617- troponin T type	7138.00	TNNT1	5.63	0.79	0.20
50012.00	B12	M-012430- F-box protein 2	26261.00	FBXO24	2.32	2.52	-0.64
50012.00	B13	M-019371- troponin T type	7139.00	TNNT2	10.82	5.98	1.52
50012.00	B14	M-031881- tetraspanin 17	26262.00	TSPAN17	9.43	4.59	1.17
50012.00	B15	M-009874- tenascin R (rest	7143.00	TNR	1.86	2.98	-0.76
50012.00	B16	M-012917- F-box protein 2	23014.00	FBXO21	3.53	1.31	-0.33
50012.00	B17	M-019434- transducer of E	10766.00	TOB2	2.33	2.51	-0.64
50012.00	B18	M-005204- F-box and leuci	54850.00	FBXL12	6.28	1.44	0.37
50012.00	B19	M-005278- topoisomerase	7150.00	TOP1	2.86	1.98	-0.51
50012.00	B20	M-003954- fatty acid synth	2194.00	FASN	12.05	7.21	1.84
50012.00	B21	M-004239- topoisomerase	7153.00	TOP2A	8.22	3.38	0.86
50012.00	B23	M-004451- Fas apoptotic in	9214.00	FAIM3	0.00	4.84	-1.24
50012.00	C02	M-015873- transducin-like	7089.00	TLE2	6.49	1.65	0.42
50012.00	C04	M-015528- transducin-like	7088.00	TLE1	1.90	2.94	-0.75
50012.00	C05	M-013770- UDP glucuronos	54659.00	UGT1A3	1.01	3.83	-0.98
50012.00	C06	M-007746- tight junction pr	7082.00	TJP1	8.43	3.59	0.91
50012.00	C07	M-019627- UDP glucuronos	54657.00	UGT1A4	7.58	2.74	0.70
50012.00	C08	M-019951- TERF1 (TRF1)-in	26277.00	TINF2	6.84	2.00	0.51

50012.00	C09	M-020196- UDP glucuronos	54578.00	UGT1A6	1.60	3.24	-0.83
50012.00	C10	M-019959- pleckstrin and S	23550.00	PSD4	1.55	3.29	-0.84
50012.00	C11	M-018274- UDP glucuronos	54576.00	UGT1A8	3.59	1.25	-0.32
50012.00	C12	M-008434- T-cell lymphom	26230.00	TIAM2	3.80	1.04	-0.27
50012.00	C13	M-014083- UDP glucuronos	54600.00	UGT1A9	2.63	2.21	-0.57
50012.00	C14	M-011921- TGFB1-induced	9220.00	TIAF1	1.85	2.99	-0.76
50012.00	C15	M-020194- UDP glucuronos	7366.00	UGT2B15	3.29	1.55	-0.40
50012.00	C16	M-015337- Thy-1 cell surfa	7070.00	THY1	1.87	2.97	-0.76
50012.00	C17	M-014139- UDP glucuronos	7363.00	UGT2B4	3.73	1.11	-0.28
50012.00	C18	M-019569- thyroid hormon	7069.00	THRSP	6.99	2.15	0.55
50012.00	C19	M-010270- UDP glycosyltra	7368.00	UGT8	11.83	6.99	1.78
50012.00	C20	M-012552- thrombopoietin	7066.00	THPO	1.85	2.99	-0.76
50012.00	C21	M-009828- uridine monoph	7372.00	UMPS	4.32	0.52	-0.13
50012.00	C23	M-011795- uracil-DNA glyc	7374.00	UNG	0.60	4.24	-1.08
50012.00	D02	M-009364- acyl-CoA synthe	2182.00	ACSL4	4.76	0.08	-0.02
50012.00	D04	M-010061- acyl-CoA synthe	2181.00	ACSL3	8.10	3.26	0.83
50012.00	D05	M-010569- TP53 activated	11257.00	TP53AP1	9.97	5.13	1.31
50012.00	D06	M-005872- coagulation fact	2158.00	F9	4.47	0.37	-0.10
50012.00	D07	M-019450- tumor protein p	9537.00	TP53I11	6.60	1.76	0.45
50012.00	D08	M-005871- coagulation fact	2155.00	F7	8.81	3.97	1.01
50012.00	D09	M-016159- tumor protein p	94241.00	TP53INP1	0.89	3.95	-1.01
50012.00	D10	M-011853- eyes absent hor	2070.00	EYA4	6.33	1.49	0.38
50012.00	D11	M-020287- TP53TG3 protei	24150.00	TP53TG3	0.73	4.11	-1.05
50012.00	D12	M-011653- eyes absent hor	2140.00	EYA3	10.61	5.77	1.47
50012.00	D13	M-004304- trophoblast glyc	7162.00	TPBG	3.78	1.06	-0.27
50012.00	D14	M-017392- eyes absent hor	2138.00	EYA1	3.49	1.35	-0.35
50012.00	D15	M-019903- tumor protein D	7163.00	TPD52	0.50	4.34	-1.11
50012.00	D16	M-013120- exonuclease 1	9156.00	EXO1	8.18	3.34	0.85
50012.00	D17	M-019567- tumor protein D	7164.00	TPD52L1	9.40	4.56	1.16
50012.00	D18	M-006626- excision repair c	2073.00	ERCC5	6.66	1.82	0.46
50012.00	D19	M-019568- tumor protein D	7165.00	TPD52L2	7.02	2.18	0.56
50012.00	D20	M-011027- excision repair c	2068.00	ERCC2	7.09	2.25	0.57
50012.00	D21	M-010548- translocated pr	7175.00	TPR	15.54	**10.70**	2.73
50012.00	D23	M-004559- tumor protein, t	7178.00	TPT1	1.20	3.64	-0.93
50012.00	E02	M-019911- THO complex 1	9984.00	THOC1	2.22	2.62	-0.67
50012.00	E04	M-017078- Theg homolog (	51298.00	THEG	4.91	0.07	0.02
50012.00	E05	M-008515- cyclin U	10309.00	CCNU	3.77	1.07	-0.27
50012.00	E06	M-019638- thrombospondi	7059.00	**THBS3**	**16.37**	**11.53**	2.94
50012.00	E07	M-006647- uridine phosph	7378.00	UPP1	2.27	2.57	-0.66
50012.00	E08	M-010544- transforming gr	7042.00	TGFB2	3.50	1.34	-0.34
50012.00	E09	M-032278- ubiquinol-cytoc	10975.00	UQCR	4.91	0.07	0.02
50012.00	E10	M-020381- TCF3 (E2A) fusi	29844.00	TFPT	3.13	1.71	-0.44
50012.00	E11	M-004748- ubiquinol-cytoc	7384.00	UQCRC1	1.36	3.49	-0.89
50012.00	E12	M-004118- testis enhanced	7009.00	TEGT	3.32	1.52	-0.39
50012.00	E13	M-008334- ubiquinol-cytoc	7385.00	UQCRC2	4.41	0.43	-0.11
50012.00	E14	M-008769- thyrotrophic em	7008.00	TEF	2.53	2.31	-0.59
50012.00	E15	M-020100- ubiquinol-cytoc	7386.00	UQCRFS1	3.09	1.75	-0.45

50012.00	E16	M-019570- TEA domain fam	7004.00	TEAD4	2.47	2.37	-0.60
50012.00	E17	M-020101- ubiquinol-cytoc	7388.00	UQCRH	7.67	2.83	0.72
50012.00	E18	M-010568- serine incorpora	10955.00	SERINC3	6.19	1.35	0.34
50012.00	E19	M-013415- uroporphyrinog	7389.00	UROD	8.40	3.56	0.91
50012.00	E20	M-019640- T-cell leukemia	6988.00	TCTA	0.73	4.11	-1.05
50012.00	E21	M-008471- uroporphyrinog	7390.00	UROS	2.34	2.50	-0.64
50012.00	E23	M-011905- vanin 1	8876.00	VNN1	1.92	2.92	-0.75
50012.00	F02	M-006311- excision repair c	2067.00	ERCC1	0.81	4.03	-1.03
50012.00	F04	M-010006- epoxide hydrola	2053.00	EPHX2	10.42	5.58	1.42
50012.00	F05	M-017630- TR4 orphan rece	126382.00	TRA16	6.14	1.30	0.33
50012.00	F06	M-011235- ectonucleoside	957.00	ENTPD5	5.84	1.00	0.25
50012.00	F07	M-017438- TNF receptor-as	7185.00	TRAF1	2.95	1.89	-0.48
50012.00	F08	M-011234- ectonucleoside	956.00	**ENTPD3**	**16.41**	**11.57**	2.95
50012.00	F09	M-018676- translocation as	23471.00	TRAM1	5.38	0.54	0.14
50012.00	F10	M-015973- ectonucleoside	953.00	ENTPD1	3.28	1.56	-0.40
50012.00	F11	M-021247- thyroid hormon	9862.00	THRAP4	4.60	0.24	-0.06
50012.00	F12	M-004540- ectonucleotide	5169.00	ENPP3	1.62	3.22	-0.82
50012.00	F13	M-012683- COP9 constituti	9318.00	COPS2	3.34	1.50	-0.38
50012.00	F14	M-005865- glutamyl amino	2028.00	ENPEP	3.02	1.82	-0.47
50012.00	F15	M-020945- SERTA domain c	9792.00	SERTAD2	2.96	1.88	-0.48
50012.00	F16	M-013961- AT hook contai	25909.00	AHCTF1	3.85	0.99	-0.25
50012.00	F17	M-006109- transient recept	8989.00	TRPA1	5.47	0.63	0.16
50012.00	F18	M-019879- etoposide induc	9538.00	EI24	4.02	0.82	-0.21
50012.00	F19	M-006516- transient recept	29850.00	TRPM5	2.38	2.46	-0.63
50012.00	F20	M-021395- ER degradation	9695.00	EDEM1	10.34	5.50	1.40
50012.00	F21	M-006517- transient recept	79054.00	TRPM8	2.73	2.11	-0.54
50012.00	F23	M-006518- transient recept	7442.00	TRPV1	4.10	0.74	-0.19
50012.00	G02	M-019892- T-cell leukemia/	9623.00	TCL1B	17.86	**13.02**	3.32
50012.00	G04	M-012608- T-cell leukemia/	8115.00	TCL1A	2.59	2.25	-0.57
50012.00	G05	M-013038- vanin 2	8875.00	**VNN2**	**16.32**	**11.48**	2.92
50012.00	G06	M-005144- transcription el	51224.00	TCEB3B	3.89	0.95	-0.24
50012.00	G07	M-009682- abhydrolase do	83451.00	ABHD11	14.05	**9.21**	2.35
50012.00	G08	M-024872- T-box 18	9096.00	TBX18	15.58	**10.74**	2.74
50012.00	G09	M-006101- X-prolyl aminop	7511.00	XPNPEP1	4.47	0.37	-0.10
50012.00	G10	M-012195- T-box 1	6899.00	TBX1	9.54	4.70	1.20
50012.00	G11	M-006104- zinc metallopep	10269.00	ZMPSTE24	7.68	2.84	0.72
50012.00	G12	M-012152- transducin (bet	6907.00	TBL1X	12.22	7.38	1.88
50012.00	G13	M-012565- ABO blood grou	28.00	ABO	5.40	0.56	0.14
50012.00	G14	M-011402- tubulin folding c	6905.00	TBCE	12.61	7.77	1.98
50012.00	G15	M-009218- amiloride bindi	26.00	ABP1	7.00	2.16	0.55
50012.00	G16	M-013416- tubulin folding c	6904.00	TBCD	6.54	1.70	0.43
50012.00	G17	M-004551- acetyl-Coenzym	31.00	ACACA	8.39	3.55	0.90
50012.00	G18	M-011401- tubulin folding c	6903.00	TBCC	14.66	**9.82**	2.50
50012.00	G19	M-004759- acetyl-Coenzym	32.00	ACACB	6.10	1.26	0.32
50012.00	G20	M-011895- tubulin folding c	6902.00	TBCA	9.74	4.90	1.25
50012.00	G21	M-010396- acyl-CoA synthe	55902.00	ACSS2	12.06	7.22	1.84
50012.00	G23	M-005754- angiotensin I co	1636.00	ACE	4.37	0.47	-0.12

50012.00	H02	M-005859- endothelin conv	9427.00	ECEL1	6.38	1.54	0.39
50012.00	H04	M-005857- endothelin conv	1889.00	ECE1	9.22	4.38	1.11
50012.00	H05	M-004453- spermatogenesi	130560.00	SPATA3	12.48	7.64	1.95
50012.00	H06	M-011023- torsin family 1,	1861.00	TOR1A	1.32	3.52	-0.90
50012.00	H07	M-003028- tuberous sclero	7248.00	TSC1	14.89	**10.05**	2.56
50012.00	H08	M-010258- dUTP pyrophos	1854.00	DUT	11.04	6.20	1.58
50012.00	H09	M-011410- tumor suppress	7260.00	TSSC1	15.52	**10.68**	2.72
50012.00	H10	M-012951- DBF4 homolog	80174.00	DBF4B	4.99	0.15	0.04
50012.00	H11	M-012155- tumor suppress	10078.00	TSSC4	11.92	7.08	1.80
50012.00	H12	M-009702- deoxynucleotid	1791.00	DNTT	7.59	2.75	0.70
50012.00	H13	M-010120- thiosulfate sulfu	7263.00	TST	7.50	2.66	0.68
50012.00	H14	M-006395- DNA (cytosine-5	1789.00	DNMT3B	15.61	**10.77**	2.74
50012.00	H15	M-019824- tetratricopeptid	7268.00	TTC4	8.72	3.88	0.99
50012.00	H16	M-006672- DNA (cytosine-5	1788.00	DNMT3A	8.78	3.94	1.00
50012.00	H17	M-017384- tubby homolog	7275.00	TUB	5.01	0.17	0.04
50012.00	H18	M-006671- tRNA aspartic a	1787.00	TRDMT1	16.88	**12.04**	3.07
50012.00	H19	M-013150- tubulin, alpha 1	7846.00	TUBA1A	18.07	**13.23**	3.37
50012.00	H20	M-004605- DNA (cytosine-5	1786.00	DNMT1	2.01	2.83	-0.72
50012.00	H21	M-009374- tubulin, alpha 8	51807.00	TUBA8	9.60	4.76	1.21
50012.00	H23	M-008265- tubulin, beta 2C	10383.00	TUBB2C	7.27	2.43	0.62
50012.00	I02	M-032269- Tax1 (human T-	10883.00	TAX1BP2	8.73	3.89	0.99
50012.00	I04	M-014003- leucine rich rep	23507.00	LRRC8B	12.22	7.38	1.88
50012.00	I05	M-009482- acetylcholineste	43.00	ACHE	2.44	2.40	-0.61
50012.00	I06	M-008948- chromodomain	1106.00	CHD2	9.37	4.53	1.15
50012.00	I07	M-014157- apoptotic chron	22985.00	ACIN1	5.91	1.07	0.27
50012.00	I08	M-009881- mitochondrial t	51102.00	MECR	6.94	2.10	0.53
50012.00	I09	M-004505- ADAM metallop	8751.00	ADAM15	7.51	2.67	0.68
50012.00	I10	M-009485- cholesteryl este	1071.00	CETP	11.73	6.89	1.75
50012.00	I11	M-003453- ADAM metallop	6868.00	ADAM17	4.17	0.67	-0.17
50012.00	I12	M-008521- chromodomain	9425.00	CDYL	5.02	0.18	0.04
50012.00	I13	M-004523- ADAM metallop	8748.00	ADAM20	3.94	0.90	-0.23
50012.00	I14	M-008566- chaperonin con	10694.00	CCT8	3.01	1.83	-0.47
50012.00	I15	M-004524- ADAM metallop	8747.00	ADAM21	6.51	1.67	0.42
50012.00	I16	M-004405- caspase 5, apop	838.00	CASP5	1.33	3.51	-0.90
50012.00	I17	M-005758- ADAM metallop	10863.00	ADAM28	7.07	2.23	0.57
50012.00	I18	M-004404- caspase 4, apop	837.00	CASP4	7.16	2.32	0.59
50012.00	I19	M-005759- ADAM metallop	11085.00	**ADAM30**	**19.70**	**14.86**	3.79
50012.00	I20	M-003465- caspase 2, apop	835.00	CASP2	7.81	2.97	0.76
50012.00	I21	M-005762- ADAM metallop	81794.00	ADAMTS1	4.75	0.09	-0.02
50012.00	I23	M-005766- ADAM metallop	170689.00	**ADAMTS1**	**18.27**	**13.43**	3.42
50012.00	J02	M-012092- dynamin 1-like	10059.00	DNM1L	4.25	0.59	-0.15
50012.00	J04	M-009667- deoxyribonucle	1777.00	DNASE2	7.66	2.82	0.72
50012.00	J05	M-009293- tubulin, gamma	27175.00	**TUBG2**	**17.43**	**12.59**	3.21
50012.00	J06	M-016280- deoxyribonucle	1773.00	DNASE1	6.56	1.72	0.44
50012.00	J07	M-020208- tubulin, gamma	10844.00	TUBGCP2	7.70	2.86	0.73
50012.00	J08	M-009551- DMC1 dosage su	11144.00	DMC1	5.01	0.17	0.04
50012.00	J09	M-011413- tubby like prote	7287.00	TULP1	4.94	0.10	0.02

50012.00	J10	M-014695- fumarylacetoac	81889.00	FAHD1	2.78	2.06	-0.53
50012.00	J11	M-011414- tubby like prote	7288.00	TULP2	2.50	2.34	-0.60
50012.00	J12	M-011477- DEAH (Asp-Glu-	8449.00	DHX16	5.18	0.34	0.09
50012.00	J13	M-006340- thioredoxin	7295.00	TXN	3.62	1.22	-0.31
50012.00	J14	M-004425- DNA fragmentat	1677.00	DFFB	3.20	1.64	-0.42
50012.00	J15	M-008236- thioredoxin red	7296.00	TXNRD1	3.59	1.25	-0.32
50012.00	J16	M-004424- DNA fragmentat	1676.00	**DFFA**	**15.20**	**10.36**	2.64
50012.00	J17	M-004717- thymidylate syn	7298.00	TYMS	6.15	1.31	0.33
50012.00	J18	M-006371- DEAD (Asp-Glu-	1656.00	DDX6	0.79	4.05	-1.03
50012.00	J19	M-017474- ubiquitin associ	51271.00	UBAP1	0.39	4.45	-1.14
50012.00	J20	M-013472- DEAD (Asp-Glu-	11218.00	DDX20	1.84	3.00	-0.77
50012.00	J21	M-013168- ubiquitin associ	55833.00	UBAP2	1.82	3.02	-0.77
50012.00	J23	M-013382- ubiquitin B	7314.00	UBB	2.78	2.06	-0.53
50012.00	K02	M-004402- caspase 10, apo	843.00	CASP10	9.27	4.43	1.13
50012.00	K04	M-009979- calpain, small su	826.00	CAPNS1	3.32	1.52	-0.39
50012.00	K05	M-005768- ADAM metallop	170691.00	ADAMTS17	2.19	2.65	-0.68
50012.00	K06	M-005804- calpain 2, (m/II)	824.00	CAPN2	4.53	0.31	-0.08
50012.00	K07	M-005770- ADAM metallop	171019.00	ADAMTS19	10.49	5.65	1.44
50012.00	K08	M-005799- calpain 1, (mu/I	823.00	CAPN1	9.78	4.94	1.26
50012.00	K09	M-005772- ADAM metallop	80070.00	ADAMTS20	3.12	1.72	-0.44
50012.00	K10	M-005244- carbonic anhydr	768.00	CA9	2.58	2.26	-0.58
50012.00	K11	M-005773- ADAM metallop	9508.00	ADAMTS3	6.09	1.25	0.32
50012.00	K12	M-003634- carbonic anhydr	771.00	CA12	8.37	3.53	0.90
50012.00	K13	M-003807- ADAM metallop	9507.00	ADAMTS4	5.25	0.41	0.10
50012.00	K14	M-013379- regulator of telo	51750.00	RTEL1	5.50	0.66	0.17
50012.00	K15	M-005776- ADAM metallop	11174.00	ADAMTS6	10.45	5.61	1.43
50012.00	K16	M-020234- ER degradation	55741.00	EDEM2	0.52	4.32	-1.10
50012.00	K17	M-005777- ADAM metallop	11173.00	ADAMTS7	8.03	3.19	0.81
50012.00	K18	M-005796- complement co	716.00	C1S	5.19	0.35	0.09
50012.00	K19	M-005779- ADAM metallop	56999.00	ADAMTS9	8.81	3.97	1.01
50012.00	K20	M-005795- complement co	715.00	C1R	8.20	3.36	0.86
50012.00	K21	M-006520- alcohol dehydro	124.00	ADH1A	7.83	2.99	0.76
50012.00	K23	M-006521- alcohol dehydro	126.00	ADH1C	9.98	5.14	1.31
50012.00	L02	M-013451- DEAD (Asp-Glu-	8886.00	DDX18	4.65	0.19	-0.05
50012.00	L04	M-011843- DEAD/H (Asp-Gl	1663.00	DDX11	12.52	7.68	1.96
50012.00	L05	M-019408- ubiquitin C	7316.00	UBC	3.43	1.41	-0.36
50012.00	L06	M-005256- dopachrome tau	1638.00	**DCT**	**18.84**	**14.00**	3.57
50012.00	L07	M-008266- ubiquitin D	10537.00	UBD	4.17	0.67	-0.17
50012.00	L08	M-010790- DNA cross-link r	9937.00	DCLRE1A	12.96	**8.12**	2.07
50012.00	L09	M-019759- ubiquitin-activa	7318.00	UBE1L	3.15	1.69	-0.43
50012.00	L10	M-008279- dihydrolipoamic	1629.00	DBT	2.97	1.87	-0.48
50012.00	L11	M-010154- ubiquitin-conjug	7326.00	UBE2G1	3.99	0.85	-0.22
50012.00	L12	M-010052- dopamine beta-	1621.00	DBH	8.03	3.19	0.81
50012.00	L13	M-008569- ubiquitin-conjug	9246.00	UBE2L6	0.17	4.67	-1.19
50012.00	L14	M-010334- aspartyl-tRNA sy	1615.00	DARS	5.52	0.68	0.17
50012.00	L15	M-004348- ubiquitin-conjug	9040.00	UBE2M	1.30	3.54	-0.90
50012.00	L16	M-009550- cytochrome P45	1565.00	CYP2D6	9.09	4.25	1.08

50012.00	L17	M-003920- ubiquitin-conjug	7334.00	UBE2N	5.32	0.48	0.12
50012.00	L18	M-008736- cytochrome P45	1557.00	CYP2C19	10.27	5.43	1.38
50012.00	L19	M-016005- SMT3 suppressc	7341.00	SUMO1	7.54	2.70	0.69
50012.00	L20	M-009709- cytochrome P45	1562.00	CYP2C18	6.47	1.63	0.41
50012.00	L21	M-012786- ubiquitin-like 3	5412.00	UBL3	7.84	3.00	0.76
50012.00	L23	M-014320- ubiquitin-like 5	59286.00	UBL5	4.87	0.03	0.01
50012.00	M02	M-017140- ER degradation	80267.00	**EDEM3**	**7.88**	3.04	0.77
50012.00	M04	M-019554- Ras association	8045.00	RASSF7	4.29	0.55	-0.14
50012.00	M05	M-008412- ADP-ribosylargi	141.00	ADPRH	8.41	3.57	0.91
50012.00	M06	M-010587- BRCA1 interacti	83990.00	**BRIP1**	**16.66**	**11.82**	3.01
50012.00	M07	M-010127- poly (ADP-ribos	10038.00	PARP2	7.81	2.97	0.76
50012.00	M08	M-007287- Bloom syndrom	641.00	BLM	12.23	7.39	1.88
50012.00	M09	M-009289- adenylosuccinat	159.00	ADSS	11.64	6.80	1.73
50012.00	M10	M-004389- NLR family, apo	4671.00	NAIP	9.87	5.03	1.28
50012.00	M11	M-005780- AFG3 ATPase fa	172.00	AFG3L1	12.14	7.30	1.86
50012.00	M12	M-009826- butyrylcholinest	590.00	**BCHE**	**18.50**	**13.66**	3.48
50012.00	M13	M-021409- activation-induc	57379.00	AICDA	9.85	5.01	1.27
50012.00	M14	M-006937- euchromatic his	10919.00	EHMT2	7.95	3.11	0.79
50012.00	M15	M-021423- AT-hook transcr	80709.00	AKNA	7.81	2.97	0.76
50012.00	M16	M-009532- acyl-CoA thioest	11332.00	ACOT7	8.21	3.37	0.86
50012.00	M17	M-009022- arachidonate lip	59344.00	ALOXE3	5.40	0.56	0.14
50012.00	M18	M-008457- AU RNA binding	549.00	AUH	5.63	0.79	0.20
50012.00	M19	M-008658- alkaline phosph	249.00	ALPL	4.70	0.14	-0.04
50012.00	M20	M-010257- argininosuccinat	445.00	ASS1	6.78	1.94	0.49
50012.00	M21	M-003455- alkaline phosph	251.00	ALPPL2	3.97	0.87	-0.22
50012.00	M23	M-013843- anaphase prom	64682.00	ANAPC1	5.79	0.95	0.24
50012.00	N02	M-011167- cytochrome P45	1549.00	CYP2A7	3.28	1.56	-0.40
50012.00	N04	M-008781- cytochrome P45	1548.00	CYP2A6	4.60	0.24	-0.06
50012.00	N05	M-014195- ubinuclein 1	29855.00	UBN1	12.01	7.17	1.83
50012.00	N06	M-009757- cytochrome P45	1594.00	CYP27B1	19.33	**14.49**	3.69
50012.00	N07	M-021183- ubiquitin family	56061.00	UBFD1	13.04	**8.20**	2.09
50012.00	N08	M-004790- cytochrome P45	1543.00	CYP1A1	4.31	0.53	-0.14
50012.00	N09	M-012942- ubiquilin 1	29979.00	UBQLN1	9.03	4.19	1.07
50012.00	N10	M-008469- cytochrome P45	1586.00	CYP17A1	11.35	6.51	1.66
50012.00	N11	M-013398- ubiquilin 3	50613.00	UBQLN3	9.74	4.90	1.25
50012.00	N12	M-009021- cytochrome P45	1585.00	CYP11B2	1.33	3.51	-0.90
50012.00	N13	M-012557- UDP glucuronos	54658.00	UGT1A1	6.74	1.90	0.48
50012.00	N14	M-008609- C-terminal bindi	1487.00	CTBP1	7.76	2.92	0.74
50012.00	N15	M-009734- unc-119 homolo	9094.00	UNC119	12.06	7.22	1.84
50012.00	N16	M-009150- crystallin, zeta (	9946.00	CRYZL1	13.71	**8.87**	2.26
50012.00	N17	M-012268- unc-13 homolog	10497.00	UNC13B	10.31	5.47	1.39
50012.00	N18	M-009891- crystallin, zeta (	1429.00	CRYZ	3.51	1.33	-0.34
50012.00	N19	M-015787- ubiquinol-cytoc	7381.00	UQCRB	7.11	2.27	0.58
50012.00	N20	M-009275- carbamoyl-phos	1373.00	CPS1	11.71	6.87	1.75
50012.00	N21	M-021440- clarin 1	7401.00	CLRN1	4.10	0.74	-0.19
50012.00	N23	M-015465- UV radiation res	7405.00	UVRAG	1.13	3.71	-0.95
50012.00	O02	M-009814- arylsulfatase B	411.00	ARSB	6.74	1.90	0.48

50012.00	O04	M-009558-	arylsulfatase A	410.00	ARSA	3.05	1.79	-0.46
50012.00	O05	M-016095-	anaphase prom	51433.00	ANAPC5	5.68	0.84	0.21
50012.00	O06	M-012083-	ADP-ribosylatio	10124.00	ARL4A	8.01	3.17	0.81
50012.00	O07	M-011206-	angiogenin, ribo	283.00	ANG	4.79	0.05	-0.01
50012.00	O08	M-009943-	ras homolog ge	23433.00	RHOQ	3.62	1.22	-0.31
50012.00	O09	M-019944-	apolipoprotein	10930.00	APOBEC2	2.87	1.97	-0.50
50012.00	O10	M-009727-	Rho family GTPa	8153.00	RND2	3.42	1.42	-0.36
50012.00	O11	M-017432-	apolipoprotein	200315.00	APOBEC3A	3.55	1.29	-0.33
50012.00	O12	M-010367-	ras homolog ge	57381.00	RHOJ	3.94	0.90	-0.23
50012.00	O13	M-013711-	apolipoprotein	27350.00	APOBEC3C	4.47	0.37	-0.09
50012.00	O14	M-008660-	DIRAS family, G	9077.00	DIRAS3	5.61	0.77	0.19
50012.00	O15	M-013072-	apolipoprotein	60489.00	APOBEC3G	4.56	0.28	-0.07
50012.00	O16	M-008995-	ras homolog ge	391.00	RHOG	1.64	3.20	-0.82
50012.00	O17	M-011583-	ADP-ribosylatio	379.00	ARL4D	5.59	0.75	0.19
50012.00	O18	M-008316-	ras homolog ge	54509.00	RHOF	4.41	0.43	-0.11
50012.00	O19	M-019250-	ADP-ribosylatio	10139.00	ARFRP1	0.72	4.12	-1.05
50012.00	O20	M-008940-	ras homolog ge	29984.00	RHOD	3.29	1.55	-0.40
50012.00	O21	M-009922-	arginase, liver	383.00	ARG1	1.63	3.22	-0.82
50012.00	O23	M-008395-	ras homolog ge	388.00	RHOB	0.77	4.07	-1.04
50012.00	P02	M-005826-	carboxypeptidas	1369.00	CPN1	2.29	2.55	-0.65
50012.00	P04	M-005825-	carboxypeptidas	1368.00	CPM	3.06	1.78	-0.45
50012.00	P05	M-013503-	vesicle-associat	8673.00	VAMP8	4.82	0.03	-0.01
50012.00	P06	M-005823-	carboxypeptidas	1363.00	CPE	3.55	1.29	-0.33
50012.00	P07	M-011419-	von Hippel-Lind	7411.00	VBP1	8.25	3.41	0.87
50012.00	P08	M-005086-	carboxypeptidas	1362.00	CPD	3.93	0.91	-0.23
50012.00	P09	M-013684-	pre-B lymphocy	29802.00	VPREB3	1.26	3.58	-0.91
50012.00	P10	M-009520-	catechol-O-met	1312.00	COMT	1.40	3.44	-0.88
50012.00	P11	M-011806-	vacuolar protei	6293.00	VPS52	1.27	3.57	-0.91
50012.00	P12	M-020338-	cyclin M4	26504.00	CNNM4	2.88	1.96	-0.50
50012.00	P13	M-020300-	catenin (cadheri	29119.00	CTNNA3	3.96	0.88	-0.23
50012.00	P14	M-008763-	ClpX caseinolyti	10845.00	CLPX	2.90	1.94	-0.50
50012.00	P15	M-016062-	visinin-like 1	7447.00	VSNL1	4.75	0.09	-0.03
50012.00	P16	M-009645-	chromatin acce	54108.00	CHRAC1	4.12	0.72	-0.19
50012.00	P17	M-017572-	WW domain bir	23558.00	WBP2	6.00	1.16	0.29
50012.00	P18	M-009775-	choline phosph	56994.00	CHPT1	1.26	3.58	-0.91
50012.00	P19	M-021349-	NOL1/NOP2/Su	55695.00	NSUN5	3.25	1.59	-0.41
50012.00	P20	M-011421-	chitinase 1 (chit	1118.00	CHIT1	0.94	3.90	-1.00
50012.00	P21	M-013967-	chitinase, acidic	27159.00	CHIA	3.11	1.73	-0.44
50012.00	P23	M-020491-	transportin 2 (ir	30000.00	TNPO2	2.47	2.37	-0.61
					mdn	4.84	2.65	
					3xMAD		7.95	
					MADc		3.92	
50012.00	C22							
50012.00	D22					35.99		24.38
50012.00	E22					37.55		23.66
50012.00	F22					37.72		20.85
						33.63		28.59

					mn	36.22	24.37
					sd	1.90	3.20
50012.00	G22						
50012.00	H22					3.32	5.18
50012.00	I22					1.76	2.13
50012.00	J22					3.68	1.02
						2.26	1.17
						2.75	2.37
						0.90	1.93
50012.00	G03	M-003290-	polo-like kinase	5347.00			
50012.00	H03	M-003290-	polo-like kinase	5347.00	PLK1 SMAR	8.12	2.86
					PLK1 SMAR	8.40	0.63
50012.00	I03	D-001206-	siControl non-targeting siRNA #2				
50012.00	J03	D-001206-	siControl non-targeting siRN			6.14	3.22
						3.26	2.52
50012.00	K03	D-001600-	siGLO RISC-free siRNA				
50012.00	L03	D-001600-	siGLO RISC-free siRNA			18.85	16.99
						17.38	17.10

% inf	abs dev	robust Z	% inf	abs dev	robust Z
0.39	3.05	-1.16	0.87	2.54	-0.94
0.16	3.28	-1.25	0.09	3.32	-1.23
2.30	1.14	-0.43	0.14	3.27	-1.21
2.12	1.32	-0.50	4.41	1.00	0.37
1.29	2.15	-0.82	0.46	2.95	-1.09
1.66	1.78	-0.67	1.10	2.31	-0.85
1.61	1.83	-0.70	3.13	0.28	-0.10
0.35	3.09	-1.17	0.65	2.76	-1.02
1.15	2.29	-0.87	0.71	2.70	-1.00
2.85	0.59	-0.22	0.80	2.61	-0.96
1.70	1.74	-0.66	2.47	0.94	-0.35
8.50	5.06	1.93	4.98	1.57	0.58
6.11	2.67	1.02	5.04	1.63	0.61
1.99	1.45	-0.55	2.16	1.25	-0.46
2.37	1.07	-0.41	1.78	1.63	-0.60
2.06	1.38	-0.52	1.96	1.45	-0.53
6.07	2.63	1.00	7.37	3.96	1.47
4.02	0.58	0.22	2.71	0.70	-0.26
0.39	3.05	-1.16	2.88	0.53	-0.19
3.92	0.48	0.18	1.98	1.43	-0.53
3.83	0.39	0.15	3.57	0.16	0.06
2.02	1.42	-0.54	2.39	1.02	-0.38
2.14	1.30	-0.49	5.91	2.50	0.93
2.40	1.04	-0.40	3.07	0.34	-0.13
1.45	1.99	-0.76	1.77	1.64	-0.61
3.14	0.30	-0.11	11.29	**7.88**	2.92
8.33	4.89	1.86	7.41	4.00	1.48
2.63	0.81	-0.31	3.18	0.23	-0.08
3.85	0.41	0.16	5.98	2.57	0.95
1.07	2.37	-0.90	0.62	2.79	-1.03
4.91	1.47	0.56	3.68	0.27	0.10
4.21	0.77	0.30	5.80	2.39	0.89
0.75	2.69	-1.02	2.54	0.87	-0.32
2.04	1.40	-0.53	1.40	2.01	-0.74
2.42	1.02	-0.39	5.13	1.72	0.64
4.87	1.43	0.55	7.02	3.61	1.34
1.21	2.23	-0.85	1.68	1.73	-0.64
4.57	1.13	0.43	15.34	**11.93**	4.42
3.92	0.48	0.18	4.36	0.95	0.35
3.27	0.17	-0.07	1.22	2.19	-0.81
6.55	3.11	1.19	3.73	0.32	0.12
3.27	0.17	-0.06	0.47	2.94	-1.09
3.53	0.09	0.03	1.72	1.69	-0.62
7.40	3.96	1.51	2.62	0.79	-0.29
1.04	2.40	-0.91	0.12	3.29	-1.22
3.92	0.48	0.19	1.39	2.02	-0.75

1.22	2.22	-0.84	2.14	1.27	-0.47	
1.33	2.11	-0.80	1.76	1.65	-0.61	
1.19	2.25	-0.85	0.20	3.21	-1.18	
2.48	0.96	-0.36	1.00	2.41	-0.89	
3.19	0.25	-0.09	1.23	2.18	-0.81	
1.05	2.39	-0.91	3.26	0.15	-0.05	
2.55	0.89	-0.34	2.70	0.71	-0.26	
1.43	2.01	-0.76	0.99	2.42	-0.89	
3.00	0.44	-0.17	2.50	0.91	-0.34	
7.93	4.49	1.71	6.16	2.75	1.02	
7.90	4.46	1.70	5.16	1.75	0.65	
0.93	2.51	-0.95	1.02	2.39	-0.88	
4.00	0.56	0.21	7.05	3.64	1.35	
0.08	3.36	-1.28	0.67	2.74	-1.01	
1.11	2.33	-0.88	2.57	0.84	-0.31	
7.55	4.11	1.56	7.71	4.30	1.59	
8.07	4.63	1.76	4.06	0.65	0.24	
3.38	0.06	-0.02	3.71	0.30	0.11	
5.47	2.03	0.77	4.38	0.97	0.36	
7.23	3.79	1.44	8.32	4.91	1.82	
1.24	2.20	-0.84	0.70	2.71	-1.00	
3.09	0.35	-0.13	3.58	0.17	0.06	
1.91	1.53	-0.58	2.78	0.63	-0.23	
2.07	1.37	-0.52	5.01	1.60	0.59	
3.20	0.24	-0.09	2.31	1.10	-0.41	
2.61	0.83	-0.32	3.02	0.39	-0.14	
1.16	2.28	-0.87	0.00	3.41	-1.26	
7.07	3.63	1.38	6.63	3.22	1.19	
4.32	0.88	0.34	2.54	0.88	-0.32	
8.05	4.61	1.75	4.08	0.67	0.25	
4.04	0.60	0.23	0.93	2.48	-0.92	
4.00	0.56	0.21	3.36	0.05	-0.02	
5.03	1.59	0.61	3.37	0.04	-0.01	
1.14	2.30	-0.87	0.48	2.93	-1.08	
3.69	0.25	0.09	4.74	1.33	0.49	
9.18	**5.74**	2.18	2.23	1.18	-0.44	
4.34	0.90	0.34	4.41	1.00	0.37	
12.02	**8.58**	3.27	**14.67**	**11.26**	4.17	y
1.62	1.82	-0.69	1.33	2.08	-0.77	
6.53	3.09	1.18	4.00	0.59	0.22	
4.29	0.85	0.32	1.87	1.54	-0.57	
5.52	2.08	0.79	1.51	1.90	-0.70	
3.53	0.09	0.03	1.21	2.20	-0.81	
4.07	0.63	0.24	2.42	0.99	-0.36	
2.51	0.93	-0.35	3.49	0.08	0.03	
2.20	1.24	-0.47	1.60	1.81	-0.67	
2.53	0.91	-0.35	0.30	3.11	-1.15	

2.30	1.14	-0.43	0.58	2.83	-1.05	
7.11	3.67	1.40	0.90	2.51	-0.93	
7.25	3.81	1.45	1.88	1.53	-0.56	
6.05	2.61	1.00	0.37	3.04	-1.12	
2.39	1.05	-0.40	0.35	3.06	-1.13	
2.41	1.03	-0.39	0.32	3.09	-1.14	
1.17	2.27	-0.86	0.38	3.03	-1.12	
2.37	1.07	-0.41	2.76	0.65	-0.24	
9.73	**6.29**	2.39	10.45	**7.04**	2.60	y
0.30	3.14	-1.19	3.22	0.19	-0.07	
4.13	0.69	0.26	6.65	3.24	1.20	
1.80	1.64	-0.62	4.10	0.69	0.26	
20.01	**16.57**	6.31	**24.74**	**21.33**	7.89	y
3.76	0.32	0.12	6.13	2.72	1.01	
1.49	1.95	-0.74	3.60	0.19	0.07	
3.14	0.30	-0.11	5.95	2.54	0.94	
3.00	0.44	-0.17	3.01	0.40	-0.15	
2.12	1.32	-0.50	2.08	1.33	-0.49	
1.66	1.78	-0.67	2.03	1.38	-0.51	
1.46	1.98	-0.75	2.63	0.78	-0.29	
1.10	2.34	-0.89	3.95	0.54	0.20	
4.95	1.51	0.57	2.46	0.95	-0.35	
5.09	1.65	0.63	2.09	1.32	-0.49	
3.10	0.34	-0.13	2.55	0.87	-0.32	
8.25	4.81	1.83	9.11	**5.70**	2.11	
3.80	0.36	0.14	1.39	2.02	-0.75	
1.16	2.28	-0.87	2.69	0.72	-0.26	
4.83	1.39	0.53	9.28	**5.87**	2.18	y
2.73	0.71	-0.27	2.22	1.19	-0.44	
9.21	**5.77**	2.20	**22.14**	**18.73**	6.93	y
0.56	2.88	-1.09	2.99	0.42	-0.15	
9.42	**5.98**	2.28	4.01	0.60	0.22	y
5.95	2.51	0.96	8.77	5.36	1.98	
2.96	0.48	-0.18	4.47	1.06	0.40	
4.55	1.11	0.42	3.14	0.27	-0.10	
10.58	**7.14**	2.72	5.50	2.09	0.78	
3.24	0.20	-0.08	4.00	0.59	0.22	
3.17	0.27	-0.10	2.65	0.76	-0.28	
6.12	2.68	1.02	7.72	4.31	1.60	
5.49	2.05	0.78	5.72	2.31	0.86	
4.03	0.59	0.23	3.91	0.50	0.19	
1.93	1.51	-0.57	4.85	1.44	0.53	
6.64	3.20	1.22	6.38	2.97	1.10	
5.18	1.74	0.66	3.78	0.37	0.14	
6.66	3.22	1.23	3.05	0.36	-0.13	
4.60	1.16	0.44	6.52	3.11	1.15	
0.76	2.68	-1.02	1.78	1.63	-0.60	

2.98	0.46	-0.17	4.28	0.87	0.32	
3.39	0.05	-0.02	7.22	3.81	1.41	
4.21	0.77	0.29	4.52	1.11	0.41	
1.87	1.57	-0.60	0.44	2.97	-1.10	
6.20	2.76	1.05	14.95	**11.54**	4.27	y
5.08	1.64	0.62	7.98	4.57	1.69	
5.91	2.47	0.94	5.70	2.29	0.85	
1.29	2.15	-0.82	2.10	1.31	-0.48	
2.96	0.48	-0.18	2.59	0.82	-0.30	
2.95	0.49	-0.19	0.99	2.42	-0.89	
2.55	0.89	-0.34	5.84	2.43	0.90	
7.58	4.14	1.58	3.84	0.43	0.16	
2.07	1.37	-0.52	4.13	0.72	0.27	
1.45	1.99	-0.76	1.71	1.70	-0.63	
2.61	0.83	-0.31	1.46	1.95	-0.72	
6.85	3.41	1.30	6.52	3.11	1.15	
6.56	3.12	1.19	7.45	4.04	1.50	
1.24	2.20	-0.84	1.15	2.26	-0.83	
3.26	0.18	-0.07	2.32	1.09	-0.40	
3.11	0.33	-0.13	1.89	1.52	-0.56	
4.96	1.52	0.58	7.53	4.12	1.52	
7.90	4.46	1.70	6.63	3.22	1.19	
3.80	0.36	0.14	2.83	0.58	-0.21	
4.75	1.31	0.50	6.81	3.40	1.26	
9.12	**5.68**	2.16	4.23	0.82	0.31	
5.12	1.68	0.64	2.50	0.91	-0.33	
4.47	1.03	0.39	2.59	0.82	-0.30	
7.99	4.55	1.73	6.59	3.18	1.18	
2.57	0.87	-0.33	1.02	2.39	-0.88	
1.45	1.99	-0.76	0.96	2.45	-0.90	
4.08	0.64	0.25	1.16	2.25	-0.83	
5.43	1.99	0.76	1.28	2.13	-0.79	
2.19	1.25	-0.47	3.64	0.23	0.09	
2.72	0.72	-0.27	0.49	2.92	-1.08	
4.04	0.60	0.23	2.95	0.46	-0.17	
2.15	1.29	-0.49	1.75	1.66	-0.61	
18.70	**15.26**	5.81	**17.28**	**13.87**	5.13	y
3.90	0.46	0.18	4.72	1.31	0.49	
2.52	0.92	-0.35	1.10	2.31	-0.85	
14.45	**11.01**	4.19	**11.91**	**8.50**	3.15	y
7.46	4.02	1.53	2.76	0.65	-0.24	
6.14	2.70	1.03	5.38	1.97	0.73	
17.42	**13.98**	5.32	**19.09**	**15.68**	5.80	y
8.90	**5.46**	2.08	8.72	5.31	1.97	
4.59	1.15	0.44	5.28	1.87	0.69	
3.06	0.38	-0.15	1.84	1.57	-0.58	
5.72	2.28	0.87	4.30	0.89	0.33	

0.76	2.68	-1.02	0.19	3.22	-1.19		
8.04	4.60	1.75	5.39	1.98	0.73		
0.94	2.50	-0.95	2.16	1.26	-0.46		
1.06	2.38	-0.90	1.71	1.70	-0.63		
5.08	1.64	0.62	2.53	0.88	-0.32		
2.21	1.23	-0.47	2.00	1.41	-0.52		
9.02	**5.58**	2.12	**11.46**	**8.05**	2.98	y	
4.26	0.82	0.31	3.96	0.55	0.21		
1.38	2.06	-0.78	0.54	2.87	-1.06		
0.90	2.54	-0.96	0.19	3.22	-1.19		
6.30	2.86	1.09	1.77	1.64	-0.61		
3.81	0.37	0.14	0.71	2.70	-1.00		
4.76	1.32	0.50	2.80	0.61	-0.22		
9.09	**5.65**	2.15	17.15	**13.74**	5.08	x	art.b
3.73	0.29	0.11	2.80	0.61	-0.22		
1.99	1.45	-0.55	4.48	1.07	0.40		
3.24	0.20	-0.08	7.29	3.88	1.44		
6.40	2.96	1.13	5.83	2.42	0.90		
3.00	0.44	-0.16	7.85	4.44	1.64		
4.35	0.91	0.35	6.74	3.33	1.23		
3.70	0.26	0.10	3.03	0.38	-0.14		
6.18	2.74	1.04	3.78	0.37	0.14		
2.45	0.99	-0.38	4.61	1.20	0.45		
7.08	3.64	1.38	10.25	**6.84**	2.53		
5.09	1.65	0.63	6.15	2.74	1.01		
6.54	3.10	1.18	8.12	4.71	1.74		
2.53	0.91	-0.34	2.78	0.63	-0.23		
5.56	2.12	0.81	6.32	2.91	1.08		
4.70	1.26	0.48	4.71	1.30	0.48		
10.65	**7.21**	2.74	9.22	**5.81**	2.15	y	
6.15	2.71	1.03	9.61	**6.20**	2.29		
5.89	2.45	0.93	8.38	4.97	1.84		
10.77	**7.33**	2.79	3.86	0.45	0.17		
5.19	1.75	0.67	2.76	0.65	-0.24		
7.14	3.70	1.41	8.12	4.71	1.75		
7.58	4.14	1.57	3.72	0.31	0.12		
18.84	**15.40**	5.86	**18.94**	**15.53**	5.75	y	
3.21	0.23	-0.09	3.01	0.40	-0.15		
13.33	**9.89**	3.76	8.75	5.34	1.98	y	
2.20	1.24	-0.47	1.72	1.69	-0.62		
4.50	1.06	0.41	3.40	0.01	0.00		
4.82	1.38	0.53	1.54	1.87	-0.69		
5.03	1.59	0.61	3.30	0.11	-0.04		
2.54	0.90	-0.34	1.13	2.28	-0.84		
2.89	0.55	-0.21	3.82	0.41	0.15		
0.67	2.77	-1.05	0.61	2.80	-1.03		
5.91	2.47	0.94	2.99	0.42	-0.15		

2.25	1.19	-0.45	5.72	2.31	0.86	
6.89	3.45	1.31	8.97	**5.56**	2.06	
8.41	4.97	1.89	6.82	3.41	1.26	
4.62	1.18	0.45	4.20	0.79	0.30	
5.07	1.63	0.62	9.52	**6.11**	2.26	
5.26	1.82	0.69	2.92	0.49	-0.18	
16.30	**12.86**	4.89	**13.49**	**10.08**	3.73	y
5.78	2.34	0.89	0.75	2.66	-0.98	
2.38	1.06	-0.40	6.99	3.58	1.33	
16.82	**13.38**	5.09	**20.60**	**17.19**	6.36	y
8.16	4.72	1.80	8.91	**5.50**	2.04	
5.52	2.08	0.79	4.72	1.31	0.48	
10.39	**6.95**	2.65	13.36	**9.95**	3.68	y
11.99	**8.55**	3.25	6.21	2.80	1.04	
5.29	1.85	0.70	5.83	2.42	0.90	
14.62	**11.18**	4.26	**7.85**	4.44	1.65	y
3.84	0.40	0.15	4.39	0.98	0.36	
6.45	3.01	1.15	3.99	0.58	0.22	
2.66	0.78	-0.30	4.16	0.75	0.28	
4.25	0.81	0.31	4.71	1.30	0.48	
3.27	0.17	-0.06	2.58	0.83	-0.31	
3.49	0.05	0.02	3.34	0.07	-0.03	
3.81	0.37	0.14	3.63	0.22	0.08	
7.67	4.23	1.61	3.03	0.38	-0.14	
5.31	1.87	0.71	5.25	1.84	0.68	
2.53	0.91	-0.34	2.48	0.93	-0.34	
0.29	3.15	-1.20	1.91	1.50	-0.55	
2.63	0.81	-0.31	3.69	0.28	0.11	
2.91	0.53	-0.20	9.45	**6.04**	2.24	
2.02	1.42	-0.54	8.47	5.06	1.88	
7.20	3.76	1.43	11.51	**8.10**	3.00	y
1.38	2.06	-0.78	6.69	3.28	1.21	
3.21	0.23	-0.09	8.84	5.43	2.01	
11.02	**7.58**	2.89	8.79	5.38	1.99	
6.49	3.05	1.16	9.26	**5.85**	2.17	
1.17	2.27	-0.86	3.41	0.00	0.00	
1.26	2.18	-0.83	2.83	0.58	-0.21	
4.02	0.58	0.22	8.05	4.64	1.72	
5.52	2.08	0.79	10.71	**7.30**	2.70	
7.09	3.65	1.39	12.42	**9.01**	3.33	y
1.85	1.59	-0.60	13.21	**9.80**	3.63	
1.59	1.85	-0.70	5.27	1.86	0.69	
3.36	0.08	-0.03	4.66	1.25	0.47	
7.40	3.96	1.51	11.54	**8.13**	3.01	
0.47	2.97	-1.13	1.82	1.59	-0.59	
0.82	2.62	-1.00	0.82	2.59	-0.96	
3.88	0.44	0.17	13.74	**10.33**	3.82	

2.22	1.22	-0.46	5.03	1.62	0.60	
2.41	1.03	-0.39	5.42	2.01	0.75	
6.99	3.55	1.35	17.39	**13.98**	5.17	
1.28	2.16	-0.82	4.73	1.32	0.49	
1.38	2.06	-0.78	2.52	0.89	-0.33	
4.32	0.88	0.33	5.05	1.64	0.61	
0.81	2.63	-1.00	2.83	0.58	-0.21	
0.86	2.58	-0.98	3.09	0.32	-0.12	
0.79	2.65	-1.01	1.48	1.93	-0.71	
0.80	2.64	-1.00	1.44	1.97	-0.73	
3.07	0.37	-0.14	9.40	**5.99**	2.22	
1.73	1.71	-0.65	9.05	**5.64**	2.09	
0.53	2.91	-1.11	2.85	0.56	-0.21	
1.69	1.75	-0.66	1.21	2.20	-0.81	
0.99	2.45	-0.93	5.93	2.52	0.93	
2.66	0.78	-0.29	2.90	0.51	-0.19	
0.97	2.47	-0.94	2.83	0.58	-0.21	
2.06	1.38	-0.52	5.60	2.19	0.81	
0.68	2.76	-1.05	2.46	0.95	-0.35	
1.02	2.42	-0.92	0.28	3.13	-1.16	
5.57	2.13	0.81	8.27	4.86	1.80	
1.30	2.14	-0.82	2.44	0.97	-0.36	
6.82	3.38	1.29	5.47	2.06	0.77	
2.57	0.87	-0.33	3.40	0.01	0.00	
5.30	1.86	0.71	4.83	1.42	0.53	
6.28	2.84	1.08	1.14	2.27	-0.84	
2.34	1.10	-0.42	1.50	1.91	-0.71	
3.51	0.07	0.03	2.69	0.72	-0.27	
2.19	1.25	-0.48	1.96	1.45	-0.53	
1.09	2.35	-0.89	1.72	1.69	-0.62	
2.07	1.37	-0.52	3.28	0.13	-0.04	
7.57	4.13	1.57	8.44	5.03	1.86	
4.14	0.70	0.27	2.71	0.70	-0.26	
1.60	1.84	-0.70	5.82	2.41	0.89	
2.82	0.62	-0.23	7.74	4.33	1.60	
3.19	0.25	-0.09	3.01	0.40	-0.15	
0.40	3.04	-1.16	3.41	0.00	0.00	
0.65	2.79	-1.06	5.16	1.75	0.65	
6.15	2.71	1.03	2.50	0.91	-0.33	
3.44	1.78		3.41	1.83		
	5.33			5.48		
	2.63			2.70		
				A	**B**	**C**
	32.22		3psSD	5.69	9.60	20.94
	21.16		3ngSD	2.69	5.79	2.05
			SumSD	8.38	15.39	22.99
	19.32		DiffMn	33.47	21.99	23.35

24.23	SmovrDiff	0.25	0.70	0.98
6.98	1minus	0.75	0.30	0.02
1.82				
0.92				
0.26				
0.52				
0.88				
0.68				
8.14				
5.13				
3.67				
0.83				
3.13				
17.21				
24.09				

						% inf	**abs dev**	**robust Z**
50013.00	A02	M-005148-	primase, poly	5558.00	PRIM2A	0.86	2.89	-0.97
50013.00	A04	M-017750-	protein phos	151987.00	PPP4R2	1.88	1.87	-0.62
50013.00	A05	M-008945-	FK506 bindin	2286.00	FKBP2	1.26	2.49	-0.83
50013.00	A06	M-024184-	protein phos	55370.00	PPP4R1L	2.76	0.99	-0.33
50013.00	A07	M-006410-	FK506 bindin	2288.00	FKBP4	0.91	2.84	-0.95
50013.00	A08	M-009869-	protein phos	5534.00	PPP3R1	0.83	2.92	-0.98
50013.00	A09	M-004224-	FK506 bindin	2289.00	FKBP5	3.36	0.39	-0.13
50013.00	A10	M-021914-	protein phos	90673.00	PPP1R3E	5.45	1.70	0.57
50013.00	A11	M-009426-	FK506 bindin	8468.00	FKBP6	2.29	1.46	-0.49
50013.00	A12	M-015361-	protein phos	5504.00	PPP1R2	0.35	3.40	-1.13
50013.00	A13	M-019253-	FK506 bindin	63943.00	FKBPL	1.39	2.36	-0.79
50013.00	A14	M-017092-	protein phos	5502.00	PPP1R1A	3.71	0.04	-0.01
50013.00	A15	M-018183-	transmembr	84866.00	TMEM25	2.69	1.06	-0.35
50013.00	A16	M-015013-	protein phos	84919.00	PPP1R15B	3.42	0.33	-0.11
50013.00	A17	M-013361-	tetratricopep	54902.00	TTC19	1.20	2.55	-0.85
50013.00	A18	M-004442-	protein phos	23645.00	PPP1R15A	3.75	0.00	0.00
50013.00	A19	M-005084-	X-ray repair c	2547.00	XRCC6	2.81	0.94	-0.31
50013.00	A20	M-015206-	protein phos	54866.00	PPP1R14D	1.68	2.07	-0.69
50013.00	A21	M-011664-	glycyl-tRNA s	2617.00	GARS	3.47	0.28	-0.09
50013.00	A23	M-005153-	guanylate bir	2633.00	GBP1	0.55	3.20	-1.07
50013.00	B02	M-009240-	nitric oxide s	4843.00	NOS2A	1.60	2.15	-0.72
50013.00	B04	M-019069-	NADH dehyd	4719.00	NDUFS1	3.16	0.59	-0.20
50013.00	B05	M-006007-	protein C (ina	5624.00	PROC	1.08	2.67	-0.89
50013.00	B06	M-009958-	similar to ne	4687.00	LOC4687	1.25	2.50	-0.84
50013.00	B07	M-010099-	protein Z, vit	8858.00	PROZ	6.97	3.22	1.07
50013.00	B08	M-008970-	lipoprotein li	4023.00	LPL	2.11	1.64	-0.55
50013.00	B09	M-006008-	protease, ser	5644.00	PRSS1	1.85	1.90	-0.63
50013.00	B10	M-008743-	lipase, hepat	3990.00	LIPC	1.44	2.31	-0.77
50013.00	B11	M-006009-	HtrA serine p	5654.00	HTRA1	4.04	0.29	0.10
50013.00	B12	M-006280-	ATPase, Ca+	9914.00	ATP2C2	3.43	0.32	-0.11
50013.00	B13	M-006012-	protease, ser	5645.00	PRSS2	1.16	2.59	-0.87
50013.00	B14	M-008139-	hydroxysterc	3295.00	HSD17B4	6.61	2.86	0.95
50013.00	B15	M-006014-	HtrA serine p	27429.00	HTRA2	2.11	1.64	-0.55
50013.00	B16	M-008601-	ATPase type	23400.00	ATP13A2	3.09	0.66	-0.22
50013.00	B17	M-010123-	proteasome	5682.00	PSMA1	5.31	1.56	0.52
50013.00	B18	M-012099-	GTPase activ	10146.00	G3BP1	8.42	4.67	1.56
50013.00	B19	M-012349-	pyrroline-5-c	5831.00	PYCR1	2.17	1.58	-0.53
50013.00	B20	M-008376-	dihydropyrim	1806.00	DPYD	1.48	2.27	-0.76
50013.00	B21	M-004667-	RAB27A, mer	5873.00	RAB27A	4.09	0.34	0.11
50013.00	B23	M-004228-	RAB27B, mer	5874.00	RAB27B	5.39	1.64	0.55
50013.00	C02	M-014682-	protein phos	81706.00	PPP1R14C	3.03	0.72	-0.24
50013.00	C04	M-026574-	protein phos	26472.00	PPP1R14B	6.37	2.62	0.88
50013.00	C05	M-011867-	guanylate bir	2634.00	GBP2	2.37	1.38	-0.46
50013.00	C06	M-021385-	protein phos	94274.00	PPP1R14A	5.50	1.75	0.58
50013.00	C07	M-016144-	G kinase ancl	80318.00	GKAP1	2.83	0.92	-0.31
50013.00	C08	M-010492-	protein phos	23368.00	PPP1R13B	6.65	2.90	0.97

50013.00	C09	M-009843-	glycerol-3-ph	2820.00	GPD2	8.00	4.25	1.42
50013.00	C10	M-013775-	protein phos	54776.00	PPP1R12C	4.04	0.29	0.10
50013.00	C11	M-009586-	glutathione s	2937.00	GSS	3.84	0.09	0.03
50013.00	C12	M-011340-	protein phos	4659.00	PPP1R12A	1.16	2.59	-0.86
50013.00	C13	M-019856-	hepatitis A vi	26762.00	HAVCR1	0.73	3.02	-1.01
50013.00	C14	M-006827-	protein phos	5501.00	PPP1CC	7.89	4.14	1.38
50013.00	C15	M-004258-	histone deac	79885.00	HDAC11	4.73	0.98	0.33
50013.00	C16	M-009613-	porcupine ho	64840.00	PORCN	5.40	1.65	0.55
50013.00	C17	M-003496-	histone deac	8841.00	HDAC3	2.40	1.35	-0.45
50013.00	C18	M-008293-	peptidylproly	9360.00	PPIG	6.58	2.83	0.94
50013.00	C19	M-003500-	histone deac	55869.00	HDAC8	10.09	**6.34**	2.12
50013.00	C20	M-008888-	peptidylproly	5481.00	PPID	4.19	0.44	0.14
50013.00	C21	M-004142-	v-Ha-ras Harv	3265.00	HRAS	2.80	0.95	-0.32
50013.00	C23	M-017609-	heat shock 7	3312.00	HSPA8	1.99	1.76	-0.59
50013.00	D02	M-009509-	dihydrolipoa	1738.00	DLD	5.18	1.43	0.48
50013.00	D04	M-010506-	DEAH (Asp-G	1659.00	DHX8	1.63	2.12	-0.71
50013.00	D05	M-008582-	RAB28, mem	9364.00	RAB28	1.66	2.09	-0.70
50013.00	D06	M-008282-	cytochrome	1545.00	CYP1B1	1.61	2.14	-0.71
50013.00	D07	M-008269-	RAB30, mem	27314.00	RAB30	1.02	2.73	-0.91
50013.00	D08	M-008276-	cytochrome	1588.00	CYP19A1	1.05	2.70	-0.90
50013.00	D09	M-009031-	RAB6C, mem	84084.00	RAB6C	3.61	0.14	-0.05
50013.00	D10	M-011550-	copine III	8895.00	CPNE3	3.08	0.67	-0.22
50013.00	D11	M-013620-	RAB, membe	11159.00	RABL2A	1.32	2.43	-0.81
50013.00	D12	M-009303-	ceruloplasmi	1356.00	CP	3.43	0.32	-0.11
50013.00	D13	M-008404-	RAB, membe	11158.00	RABL2B	1.59	2.16	-0.72
50013.00	D14	M-011837-	COX11 homo	1353.00	COX11	1.92	1.83	-0.61
50013.00	D15	M-007741-	ras-related C	5880.00	RAC2	0.86	2.89	-0.97
50013.00	D16	M-020426-	ATPase type	57130.00	ATP13A1	4.20	0.45	0.15
50013.00	D17	M-003293-	RAD1 homol	5810.00	RAD1	2.76	0.99	-0.33
50013.00	D18	M-006425-	cystic fibrosis	1080.00	CFTR	8.10	4.35	1.45
50013.00	D19	M-005232-	RAD50 homo	10111.00	RAD50	8.62	4.87	1.62
50013.00	D20	M-008954-	copper chape	9973.00	CCS	2.43	1.32	-0.44
50013.00	D21	M-010534-	RAD51 homo	5889.00	RAD51C	7.05	3.30	1.10
50013.00	D23	M-011373-	RAD51-like 1	5890.00	RAD51L1	3.96	0.21	0.07
50013.00	E02	M-022098-	protein tyros	8497.00	PPFIA4	1.65	2.10	-0.70
50013.00	E04	M-012612-	protein tyros	8541.00	PPFIA3	3.96	0.21	0.07
50013.00	E05	M-019543-	interferon in	8519.00	IFITM1	1.68	2.07	-0.69
50013.00	E06	M-011485-	protein tyros	8499.00	PPFIA2	5.71	1.96	0.65
50013.00	E07	M-019657-	immunoglob	3508.00	IGHMBP2	2.04	1.71	-0.57
50013.00	E08	M-011486-	protein tyros	8500.00	PPFIA1	5.52	1.77	0.59
50013.00	E09	M-010172-	inositol(myo)	3612.00	IMPA1	3.97	0.22	0.07
50013.00	E10	M-006003-	phosphoribo	5471.00	PPAT	13.54	**9.79**	3.27
50013.00	E11	M-008348-	inositol(myo)	3613.00	IMPA2	5.38	1.63	0.54
50013.00	E12	M-017891-	peter pan ho	56342.00	PPAN	4.06	0.31	0.10
50013.00	E13	M-008505-	inositol polyp	3628.00	INPP1	8.89	5.14	1.72
50013.00	E14	M-013134-	pyrophospha	5464.00	PPA1	1.85	1.90	-0.63
50013.00	E15	M-021154-	NFKB inhibito	28512.00	NKIRAS1	4.49	0.74	0.25

50013.00	E16	M-020046-	processing o	10775.00	POP4	2.64	1.11	-0.37
50013.00	E17	M-015340-	NFKB inhibit	28511.00	NKIRAS2	4.13	0.38	0.13
50013.00	E18	M-009807-	polymerase (	11044.00	**POLS**	**16.70**	**12.95**	4.32
50013.00	E19	M-026388-	La ribonucle	23185.00	LARP5	5.00	1.25	0.42
50013.00	E20	M-011357-	polymerase (	5436.00	POLR2G	3.44	0.31	-0.10
50013.00	E21	M-004630-	microtubule	23227.00	MAST4	2.16	1.59	-0.53
50013.00	E23	M-004049-	receptor inte	25778.00	RIPK5	5.32	1.57	0.52
50013.00	F02	M-024177-	ATPase, Clas	10079.00	ATP9A	7.50	3.75	1.25
50013.00	F04	M-019995-	ATPase, Clas	5205.00	ATP8B1	9.36	5.61	1.87
50013.00	F05	M-017467-	RAD51-like 3	5892.00	RAD51L3	6.71	2.96	0.99
50013.00	F06	M-010164-	ATPase, ami	51761.00	ATP8A2	2.88	0.87	-0.29
50013.00	F07	M-010572-	RAD54 homo	25788.00	RAD54B	7.50	3.75	1.25
50013.00	F08	M-008166-	ATPase, ami	10396.00	ATP8A1	3.42	0.33	-0.11
50013.00	F09	M-012548-	recombinati	5897.00	RAG2	3.81	0.06	0.02
50013.00	F10	M-019281-	ATPase, Cu+	540.00	ATP7B	6.86	3.11	1.04
50013.00	F11	M-004746-	RAN binding	5903.00	RANBP2	10.10	**6.35**	2.12
50013.00	F12	M-019280-	ATPase, Cu+	538.00	ATP7A	3.77	0.02	0.01
50013.00	F13	M-003623-	RAP1A, mem	5906.00	RAP1A	2.49	1.26	-0.42
50013.00	F14	M-010930-	ATPase, H+ t	51606.00	ATP6V1H	3.69	0.06	-0.02
50013.00	F15	M-010081-	RAP2A, mem	5911.00	RAP2A	0.32	3.43	-1.14
50013.00	F16	M-011588-	ATPase, H+ t	525.00	ATP6V1B1	1.17	2.58	-0.86
50013.00	F17	M-008073-	retinol bindi	5949.00	RBP3	3.16	0.59	-0.20
50013.00	F18	M-006114-	ATPase, Ca+	489.00	ATP2A3	0.62	3.13	-1.05
50013.00	F19	M-010559-	RecQ protei	9401.00	RECQL4	0.61	3.14	-1.05
50013.00	F20	M-006113-	ATPase, Ca+	487.00	ATP2A1	0.71	3.04	-1.01
50013.00	F21	M-019338-	RecQ protei	9400.00	RECQL5	7.27	3.52	1.17
50013.00	F23	M-011763-	UPF1 regulat	5976.00	UPF1	7.64	3.89	1.30
50013.00	G02	M-011187-	polymerase (	5431.00	POLR2B	4.65	0.90	0.30
50013.00	G04	M-011186-	polymerase (	5430.00	POLR2A	1.50	2.25	-0.75
50013.00	G05	M-005069-	v-Ki-ras2 Kirs	3845.00	KRAS	3.25	0.50	-0.17
50013.00	G06	M-008746-	polymerase (	27343.00	POLL	1.90	1.85	-0.62
50013.00	G07	M-003570-	kinase suppr	8844.00	KSR1	10.19	**6.44**	2.15
50013.00	G08	M-006454-	polymerase (	5429.00	POLH	4.93	1.18	0.39
50013.00	G09	M-005923-	leucine amin	51056.00	LAP3	5.90	2.15	0.72
50013.00	G10	M-012649-	polymerase (	5428.00	POLG	3.31	0.44	-0.15
50013.00	G11	M-009623-	lecithin-chol	3931.00	LCAT	4.87	1.12	0.37
50013.00	G12	M-020132-	polymerase (	5426.00	POLE	7.86	4.11	1.37
50013.00	G13	M-010582-	likely orthol	79132.00	LGP2	4.70	0.95	0.32
50013.00	G14	M-019687-	polymerase (	5424.00	POLD1	3.32	0.43	-0.14
50013.00	G15	M-011076-	ligase I, DNA,	3978.00	**LIG1**	**8.84**	5.09	1.70
50013.00	G16	M-020856-	polymerase (	5422.00	POLA1	8.82	5.07	1.69
50013.00	G17	M-009060-	lipase, gastri	8513.00	**LIPF**	**23.76**	**20.01**	6.68
50013.00	G18	M-017120-	pyridoxal (py	57026.00	PDXP	7.43	3.68	1.23
50013.00	G19	M-009601-	lipase, endot	9388.00	**LIPG**	**15.11**	**11.36**	3.79
50013.00	G20	M-006001-	plasminogen	5340.00	PLG	1.78	1.97	-0.66
50013.00	G21	M-005926-	leucyl/cystin	4012.00	LNPEP	5.76	2.01	0.67
50013.00	G23	M-009810-	lysyl oxidase	4015.00	LOX	2.57	1.18	-0.39

50013.00	H02	M-006112-	ATPase, Na+,	477.00	ATP1A2	11.96	**8.21**	2.74
50013.00	H04	M-023660-	ATPase, Clas	23200.00	ATP11B	6.49	2.74	0.91
50013.00	H05	M-008234-	REV1 homol	51455.00	REV1	2.48	1.27	-0.43
50013.00	H06	M-008291-	aldehyde oxi	316.00	AOX1	8.50	4.75	1.58
50013.00	H07	M-006302-	REV3-like, ca	5980.00	REV3L	6.63	2.88	0.96
50013.00	H08	M-009026-	arachidonate	247.00	ALOX15B	3.91	0.16	0.05
50013.00	H09	M-008929-	Rho family G	27289.00	RND1	5.56	1.81	0.61
50013.00	H10	M-009025-	arachidonate	242.00	ALOX12B	3.53	0.22	-0.07
50013.00	H11	M-020480-	Rho-related	22836.00	RHOBTB3	3.70	0.05	-0.02
50013.00	H12	M-008503-	aldo-keto re	1646.00	AKR1C2	11.89	**8.14**	2.72
50013.00	H13	M-008510-	Ras-like with	6014.00	**RIT2**	**9.11**	5.36	1.79
50013.00	H14	M-009151-	aldo-keto re	1645.00	AKR1C1	3.40	0.35	-0.12
50013.00	H15	M-009282-	ribonuclease	8635.00	RNASET2	6.70	2.95	0.99
50013.00	H16	M-008131-	ATPase type	79572.00	ATP13A3	7.01	3.26	1.09
50013.00	H17	M-019525-	RNA (guanin	8731.00	RNMT	12.63	**8.88**	2.96
50013.00	H18	M-008115-	alcohol dehy	131.00	ADH7	0.70	3.05	-1.02
50013.00	H19	M-006031-	arginyl amin	6051.00	RNPEP	8.23	4.48	1.49
50013.00	H20	M-008939-	alcohol dehy	130.00	ADH6	8.21	4.46	1.49
50013.00	H21	M-007793-	Ras-related	6236.00	RRAD	5.32	1.57	0.52
50013.00	H23	M-010352-	related RAS	6237.00	RRAS	1.27	2.48	-0.83
50013.00	I02	M-004903-	phospholipa	7941.00	PLA2G7	0.97	2.78	-0.93
50013.00	I04	M-010110-	phospholipa	5322.00	**PLA2G5**	**9.59**	5.84	1.95
50013.00	I05	M-009695-	leukotriene	22949.00	LTB4DH	10.49	**6.74**	2.25
50013.00	I06	M-009545-	phospholipa	50487.00	PLA2G3	3.05	0.70	-0.24
50013.00	I07	M-019661-	lactotransfer	4057.00	LTF	10.36	**6.61**	2.21
50013.00	I08	M-010283-	phospholipa	30814.00	PLA2G2E	1.21	2.54	-0.85
50013.00	I09	M-019883-	ectonucleosi	9583.00	ENTPD4	6.17	2.42	0.81
50013.00	I10	M-010281-	phospholipa	26279.00	PLA2G2D	10.42	**6.67**	2.23
50013.00	I11	M-008496-	methionine	4143.00	MAT1A	1.52	2.23	-0.74
50013.00	I12	M-009901-	phospholipa	5320.00	PLA2G2A	5.08	1.33	0.44
50013.00	I13	M-011554-	methyl-CpG	8930.00	MBD4	3.35	0.40	-0.13
50013.00	I14	M-008873-	phospholipa	5319.00	PLA2G1B	0.77	2.98	-1.00
50013.00	I15	M-005940-	membrane-b	51360.00	MBTPS2	5.77	2.02	0.67
50013.00	I16	M-003291-	protein (pep	5300.00	PIN1	4.32	0.57	0.19
50013.00	I17	M-009429-	methylcroto	56922.00	MCCC1	4.56	0.81	0.27
50013.00	I18	M-009518-	phosphoglyc	26227.00	PHGDH	4.08	0.33	0.11
50013.00	I19	M-003273-	minichromos	4171.00	MCM2	7.36	3.61	1.20
50013.00	I20	M-005995-	phosphate re	5251.00	PHEX	5.13	1.38	0.46
50013.00	I21	M-003274-	minichromos	4172.00	MCM3	3.72	0.03	-0.01
50013.00	I23	M-003275-	minichromos	4173.00	MCM4	2.13	1.62	-0.54
50013.00	J02	M-009924-	ATP-binding	9429.00	ABCG2	2.79	0.96	-0.32
50013.00	J04	M-005160-	tubulin, gam	7283.00	TUBG1	1.70	2.05	-0.68
50013.00	J05	M-010358-	related RAS	22800.00	RRAS2	5.30	1.55	0.52
50013.00	J06	M-006844-	tubulin, epsil	51175.00	TUBE1	2.82	0.93	-0.31
50013.00	J07	M-009557-	RAS-like, fam	10633.00	RASL10A	5.42	1.67	0.56
50013.00	J08	M-006843-	tubulin, delta	51174.00	TUBD1	4.34	0.59	0.20
50013.00	J09	M-008977-	RuvB-like 1 (	8607.00	RUVBL1	11.22	**7.47**	2.49

50013.00	J10	M-010111- tubulin, beta	56604.00	TUBB4Q	1.78	1.97	-0.66
50013.00	J11	M-012299- RuvB-like 2 (	10856.00	RUVBL2	4.24	0.49	0.16
50013.00	J12	M-020099- tubulin, beta	10381.00	TUBB3	11.82	8.07	2.69
50013.00	J13	M-005061- stearoyl-CoA	6319.00	SCD	3.15	0.60	-0.20
50013.00	J14	M-009589- tubulin, beta	81027.00	TUBB1	1.37	2.38	-0.79
50013.00	J15	M-014751- SET domain,	83852.00	SETDB2	5.37	1.62	0.54
50013.00	J16	M-009279- tubulin, alph	7278.00	TUBA3C	4.87	1.12	0.37
50013.00	J17	M-020013- SET domain a	6419.00	SETMAR	3.90	0.15	0.05
50013.00	J18	M-008779- tubulin, alph	7277.00	TUBA4A	3.41	0.34	-0.11
50013.00	J19	M-012597- SH3-domain	6456.00	SH3GL2	5.98	2.23	0.74
50013.00	J20	M-040894- ribosomal pr	58988.00	Rps6kb2	1.44	2.31	-0.77
50013.00	J21	M-021353- split hand/fo	7979.00	SHFM1	0.96	2.79	-0.93
50013.00	J23	M-003540- sirtuin (silent	23411.00	SIRT1	7.38	3.63	1.21
50013.00	K02	M-004902- peroxisomal	5190.00	PEX6	6.51	2.76	0.92
50013.00	K04	M-003820- phosphodies	5152.00	PDE9A	5.83	2.08	0.69
50013.00	K05	M-003276- minichromos	4174.00	MCM5	3.09	0.66	-0.22
50013.00	K06	M-007667- phosphodies	8654.00	PDE5A	10.59	6.84	2.28
50013.00	K07	M-003277- minichromos	4175.00	MCM6	10.57	6.82	2.27
50013.00	K08	M-007643- phosphodies	5137.00	PDE1C	5.58	1.83	0.61
50013.00	K09	M-003278- minichromos	4176.00	**MCM7**	**12.97**	9.22	3.08
50013.00	K10	M-007642- phosphodies	5153.00	PDE1B	3.14	0.61	-0.21
50013.00	K11	M-005941- meprin A, alp	4224.00	MEP1A	4.79	1.04	0.35
50013.00	K12	M-007641- phosphodies	5136.00	PDE1A	1.03	2.72	-0.91
50013.00	K13	M-005949- mitochondri	4285.00	MIPEP	0.75	3.00	-1.00
50013.00	K14	M-010339- chromatin m	5119.00	CHMP1A	3.24	0.51	-0.17
50013.00	K15	M-005951- matrix metal	4312.00	MMP1	4.44	0.69	0.23
50013.00	K16	M-003289- proliferating	5111.00	PCNA	5.47	1.72	0.57
50013.00	K17	M-005952- matrix metal	4319.00	MMP10	7.62	3.87	1.29
50013.00	K18	M-005165- pericentriola	5108.00	PCM1	1.90	1.85	-0.62
50013.00	K19	M-005953- matrix metal	4320.00	MMP11	4.83	1.08	0.36
50013.00	K20	M-008965- propionyl Co	5095.00	PCCA	1.22	2.53	-0.85
50013.00	K21	M-005954- matrix metal	4321.00	MMP12	3.11	0.65	-0.22
50013.00	K23	M-005955- matrix metal	4322.00	MMP13	2.85	0.90	-0.30
50013.00	L02	M-012005- reelin	5649.00	RELN	11.44	7.69	2.57
50013.00	L04	M-008969- protein tyros	5771.00	PTPN2	2.10	1.65	-0.55
50013.00	L05	M-004826- sirtuin (silent	22933.00	SIRT2	3.75	0.00	0.00
50013.00	L06	M-011886- septin 4	5414.00	SEPT4	2.58	1.17	-0.39
50013.00	L07	M-013801- SWI/SNF-rela	56916.00	SMARCAD1	13.36	9.61	3.21
50013.00	L08	M-013234- septin 5	5413.00	SEPT5	7.78	4.03	1.35
50013.00	L09	M-013058- SWI/SNF rela	50485.00	SMARCAL1	6.58	2.83	0.94
50013.00	L10	M-012184- NEL-like 1 (ch	4745.00	NELL1	0.41	3.34	-1.11
50013.00	L11	M-009784- superoxide d	6648.00	SOD2	4.46	0.71	0.24
50013.00	L12	M-008981- tubulin, beta	84617.00	TUBB6	0.71	3.04	-1.01
50013.00	L13	M-017294- sperm adhes	6677.00	SPAM1	10.49	6.74	2.25
50013.00	L14	M-020062- tubulin, alph	10376.00	TUBA1B	3.49	0.26	-0.09
50013.00	L15	M-010946- spastic parap	51062.00	**SPG3A**	**17.95**	14.20	4.74
50013.00	L16	M-005763- ADAM metal	81792.00	ADAMTS12	8.59	4.84	1.61

50013.00	L17	M-006039-	spastic parap	6687.00	SPG7	3.26	0.49	-0.16
50013.00	L18	M-017387-	TAP binding	6892.00	TAPBP	0.33	3.42	-1.14
50013.00	L19	M-020043-	SPO11 meiot	23626.00	SPO11	3.16	0.59	-0.20
50013.00	L20	M-007635-	transporter 2	6891.00	TAP2	8.02	4.27	1.42
50013.00	L21	M-009738-	sulfotransfer	6783.00	**SULT1E1**	**13.47**	**9.72**	3.24
50013.00	L23	M-009602-	steroid sulfat	412.00	STS	3.31	0.44	-0.15
50013.00	M02	M-008950-	pyruvate carl	5091.00	PC	1.30	2.45	-0.82
50013.00	M04	M-005130-	pregnancy-as	5069.00	PAPPA	7.15	3.40	1.13
50013.00	M05	M-004048-	matrix metal	4327.00	MMP19	3.33	0.42	-0.14
50013.00	M06	M-003797-	pantothenate	80025.00	PANK2	8.73	4.98	1.66
50013.00	M07	M-005959-	matrix metal	4313.00	MMP2	7.77	4.02	1.34
50013.00	M08	M-008898-	phenylalanin	5053.00	PAH	4.91	1.16	0.39
50013.00	M09	M-005960-	matrix metal	9313.00	MMP20	14.33	**10.58**	3.53
50013.00	M10	M-008583-	platelet-activ	5051.00	**PAFAH2**	**19.77**	**16.02**	5.35
50013.00	M11	M-009245-	matrix metal	8511.00	MMP23A	10.59	**6.84**	2.28
50013.00	M12	M-009291-	ornithine car	5009.00	OTC	11.20	**7.45**	2.48
50013.00	M13	M-005962-	matrix metal	8510.00	MMP23B	11.69	**7.94**	2.65
50013.00	M14	M-019111-	O-linked N-a	8473.00	OGT	6.42	2.67	0.89
50013.00	M15	M-005964-	matrix metal	64386.00	MMP25	2.76	0.99	-0.33
50013.00	M16	M-005147-	8-oxoguanin	4968.00	OGG1	2.60	1.15	-0.38
50013.00	M17	M-005965-	matrix metal	56547.00	MMP26	4.16	0.41	0.14
50013.00	M18	M-019216-	ornithine dec	4946.00	OAZ1	9.66	5.91	1.97
50013.00	M19	M-005967-	matrix metal	79148.00	MMP28	6.87	3.12	1.04
50013.00	M20	M-009767-	2'-5'-oligoad	4940.00	OAS3	2.70	1.05	-0.35
50013.00	M21	M-005968-	matrix metal	4314.00	MMP3	3.06	0.69	-0.23
50013.00	M23	M-003782-	matrix metal	4316.00	MMP7	3.86	0.11	0.04
50013.00	N02	M-006235-	potassium vo	27133.00	KCNH5	2.17	1.58	-0.53
50013.00	N04	M-006232-	potassium vo	3756.00	KCNH1	8.03	4.28	1.43
50013.00	N05	M-008310-	sulfite oxidas	6821.00	SUOX	3.12	0.63	-0.21
50013.00	N06	M-006119-	ATPase, Ca++	27032.00	ATP2C1	5.65	1.90	0.63
50013.00	N07	M-009604-	suppressor o	6839.00	SUV39H1	5.60	1.85	0.62
50013.00	N08	M-005778-	ADAM metal	11095.00	ADAMTS8	1.15	2.60	-0.87
50013.00	N09	M-008512-	suppressor o	79723.00	SUV39H2	0.97	2.78	-0.93
50013.00	N10	M-009652-	tubulin, beta	10382.00	TUBB4	1.29	2.46	-0.82
50013.00	N11	M-019486-	synaptojanin	8867.00	SYNJ1	1.36	2.39	-0.80
50013.00	N12	M-008260-	tubulin, beta	7280.00	TUBB2A	4.33	0.58	0.19
50013.00	N13	M-012151-	Tar (HIV-1) R	6894.00	TARBP1	1.72	2.03	-0.68
50013.00	N14	M-010325-	tubulin, beta	203068.00	TUBB	8.19	4.44	1.48
50013.00	N15	M-008336-	tyrosine ami	6898.00	TAT	6.08	2.33	0.78
50013.00	N16	M-031724-	zinc finger pr	84914.00	ZNF587	13.47	**9.72**	3.24
50013.00	N17	M-004496-	prostaglandi	10728.00	PTGES3	9.58	5.83	1.95
50013.00	N18	M-006103-	YME1-like 1 (	10730.00	YME1L1	14.65	**10.90**	3.64
50013.00	N19	M-012377-	telomerase-a	7011.00	TEP1	3.41	0.34	-0.12
50013.00	N20	M-012067-	X-ray repair c	7517.00	XRCC3	4.16	0.41	0.14
50013.00	N21	M-003547-	telomerase r	7015.00	TERT	3.67	0.08	-0.03
50013.00	N23	M-004575-	transglutami	7051.00	TGM1	5.04	1.29	0.43
50013.00	O02	M-009768-	2'-5'-oligoad	4939.00	OAS2	0.99	2.76	-0.92

50013.00	O04	M-011344-	2',5'-oligoade	4938.00	OAS1	4.34	0.59	0.20
50013.00	O05	M-005969-	matrix metal	4317.00	MMP8	4.90	1.15	0.38
50013.00	O06	M-009345-	nth endonuc	4913.00	NTHL1	6.44	2.69	0.90
50013.00	O07	M-005970-	matrix metal	4318.00	MMP9	8.24	4.49	1.50
50013.00	O08	M-003919-	neuroblastor	4893.00	NRAS	5.85	2.10	0.70
50013.00	O09	M-004430-	modulator of	64112.00	MOAP1	4.20	0.45	0.15
50013.00	O10	M-005979-	aminopeptid	9520.00	NPEPPS	7.58	3.83	1.28
50013.00	O11	M-005146-	N-methylpur	4350.00	MPG	1.85	1.90	-0.63
50013.00	O12	M-005977-	neurolysin (n	57486.00	NLN	4.63	0.88	0.29
50013.00	O13	M-011729-	mannose pho	4351.00	MPI	3.95	0.20	0.07
50013.00	O14	M-010614-	septin 2	4735.00	SEPT2	3.43	0.32	-0.11
50013.00	O15	M-008586-	muscle RAS o	22808.00	MRAS	3.90	0.15	0.05
50013.00	O16	M-019063-	Nedd4 bindir	55728.00	N4BP2	3.91	0.16	0.05
50013.00	O17	M-009271-	MRE11 meio	4361.00	MRE11A	4.16	0.41	0.14
50013.00	O18	M-020341-	MYB binding	10514.00	MYBBP1A	3.41	0.34	-0.12
50013.00	O19	M-008946-	macrophage	4485.00	MST1	0.86	2.89	-0.97
50013.00	O20	M-011736-	myxovirus (ir	4600.00	MX2	1.23	2.52	-0.84
50013.00	O21	M-019244-	myotubularir	66036.00	MTMR9	2.93	0.82	-0.27
50013.00	O23	M-008429-	methylmalor	4594.00	MUT	0.76	2.99	-1.00
50013.00	P02	M-006102-	X-prolyl amir	7512.00	XPNPEP2	3.15	0.60	-0.20
50013.00	P04	M-010378-	Werner synd	7486.00	WRN	0.63	3.13	-1.04
50013.00	P05	M-004971-	transglutami	7052.00	TGM2	3.46	0.29	-0.10
50013.00	P06	M-008322-	tryptophanyl	7453.00	WARS	1.56	2.19	-0.73
50013.00	P07	M-009041-	tyrosine hydr	7054.00	TH	4.04	0.29	0.10
50013.00	P08	M-010384-	ubiquitin-cor	7332.00	UBE2L3	2.25	1.50	-0.50
50013.00	P09	M-004734-	transketolase	7086.00	TKT	1.27	2.48	-0.83
50013.00	P10	M-014161-	activating sig	23020.00	ASCC3L1	0.92	2.83	-0.95
50013.00	P11	M-004736-	transketolase	8277.00	TKTL1	0.18	3.57	-1.19
50013.00	P12	M-015850-	tRNA nucleot	51095.00	TRNT1	1.47	2.28	-0.76
50013.00	P13	M-006046-	tolloid-like 1	7092.00	TLL1	0.39	3.36	-1.12
50013.00	P14	M-010011-	PAP associat	64282.00	PAPD5	1.99	1.77	-0.59
50013.00	P15	M-009976-	tensin 1	7145.00	TNS1	2.62	1.13	-0.38
50013.00	P16	M-032280-	three prime r	11219.00	TREX2	0.99	2.76	-0.92
50013.00	P17	M-009086-	topoisomera	116447.00	TOP1MT	0.45	3.30	-1.10
50013.00	P18	M-013239-	three prime r	11277.00	TREX1	0.12	3.63	-1.21
50013.00	P19	M-004240-	topoisomera	7155.00	TOP2B	1.52	2.23	-0.74
50013.00	P20	M-012358-	topoisomera	11073.00	TOPBP1	4.26	0.51	0.17
50013.00	P21	M-005279-	topoisomera	7156.00	TOP3A	0.28	3.47	-1.16
50013.00	P23	M-005282-	topoisomera	8940.00	TOP3B	0.41	3.34	-1.11
50013.00					mdn	3.75	2.02	
50013.00					3XMAD		6.07	
50013.00					MADc		3.00	
50013.00								
50013.00	C22					40.99		33.18
50013.00	D22					32.13		35.21
	E22					29.82		25.44
	F22					29.07		36.32

						33.00	32.54
						5.48	4.91
50013.00							
50013.00	G22					0.69	4.83
50013.00	H22					3.15	1.09
50013.00	I22					1.43	2.23
	J22					1.30	0.87
						1.64	2.25
						1.05	1.81
50013.00							
50013.00	G03	M-003290-	polo-like kin	5347.00	PLK1 SMA	5.29	8.15
50013.00	H03	M-003290-	polo-like kin	5347.00	PLK1 SMA	6.77	3.42
50013.00							
	I03	D-001206-	siControl non-targeting s			9.72	3.31
	J03	D-001206-	siControl non-targeting s			2.07	5.76
	K03	D-001600-	siGLO RISC-free siRNA			21.96	17.21
	L03	D-001600-	siGLO RISC-free siRNA			17.83	7.40

% inf	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**
1.77	0.72	-0.35	3.44	0.12	-0.05
0.09	2.40	-1.18	0.62	2.94	-1.19
0.87	1.62	-0.80	0.89	2.67	-1.09
0.81	1.68	-0.82	0.98	2.58	-1.05
0.71	1.78	-0.87	0.58	2.98	-1.21
0.14	2.35	-1.16	1.65	1.91	-0.78
0.91	1.58	-0.78	4.12	0.56	0.23
2.41	0.08	-0.04	4.05	0.49	0.20
1.64	0.85	-0.42	3.11	0.45	-0.18
1.84	0.65	-0.32	0.33	3.23	-1.32
1.34	1.15	-0.56	1.97	1.59	-0.65
2.34	0.15	-0.07	3.39	0.17	-0.07
0.82	1.67	-0.82	1.45	2.11	-0.86
1.36	1.13	-0.56	2.67	0.89	-0.36
0.74	1.75	-0.86	1.32	2.24	-0.91
1.12	1.37	-0.67	2.73	0.83	-0.34
2.38	0.11	-0.05	2.35	1.21	-0.49
4.58	2.09	1.03	5.70	2.14	0.87
0.35	2.14	-1.05	3.21	0.35	-0.14
1.56	0.93	-0.46	10.86	7.30	2.96
1.00	1.49	-0.73	2.09	1.47	-0.60
1.97	0.52	-0.26	1.83	1.73	-0.70
0.89	1.60	-0.79	1.88	1.68	-0.69
0.36	2.13	-1.05	0.32	3.24	-1.32
8.41	5.92	2.92	4.79	1.23	0.50
0.32	2.17	-1.07	0.56	3.00	-1.22
3.97	1.48	0.73	3.30	0.26	-0.11
0.23	2.26	-1.11	0.28	3.28	-1.33
1.07	1.42	-0.70	0.32	3.24	-1.32
0.93	1.56	-0.77	3.43	0.13	-0.06
0.16	2.33	-1.15	1.13	2.43	-0.99
0.65	1.84	-0.90	2.63	0.93	-0.38
0.39	2.10	-1.04	1.68	1.88	-0.77
0.43	2.06	-1.01	1.65	1.91	-0.78
3.34	0.85	0.42	1.42	2.14	-0.87
2.07	0.42	-0.21	6.99	3.43	1.39
1.51	0.98	-0.48	4.11	0.55	0.22
1.44	1.05	-0.51	3.90	0.34	0.14
3.56	1.07	0.53	5.64	2.08	0.84
3.96	1.47	0.72	6.68	3.12	1.26
2.01	0.48	-0.24	3.66	0.10	0.04
2.33	0.16	-0.08	2.37	1.19	-0.49
1.99	0.50	-0.25	3.60	0.04	0.02
3.06	0.57	0.28	1.34	2.22	-0.90
1.63	0.86	-0.42	1.32	2.24	-0.91
8.67	6.18	3.04	3.24	0.32	-0.13

8.34	**5.85**	2.88	6.49	2.93	1.19
3.36	0.87	0.43	3.20	0.36	-0.15
3.45	0.96	0.47	2.87	0.69	-0.28
1.75	0.74	-0.36	1.07	2.49	-1.01
0.61	1.88	-0.92	1.58	1.98	-0.81
0.55	1.94	-0.96	2.08	1.48	-0.60
7.42	**4.93**	2.43	5.17	1.61	0.65
2.80	0.31	0.15	2.42	1.14	-0.46
1.01	1.48	-0.73	0.53	3.03	-1.23
3.99	1.50	0.74	5.98	2.42	0.98
4.17	1.68	0.83	4.55	0.99	0.40
2.35	0.14	-0.07	3.93	0.37	0.15
1.32	1.17	-0.58	3.18	0.38	-0.16
0.72	1.77	-0.87	1.92	1.64	-0.67
6.47	3.98	1.96	6.56	3.00	1.22
4.29	1.80	0.89	3.43	0.13	-0.05
2.50	0.01	0.01	3.50	0.06	-0.02
1.60	0.89	-0.44	1.45	2.11	-0.86
2.45	0.04	-0.02	1.10	2.46	-1.00
0.31	2.18	-1.07	0.70	2.86	-1.16
3.58	1.09	0.54	2.89	0.67	-0.27
4.03	1.54	0.76	3.22	0.34	-0.14
1.52	0.97	-0.48	0.35	3.21	-1.31
0.43	2.06	-1.01	1.32	2.24	-0.91
1.71	0.78	-0.38	2.21	1.35	-0.55
2.65	0.16	0.08	1.29	2.27	-0.92
2.38	0.11	-0.05	1.64	1.92	-0.78
1.66	0.83	-0.41	2.78	0.78	-0.32
7.08	**4.59**	2.26	2.86	0.70	-0.28
7.27	**4.78**	2.35	4.81	1.25	0.51
5.76	3.27	1.61	6.94	3.38	1.37
4.22	1.73	0.85	2.62	0.94	-0.38
13.18	**10.69**	5.26	6.60	3.04	1.23
5.45	2.96	1.46	5.29	1.73	0.70
1.41	1.08	-0.53	0.43	3.13	-1.27
4.15	1.66	0.82	1.00	2.56	-1.04
3.14	0.65	0.32	1.78	1.78	-0.73
7.12	**4.63**	2.28	1.35	2.21	-0.90
2.62	0.13	0.07	2.01	1.55	-0.63
4.64	2.15	1.06	3.55	0.01	0.00
2.54	0.05	0.03	0.56	3.00	-1.22
5.02	2.53	1.25	2.85	0.71	-0.29
1.87	0.62	-0.31	3.41	0.15	-0.06
1.01	1.48	-0.73	0.64	2.92	-1.19
2.88	0.39	0.20	3.45	0.11	-0.05
0.23	2.26	-1.11	0.32	3.24	-1.32
2.05	0.44	-0.22	1.26	2.30	-0.94

1.07	1.42	-0.70	1.26	2.30	-0.94	
0.55	1.94	-0.95	2.06	1.50	-0.61	
4.08	1.59	0.79	**12.20**	**8.64**	3.51	y
2.20	0.29	-0.14	5.07	1.51	0.61	
0.70	1.79	-0.88	0.85	2.71	-1.10	
1.08	1.41	-0.70	1.95	1.61	-0.66	
1.52	0.97	-0.48	5.14	1.58	0.64	
0.45	2.04	-1.00	2.70	0.86	-0.35	
2.64	0.15	0.08	5.03	1.47	0.60	
3.71	1.22	0.60	6.24	2.68	1.09	
5.06	2.57	1.26	2.00	1.56	-0.63	
5.87	3.38	1.67	2.23	1.33	-0.54	
3.88	1.39	0.68	3.37	0.19	-0.08	
2.20	0.29	-0.14	1.96	1.60	-0.65	
11.01	**8.52**	4.20	4.21	0.65	0.26	
7.58	**5.09**	2.51	10.90	**7.34**	2.98	y
1.13	1.36	-0.67	1.21	2.35	-0.96	
1.69	0.80	-0.39	1.74	1.82	-0.74	
1.36	1.13	-0.56	2.95	0.61	-0.25	
3.02	0.53	0.26	3.12	0.44	-0.18	
3.26	0.77	0.38	5.09	1.53	0.62	
2.10	0.39	-0.19	4.05	0.49	0.20	
1.19	1.30	-0.64	4.47	0.91	0.37	
0.72	1.77	-0.87	1.25	2.31	-0.94	
2.82	0.33	0.16	3.81	0.25	0.10	
5.16	2.67	1.31	12.05	**8.49**	3.44	
4.22	1.73	0.85	7.15	3.59	1.46	
0.92	1.57	-0.77	1.94	1.62	-0.66	
2.48	0.01	0.00	3.76	0.20	0.08	
4.16	1.67	0.82	3.41	0.15	-0.06	
2.52	0.03	0.02	1.75	1.81	-0.73	
13.83	**11.34**	5.59	4.56	1.00	0.40	y
9.89	**7.40**	3.65	1.95	1.61	-0.66	
4.45	1.96	0.97	3.24	0.32	-0.13	
6.70	**4.21**	2.08	1.38	2.18	-0.89	
6.79	**4.30**	2.12	4.09	0.53	0.21	
7.22	**4.73**	2.33	4.34	0.78	0.31	
3.58	1.09	0.54	5.93	2.37	0.96	
3.71	1.22	0.60	9.58	**6.02**	2.44	
14.56	**12.07**	5.94	**13.93**	**10.37**	4.21	y
12.92	**10.43**	5.14	9.83	**6.27**	2.55	y
23.33	**20.84**	10.26	**25.92**	**22.36**	9.08	y
10.39	**7.90**	3.89	7.86	4.30	1.74	
16.22	**13.73**	6.76	**12.66**	**9.10**	3.70	y
2.04	0.45	-0.22	2.49	1.07	-0.44	
3.02	0.53	0.26	3.56	0.00	0.00	
5.59	3.10	1.53	10.86	**7.30**	2.96	

3.52	1.03	0.51	7.78	4.22	1.71		
8.67	**6.18**	3.04	9.61	**6.05**	2.46	y	
2.11	0.38	-0.19	1.92	1.64	-0.67		
7.91	**5.42**	2.67	7.93	4.37	1.77		
7.89	**5.40**	2.66	11.29	**7.73**	3.14	y	
1.15	1.34	-0.66	4.15	0.59	0.24		
7.16	**4.67**	2.30	7.27	3.71	1.50		
1.45	1.04	-0.51	3.80	0.24	0.10		
2.44	0.05	-0.02	11.88	**8.32**	3.38		
5.85	3.36	1.66	8.50	4.94	2.01		
8.67	**6.18**	3.04	**14.84**	**11.28**	4.58	y	
4.91	2.42	1.19	8.68	**5.12**	2.08		
4.22	1.73	0.85	9.28	**5.72**	2.32		
3.11	0.62	0.31	9.81	**6.25**	2.54		
6.20	3.71	1.83	10.88	**7.32**	2.97	y	
5.61	3.12	1.54	6.68	3.12	1.26		
4.07	1.58	0.78	14.25	**10.69**	4.34		
2.84	0.35	0.17	9.65	**6.09**	2.47		
2.08	0.41	-0.20	7.10	3.54	1.43		
0.36	2.13	-1.05	5.72	2.16	0.87		
1.14	1.35	-0.66	5.02	1.46	0.59		
9.02	**6.53**	3.22	**11.22**	**7.66**	3.11	y	
7.53	**5.04**	2.48	4.01	0.45	0.18	y	
0.50	1.99	-0.98	2.30	1.26	-0.51		
6.91	**4.42**	2.18	6.67	3.11	1.26	x	txc a,b,c
0.68	1.81	-0.89	2.81	0.75	-0.30		
3.06	0.57	0.28	4.80	1.24	0.50		
2.62	0.13	0.07	2.78	0.78	-0.32		
1.13	1.36	-0.67	1.36	2.20	-0.90		
2.92	0.43	0.21	3.36	0.20	-0.08		
3.14	0.65	0.32	0.98	2.58	-1.05		
1.12	1.37	-0.67	2.51	1.05	-0.43		
6.55	4.06	2.00	5.28	1.72	0.70		
2.49	0.00	0.00	2.92	0.64	-0.26		
6.53	4.04	1.99	5.41	1.85	0.75		
2.88	0.39	0.19	4.29	0.73	0.29		
4.18	1.69	0.83	5.29	1.73	0.70		
3.18	0.69	0.34	2.79	0.77	-0.31		
4.05	1.56	0.77	8.67	**5.11**	2.07		
2.99	0.50	0.25	7.28	3.72	1.51		
1.06	1.43	-0.70	2.32	1.24	-0.50		
2.31	0.18	-0.09	1.08	2.48	-1.01		
5.97	3.48	1.71	3.63	0.07	0.03		
1.72	0.77	-0.38	2.77	0.79	-0.32		
1.74	0.75	-0.37	3.78	0.22	0.09		
1.59	0.90	-0.44	2.41	1.15	-0.47		
4.58	2.09	1.03	4.66	1.10	0.45		

1.18	1.31	-0.64	1.94	1.62	-0.66	
2.09	0.40	-0.19	6.48	2.92	1.18	
1.94	0.55	-0.27	3.83	0.27	0.11	
0.94	1.55	-0.76	6.36	2.80	1.13	
1.47	1.02	-0.50	2.28	1.28	-0.52	
2.81	0.32	0.16	1.09	2.47	-1.01	
5.56	3.07	1.51	5.33	1.77	0.72	
2.87	0.38	0.19	0.76	2.80	-1.14	
2.86	0.37	0.18	2.81	0.75	-0.30	
4.39	1.90	0.94	6.26	2.70	1.10	
1.73	0.76	-0.37	5.05	1.49	0.60	
1.34	1.15	-0.56	1.64	1.92	-0.78	
5.75	3.26	1.61	19.12	**15.56**	6.32	
1.12	1.37	-0.67	2.88	0.68	-0.28	
6.76	**4.27**	2.10	2.20	1.36	-0.55	
1.74	0.75	-0.37	4.66	1.10	0.45	
10.13	**7.64**	3.76	7.57	4.01	1.63	y
5.84	3.35	1.65	7.65	4.09	1.66	
2.46	0.03	-0.01	5.49	1.93	0.78	
9.07	**6.58**	3.24	**11.08**	**7.52**	3.05	y
3.68	1.19	0.59	2.71	0.85	-0.34	
4.39	1.90	0.94	6.24	2.68	1.09	
2.48	0.01	-0.01	2.87	0.69	-0.28	
0.39	2.10	-1.03	1.03	2.53	-1.03	
2.17	0.32	-0.16	2.78	0.78	-0.32	
0.86	1.63	-0.80	3.20	0.36	-0.15	
7.16	**4.67**	2.30	6.20	2.64	1.07	
2.92	0.43	0.21	5.26	1.70	0.69	
2.21	0.28	-0.14	3.85	0.29	0.11	
1.35	1.14	-0.56	4.41	0.85	0.34	
1.27	1.22	-0.60	2.30	1.26	-0.51	
1.48	1.01	-0.50	6.20	2.64	1.07	
1.08	1.41	-0.69	3.30	0.26	-0.11	
4.37	1.88	0.93	6.69	3.13	1.27	
0.38	2.11	-1.04	0.56	3.00	-1.22	
1.95	0.54	-0.26	3.16	0.40	-0.16	
6.51	4.02	1.98	0.39	3.17	-1.29	
7.45	**4.96**	2.44	5.25	1.69	0.69	y
3.23	0.74	0.37	3.76	0.20	0.08	
2.02	0.47	-0.23	3.23	0.33	-0.14	
4.26	1.77	0.87	0.64	2.92	-1.19	
2.73	0.24	0.12	4.41	0.85	0.34	
0.40	2.09	-1.03	1.64	1.92	-0.78	
5.23	2.74	1.35	4.98	1.42	0.58	
2.67	0.18	0.09	1.14	2.42	-0.98	
8.98	**6.49**	3.20	**12.02**	**8.46**	3.43	y
6.72	**4.23**	2.09	2.96	0.60	-0.25	

2.98	0.49	0.24	3.25	0.31	-0.13	
1.59	0.90	-0.44	3.19	0.37	-0.15	
0.86	1.63	-0.80	4.06	0.50	0.20	
2.53	0.04	0.02	5.16	1.60	0.65	
12.08	**9.59**	4.72	**9.03**	**5.47**	2.22	y
5.23	2.74	1.35	5.80	2.24	0.91	
0.83	1.66	-0.82	1.28	2.28	-0.93	
4.91	2.42	1.19	4.95	1.39	0.56	
2.19	0.30	-0.14	6.02	2.46	1.00	
3.40	0.91	0.45	6.77	3.21	1.30	
1.63	0.86	-0.42	7.32	3.76	1.52	
4.59	2.10	1.04	2.77	0.79	-0.32	
5.03	2.54	1.25	9.66	**6.10**	2.48	y
12.66	**10.17**	5.01	**18.47**	**14.91**	6.05	y
5.66	3.17	1.56	8.20	4.64	1.88	
5.15	2.66	1.31	11.24	**7.68**	3.12	y
5.43	2.94	1.45	5.34	1.78	0.72	
1.60	0.89	-0.44	4.11	0.55	0.22	
1.12	1.37	-0.67	2.15	1.41	-0.58	
1.14	1.35	-0.66	7.60	4.04	1.64	
1.24	1.25	-0.61	2.43	1.13	-0.46	
4.23	1.74	0.86	8.55	**4.99**	2.03	
1.97	0.52	-0.26	5.08	1.52	0.61	
1.10	1.39	-0.68	1.15	2.41	-0.98	
0.85	1.64	-0.81	2.38	1.18	-0.48	
0.80	1.69	-0.83	4.50	0.94	0.38	
0.85	1.64	-0.81	4.61	1.05	0.42	
2.73	0.24	0.12	3.73	0.17	0.07	
3.94	1.45	0.72	0.73	2.83	-1.15	
2.30	0.19	-0.09	6.59	3.03	1.23	
1.67	0.82	-0.40	3.53	0.03	-0.01	
2.17	0.32	-0.16	5.33	1.77	0.72	
1.31	1.18	-0.58	2.88	0.68	-0.28	
1.05	1.44	-0.71	2.92	0.64	-0.26	
1.92	0.57	-0.28	3.52	0.04	-0.02	
2.52	0.03	0.02	6.20	2.64	1.07	
4.55	2.06	1.01	4.62	1.06	0.43	
1.95	0.54	-0.27	4.05	0.49	0.20	
2.78	0.29	0.14	4.74	1.18	0.48	
6.57	4.08	2.01	7.36	3.80	1.54	
1.79	0.70	-0.34	8.99	**5.43**	2.20	
4.54	2.05	1.01	4.09	0.53	0.22	
3.51	1.02	0.51	2.72	0.84	-0.34	
5.96	3.47	1.71	4.91	1.35	0.55	
1.21	1.28	-0.63	1.38	2.18	-0.89	
1.60	0.89	-0.44	5.83	2.27	0.92	
1.14	1.35	-0.66	5.41	1.85	0.75	

1.66	0.84	-0.41	2.96	0.60	-0.24	
3.54	1.05	0.52	2.38	1.18	-0.48	
6.43	3.94	1.94	4.68	1.12	0.45	
4.46	1.97	0.97	8.32	4.76	1.93	
3.24	0.75	0.37	4.35	0.79	0.32	
4.52	2.03	1.00	5.45	1.89	0.77	
3.72	1.23	0.61	8.00	4.44	1.80	
1.63	0.86	-0.42	2.37	1.19	-0.48	
1.91	0.58	-0.28	2.67	0.89	-0.36	
2.14	0.35	-0.17	2.83	0.73	-0.30	
1.15	1.34	-0.66	5.80	2.24	0.91	
1.79	0.70	-0.34	12.73	**9.17**	3.72	
3.74	1.25	0.62	12.50	**8.94**	3.63	
2.45	0.04	-0.02	5.19	1.63	0.66	
1.32	1.17	-0.57	5.90	2.34	0.95	
2.21	0.28	-0.14	8.29	4.73	1.92	
1.05	1.44	-0.71	3.35	0.21	-0.09	
4.50	2.01	0.99	5.88	2.32	0.94	
0.57	1.92	-0.94	4.99	1.43	0.58	
2.57	0.08	0.04	1.67	1.89	-0.77	
3.41	0.92	0.45	3.62	0.06	0.02	
2.94	0.45	0.22	4.50	0.94	0.38	
1.54	0.95	-0.47	2.60	0.96	-0.39	
1.33	1.16	-0.57	3.93	0.37	0.15	
0.88	1.61	-0.79	4.42	0.86	0.35	
5.42	2.93	1.44	3.91	0.35	0.14	
1.15	1.34	-0.66	2.70	0.86	-0.35	
2.31	0.18	-0.09	3.40	0.16	-0.07	
2.87	0.38	0.19	1.44	2.12	-0.86	
0.43	2.06	-1.01	1.58	1.98	-0.81	
2.07	0.42	-0.21	5.60	2.04	0.83	
5.86	3.37	1.66	10.52	**6.96**	2.82	
1.64	0.85	-0.42	3.08	0.48	-0.20	
1.35	1.14	-0.56	3.57	0.01	0.00	
1.12	1.37	-0.67	2.49	1.07	-0.44	
3.44	0.95	0.47	3.68	0.12	0.05	
7.58	**5.09**	2.51	15.41	**11.85**	4.81	y
4.28	1.79	0.88	5.39	1.83	0.74	
4.40	1.91	0.94	2.81	0.75	-0.31	
2.49	1.37		3.56	1.66		
	4.12			4.99		
	2.03			2.46		
	34.37					
	37.70					
	24.59					
	34.97					

32.91
5.73

3.87
3.94
0.80
6.46
3.77
2.32

2.94
3.92

3.13
2.02

13.60
10.42

	A	B	C
3psSD	16.44	14.72	17.19
3ngSD	3.16	5.44	6.96
SumSD	19.60	20.16	24.14
DiffMn	31.36	30.28	29.14
SmovrDiff	0.63	0.67	0.83
1minus	0.37	0.33	0.17

						% inf	abs dev	robust Z
50014.00	A02	M-020011-	lipoprotein, Lp(a)	4018.00	LPA	3.51	1.13	-0.37
50014.00	A04	M-010972-	apolipoprotein C-II	344.00	APOC2	2.04	2.60	-0.86
50014.00	A05	M-010195-	NADPH oxidase, EF-h	79400.00	NOX5	1.03	3.61	-1.20
50014.00	A06	M-016221-	SRB7 suppressor of R	9412.00	SURB7	1.51	3.13	-1.03
50014.00	A07	M-009752-	pyruvate dehydrogen	8050.00	PDHX	10.08	5.44	1.80
50014.00	A08	M-003759-	nuclear receptor coa	8202.00	NCOA3	2.73	1.91	-0.63
50014.00	A09	M-009698-	prostaglandin D2 syn	5730.00	PTGDS	6.35	1.71	0.56
50014.00	A10	M-003477-	CREB binding protein	1387.00	CREBBP	6.40	1.76	0.58
50014.00	A11	M-012689-	putative neuronal cel	9543.00	PUNC	7.87	3.23	1.07
50014.00	A12	M-004429-	MAP-kinase activatin	8567.00	MADD	4.92	0.28	0.09
50014.00	A13	M-004726-	RAB11A, member RA	8766.00	RAB11A	2.61	2.03	-0.67
50014.00	A14	M-004401-	caspase 1, apoptosis-	834.00	CASP1	4.47	0.17	-0.06
50014.00	A15	M-004727-	RAB11B, member RA	9230.00	RAB11B	2.57	2.07	-0.68
50014.00	A16	M-019737-	transforming growth	7039.00	TGFA	2.78	1.86	-0.61
50014.00	A17	M-008389-	RAB13, member RAS	5872.00	RAB13	6.41	1.77	0.58
50014.00	A18	M-008438-	scavenger receptor c	136853.00	SRCRB4D	8.14	3.50	1.16
50014.00	A19	M-010824-	RAB18, member RAS	22931.00	RAB18	5.06	0.42	0.14
50014.00	A20	M-008339-	phospholipase C, gam	5336.00	PLCG2	6.43	1.79	0.59
50014.00	A21	M-008283-	RAB1A, member RAS	5861.00	RAB1A	4.02	0.62	-0.21
50014.00	A23	M-009553-	RAB36, member RAS	9609.00	RAB36	8.01	3.37	1.12
50014.00	B02	M-011126-	CD79b molecule, imm	974.00	CD79B	16.45	**11.81**	3.90
50014.00	B04	M-011606-	CD79a molecule, imm	973.00	CD79A	6.78	2.14	0.71
50014.00	B05	M-011097-	oculocutaneous albin	4948.00	OCA2	1.63	3.01	-1.00
50014.00	B06	M-012667-	CD74 molecule, majo	972.00	CD74	5.21	0.57	0.19
50014.00	B07	M-006004-	cathepsin A	5476.00	CTSA	3.46	1.18	-0.39
50014.00	B08	M-007849-	CD5 molecule-like	922.00	CD5L	1.46	3.18	-1.05
50014.00	B09	M-008611-	active BCR-related ge	29.00	ABR	4.13	0.51	-0.17
50014.00	B10	M-017239-	CD200 receptor 1	131450.00	CD200R1	2.26	2.38	-0.79
50014.00	B11	M-014168-	amyotrophic lateral s	57679.00	ALS2	4.17	0.47	-0.16
50014.00	B12	M-017576-	CD19 molecule	930.00	CD19	3.43	1.21	-0.40
50014.00	B13	M-007807-	angiopoietin-like 4	51129.00	ANGPTL4	1.99	2.65	-0.88
50014.00	B14	M-007847-	CD163 molecule	9332.00	CD163	6.84	2.20	0.73
50014.00	B15	M-012208-	ADP-ribosylation fact	10564.00	ARFGEF2	3.16	1.48	-0.49
50014.00	B16	M-011599-	butyrophilin, subfami	696.00	BTN1A1	4.02	0.62	-0.20
50014.00	B17	M-010893-	Rho GDP dissociation	397.00	ARHGDIB	2.58	2.06	-0.68
50014.00	B18	M-010737-	basigin (Ok blood gro	682.00	BSG	3.07	1.57	-0.52
50014.00	B19	M-012566-	Rho GDP dissociation	398.00	ARHGDIG	5.61	0.97	0.32
50014.00	B20	M-008809-	axin 2 (conductin, axi	8313.00	AXIN2	1.46	3.18	-1.05
50014.00	B21	M-013243-	Rho guanine nucleoti	50650.00	ARHGEF3	4.75	0.11	0.03
50014.00	B23	M-008235-	Rho guanine nucleoti	50649.00	ARHGEF4	6.51	1.87	0.62
50014.00	C02	M-003559-	phospholipase C, gam	5335.00	PLCG1	4.30	0.34	-0.11
50014.00	C04	M-009149-	phospholipase C, delt	5333.00	PLCD1	2.46	2.18	-0.72
50014.00	C05	M-010059-	RAB38, member RAS	23682.00	RAB38	4.08	0.56	-0.19

50014.00	C06	M-009249-	peptidoglycan recogn	8993.00	PGLYRP1	3.74	0.90	-0.30
50014.00	C07	M-009668-	RAB3A, member RAS	5864.00	RAB3A	4.77	0.13	0.04
50014.00	C08	M-007661-	phosphodiesterase 8	8622.00	PDE8B	7.27	2.63	0.87
50014.00	C09	M-008825-	RAB3B, member RAS	5865.00	RAB3B	8.45	3.81	1.26
50014.00	C10	M-003824-	phosphodiesterase 8	5151.00	PDE8A	8.72	4.08	1.35
50014.00	C11	M-004009-	RAB5A, member RAS	5868.00	RAB5A	7.89	3.25	1.08
50014.00	C12	M-004581-	pre-B-cell colony enh	10135.00	PBEF1	6.51	1.87	0.62
50014.00	C13	M-004011-	RAB5C, member RAS	5878.00	RAB5C	4.25	0.39	-0.13
50014.00	C14	M-012617-	2'-5'-oligoadenylate s	8638.00	OASL	3.79	0.85	-0.28
50014.00	C15	M-008975-	RAB6A, member RAS	5870.00	RAB6A	2.94	1.70	-0.56
50014.00	C16	M-020126-	mannosidase, alpha,	10905.00	MAN1A2	4.40	0.24	-0.08
50014.00	C17	M-008548-	RAB6B, member RAS	51560.00	RAB6B	8.13	3.49	1.15
50014.00	C18	M-011939-	zinc finger, FYVE dom	9372.00	ZFYVE9	3.04	1.60	-0.53
50014.00	C19	M-010388-	RAB7A, member RAS	7879.00	RAB7A	8.62	3.98	1.31
50014.00	C20	M-011127-	latent transforming g	4052.00	LTBP1	9.38	4.74	1.57
50014.00	C21	M-010556-	RAB7, member RAS o	8934.00	RAB7L1	11.21	**6.57**	2.17
50014.00	C23	M-004177-	RAB9A, member RAS	9367.00	RAB9A	3.78	0.86	-0.28
50014.00	D02	M-009625-	axin 1	8312.00	AXIN1	4.41	0.23	-0.08
50014.00	D04	M-010566-	SH2B adaptor protein	10603.00	SH2B2	3.10	1.54	-0.51
50014.00	D05	M-010231-	Rac/Cdc42 guanine n	9459.00	ARHGEF6	1.93	2.71	-0.90
50014.00	D06	M-013308-	apolipoprotein B48 re	55911.00	APOB48R	4.73	0.09	0.03
50014.00	D07	M-009616-	Rho guanine nucleoti	8874.00	ARHGEF7	5.27	0.63	0.21
50014.00	D08	M-010126-	aryl hydrocarbon rece	23746.00	AIPL1	3.41	1.24	-0.41
50014.00	D09	M-012158-	arginine-rich, mutate	7873.00	ARMET	2.71	1.93	-0.64
50014.00	D10	M-009337-	aryl-hydrocarbon rece	57491.00	AHRR	4.43	0.21	-0.07
50014.00	D11	M-011469-	breast cancer anti-est	8412.00	BCAR3	6.41	1.77	0.59
50014.00	D12	M-003625-	advanced glycosylatic	177.00	AGER	2.20	2.44	-0.81
50014.00	D13	M-020290-	BCL2-like 13 (apoptos	23786.00	BCL2L13	12.02	**7.38**	2.44
50014.00	D14	M-010178-	vav 3 oncogene	10451.00	VAV3	12.51	**7.87**	2.60
50014.00	D15	M-012207-	ADP-ribosylation fact	10565.00	ARFGEF1	6.88	2.24	0.74
50014.00	D16	M-017577-	tumor necrosis factor	8740.00	TNFSF14	6.70	2.06	0.68
50014.00	D17	M-011814-	BCL2/adenovirus E1B	663.00	BNIP2	6.13	1.49	0.49
50014.00	D18	M-003932-	T-cell lymphoma inva	7074.00	TIAM1	11.15	**6.51**	2.15
50014.00	D19	M-011002-	complement compon	720.00	C4A	7.00	2.36	0.78
50014.00	D20	M-016680-	secretoglobin, family	7356.00	SCGB1A1	9.66	5.02	1.66
50014.00	D21	M-012436-	calcium binding tyros	26256.00	CABYR	7.91	3.27	1.08
50014.00	D23	M-013446-	nitric oxide synthase	9722.00	NOS1AP	4.35	0.29	-0.10
50014.00	E02	M-008021-	lysyl oxidase-like 3	84695.00	LOXL3	2.73	1.91	-0.63
50014.00	E04	M-003302-	interleukin-1 recepto	51135.00	IRAK4	4.50	0.14	-0.05
50014.00	E05	M-010353-	RAN, member RAS on	5901.00	RAN	27.99	**23.35**	7.72
50014.00	E06	M-005901-	Indian hedgehog hom	3549.00	IHH	7.61	2.97	0.98
50014.00	E07	M-011773-	succinate dehydroger	6390.00	SDHB	8.75	4.11	1.36
50014.00	E08	M-006650-	hepatocyte growth fa	3082.00	HGF	7.88	3.24	1.07
50014.00	E09	M-026181-	thioredoxin domain c	23071.00	TXNDC4	8.80	4.16	1.37

50014.00	E10	M-004900- glucose phosphate isc	2821.00	GPI	14.19	**9.55**	3.16
50014.00	E11	M-003961- WW domain containi	51741.00	WWOX	3.66	0.98	-0.32
50014.00	E12	M-003897- guanine nucleotide bi	2771.00	GNAI2	5.26	0.62	0.20
50014.00	E13	M-010021- catalase	847.00	CAT	4.70	0.06	0.02
50014.00	E14	M-010860- guanine nucleotide bi	2767.00	GNA11	12.85	**8.21**	2.72
50014.00	E15	M-010009- eosinophil peroxidase	8288.00	EPX	6.24	1.60	0.53
50014.00	E16	M-009568- FK506 binding protei	2287.00	FKBP3	4.16	0.48	-0.16
50014.00	E17	M-011675- glutathione peroxidas	2877.00	GPX2	3.68	0.96	-0.32
50014.00	E18	M-009494- FK506 binding protei	2280.00	FKBP1A	14.95	**10.31**	3.41
50014.00	E19	M-011290- glutathione transfera	2954.00	GSTZ1	12.76	**8.12**	2.68
50014.00	E20	M-009907- fatty acid amide hydr	2166.00	FAAH	12.31	**7.67**	2.53
50014.00	E21	M-010338- peroxiredoxin 1	5052.00	PRDX1	9.83	5.19	1.72
50014.00	E23	M-008178- peroxiredoxin 2	7001.00	PRDX2	19.02	**14.38**	4.76
50014.00	F02	M-008517- RAS guanyl releasing	25780.00	RASGRP3	2.32	2.32	-0.77
50014.00	F04	M-019268- pleckstrin homology,	9265.00	PSCD3	2.24	2.40	-0.79
50014.00	F05	M-017433- calpastatin	831.00	CAST	14.23	**9.59**	3.17
50014.00	F06	M-006304- prolactin receptor	5618.00	PRLR	4.93	0.29	0.10
50014.00	F07	M-010020- cystatin A (stefin A)	1475.00	CSTA	60.97	**56.33**	18.63
50014.00	F08	M-009742- Rap guanine nucleoti	9693.00	RAPGEF2	5.18	0.54	0.18
50014.00	F09	M-017240- cystatin B (stefin B)	1476.00	CSTB	8.01	3.37	1.11
50014.00	F10	M-004608- neuregulin 1	3084.00	NRG1	2.95	1.69	-0.56
50014.00	F11	M-005281- dynein, light chain, LC	8655.00	DYNLL1	5.87	1.23	0.41
50014.00	F12	M-006440- fibroblast growth fact	10818.00	FRS2	7.62	2.98	0.98
50014.00	F13	M-011253- dedicator of cytokine	1793.00	DOCK1	4.34	0.30	-0.10
50014.00	F14	M-019915- dedicator of cytokine	1794.00	DOCK2	4.19	0.45	-0.15
50014.00	F15	M-021495- estrogen receptor bin	9166.00	EBAG9	1.62	3.02	-1.00
50014.00	F16	M-004398- nucleotide-binding oli	10392.00	NOD1	4.91	0.27	0.09
50014.00	F17	M-012435- F-box protein 8	26269.00	FBXO8	4.85	0.21	0.07
50014.00	F18	M-008480- Rho guanine nucleoti	23365.00	ARHGEF12	6.67	2.03	0.67
50014.00	F19	M-009877- Ral GEF with PH doma	55103.00	RALGPS2	3.09	1.55	-0.51
50014.00	F20	M-010360- Rho guanine nucleoti	9826.00	ARHGEF11	5.24	0.60	0.20
50014.00	F21	M-011281- growth arrest-specific	2622.00	GAS8	6.16	1.52	0.50
50014.00	F23	M-011286- GDP dissociation inhi	2664.00	GDI1	1.57	3.07	-1.02
50014.00	G02	M-005870- coagulation factor II (	2147.00	F2	7.15	2.51	0.83
50014.00	G04	M-013298- EDAR-associated deat	128178.00	EDARADD	10.09	5.45	1.80
50014.00	G05	M-010355- peroxiredoxin 3	10935.00	PRDX3	4.18	0.46	-0.15
50014.00	G06	M-009281- endothelial cell growt	1890.00	ECGF1	8.63	3.99	1.32
50014.00	G07	M-012204- peroxiredoxin 4	10549.00	PRDX4	5.53	0.89	0.29
50014.00	G08	M-004070- dishevelled, dsh hom	1857.00	DVL3	5.11	0.47	0.15
50014.00	G09	M-019173- peroxiredoxin 6	9588.00	PRDX6	4.00	0.64	-0.21
50014.00	G10	M-007880- chemokine (C-X-C mo	6372.00	CXCL6	14.58	**9.94**	3.29
50014.00	G11	M-004556- prostaglandin-endope	5742.00	PTGS1	3.93	0.71	-0.24
50014.00	G12	M-005830- carboxypeptidase Z	8532.00	CPZ	7.95	3.31	1.10
50014.00	G13	M-004557- prostaglandin-endope	5743.00	PTGS2	5.27	0.63	0.21

50014.00	G14	M-003772- CASP8 and FADD-like	8837.00	CFLAR	11.17	**6.53**	2.16
50014.00	G15	M-009089- thioredoxin reductas	10587.00	TXNRD2	24.50	**19.86**	6.57
50014.00	G16	M-003466- caspase 8, apoptosis-	841.00	CASP8	9.59	4.95	1.64
50014.00	G17	M-022772- peroxidasin homolog	7837.00	PXDN	8.85	4.21	1.39
50014.00	G18	M-005805- calpain 3, (p94)	825.00	CAPN3	19.74	**15.10**	4.99
50014.00	G19	M-008324- dual oxidase 2	50506.00	DUOX2	32.01	**27.37**	9.05
50014.00	G20	M-005794- bone morphogenetic	649.00	BMP1	8.19	3.55	1.17
50014.00	G21	M-009228- myeloperoxidase	4353.00	MPO	20.92	**16.28**	5.38
50014.00	G23	M-009741- superoxide dismutas	6649.00	SOD3	9.82	5.18	1.71
50014.00	H02	M-008966- Rho GTPase activatin	392.00	ARHGAP1	4.66	0.02	0.01
50014.00	H04	M-007806- angiopoietin-like 3	27329.00	ANGPTL3	3.37	1.27	-0.42
50014.00	H05	M-010596- GDP dissociation inhi	2665.00	GDI2	6.91	2.27	0.75
50014.00	H06	M-010988- angiotensinogen (ser	183.00	AGT	12.45	**7.81**	2.58
50014.00	H07	M-011044- GM2 ganglioside acti	2760.00	GM2A	2.47	2.17	-0.72
50014.00	H08	M-006355- myosin VI	4646.00	MYO6	10.65	6.01	1.99
50014.00	H09	M-004329- G protein pathway su	2874.00	GPS2	4.79	0.15	0.05
50014.00	H10	M-013160- myosin XVA	51168.00	MYO15A	2.12	2.52	-0.83
50014.00	H11	M-008426- Rho GTPase activatin	23092.00	ARHGAP26	5.30	0.66	0.22
50014.00	H12	M-012646- myosin, heavy chain	4626.00	MYH8	4.20	0.44	-0.15
50014.00	H13	M-012777- guanylate cyclase acti	2981.00	GUCA2B	5.48	0.84	0.28
50014.00	H14	M-011086- myosin, heavy chain	4625.00	MYH7	7.46	2.82	0.93
50014.00	H15	M-010019- kalirin, RhoGEF kinas	8997.00	KALRN	5.41	0.77	0.25
50014.00	H16	M-008243- actin-like 6A	86.00	ACTL6A	7.35	2.71	0.90
50014.00	H17	M-012962- protein phosphatase	80316.00	PPP1R2P9	2.10	2.54	-0.84
50014.00	H18	M-005273- optic atrophy 1 (auto	4976.00	OPA1	15.95	**11.31**	3.74
50014.00	H19	M-011298- immunoglobulin (CD	3476.00	IGBP1	17.95	**13.31**	4.40
50014.00	H20	M-019330- myosin VIIA	4647.00	MYO7A	6.41	1.77	0.58
50014.00	H21	M-009710- Rap guanine nucleoti	51195.00	RAPGEFL1	8.43	3.79	1.25
50014.00	H23	M-014315- mitogen-activated pr	79109.00	MAPKAP1	4.00	0.64	-0.21
50014.00	I02	M-012664- acetylserotonin O-me	438.00	ASMT	1.23	3.41	-1.13
50014.00	I04	M-005787- type 1 tumor necrosi	51752.00	ARTS-1	3.78	0.86	-0.28
50014.00	I05	M-009863- thyroid peroxidase	7173.00	TPO	3.36	1.28	-0.42
50014.00	I06	M-008555- ras homolog gene fan	389.00	RHOC	4.05	0.59	-0.20
50014.00	I07	M-011804- annexin A3	306.00	ANXA3	5.83	1.19	0.39
50014.00	I08	M-005775- ADAM metallopeptid	11096.00	ADAMTS5	23.85	**19.21**	6.35
50014.00	I09	M-003309- caspase 9, apoptosis-	842.00	CASP9	3.85	0.79	-0.26
50014.00	I10	M-005764- ADAM metallopeptid	11093.00	ADAMTS13	5.29	0.65	0.21
50014.00	I11	M-005867- coagulation factor X	2159.00	F10	1.81	2.83	-0.94
50014.00	I12	M-005761- ADAM metallopeptid	9510.00	ADAMTS1	9.06	4.42	1.46
50014.00	I13	M-005956- matrix metallopeptid	4324.00	MMP15	7.84	3.20	1.06
50014.00	I14	M-005760- ADAM-like, decysin 1	27299.00	ADAMDEC1	3.80	0.84	-0.28
50014.00	I15	M-005957- matrix metallopeptid	4325.00	MMP16	3.16	1.48	-0.49
50014.00	I16	M-010700- ADAM metallopeptid	8745.00	ADAM23	4.62	0.02	-0.01
50014.00	I17	M-005958- matrix metallopeptid	4326.00	MMP17	5.66	1.02	0.34

50014.00	I18	M-009246- ADAM metallopeptid	53616.00	ADAM22	7.14	2.50	0.82
50014.00	I19	M-005963- matrix metallopeptid	10893.00	MMP24	7.36	2.72	0.90
50014.00	I20	M-010696- ADAM metallopeptid	2515.00	ADAM2	5.08	0.44	0.15
50014.00	I21	M-009535- myosin IXB	4650.00	MYO9B	6.67	2.03	0.67
50014.00	I23	M-010903- protein phosphatase	5511.00	PPP1R8	6.42	1.78	0.59
50014.00	J02	M-019321- myosin VA (heavy ch	4644.00	MYO5A	1.59	3.05	-1.01
50014.00	J04	M-021478- myosin, light chain 7,	58498.00	MYL7	15.43	**10.79**	3.57
50014.00	J05	M-013109- microtubule-associat	22924.00	MAPRE3	3.20	1.44	-0.48
50014.00	J06	M-021250- myosin, heavy chain	4622.00	MYH4	1.04	3.60	-1.19
50014.00	J07	M-003904- MCF.2 cell line derive	4168.00	MCF2	7.45	2.81	0.93
50014.00	J08	M-012644- myosin, heavy chain	4621.00	MYH3	4.67	0.03	0.01
50014.00	J09	M-003916- neurofibromin 1 (neu	4763.00	NF1	4.61	0.03	-0.01
50014.00	J10	M-006828- dynein, cytoplasmic 1	1778.00	DYNC1H1	1.75	2.89	-0.96
50014.00	J11	M-011742- ornithine decarboxyl	4947.00	OAZ2	2.13	2.51	-0.83
50014.00	J12	M-019964- dynein, light chain, T	6993.00	DYNLT1	6.75	2.11	0.70
50014.00	J13	M-013344- ornithine decarboxyl	51686.00	OAZ3	2.69	1.95	-0.65
50014.00	J14	M-019482- kinesin light chain 1	3831.00	KLC1	4.61	0.03	-0.01
50014.00	J15	M-009444- oligophrenin 1	4983.00	OPHN1	2.04	2.60	-0.86
50014.00	J16	M-016063- kinesin light chain 3	147700.00	KLC3	3.90	0.74	-0.24
50014.00	J17	M-008277- Rho GTPase activatin	9411.00	ARHGAP29	1.93	2.71	-0.90
50014.00	J18	M-014218- kinesin light chain 2	64837.00	KLC2	1.66	2.98	-0.99
50014.00	J19	M-017218- protein kinase (cAMP	11142.00	PKIG	7.32	2.68	0.89
50014.00	J20	M-012574- dynein, cytoplasmic 1	1781.00	DYNC1I2	6.18	1.54	0.51
50014.00	J21	M-018693- transmembrane prot	11070.00	TMEM115	4.56	0.08	-0.03
50014.00	J23	M-016215- phospholipase A2-act	9373.00	PLAA	2.68	1.96	-0.65
50014.00	K02	M-009399- ADAM metallopeptid	4185.00	ADAM11	14.19	**9.55**	3.16
50014.00	K04	M-004503- ADAM metallopeptid	102.00	ADAM10	4.17	0.47	-0.15
50014.00	K05	M-004824- protein phosphatase	5520.00	PPP2R2A	17.81	**13.17**	4.35
50014.00	K06	M-010561- abl interactor 2	10152.00	ABI2	9.27	4.63	1.53
50014.00	K07	M-019459- protein phosphatase	28227.00	PPP2R3B	19.23	**14.59**	4.82
50014.00	K08	M-009085- phospholipase A2, gr	8398.00	PLA2G6	7.60	2.96	0.98
50014.00	K09	M-019863- general transcription	9329.00	GTF3C4	4.20	0.44	-0.15
50014.00	K10	M-010284- patatin-like phosphol	50640.00	PNPLA8	5.14	0.50	0.16
50014.00	K11	M-012628- BTAF1 RNA polymera	9044.00	BTAF1	11.56	**6.92**	2.29
50014.00	K12	M-010271- patatin-like phosphol	8228.00	PNPLA4	12.86	**8.22**	2.72
50014.00	K13	M-004034- enolase 1, (alpha)	2023.00	ENO1	9.41	4.77	1.58
50014.00	K14	M-019376- serpin peptidase inhi	5054.00	SERPINE1	3.04	1.60	-0.53
50014.00	K15	M-003486- E1A binding protein p	2033.00	EP300	7.70	3.06	1.01
50014.00	K16	M-010859- serpin peptidase inhi	5055.00	SERPINB2	5.08	0.44	0.15
50014.00	K17	M-004888- excision repair cross-	2074.00	ERCC6	5.56	0.92	0.30
50014.00	K18	M-013082- renin binding protein	5973.00	RENBP	3.41	1.23	-0.41
50014.00	K19	M-009643- ubiquitin-conjugating	55284.00	UBE2W	9.71	5.07	1.68
50014.00	K20	M-010532- protein phosphatase	5506.00	PPP1R3A	5.99	1.35	0.45
50014.00	K21	M-019646- general transcription	2962.00	GTF2F1	3.68	0.96	-0.32

50014.00	K23	M-010898-	general transcription	2963.00	GTF2F2	5.71	1.07	0.35
50014.00	L02	M-019799-	dynein, cytoplasmic 1	1780.00	DYNC1I1	1.88	2.76	-0.91
50014.00	L04	M-012419-	dynein, axonemal, int	27019.00	DNAI1	9.35	4.71	1.56
50014.00	L05	M-011917-	protein phosphatase	6992.00	PPP1R11	4.84	0.20	0.07
50014.00	L06	M-006493-	dynein, light chain, LC	140735.00	DYNLL2	1.77	2.87	-0.95
50014.00	L07	M-013547-	protein phosphatase	4660.00	PPP1R12B	1.83	2.81	-0.93
50014.00	L08	M-012874-	dynactin 1 (p150, glu	1639.00	DCTN1	1.77	2.87	-0.95
50014.00	L09	M-019589-	protein phosphatase	5510.00	PPP1R7	11.54	**6.90**	2.28
50014.00	L10	M-013316-	amyloid beta precurs	10513.00	APPBP2	2.74	1.90	-0.63
50014.00	L11	M-019167-	protein phosphatase	5522.00	PPP2R2C	1.16	3.48	-1.15
50014.00	L12	M-012075-	ARP1 actin-related pr	10120.00	ACTR1B	5.57	0.93	0.31
50014.00	L13	M-005214-	protein phosphatase	5524.00	PPP2R4	1.92	2.72	-0.90
50014.00	L14	M-009422-	actin-like 6B	51412.00	ACTL6B	6.22	1.58	0.52
50014.00	L15	M-011926-	pleckstrin homology,	9267.00	PSCD1	6.88	2.24	0.74
50014.00	L16	M-011567-	actin, gamma 2, smoo	72.00	ACTG2	2.67	1.97	-0.65
50014.00	L17	M-011925-	pleckstrin homology,	9266.00	PSCD2	1.99	2.65	-0.88
50014.00	L18	M-005265-	actin, gamma 1	71.00	ACTG1	2.40	2.24	-0.74
50014.00	L19	M-012254-	proteasome (prosom	5720.00	PSME1	5.47	0.83	0.27
50014.00	L20	M-012015-	actin, alpha, cardiac m	70.00	ACTC1	2.43	2.21	-0.73
50014.00	L21	M-009321-	ral guanine nucleotid	5863.00	RGL2	2.30	2.34	-0.77
50014.00	L23	M-032255-	RAB3 GTPase activati	25782.00	RAB3GAP2	1.23	3.41	-1.13
50014.00	M02	M-005211-	protein phosphatase	51400.00	PPME1	2.66	1.98	-0.65
50014.00	M04	M-005075-	pitrilysin metallopept	10531.00	PITRM1	5.65	1.01	0.33
50014.00	M05	M-003493-	histone deacetylase 1	3065.00	HDAC1	11.00	**6.36**	2.10
50014.00	M06	M-007656-	phosphodiesterase 6	5149.00	PDE6H	1.49	3.15	-1.04
50014.00	M07	M-004072-	histone deacetylase 1	83933.00	HDAC10	5.86	1.22	0.40
50014.00	M08	M-007655-	phosphodiesterase 6	5148.00	PDE6G	1.52	3.12	-1.03
50014.00	M09	M-003495-	histone deacetylase 2	3066.00	HDAC2	8.07	3.43	1.13
50014.00	M10	M-009475-	microsomal glutathio	4258.00	MGST2	3.73	0.91	-0.30
50014.00	M11	M-003498-	histone deacetylase 5	10014.00	HDAC5	3.61	1.03	-0.34
50014.00	M12	M-011610-	choroideremia-like (R	1122.00	CHML	4.28	0.36	-0.12
50014.00	M13	M-009330-	histone deacetylase 7	51564.00	HDAC7A	0.94	3.70	-1.22
50014.00	M14	M-009414-	choroideremia (Rab e	1121.00	CHM	9.25	4.61	1.53
50014.00	M15	M-005241-	histone deacetylase 9	9734.00	HDAC9	1.56	3.08	-1.02
50014.00	M16	M-013857-	baculoviral IAP repea	57448.00	BIRC6	2.46	2.18	-0.72
50014.00	M17	M-009431-	huntingtin interactin	3093.00	HIP2	3.25	1.39	-0.46
50014.00	M18	M-009580-	Rho GTPase activatin	394.00	ARHGAP5	1.20	3.44	-1.14
50014.00	M19	M-006301-	HIV-1 Tat interacting	10524.00	HTATIP	1.81	2.83	-0.94
50014.00	M20	M-019820-	PET112-like (yeast)	5188.00	PET112L	4.37	0.27	-0.09
50014.00	M21	M-017599-	interleukin enhancer	3608.00	ILF2	2.70	1.94	-0.64
50014.00	M23	M-019680-	pre-B-cell leukemia h	5087.00	PBX1	1.20	3.44	-1.14
50014.00	N02	M-003451-	actin, beta	60.00	ACTB	26.10	**21.46**	7.10
50014.00	N04	M-003450-	actin, alpha 2, smoot	59.00	ACTA2	1.88	2.76	-0.91
50014.00	N05	M-005193-	ral guanine nucleotid	5900.00	RALGDS	3.75	0.89	-0.29

50014.00	N06	M-011194- actin, alpha 1, skeleta	58.00	ACTA1	4.27	0.37	-0.12
50014.00	N07	M-006846- Ran GTPase activatin	5905.00	RANGAP1	1.13	3.51	-1.16
50014.00	N08	M-013097- WAP four-disulfide cc	58189.00	WFDC1	5.35	0.71	0.24
50014.00	N09	M-019706- RAP1 GTPase activati	5909.00	RAP1GAP	4.37	0.27	-0.09
50014.00	N10	M-028294- Wiskott-Aldrich syndr	7454.00	WAS	8.45	3.81	1.26
50014.00	N11	M-015881- RAP1, GTP-GDP disso	5910.00	RAP1GDS1	4.17	0.47	-0.16
50014.00	N12	M-011406- TIMP metallopeptida	7079.00	TIMP4	6.50	1.86	0.62
50014.00	N13	M-005276- RAS p21 protein activ	5921.00	RASA1	4.39	0.25	-0.08
50014.00	N14	M-011111- TIMP metallopeptida	7078.00	TIMP3	3.74	0.90	-0.30
50014.00	N15	M-004333- RAS p21 protein activ	5922.00	RASA2	3.73	0.91	-0.30
50014.00	N16	M-011793- TIMP metallopeptida	7077.00	TIMP2	5.74	1.10	0.36
50014.00	N17	M-009117- RAS p21 protein activ	22821.00	RASA3	2.62	2.02	-0.67
50014.00	N18	M-011792- TIMP metallopeptida	7076.00	TIMP1	3.79	0.85	-0.28
50014.00	N19	M-009411- RAS protein activator	9462.00	RASAL2	8.36	3.72	1.23
50014.00	N20	M-019922- tissue factor pathway	7035.00	TFPI	4.84	0.20	0.07
50014.00	N21	M-009323- Ras protein-specific g	5923.00	RASGRF1	12.22	7.58	2.50
50014.00	N23	M-011474- reversion-inducing-cy	8434.00	RECK	3.52	1.12	-0.37
50014.00	O02	M-021336- eukaryotic translatio	1983.00	EIF5	3.24	1.40	-0.46
50014.00	O04	M-004208- eukaryotic translatio	8891.00	EIF2B3	4.49	0.15	-0.05
50014.00	O05	M-011746- pre-B-cell leukemia h	5089.00	PBX2	4.73	0.09	0.03
50014.00	O06	M-021264- REX4, RNA exonuclea	57109.00	REXO4	2.75	1.89	-0.62
50014.00	O07	M-020121- pre-B-cell leukemia h	5090.00	PBX3	1.52	3.12	-1.03
50014.00	O08	M-010064- ubiquitin-conjugating	7335.00	UBE2V1	2.86	1.78	-0.59
50014.00	O09	M-012969- pre-B-cell leukemia h	80714.00	PBX4	8.32	3.68	1.22
50014.00	O10	M-015316- transcription termina	8458.00	TTF2	2.84	1.80	-0.60
50014.00	O11	M-005055- p300/CBP-associated	8850.00	PCAF	4.62	0.02	-0.01
50014.00	O12	M-003549- tumor susceptibility g	7251.00	TSG101	1.57	3.07	-1.02
50014.00	O13	M-016286- methionine sulfoxide	22921.00	MSRB2	3.60	1.04	-0.35
50014.00	O14	M-003329- tumor protein p53	7157.00	TP53	2.56	2.08	-0.69
50014.00	O15	M-019109- peroxisomal prolifera	85441.00	PRIC285	9.45	4.81	1.59
50014.00	O16	M-012847- NMDA receptor regul	80155.00	NARG1	1.25	3.39	-1.12
50014.00	O17	M-007772- recombination signal	3516.00	RBPJ	1.58	3.06	-1.01
50014.00	O18	M-010540- suppressor of Ty 6 ho	6830.00	SUPT6H	1.65	2.99	-0.99
50014.00	O19	M-017253- SWI/SNF related, mat	6595.00	SMARCA2	0.77	3.87	-1.28
50014.00	O20	M-004830- Snf2-related CBP acti	10847.00	SRCAP	0.25	4.39	-1.45
50014.00	O21	M-010431- SWI/SNF related, mat	6597.00	SMARCA4	0.68	3.96	-1.31
50014.00	O23	M-011478- SWI/SNF related, mat	8467.00	SMARCA5	1.02	3.62	-1.20
50014.00	P02	M-010216- serine peptidase inhil	10653.00	SPINT2	18.32	13.68	4.52
50014.00	P04	M-012327- serine peptidase inhil	11005.00	SPINK5	9.00	4.36	1.44
50014.00	P05	M-008387- ral guanine nucleotid	23179.00	RGL1	5.18	0.54	0.18
50014.00	P06	M-019724- serine peptidase inhil	6690.00	SPINK1	7.99	3.35	1.11
50014.00	P07	M-008607- Ral-GDS related prote	266747.00	Rgr	3.54	1.10	-0.36
50014.00	P08	M-005195- son of sevenless hom	6655.00	SOS2	2.75	1.89	-0.63
50014.00	P09	M-016048- ribonuclease/angioge	6050.00	RNH1	5.85	1.21	0.40

50014.00	P10	M-011391-	secretory leukocyte p	6590.00	SLPI	4.48	0.16	-0.05
50014.00	P11	M-021066-	serpin peptidase inhi	51156.00	SERPINA10	10.45	5.81	1.92
50014.00	P12	M-019971-	SH2 domain containi	10044.00	SH2D3C	1.35	3.29	-1.09
50014.00	P13	M-015832-	serpin peptidase inhi	5104.00	SERPINA5	3.11	1.53	-0.51
50014.00	P14	M-012246-	serpin peptidase inhi	5276.00	SERPINI2	3.10	1.54	-0.51
50014.00	P15	M-016240-	serpin peptidase inhi	1992.00	SERPINB1	3.63	1.01	-0.34
50014.00	P16	M-019901-	serpin peptidase inhi	5274.00	SERPINI1	4.55	0.09	-0.03
50014.00	P17	M-015331-	serpin peptidase inhi	5275.00	SERPINB13	6.52	1.88	0.62
50014.00	P18	M-010999-	serpin peptidase inhi	710.00	SERPING1	3.53	1.11	-0.37
50014.00	P19	M-012768-	serpin peptidase inhi	6317.00	SERPINB3	2.39	2.25	-0.75
50014.00	P20	M-010153-	serpin peptidase inhi	5176.00	SERPINF1	1.96	2.68	-0.89
50014.00	P21	M-012596-	serpin peptidase inhi	6318.00	SERPINB4	4.67	0.03	0.01
50014.00	P23	M-019684-	serpin peptidase inhi	5268.00	SERPINB5	2.56	2.08	-0.69
					mdn	4.64	2.04	
					3xMAD		6.13	
					MADc		3.02	
50014.00	C22					26.08		19.28
50014.00	D22					28.86		22.48
50014.00	E22					26.63		17.50
50014.00	F22					25.17		22.01
					mn	26.68		20.32
					sd	1.57		2.35
50014.00	G22					5.71		1.38
50014.00	H22				20.13			4.79
50014.00	I22					6.92		3.24
50014.00	J22					0.67		1.85
					mn	4.43		2.81
					sd	3.32		1.54

3psSD	4.71		7.05
3ngSD	9.96		4.61
SumSD	14.67		11.66
DiffMn	22.25		17.50
SmovrDiff	0.66		0.67
1minus	0.34		0.33

50014.00	G03	M-003290-	polo-like kinase 1 (Dr	5347.00	PLK1 SMAR	28.96		6.90
50014.00	H03	M-003290-	polo-like kinase 1 (Dr	5347.00		23.47		4.55
50014.00	I03	D-001206-	siControl non-targeting siRNA #2			5.78		1.26
50014.00	J03	D-001206-	siControl non-targeting siRNA #2			4.33		1.94
50014.00	K03	D-001600-	siGLO RISC-free siRNA			9.98		10.43
50014.00	L03	D-001600-	siGLO RISC-free siRNA			10.72		8.52

% inf	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**		
20.69	**17.46**	6.80	10.56	**6.48**	2.21	x	toxic a,b,c
2.38	0.85	-0.33	3.14	0.94	-0.32		
1.66	1.57	-0.61	4.20	0.12	0.04		
3.36	0.13	0.05	3.96	0.12	-0.04		
8.37	5.14	2.00	13.43	**9.35**	3.19	x	toxic a,b,c
2.94	0.29	-0.11	4.80	0.72	0.24		
3.66	0.43	0.17	5.16	1.08	0.37		
1.68	1.55	-0.60	4.06	0.02	0.00		
5.15	1.92	0.75	7.00	2.92	1.00		
1.54	1.69	-0.66	2.92	1.16	-0.40		
1.86	1.37	-0.53	7.20	3.12	1.06		
7.76	4.53	1.76	13.26	**9.18**	3.14		
2.34	0.89	-0.34	4.96	0.88	0.30		
4.36	1.13	0.44	10.35	**6.27**	2.14		
3.32	0.09	0.04	19.49	**15.41**	5.26		
0.99	2.24	-0.87	19.32	**15.24**	5.20		
3.31	0.08	0.03	14.72	**10.64**	3.63		
4.70	1.47	0.57	15.77	**11.69**	3.99		
4.50	1.27	0.50	9.70	5.62	1.92		
12.94	**9.71**	3.78	21.33	**17.25**	5.89	x	toxic a,b,c
11.74	**8.51**	3.32	13.33	**9.25**	3.16	x	toxic a,b,c
3.06	0.17	-0.06	8.08	4.00	1.37		
2.14	1.09	-0.43	4.38	0.30	0.10		
2.57	0.66	-0.26	3.42	0.66	-0.22		
2.28	0.95	-0.37	9.58	5.50	1.88		
0.80	2.43	-0.95	2.37	1.71	-0.58		
1.03	2.20	-0.86	1.20	2.88	-0.98		
0.74	2.49	-0.97	4.22	0.14	0.05		
5.17	1.94	0.76	4.09	0.01	0.00		
0.94	2.29	-0.89	2.94	1.14	-0.39		
1.49	1.74	-0.68	3.54	0.54	-0.18		
0.16	3.07	-1.19	6.43	2.35	0.80		
1.68	1.55	-0.60	6.09	2.01	0.69		
0.11	3.12	-1.21	2.21	1.87	-0.64		
2.79	0.44	-0.17	4.12	0.04	0.01		
1.77	1.46	-0.57	7.30	3.22	1.10		
1.30	1.93	-0.75	5.50	1.42	0.49		
0.25	2.98	-1.16	5.73	1.65	0.57		
1.16	2.07	-0.81	8.53	4.45	1.52		
2.35	0.88	-0.34	19.75	**15.67**	5.35		
1.77	1.46	-0.57	2.10	1.98	-0.68		
2.31	0.92	-0.36	1.48	2.60	-0.89		
0.90	2.33	-0.91	1.21	2.87	-0.98		

2.70	0.53	-0.21	1.61	2.47	-0.84
1.57	1.66	-0.64	1.25	2.83	-0.97
4.79	1.56	0.61	4.02	0.06	-0.02
3.91	0.68	0.27	2.59	1.49	-0.51
3.52	0.29	0.11	0.97	3.11	-1.06
3.47	0.24	0.09	3.53	0.55	-0.19
1.84	1.39	-0.54	1.42	2.66	-0.91
1.54	1.69	-0.66	0.89	3.19	-1.09
4.23	1.00	0.39	0.13	3.95	-1.35
2.98	0.25	-0.10	1.79	2.29	-0.78
0.98	2.25	-0.88	1.45	2.63	-0.90
3.21	0.02	0.00	2.64	1.44	-0.49
2.51	0.72	-0.28	0.91	3.17	-1.08
4.58	1.35	0.53	0.99	3.09	-1.06
1.61	1.62	-0.63	0.79	3.29	-1.12
3.55	0.32	0.12	3.40	0.68	-0.23
2.70	0.53	-0.21	3.47	0.61	-0.21
0.99	2.24	-0.87	0.26	3.82	-1.30
0.48	2.75	-1.07	1.78	2.30	-0.78
2.30	0.93	-0.36	1.34	2.74	-0.94
2.52	0.71	-0.28	4.60	0.52	0.18
3.51	0.28	0.11	1.73	2.35	-0.80
3.07	0.16	-0.06	0.94	3.14	-1.07
1.83	1.40	-0.54	0.96	3.12	-1.07
3.44	0.21	0.08	0.91	3.17	-1.08
8.21	4.98	1.94	2.62	1.46	-0.50
1.60	1.63	-0.64	0.65	3.43	-1.17
4.88	1.65	0.64	8.83	4.75	1.62
5.85	2.62	1.02	7.50	3.42	1.17
3.88	0.65	0.26	3.55	0.53	-0.18
1.77	1.46	-0.57	2.39	1.69	-0.58
6.16	2.93	1.14	4.76	0.68	0.23
5.66	2.43	0.95	6.23	2.15	0.73
5.70	2.47	0.96	2.12	1.96	-0.67
2.83	0.40	-0.15	1.83	2.25	-0.77
7.51	4.28	1.67	2.81	1.27	-0.43
5.75	2.52	0.98	1.18	2.90	-0.99
1.14	2.09	-0.81	0.82	3.26	-1.11
1.50	1.73	-0.67	2.62	1.46	-0.50
1.26	1.97	-0.77	4.35	0.27	0.09
3.77	0.54	0.21	3.41	0.67	-0.23
4.77	1.54	0.60	1.53	2.55	-0.87
2.22	1.01	-0.39	1.40	2.68	-0.91
2.31	0.92	-0.36	3.63	0.45	-0.15

12.37	**9.14**	3.56	16.76	**12.68**	4.33	x	toxic a,b,c
4.53	1.30	0.51	3.71	0.37	-0.12		
3.43	0.20	0.08	2.26	1.82	-0.62		
4.51	1.28	0.50	6.91	2.83	0.97		
5.14	1.91	0.74	8.95	4.87	1.66		
4.47	1.24	0.48	3.82	0.26	-0.09		
3.13	0.10	-0.04	1.34	2.74	-0.94		
3.05	0.18	-0.07	7.12	3.04	1.04		
9.32	**6.09**	2.37	13.97	**9.89**	3.38	x	toxic a,b,c
6.74	3.51	1.37	8.52	4.44	1.52		
9.75	**6.52**	2.54	11.58	**7.50**	2.56	x	toxic a,b,c
8.46	**5.23**	2.04	12.64	**8.56**	2.92	y	
3.66	0.43	0.17	3.67	0.41	-0.14		
0.90	2.33	-0.91	3.63	0.45	-0.15		
0.38	2.85	-1.11	4.27	0.19	0.06		
2.24	0.99	-0.38	3.52	0.56	-0.19		
2.78	0.45	-0.17	2.22	1.86	-0.63		
19.29	**16.06**	6.26	50.36	**46.28**	15.80	x	toxic a,b,c
1.50	1.73	-0.67	5.18	1.10	0.38		
3.44	0.21	0.08	4.10	0.02	0.01		
7.54	4.31	1.68	4.53	0.45	0.15		
4.97	1.74	0.68	7.65	3.57	1.22		
3.10	0.13	-0.05	13.98	**9.90**	3.38		
2.33	0.90	-0.35	4.73	0.65	0.22		
1.33	1.90	-0.74	3.49	0.59	-0.20		
1.30	1.93	-0.75	3.41	0.67	-0.23		
0.97	2.26	-0.88	9.61	5.53	1.89		
4.57	1.34	0.52	4.93	0.85	0.29		
5.60	2.37	0.93	12.39	**8.31**	2.84		
3.76	0.53	0.21	5.49	1.41	0.48		
5.23	2.00	0.78	5.81	1.73	0.59		
3.57	0.34	0.13	6.51	2.43	0.83		
2.01	1.22	-0.47	3.50	0.58	-0.20		
0.62	2.61	-1.02	2.51	1.57	-0.53		
5.96	2.73	1.07	4.35	0.27	0.09		
2.55	0.68	-0.26	1.50	2.58	-0.88		
2.23	1.00	-0.39	5.47	1.39	0.48		
1.60	1.63	-0.64	3.35	0.73	-0.25		
1.63	1.60	-0.62	3.59	0.49	-0.17		
2.56	0.67	-0.26	3.42	0.66	-0.23		
7.23	4.00	1.56	10.72	**6.64**	2.27	x	toxic a
0.93	2.30	-0.89	4.22	0.14	0.05		
1.98	1.25	-0.49	3.69	0.39	-0.13		
2.23	1.00	-0.39	4.82	0.74	0.25		

4.38	1.15	0.45	13.99	**9.91**	3.38	x	toxic a
7.24	4.01	1.56	5.48	1.40	0.48		
3.89	0.66	0.26	7.42	3.34	1.14		
2.79	0.44	-0.17	1.67	2.41	-0.82		
4.84	1.61	0.63	7.30	3.22	1.10		
3.89	0.66	0.26	12.57	**8.49**	2.90	x	toxic a,b
2.64	0.59	-0.23	2.21	1.87	-0.64		
0.74	2.49	-0.97	5.28	1.20	0.41		
2.57	0.66	-0.26	5.15	1.07	0.37		
1.14	2.09	-0.81	3.50	0.58	-0.20		
3.18	0.05	-0.02	7.43	3.35	1.15		
3.01	0.22	-0.08	8.32	4.24	1.45		
0.50	2.73	-1.06	6.00	1.92	0.66		
1.22	2.01	-0.78	2.40	1.68	-0.57		
4.81	1.58	0.62	11.27	**7.19**	2.46		
0.57	2.66	-1.03	3.37	0.71	-0.24		
2.16	1.07	-0.41	2.77	1.31	-0.45		
2.39	0.84	-0.33	6.81	2.73	0.93		
2.62	0.61	-0.24	4.87	0.79	0.27		
1.48	1.75	-0.68	4.75	0.67	0.23		
1.30	1.93	-0.75	2.03	2.05	-0.70		
3.56	0.33	0.13	5.51	1.43	0.49		
4.22	0.99	0.39	3.05	1.03	-0.35		
1.06	2.17	-0.84	2.21	1.87	-0.64		
6.68	3.45	1.34	3.18	0.90	-0.31		
8.64	**5.41**	2.11	6.91	2.83	0.97	x	toxic a
5.98	2.75	1.07	6.38	2.30	0.79		
6.81	3.58	1.40	9.29	5.21	1.78		
5.92	2.69	1.05	3.67	0.41	-0.14		
0.73	2.50	-0.97	0.46	3.62	-1.24		
3.08	0.15	-0.06	2.56	1.52	-0.52		
2.88	0.35	-0.13	2.11	1.97	-0.67		
0.66	2.57	-1.00	4.79	0.71	0.24		
1.25	1.98	-0.77	1.77	2.31	-0.79		
0.06	3.17	-1.24	1.65	2.43	-0.83		
0.67	2.56	-1.00	3.69	0.39	-0.13		
2.97	0.26	-0.10	7.80	3.72	1.27		
1.21	2.02	-0.79	6.00	1.92	0.66		
2.28	0.95	-0.37	15.27	**11.19**	3.82		
1.23	2.00	-0.78	28.30	**24.22**	8.27		
2.00	1.23	-0.48	8.40	4.32	1.47		
2.01	1.22	-0.47	2.35	1.73	-0.59		
5.70	2.47	0.96	8.53	4.45	1.52		
0.24	2.99	-1.16	10.81	**6.73**	2.30		

2.49	0.74	-0.29	11.41	**7.33**	2.50	
1.29	1.94	-0.76	10.78	**6.70**	2.29	
0.49	2.74	-1.07	7.21	3.13	1.07	
0.79	2.44	-0.95	5.03	0.95	0.33	
0.48	2.75	-1.07	6.73	2.65	0.91	
1.34	1.89	-0.74	2.47	1.61	-0.55	
1.55	1.68	-0.65	5.01	0.93	0.32	
0.78	2.45	-0.95	2.35	1.73	-0.59	
0.28	2.95	-1.15	1.51	2.57	-0.88	
4.92	1.69	0.66	13.47	**9.39**	3.20	
4.38	1.15	0.45	5.89	1.81	0.62	
2.01	1.22	-0.47	6.54	2.46	0.84	
1.09	2.14	-0.83	2.61	1.47	-0.50	
0.63	2.61	-1.01	3.06	1.02	-0.35	
1.68	1.55	-0.60	7.04	2.96	1.01	
0.75	2.48	-0.97	2.54	1.54	-0.52	
3.32	0.09	0.04	7.19	3.11	1.06	
2.62	0.61	-0.24	4.39	0.31	0.11	
4.93	1.70	0.66	5.26	1.18	0.40	
1.27	1.96	-0.76	4.65	0.57	0.19	
1.56	1.67	-0.65	5.35	1.27	0.43	
1.61	1.62	-0.63	4.78	0.70	0.24	
2.35	0.88	-0.34	12.22	**8.14**	2.78	
0.98	2.25	-0.88	5.26	1.18	0.40	
5.30	2.07	0.81	7.39	3.31	1.13	
3.17	0.06	-0.02	3.74	0.34	-0.11	
3.69	0.46	0.18	2.65	1.43	-0.49	
15.17	**11.94**	4.65	8.86	4.78	1.63	y
14.31	**11.08**	4.32	5.73	1.65	0.56	
4.47	1.24	0.48	3.47	0.61	-0.21	
2.74	0.49	-0.19	6.80	2.72	0.93	
3.21	0.02	-0.01	8.35	4.27	1.46	
3.48	0.25	0.10	4.72	0.64	0.22	
5.74	2.51	0.98	2.31	1.77	-0.61	
7.10	3.87	1.51	16.37	**12.29**	4.20	y
4.72	1.49	0.58	8.88	4.80	1.64	
2.49	0.74	-0.29	7.27	3.19	1.09	
3.51	0.28	0.11	2.46	1.63	-0.55	
0.70	2.53	-0.98	1.67	2.41	-0.82	
4.90	1.67	0.65	3.25	0.83	-0.28	
3.00	0.23	-0.09	1.87	2.21	-0.75	
5.46	2.23	0.87	5.20	1.12	0.38	
7.93	4.70	1.83	5.41	1.33	0.45	
4.06	0.83	0.32	1.95	2.13	-0.73	

6.04	2.81	1.10	5.07	0.99	0.34
4.03	0.80	0.31	0.77	3.31	-1.13
3.34	0.11	0.04	2.10	1.98	-0.67
3.83	0.60	0.24	1.35	2.73	-0.93
5.33	2.10	0.82	1.27	2.81	-0.96
2.46	0.77	-0.30	0.64	3.44	-1.17
3.15	0.08	-0.03	0.76	3.32	-1.13
3.97	0.74	0.29	3.33	0.75	-0.26
4.93	1.70	0.66	0.69	3.39	-1.16
3.93	0.70	0.27	1.48	2.60	-0.89
4.73	1.50	0.59	2.24	1.84	-0.63
1.83	1.40	-0.54	1.67	2.41	-0.82
5.05	1.82	0.71	3.12	0.96	-0.33
4.62	1.39	0.54	2.43	1.65	-0.56
3.78	0.55	0.22	4.24	0.16	0.05
3.97	0.74	0.29	0.82	3.26	-1.11
10.80	**7.57**	2.95	1.48	2.60	-0.89
3.56	0.33	0.13	4.37	0.29	0.10
3.01	0.22	-0.09	0.60	3.48	-1.19
3.85	0.62	0.24	1.02	3.06	-1.05
4.75	1.52	0.59	4.53	0.45	0.15
3.80	0.57	0.22	6.18	2.10	0.72
1.44	1.79	-0.69	3.73	0.35	-0.12
6.18	2.95	1.15	6.19	2.11	0.72
2.09	1.14	-0.44	1.56	2.52	-0.86
5.25	2.02	0.79	2.60	1.48	-0.51
2.07	1.16	-0.45	0.53	3.55	-1.21
6.13	2.90	1.13	7.05	2.97	1.01
3.41	0.18	0.07	1.89	2.19	-0.75
2.03	1.20	-0.47	1.35	2.73	-0.93
6.02	2.79	1.09	2.80	1.28	-0.44
4.96	1.73	0.67	0.93	3.15	-1.07
12.23	**9.00**	3.51	4.87	0.79	0.27
3.28	0.05	0.02	4.06	0.02	-0.01
12.81	**9.58**	3.74	6.20	2.12	0.73
8.36	5.13	2.00	4.60	0.52	0.18
1.77	1.46	-0.57	0.88	3.20	-1.09
7.56	4.33	1.69	1.39	2.69	-0.92
10.94	**7.71**	3.01	3.17	0.91	-0.31
6.56	3.33	1.30	1.91	2.17	-0.74
3.24	0.01	0.00	1.46	2.62	-0.89
1.14	2.09	-0.81	2.40	1.68	-0.57
3.02	0.21	-0.08	2.02	2.06	-0.70
1.11	2.12	-0.82	4.56	0.48	0.16

1.34	1.89	-0.73	4.17	0.09	0.03		
1.20	2.03	-0.79	2.42	1.66	-0.57		
2.56	0.67	-0.26	5.62	1.54	0.53		
0.42	2.81	-1.09	1.89	2.19	-0.75		
1.01	2.22	-0.87	4.30	0.22	0.07		
0.65	2.58	-1.00	2.40	1.68	-0.57		
1.22	2.01	-0.78	5.12	1.04	0.35		
3.09	0.14	-0.05	4.62	0.54	0.18		
1.03	2.20	-0.86	2.35	1.73	-0.59		
2.34	0.89	-0.35	11.49	**7.41**	2.53		
2.05	1.18	-0.46	3.51	0.57	-0.19		
0.35	2.88	-1.12	2.59	1.49	-0.51		
1.76	1.47	-0.57	4.05	0.03	-0.01		
2.37	0.86	-0.33	31.29	**27.21**	9.29		
1.58	1.65	-0.64	2.71	1.37	-0.47		
9.88	**6.65**	2.59	9.33	5.25	1.79		
1.22	2.01	-0.78	0.85	3.23	-1.10		
10.42	**7.19**	2.80	2.42	1.66	-0.57		
14.12	**10.89**	4.24	1.28	2.80	-0.95		
9.05	**5.82**	2.27	5.54	1.46	0.50		
8.06	4.83	1.88	0.74	3.34	-1.14		
14.09	**10.86**	4.23	2.69	1.39	-0.47		
9.82	**6.59**	2.57	4.07	0.01	0.00		
12.84	**9.61**	3.75	2.87	1.21	-0.41		
9.12	**5.89**	2.30	4.40	0.32	0.11		
2.28	0.96	-0.37	4.55	0.47	0.16		
5.17	1.94	0.76	5.11	1.03	0.35		
16.29	**13.06**	5.09	7.87	3.79	1.29		
6.12	2.89	1.13	3.26	0.82	-0.28		
13.80	**10.57**	4.12	19.82	**15.74**	5.37	y	
6.93	3.70	1.44	3.31	0.77	-0.26		
7.56	4.33	1.69	2.95	1.13	-0.38		
11.74	**8.51**	3.32	1.95	2.13	-0.73		
9.45	**6.22**	2.43	5.58	1.50	0.51		
11.79	**8.56**	3.34	4.94	0.86	0.29		
8.07	4.84	1.89	2.78	1.30	-0.44		
21.25	**18.02**	7.02	8.57	4.49	1.53		
12.83	**9.60**	3.74	12.83	**8.75**	2.99	x	toxic a,b
8.65	**5.42**	2.11	3.78	0.30	-0.10		
17.35	**14.12**	5.50	15.56	**11.48**	3.92	x	toxic a,b
19.35	**16.12**	6.28	7.08	3.00	1.02		
21.61	**18.38**	7.16	3.17	0.91	-0.31		
8.19	4.96	1.93	6.18	2.10	0.72		
5.63	2.40	0.94	13.95	**9.87**	3.37		

6.94	3.71	1.45	2.59	1.49	-0.51		
28.68	**25.45**	9.91	17.57	**13.49**	4.60	x	toxic a,b
10.68	**7.45**	2.90	6.58	2.50	0.85		
43.62	**40.39**	15.74	13.92	**9.84**	3.36	x	toxic a,b
10.66	**7.43**	2.90	2.32	1.76	-0.60		
10.35	**7.12**	2.78	8.01	3.93	1.34		
5.93	2.70	1.05	2.79	1.29	-0.44		
20.14	**16.91**	6.59	9.37	5.29	1.81		
9.26	**6.03**	2.35	7.89	3.81	1.30		
40.71	**37.48**	14.60	4.37	0.29	0.10		
5.71	2.48	0.97	0.91	3.17	-1.08		
18.00	**14.77**	5.75	4.39	0.31	0.11		
25.81	**22.58**	8.80	12.63	**8.55**	2.92	x	toxic a,b
3.23	1.73		4.08	1.98			
	5.20			5.94			
	2.57			2.93			
	21.31						
	33.29						
	27.79						
	35.20						
	29.40						
	6.24						
	2.43						
	2.67						
	9.23						
	9.15						
	5.87						
	3.84						
	18.72						
	11.51						
	30.23						
	23.53						
	1.28						
	-0.28						
	6.32						
	16.09						
	1.00						
	3.76						
	12.65						
	8.35						

						% inf	**abs dev**	**robust Z**
50015.00	A02	M-007178-	neural prec	4734.00	NEDD4	6.39	1.44	0.48
50015.00	A04	M-007039-	myeloid/lyn	58508.00	MLL3	3.32	1.63	-0.54
50015.00	A05	M-005791-	BRCA1 asso	8314.00	BAP1	14.24	**9.29**	3.09
50015.00	A06	M-007161-	membrane-	220972.00	MARCH8	5.12	0.17	0.05
50015.00	A07	M-006597-	BRCA1 asso	8315.00	BRAP	17.00	**12.05**	4.00
50015.00	A08	M-007186-	HECT, C2 an	23072.00	HECW1	2.92	2.03	-0.68
50015.00	A09	M-004609-	cylindromat	1540.00	CYLD	4.29	0.66	-0.22
50015.00	A10	M-007183-	ubiquitin pr	9690.00	UBE3C	7.03	2.08	0.69
50015.00	A11	M-017741-	ubiquitin sp	10208.00	USPL1	17.95	**13.00**	4.32
50015.00	A12	M-007196-	itchy homol	83737.00	ITCH	6.50	1.55	0.51
50015.00	A13	M-003497-	histone dea	9759.00	HDAC4	10.10	5.15	1.71
50015.00	A14	M-007181-	hect (homo	8925.00	HERC1	6.18	1.23	0.41
50015.00	A15	M-003499-	histone dea	10013.00	HDAC6	10.66	5.71	1.90
50015.00	A16	M-007188-	HECT doma	25831.00	HECTD1	4.43	0.52	-0.17
50015.00	A17	M-016888-	TL132 prote	220594.00	LOC22059	2.68	2.27	-0.76
50015.00	A18	M-015377-	fizzy/cell di	51343.00	FZR1	4.88	0.07	-0.03
50015.00	A19	M-021061-	OTU domai	55611.00	OTUB1	20.08	**15.13**	5.03
50015.00	A20	M-014244-	chromosom	65259.00	C16orf28	8.52	3.57	1.18
50015.00	A21	M-009919-	tumor necr	7128.00	TNFAIP3	5.27	0.32	0.11
50015.00	A23	M-004309-	ubiquitin ca	7345.00	UCHL1	9.51	4.56	1.52
50015.00	B02	M-008030-	CDC14 cell	168448.00	CDC14C	1.48	3.47	-1.15
50015.00	B04	M-008027-	dual specifi	78986.00	DUSP26	1.32	3.63	-1.21
50015.00	B05	M-007187-	neural prec	23327.00	NEDD4L	10.12	5.17	1.72
50015.00	B06	M-027012-	protein pho	57460.00	PPM1H	1.55	3.40	-1.13
50015.00	B07	M-020081-	neural prec	4738.00	NEDD8	1.60	3.35	-1.11
50015.00	B08	M-008782-	glycerol-3-p	2819.00	GPD1	5.94	0.99	0.33
50015.00	B09	M-016715-	neuralized	9148.00	NEURL	2.96	1.99	-0.66
50015.00	B10	M-007909-	dual specifi	54935.00	DUSP23	1.95	3.00	-1.00
50015.00	B11	M-014128-	p53-associa	23113.00	PARC	3.22	1.73	-0.58
50015.00	B12	M-014501-	plasticity-re	79948.00	PRG2	3.30	1.65	-0.55
50015.00	B13	M-003530-	RAD51 hom	5888.00	RAD51	12.70	**7.75**	2.58
50015.00	B14	M-009673-	FK506 bindi	23770.00	FKBP8	2.83	2.12	-0.71
50015.00	B15	M-006550-	receptor-as	5913.00	RAPSN	6.24	1.29	0.43
50015.00	B16	M-003569-	dual specifi	1852.00	DUSP9	1.06	3.89	-1.29
50015.00	B17	M-004087-	ring-box 1	9978.00	RBX1	2.32	2.63	-0.88
50015.00	B18	M-007894-	dual specifi	1845.00	DUSP3	1.93	3.02	-1.01
50015.00	B19	M-006923-	tripartite m	10206.00	TRIM13	8.96	4.01	1.33
50015.00	B20	M-007893-	dual specifi	63904.00	DUSP21	6.84	1.89	0.63
50015.00	B21	M-006584-	polycomb g	7703.00	PCGF2	2.31	2.64	-0.88
50015.00	B23	M-006942-	ring finger	11236.00	RNF139	6.56	1.61	0.53
50015.00	C02	M-012431-	F-box and	26259.00	FBXW8	2.24	2.71	-0.90
50015.00	C04	M-004264-	F-box and	55294.00	FBXW7	4.27	0.68	-0.23
50015.00	C05	M-006059-	ubiquitin ca	7347.00	UCHL3	26.31	**21.36**	7.10

50015.00	C06	M-009706-	split hand/f	26226.00	SHFM3P1	4.82	0.13	-0.05
50015.00	C07	M-006060-	ubiquitin ca	51377.00	UCHL5	4.21	0.74	-0.25
50015.00	C08	M-012427-	F-box and W	26190.00	FBXW2	3.48	1.47	-0.49
50015.00	C09	M-006061-	ubiquitin sp	7398.00	USP1	1.19	3.76	-1.25
50015.00	C10	M-012469-	F-box prote	26268.00	FBXO9	3.56	1.39	-0.46
50015.00	C11	M-006062-	ubiquitin sp	9100.00	USP10	2.57	2.38	-0.79
50015.00	C12	M-013606-	F-box prote	25793.00	FBXO7	3.90	1.05	-0.35
50015.00	C13	M-006063-	ubiquitin sp	8237.00	USP11	2.23	2.72	-0.90
50015.00	C14	M-013314-	F-box prote	26270.00	FBXO6	14.89	9.94	3.30
50015.00	C15	M-027148-	ubiquitin sp	219333.00	USP12	6.16	1.21	0.40
50015.00	C16	M-012434-	F-box prote	26271.00	FBXO5	1.30	3.65	-1.21
50015.00	C17	M-006064-	ubiquitin sp	8975.00	USP13	2.14	2.81	-0.93
50015.00	C18	M-012433-	F-box prote	26272.00	FBXO4	2.61	2.34	-0.78
50015.00	C19	M-006065-	ubiquitin sp	9097.00	USP14	3.26	1.69	-0.56
50015.00	C20	M-012432-	F-box prote	26273.00	FBXO3	6.40	1.45	0.48
50015.00	C21	M-006066-	ubiquitin sp	9958.00	USP15	3.28	1.67	-0.56
50015.00	C23	M-006067-	ubiquitin sp	10600.00	USP16	3.50	1.45	-0.48
50015.00	D02	M-007892-	dual specifi	142679.00	DUSP19	7.12	2.17	0.72
50015.00	D04	M-007891-	dual specifi	150290.00	DUSP18	2.42	2.53	-0.84
50015.00	D05	M-006912-	ring finger p	9781.00	RNF144	3.61	1.34	-0.45
50015.00	D06	M-007890-	dual specifi	80824.00	DUSP16	2.12	2.83	-0.94
50015.00	D07	M-021419-	ring finger p	55072.00	RNF31	1.91	3.04	-1.01
50015.00	D08	M-008484-	dual specifi	128853.00	DUSP15	7.08	2.13	0.71
50015.00	D09	M-007136-	ring finger p	140545.00	RNF32	13.04	8.09	2.69
50015.00	D10	M-007888-	dual specifi	11072.00	DUSP14	10.55	5.60	1.86
50015.00	D11	M-007144-	ring finger p	152006.00	RNF38	3.15	1.80	-0.60
50015.00	D12	M-007887-	dual specifi	51207.00	DUSP13	3.16	1.79	-0.60
50015.00	D13	M-006559-	ring finger p	6049.00	RNF6	4.17	0.78	-0.26
50015.00	D14	M-007886-	dual specifi	11266.00	DUSP12	10.13	5.18	1.72
50015.00	D15	M-006907-	ring finger p	9616.00	RNF7	8.01	3.06	1.02
50015.00	D16	M-017951-	dolichyl pyr	57171.00	DOLPP1	11.67	6.72	2.23
50015.00	D17	M-006900-	ring finger p	9025.00	RNF8	7.24	2.29	0.76
50015.00	D18	M-009326-	CTD (carbox	9150.00	CTDP1	4.13	0.82	-0.27
50015.00	D19	M-013956-	F-box and W	6468.00	FBXW4	4.32	0.63	-0.21
50015.00	D20	M-008107-	transmemb	93492.00	TPTE2	5.18	0.23	0.07
50015.00	D21	M-012598-	seven in abs	6477.00	SIAH1	7.10	2.15	0.71
50015.00	D23	M-003323-	S-phase kin	6500.00	SKP1A	2.21	2.74	-0.91
50015.00	E02	M-019192-	F-box prote	26260.00	FBXO25	6.26	1.31	0.43
50015.00	E04	M-010812-	F-box prote	26263.00	FBXO22	8.62	3.67	1.22
50015.00	E05	M-004236-	ubiquitin sp	11274.00	USP18	1.75	3.20	-1.06
50015.00	E06	M-012429-	F-box prote	26232.00	FBXO2	10.73	5.78	1.92
50015.00	E07	M-006068-	ubiquitin sp	10869.00	USP19	9.42	4.47	1.48
50015.00	E08	M-012428-	F-box prote	80204.00	FBXO11	1.82	3.13	-1.04
50015.00	E09	M-006069-	ubiquitin sp	9099.00	USP2	4.33	0.62	-0.21

50015.00	E10	M-026138-	F-box prote	26267.00	FBXO10	13.95	**9.00**	2.99
50015.00	E11	M-006070-	ubiquitin sp	10868.00	USP20	3.21	1.74	-0.58
50015.00	E12	M-012426-	leucine rich	26231.00	LRRC29	5.80	0.85	0.28
50015.00	E13	M-006071-	ubiquitin sp	27005.00	USP21	16.86	**11.91**	3.96
50015.00	E14	M-012457-	F-box and le	23194.00	FBXL7	5.53	0.58	0.19
50015.00	E15	M-006072-	ubiquitin sp	23326.00	USP22	9.65	4.70	1.56
50015.00	E16	M-012425-	F-box and le	26233.00	FBXL6	1.26	3.69	-1.23
50015.00	E17	M-006073-	ubiquitin sp	23358.00	USP24	3.06	1.89	-0.63
50015.00	E18	M-012424-	F-box and le	26234.00	FBXL5	7.86	2.91	0.97
50015.00	E19	M-006074-	ubiquitin sp	29761.00	USP25	8.09	3.14	1.04
50015.00	E20	M-013564-	F-box and le	26235.00	FBXL4	4.44	0.51	-0.17
50015.00	E21	M-006075-	ubiquitin sp	83844.00	USP26	7.00	2.05	0.68
50015.00	E23	M-006076-	ubiquitin sp	57646.00	USP28	1.87	3.08	-1.02
50015.00	F02	M-009328-	protein tyro	10076.00	PTPRU	6.46	1.51	0.50
50015.00	F04	M-008509-	protein tyro	5784.00	PTPN14	4.94	0.01	0.00
50015.00	F05	M-003324-	S-phase kina	6502.00	SKP2	19.03	**14.08**	4.68
50015.00	F06	M-032265-	phosphatas	11191.00	PTENP1	6.31	1.36	0.45
50015.00	F07	M-006448-	helicase-like	6596.00	HLTF	6.83	1.88	0.62
50015.00	F08	M-003023-	phosphatas	5728.00	PTEN	3.93	1.02	-0.34
50015.00	F09	M-007191-	SMAD speci	57154.00	SMURF1	1.45	3.50	-1.17
50015.00	F10	M-032264-	phosphoser	8781.00	PSPHL	2.06	2.89	-0.96
50015.00	F11	M-007194-	SMAD speci	64750.00	SMURF2	4.80	0.15	-0.05
50015.00	F12	M-017077-	protein pho	5507.00	PPP1R3C	4.31	0.64	-0.21
50015.00	F13	M-006563-	tripartite m	6737.00	TRIM21	8.48	3.53	1.17
50015.00	F14	M-004554-	protein pho	8493.00	PPM1D	14.77	**9.82**	3.26
50015.00	F15	M-007201-	STIP1 homo	10273.00	STUB1	3.48	1.47	-0.49
50015.00	F16	M-011500-	phosphatidi	8612.00	PPAP2C	4.90	0.05	-0.02
50015.00	F17	M-010541-	transcriptio	6921.00	TCEB1	4.82	0.13	-0.05
50015.00	F18	M-017312-	phosphatidi	8613.00	PPAP2B	4.28	0.67	-0.22
50015.00	F19	M-020048-	topoisomer	10210.00	TOPORS	6.95	2.00	0.66
50015.00	F20	M-008036-	myotubular	4534.00	MTM1	14.57	**9.62**	3.19
50015.00	F21	M-017305-	TRIAD3 prot	54476.00	TRIAD3	41.87	**36.92**	12.27
50015.00	F23	M-005392-	tripartite m	51592.00	TRIM33	12.92	**7.97**	2.65
50015.00	G02	M-012423-	F-box and le	26223.00	FBXL21	5.60	0.65	0.21
50015.00	G04	M-012422-	F-box and le	26224.00	FBXL3	0.78	4.17	-1.39
50015.00	G05	M-006077-	ubiquitin sp	57663.00	USP29	13.57	**8.62**	2.86
50015.00	G06	M-013562-	F-box and le	25827.00	FBXL2	1.05	3.90	-1.30
50015.00	G07	M-006078-	ubiquitin sp	9960.00	USP3	6.98	2.03	0.67
50015.00	G08	M-012458-	F-box and le	22992.00	FBXL11	5.26	0.31	0.10
50015.00	G09	M-021294-	ubiquitin sp	84749.00	USP30	5.99	1.04	0.35
50015.00	G10	M-021426-	hect domair	26091.00	HERC4	5.28	0.33	0.11
50015.00	G11	M-022513-	ubiquitin sp	57478.00	USP31	6.62	1.67	0.55
50015.00	G12	M-007189-	E3 ubiquitin	51366.00	EDD1	3.18	1.77	-0.59
50015.00	G13	M-006081-	ubiquitin sp	23032.00	USP33	5.70	0.75	0.25

50015.00	G14	M-020323-	CCR4-NOT t	4850.00	CNOT4	11.90	**6.95**	2.31
50015.00	G15	M-006083-	ubiquitin sp	57558.00	USP35	2.46	2.49	-0.83
50015.00	G16	M-007018-	checkpoint	55743.00	CHFR	5.19	0.24	0.08
50015.00	G17	M-006084-	ubiquitin sp	57602.00	USP36	1.70	3.25	-1.08
50015.00	G18	M-009774-	chromodom	1108.00	CHD4	6.62	1.67	0.55
50015.00	G19	M-006085-	ubiquitin sp	57695.00	USP37	2.70	2.25	-0.75
50015.00	G20	M-005174-	hect domai	51191.00	HERC5	6.41	1.46	0.48
50015.00	G21	M-006086-	ubiquitin sp	84640.00	USP38	9.07	4.12	1.37
50015.00	G23	M-004974-	ubiquitin sp	7375.00	USP4	2.37	2.58	-0.86
50015.00	H02	M-021508-	protein pho	333926.00	PPM1J	0.60	4.35	-1.45
50015.00	H04	M-029988-	protein tyro	114971.00	PTPMT1	4.57	0.38	-0.13
50015.00	H05	M-006538-	tripartite m	4591.00	TRIM37	3.18	1.77	-0.59
50015.00	H06	M-004152-	inositol poly	3636.00	INPPL1	2.84	2.11	-0.70
50015.00	H07	M-006924-	TRAF intera	10293.00	TRAIP	4.53	0.42	-0.14
50015.00	H08	M-006896-	epilepsy, pr	7957.00	EPM2A	2.71	2.24	-0.75
50015.00	H09	M-006949-	U-box doma	22888.00	UBOX5	3.54	1.41	-0.47
50015.00	H10	M-007885-	dual specifi	8446.00	DUSP11	4.90	0.05	-0.02
50015.00	H11	M-007197-	ubiquitin pr	89910.00	UBE3B	2.06	2.89	-0.96
50015.00	H12	M-013777-	CTD (carbox	58190.00	CTDSP1	8.19	3.24	1.07
50015.00	H13	M-007202-	ubiquitinati	10277.00	UBE4B	1.92	3.03	-1.01
50015.00	H14	M-003228-	cell division	995.00	CDC25C	5.56	0.61	0.20
50015.00	H15	M-010691-	ubiquitin pr	197131.00	UBR1	0.65	4.30	-1.43
50015.00	H16	M-003227-	cell division	994.00	CDC25B	3.34	1.61	-0.54
50015.00	H17	M-006977-	ubiquitin-lik	29128.00	UHRF1	4.35	0.60	-0.20
50015.00	H18	M-003226-	cell division	993.00	CDC25A	3.06	1.89	-0.63
50015.00	H19	M-006571-	Wolf-Hirsch	7468.00	WHSC1	3.53	1.42	-0.47
50015.00	H20	M-003470-	CDC14 cell c	8555.00	CDC14B	8.63	3.68	1.22
50015.00	H21	M-004251-	WW domai	11059.00	WWP1	13.67	**8.72**	2.90
50015.00	H23	M-004252-	WW domai	11060.00	WWP2	4.47	0.48	-0.16
50015.00	I02	M-006962-	Cas-Br-M (m	23624.00	CBLC	2.15	2.80	-0.93
50015.00	I04	M-006954-	ubiquitin pr	23304.00	UBR2	6.85	1.90	0.63
50015.00	I05	M-006089-	ubiquitin sp	84132.00	USP42	3.78	1.17	-0.39
50015.00	I06	M-006932-	RanBP-type	10616.00	RBCK1	1.43	3.52	-1.17
50015.00	I07	M-006091-	ubiquitin sp	84101.00	USP44	9.06	4.11	1.36
50015.00	I08	M-003463-	beta-transd	8945.00	BTRC	5.19	0.24	0.08
50015.00	I09	M-006092-	ubiquitin sp	64854.00	USP46	6.10	1.15	0.38
50015.00	I10	M-003461-	breast canc	672.00	BRCA1	1.61	3.34	-1.11
50015.00	I11	M-006095-	ubiquitin sp	8078.00	USP5	6.86	1.91	0.63
50015.00	I12	M-005230-	BMI1 polyco	648.00	BMI1	8.39	3.44	1.14
50015.00	I13	M-021192-	ubiquitin sp	9924.00	USP52	8.13	3.18	1.06
50015.00	I14	M-004392-	baculoviral	112401.00	BIRC8	4.17	0.78	-0.26
50015.00	I15	M-006096-	ubiquitin sp	9098.00	USP6	2.27	2.68	-0.89
50015.00	I16	M-006988-	PHD finger	51317.00	PHF21A	1.58	3.37	-1.12
50015.00	I17	M-006097-	ubiquitin sp	7874.00	USP7	5.34	0.39	0.13

50015.00	I18	M-004386-	bifunctional	51283.00	BFAR	8.43	3.48	1.15
50015.00	I19	M-005203-	ubiquitin sp	9101.00	USP8	3.97	0.98	-0.33
50015.00	I20	M-019984-	ariadne hon	25820.00	ARIH1	4.48	0.47	-0.16
50015.00	I21	M-006099-	ubiquitin sp	8239.00	USP9X	5.40	0.45	0.15
50015.00	I23	M-006100-	ubiquitin sp	8287.00	USP9Y	7.24	2.29	0.76
50015.00	J02	M-003469-	CDC14 cell c	8556.00	CDC14A	4.63	0.32	-0.11
50015.00	J04	M-009262-	acid phosph	55.00	ACPP	3.88	1.07	-0.36
50015.00	J05	M-007180-	hect domair	8924.00	HERC2	5.15	0.20	0.07
50015.00	J06	M-019058-	acid phosph	52.00	ACP1	3.45	1.50	-0.50
50015.00	J07	M-006541-	nuclear trar	4799.00	NFX1	11.46	6.51	2.16
50015.00	J08	M-011888-	phosphoser	5723.00	PSPH	11.21	6.26	2.08
50015.00	J09	M-006906-	ring finger p	9604.00	RNF14	1.67	3.28	-1.09
50015.00	J10	M-016119-	protein pho	5535.00	PPP3R2	2.67	2.28	-0.76
50015.00	J11	M-006561-	seven in abs	6478.00	SIAH2	2.20	2.75	-0.92
50015.00	J12	M-012261-	calcium and	10519.00	CIB1	3.88	1.07	-0.36
50015.00	J13	M-006522-	autocrine m	267.00	AMFR	9.86	4.91	1.63
50015.00	J14	M-008300-	protein pho	5530.00	PPP3CA	7.84	2.89	0.96
50015.00	J15	M-007182-	thyroid horr	9320.00	TRIP12	6.23	1.28	0.43
50015.00	J16	M-009615-	acid phosph	54.00	ACP5	6.25	1.30	0.43
50015.00	J17	M-003003-	Cas-Br-M (n	867.00	CBL	10.19	5.24	1.74
50015.00	J18	M-009595-	kinesin fami	9371.00	KIF3B	5.34	0.39	0.13
50015.00	J19	M-005198-	TNF recepto	7186.00	TRAF2	9.82	4.87	1.62
50015.00	J20	M-006849-	kinesin fami	81930.00	KIF18A	3.10	1.85	-0.62
50015.00	J21	M-005252-	TNF recepto	7187.00	TRAF3	7.17	2.22	0.74
50015.00	J23	M-006568-	TNF recepto	7188.00	TRAF5	6.30	1.35	0.45
50015.00	K02	M-003200-	anaphase pr	29882.00	ANAPC2	10.34	5.39	1.79
50015.00	K04	M-021035-	anaphase pr	51434.00	ANAPC7	5.11	0.16	0.05
50015.00	K05	M-007179-	hect domair	8916.00	HERC3	10.31	5.36	1.78
50015.00	K06	M-013642-	anaphase pr	29945.00	ANAPC4	12.06	7.11	2.36
50015.00	K07	M-015029-	F-box and le	84961.00	FBXL20	1.96	2.99	-1.00
50015.00	K08	M-006992-	APC11 anap	51529.00	ANAPC11	2.80	2.15	-0.71
50015.00	K09	M-006523-	tripartite m	373.00	TRIM23	3.33	1.62	-0.54
50015.00	K10	M-007200-	ubiquitinati	9354.00	UBE4A	6.78	1.83	0.61
50015.00	K11	M-003873-	BRCA1 asso	580.00	BARD1	6.31	1.36	0.45
50015.00	K12	M-009387-	ubiquitin-co	7321.00	UBE2D1	5.74	0.79	0.26
50015.00	K13	M-023015-	chromodom	1107.00	CHD3	2.46	2.49	-0.83
50015.00	K14	M-003603-	Parkinson d	5071.00	PARK2	6.11	1.16	0.38
50015.00	K15	M-004086-	cullin 1	8454.00	CUL1	7.80	2.85	0.95
50015.00	K16	M-006536-	Mdm4, tran	4194.00	MDM4	4.72	0.23	-0.08
50015.00	K17	M-007277-	cullin 2	8453.00	CUL2	5.77	0.82	0.27
50015.00	K18	M-003279-	Mdm2 p53	4193.00	MDM2	8.81	3.86	1.28
50015.00	K19	M-010224-	cullin 3	8452.00	CUL3	3.29	1.66	-0.55
50015.00	K20	M-003230-	cell division	997.00	CDC34	5.74	0.79	0.26
50015.00	K21	M-012610-	cullin 4A	8451.00	CUL4A	7.52	2.57	0.85

50015.00	K23	M-017965-	cullin 4B	8450.00	CUL4B	4.86	0.09	-0.03
50015.00	L02	M-008559-	kinesin fami	3798.00	KIF5A	3.24	1.71	-0.57
50015.00	L04	M-004956-	kinesin fami	9493.00	KIF23	8.91	3.96	1.31
50015.00	L05	M-004712-	TNF recept	7189.00	TRAF6	6.84	1.89	0.63
50015.00	L06	M-004957-	kinesin fami	10112.00	KIF20A	3.03	1.92	-0.64
50015.00	L07	M-006525-	deltex hom	1840.00	DTX1	3.74	1.21	-0.40
50015.00	L08	M-022067-	kinesin fami	57576.00	KIF17	1.23	3.72	-1.24
50015.00	L09	M-005387-	tripartite m	8805.00	TRIM24	4.06	0.89	-0.30
50015.00	L10	M-003319-	kinesin fami	9928.00	KIF14	6.00	1.05	0.35
50015.00	L11	M-022564-	ring finger a	89970.00	RSPRY1	3.90	1.05	-0.35
50015.00	L12	M-010236-	kinesin fami	547.00	KIF1A	6.02	1.07	0.35
50015.00	L13	M-005478-	dopamine r	1813.00	DRD2	7.93	2.98	0.99
50015.00	L14	M-003318-	M-phase ph	9585.00	MPHOSPH	7.36	2.41	0.80
50015.00	L15	M-005479-	dopamine r	1814.00	DRD3	3.25	1.70	-0.57
50015.00	L16	M-009317-	kinesin fami	23095.00	KIF1B	3.07	1.88	-0.63
50015.00	L17	M-005480-	dopamine r	1815.00	DRD4	4.81	0.14	-0.05
50015.00	L18	M-008345-	kinesin fami	84643.00	KIF2B	3.27	1.68	-0.56
50015.00	L19	M-005488-	egf-like mo	30817.00	EMR2	7.65	2.70	0.90
50015.00	L20	M-004960-	kinesin fami	56992.00	KIF15	2.76	2.19	-0.73
50015.00	L21	M-005639-	5-hydroxytr	3357.00	HTR2B	7.67	2.72	0.90
50015.00	L23	M-027433-	olfactory re	26245.00	OR2M4	3.58	1.37	-0.46
50015.00	M02	M-006950-	tripartite m	22954.00	TRIM32	1.02	3.93	-1.31
50015.00	M04	M-005046-	tripartite m	10155.00	TRIM28	5.77	0.82	0.27
50015.00	M05	M-005175-	hect domai	55008.00	HERC6	2.27	2.68	-0.89
50015.00	M06	M-006557-	ring finger p	6047.00	RNF4	6.87	1.92	0.64
50015.00	M07	M-007094-	polycomb g	84759.00	PCGF1	4.53	0.42	-0.14
50015.00	M08	M-006554-	ring finger p	6015.00	RING1	3.06	1.89	-0.63
50015.00	M09	M-006549-	recombinat	5896.00	RAG1	3.26	1.69	-0.56
50015.00	M10	M-006547-	promyelocy	5371.00	PML	2.58	2.37	-0.79
50015.00	M11	M-005137-	ubiquitin pr	7337.00	UBE3A	5.95	1.00	0.33
50015.00	M12	M-004828-	myeloid/lyn	8085.00	MLL2	3.33	1.62	-0.54
50015.00	M13	M-007185-	HECT, UBA	10075.00	HUWE1	3.32	1.63	-0.54
50015.00	M14	M-011291-	general tra	2966.00	GTF2H2	3.49	1.46	-0.49
50015.00	M15	M-003936-	von Hippel-	7428.00	VHL	8.98	4.03	1.34
50015.00	M16	M-004098-	baculoviral	331.00	BIRC4	8.42	3.47	1.15
50015.00	M17	M-008701-	anaphase pr	10393.00	ANAPC10	4.53	0.42	-0.14
50015.00	M18	M-004099-	baculoviral	330.00	BIRC3	3.29	1.66	-0.55
50015.00	M19	M-006936-	zinc finger,	10771.00	ZMYND11	5.98	1.03	0.34
50015.00	M20	M-004390-	baculoviral	329.00	BIRC2	10.32	5.37	1.78
50015.00	M21	M-006933-	cell growth	10668.00	CGRRF1	7.68	2.73	0.91
50015.00	M23	M-004444-	D4, zinc an	5977.00	DPF2	7.32	2.37	0.78
50015.00	N02	M-008338-	kinesin fami	3801.00	KIFC3	6.20	1.25	0.41
50015.00	N04	M-004958-	kinesin fami	3833.00	KIFC1	1.85	3.10	-1.03
50015.00	N05	M-011185-	oxytocin, pr	5020.00	OXT	4.97	0.02	0.00

50015.00	N06	M-004967-	kinesin fami	64147.00	KIF9	1.53	3.42	-1.14
50015.00	N07	M-003688-	purinergic r	5029.00	P2RY2	5.27	0.32	0.11
50015.00	N08	M-019811-	kinesin fami	3800.00	KIF5C	7.24	2.29	0.76
50015.00	N09	M-004576-	G protein-c	9052.00	GPRC5A	3.06	1.89	-0.63
50015.00	N10	M-008867-	kinesin fami	3799.00	KIF5B	3.33	1.62	-0.54
50015.00	N11	M-011781-	signal seque	6745.00	SSR1	7.23	2.28	0.76
50015.00	N12	M-004961-	kinesin fami	24137.00	KIF4A	3.66	1.29	-0.43
50015.00	N13	M-011782-	signal seque	6746.00	SSR2	3.59	1.36	-0.45
50015.00	N14	M-009469-	kinesin fami	3797.00	KIF3C	11.29	**6.34**	2.10
50015.00	N15	M-005466-	cholinergic	1133.00	CHRM5	1.83	3.12	-1.04
50015.00	N16	M-004964-	kinesin fami	11127.00	KIF3A	4.43	0.52	-0.18
50015.00	N17	M-005447-	cholecystok	887.00	CCKBR	4.40	0.55	-0.18
50015.00	N18	M-004955-	kinesin fami	11004.00	KIF2C	3.10	1.85	-0.62
50015.00	N19	M-005535-	G protein-c	221188.00	GPR114	0.58	4.37	-1.45
50015.00	N20	M-010082-	kinesin fami	3834.00	KIF25	5.92	0.97	0.32
50015.00	N21	M-005648-	leucine-rich	59352.00	LGR6	8.01	3.06	1.02
50015.00	N23	M-029816-	olfactory re	26492.00	OR8G2	6.67	1.72	0.57
50015.00	O02	M-012875-	Wolf-Hirsch	54904.00	WHSC1L1	2.48	2.47	-0.82
50015.00	O04	M-007076-	tripartite m	81603.00	TRIM8	2.25	2.70	-0.90
50015.00	O05	M-007114-	deltex hom	113878.00	DTX2	1.95	3.00	-1.00
50015.00	O06	M-006587-	tripartite m	7726.00	TRIM26	1.20	3.75	-1.25
50015.00	O07	M-013005-	F-box prote	114907.00	FBXO32	4.84	0.11	-0.04
50015.00	O08	M-006927-	tripartite m	10346.00	TRIM22	3.04	1.91	-0.64
50015.00	O09	M-019252-	LIM domain	4008.00	LMO7	2.69	2.26	-0.75
50015.00	O10	M-006908-	TNF recepto	9618.00	TRAF4	4.67	0.28	-0.10
50015.00	O11	M-014940-	ligand of nu	84708.00	LNX1	8.31	3.36	1.12
50015.00	O12	M-006551-	retinoblasto	5930.00	RBBP6	6.87	1.92	0.64
50015.00	O13	M-007120-	ring finger a	117584.00	RFFL	6.41	1.46	0.48
50015.00	O14	M-004591-	RAD18 hom	56852.00	RAD18	2.46	2.49	-0.83
50015.00	O15	M-014033-	mindbomb	57534.00	MIB1	2.81	2.14	-0.71
50015.00	O16	M-006548-	peroxisoma	5828.00	PXMP3	4.93	0.02	-0.01
50015.00	O17	M-006537-	midline 1 (C	4281.00	MID1	3.14	1.81	-0.60
50015.00	O18	M-019337-	peroxisoma	5193.00	PEX12	7.51	2.56	0.85
50015.00	O19	M-003281-	menage a tr	4331.00	MNAT1	13.80	**8.85**	2.94
50015.00	O20	M-006545-	peroxisome	5192.00	PEX10	13.98	**9.03**	3.00
50015.00	O21	M-007117-	ubiquitin-lik	115426.00	UHRF2	13.73	**8.78**	2.92
50015.00	O23	M-007048-	nuclear rece	64324.00	NSD1	17.23	**12.28**	4.08
50015.00	P02	M-004962-	kinesin fami	3835.00	KIF22	5.01	0.06	0.02
50015.00	P04	M-004969-	kinesin fami	55605.00	KIF21A	4.27	0.68	-0.23
50015.00	P05	M-005703-	G protein-c	338557.00	GPR120	4.36	0.59	-0.20
50015.00	P06	M-004959-	kinesin hea	3796.00	KIF2A	11.47	**6.52**	2.16
50015.00	P07	M-005746-	G protein-c	131601.00	GPR175	5.94	0.99	0.33
50015.00	P08	M-010354-	kinesin fami	10749.00	KIF1C	5.98	1.03	0.34
50015.00	P09	M-005446-	cholecystok	886.00	CCKAR	6.81	1.86	0.62

50015.00	P10	M-008257-	kinesin fami	63971.00	KIF13A	9.46	4.51	1.50
50015.00	P11	M-005465-	cholinergic	1132.00	CHRM4	3.80	1.15	-0.39
50015.00	P12	M-008252-	kinesin fami	113220.00	KIF12	15.85	**10.90**	3.62
50015.00	P13	M-005510-	galanin rece	2587.00	GALR1	10.56	5.61	1.86
50015.00	P14	M-003317-	kinesin fami	3832.00	KIF11	17.93	**12.98**	4.31
50015.00	P15	M-004141-	galanin rece	8484.00	GALR3	6.55	1.60	0.53
50015.00	P16	M-009495-	chromosom	55614.00	C20orf23	6.40	1.45	0.48
50015.00	P17	M-011292-	hypocretin	3060.00	HCRT	4.15	0.80	-0.27
50015.00	P18	M-022010-	kinesin fami	26153.00	KIF26A	9.92	4.97	1.65
50015.00	P19	M-005626-	hypocretin	3061.00	HCRTR1	16.77	**11.82**	3.93
50015.00	P20	M-003252-	centromere	1062.00	CENPE	25.03	**20.08**	6.67
50015.00	P21	M-005627-	hypocretin	3062.00	HCRTR2	24.59	**19.64**	6.53
50015.00	P23	M-008406-	GULP, engu	51454.00	GULP1	27.81	**22.86**	7.60
					mdn	4.95	2.03	
					3xmad		6.10	
					MADc		3.01	
50015.00	C22					24.04		22.15
50015.00	D22		2395.00	10.40		24.98		
50015.00	E22					25.54		20.35
50015.00	F22					28.74		31.11
					mn	25.83		24.54
					sd	2.04		5.76
50015.00	G22					4.68		2.74
50015.00	H22					2.75		1.49
50015.00	I22					5.45		3.04
50015.00	J22					4.11		3.35
					mn	4.25		2.65
					sd	1.14		0.81
						6.13		17.28
						3.42		2.44
						9.54		19.73
						21.58		21.88
						0.44		0.90
						0.56		0.10
50015.00	G03	M-003290-	polo-like kir	5347.00	PLK1 SMAF	3.15		38.46
50015.00	H03	M-003290-	polo-like kir	5347.00	PLK1 SMAF	5.98		3.00
50015.00	I03	D-001206-	siControl non-targeting			1.36		1.26
50015.00	J03	D-001206-	siControl non-targeting			5.54		2.12
50015.00	K03	D-001600-	siGLO RISC-free siRNA			11.88		5.54
50015.00	L03	D-001600-	siGLO RISC-free siRNA			11.38		4.05

% inf	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**		
16.34	**12.27**	4.21	7.48	1.57	0.50		
2.45	1.62	-0.55	1.45	4.46	-1.22		
8.67	4.60	1.58	9.37	3.46	1.04		
7.47	3.40	1.17	11.93	6.02	1.77		
5.04	0.97	0.33	8.22	2.31	0.71		
2.69	1.38	-0.47	2.66	3.25	-0.88		
16.10	**12.03**	4.13	5.36	0.55	-0.11		
6.93	2.86	0.98	5.14	0.77	-0.17		
9.78	5.71	1.96	10.66	4.75	1.41		
3.19	0.88	-0.30	11.09	5.18	1.53		
8.98	4.91	1.69	13.47	**7.56**	2.21		
2.88	1.19	-0.41	7.14	1.23	0.40		
7.81	3.74	1.29	9.72	3.81	1.14		
4.14	0.07	0.03	13.67	**7.76**	2.27		
0.86	3.21	-1.10	6.31	0.40	0.17		
1.76	2.31	-0.79	6.87	0.96	0.32		
16.91	**12.84**	4.41	40.11	**34.20**	9.83	y	
5.24	1.17	0.40	35.68	**29.77**	8.56		
1.84	2.23	-0.76	7.93	2.02	0.63		
0.83	3.24	-1.11	4.05	1.86	-0.48		
1.05	3.02	-1.03	7.37	1.46	0.47		
1.81	2.26	-0.78	4.51	1.40	-0.35		
4.18	0.11	0.04	10.20	4.29	1.28		
0.88	3.19	-1.09	7.72	1.81	0.57		
0.71	3.36	-1.15	6.59	0.68	0.25		
2.57	1.50	-0.51	7.66	1.75	0.55		
2.23	1.84	-0.63	2.10	3.81	-1.04		
1.50	2.57	-0.88	8.78	2.87	0.87		
3.02	1.05	-0.36	2.25	3.66	-1.00		
1.14	2.93	-1.00	3.15	2.76	-0.74		
4.22	0.15	0.05	21.47	**15.56**	4.50	x	toxic a,b
3.19	0.88	-0.30	4.37	1.54	-0.39		
3.24	0.83	-0.28	3.40	2.51	-0.67		
2.05	2.02	-0.69	6.43	0.52	0.20		
2.04	2.03	-0.69	0.32	5.59	-1.55		
2.61	1.46	-0.50	3.32	2.59	-0.69		
3.39	0.68	-0.23	10.65	4.74	1.41		
6.23	2.16	0.74	7.63	1.72	0.54		
0.29	3.78	-1.30	3.73	2.18	-0.57		
2.07	2.00	-0.68	6.56	0.65	0.24		
1.81	2.26	-0.77	3.97	1.94	-0.50		
3.01	1.06	-0.36	3.62	2.29	-0.60		
10.20	**6.13**	2.11	23.99	**18.08**	5.22	y	

6.23	2.16	0.74	8.64	2.73	0.83	
2.78	1.29	-0.44	7.43	1.52	0.49	
5.51	1.44	0.49	1.20	4.71	-1.30	
4.37	0.30	0.10	3.41	2.50	-0.67	
2.26	1.81	-0.62	6.78	0.87	0.30	
3.39	0.68	-0.23	1.33	4.58	-1.26	
5.46	1.39	0.48	4.83	1.08	-0.26	
2.44	1.63	-0.56	1.09	4.82	-1.33	
12.65	**8.58**	2.95	12.52	6.61	1.94	y
7.65	3.58	1.23	7.25	1.34	0.43	
8.02	3.95	1.36	5.51	0.40	-0.06	
5.07	1.00	0.34	3.94	1.97	-0.51	
10.14	**6.07**	2.08	2.86	3.05	-0.82	
7.16	3.09	1.06	5.64	0.27	-0.03	
6.94	2.87	0.98	6.33	0.42	0.17	
10.64	**6.57**	2.25	7.34	1.43	0.46	
4.19	0.12	0.04	4.11	1.80	-0.46	
5.49	1.42	0.49	2.55	3.36	-0.91	
4.52	0.45	0.15	2.19	3.72	-1.01	
3.74	0.33	-0.11	2.83	3.08	-0.83	
8.63	4.56	1.56	2.36	3.55	-0.97	
1.56	2.51	-0.86	1.19	4.72	-1.30	
6.28	2.21	0.76	2.93	2.98	-0.80	
11.37	**7.30**	2.51	10.78	4.87	1.44	y
4.69	0.62	0.21	2.79	3.12	-0.84	
10.64	**6.57**	2.25	1.92	3.99	-1.09	
3.10	0.97	-0.33	1.15	4.76	-1.31	
2.81	1.26	-0.43	2.26	3.65	-0.99	
13.51	**9.44**	3.24	8.63	2.72	0.83	
2.63	1.44	-0.49	3.18	2.73	-0.73	
7.51	3.44	1.18	3.26	2.65	-0.71	
8.64	4.57	1.57	5.11	0.80	-0.18	
4.59	0.52	0.18	5.96	0.05	0.06	
6.67	2.60	0.89	2.78	3.13	-0.84	
6.38	2.31	0.79	2.10	3.81	-1.04	
3.59	0.48	-0.16	8.48	2.57	0.79	
1.84	2.23	-0.76	1.38	4.53	-1.24	
4.60	0.53	0.18	10.02	4.11	1.22	
5.47	1.40	0.48	7.35	1.44	0.46	
0.83	3.24	-1.11	1.49	4.42	-1.21	
3.98	0.09	-0.03	11.18	5.27	1.56	
2.43	1.64	-0.56	5.72	0.20	-0.01	
2.11	1.96	-0.67	1.37	4.54	-1.25	
0.32	3.75	-1.29	4.19	1.72	-0.44	

3.45	0.62	-0.21	12.53	6.62	1.94		
1.93	2.14	-0.73	2.21	3.70	-1.01		
1.25	2.82	-0.96	5.09	0.82	-0.18		
8.05	3.98	1.37	9.29	3.38	1.02		
1.18	2.89	-0.99	7.84	1.93	0.60		
6.61	2.54	0.87	10.51	4.60	1.37		
2.30	1.77	-0.60	4.08	1.83	-0.47		
4.07	0.00	0.00	1.63	4.28	-1.17		
6.60	2.53	0.87	7.26	1.35	0.44		
6.50	2.43	0.84	7.45	1.54	0.49		
4.65	0.58	0.20	3.94	1.97	-0.51		
7.56	3.49	1.20	7.30	1.39	0.45		
2.38	1.69	-0.58	2.58	3.33	-0.90		
3.12	0.95	-0.33	1.87	4.04	-1.10		
8.97	4.90	1.68	6.03	0.12	0.08		
18.66	**14.59**	5.01	25.36	**19.45**	5.61	y	
5.26	1.19	0.41	7.88	1.97	0.61		
4.08	0.01	0.00	5.89	0.02	0.04		
3.45	0.62	-0.21	13.02	**7.11**	2.08		
7.39	3.32	1.14	8.20	2.29	0.70		
4.16	0.09	0.03	4.78	1.13	-0.27		
8.70	4.63	1.59	5.50	0.41	-0.07		
5.09	1.02	0.35	4.25	1.66	-0.43		
3.68	0.39	-0.13	7.93	2.02	0.63		
14.06	**9.99**	3.43	10.96	5.05	1.49	y	
3.27	0.80	-0.27	6.02	0.11	0.08		
4.34	0.27	0.09	5.16	0.75	-0.16		
6.87	2.80	0.96	6.77	0.86	0.30		
3.52	0.55	-0.19	6.74	0.83	0.29		
6.43	2.36	0.81	6.33	0.42	0.17		
8.21	4.14	1.42	9.09	3.18	0.96		
10.43	**6.36**	2.18	12.59	6.68	1.96	x	debris b,c
9.92	5.85	2.01	13.70	**7.79**	2.28	y	
4.06	0.01	0.00	6.29	0.38	0.16		
6.69	2.62	0.90	4.17	1.74	-0.45		
10.04	**5.97**	2.05	7.90	1.99	0.62	x	debris b,c
6.00	1.93	0.66	2.07	3.84	-1.05		
3.22	0.85	-0.29	7.72	1.81	0.57		
3.97	0.10	-0.03	6.06	0.15	0.09		
1.54	2.53	-0.87	2.99	2.92	-0.78		
7.83	3.76	1.29	5.60	0.31	-0.04		
4.46	0.39	0.13	7.94	2.03	0.63		
5.78	1.71	0.59	3.03	2.88	-0.77		
5.73	1.66	0.57	7.69	1.78	0.56		

9.72	5.65	1.94	9.57	3.66	1.10
2.19	1.88	-0.64	5.50	0.41	-0.07
13.26	**9.19**	3.15	4.59	1.32	-0.33
4.90	0.83	0.28	2.65	3.26	-0.88
24.57	**20.50**	7.03	7.95	2.04	0.63
5.86	1.79	0.61	2.70	3.21	-0.87
9.65	5.58	1.91	4.67	1.24	-0.30
13.84	**9.77**	3.35	10.25	4.34	1.29
2.56	1.51	-0.52	4.06	1.85	-0.48
1.57	2.50	-0.86	3.43	2.49	-0.66
3.61	0.46	-0.16	5.98	0.07	0.07
3.58	0.49	-0.17	1.79	4.12	-1.13
2.40	1.67	-0.57	3.47	2.44	-0.65
4.53	0.46	0.16	1.04	4.87	-1.34
1.44	2.63	-0.90	2.15	3.76	-1.02
3.10	0.97	-0.33	1.27	4.64	-1.28
4.35	0.28	0.10	4.16	1.75	-0.45
2.49	1.58	-0.54	2.45	3.46	-0.94
1.69	2.38	-0.81	3.95	1.96	-0.51
1.86	2.21	-0.76	0.79	5.12	-1.41
5.47	1.40	0.48	3.24	2.67	-0.71
1.04	3.03	-1.04	0.72	5.19	-1.43
3.51	0.56	-0.19	1.62	4.29	-1.18
3.37	0.70	-0.24	4.04	1.87	-0.49
0.60	3.47	-1.19	0.38	5.53	-1.53
1.61	2.46	-0.84	4.25	1.66	-0.42
6.80	2.73	0.94	3.67	2.24	-0.59
5.76	1.69	0.58	5.81	0.10	0.02
5.92	1.85	0.64	3.12	2.79	-0.75
1.48	2.59	-0.89	3.84	2.07	-0.54
2.44	1.63	-0.56	12.03	6.12	1.80
1.37	2.70	-0.93	6.23	0.32	0.14
3.02	1.05	-0.36	6.00	0.09	0.08
5.19	1.12	0.38	10.94	5.03	1.49
1.34	2.73	-0.93	8.27	2.36	0.73
1.87	2.20	-0.75	4.24	1.67	-0.43
1.77	2.30	-0.79	8.24	2.33	0.72
7.12	3.05	1.05	4.59	1.32	-0.33
4.58	0.51	0.17	6.03	0.12	0.09
2.69	1.38	-0.47	4.87	1.04	-0.25
1.61	2.46	-0.84	5.24	0.67	-0.14
3.98	0.09	-0.03	10.21	4.30	1.28
1.07	3.00	-1.03	6.87	0.96	0.32
5.40	1.33	0.46	5.06	0.85	-0.19

4.95	0.88	0.30	4.73	1.18	-0.29		
3.23	0.84	-0.29	4.83	1.08	-0.26		
2.34	1.73	-0.59	5.70	0.21	-0.01		
3.88	0.19	-0.07	5.75	0.16	0.01		
3.34	0.73	-0.25	9.90	3.99	1.19		
3.29	0.78	-0.27	3.77	2.14	-0.56		
3.69	0.38	-0.13	4.84	1.07	-0.26		
5.86	1.79	0.61	6.06	0.15	0.09		
3.78	0.29	-0.10	3.40	2.51	-0.67		
11.87	**7.80**	2.68	23.40	**17.49**	5.05	y	
6.94	2.87	0.98	9.73	3.82	1.14		
0.78	3.29	-1.13	3.97	1.94	-0.50		
1.98	2.09	-0.72	3.53	2.38	-0.63		
1.55	2.52	-0.86	1.79	4.12	-1.13		
0.71	3.36	-1.15	6.46	0.55	0.21		
5.35	1.28	0.44	12.72	6.81	2.00		
6.40	2.33	0.80	8.76	2.85	0.87		
6.21	2.14	0.74	6.98	1.07	0.36		
5.87	1.80	0.62	10.74	4.83	1.43		
9.03	4.96	1.70	6.71	0.80	0.28		
3.50	0.57	-0.19	2.24	3.67	-1.00		
5.01	0.94	0.32	6.52	0.61	0.22		
2.27	1.80	-0.62	3.50	2.41	-0.64		
2.49	1.58	-0.54	3.55	2.36	-0.63		
2.74	1.33	-0.45	6.55	0.64	0.23		
1.86	2.21	-0.76	10.22	4.31	1.28		
3.33	0.74	-0.25	11.47	5.56	1.64		
2.76	1.31	-0.45	6.22	0.31	0.14		
8.06	3.99	1.37	14.31	**8.40**	2.45	x	toxic b,c
2.85	1.22	-0.42	4.04	1.87	-0.48		
3.98	0.09	-0.03	4.47	1.44	-0.36		
3.30	0.77	-0.26	3.48	2.43	-0.64		
3.46	0.61	-0.21	6.16	0.25	0.12		
2.66	1.41	-0.48	9.83	3.92	1.17		
3.96	0.11	-0.04	7.46	1.55	0.49		
6.24	2.17	0.75	2.96	2.95	-0.79		
10.66	**6.59**	2.26	5.83	0.08	0.03		
6.05	1.98	0.68	10.47	4.56	1.35		
7.71	3.64	1.25	5.94	0.03	0.06		
4.37	0.30	0.10	8.64	2.73	0.83		
6.54	2.47	0.85	15.08	**9.17**	2.67		
7.58	3.51	1.20	4.89	1.02	-0.24		
4.75	0.68	0.23	8.71	2.80	0.85		
12.42	**8.35**	2.87	10.06	4.15	1.24		

5.33	1.26	0.43	4.47	1.44	-0.36
2.73	1.34	-0.46	3.26	2.65	-0.71
5.84	1.77	0.61	6.61	0.70	0.25
3.71	0.36	-0.12	5.88	0.03	0.04
1.07	3.00	-1.03	3.26	2.65	-0.71
1.60	2.47	-0.85	5.63	0.28	-0.03
0.12	3.95	-1.35	1.96	3.95	-1.08
6.55	2.48	0.85	11.66	5.75	1.69
7.84	3.77	1.30	8.45	2.54	0.78
2.91	1.16	-0.40	3.18	2.73	-0.73
2.79	1.28	-0.44	9.33	3.42	1.03
5.95	1.88	0.65	19.60	**13.69**	3.97
9.76	5.69	1.95	8.27	2.36	0.72
1.33	2.74	-0.94	4.69	1.22	-0.30
4.45	0.38	0.13	2.65	3.26	-0.88
7.04	2.97	1.02	6.59	0.68	0.24
10.94	**6.87**	2.36	9.44	3.53	1.06
8.90	4.83	1.66	4.39	1.52	-0.39
3.41	0.66	-0.22	9.52	3.61	1.08
16.16	**12.09**	4.15	6.42	0.51	0.20
9.42	5.35	1.84	3.40	2.51	-0.67
0.25	3.82	-1.31	1.69	4.22	-1.16
2.33	1.74	-0.59	7.54	1.63	0.52
2.67	1.40	-0.48	2.77	3.14	-0.85
3.48	0.59	-0.20	8.71	2.80	0.85
1.66	2.41	-0.82	3.38	2.53	-0.67
1.74	2.33	-0.80	4.71	1.20	-0.29
3.06	1.01	-0.35	6.42	0.51	0.20
2.23	1.84	-0.63	0.87	5.04	-1.39
5.08	1.01	0.35	6.22	0.31	0.14
1.68	2.39	-0.82	4.37	1.54	-0.39
7.09	3.02	1.04	10.17	4.26	1.27
3.16	0.91	-0.31	4.03	1.88	-0.49
5.87	1.80	0.62	4.84	1.07	-0.26
8.40	4.33	1.49	4.10	1.81	-0.47
7.36	3.29	1.13	2.13	3.78	-1.03
4.35	0.28	0.10	2.46	3.45	-0.93
6.36	2.29	0.79	2.00	3.91	-1.07
8.74	4.67	1.60	1.28	4.63	-1.27
17.58	**13.51**	4.64	6.02	0.11	0.08
13.70	**9.63**	3.30	9.08	3.17	0.96
1.07	3.00	-1.03	0.92	4.99	-1.38
0.94	3.13	-1.07	2.39	3.52	-0.96
3.20	0.87	-0.30	2.48	3.43	-0.93

1.05	3.02	-1.03	5.23	0.68	-0.14		
2.53	1.54	-0.53	1.97	3.94	-1.08		
1.90	2.17	-0.74	3.68	2.23	-0.59		
2.61	1.46	-0.50	4.85	1.06	-0.25		
0.37	3.70	-1.27	4.91	1.00	-0.24		
3.98	0.09	-0.03	7.53	1.62	0.51		
4.64	0.57	0.20	4.96	0.95	-0.22		
2.53	1.54	-0.53	2.75	3.16	-0.85		
10.18	**6.11**	2.10	6.74	0.83	0.29	x	toxic a,c
3.49	0.58	-0.20	7.53	1.62	0.51		
2.11	1.96	-0.67	3.90	2.01	-0.52		
2.71	1.36	-0.47	5.20	0.71	-0.15		
3.59	0.48	-0.16	7.94	2.03	0.63		
3.68	0.39	-0.13	2.41	3.50	-0.95		
4.63	0.56	0.19	2.44	3.47	-0.94		
11.32	**7.25**	2.49	6.86	0.95	0.32		
2.85	1.22	-0.42	8.35	2.44	0.75		
1.93	2.14	-0.73	4.41	1.50	-0.38		
1.15	2.92	-1.00	3.67	2.24	-0.59		
2.04	2.03	-0.70	6.46	0.55	0.21		
0.93	3.14	-1.08	4.07	1.84	-0.48		
5.99	1.92	0.66	9.66	3.75	1.12		
4.07	0.00	0.00	4.43	1.48	-0.37		
4.94	0.87	0.30	8.23	2.32	0.71		
6.65	2.58	0.89	10.67	4.76	1.41		
5.54	1.47	0.51	14.91	**9.00**	2.63		
6.07	2.00	0.69	7.32	1.41	0.45		
9.47	5.40	1.85	10.70	4.79	1.42		
4.82	0.75	0.26	7.21	1.30	0.42		
2.36	1.71	-0.59	4.63	1.28	-0.32		
2.65	1.42	-0.48	14.42	**8.51**	2.48		
7.05	2.98	1.02	3.46	2.45	-0.65		
11.65	**7.58**	2.60	7.70	1.79	0.56		
19.26	**15.19**	5.21	15.63	**9.72**	2.83	x	toxic a,b
14.29	**10.22**	3.51	6.35	0.44	0.18	x	toxic a,b
14.57	**10.50**	3.60	12.35	6.44	1.89	y	
5.83	1.76	0.61	3.01	2.90	-0.78		
3.84	0.23	-0.08	1.96	3.95	-1.08		
4.54	0.47	0.16	5.42	0.49	-0.09		
5.78	1.71	0.59	8.16	2.25	0.69		
6.62	2.55	0.88	17.40	**11.49**	3.34	x	toxic a,b,c
0.79	3.28	-1.13	4.87	1.04	-0.25		
1.18	2.89	-0.99	7.10	1.19	0.39		
5.93	1.86	0.64	7.26	1.35	0.44		

2.65	1.42	-0.49	10.17	4.26	1.27		
1.40	2.67	-0.91	6.62	0.71	0.25		
16.07	**12.00**	4.12	26.96	**21.05**	6.07	x	toxic a,b,c
4.23	0.16	0.06	8.67	2.76	0.84		
4.79	0.72	0.25	16.13	**10.22**	2.97	x	toxic a,b,c
4.02	0.05	-0.01	7.35	1.44	0.46		
1.27	2.80	-0.96	4.85	1.06	-0.25		
1.07	3.00	-1.03	1.96	3.95	-1.08		
2.87	1.20	-0.41	2.90	3.01	-0.81		
8.31	4.24	1.46	5.93	0.02	0.06		
3.27	0.80	-0.27	9.25	3.34	1.01		
7.54	3.47	1.19	12.39	6.48	1.90		
8.53	4.46	1.53	4.87	1.04	-0.25		
4.07	1.97		5.73	2.36			
	5.91			7.09			
	2.91			3.50			
	25.67						
	22.92						
	26.45						
	31.71						
	26.69						
	3.68						
	2.06						
	1.82						
	4.58						
	3.49						
	2.99						
	1.29						
	11.03						
	10.20						
	21.23						
	23.70						
	0.90						
	0.10						
	12.20						
	5.08						
	8.83						
	6.02						
	11.14						
	12.94						

						% inf	abs dev	robust Z	% inf
50016.00	A02	M-011688-	major histc	3123.00	HLA-DRB1	10.98	3.06	0.68	5.59
50016.00	A04	M-020310-	killer cell ir	57292.00	KIR2DL5A	10.92	3.00	0.67	7.43
50016.00	A05	M-008031-	serine/thre	51657.00	STYXL1	10.33	2.41	0.53	3.38
50016.00	A06	M-012316-	KDEL (Lys-/	11015.00	KDELR3	17.19	9.27	2.06	12.18
50016.00	A07	M-008037-	myotubula	8776.00	MTMR1	7.48	0.44	-0.10	6.35
50016.00	A08	M-006238-	potassium	131096.00	KCNH8	4.57	3.35	-0.74	3.92
50016.00	A09	M-008038-	myotubula	8898.00	MTMR2	7.65	0.27	-0.06	9.31
50016.00	A10	M-006237-	potassium	90134.00	KCNH7	8.18	0.26	0.06	4.45
50016.00	A11	M-008040-	myotubula	9110.00	MTMR4	5.57	2.35	-0.52	6.60
50016.00	A12	M-006234-	potassium	23415.00	KCNH4	5.55	2.37	-0.53	2.07
50016.00	A13	M-008309-	myotubula	9107.00	MTMR6	14.56	6.64	1.48	7.26
50016.00	A14	M-010707-	potassium	23416.00	KCNH3	7.38	0.54	-0.12	3.96
50016.00	A15	M-008041-	myotubula	9108.00	MTMR7	9.87	1.95	0.43	2.79
50016.00	A16	M-006233-	potassium	3757.00	KCNH2	8.40	0.48	0.11	5.61
50016.00	A17	M-008042-	myotubula	55613.00	MTMR8	8.82	0.90	0.20	5.74
50016.00	A18	M-006209-	inositol 1,4	3710.00	ITPR3	1.28	6.64	-1.48	2.41
50016.00	A19	M-022572-	pyruvate d	57546.00	PDP2	9.23	1.31	0.29	4.84
50016.00	A20	M-006207-	inositol 1,4	3708.00	ITPR1	7.49	0.43	-0.10	7.14
50016.00	A21	M-019103-	PH domain	23239.00	PHLPP	7.19	0.73	-0.16	3.87
50016.00	A23	M-009479-	protein ph	5475.00	PPEF1	10.69	2.77	0.61	3.68
50016.00	B02	M-004379-	BCL2-assoc	9530.00	BAG4	4.21	3.71	-0.83	1.75
50016.00	B04	M-010997-	arginine va	551.00	AVP	4.57	3.35	-0.75	2.44
50016.00	B05	M-013303-	ribosomal	3921.00	RPSA	11.41	3.49	0.77	4.14
50016.00	B06	M-011587-	agouti sign	434.00	ASIP	3.24	4.68	-1.04	4.86
50016.00	B07	M-020541-	linker for a	27040.00	LAT	5.47	2.45	-0.55	3.31
50016.00	B08	M-011215-	asialoglyco	433.00	ASGR2	1.55	6.37	-1.42	6.01
50016.00	B09	M-008015-	leptin rece	3953.00	LEPR	4.71	3.21	-0.72	2.17
50016.00	B10	M-017435-	amphiregu	374.00	AREG	14.69	6.77	1.50	3.52
50016.00	B11	M-011720-	leukemia ir	3976.00	LIF	15.84	7.92	1.76	5.91
50016.00	B12	M-017407-	apolipopro	23780.00	APOL2	5.86	2.06	-0.46	1.76
50016.00	B13	M-017168-	leukocyte i	10859.00	LILRB1	5.00	2.93	-0.65	2.36
50016.00	B14	M-007805-	angiopoiet	23452.00	ANGPTL2	2.72	5.20	-1.16	2.69
50016.00	B15	M-020017-	leukocyte i	10288.00	LILRB2	4.25	3.67	-0.82	2.95
50016.00	B16	M-007804-	angiopoiet	9068.00	ANGPTL1	13.35	5.43	1.21	3.35
50016.00	B17	M-017091-	leukocyte i	11006.00	LILRB4	3.41	4.51	-1.00	1.08
50016.00	B18	M-006315-	angiopoiet	285.00	ANGPT2	6.89	1.03	-0.23	3.75
50016.00	B19	M-017687-	leukocyte i	10990.00	LILRB5	8.10	0.18	0.04	3.02
50016.00	B20	M-007802-	angiopoiet	284.00	ANGPT1	5.61	2.31	-0.51	1.64
50016.00	B21	M-020750-	limb regior	55716.00	LMBR1L	3.48	4.44	-0.99	1.82
50016.00	B23	M-019609-	low density	4037.00	LRP3	9.53	1.61	0.36	6.95
50016.00	C02	M-017895-	CD300e mo	342510.00	CD300E	5.35	2.57	-0.57	4.63
50016.00	C04	M-012449-	leukocyte i	23547.00	LILRA4	8.37	0.45	0.10	3.92
50016.00	C05	M-012250-	protein ph	5470.00	PPEF2	3.97	3.95	-0.88	3.90

50016.00	C06	M-007981-	interleukin	163702.00	IL28RA	2.48	5.44	-1.21	3.32
50016.00	C07	M-008281-	protein ph	5495.00	PPM1B	3.68	4.24	-0.94	3.51
50016.00	C08	M-007976-	interleukin	149233.00	IL23R	3.97	3.95	-0.88	1.05
50016.00	C09	M-008964-	protein ph	22843.00	PPM1E	4.29	3.63	-0.81	4.28
50016.00	C10	M-007974-	interleukin	116379.00	IL22RA2	3.17	4.75	-1.06	4.11
50016.00	C11	M-009544-	protein ph	9647.00	PPM1F	7.27	0.65	-0.14	1.33
50016.00	C12	M-007969-	interleukin	53832.00	IL20RA	4.90	3.02	-0.67	4.66
50016.00	C13	M-005264-	protein ph	5496.00	PPM1G	3.27	4.65	-1.03	2.79
50016.00	C14	M-007961-	interleukin	11141.00	IL1RAPL1	4.71	3.21	-0.71	1.76
50016.00	C15	M-008679-	protein ph	151742.00	PPM1L	3.90	4.02	-0.89	3.25
50016.00	C16	M-007950-	interleukin	8807.00	IL18RAP	5.12	2.80	-0.62	1.31
50016.00	C17	M-008718-	protein ph	54704.00	PPM2C	14.49	6.57	1.46	3.71
50016.00	C18	M-007933-	interleukin	3597.00	IL13RA1	5.13	2.79	-0.62	7.89
50016.00	C19	M-008927-	protein ph	5499.00	PPP1CA	8.02	0.10	0.02	0.91
50016.00	C20	M-007928-	interleukin	3590.00	IL11RA	5.91	2.01	-0.45	1.39
50016.00	C21	M-008685-	protein ph	5500.00	PPP1CB	13.24	5.32	1.18	5.19
50016.00	C23	M-018795-	protein ph	84988.00	PPP1R16A	8.83	0.91	0.20	1.92
50016.00	D02	M-010991-	anti-Mulle	268.00	AMH	8.73	0.81	0.18	1.77
50016.00	D04	M-004574-	activated l	214.00	ALCAM	7.65	0.27	-0.06	1.86
50016.00	D05	M-003844-	low density	4041.00	LRP5	21.91	**13.99**	3.11	2.80
50016.00	D06	M-017362-	A kinase (P	10142.00	AKAP9	13.40	5.48	1.22	4.04
50016.00	D07	M-010608-	basal cell a	4059.00	BCAM	12.54	4.62	1.03	3.45
50016.00	D08	M-017300-	A kinase (P	11216.00	AKAP10	4.43	3.49	-0.78	0.62
50016.00	D09	M-008024-	CD163 mol	283316.00	CD163L1	6.82	1.10	-0.25	3.61
50016.00	D10	M-011204-	agouti rela	181.00	AGRP	3.67	4.25	-0.95	1.30
50016.00	D11	M-010611-	mannose-	4074.00	M6PR	6.72	1.20	-0.27	5.14
50016.00	D12	M-011199-	adrenome	133.00	ADM	5.63	2.29	-0.51	2.16
50016.00	D13	M-013568-	mastermin	84441.00	MAML2	4.69	3.23	-0.72	1.81
50016.00	D14	M-011403-	zona pellu	7783.00	ZP2	7.31	0.61	-0.14	2.81
50016.00	D15	M-008025-	macropha	8685.00	MARCO	8.81	0.89	0.20	4.39
50016.00	D16	M-008108-	interleukin	9466.00	IL27RA	8.29	0.37	0.08	4.46
50016.00	D17	M-010523-	mutated in	4163.00	MCC	6.76	1.16	-0.26	6.42
50016.00	D18	M-008592-	wingless-t	7484.00	WNT9B	3.18	4.74	-1.05	1.99
50016.00	D19	M-004570-	CD46 mole	4179.00	CD46	9.60	1.68	0.37	6.80
50016.00	D20	M-008392-	wingless-t	7483.00	WNT9A	4.17	3.75	-0.83	1.01
50016.00	D21	M-003908-	myeloproli	4352.00	MPL	10.39	2.47	0.55	2.34
50016.00	D23	M-008033-	progestin	164091.00	PAQR7	4.72	3.20	-0.71	1.91
50016.00	E02	M-009122-	taste rece	353164.00	TAS2R42	7.71	0.21	-0.05	0.41
50016.00	E04	M-017490-	HLA-G hist	3135.00	HLA-G	16.28	8.36	1.86	4.83
50016.00	E05	M-014386-	protein ph	79660.00	PPP1R3B	4.73	3.19	-0.71	0.70
50016.00	E06	M-012106-	major hist	3133.00	HLA-E	3.86	4.06	-0.90	1.71
50016.00	E07	M-021439-	protein ph	5509.00	PPP1R3D	7.29	0.63	-0.14	1.51
50016.00	E08	M-013204-	major hist	3125.00	HLA-DRB3	13.13	5.21	1.16	0.95
50016.00	E09	M-010259-	protein ph	5518.00	PPP2R1A	6.19	1.73	-0.38	2.54

50016.00	E10	M-013296-	major histo	3122.00	HLA-DRA	4.81	3.12	-0.69	1.24
50016.00	E11	M-017592-	protein ph	5519.00	PPP2R1B	3.90	4.02	-0.89	0.64
50016.00	E12	M-011687-	major histo	3119.00	HLA-DQB1	10.34	2.42	0.54	3.62
50016.00	E13	M-009352-	protein ph	5525.00	PPP2R5A	7.40	0.52	-0.12	2.22
50016.00	E14	M-013228-	major histo	3117.00	HLA-DQA1	11.29	3.37	0.75	4.04
50016.00	E15	M-009366-	protein ph	5526.00	PPP2R5B	13.37	5.45	1.21	6.73
50016.00	E16	M-013229-	major histo	3115.00	HLA-DPB1	3.99	3.93	-0.87	1.21
50016.00	E17	M-009433-	protein ph	5527.00	PPP2R5C	7.19	0.73	-0.16	4.37
50016.00	E18	M-011686-	major histo	3112.00	HLA-DOB	4.54	3.38	-0.75	3.00
50016.00	E19	M-009799-	protein ph	5528.00	PPP2R5D	10.06	2.14	0.48	3.96
50016.00	E20	M-019456-	major histo	3111.00	HLA-DOA	8.65	0.73	0.16	5.49
50016.00	E21	M-008531-	protein ph	5529.00	PPP2R5E	3.18	4.74	-1.06	3.33
50016.00	E23	M-010005-	protein ph	5533.00	PPP3CC	5.09	2.83	-0.63	2.17
50016.00	F02	M-009409-	wingless-ty	7479.00	WNT8B	3.89	4.03	-0.90	1.28
50016.00	F04	M-009331-	wingless-ty	7478.00	WNT8A	6.17	1.75	-0.39	1.39
50016.00	F05	M-012214-	membrane	931.00	MS4A1	9.63	1.71	0.38	3.65
50016.00	F06	M-003722-	wingless-ty	7477.00	WNT7B	3.69	4.23	-0.94	1.02
50016.00	F07	M-012893-	membrane	64231.00	MS4A6A	6.82	1.10	-0.25	1.24
50016.00	F08	M-009860-	wingless-ty	7475.00	WNT6	4.09	3.83	-0.85	1.90
50016.00	F09	M-003644-	membrane	58475.00	MS4A7	3.06	4.86	-1.08	2.09
50016.00	F10	M-009761-	wingless-ty	81029.00	WNT5B	4.62	3.30	-0.73	2.49
50016.00	F11	M-008767-	membrane	83661.00	MS4A8B	8.38	0.46	0.10	3.75
50016.00	F12	M-008659-	wingless-ty	54361.00	WNT4	2.30	5.62	-1.25	1.11
50016.00	F13	M-008035-	macrophag	4481.00	MSR1	4.79	3.13	-0.70	3.60
50016.00	F14	M-008538-	wingless-ty	89780.00	WNT3A	8.56	0.64	0.14	7.07
50016.00	F15	M-016944-	family with	23625.00	FAM89B	3.95	3.97	-0.88	1.11
50016.00	F16	M-009712-	wingless-ty	7473.00	WNT3	10.31	2.39	0.53	9.17
50016.00	F17	M-011089-	myocilin, t	4653.00	MYOC	6.21	1.71	-0.38	3.97
50016.00	F18	M-010345-	wingless-ty	7482.00	WNT2B	5.34	2.58	-0.57	1.83
50016.00	F19	M-020866-	natural cyt	9437.00	NCR1	6.93	0.99	-0.22	2.60
50016.00	F20	M-003938-	wingless-ty	7472.00	WNT2	7.46	0.46	-0.10	2.36
50016.00	F21	M-016894-	natural cyt	259197.00	NCR3	11.07	3.15	0.70	4.05
50016.00	F23	M-009340-	nerve grow	4804.00	NGFR	4.48	3.44	-0.76	2.73
50016.00	G02	M-013238-	major histo	3109.00	HLA-DMB	3.16	4.76	-1.06	8.78
50016.00	G04	M-017513-	major histo	3107.00	HLA-C	4.04	3.88	-0.86	4.33
50016.00	G05	M-019912-	protein ph	9989.00	PPP4R1	3.20	4.72	-1.05	3.29
50016.00	G06	M-013203-	major histo	3106.00	HLA-B	5.57	2.35	-0.52	1.70
50016.00	G07	M-009259-	protein ph	5536.00	PPP5C	7.96	0.04	0.01	2.79
50016.00	G08	M-012850-	major histo	3105.00	HLA-A	6.18	1.74	-0.39	1.51
50016.00	G09	M-009935-	protein ph	5537.00	PPP6C	5.18	2.74	-0.61	0.75
50016.00	G10	M-011051-	hemochro	3077.00	HFE	3.60	4.32	-0.96	1.88
50016.00	G11	M-006333-	protein tyr	7803.00	PTP4A1	7.25	0.67	-0.15	4.64
50016.00	G12	M-016696-	hepatitis A	84868.00	HAVCR2	5.58	2.34	-0.52	8.84
50016.00	G13	M-009078-	protein tyr	8073.00	PTP4A2	7.73	0.19	-0.04	2.70

50016.00	G14	M-007919-	glutamate	81488.00	GRINL1A	15.83	7.91	1.76	1.56
50016.00	G15	M-006859-	protein tyr	11156.00	PTP4A3	9.42	1.50	0.33	3.26
50016.00	G16	M-006199-	glutamate	116443.00	GRIN3A	9.16	1.24	0.27	3.02
50016.00	G17	M-008584-	protein tyr	138639.00	PTPDC1	6.15	1.77	-0.39	1.84
50016.00	G18	M-006193-	glutamate	2901.00	GRIK5	13.41	5.49	1.22	2.37
50016.00	G19	M-008742-	protein tyr	9200.00	PTPLA	12.35	4.43	0.98	1.72
50016.00	G20	M-006192-	glutamate	2900.00	GRIK4	30.56	**22.64**	5.03	4.48
50016.00	G21	M-027184-	protein tyr	201562.00	PTPLB	26.37	**18.45**	4.10	1.97
50016.00	G23	M-003529-	protein tyr	5770.00	PTPN1	16.19	8.27	1.84	0.94
50016.00	H02	M-010821-	wingless-ty	51384.00	WNT16	6.14	1.78	-0.40	6.48
50016.00	H04	M-009474-	wingless-ty	7481.00	WNT11	2.94	4.98	-1.11	1.24
50016.00	H05	M-008045-	reticulon 4	349667.00	RTN4RL2	1.23	6.69	-1.49	3.19
50016.00	H06	M-007759-	wingless-ty	7480.00	WNT10B	1.82	6.10	-1.36	1.56
50016.00	H07	M-008046-	reticulon 4	146760.00	RTN4RL1	6.65	1.27	-0.28	11.70
50016.00	H08	M-008232-	wingless-ty	80326.00	WNT10A	7.60	0.32	-0.07	3.33
50016.00	H09	M-016694-	CD300 mol	146722.00	CD300LF	8.06	0.14	0.03	8.40
50016.00	H10	M-003937-	wingless-ty	7471.00	WNT1	6.40	1.52	-0.34	4.15
50016.00	H11	M-008047-	Niemann-P	4864.00	NPC1	13.04	5.12	1.14	4.11
50016.00	H12	M-012141-	WAS prote	10163.00	WASF2	4.25	3.67	-0.82	11.20
50016.00	H13	M-012507-	neuronal p	23467.00	NPTXR	4.21	3.71	-0.82	4.84
50016.00	H14	M-010628-	unc-5 hom	8633.00	UNC5C	5.23	2.69	-0.60	2.65
50016.00	H15	M-017721-	neuropilin	8828.00	NRP2	10.84	2.92	0.65	3.95
50016.00	H16	M-021392-	unc-5 hom	219699.00	UNC5B	8.25	0.33	0.07	2.52
50016.00	H17	M-017920-	neutral sph	8439.00	NSMAF	17.28	**9.36**	2.08	4.34
50016.00	H18	M-012607-	TYRO prote	7305.00	TYROBP	6.91	1.01	-0.22	3.41
50016.00	H19	M-017889-	neuronal P	266743.00	NPAS4	9.30	1.38	0.31	2.86
50016.00	H20	M-005263-	transient r	162514.00	TRPV3	14.56	6.64	1.48	8.86
50016.00	H21	M-012922-	osteoclast-	126014.00	OSCAR	4.44	3.48	-0.77	1.39
50016.00	H23	M-008050-	oncostatin	9180.00	OSMR	6.93	0.99	-0.22	1.62
50016.00	I02	M-006191-	glutamate	2899.00	GRIK3	3.64	4.28	-0.95	4.80
50016.00	I04	M-006190-	glutamate	2898.00	GRIK2	53.73	**45.81**	10.18	5.45
50016.00	I05	M-003947-	protein tyr	5781.00	PTPN11	6.70	1.22	-0.27	6.25
50016.00	I06	M-006188-	glutamate	2895.00	GRID2	13.35	5.43	1.21	7.43
50016.00	I07	M-008064-	protein tyr	5782.00	PTPN12	10.93	3.01	0.67	6.53
50016.00	I08	M-006187-	glutamate	2893.00	GRIA4	5.88	2.04	-0.45	3.40
50016.00	I09	M-008065-	protein tyr	5783.00	PTPN13	20.84	**12.92**	2.87	10.91
50016.00	I10	M-006186-	glutamate	2892.00	GRIA3	9.78	1.86	0.41	9.30
50016.00	I11	M-009379-	protein tyr	11099.00	PTPN21	9.84	1.92	0.43	4.81
50016.00	I12	M-006185-	glutamate	2891.00	GRIA2	7.57	0.35	-0.08	4.64
50016.00	I13	M-008066-	protein tyr	26191.00	PTPN22	4.09	3.83	-0.85	2.77
50016.00	I14	M-006184-	glutamate	2890.00	GRIA1	8.07	0.15	0.03	8.33
50016.00	I15	M-009417-	protein tyr	25930.00	PTPN23	5.38	2.54	-0.57	5.55
50016.00	I16	M-012701-	growth fac	2886.00	GRB7	8.39	0.47	0.10	3.67
50016.00	I17	M-009372-	protein tyr	5774.00	PTPN3	8.16	0.24	0.05	3.88

50016.00	I18	M-019810- growth fac	2888.00	GRB14	9.16	1.24	0.27	6.43
50016.00	I19	M-009489- protein tyr	5775.00	PTPN4	9.94	2.02	0.45	13.43
50016.00	I20	M-015313- growth fac	2887.00	GRB10	11.08	3.16	0.70	6.55
50016.00	I21	M-008394- protein tyr	5778.00	PTPN7	15.96	8.04	1.79	8.35
50016.00	I23	M-008832- protein tyr	5780.00	PTPN9	10.70	2.78	0.62	7.63
50016.00	J02	M-004194- transient re	51393.00	TRPV2	4.25	3.67	-0.82	1.00
50016.00	J04	M-006515- transient re	54795.00	TRPM4	13.04	5.12	1.14	10.12
50016.00	J05	M-004435- programm	5133.00	PDCD1	2.52	5.40	-1.20	1.87
50016.00	J06	M-006512- transient re	57113.00	TRPC7	14.24	6.32	1.40	9.75
50016.00	J07	M-011350- period hon	5187.00	PER1	13.29	5.37	1.19	6.95
50016.00	J08	M-006510- transient re	7223.00	TRPC4	10.43	2.51	0.56	2.86
50016.00	J09	M-012977- period hon	8864.00	PER2	5.69	2.23	-0.50	2.80
50016.00	J10	M-017772- CD300 mol	124599.00	CD300LB	15.99	8.07	1.79	6.58
50016.00	J11	M-017225- polycystic l	5314.00	PKHD1	13.18	5.26	1.17	3.73
50016.00	J12	M-021235- triggering r	54209.00	TREM2	10.21	2.29	0.51	16.55
50016.00	J13	M-006388- plasminoge	5329.00	PLAUR	13.32	5.40	1.20	7.78
50016.00	J14	M-017974- triggering r	54210.00	TREM1	4.42	3.50	-0.78	2.68
50016.00	J15	M-020933- plexin A3	55558.00	PLXNA3	7.83	0.09	-0.02	8.68
50016.00	J16	M-004452- TNFRSF1A-	8717.00	TRADD	6.68	1.24	-0.28	1.87
50016.00	J17	M-007752- plexin B3	5365.00	PLXNB3	9.48	1.56	0.35	5.98
50016.00	J18	M-004753- tumor prot	7159.00	TP53BP2	8.44	0.52	0.12	8.21
50016.00	J19	M-015670- proline-rich	55629.00	PNRC2	16.95	9.03	2.01	10.91
50016.00	J20	M-008105- tumor necr	3604.00	TNFRSF9	6.47	1.45	-0.32	3.82
50016.00	J21	M-015166- transmemb	114908.00	TMEM123	17.60	**9.68**	2.15	11.66
50016.00	J23	M-014182- proline-rich	5544.00	PRB3	7.34	0.58	-0.13	6.10
50016.00	K02	M-017406- GRB2-relat	9402.00	GRAP2	9.95	2.03	0.45	4.38
50016.00	K04	M-012285- GRB2-relat	10750.00	GRAP	4.02	3.90	-0.87	3.77
50016.00	K05	M-004519- protein tyr	5786.00	PTPRA	8.76	0.84	0.19	7.52
50016.00	K06	M-005546- G protein-c	350383.00	GPR142	7.04	0.88	-0.20	4.78
50016.00	K07	M-004994- protein tyr	5787.00	PTPRB	7.63	0.29	-0.06	3.20
50016.00	K08	M-005645- G protein-c	64582.00	GPR135	12.19	4.27	0.95	7.43
50016.00	K09	M-008067- protein tyr	5788.00	PTPRC	23.44	**15.52**	3.45	13.57
50016.00	K10	M-010980- golgi SNAP	9570.00	GOSR2	7.59	0.33	-0.07	8.25
50016.00	K11	M-008527- protein tyr	5789.00	PTPRD	21.59	**13.67**	3.04	15.25
50016.00	K12	M-011959- golgi SNAP	9527.00	GOSR1	9.51	1.59	0.35	53.01
50016.00	K13	M-008068- protein tyr	5791.00	PTPRE	18.50	**10.58**	2.35	9.59
50016.00	K14	M-011042- gap junctio	2697.00	GJA1	22.51	**14.59**	3.24	15.67
50016.00	K15	M-008375- protein tyr	5792.00	PTPRF	8.20	0.28	0.06	3.74
50016.00	K16	M-010402- growth hor	2690.00	GHR	10.67	2.75	0.61	6.04
50016.00	K17	M-009448- protein tyr	5794.00	PTPRH	29.74	**21.82**	4.85	11.09
50016.00	K18	M-007916- GDNF fami	64096.00	GFRA4	27.12	**19.20**	4.27	15.76
50016.00	K19	M-004204- protein tyr	5796.00	PTPRK	14.19	6.27	1.39	9.47
50016.00	K20	M-007913- GDNF fami	2674.00	GFRA1	15.02	7.10	1.58	9.22
50016.00	K21	M-006326- protein tyr	5797.00	PTPRM	14.21	6.29	1.40	8.49

50016.00	K23	M-009315-	protein tyr	5798.00	PTPRN	34.02	**26.10**	5.80	3.84
50016.00	L02	M-008104-	tumor necı	943.00	TNFRSF8	4.74	3.18	-0.71	5.10
50016.00	L04	M-003776-	Fas (TNF re	355.00	FAS	3.53	4.39	-0.98	3.58
50016.00	L05	M-017326-	protein C r	10544.00	PROCR	5.19	2.73	-0.61	3.45
50016.00	L06	M-008101-	CD40 mole	958.00	CD40	6.93	0.99	-0.22	5.66
50016.00	L07	M-021388-	pleckstrin a	5662.00	PSD	5.28	2.64	-0.59	2.73
50016.00	L08	M-004450-	tumor necı	27242.00	TNFRSF21	7.14	0.78	-0.17	10.18
50016.00	L09	M-008062-	seizure rela	26470.00	SEZ6L2	4.85	3.07	-0.68	6.32
50016.00	L10	M-008099-	tumor necı	84957.00	TNFRSF19L	11.50	3.58	0.79	9.51
50016.00	L11	M-003924-	patched hc	5727.00	PTCH1	10.68	2.76	0.61	7.29
50016.00	L12	M-011217-	tumor necı	608.00	TNFRSF17	2.16	5.76	-1.28	12.20
50016.00	L13	M-008063-	patched hc	8643.00	PTCH2	5.25	2.67	-0.59	4.36
50016.00	L14	M-008095-	tumor necı	23495.00	TNFRSF13E	4.60	3.32	-0.74	11.20
50016.00	L15	M-015323-	poliovirus ı	5817.00	PVR	6.81	1.11	-0.25	5.79
50016.00	L16	M-008093-	tumor necı	8792.00	TNFRSF11A	3.95	3.97	-0.88	8.15
50016.00	L17	M-003699-	poliovirus ı	5819.00	PVRL2	7.22	0.70	-0.16	10.20
50016.00	L18	M-008092-	tumor necı	8793.00	TNFRSF10D	14.62	6.70	1.49	16.60
50016.00	L19	M-003701-	receptor (G	10266.00	RAMP2	7.49	0.43	-0.10	11.06
50016.00	L20	M-008091-	tumor necı	8794.00	TNFRSF10C	16.51	8.59	1.91	9.15
50016.00	L21	M-003702-	receptor (G	10268.00	RAMP3	13.94	6.02	1.34	13.66
50016.00	L23	M-006995-	ubiquitin ir	51720.00	UIMC1	7.90	0.02	-0.01	3.57
50016.00	M02	M-012221-	follistatin	10468.00	FST	5.95	1.97	-0.44	8.68
50016.00	M04	M-014978-	Fc receptoı	84824.00	FCRLA	5.57	2.35	-0.52	2.96
50016.00	M05	M-008070-	protein tyr	5799.00	PTPRN2	6.11	1.81	-0.40	5.66
50016.00	M06	M-020219-	FGF recept	27315.00	FRAG1	6.10	1.82	-0.40	6.60
50016.00	M07	M-008500-	protein tyr	5800.00	PTPRO	7.15	0.77	-0.17	6.18
50016.00	M08	M-020584-	feline leuke	28982.00	FLVCR	13.10	5.18	1.15	8.23
50016.00	M09	M-009662-	protein tyr	5802.00	PTPRS	7.05	0.87	-0.19	4.56
50016.00	M10	M-016705-	Fc receptoı	115352.00	FCRL3	6.02	1.90	-0.42	4.73
50016.00	M11	M-009685-	protein tyr	5803.00	PTPRZ1	15.28	7.36	1.64	10.43
50016.00	M12	M-018732-	Fc receptoı	115350.00	FCRL1	9.83	1.91	0.42	5.62
50016.00	M13	M-009782-	RNA guany	8732.00	RNGTT	14.37	6.45	1.43	13.87
50016.00	M14	M-004462-	coagulatioı	2152.00	F3	4.08	3.84	-0.85	4.62
50016.00	M15	M-008083-	slingshot h	54434.00	SSH1	9.80	1.88	0.42	11.16
50016.00	M16	M-014034-	ectodyspla	10913.00	EDAR	9.63	1.71	0.38	6.91
50016.00	M17	M-008084-	slingshot h	85464.00	SSH2	19.26	**11.34**	2.52	19.32
50016.00	M18	M-012282-	emopamil	10682.00	EBP	10.16	2.24	0.50	4.68
50016.00	M19	M-008937-	slingshot h	54961.00	SSH3	7.95	0.03	0.01	4.75
50016.00	M20	M-003880-	deleted in	1630.00	DCC	6.88	1.04	-0.23	5.16
50016.00	M21	M-009571-	serine/thre	6815.00	STYX	13.25	5.33	1.18	6.07
50016.00	M23	M-017008-	PTC7 prote	160760.00	PPTC7	12.21	4.29	0.95	5.32
50016.00	N02	M-004066-	toll-like rec	54106.00	TLR9	4.18	3.74	-0.83	4.30
50016.00	N04	M-004714-	toll-like rec	51284.00	TLR7	3.92	4.00	-0.89	2.84
50016.00	N05	M-009513-	regulator c	26575.00	RGS17	4.79	3.13	-0.70	5.53

50016.00	N06	M-008089-	toll-like rec	7100.00	TLR5	4.20	3.72	-0.83	2.98
50016.00	N07	M-011381-	roundabou	6091.00	ROBO1	3.12	4.80	-1.07	0.52
50016.00	N08	M-008087-	toll-like rec	81793.00	TLR10	10.71	2.79	0.62	5.63
50016.00	N09	M-008075-	reticulon 4	65078.00	RTN4R	13.91	5.99	1.33	5.11
50016.00	N10	M-004713-	toll-interle	114609.00	TIRAP	13.22	5.30	1.18	4.81
50016.00	N11	M-011556-	src kinase a	8935.00	SKAP2	10.89	2.97	0.66	3.38
50016.00	N12	M-015979-	mannose-6	10226.00	M6PRBP1	5.72	2.20	-0.49	12.61
50016.00	N13	M-010592-	scavenger	949.00	SCARB1	6.78	1.14	-0.25	2.24
50016.00	N14	M-006903-	transformi	9392.00	TGFBRAP1	9.82	1.90	0.42	2.83
50016.00	N15	M-013710-	secretogra	29106.00	SCG3	60.68	**52.76**	11.73	19.15
50016.00	N16	M-016366-	TRK-fused	10342.00	TFG	15.16	7.24	1.61	5.54
50016.00	N17	M-012477-	neuroplast	27020.00	NPTN	10.06	2.14	0.47	6.46
50016.00	N18	M-018451-	taste recep	5726.00	TAS2R38	16.09	8.17	1.82	6.41
50016.00	N19	M-020091-	sema doma	10371.00	SEMA3A	14.28	6.36	1.41	5.98
50016.00	N20	M-010609-	tumor-asso	4070.00	TACSTD2	12.66	4.74	1.05	3.74
50016.00	N21	M-017644-	sema doma	6405.00	SEMA3F	11.86	3.94	0.88	5.68
50016.00	N23	M-019442-	sema doma	10507.00	SEMA4D	10.67	2.75	0.61	2.26
50016.00	O02	M-003650-	coxsackie v	1525.00	CXADR	14.18	6.26	1.39	5.66
50016.00	O04	M-007864-	colony stim	1438.00	CSF2RA	11.14	3.22	0.71	7.08
50016.00	O05	M-009977-	tensin like	23371.00	TENC1	13.39	5.47	1.22	5.24
50016.00	O06	M-015312-	cytokine re	64109.00	CRLF2	5.90	2.02	-0.45	3.08
50016.00	O07	M-023692-	translocase	92609.00	TIMM50	13.19	5.27	1.17	9.26
50016.00	O08	M-010503-	v-crk sarco	1398.00	CRK	12.23	4.31	0.96	10.19
50016.00	O09	M-008745-	transmemb	7179.00	TPTE	10.42	2.50	0.56	9.79
50016.00	O10	M-007856-	ciliary neur	1271.00	CNTFR	6.97	0.95	-0.21	2.70
50016.00	O11	M-008039-	myotubula	8897.00	MTMR3	7.84	0.08	-0.02	5.32
50016.00	O12	M-017088-	CD300c mo	10871.00	CD300C	20.54	**12.62**	2.80	17.19
50016.00	O13	M-009574-	protein pho	5494.00	PPM1A	15.57	7.65	1.70	15.82
50016.00	O14	M-011611-	clathrin, he	8218.00	CLTCL1	5.47	2.45	-0.54	7.94
50016.00	O15	M-009704-	protein pho	5532.00	PPP3CB	11.97	4.05	0.90	12.23
50016.00	O16	M-013612-	claudin 4	1364.00	CLDN4	11.45	3.53	0.78	1.38
50016.00	O17	M-004770-	mitogen-ac	10454.00	MAP3K7IP	11.18	3.26	0.72	9.82
50016.00	O18	M-017303-	claudin 3	1365.00	CLDN3	0.98	6.94	-1.54	4.88
50016.00	O19	M-003022-	protein pho	5521.00	PPP2R2B	18.94	**11.02**	2.45	15.75
50016.00	O20	M-009385-	protein tyr	26469.00	PTPN18	7.71	0.21	-0.05	7.88
50016.00	O21	M-009705-	multiple in	9562.00	MINPP1	9.00	1.08	0.24	3.34
50016.00	O23	M-012572-	catenin (ca	1500.00	CTNND1	12.49	4.57	1.01	3.99
50016.00	P02	M-005152-	stathmin 1,	3925.00	STMN1	6.35	1.57	-0.35	12.47
50016.00	P04	M-011423-	signal trans	8027.00	STAM	7.83	0.09	-0.02	4.93
50016.00	P05	M-013211-	sema doma	10501.00	SEMA6B	8.71	0.79	0.17	4.22
50016.00	P06	M-016490-	Fc receptor	79368.00	FCRL2	27.08	**19.16**	4.26	6.95
50016.00	P07	M-004600-	secreted fr	6422.00	SFRP1	11.87	3.95	0.88	2.70
50016.00	P08	M-004722-	sortilin-rela	6653.00	SORL1	33.33	**25.41**	5.65	7.94
50016.00	P09	M-024062-	secreted fr	6423.00	SFRP2	9.57	1.65	0.37	4.30

50016.00	P10	M-017335-	sorting nex	51429.00	SNX9	12.42	4.50	1.00	1.42
50016.00	P11	M-011388-	secreted fr	6424.00	SFRP4	10.39	2.47	0.55	1.81
50016.00	P12	M-013423-	SLAM fami	114836.00	SLAMF6	10.54	2.62	0.58	2.11
50016.00	P13	M-011389-	secreted fr	6425.00	SFRP5	8.65	0.73	0.16	4.76
50016.00	P14	M-010815-	Src-like-ad	6503.00	SLA	8.22	0.30	0.07	1.34
50016.00	P15	M-005725-	G protein-c	51463.00	GPR89A	30.82	**22.90**	5.09	2.80
50016.00	P16	M-012262-	SIVA1, apo	10572.00	SIVA1	13.01	5.09	1.13	2.96
50016.00	P17	M-010430-	SH2 domai	4068.00	SH2D1A	18.19	**10.27**	2.28	3.28
50016.00	P18	M-017022-	SHC (Src hc	53358.00	SHC3	10.84	2.92	0.65	1.10
50016.00	P19	M-019973-	SH3 domai	6450.00	SH3BGR	16.05	8.13	1.81	4.99
50016.00	P20	M-019715-	Src homolc	6461.00	SHB	10.20	2.28	0.51	6.53
50016.00	P21	M-019869-	SH3-domai	9467.00	SH3BP5	14.42	6.50	1.44	6.19
50016.00	P23	M-018707-	calcium act	124583.00	CANT1	5.63	2.30	-0.51	2.66
					mdn	7.92	3.04		4.19
					3MAD		9.12		
					MADc		4.50		
50016.00	C22					21.35		28.02	
50016.00	D22					29.29		22.70	
50016.00	E22					32.84		20.47	
50016.00	F22					32.89		28.12	
					mn	29.09		24.83	
					sd	5.43		3.85	
50016.00	G22					7.97		2.38	
50016.00	H22					8.91		4.92	
50016.00	I22					9.67		2.40	
50016.00	J22					14.06		8.95	
					mn	10.16		4.66	
					sd	2.70		3.10	
						16.30		11.55	
						8.09		9.29	
						24.39		20.85	
						18.94		20.17	
						1.29		1.03	
						-0.29		-0.03	

50016.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	24.20		17.19	
50016.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	16.11		27.64	
50016.00	I03	D-001206-	siControl non-targeting			14.20		6.64	
50016.00	J03	D-001206-	siControl non-targeting			8.55		4.15	
50016.00	K03	D-001600-	siGLO RISC-free siRNA			17.68		6.44	

50016.00	L03	D-001600-	siGLO RISC-free siRNA	15.34	12.96

abs dev	robust Z	% inf	abs dev	robust Z		
1.40	0.48	6.10	2.26	0.81		
3.24	1.11	3.57	0.27	-0.09		
0.81	-0.27	2.57	1.27	-0.46		
7.99	2.73	9.98	**6.14**	2.21	x	toxic a,b,c
2.16	0.74	9.64	**5.80**	2.08		
0.27	-0.09	2.03	1.81	-0.65		
5.12	1.75	6.52	2.68	0.97		
0.26	0.09	3.81	0.03	-0.01		
2.41	0.82	6.69	2.85	1.02		
2.12	-0.72	7.64	3.80	1.37		
3.07	1.05	3.22	0.62	-0.22		
0.23	-0.08	2.43	1.41	-0.51		
1.40	-0.48	1.65	2.19	-0.79		
1.42	0.48	3.25	0.59	-0.21		
1.55	0.53	4.98	1.14	0.41		
1.78	-0.60	1.12	2.72	-0.98		
0.65	0.22	5.36	1.52	0.55		
2.95	1.01	6.17	2.33	0.84		
0.32	-0.11	1.75	2.09	-0.75		
0.51	-0.17	22.52	**18.68**	6.71		
2.44	-0.83	2.26	1.58	-0.57		
1.75	-0.60	1.22	2.62	-0.94		
0.05	-0.02	2.00	1.84	-0.66		
0.67	0.23	0.28	3.56	-1.28		
0.88	-0.30	2.83	1.01	-0.36		
1.82	0.62	0.68	3.16	-1.14		
2.02	-0.69	1.58	2.26	-0.81		
0.67	-0.23	3.60	0.24	-0.09		
1.72	0.59	5.79	1.95	0.70		
2.43	-0.83	1.04	2.80	-1.00		
1.83	-0.62	1.11	2.74	-0.98		
1.50	-0.51	0.71	3.13	-1.12		
1.24	-0.42	0.77	3.07	-1.10		
0.84	-0.28	3.05	0.79	-0.28		
3.11	-1.06	1.94	1.90	-0.68		
0.44	-0.15	1.08	2.76	-0.99		
1.17	-0.40	1.57	2.27	-0.81		
2.55	-0.87	2.05	1.79	-0.64		
2.37	-0.81	1.30	2.54	-0.91		
2.76	0.94	1.79	2.05	-0.74		
0.44	0.15	3.67	0.17	-0.06		
0.27	-0.09	8.62	4.78	1.72		
0.29	-0.10	2.69	1.15	-0.41		

0.87	-0.30	1.52	2.32	-0.83
0.68	-0.23	0.75	3.09	-1.11
3.14	-1.07	1.98	1.86	-0.67
0.09	0.03	7.67	3.83	1.38
0.08	-0.03	5.94	2.10	0.76
2.86	-0.97	2.18	1.66	-0.60
0.47	0.16	8.28	4.44	1.60
1.40	-0.48	3.69	0.15	-0.05
2.43	-0.83	3.48	0.36	-0.13
0.94	-0.32	3.56	0.28	-0.10
2.88	-0.98	4.11	0.27	0.10
0.48	-0.16	14.10	**10.26**	3.69
3.70	1.26	5.18	1.34	0.48
3.28	-1.12	5.74	1.90	0.69
2.80	-0.95	6.58	2.74	0.99
1.00	0.34	8.53	4.69	1.68
2.27	-0.77	2.21	1.63	-0.58
2.42	-0.83	1.32	2.52	-0.90
2.33	-0.79	4.05	0.21	0.08
1.39	-0.47	3.85	0.01	0.00
0.15	-0.05	8.68	4.84	1.74
0.74	-0.25	7.06	3.22	1.16
3.57	-1.22	1.05	2.79	-1.00
0.58	-0.20	2.95	0.89	-0.32
2.89	-0.99	1.04	2.80	-1.00
0.95	0.32	3.33	0.51	-0.18
2.03	-0.69	2.29	1.55	-0.56
2.38	-0.81	3.23	0.61	-0.22
1.38	-0.47	7.51	3.67	1.32
0.20	0.07	11.12	**7.28**	2.62
0.27	0.09	3.48	0.36	-0.13
2.23	0.76	8.41	4.57	1.64
2.20	-0.75	2.12	1.72	-0.62
2.61	0.89	4.44	0.60	0.22
3.18	-1.08	3.19	0.65	-0.23
1.85	-0.63	4.38	0.54	0.20
2.28	-0.78	2.67	1.17	-0.42
3.78	-1.29	3.96	0.12	0.04
0.64	0.22	3.50	0.34	-0.12
3.49	-1.19	0.84	3.00	-1.08
2.48	-0.84	2.85	0.99	-0.36
2.68	-0.91	3.22	0.62	-0.22
3.24	-1.10	0.77	3.07	-1.10
1.65	-0.56	1.79	2.05	-0.74

2.95	-1.00	0.43	3.41	-1.22
3.55	-1.21	2.07	1.77	-0.64
0.57	-0.19	1.94	1.90	-0.68
1.97	-0.67	1.71	2.13	-0.77
0.15	-0.05	5.57	1.73	0.62
2.54	0.87	18.65	**14.81**	5.32
2.98	-1.01	0.73	3.11	-1.12
0.18	0.06	4.86	1.02	0.37
1.19	-0.40	3.02	0.82	-0.29
0.23	-0.08	5.16	1.32	0.47
1.30	0.44	7.06	3.22	1.16
0.86	-0.29	0.51	3.33	-1.20
2.02	-0.69	0.92	2.92	-1.05
2.91	-0.99	3.02	0.82	-0.29
2.80	-0.95	1.75	2.09	-0.75
0.54	-0.18	5.03	1.19	0.43
3.17	-1.08	2.68	1.16	-0.42
2.95	-1.00	1.37	2.47	-0.89
2.29	-0.78	2.22	1.62	-0.58
2.10	-0.71	0.56	3.28	-1.18
1.70	-0.58	1.39	2.45	-0.88
0.44	-0.15	2.52	1.32	-0.47
3.08	-1.05	0.53	3.31	-1.19
0.59	-0.20	1.56	2.28	-0.82
2.88	0.98	3.63	0.21	-0.08
3.08	-1.05	0.78	3.06	-1.10
4.98	1.70	6.33	2.49	0.90
0.22	-0.07	1.55	2.29	-0.82
2.36	-0.80	2.29	1.55	-0.55
1.59	-0.54	2.15	1.69	-0.61
1.83	-0.62	2.13	1.71	-0.62
0.14	-0.05	3.46	0.38	-0.14
1.46	-0.50	1.51	2.33	-0.84
4.59	1.57	2.20	1.64	-0.59
0.14	0.05	1.28	2.56	-0.92
0.90	-0.30	1.59	2.25	-0.81
2.49	-0.85	4.16	0.32	0.12
1.40	-0.48	1.71	2.13	-0.76
2.68	-0.91	6.30	2.46	0.88
3.44	-1.17	2.64	1.20	-0.43
2.31	-0.79	2.36	1.48	-0.53
0.45	0.15	4.86	1.02	0.37
4.65	1.59	1.78	2.06	-0.74
1.49	-0.51	2.27	1.57	-0.56

2.63	-0.90	1.26	2.58	-0.93		
0.93	-0.32	3.79	0.05	-0.02		
1.17	-0.40	8.20	4.36	1.57		
2.35	-0.80	2.75	1.09	-0.39		
1.82	-0.62	4.05	0.21	0.08		
2.47	-0.84	7.27	3.43	1.23		
0.29	0.10	2.22	1.62	-0.58		
2.22	-0.76	8.50	4.66	1.68		
3.25	-1.11	3.71	0.13	-0.04		
2.29	0.78	3.59	0.25	-0.09		
2.95	-1.00	1.96	1.88	-0.67		
1.00	-0.34	5.55	1.71	0.62		
2.63	-0.89	4.01	0.17	0.06		
7.51	2.56	3.86	0.02	0.01		
0.86	-0.29	5.51	1.67	0.60		
4.21	1.44	7.41	3.57	1.28		
0.04	-0.01	9.40	5.56	2.00		
0.08	-0.03	8.10	4.26	1.53		
7.01	2.39	4.51	0.67	0.24		
0.65	0.22	6.57	2.73	0.98		
1.54	-0.52	2.32	1.52	-0.54		
0.24	-0.08	4.04	0.20	0.07		
1.67	-0.57	5.14	1.30	0.47		
0.15	0.05	11.22	**7.38**	2.65	x	art b,c
0.78	-0.27	3.27	0.57	-0.20		
1.33	-0.45	6.81	2.97	1.07		
4.67	1.59	11.21	**7.37**	2.65		
2.80	-0.96	3.07	0.77	-0.28		
2.57	-0.87	3.04	0.80	-0.29		
0.61	0.21	1.05	2.79	-1.00		
1.26	0.43	12.56	**8.72**	3.13	x	toxic a
2.06	0.70	3.70	0.14	-0.05		
3.24	1.11	8.74	4.90	1.76		
2.34	0.80	6.52	2.68	0.96		
0.79	-0.27	3.00	0.84	-0.30		
6.72	2.29	18.63	**14.79**	5.31	y	
5.11	1.74	4.16	0.32	0.12		
0.62	0.21	8.56	4.72	1.70		
0.45	0.15	6.60	2.76	0.99		
1.42	-0.48	0.93	2.91	-1.04		
4.14	1.41	4.62	0.78	0.28		
1.36	0.46	1.11	2.73	-0.98		
0.52	-0.18	3.83	0.01	0.00		
0.31	-0.11	3.62	0.22	-0.08		

2.24	0.76	4.05	0.21	0.07	
9.24	3.15	15.78	**11.94**	4.29	y
2.36	0.80	7.11	3.27	1.18	
4.16	1.42	10.55	**6.71**	2.41	
3.44	1.17	6.13	2.29	0.82	
3.19	-1.09	1.21	2.63	-0.94	
5.93	2.02	4.96	1.12	0.40	
2.32	-0.79	0.27	3.57	-1.28	
5.56	1.90	5.25	1.41	0.51	
2.76	0.94	4.37	0.53	0.19	
1.33	-0.45	1.44	2.40	-0.86	
1.39	-0.47	0.31	3.53	-1.27	
2.39	0.82	5.57	1.73	0.62	
0.46	-0.15	5.59	1.75	0.63	
12.36	4.22	3.20	0.64	-0.23	
3.59	1.23	4.41	0.57	0.21	
1.51	-0.51	2.97	0.87	-0.31	
4.49	1.53	5.29	1.45	0.52	
2.32	-0.79	3.20	0.64	-0.23	
1.79	0.61	2.27	1.57	-0.56	
4.02	1.37	1.42	2.42	-0.87	
6.72	2.29	3.31	0.53	-0.19	
0.37	-0.12	1.72	2.12	-0.76	
7.47	2.55	3.65	0.19	-0.07	y
1.91	0.65	2.61	1.23	-0.44	
0.19	0.06	5.73	1.89	0.68	
0.42	-0.14	4.34	0.50	0.18	
3.33	1.14	5.74	1.90	0.68	
0.59	0.20	7.46	3.62	1.30	
0.99	-0.34	2.58	1.26	-0.45	
3.24	1.11	1.96	1.88	-0.67	
9.38	3.20	13.10	**9.26**	3.33	y
4.06	1.38	4.78	0.94	0.34	
11.06	3.77	14.65	**10.81**	3.89	y
48.82	16.65	5.53	1.69	0.61	
5.40	1.84	5.40	1.56	0.56	
11.48	3.92	12.30	**8.46**	3.04	y
0.45	-0.15	4.47	0.63	0.23	
1.85	0.63	3.09	0.75	-0.27	
6.90	2.35	12.55	**8.71**	3.13	y
11.57	3.95	26.44	**22.60**	8.12	y
5.28	1.80	6.68	2.84	1.02	
5.03	1.72	4.74	0.90	0.32	
4.30	1.47	6.93	3.09	1.11	

0.35	-0.12	5.06	1.22	0.44	
0.91	0.31	3.90	0.06	0.02	
0.61	-0.21	5.34	1.50	0.54	
0.74	-0.25	2.94	0.90	-0.32	
1.47	0.50	3.24	0.60	-0.22	
1.46	-0.50	1.56	2.28	-0.82	
5.99	2.04	4.43	0.59	0.21	
2.13	0.73	3.64	0.20	-0.07	
5.32	1.82	4.10	0.26	0.10	
3.10	1.06	3.02	0.82	-0.29	
8.01	2.73	0.37	3.47	-1.24	
0.17	0.06	2.11	1.73	-0.62	
7.01	2.39	5.59	1.75	0.63	
1.60	0.55	2.93	0.91	-0.33	
3.96	1.35	0.92	2.92	-1.05	
6.01	2.05	3.06	0.78	-0.28	
12.41	4.23	6.65	2.81	1.01	
6.87	2.35	7.50	3.66	1.32	
4.96	1.69	6.82	2.98	1.07	
9.47	3.23	8.24	4.40	1.58	
0.62	-0.21	2.99	0.85	-0.30	
4.49	1.53	2.68	1.16	-0.42	
1.23	-0.42	4.32	0.48	0.17	
1.47	0.50	8.99	5.15	1.85	
2.41	0.82	5.49	1.65	0.59	
1.99	0.68	9.00	5.16	1.86	
4.04	1.38	12.00	**8.16**	2.93	
0.37	0.13	4.85	1.01	0.36	
0.54	0.18	5.28	1.44	0.52	
6.24	2.13	8.78	4.94	1.77	
1.43	0.49	6.21	2.37	0.85	
9.68	3.30	13.79	**9.95**	3.57	y
0.43	0.15	6.12	2.28	0.82	
6.97	2.38	9.89	**6.05**	2.17	y
2.72	0.93	10.92	**7.08**	2.54	
15.13	5.16	23.33	**19.49**	7.00	y
0.49	0.17	5.62	1.78	0.64	
0.56	0.19	7.45	3.61	1.30	
0.97	0.33	5.22	1.38	0.50	
1.88	0.64	8.48	4.64	1.67	
1.13	0.39	4.30	0.46	0.16	
0.11	0.04	1.67	2.17	-0.78	
1.35	-0.46	3.10	0.74	-0.26	
1.34	0.46	4.05	0.21	0.08	

1.21	-0.41	3.72	0.12	-0.04		
3.67	-1.25	1.68	2.16	-0.78		
1.44	0.49	8.84	5.00	1.80		
0.92	0.32	6.64	2.80	1.01		
0.62	0.21	7.11	3.27	1.18		
0.81	-0.28	3.04	0.80	-0.29		
8.42	2.87	3.34	0.50	-0.18		
1.95	-0.66	2.42	1.42	-0.51		
1.36	-0.46	2.93	0.91	-0.33		
14.96	5.10	4.75	0.91	0.33	x	toxic a,b,c
1.35	0.46	8.91	5.07	1.82		
2.27	0.78	9.16	5.32	1.91		
2.22	0.76	9.85	**6.01**	2.16		
1.79	0.61	9.17	5.33	1.92		
0.45	-0.15	9.74	**5.90**	2.12		
1.49	0.51	7.50	3.66	1.31		
1.93	-0.66	4.54	0.70	0.25		
1.47	0.50	8.36	4.52	1.62		
2.89	0.99	9.53	**5.69**	2.05		
1.05	0.36	8.75	4.91	1.77		
1.11	-0.38	5.78	1.94	0.70		
5.07	1.73	7.07	3.23	1.16		
6.00	2.05	8.85	5.01	1.80		
5.60	1.91	10.84	**7.00**	2.51		
1.49	-0.51	4.35	0.51	0.18		
1.13	0.39	7.08	3.24	1.17		
13.00	4.43	4.57	0.73	0.26	x	toxic a,b,c
11.63	3.97	5.72	1.88	0.68		
3.75	1.28	2.80	1.04	-0.37		
8.04	2.74	12.80	**8.96**	3.22	y	
2.81	-0.96	2.84	1.00	-0.36		
5.63	1.92	2.43	1.41	-0.50		
0.69	0.24	3.09	0.75	-0.27		
11.56	3.94	21.48	**17.64**	6.34	y	
3.69	1.26	3.16	0.68	-0.24		
0.85	-0.29	4.36	0.52	0.19		
0.20	-0.07	4.95	1.11	0.40		
8.28	2.83	1.31	2.53	-0.91		
0.74	0.25	0.83	3.01	-1.08		
0.03	0.01	1.40	2.44	-0.88		
2.76	0.94	4.40	0.56	0.20		
1.49	-0.51	5.26	1.42	0.51		
3.75	1.28	5.79	1.95	0.70		
0.11	0.04	2.64	1.20	-0.43		

2.77	-0.94	0.80	3.04	-1.09
2.38	-0.81	1.57	2.27	-0.81
2.08	-0.71	4.60	0.76	0.27
0.57	0.20	6.10	2.26	0.81
2.85	-0.97	2.83	1.01	-0.36
1.39	-0.47	7.61	3.77	1.36
1.23	-0.42	3.42	0.42	-0.15
0.91	-0.31	9.12	5.28	1.90
3.09	-1.05	2.52	1.32	-0.47
0.80	0.27	3.00	0.84	-0.30
2.34	0.80	3.65	0.19	-0.07
2.00	0.68	8.17	4.33	1.56
1.53	-0.52	4.46	0.62	0.23
1.98		3.84	1.88	
5.94			5.64	
2.93			2.78	
21.55				
21.78				
21.22				
21.67				
21.55				
0.24				
3.32				
5.11				
5.57				
2.01				
4.01				
1.64				
0.72				
4.56				
5.28				
17.55				
0.30				
0.70				

2.79
11.74
5.63
2.32
9.61

20.60

					% inf	**abs dev**
50017.00	A02	M-007953- interleukin 1, beta	3553.00	IL1B	0.16	3.67
50017.00	A04	M-007952- interleukin 1, alpha	3552.00	IL1A	3.66	0.17
50017.00	A05	M-004381- B-cell CLL/lymphoma 10	8915.00	BCL10	2.58	1.25
50017.00	A06	M-007951- interleukin 19	29949.00	IL19	3.09	0.74
50017.00	A07	M-017626- brain-derived neurotrophic f	627.00	BDNF	0.68	3.15
50017.00	A08	M-007949- interleukin 18 receptor 1	8809.00	IL18R1	2.07	1.76
50017.00	A09	M-012018- bone morphogenetic protei	9210.00	BMP15	1.10	2.73
50017.00	A10	M-017446- interleukin 18 binding protei	10068.00	IL18BP	1.29	2.54
50017.00	A11	M-011219- bone morphogenetic protei	650.00	BMP2	1.86	1.97
50017.00	A12	M-007948- interleukin 18 (interferon-ga	3606.00	IL18	2.41	1.42
50017.00	A13	M-011220- bone morphogenetic protei	651.00	BMP3	3.12	0.71
50017.00	A14	M-007944- interleukin 17 receptor B	55540.00	IL17RB	10.64	6.81
50017.00	A15	M-011221- bone morphogenetic protei	652.00	BMP4	1.94	1.89
50017.00	A16	M-007943- interleukin 17 receptor A	23765.00	IL17RA	5.06	1.23
50017.00	A17	M-017549- bone morphogenetic protei	653.00	BMP5	2.36	1.47
50017.00	A18	M-007939- interleukin 17C	27189.00	IL17C	5.14	1.31
50017.00	A19	M-021475- bone morphogenetic protei	654.00	BMP6	1.90	1.93
50017.00	A20	M-007938- interleukin 17B	27190.00	IL17B	5.89	2.06
50017.00	A21	M-011592- bone morphogenetic protei	655.00	BMP7	4.45	0.62
50017.00	A23	M-011593- bone morphogenetic protei	656.00	BMP8B	8.90	5.07
50017.00	B02	M-011173- folate receptor 2 (fetal)	2350.00	FOLR2	0.28	3.55
50017.00	B04	M-010403- folate receptor 1 (adult)	2348.00	FOLR1	0.66	3.17
50017.00	B05	M-007955- interleukin 1 family, membe	26525.00	IL1F5	1.68	2.15
50017.00	B06	M-020176- fms-related tyrosine kinase	2323.00	FLT3LG	3.19	0.64
50017.00	B07	M-007956- interleukin 1 family, membe	27179.00	IL1F6	0.79	3.04
50017.00	B08	M-012579- filamin A, alpha (actin bindin	2316.00	FLNA	2.57	1.26
50017.00	B09	M-007957- interleukin 1 family, membe	27178.00	IL1F7	3.54	0.29
50017.00	B10	M-017552- c-fos induced growth factor	2277.00	FIGF	3.48	0.35
50017.00	B11	M-007958- interleukin 1 family, membe	27177.00	IL1F8	3.98	0.15
50017.00	B12	M-011660- fibroblast growth factor 9 (gl	2254.00	FGF9	3.49	0.34
50017.00	B13	M-007959- interleukin 1 family, membe	56300.00	IL1F9	1.89	1.94
50017.00	B14	M-013693- fibroblast growth factor 8 (a	2253.00	FGF8	3.88	0.05
50017.00	B15	M-005188- interleukin 1 receptor, type I	3554.00	IL1R1	3.74	0.09
50017.00	B16	M-011659- fibroblast growth factor 7 (k	2252.00	FGF7	2.08	1.75
50017.00	B17	M-007960- interleukin 1 receptor, type I	7850.00	IL1R2	0.98	2.85
50017.00	B18	M-003891- fibroblast growth factor 6	2251.00	FGF6	1.50	2.33
50017.00	B19	M-003504- interleukin 1 receptor access	3556.00	IL1RAP	6.13	2.30
50017.00	B20	M-011972- fibroblast growth factor 5	2250.00	FGF5	3.52	0.31
50017.00	B21	M-007962- interleukin 1 receptor access	26280.00	IL1RAPL2	8.26	4.43
50017.00	B23	M-007963- interleukin 1 receptor-like 1	9173.00	IL1RL1	3.20	0.63
50017.00	C02	M-007937- interleukin 17A	3605.00	IL17A	1.06	2.77
50017.00	C04	M-007936- interleukin 16 (lymphocyte c	3603.00	IL16	4.11	0.28
50017.00	C05	M-019846- benzodiazapine receptor (pe	9256.00	BZRAP1	4.06	0.23

50017.00	C06	M-007935-	interleukin 15 receptor, alph	3601.00	IL15RA	3.64	0.19
50017.00	C07	M-009559-	translocator protein (18kDa)	706.00	TSPO	0.78	3.05
50017.00	C08	M-007934-	interleukin 15	3600.00	IL15	6.25	2.42
50017.00	C09	M-021221-	cytokine-like 1	54360.00	CYTL1	1.79	2.04
50017.00	C10	M-004598-	interleukin 13 receptor, alph	3598.00	IL13RA2	2.02	1.81
50017.00	C11	M-007815-	CD93 molecule	22918.00	CD93	2.90	0.93
50017.00	C12	M-007932-	interleukin 12 receptor, beta	3595.00	IL12RB2	2.57	1.26
50017.00	C13	M-011163-	cholecystokinin	885.00	CCK	3.01	0.82
50017.00	C14	M-007931-	interleukin 12 receptor, beta	3594.00	IL12RB1	2.81	1.02
50017.00	C15	M-007822-	chemokine (C-C motif) liganc	6346.00	CCL1	2.13	1.70
50017.00	C16	M-007930-	interleukin 12B (natural kille	3593.00	IL12B	4.25	0.42
50017.00	C17	M-007823-	chemokine (C-C motif) liganc	6356.00	CCL11	5.54	1.71
50017.00	C18	M-007927-	interleukin 11	3589.00	IL11	1.70	2.13
50017.00	C19	M-007824-	chemokine (C-C motif) liganc	6357.00	CCL13	4.01	0.18
50017.00	C20	M-007926-	interleukin 10 receptor, beta	3588.00	IL10RB	12.22	**8.39**
50017.00	C21	M-007825-	chemokine (C-C motif) liganc	6358.00	CCL14	2.06	1.77
50017.00	C23	M-007826-	chemokine (C-C motif) liganc	6359.00	CCL15	6.83	3.00
50017.00	D02	M-003890-	fibroblast growth factor 4 (h	2249.00	FGF4	1.20	2.63
50017.00	D04	M-003889-	fibroblast growth factor 3 (m	2248.00	FGF3	7.80	3.97
50017.00	D05	M-007965-	interleukin 1 receptor-like 2	8808.00	IL1RL2	5.00	1.17
50017.00	D06	M-013172-	fibroblast growth factor 23	8074.00	FGF23	5.11	1.28
50017.00	D07	M-007966-	interleukin 1 receptor antag	3557.00	IL1RN	2.29	1.54
50017.00	D08	M-013305-	fibroblast growth factor 21	26291.00	FGF21	2.97	0.86
50017.00	D09	M-007971-	interleukin 21 receptor	50615.00	IL21R	2.14	1.69
50017.00	D10	M-013235-	fibroblast growth factor 20	26281.00	FGF20	5.46	1.63
50017.00	D11	M-007972-	interleukin 22	50616.00	IL22	5.90	2.07
50017.00	D12	M-013670-	fibroblast growth factor 19	9965.00	FGF19	3.44	0.39
50017.00	D13	M-007973-	interleukin 22 receptor, alph	58985.00	IL22RA1	2.42	1.41
50017.00	D14	M-011537-	fibroblast growth factor 18	8817.00	FGF18	7.39	3.56
50017.00	D15	M-007977-	interleukin 24	11009.00	IL24	4.83	1.00
50017.00	D16	M-011540-	fibroblast growth factor 17	8822.00	FGF17	7.06	3.23
50017.00	D17	M-007978-	interleukin 26	55801.00	IL26	5.94	2.11
50017.00	D18	M-011541-	fibroblast growth factor 16	8823.00	FGF16	9.05	**5.22**
50017.00	D19	M-007983-	interleukin 2 receptor, alpha	3559.00	IL2RA	3.43	0.40
50017.00	D20	M-011860-	fibroblast growth factor 14	2259.00	FGF14	11.37	**7.54**
50017.00	D21	M-007984-	interleukin 2 receptor, beta	3560.00	IL2RB	12.01	**8.18**
50017.00	D23	M-007985-	interleukin 2 receptor, gamn	3561.00	IL2RG	4.38	0.55
50017.00	E02	M-007925-	interleukin 10 receptor, alph	3587.00	IL10RA	2.66	1.17
50017.00	E04	M-005066-	interleukin 10	3586.00	IL10	2.64	1.19
50017.00	E05	M-007827-	chemokine (C-C motif) liganc	6360.00	CCL16	4.11	0.28
50017.00	E06	M-003767-	inhibitor of kappa light polyp	8517.00	IKBKG	1.81	2.02
50017.00	E07	M-007829-	chemokine (C-C motif) liganc	6362.00	CCL18	4.07	0.24
50017.00	E08	M-012190-	IK cytokine, down-regulator	3550.00	IK	8.53	4.70
50017.00	E09	M-007830-	chemokine (C-C motif) liganc	6363.00	CCL19	4.72	0.89

50017.00	E10	M-004093- insulin-like growth factor 2 (	3481.00	IGF2	2.44	1.39
50017.00	E11	M-007832- chemokine (C-C motif) ligan	6364.00	CCL20	3.37	0.46
50017.00	E12	M-003011- insulin-like growth factor 1 (	3479.00	IGF1	9.97	**6.14**
50017.00	E13	M-007833- chemokine (C-C motif) ligan	6366.00	CCL21	3.97	0.14
50017.00	E14	M-012638- interferon, omega 1	3467.00	IFNW1	3.51	0.32
50017.00	E15	M-007834- chemokine (C-C motif) ligan	6367.00	CCL22	8.88	5.05
50017.00	E16	M-011057- interferon gamma receptor	3459.00	IFNGR1	14.36	**10.53**
50017.00	E17	M-007836- chemokine (C-C motif) ligan	6369.00	CCL24	12.80	**8.97**
50017.00	E18	M-019379- interferon, gamma	3458.00	IFNG	5.62	1.79
50017.00	E19	M-007838- chemokine (C-C motif) ligan	10344.00	CCL26	10.57	**6.74**
50017.00	E20	M-019656- interferon, beta 1, fibroblast	3456.00	IFNB1	4.11	0.28
50017.00	E21	M-007839- chemokine (C-C motif) ligan	10850.00	CCL27	9.39	**5.56**
50017.00	E23	M-007840- chemokine (C-C motif) ligan	56477.00	CCL28	7.25	3.42
50017.00	F02	M-011859- fibroblast growth factor 13	2258.00	FGF13	4.06	0.23
50017.00	F04	M-011858- fibroblast growth factor 11	2256.00	FGF11	2.06	1.77
50017.00	F05	M-007986- interleukin 3 (colony-stimula	3562.00	IL3	5.22	1.39
50017.00	F06	M-011857- fibroblast growth factor 10	2255.00	FGF10	3.21	0.62
50017.00	F07	M-007988- interleukin 3 receptor, alpha	3563.00	IL3RA	1.98	1.85
50017.00	F08	M-011172- fibroblast growth factor 1 (a	2246.00	FGF1	3.10	0.73
50017.00	F09	M-007989- interleukin 4	3565.00	IL4	1.96	1.87
50017.00	F10	M-015838- fem-1 homolog b (C. elegans	10116.00	FEM1B	3.26	0.57
50017.00	F11	M-007990- interleukin 4 receptor	3566.00	IL4R	2.29	1.54
50017.00	F12	M-017906- Fc fragment of IgG, receptor	2217.00	FCGRT	5.37	1.54
50017.00	F13	M-007991- interleukin 5 (colony-stimula	3567.00	IL5	3.55	0.28
50017.00	F14	M-019374- Fc fragment of IgG, low affin	2215.00	FCGR3B	4.46	0.63
50017.00	F15	M-007992- interleukin 5 receptor, alpha	3568.00	IL5RA	2.51	1.32
50017.00	F16	M-015823- Fc fragment of IgG, low affin	2213.00	FCGR2B	5.49	1.66
50017.00	F17	M-007993- interleukin 6 (interferon, bet	3569.00	IL6	8.34	4.51
50017.00	F18	M-014152- Fc fragment of IgG, low affin	2212.00	FCGR2A	14.84	**11.01**
50017.00	F19	M-007994- interleukin 6 receptor	3570.00	IL6R	11.86	**8.03**
50017.00	F20	M-015650- Fc fragment of IgG, high affi	2209.00	FCGR1A	16.86	**13.03**
50017.00	F21	M-005166- interleukin 6 signal transduc	3572.00	IL6ST	7.47	3.64
50017.00	F23	M-007995- interleukin 7	3574.00	IL7	7.33	3.50
50017.00	G02	M-015411- interferon (alpha, beta and	3455.00	IFNAR2	8.13	4.30
50017.00	G04	M-020209- interferon (alpha, beta and	3454.00	IFNAR1	25.41	**21.58**
50017.00	G05	M-007842- chemokine (C-C motif) ligan	6349.00	CCL3L1	2.68	1.15
50017.00	G06	M-019655- interferon, alpha 8	3445.00	IFNA8	3.59	0.24
50017.00	G07	M-007844- chemokine (C-C motif) ligan	6352.00	CCL5	2.77	1.06
50017.00	G08	M-014155- interferon, alpha 6	3443.00	IFNA6	0.99	2.84
50017.00	G09	M-007845- chemokine (C-C motif) ligan	6354.00	CCL7	1.90	1.93
50017.00	G10	M-012637- interferon, alpha 5	3442.00	IFNA5	5.64	1.81
50017.00	G11	M-007846- chemokine (C-C motif) ligan	6355.00	CCL8	0.89	2.94
50017.00	G12	M-014154- interferon, alpha 4	3441.00	IFNA4	6.47	2.64
50017.00	G13	M-011121- CD14 molecule	929.00	CD14	3.18	0.65

50017.00	G14	M-019654-	interferon, alpha 21	3452.00	IFNA21	4.64	0.81
50017.00	G15	M-019429-	CD1d molecule	912.00	CD1D	4.12	0.29
50017.00	G16	M-013809-	interferon, alpha 2	3440.00	IFNA2	6.46	2.63
50017.00	G17	M-017854-	CD2 molecule	914.00	CD2	5.81	1.98
50017.00	G18	M-014147-	interferon, alpha 17	3451.00	IFNA17	3.26	0.57
50017.00	G19	M-016287-	C-type lectin domain family	10332.00	CLEC4M	4.56	0.73
50017.00	G20	M-019653-	interferon, alpha 16	3449.00	IFNA16	6.45	2.62
50017.00	G21	M-012734-	CD28 molecule	940.00	CD28	4.26	0.43
50017.00	G23	M-019502-	CD33 molecule	945.00	CD33	5.24	1.41
50017.00	H02	M-016242-	Fc fragment of IgE, low affini	2208.00	FCER2	3.52	0.31
50017.00	H04	M-011856-	Fc fragment of IgE, high affin	2207.00	FCER1G	14.03	**10.20**
50017.00	H05	M-007996-	interleukin 7 receptor	3575.00	IL7R	3.68	0.15
50017.00	H06	M-011658-	Fc fragment of IgE, high affin	2205.00	FCER1A	4.68	0.85
50017.00	H07	M-007997-	interleukin 9	3578.00	IL9	4.00	0.17
50017.00	H08	M-011657-	Fc fragment of IgA, receptor	2204.00	FCAR	1.35	2.48
50017.00	H09	M-007998-	interleukin 9 receptor	3581.00	IL9R	0.76	3.07
50017.00	H10	M-003800-	Fas (TNFRSF6)-associated vi	8772.00	FADD	3.90	0.07
50017.00	H11	M-011700-	inhibin, alpha	3623.00	INHA	1.67	2.16
50017.00	H12	M-012338-	endothelial cell-specific mol	11082.00	ESM1	2.11	1.72
50017.00	H13	M-011701-	inhibin, beta A (activin A, act	3624.00	INHBA	1.34	2.49
50017.00	H14	M-011268-	epiregulin	2069.00	EREG	2.30	1.53
50017.00	H15	M-011702-	inhibin, beta B (activin AB be	3625.00	INHBB	0.93	2.90
50017.00	H16	M-004006-	epidermal growth factor rec	58513.00	EPS15L1	2.08	1.75
50017.00	H17	M-012113-	inhibin, beta C	3626.00	INHBC	4.36	0.53
50017.00	H18	M-020204-	erythropoietin	2056.00	EPO	7.85	4.02
50017.00	H19	M-011058-	insulin	3630.00	INS	2.10	1.73
50017.00	H20	M-012994-	EGF-like-domain, multiple 6	25975.00	EGFL6	2.61	1.22
50017.00	H21	M-020006-	insulin-like 3 (Leydig cell)	3640.00	INSL3	1.80	2.03
50017.00	H23	M-011703-	insulin-like 4 (placenta)	3641.00	INSL4	3.56	0.27
50017.00	I02	M-019652-	interferon, alpha 14	3448.00	IFNA14	1.77	2.06
50017.00	I04	M-014265-	interferon, alpha 13	3447.00	IFNA13	2.43	1.40
50017.00	I05	M-010206-	CD36 molecule (thrombosp	948.00	CD36	6.12	2.29
50017.00	I06	M-019651-	interferon, alpha 10	3446.00	IFNA10	0.94	2.89
50017.00	I07	M-020205-	CD3d molecule, delta (CD3-T	915.00	CD3D	4.58	0.75
50017.00	I08	M-011698-	intercellular adhesion molec	3385.00	ICAM3	8.41	4.58
50017.00	I09	M-011005-	CD3g molecule, gamma (CD	917.00	CD3G	2.52	1.31
50017.00	I10	M-011182-	intercellular adhesion molec	3384.00	ICAM2	5.00	1.17
50017.00	I11	M-004257-	CD247 molecule	919.00	CD247	1.74	2.09
50017.00	I12	M-003502-	intercellular adhesion molec	3383.00	ICAM1	1.87	1.96
50017.00	I13	M-009999-	CD44 molecule (Indian bloo	960.00	CD44	3.86	0.03
50017.00	I14	M-007790-	islet amyloid polypeptide	3375.00	IAPP	3.13	0.70
50017.00	I15	M-007848-	CD5 molecule	921.00	CD5	2.63	1.20
50017.00	I16	M-011932-	high mobility group nucleos	9324.00	HMGN3	1.29	2.54
50017.00	I17	M-007850-	CD6 molecule	923.00	CD6	2.00	1.83

50017.00	I18	M-012105-	major histocompatibility com	3108.00	HLA-DMA	3.00	0.83
50017.00	I19	M-006359-	CD69 molecule	969.00	CD69	1.57	2.26
50017.00	I20	M-019782-	hepatoma-derived growth fa	3068.00	HDGF	5.14	1.31
50017.00	I21	M-019508-	CD72 molecule	971.00	CD72	5.85	2.02
50017.00	I23	M-017568-	CD8a molecule	925.00	CD8A	1.35	2.48
50017.00	J02	M-011650-	epidermal growth factor (be	1950.00	EGF	2.32	1.51
50017.00	J04	M-003659-	ephrin-B2	1948.00	EFNB2	1.99	1.84
50017.00	J05	M-019960-	insulin-like 5	10022.00	INSL5	5.33	1.50
50017.00	J06	M-003658-	ephrin-B1	1947.00	EFNB1	2.84	0.99
50017.00	J07	M-019675-	insulin-like 6	11172.00	INSL6	3.74	0.09
50017.00	J08	M-011649-	ephrin-A5	1946.00	EFNA5	1.15	2.68
50017.00	J09	M-003554-	insulin receptor substrate 2	8660.00	IRS2	3.86	0.03
50017.00	J10	M-011260-	ephrin-A2	1943.00	EFNA2	4.88	1.05
50017.00	J11	M-011480-	insulin receptor substrate 4	8471.00	IRS4	1.93	1.90
50017.00	J12	M-006369-	ephrin-A1	1942.00	EFNA1	2.63	1.20
50017.00	J13	M-007999-	integrin, alpha 10	8515.00	ITGA10	3.79	0.04
50017.00	J14	M-011024-	endothelin 3	1908.00	EDN3	1.93	1.90
50017.00	J15	M-004566-	integrin, alpha 2 (CD49B, alp	3673.00	ITGA2	2.07	1.76
50017.00	J16	M-016692-	endothelin 1	1906.00	EDN1	0.88	2.95
50017.00	J17	M-008001-	integrin, alpha 2b (platelet g	3674.00	ITGA2B	5.64	1.81
50017.00	J18	M-017593-	EGF-like repeats and discoidi	10085.00	EDIL3	3.56	0.27
50017.00	J19	M-004571-	integrin, alpha 3 (antigen CD	3675.00	ITGA3	7.10	3.27
50017.00	J20	M-003654-	ectodysplasin A	1896.00	EDA	10.19	**6.36**
50017.00	J21	M-005189-	integrin, alpha 4 (antigen CD	3676.00	ITGA4	13.49	**9.66**
50017.00	J23	M-008003-	integrin, alpha 5 (fibronectin	3678.00	ITGA5	5.47	1.64
50017.00	K02	M-014014-	hepcidin antimicrobial pepti	57817.00	HAMP	2.47	1.36
50017.00	K04	M-017724-	gastrin-releasing peptide	2922.00	GRP	3.49	0.34
50017.00	K05	M-011975-	CD8b molecule	926.00	CD8B	5.76	1.93
50017.00	K06	M-019220-	growth factor receptor-bour	2885.00	GRB2	7.92	4.09
50017.00	K07	M-011902-	CDK2-associated protein 1	8099.00	CDK2AP1	4.37	0.54
50017.00	K08	M-021356-	glycoprotein VI (platelet)	51206.00	GP6	7.58	3.75
50017.00	K09	M-013210-	glycoprotein hormones, alph	1081.00	CGA	5.27	1.44
50017.00	K10	M-011045-	glycoprotein Ib (platelet), alp	2811.00	GP1BA	1.95	1.88
50017.00	K11	M-011609-	chromogranin B (secretogra	1114.00	CHGB	3.53	0.30
50017.00	K12	M-011288-	gonadotropin-releasing horm	2797.00	GNRH2	9.45	**5.62**
50017.00	K13	M-010709-	chemokine-like factor	51192.00	CKLF	5.77	1.94
50017.00	K14	M-015410-	gonadotropin-releasing horm	2796.00	GNRH1	4.75	0.92
50017.00	K15	M-010749-	CKLF-like MARVEL transmem	112616.00	CMTM7	4.28	0.45
50017.00	K16	M-010597-	golgi apparatus protein 1	2734.00	GLG1	3.72	0.11
50017.00	K17	M-020622-	cardiotrophin-like cytokine f	23529.00	CLCF1	5.34	1.51
50017.00	K18	M-019781-	gastric inhibitory polypeptid	2695.00	GIP	2.91	0.92
50017.00	K19	M-021142-	C-type lectin domain family	51266.00	CLEC1B	14.50	**10.67**
50017.00	K20	M-020860-	ghrelin/obestatin preprohor	51738.00	GHRL	10.42	**6.59**
50017.00	K21	M-021373-	C-type lectin domain family	338339.00	CLEC4D	15.31	**11.48**

50017.00	K23	M-011125- ciliary neurotrophic factor	1270.00	CNTF	5.77	1.94
50017.00	L02	M-004069- dishevelled, dsh homolog 2 (	1856.00	DVL2	2.18	1.65
50017.00	L04	M-004068- dishevelled, dsh homolog 1 (	1855.00	DVL1	4.12	0.29
50017.00	L05	M-007214- integrin, alpha 6	3655.00	ITGA6	8.08	4.25
50017.00	L06	M-019624- heparin-binding EGF-like gro	1839.00	HBEGF	3.77	0.06
50017.00	L07	M-008004- integrin, alpha 7	3679.00	ITGA7	5.56	1.73
50017.00	L08	M-019050- docking protein 5	55816.00	DOK5	4.57	0.74
50017.00	L09	M-010699- integrin, alpha 8	8516.00	ITGA8	6.76	2.93
50017.00	L10	M-015871- docking protein 4	55715.00	DOK4	3.29	0.54
50017.00	L11	M-008005- integrin, alpha 9	3680.00	ITGA9	5.59	1.76
50017.00	L12	M-011562- docking protein 2, 56kDa	9046.00	DOK2	3.13	0.70
50017.00	L13	M-008006- integrin, alpha E (antigen CD	3682.00	ITGAE	3.23	0.60
50017.00	L14	M-007883- deleted in malignant brain tu	1755.00	DMBT1	8.50	4.67
50017.00	L15	M-008007- integrin, alpha L (antigen CD	3683.00	ITGAL	9.25	**5.42**
50017.00	L16	M-010490- delta-like 4 (Drosophila)	54567.00	DLL4	2.58	1.25
50017.00	L17	M-008008- integrin, alpha M (compleme	3684.00	ITGAM	3.34	0.49
50017.00	L18	M-013247- glycoprotein Ib (platelet), be	2812.00	GP1BB	3.11	0.72
50017.00	L19	M-008009- integrin, alpha X (compleme	3687.00	ITGAX	11.74	**7.91**
50017.00	L20	M-017473- left-right determination fact	7044.00	LEFTY2	4.74	0.91
50017.00	L21	M-004506- integrin, beta 1 (fibronectin	3688.00	ITGB1	18.25	**14.42**
50017.00	L23	M-008010- integrin, beta 2 (complemen	3689.00	ITGB2	5.94	2.11
50017.00	M02	M-019005- growth hormone releasing h	2691.00	GHRH	2.11	1.72
50017.00	M04	M-011668- growth hormone 2	2689.00	GH2	5.27	1.44
50017.00	M05	M-007859- complement component (3b	1378.00	CR1	5.17	1.34
50017.00	M06	M-007915- GDNF family receptor alpha	2676.00	GFRA3	6.54	2.71
50017.00	M07	M-007861- complement component (3d	1380.00	CR2	4.82	0.99
50017.00	M08	M-011040- glial cell derived neurotrophi	2668.00	GDNF	6.28	2.45
50017.00	M09	M-011165- corticotropin releasing horm	1392.00	CRH	8.55	4.72
50017.00	M10	M-012040- growth differentiation factor	2661.00	GDF9	4.22	0.39
50017.00	M11	M-017514- colony stimulating factor 1 (	1435.00	CSF1	4.88	1.05
50017.00	M12	M-012039- growth differentiation factor	2660.00	GDF8	8.45	4.62
50017.00	M13	M-011166- colony stimulating factor 2 (	1437.00	CSF2	12.89	**9.06**
50017.00	M14	M-012271- growth differentiation factor	8200.00	GDF5	6.93	3.10
50017.00	M15	M-007865- colony stimulating factor 2 r	1439.00	CSF2RB	8.36	4.53
50017.00	M16	M-013233- growth differentiation factor	2658.00	GDF2	3.15	0.68
50017.00	M17	M-007866- colony stimulating factor 3 (	1440.00	CSF3	4.09	0.26
50017.00	M18	M-019875- growth differentiation factor	9518.00	GDF15	1.41	2.42
50017.00	M19	M-007867- colony stimulating factor 3 r	1441.00	CSF3R	10.54	**6.71**
50017.00	M20	M-012086- growth differentiation factor	10220.00	GDF11	7.77	3.94
50017.00	M21	M-010962- chorionic somatomammotro	1444.00	CSHL1	2.15	1.68
50017.00	M23	M-020183- cardiotrophin 1	1489.00	CTF1	1.99	1.84
50017.00	N02	M-020079- neuromedin U	10874.00	NMU	2.43	1.40
50017.00	N04	M-003950- neuromedin B	4828.00	NMB	2.66	1.17
50017.00	N05	M-004124- integrin, beta 3 (platelet glyc	3690.00	ITGB3	2.38	1.45

50017.00	N06	M-019673-	nerve growth factor, beta pc	4803.00	NGFB	4.80	0.97
50017.00	N07	M-017722-	integrin beta 3 binding prote	23421.00	ITGB3BP	3.48	0.35
50017.00	N08	M-011091-	Norrie disease (pseudogliom	4693.00	NDP	4.12	0.29
50017.00	N09	M-008011-	integrin, beta 4	3691.00	ITGB4	4.97	1.14
50017.00	N10	M-019547-	NCK adaptor protein 2	8440.00	NCK2	4.20	0.37
50017.00	N11	M-004125-	integrin, beta 5	3693.00	ITGB5	8.12	4.29
50017.00	N12	M-006354-	NCK adaptor protein 1	4690.00	NCK1	4.11	0.28
50017.00	N13	M-008012-	integrin, beta 6	3694.00	ITGB6	7.38	3.55
50017.00	N14	M-004769-	myeloid differentiation prim	4615.00	MYD88	11.57	**7.74**
50017.00	N15	M-017187-	jagged 2	3714.00	JAG2	8.57	4.74
50017.00	N16	M-011730-	mannose receptor, C type 1	4360.00	MRC1	2.07	1.76
50017.00	N17	M-011184-	KIT ligand	4254.00	KITLG	10.81	**6.98**
50017.00	N18	M-020116-	melanoma inhibitory activity	8190.00	MIA	4.36	0.53
50017.00	N19	M-020139-	killer cell lectin-like receptor	10748.00	KLRA1	10.00	**6.17**
50017.00	N20	M-003677-	midkine (neurite growth-pro	4192.00	MDK	7.40	3.57
50017.00	N21	M-013593-	killer cell lectin-like receptor	8302.00	KLRC4	19.58	**15.75**
50017.00	N23	M-011304-	killer cell lectin-like receptor	3824.00	KLRD1	14.37	**10.54**
50017.00	O02	M-011976-	growth differentiation factor	2662.00	GDF10	2.26	1.57
50017.00	O04	M-013088-	growth differentiation factor	2657.00	GDF1	7.47	3.64
50017.00	O05	M-007870-	chemokine (C-X3-C motif) lig	6376.00	CX3CL1	0.90	2.93
50017.00	O06	M-011174-	gastrin	2520.00	GAST	2.40	1.43
50017.00	O07	M-007872-	chemokine (C-X-C motif) liga	6373.00	CXCL11	1.37	2.46
50017.00	O08	M-003553-	GRB2-associated binding prc	2549.00	GAB1	8.15	4.32
50017.00	O09	M-007874-	chemokine (C-X-C motif) liga	10563.00	CXCL13	2.28	1.55
50017.00	O10	M-012537-	follicle stimulating hormone,	2488.00	FSHB	8.88	5.05
50017.00	O11	M-021477-	cytoplasmic FMR1 interactin	26999.00	CYFIP2	5.02	1.19
50017.00	O12	M-020173-	frizzled-related protein	2487.00	FRZB	2.39	1.44
50017.00	O13	M-010452-	dystroglycan 1 (dystrophin-a	1605.00	DAG1	1.36	2.47
50017.00	O14	M-019038-	fibroblast growth factor rece	10817.00	FRS3	3.42	0.41
50017.00	O15	M-006488-	diazepam binding inhibitor (	1622.00	DBI	4.46	0.63
50017.00	O16	M-011190-	folate receptor 3 (gamma)	2352.00	FOLR3	4.99	1.16
50017.00	O17	M-018909-	CD302 molecule	9936.00	CD302	1.88	1.95
50017.00	O18	M-009506-	delta-like 3 (Drosophila)	10683.00	DLL3	3.25	0.58
50017.00	O19	M-011986-	DiGeorge syndrome critical r	9993.00	DGCR2	5.79	1.96
50017.00	O20	M-008495-	discs, large homolog 5 (Dros	9231.00	DLG5	4.80	0.97
50017.00	O21	M-010347-	diaphanous homolog 1 (Dros	1729.00	DIAPH1	2.90	0.93
50017.00	O23	M-027334-	cortistatin	1325.00	CORT	1.96	1.87
50017.00	P02	M-015362-	SMAD family member 6	4091.00	SMAD6	2.05	1.78
50017.00	P04	M-020015-	CD180 molecule	4064.00	CD180	10.97	**7.14**
50017.00	P05	M-020680-	killer cell lectin-like receptor	51348.00	KLRF1	3.52	0.31
50017.00	P06	M-008023-	lymphotoxin beta receptor (	4055.00	LTBR	4.36	0.53
50017.00	P07	M-021505-	lamin B receptor	3930.00	LBR	1.81	2.02
50017.00	P08	M-019552-	latent transforming growth f	8425.00	LTBP4	2.04	1.79
50017.00	P09	M-011074-	leptin (obesity homolog, mo	3952.00	LEP	2.28	1.55

50017.00	P10	M-010521-	lymphotoxin beta (TNF supe	4050.00	LTB	2.66	1.17
50017.00	P11	M-011718-	lectin, galactoside-binding, s	3956.00	LGALS1	9.07	**5.24**
50017.00	P12	M-010520-	lymphotoxin alpha (TNF supe	4049.00	LTA	2.45	1.38
50017.00	P13	M-008016-	lectin, galactoside-binding, s	3959.00	LGALS3BP	3.23	0.60
50017.00	P14	M-012640-	lymphocyte-specific protein	4046.00	LSP1	2.12	1.71
50017.00	P15	M-011319-	lectin, galactoside-binding, s	3965.00	LGALS9	3.28	0.55
50017.00	P16	M-003610-	low density lipoprotein rece	4043.00	LRPAP1	5.81	1.98
50017.00	P17	M-011183-	luteinizing hormone beta po	3972.00	LHB	2.16	1.67
50017.00	P18	M-011802-	low density lipoprotein rece	7804.00	LRP8	4.19	0.36
50017.00	P19	M-012491-	C-type lectin domain family	29121.00	CLEC2D	10.12	**6.29**
50017.00	P20	M-003845-	low density lipoprotein rece	4040.00	LRP6	3.67	0.16
50017.00	P21	M-010665-	low density lipoprotein-relat	53353.00	LRP1B	3.98	0.15
50017.00	P23	M-012673-	low density lipoprotein-relat	4036.00	LRP2	3.09	0.74
					mdmdMAD	3.83	1.69
					3MAD	11.48	5.08
					MADc		2.51
50017.00	C22		2198.00	12.06			
50017.00	D22					21.81	
50017.00	E22					32.56	
50017.00	F22					24.49	
					mn	26.28	
					sd	5.60	
50017.00	G22		456.00	16.67		4.47	
50017.00	H22					2.67	
50017.00	I22					1.60	
50017.00	J22					0.74	
					mn	2.37	
					sd	1.61	
						16.79	
						4.82	
						21.61	
						23.91	
						0.90	
						0.10	

50017.00	G03	M-003290-	polo-like kinase 1 (Drosophil	5347.00	PLK1 SMAF	2.38
50017.00	H03	M-003290-	polo-like kinase 1 (Drosophil	5347.00	PLK1 SMAF	1.66
50017.00	I03	D-001206-	siControl non-targeting siRNA #2			1.42
50017.00	J03	D-001206-	siControl non-targeting siRNA #2			3.82

50017.00	K03	D-001600-(	siGLO RISC-free siRNA	11.49
50017.00	L03	D-001600-(	siGLO RISC-free siRNA	9.11

robust Z	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**		
-1.46	1.24	4.93	-1.24	2.55	3.25	-0.92		
-0.07	5.11	1.06	-0.27	5.10	0.70	-0.20		
-0.50	14.36	**8.19**	2.07	15.25	**9.45**	2.69	x	toxic a,b
-0.29	3.31	2.86	-0.72	7.98	2.18	0.62		
-1.25	1.53	4.64	-1.17	3.33	2.47	-0.70		
-0.70	1.96	4.21	-1.06	4.94	0.86	-0.24		
-1.09	4.10	2.07	-0.52	8.26	2.46	0.70		
-1.01	2.83	3.34	-0.84	3.08	2.72	-0.77		
-0.78	5.59	0.58	-0.15	4.51	1.29	-0.37		
-0.56	6.12	0.05	-0.01	9.35	3.55	1.01		
-0.28	6.49	0.32	0.08	5.61	0.19	-0.05		
2.72	14.59	**8.42**	2.12	15.21	**9.41**	2.68	y	
-0.75	6.81	0.64	0.16	5.48	0.32	-0.09		
0.49	7.14	0.97	0.24	12.28	6.48	1.85		
-0.58	5.79	0.38	-0.10	4.20	1.60	-0.46		
0.52	6.43	0.26	0.07	13.13	**7.33**	2.09		
-0.77	11.10	4.93	1.24	10.95	5.15	1.47		
0.82	13.26	7.09	1.79	24.21	**18.41**	5.24		
0.25	14.94	**8.77**	2.21	12.40	6.60	1.88		
2.02	20.55	**14.38**	3.63	10.50	4.70	1.34	x	toxic a,b,c
-1.42	11.39	5.22	1.32	0.41	5.39	-1.53		
-1.26	4.42	1.75	-0.44	0.64	5.16	-1.47		
-0.86	4.72	1.45	-0.37	2.05	3.75	-1.07		
-0.26	6.79	0.62	0.16	3.43	2.37	-0.67		
-1.21	7.42	1.25	0.32	0.73	5.07	-1.44		
-0.50	14.84	**8.67**	2.19	10.07	4.27	1.21		
-0.11	13.60	7.43	1.87	3.20	2.60	-0.74		
-0.14	6.51	0.34	0.09	1.24	4.56	-1.30		
0.06	11.01	4.84	1.22	3.37	2.43	-0.69		
-0.13	10.56	4.39	1.11	4.48	1.32	-0.38		
-0.77	5.21	0.96	-0.24	3.73	2.07	-0.59		
0.02	3.71	2.46	-0.62	1.40	4.40	-1.25		
-0.03	7.10	0.93	0.23	2.94	2.86	-0.81		
-0.69	3.38	2.79	-0.70	2.53	3.27	-0.93		
-1.13	3.53	2.64	-0.67	4.81	0.99	-0.28		
-0.93	3.55	2.62	-0.66	3.66	2.14	-0.61		
0.92	4.49	1.68	-0.42	12.26	6.46	1.84		
-0.12	1.98	4.19	-1.06	10.07	4.27	1.21		
1.77	3.47	2.70	-0.68	11.75	5.95	1.69		
-0.25	5.59	0.58	-0.15	8.91	3.11	0.89		
-1.10	4.12	2.05	-0.52	1.24	4.56	-1.30		
0.11	2.79	3.38	-0.85	2.89	2.91	-0.83		
0.09	3.26	2.91	-0.73	2.35	3.45	-0.98		

-0.07	5.21	0.96	-0.24	1.67	4.13	-1.18	
-1.21	1.69	4.48	-1.13	0.76	5.04	-1.43	
0.97	9.80	3.63	0.92	13.12	**7.32**	2.08	
-0.81	4.48	1.69	-0.43	1.37	4.43	-1.26	
-0.72	6.57	0.40	0.10	2.26	3.54	-1.01	
-0.37	5.87	0.30	-0.08	3.76	2.04	-0.58	
-0.50	12.50	6.33	1.60	8.49	2.69	0.77	
-0.32	2.17	4.00	-1.01	5.94	0.14	0.04	
-0.41	4.88	1.29	-0.32	3.54	2.26	-0.64	
-0.68	3.75	2.42	-0.61	2.62	3.18	-0.90	
0.17	8.83	2.66	0.67	4.88	0.92	-0.26	
0.68	3.98	2.19	-0.55	6.89	1.09	0.31	
-0.85	4.30	1.87	-0.47	8.38	2.58	0.74	
0.07	8.55	2.38	0.60	6.03	0.23	0.07	
3.35	19.36	**13.19**	3.33	22.11	**16.31**	4.64	y
-0.70	5.55	0.62	-0.16	6.46	0.66	0.19	
1.20	16.27	**10.10**	2.55	5.42	0.38	-0.11	
-1.05	0.36	5.81	-1.47	1.36	4.44	-1.26	
1.58	9.93	3.76	0.95	7.51	1.71	0.49	
0.47	2.62	3.55	-0.90	2.55	3.25	-0.92	
0.51	2.16	4.01	-1.01	0.91	4.89	-1.39	
-0.61	1.42	4.75	-1.20	1.39	4.41	-1.25	
-0.34	4.12	2.05	-0.52	3.88	1.92	-0.55	
-0.67	2.16	4.01	-1.01	3.44	2.36	-0.67	
0.65	2.50	3.67	-0.92	2.08	3.72	-1.06	
0.83	2.28	3.89	-0.98	1.48	4.32	-1.23	
-0.15	3.19	2.98	-0.75	2.49	3.31	-0.94	
-0.56	1.09	5.08	-1.28	2.69	3.11	-0.89	
1.42	5.85	0.32	-0.08	4.68	1.12	-0.32	
0.40	1.94	4.23	-1.07	0.30	5.50	-1.57	
1.29	3.01	3.16	-0.80	3.20	2.60	-0.74	
0.84	3.61	2.56	-0.65	4.33	1.47	-0.42	
2.08	1.77	4.40	-1.11	3.64	2.16	-0.61	
-0.16	4.86	1.31	-0.33	6.44	0.64	0.18	
3.01	6.56	0.39	0.10	3.42	2.38	-0.68	
3.26	1.86	4.31	-1.09	11.37	5.57	1.59	
0.22	2.61	3.57	-0.90	4.28	1.52	-0.43	
-0.46	3.52	2.65	-0.67	2.53	3.27	-0.93	
-0.47	3.94	2.23	-0.56	0.51	5.29	-1.50	
0.11	7.45	1.28	0.32	6.85	1.05	0.30	
-0.80	2.84	3.33	-0.84	2.01	3.79	-1.08	
0.10	5.68	0.49	-0.12	4.34	1.46	-0.42	
1.88	30.40	**24.23**	6.11	4.46	1.34	-0.38	
0.36	5.31	0.86	-0.22	3.43	2.37	-0.67	

-0.55	2.18	3.99	-1.01	0.75	5.05	-1.44	
-0.18	10.73	4.56	1.15	3.19	2.61	-0.74	
2.45	8.92	2.75	0.69	10.55	4.75	1.35	
0.06	2.90	3.27	-0.82	1.38	4.42	-1.26	
-0.13	9.23	3.06	0.77	4.82	0.98	-0.28	
2.01	15.56	**9.39**	2.37	11.12	5.32	1.51	
4.20	11.66	5.49	1.38	18.52	**12.72**	3.62	y
3.58	9.50	3.33	0.84	5.06	0.74	-0.21	
0.71	6.78	0.61	0.15	7.41	1.61	0.46	
2.69	15.75	**9.58**	2.42	12.82	7.02	2.00	y
0.11	2.12	4.05	-1.02	4.32	1.48	-0.42	
2.22	10.52	4.35	1.10	12.71	6.91	1.97	
1.36	13.93	7.76	1.96	5.88	0.08	0.02	
0.09	3.51	2.66	-0.67	3.28	2.52	-0.72	
-0.70	3.46	2.71	-0.68	5.17	0.63	-0.18	
0.55	8.99	2.82	0.71	5.31	0.49	-0.14	
-0.24	6.27	0.10	0.03	7.42	1.62	0.46	
-0.74	2.70	3.47	-0.87	6.67	0.87	0.25	
-0.29	6.19	0.02	0.01	4.26	1.54	-0.44	
-0.75	1.88	4.29	-1.08	3.92	1.88	-0.53	
-0.22	7.54	1.37	0.35	6.57	0.77	0.22	
-0.61	3.29	2.88	-0.73	4.36	1.44	-0.41	
0.62	3.44	2.73	-0.69	2.30	3.50	-1.00	
-0.11	5.54	0.63	-0.16	7.84	2.04	0.58	
0.25	10.02	3.85	0.97	6.95	1.15	0.33	
-0.52	5.94	0.24	-0.06	4.18	1.62	-0.46	
0.66	16.43	**10.26**	2.59	4.91	0.89	-0.25	
1.80	8.97	2.80	0.71	4.97	0.83	-0.24	
4.39	9.01	2.84	0.72	4.25	1.55	-0.44	
3.20	6.86	0.69	0.17	5.30	0.50	-0.14	
5.20	12.54	6.37	1.61	8.56	2.76	0.79	
1.45	4.34	1.83	-0.46	4.06	1.74	-0.49	
1.40	3.77	2.40	-0.60	4.62	1.18	-0.34	
1.71	14.58	**8.41**	2.12	19.47	**13.67**	3.89	y
8.61	26.46	**20.29**	5.12	39.26	**33.46**	9.52	y
-0.46	0.79	5.38	-1.36	4.18	1.62	-0.46	
-0.09	7.27	1.10	0.28	10.12	4.32	1.23	
-0.42	3.42	2.75	-0.69	8.48	2.68	0.76	
-1.13	9.64	3.47	0.88	3.70	2.10	-0.60	
-0.77	5.08	1.09	-0.28	5.82	0.02	0.01	
0.72	11.58	5.41	1.36	14.53	**8.73**	2.49	
-1.17	10.94	4.77	1.20	8.12	2.32	0.66	
1.05	9.04	2.87	0.72	8.32	2.52	0.72	
-0.26	6.55	0.38	0.10	12.47	6.67	1.90	

0.33	7.35	1.18	0.30	7.97	2.17	0.62		
0.12	4.56	1.61	-0.41	6.04	0.24	0.07		
1.05	6.31	0.14	0.04	9.65	3.85	1.10		
0.79	10.28	4.11	1.04	11.08	5.28	1.50		
-0.23	7.36	1.19	0.30	6.36	0.56	0.16		
0.29	10.80	4.63	1.17	6.91	1.11	0.32		
1.05	9.01	2.84	0.72	7.02	1.22	0.35		
0.18	4.33	1.84	-0.46	2.78	3.02	-0.86		
0.56	8.59	2.42	0.61	9.03	3.23	0.92		
-0.12	8.90	2.73	0.69	7.22	1.42	0.41		
4.07	21.00	**14.83**	3.74	18.48	**12.68**	3.61	y	
-0.06	5.95	0.22	-0.05	5.79	0.01	0.00		
0.34	8.38	2.21	0.56	8.32	2.52	0.72		
0.07	14.29	**8.12**	2.05	10.15	4.35	1.24		
-0.99	10.81	4.64	1.17	1.10	4.70	-1.34		
-1.22	3.53	2.64	-0.67	4.55	1.25	-0.36		
0.03	8.81	2.64	0.67	15.78	**9.98**	2.84		
-0.86	6.85	0.68	0.17	8.04	2.24	0.64		
-0.69	3.46	2.71	-0.68	7.19	1.39	0.40		
-0.99	4.76	1.41	-0.35	1.61	4.19	-1.19		
-0.61	5.24	0.93	-0.23	4.09	1.71	-0.49		
-1.15	5.90	0.27	-0.07	4.63	1.17	-0.33		
-0.70	6.09	0.08	-0.02	5.84	0.04	0.01		
0.21	6.75	0.58	0.15	5.91	0.11	0.03		
1.60	16.45	**10.28**	2.59	16.63	**10.83**	3.08	y	
-0.69	7.56	1.39	0.35	5.04	0.76	-0.22		
-0.48	14.05	7.88	1.99	2.51	3.29	-0.94		
-0.81	5.24	0.93	-0.24	2.42	3.38	-0.96		
-0.10	7.25	1.08	0.27	5.50	0.30	-0.08		
-0.82	6.91	0.74	0.19	6.44	0.64	0.18		
-0.56	12.96	6.79	1.71	5.26	0.54	-0.15		
0.91	15.12	**8.95**	2.26	13.23	**7.43**	2.12	x	toxic a,b
-1.15	7.27	1.10	0.28	1.66	4.14	-1.18		
0.30	5.02	1.15	-0.29	5.70	0.10	-0.03		
1.83	22.92	**16.75**	4.22	16.03	**10.23**	2.91	y	
-0.52	10.46	4.29	1.08	10.93	5.13	1.46		
0.47	13.62	7.45	1.88	9.21	3.41	0.97		
-0.83	5.72	0.45	-0.11	3.65	2.15	-0.61		
-0.78	17.00	**10.83**	2.73	7.81	2.01	0.57		
0.01	8.61	2.44	0.62	4.20	1.60	-0.46		
-0.28	8.52	2.35	0.59	5.91	0.11	0.03		
-0.48	12.29	6.12	1.54	5.32	0.48	-0.14		
-1.01	5.15	1.02	-0.26	5.67	0.13	-0.04		
-0.73	7.16	0.99	0.25	6.10	0.30	0.09		

-0.33	9.47	3.30	0.83	11.17	5.37	1.53		
-0.90	6.01	0.16	-0.04	4.78	1.02	-0.29		
0.53	6.75	0.58	0.15	8.84	3.04	0.86		
0.81	12.07	5.90	1.49	5.97	0.17	0.05		
-0.99	10.50	4.33	1.09	2.44	3.36	-0.96		
-0.60	5.82	0.35	-0.09	7.59	1.79	0.51		
-0.73	7.11	0.94	0.24	2.70	3.10	-0.88		
0.60	11.36	5.19	1.31	8.81	3.01	0.86		
-0.39	6.81	0.64	0.16	3.55	2.25	-0.64		
-0.04	8.42	2.25	0.57	11.59	5.79	1.65		
-1.07	4.02	2.15	-0.54	2.22	3.58	-1.02		
0.01	4.69	1.48	-0.37	3.59	2.21	-0.63		
0.42	7.62	1.45	0.36	12.09	6.29	1.79		
-0.76	5.37	0.80	-0.20	2.86	2.94	-0.84		
-0.48	7.20	1.03	0.26	7.70	1.90	0.54		
-0.01	5.17	1.00	-0.25	6.46	0.66	0.19		
-0.75	4.14	2.03	-0.51	3.26	2.54	-0.72		
-0.70	13.33	7.16	1.81	7.97	2.17	0.62		
-1.17	8.51	2.34	0.59	1.94	3.86	-1.10		
0.72	10.83	4.66	1.18	5.48	0.32	-0.09		
-0.11	5.07	1.10	-0.28	7.32	1.52	0.43		
1.31	8.16	1.99	0.50	8.54	2.74	0.78		
2.54	11.81	5.64	1.42	15.70	**9.90**	2.82	y	
3.85	14.41	**8.24**	2.08	14.11	**8.31**	2.37	y	
0.66	11.01	4.84	1.22	8.26	2.46	0.70		
-0.54	2.34	3.83	-0.97	3.87	1.93	-0.55		
-0.13	9.34	3.17	0.80	6.41	0.61	0.17		
0.77	7.96	1.79	0.45	8.97	3.17	0.90		
1.63	11.20	5.03	1.27	11.18	5.38	1.53		
0.22	5.99	0.18	-0.05	6.95	1.15	0.33		
1.50	9.08	2.91	0.73	12.03	6.23	1.77		
0.58	10.65	4.48	1.13	8.16	2.36	0.67		
-0.75	7.04	0.87	0.22	9.16	3.36	0.96		
-0.12	3.24	2.93	-0.74	9.08	3.28	0.94		
2.24	11.84	5.67	1.43	21.45	**15.65**	4.45	x	toxic a,b
0.78	4.16	2.01	-0.51	11.21	5.41	1.54		
0.37	8.13	1.96	0.49	7.68	1.88	0.53		
0.18	8.21	2.04	0.51	15.47	**9.67**	2.75		
-0.04	3.52	2.65	-0.67	4.42	1.38	-0.39		
0.60	7.78	1.61	0.41	5.84	0.04	0.01		
-0.36	6.13	0.04	-0.01	8.08	2.28	0.65		
4.26	9.19	3.02	0.76	14.81	**9.01**	2.56	y	
2.63	7.73	1.56	0.39	14.21	**8.41**	2.39	x	debris B,c
4.58	9.33	3.16	0.80	11.90	6.10	1.74		

0.78	5.77	0.40	-0.10	6.35	0.55	0.16	
-0.66	6.15	0.02	-0.01	5.60	0.20	-0.06	
0.12	6.84	0.67	0.17	2.86	2.94	-0.83	
1.70	9.74	3.57	0.90	20.10	**14.30**	4.07	
-0.02	5.65	0.52	-0.13	4.74	1.06	-0.30	
0.69	2.97	3.20	-0.81	4.76	1.04	-0.30	
0.30	3.05	3.12	-0.79	8.07	2.27	0.65	
1.17	5.08	1.09	-0.28	9.69	3.89	1.11	
-0.21	2.28	3.89	-0.98	3.95	1.85	-0.53	
0.70	2.94	3.23	-0.81	4.48	1.32	-0.38	
-0.28	1.73	4.44	-1.12	5.63	0.17	-0.05	
-0.24	1.77	4.40	-1.11	2.96	2.84	-0.81	
1.87	4.00	2.17	-0.55	2.61	3.19	-0.91	
2.16	5.39	0.78	-0.20	5.09	0.71	-0.20	
-0.50	1.33	4.84	-1.22	2.12	3.68	-1.05	
-0.19	5.81	0.36	-0.09	7.50	1.70	0.48	
-0.28	2.47	3.70	-0.93	4.21	1.59	-0.45	
3.16	15.06	**8.89**	2.24	10.80	5.00	1.42	y
0.37	4.66	1.51	-0.38	5.41	0.39	-0.11	
5.75	19.05	**12.88**	3.25	21.82	**16.02**	4.56	y
0.84	8.13	1.96	0.50	8.57	2.77	0.79	
-0.68	3.00	3.17	-0.80	2.66	3.14	-0.89	
0.58	6.39	0.22	0.06	4.67	1.13	-0.32	
0.54	5.32	0.85	-0.21	6.57	0.77	0.22	
1.08	5.51	0.66	-0.17	5.25	0.55	-0.15	
0.39	4.94	1.23	-0.31	6.34	0.54	0.16	
0.98	2.92	3.25	-0.82	4.23	1.57	-0.45	
1.88	11.76	5.59	1.41	10.36	4.56	1.30	
0.16	5.78	0.39	-0.10	6.54	0.74	0.21	
0.42	4.93	1.24	-0.31	8.58	2.78	0.79	
1.84	3.00	3.17	-0.80	7.01	1.21	0.34	
3.61	13.79	7.62	1.92	16.26	**10.46**	2.98	y
1.24	2.67	3.50	-0.88	5.77	0.03	-0.01	
1.81	8.44	2.27	0.57	11.47	5.67	1.61	
-0.27	3.25	2.92	-0.74	6.70	0.90	0.26	
0.10	5.20	0.97	-0.25	8.05	2.25	0.64	
-0.96	2.64	3.53	-0.89	6.80	1.00	0.28	
2.68	10.33	4.16	1.05	16.28	**10.48**	2.98	y
1.57	6.62	0.45	0.11	11.00	5.20	1.48	
-0.67	2.30	3.87	-0.98	3.27	2.53	-0.72	
-0.73	3.80	2.37	-0.60	4.44	1.36	-0.39	
-0.55	5.34	0.83	-0.21	7.60	1.80	0.51	
-0.47	1.79	4.38	-1.10	1.58	4.22	-1.20	
-0.57	7.98	1.81	0.46	5.80	0.00	0.00	

0.39	6.55	0.38	0.10	5.45	0.35	-0.10		
-0.14	3.27	2.90	-0.73	5.57	0.23	-0.06		
0.12	12.28	6.11	1.54	6.22	0.42	0.12		
0.46	5.89	0.28	-0.07	3.19	2.61	-0.74		
0.15	5.85	0.32	-0.08	6.60	0.80	0.23		
1.71	8.35	2.18	0.55	12.31	6.51	1.85		
0.11	3.81	2.36	-0.59	4.04	1.76	-0.50		
1.42	4.95	1.22	-0.31	4.39	1.41	-0.40		
3.09	7.52	1.35	0.34	4.54	1.26	-0.36		
1.89	10.72	4.55	1.15	5.01	0.79	-0.22		
-0.70	1.47	4.70	-1.19	2.22	3.58	-1.02		
2.78	11.29	5.12	1.29	8.54	2.74	0.78		
0.21	4.61	1.56	-0.39	2.72	3.08	-0.88		
2.46	3.91	2.26	-0.57	6.08	0.28	0.08		
1.42	4.93	1.24	-0.31	6.49	0.69	0.20		
6.28	14.41	**8.24**	2.08	9.10	3.30	0.94	x	toxic a,b
4.20	3.19	2.98	-0.75	13.34	**7.54**	2.15	x	art a,b
-0.63	4.56	1.61	-0.41	4.16	1.64	-0.47		
1.45	23.04	**16.87**	4.26	19.76	**13.96**	3.97	x	toxic a,b,c
-1.17	7.66	1.49	0.38	4.96	0.84	-0.24		
-0.57	11.90	5.73	1.44	4.52	1.28	-0.36		
-0.98	7.19	1.02	0.26	5.39	0.41	-0.12		
1.72	5.76	0.41	-0.10	6.37	0.57	0.16		
-0.62	5.83	0.34	-0.09	5.24	0.56	-0.16		
2.01	16.64	**10.47**	2.64	9.94	4.14	1.18		
0.48	4.14	2.03	-0.51	4.16	1.64	-0.47		
-0.57	5.11	1.06	-0.27	5.95	0.15	0.04		
-0.98	11.33	5.16	1.30	6.35	0.55	0.16		
-0.16	6.50	0.33	0.08	3.50	2.30	-0.65		
0.25	4.65	1.52	-0.38	3.69	2.11	-0.60		
0.47	6.71	0.54	0.14	2.06	3.74	-1.06		
-0.78	8.70	2.53	0.64	4.44	1.36	-0.39		
-0.23	14.42	**8.25**	2.08	4.20	1.60	-0.45		
0.78	3.17	3.00	-0.76	2.25	3.55	-1.01		
0.39	10.70	4.53	1.14	2.55	3.25	-0.92		
-0.37	7.32	1.15	0.29	2.49	3.31	-0.94		
-0.75	10.92	4.75	1.20	5.85	0.05	0.02		
-0.71	3.54	2.63	-0.66	2.77	3.03	-0.86		
2.85	11.77	5.60	1.41	15.33	**9.53**	2.71	x	toxic a,b,c
-0.12	1.35	4.82	-1.22	5.77	0.03	-0.01		
0.21	12.90	6.73	1.70	13.06	**7.26**	2.07		
-0.81	7.29	1.12	0.28	7.91	2.11	0.60		
-0.71	5.87	0.30	-0.08	1.99	3.81	-1.08		
-0.62	4.96	1.21	-0.31	13.72	**7.92**	2.25		

-0.46	5.94	0.23	-0.06	7.80	2.00	0.57		
2.09	15.66	**9.49**	2.39	19.62	**13.82**	3.93	x	toxic a,b,c
-0.55	0.24	5.93	-1.50	8.46	2.66	0.76		
-0.24	0.86	5.31	-1.34	15.18	**9.38**	2.67		
-0.68	12.65	6.48	1.64	3.68	2.12	-0.60		
-0.22	7.00	0.83	0.21	7.81	2.01	0.57		
0.79	1.87	4.30	-1.08	3.82	1.98	-0.56		
-0.66	1.80	4.37	-1.10	14.83	**9.03**	2.57		
0.15	15.72	**9.55**	2.41	11.79	5.99	1.71		
2.51	19.70	**13.53**	3.41	14.07	**8.27**	2.36	x	toxic a,b,c
-0.06	9.36	3.19	0.81	6.47	0.67	0.19		
0.06	0.44	5.73	-1.45	6.09	0.29	0.08		
-0.29	5.99	0.18	-0.05	8.60	2.80	0.80		
	6.17	2.68		5.80	2.37			
		8.04			7.12			
		3.96			3.51			
21.77		35.73						
21.20		30.22						
23.28		37.68						
17.56		21.54						
20.95		31.30						
2.42		7.23						
		7.94						
5.08		4.88						
6.96		1.93						
8.52		4.71						
6.85		4.87						
1.72		2.45						
7.27		21.68						
5.17		5.00						
12.45		26.69						
14.10		26.43						
0.88		1.01						
0.12		-0.01						

26.85		9.59
46.04		33.20
8.77		7.44
7.14		4.97

12.15	11.98
10.31	14.86

					% inf
50018.00	A02	M-003429- nuclear receptor subfamily 5, g	2516.00	NR5A1	1717.00
50018.00	A04	M-003428- nuclear receptor subfamily 4, g	8013.00	NR4A3	2091.00
50018.00	A05	M-010527- nephroblastoma overexpresse	4856.00	NOV	1558.00
50018.00	A06	M-003427- nuclear receptor subfamily 4, g	4929.00	NR4A2	1469.00
50018.00	A07	M-012729- natriuretic peptide precursor A	4878.00	NPPA	884.00
50018.00	A08	M-003426- nuclear receptor subfamily 4, g	3164.00	NR4A1	715.00
50018.00	A09	M-008100- tumor necrosis factor receptor	7293.00	TNFRSF4	1146.00
50018.00	A10	M-003425- nuclear receptor subfamily 3, g	4306.00	NR3C2	1516.00
50018.00	A11	M-011524- tumor necrosis factor (ligand) s	8743.00	TNFSF10	463.00
50018.00	A12	M-003424- nuclear receptor subfamily 3, g	2908.00	NR3C1	513.00
50018.00	A13	M-011499- tumor necrosis factor (ligand) s	8600.00	TNFSF11	762.00
50018.00	A14	M-003423- nuclear receptor subfamily 2, g	2063.00	NR2F6	754.00
50018.00	A15	M-010629- tumor necrosis factor (ligand) s	8742.00	TNFSF12	1342.00
50018.00	A16	M-003422- nuclear receptor subfamily 2, g	7026.00	NR2F2	800.00
50018.00	A17	M-011523- tumor necrosis factor (ligand) s	8741.00	TNFSF13	686.00
50018.00	A18	M-003421- nuclear receptor subfamily 2, g	7025.00	NR2F1	1896.00
50018.00	A19	M-017586- tumor necrosis factor (ligand) s	10673.00	TNFSF13B	803.00
50018.00	A20	M-003420- nuclear receptor subfamily 2, g	10002.00	NR2E3	661.00
50018.00	A21	M-017588- tumor necrosis factor (ligand) s	9966.00	TNFSF15	1567.00
50018.00	A23	M-011981- tumor necrosis factor (ligand) s	8995.00	TNFSF18	1025.00
50018.00	B02	M-011849- extracellular matrix protein 1	1893.00	ECM1	1057.00
50018.00	B04	M-019800- desmoplakin	1832.00	DSP	1627.00
50018.00	B05	M-003430- nuclear receptor subfamily 5, g	2494.00	NR5A2	2427.00
50018.00	B06	M-012365- dynactin 3 (p22)	11258.00	DCTN3	1861.00
50018.00	B07	M-003431- nuclear receptor subfamily 6, g	2649.00	NR6A1	893.00
50018.00	B08	M-004416- death associated protein 3	7818.00	DAP3	999.00
50018.00	B09	M-003778- paired box gene 8	7849.00	PAX8	836.00
50018.00	B10	M-010551- coiled-coil domain containing 6	8030.00	CCDC6	538.00
50018.00	B11	M-008556- peroxisome proliferator-activa	133522.00	PPARGC1B	1632.00
50018.00	B12	M-013142- crystallin, gamma C	1420.00	CRYGC	1456.00
50018.00	B13	M-003433- progesterone receptor	5241.00	PGR	1140.00
50018.00	B14	M-012025- crystallin, gamma B	1419.00	CRYGB	2909.00
50018.00	B15	M-019593- pleiotropic regulator 1 (PRL1 h	5356.00	PLRG1	1458.00
50018.00	B16	M-006480- crystallin, beta B3	1417.00	CRYBB3	1295.00
50018.00	B17	M-003434- peroxisome proliferator-activa	5465.00	PPARA	1851.00
50018.00	B18	M-012024- crystallin, beta A2	1412.00	CRYBA2	600.00
50018.00	B19	M-004126- PPAR binding protein	5469.00	PPARBP	1432.00
50018.00	B20	M-013067- crystallin, beta A1	1411.00	CRYBA1	1912.00
50018.00	B21	M-003435- peroxisome proliferator-activa	5467.00	PPARD	1007.00
50018.00	B23	M-003436- peroxisome proliferator-activa	5468.00	PPARG	1987.00
50018.00	C02	M-003419- nuclear receptor subfamily 2, g	7101.00	NR2E1	3156.00
50018.00	C04	M-003418- nuclear receptor subfamily 2, g	7182.00	NR2C2	1911.00
50018.00	C05	M-011416- tumor necrosis factor (ligand) s	7292.00	TNFSF4	2362.00
50018.00	C06	M-003417- nuclear receptor subfamily 2, g	7181.00	NR2C1	1089.00
50018.00	C07	M-011006- CD40 ligand (TNF superfamily,	959.00	CD40LG	3395.00
50018.00	C08	M-003416- nuclear receptor subfamily 1, g	9970.00	NR1I3	1158.00

50018.00	C09	M-011130-	Fas ligand (TNF superfamily, m	356.00	FASLG	1783.00
50018.00	C10	M-003415-	nuclear receptor subfamily 1, g	8856.00	NR1I2	1850.00
50018.00	C11	M-009952-	CD70 molecule	970.00	CD70	1663.00
50018.00	C12	M-003414-	nuclear receptor subfamily 1, g	9971.00	NR1H4	1290.00
50018.00	C13	M-011231-	tumor necrosis factor (ligand) s	944.00	TNFSF8	1805.00
50018.00	C14	M-003413-	nuclear receptor subfamily 1, g	10062.00	NR1H3	1878.00
50018.00	C15	M-011525-	tumor necrosis factor (ligand) s	8744.00	TNFSF9	1820.00
50018.00	C16	M-003412-	nuclear receptor subfamily 1, g	7376.00	NR1H2	680.00
50018.00	C17	M-010560-	transducer of ERBB2, 1	10140.00	TOB1	1745.00
50018.00	C18	M-003432-	nuclear receptor subfamily 1, g	9975.00	NR1D2	1615.00
50018.00	C19	M-016930-	toll interacting protein	54472.00	TOLLIP	720.00
50018.00	C20	M-003411-	nuclear receptor subfamily 1, g	9572.00	NR1D1	1656.00
50018.00	C21	M-009840-	tumor protein p53 inducible pr	9540.00	TP53I3	1994.00
50018.00	C23	M-010104-	TNF receptor-associated protei	10131.00	TRAP1	3040.00
50018.00	D02	M-009743-	crystallin, alpha B	1410.00	CRYAB	1659.00
50018.00	D04	M-013473-	crystallin, alpha A	1409.00	CRYAA	2799.00
50018.00	D05	M-003437-	retinoic acid receptor, alpha	5914.00	RARA	846.00
50018.00	D06	M-011624-	collagen, type IX, alpha 3	1299.00	COL9A3	455.00
50018.00	D07	M-003438-	retinoic acid receptor, beta	5915.00	RARB	1198.00
50018.00	D08	M-011623-	collagen, type IX, alpha 2	1298.00	COL9A2	703.00
50018.00	D09	M-003439-	retinoic acid receptor, gamma	5916.00	RARG	1079.00
50018.00	D10	M-011622-	collagen, type IX, alpha 1	1297.00	COL9A1	547.00
50018.00	D11	M-004768-	v-rel reticuloendotheliosis viral	5966.00	REL	441.00
50018.00	D12	M-013060-	collagen, type V, alpha 3	50509.00	COL5A3	793.00
50018.00	D13	M-003533-	v-rel reticuloendotheliosis viral	5970.00	RELA	2193.00
50018.00	D14	M-011016-	collagen, type V, alpha 2	1290.00	COL5A2	2096.00
50018.00	D15	M-003440-	RAR-related orphan receptor A	6095.00	RORA	737.00
50018.00	D16	M-011014-	collagen, type IV, alpha 5 (Alpo	1287.00	COL4A5	1192.00
50018.00	D17	M-003441-	RAR-related orphan receptor B	6096.00	RORB	1007.00
50018.00	D18	M-021363-	collagen, type IV, alpha 4	1286.00	COL4A4	1566.00
50018.00	D19	M-003442-	RAR-related orphan receptor C	6097.00	RORC	1964.00
50018.00	D20	M-003645-	collagen, type IV, alpha 2	1284.00	COL4A2	2075.00
50018.00	D21	M-003443-	retinoid X receptor, alpha	6256.00	RXRA	1420.00
50018.00	D23	M-003444-	retinoid X receptor, beta	6257.00	RXRB	2956.00
50018.00	E02	M-003410-	nuclear receptor subfamily 0, g	8431.00	NR0B2	2678.00
50018.00	E04	M-003409-	nuclear receptor subfamily 0, g	190.00	NR0B1	2772.00
50018.00	E05	M-019629-	thyrotropin-releasing hormone	7200.00	TRH	1725.00
50018.00	E06	M-010317-	neuronal PAS domain protein 1	4861.00	NPAS1	3936.00
50018.00	E07	M-012605-	thyroid hormone receptor inte	7205.00	TRIP6	2506.00
50018.00	E08	M-011883-	Notch homolog 4 (Drosophila)	4855.00	NOTCH4	1600.00
50018.00	E09	M-012686-	jumonji domain containing 1C	221037.00	JMJD1C	3475.00
50018.00	E10	M-011093-	Notch homolog 3 (Drosophila)	4854.00	NOTCH3	1197.00
50018.00	E11	M-011418-	urocortin	7349.00	UCN	1906.00
50018.00	E12	M-012235-	Notch homolog 2 (Drosophila)	4853.00	NOTCH2	1926.00
50018.00	E13	M-003550-	vascular endothelial growth fac	7422.00	VEGFA	1720.00
50018.00	E14	M-007771-	Notch homolog 1, translocatio	4851.00	NOTCH1	2763.00
50018.00	E15	M-015731-	vascular endothelial growth fac	7423.00	VEGFB	1430.00

50018.00	E16	M-015757- nuclear factor of kappa light pc	4793.00	NFKBIB	1276.00
50018.00	E17	M-012071- vascular endothelial growth fac	7424.00	VEGFC	3333.00
50018.00	E18	M-019107- nuclear receptor coactivator 6	23054.00	NCOA6	4046.00
50018.00	E19	M-012861- VGF nerve growth factor induc	7425.00	VGF	3155.00
50018.00	E20	M-020159- nuclear receptor coactivator 2	10499.00	NCOA2	2985.00
50018.00	E21	M-011542- WNT1 inducible signaling path	8838.00	WISP3	1232.00
50018.00	E23	M-008543- wingless-type MMTV integratio	7476.00	WNT7A	4761.00
50018.00	F02	M-011618- collagen, type IV, alpha 1	1282.00	COL4A1	2059.00
50018.00	F04	M-011012- collagen, type III, alpha 1 (Ehle	1281.00	COL3A1	1721.00
50018.00	F05	M-003445- retinoid X receptor, gamma	6258.00	RXRG	3234.00
50018.00	F06	M-004758- collagen, type I, alpha 2	1278.00	COL1A2	1845.00
50018.00	F07	M-011884- neurturin	4902.00	NRTN	2702.00
50018.00	F08	M-010502- collagen, type I, alpha 1	1277.00	COL1A1	2068.00
50018.00	F09	M-019676- natriuretic peptide precursor B	4879.00	NPPB	1647.00
50018.00	F10	M-011010- collagen, type XVII, alpha 1	1308.00	COL17A1	1107.00
50018.00	F11	M-014648- nuclear receptor binding facto	29982.00	NRBF2	1710.00
50018.00	F12	M-011616- collagen, type XVI, alpha 1	1307.00	COL16A1	1965.00
50018.00	F13	M-013405- neurotrophin 3	4908.00	NTF3	740.00
50018.00	F14	M-011834- collagen, type XII, alpha 1	1303.00	COL12A1	3891.00
50018.00	F15	M-012236- neurotrophin 5 (neurotrophin	4909.00	NTF5	1829.00
50018.00	F16	M-013352- collagen, type XI, alpha 2	1302.00	COL11A2	930.00
50018.00	F17	M-010170- neurotensin	4922.00	NTS	1943.00
50018.00	F18	M-011009- collagen, type X, alpha 1(Schmi	1300.00	COL10A1	1100.00
50018.00	F19	M-019185- opioid growth factor receptor	11054.00	OGFR	1622.00
50018.00	F20	M-011409- claudin 5 (transmembrane pro	7122.00	CLDN5	1805.00
50018.00	F21	M-003804- oxidized low density lipoprotei	4973.00	OLR1	2672.00
50018.00	F23	M-011743- opioid binding protein/cell adh	4978.00	OPCML	2935.00
50018.00	G02	M-005196- nuclear receptor coactivator 1	8648.00	NCOA1	4588.00
50018.00	G04	M-021258- centrosomal protein 170kDa	9859.00	CEP170	3286.00
50018.00	G05	M-007889- chemokine (C motif) ligand 1	6375.00	XCL1	2230.00
50018.00	G06	M-003407- hepatocyte nuclear factor 4, ga	3174.00	HNF4G	2390.00
50018.00	G07	M-007898- chemokine (C motif) ligand 2	6846.00	XCL2	2508.00
50018.00	G08	M-004597- high mobility group AT-hook 1	3159.00	HMGA1	1761.00
50018.00	G09	M-008044- ectodysplasin A2 receptor	60401.00	EDA2R	2103.00
50018.00	G10	M-010068- hypoxia inducible factor 3, alph	64344.00	HIF3A	933.00
50018.00	G11	M-017571- zona pellucida glycoprotein 3 (	7784.00	ZP3	3191.00
50018.00	G12	M-004018- hypoxia-inducible factor 1, alph	3091.00	HIF1A	1697.00
50018.00	G13	M-013212- chemokine (C-X-C motif) recep	57007.00	CXCR7	1027.00
50018.00	G14	M-003405- estrogen-related receptor gam	2104.00	ESRRG	1296.00
50018.00	G15	M-007316- ATP-binding cassette, sub-fami	10060.00	ABCC9	2020.00
50018.00	G16	M-003404- estrogen-related receptor beta	2103.00	ESRRB	1790.00
50018.00	G17	M-014141- trafficking protein, kinesin binc	66008.00	TRAK2	1778.00
50018.00	G18	M-003403- estrogen-related receptor alph	2101.00	ESRRA	1242.00
50018.00	G19	M-013434- apolipoprotein L, 3	80833.00	APOL3	1323.00
50018.00	G20	M-003402- estrogen receptor 2 (ER beta)	2100.00	ESR2	3510.00
50018.00	G21	M-015338- cyclic AMP phosphoprotein, 19	10776.00	ARPP-19	1335.00
50018.00	G23	M-006134- cholinergic receptor, nicotinic,	1134.00	CHRNA1	2056.00

50018.00	H02	M-020781-	claudin 2	9075.00	CLDN2	1367.00
50018.00	H04	M-017304-	claudin 14	23562.00	CLDN14	2045.00
50018.00	H05	M-010528-	oncostatin M	5008.00	OSM	3342.00
50018.00	H06	M-021307-	claudin 12	9069.00	CLDN12	1083.00
50018.00	H07	M-011748-	platelet-derived growth factor	5154.00	PDGFA	2850.00
50018.00	H08	M-019258-	claudin 11 (oligodendrocyte tra	5010.00	CLDN11	2419.00
50018.00	H09	M-011749-	platelet-derived growth factor	5155.00	PDGFB	1089.00
50018.00	H10	M-019255-	claudin 10	9071.00	CLDN10	1942.00
50018.00	H11	M-020123-	proenkephalin	5179.00	PENK	566.00
50018.00	H12	M-017369-	claudin 1	9076.00	CLDN1	2257.00
50018.00	H13	M-008058-	platelet factor 4 (chemokine (C	5196.00	PF4	1459.00
50018.00	H14	M-003467-	caveolin 1, caveolae protein, 2	857.00	CAV1	2294.00
50018.00	H15	M-016246-	placental growth factor, vascul	5228.00	PGF	2355.00
50018.00	H16	M-021493-	biglycan	633.00	BGN	2302.00
50018.00	H17	M-010639-	progesterone receptor membr	10424.00	PGRMC2	2346.00
50018.00	H18	M-005284-	actin related protein 2/3 comp	10094.00	ARPC3	1748.00
50018.00	H19	M-019291-	pleckstrin homology domain in	55023.00	PHIP	2514.00
50018.00	H20	M-012081-	actin related protein 2/3 comp	10109.00	ARPC2	1050.00
50018.00	H21	M-019590-	plexin B1	5364.00	PLXNB1	2784.00
50018.00	H23	M-007753-	plexin C1	10154.00	PLXNC1	1921.00
50018.00	I02	M-003886-	v-ets erythroblastosis virus E26	2078.00	ERG	3963.00
50018.00	I04	M-004814-	endothelial PAS domain protei	2034.00	EPAS1	3017.00
50018.00	I05	M-006135-	cholinergic receptor, nicotinic,	57053.00	CHRNA10	307.00
50018.00	I06	M-017313-	cofactor required for Sp1 trans	9443.00	CRSP9	1527.00
50018.00	I07	M-006136-	cholinergic receptor, nicotinic,	1135.00	CHRNA2	2134.00
50018.00	I08	M-011948-	cofactor required for Sp1 trans	9441.00	CRSP7	2078.00
50018.00	I09	M-006137-	cholinergic receptor, nicotinic,	1136.00	CHRNA3	2412.00
50018.00	I10	M-006312-	cofactor required for Sp1 trans	9440.00	CRSP6	2223.00
50018.00	I11	M-006138-	cholinergic receptor, nicotinic,	1137.00	CHRNA4	2120.00
50018.00	I12	M-011928-	cofactor required for Sp1 trans	9282.00	CRSP2	1285.00
50018.00	I13	M-006139-	cholinergic receptor, nicotinic,	1138.00	CHRNA5	1869.00
50018.00	I14	M-007862-	interleukin 31 receptor A	133396.00	IL31RA	1766.00
50018.00	I15	M-006140-	cholinergic receptor, nicotinic,	8973.00	CHRNA6	1833.00
50018.00	I16	M-012897-	CCR4-NOT transcription compl	29883.00	CNOT7	2212.00
50018.00	I17	M-004143-	cholinergic receptor, nicotinic,	1139.00	CHRNA7	2007.00
50018.00	I18	M-008212-	clock homolog (mouse)	9575.00	CLOCK	2765.00
50018.00	I19	M-006141-	cholinergic receptor, nicotinic,	55584.00	CHRNA9	2724.00
50018.00	I20	M-007852-	CD86 molecule	942.00	CD86	3314.00
50018.00	I21	M-006142-	cholinergic receptor, nicotinic,	1140.00	CHRNB1	3333.00
50018.00	I23	M-006143-	cholinergic receptor, nicotinic,	1141.00	CHRNB2	2669.00
50018.00	J02	M-012082-	actin related protein 2/3 comp	10095.00	ARPC1B	3290.00
50018.00	J04	M-011207-	ankyrin 3, node of Ranvier (ank	288.00	ANK3	2553.00
50018.00	J05	M-019685-	pro-melanin-concentrating hor	5367.00	PMCH	2516.00
50018.00	J06	M-008417-	ankyrin 2, neuronal	287.00	ANK2	2784.00
50018.00	J07	M-020201-	proopiomelanocortin (adrenoc	5443.00	POMC	1627.00
50018.00	J08	M-012489-	amelogenin (amelogenesis imp	265.00	AMELX	2350.00
50018.00	J09	M-006393-	prolactin	5617.00	PRL	2320.00

50018.00	J10	M-012274- actin-like 7B	10880.00	ACTL7B	2015.00
50018.00	J11	M-014883- prokineticin 1	84432.00	PROK1	2702.00
50018.00	J12	M-012273- actin-like 7A	10881.00	ACTL7A	2057.00
50018.00	J13	M-011887- persephin	5623.00	PSPN	2296.00
50018.00	J14	M-020264- gamma tubulin ring complex pı	27229.00	76P	1525.00
50018.00	J15	M-003698- parathyroid hormone-like horn	5744.00	PTHLH	1850.00
50018.00	J16	M-019963- mediator of RNA polymerase II	10001.00	MED6	2194.00
50018.00	J17	M-004300- poliovirus receptor-related 1 (h	5818.00	PVRL1	3171.00
50018.00	J18	M-015791- SMAD family member 5	4090.00	SMAD5	3172.00
50018.00	J19	M-018703- prohibitin 2	11331.00	PHB2	630.00
50018.00	J20	M-019874- lipopolysaccharide-induced TN	9516.00	LITAF	4083.00
50018.00	J21	M-017403- relaxin 1	6013.00	RLN1	4284.00
50018.00	J23	M-017400- relaxin 2	6019.00	RLN2	3932.00
50018.00	K02	M-007851- CD80 molecule	941.00	CD80	4508.00
50018.00	K04	M-009284- aryl hydrocarbon receptor nucl	56938.00	ARNTL2	2958.00
50018.00	K05	M-006144- cholinergic receptor, nicotinic,	1142.00	CHRNB3	166.00
50018.00	K06	M-010261- aryl hydrocarbon receptor nucl	406.00	ARNTL	2136.00
50018.00	K07	M-006146- cholinergic receptor, nicotinic,	1144.00	CHRND	2941.00
50018.00	K08	M-008920- aryl-hydrocarbon receptor nuc	9915.00	ARNT2	2929.00
50018.00	K09	M-006147- cholinergic receptor, nicotinic,	1145.00	CHRNE	1594.00
50018.00	K10	M-007207- aryl hydrocarbon receptor nucl	405.00	ARNT	3290.00
50018.00	K11	M-011175- cubilin (intrinsic factor-cobalan	8029.00	CUBN	2122.00
50018.00	K12	M-003400- androgen receptor (dihydrotes	367.00	AR	940.00
50018.00	K13	M-006162- gamma-aminobutyric acid (GAI	2554.00	GABRA1	2124.00
50018.00	K14	M-006325- aryl hydrocarbon receptor inte	9049.00	AIP	2101.00
50018.00	K15	M-006163- gamma-aminobutyric acid (GAI	2555.00	GABRA2	4251.00
50018.00	K16	M-004990- aryl hydrocarbon receptor	196.00	AHR	2781.00
50018.00	K17	M-006164- gamma-aminobutyric acid (GAI	2556.00	GABRA3	1310.00
50018.00	K18	M-003401- estrogen receptor 1	2099.00	ESR1	1100.00
50018.00	K19	M-006165- gamma-aminobutyric acid (GAI	2557.00	GABRA4	3211.00
50018.00	K20	M-008103- CD27 molecule	939.00	CD27	2491.00
50018.00	K21	M-006166- gamma-aminobutyric acid (GAI	2558.00	GABRA5	3595.00
50018.00	K23	M-006167- gamma-aminobutyric acid (GAI	2559.00	GABRA6	4808.00
50018.00	L02	M-019853- slit homolog 2 (Drosophila)	9353.00	SLIT2	2036.00
50018.00	L04	M-017502- scavenger receptor class F, me	91179.00	SCARF2	1882.00
50018.00	L05	M-013463- S100 calcium binding protein A	6277.00	S100A6	1705.00
50018.00	L06	M-011060- jagged 1 (Alagille syndrome)	182.00	JAG1	2150.00
50018.00	L07	M-011384- S100 calcium binding protein A	6280.00	S100A9	1323.00
50018.00	L08	M-003482- catenin (cadherin-associated p	1499.00	CTNNB1	826.00
50018.00	L09	M-021415- C-type lectin domain family 11,	6320.00	CLEC11A	2645.00
50018.00	L10	M-011596- dystonin	667.00	DST	2657.00
50018.00	L11	M-011924- small inducible cytokine subfar	9255.00	SCYE1	1272.00
50018.00	L12	M-007895- erythropoietin receptor	2057.00	EPOR	1121.00
50018.00	L13	M-011774- selectin P ligand	6404.00	SELPLG	1900.00
50018.00	L14	M-006450- epithelial cell transforming seq	1894.00	ECT2	1305.00
50018.00	L15	M-019583- signaling lymphocytic activatio	6504.00	SLAMF1	2958.00

50018.00	L16	M-009421- Rho guanine nucleotide excha	9138.00	ARHGEF1	2740.00
50018.00	L17	M-017604- suppressor of cytokine signalin	8835.00	SOCS2	2115.00
50018.00	L18	M-009304- Rho GTPase activating protein	395.00	ARHGAP6	1300.00
50018.00	L19	M-027326- sialophorin (leukosialin, CD43)	6693.00	SPN	2190.00
50018.00	L20	M-003628- Rho GTPase activating protein	393.00	ARHGAP4	3817.00
50018.00	L21	M-016717- signal recognition particle rece	6734.00	SRPR	2705.00
50018.00	L23	M-010233- low density lipoprotein-related	29967.00	LRP12	2839.00
50018.00	M02	M-003721- very low density lipoprotein re	7436.00	VLDLR	3108.00
50018.00	M04	M-003607- transient receptor potential ca	55503.00	TRPV6	1864.00
50018.00	M05	M-006168- gamma-aminobutyric acid (GA	2560.00	GABRB1	2033.00
50018.00	M06	M-004196- transient receptor potential ca	56302.00	TRPV5	2175.00
50018.00	M07	M-006169- gamma-aminobutyric acid (GA	2561.00	GABRB2	2128.00
50018.00	M08	M-006902- zinc finger, HIT type 3	9326.00	ZNHIT3	1447.00
50018.00	M09	M-006170- gamma-aminobutyric acid (GA	2562.00	GABRB3	2927.00
50018.00	M10	M-012934- sortilin-related VPS10 domain	22986.00	SORCS3	2726.00
50018.00	M11	M-006171- gamma-aminobutyric acid (GA	2563.00	GABRD	2211.00
50018.00	M12	M-013162- sortilin-related VPS10 domain	57537.00	SORCS2	1247.00
50018.00	M13	M-006172- gamma-aminobutyric acid (GA	2564.00	GABRE	1844.00
50018.00	M14	M-013422- sortilin-related VPS10 domain	114815.00	SORCS1	2683.00
50018.00	M15	M-006173- gamma-aminobutyric acid (GA	2565.00	GABRG1	3509.00
50018.00	M16	M-006294- ryanodine receptor 3	6263.00	RYR3	2220.00
50018.00	M17	M-006174- gamma-aminobutyric acid (GA	2566.00	GABRG2	2409.00
50018.00	M18	M-006293- ryanodine receptor 2 (cardiac)	6262.00	RYR2	3829.00
50018.00	M19	M-006175- gamma-aminobutyric acid (GA	2567.00	GABRG3	3445.00
50018.00	M20	M-015788- peroxisomal biogenesis factor	5830.00	PEX5	3388.00
50018.00	M21	M-006176- gamma-aminobutyric acid (GA	2568.00	GABRP	3957.00
50018.00	M23	M-006177- gamma-aminobutyric acid (GA	55879.00	GABRQ	3360.00
50018.00	N02	M-020687- mediator of RNA polymerase II	29079.00	MED4	2286.00
50018.00	N04	M-003448- vitamin D (1,25- dihydroxyvita	7421.00	VDR	2868.00
50018.00	N05	M-011788- tachykinin, precursor 1 (substa	6863.00	TAC1	3532.00
50018.00	N06	M-017578- TRAF and TNF receptor associa	51567.00	TTRAP	1736.00
50018.00	N07	M-008764- tachykinin 3 (neuromedin K, ne	6866.00	TAC3	1212.00
50018.00	N08	M-009632- thyroid hormone receptor inte	9325.00	TRIP4	1264.00
50018.00	N09	M-004832- teratocarcinoma-derived grow	6997.00	TDGF1	3644.00
50018.00	N10	M-016262- thyroid hormone receptor inte	9319.00	TRIP13	1355.00
50018.00	N11	M-009299- thyroglobulin	7038.00	TG	2490.00
50018.00	N12	M-003736- thyroid hormone receptor ass	10025.00	THRAP5	1159.00
50018.00	N13	M-012562- transforming growth factor, be	7040.00	TGFB1	1883.00
50018.00	N14	M-019908- thyroid hormone receptor ass	9969.00	THRAP1	1856.00
50018.00	N15	M-019740- transforming growth factor, be	7043.00	TGFB3	932.00
50018.00	N16	M-019907- thyroid hormone receptor ass	9967.00	THRAP3	1966.00
50018.00	N17	M-019370- transforming growth factor, be	7045.00	TGFBI	2961.00
50018.00	N18	M-009092- mediator of RNA polymerase II	9968.00	MED12	1312.00
50018.00	N19	M-010545- transforming growth factor, be	7049.00	TGFBR3	2268.00
50018.00	N20	M-003447- thyroid hormone receptor, bet	7068.00	THRB	951.00
50018.00	N21	M-012551- thrombomodulin	7056.00	THBD	2413.00
50018.00	N23	M-005120- toll-like receptor 2	7097.00	TLR2	1624.00

50018.00	O02	M-012544- peroxisomal biogenesis factor	5191.00	PEX7	2136.00
50018.00	O04	M-003728- purinergic receptor P2X, ligand	5027.00	P2RX7	1550.00
50018.00	O05	M-006178- gamma-aminobutyric acid (GA	2569.00	GABRR1	763.00
50018.00	O06	M-006285- purinergic receptor P2X, ligand	5025.00	P2RX4	2013.00
50018.00	O07	M-006179- gamma-aminobutyric acid (GA	2570.00	GABRR2	1797.00
50018.00	O08	M-006284- purinergic receptor P2X, ligand	5024.00	P2RX3	2240.00
50018.00	O09	M-006180- glycine receptor, alpha 1 (start	2741.00	GLRA1	2157.00
50018.00	O10	M-006283- purinergic receptor P2X, ligand	22953.00	P2RX2	1580.00
50018.00	O11	M-006181- glycine receptor, alpha 2	2742.00	GLRA2	1854.00
50018.00	O12	M-005098- purinergic receptor P2X, ligand	5023.00	P2RX1	1361.00
50018.00	O13	M-006182- glycine receptor, alpha 3	8001.00	GLRA3	1804.00
50018.00	O14	M-004721- low density lipoprotein-related	4035.00	LRP1	881.00
50018.00	O15	M-006194- glutamate receptor, ionotropic	2902.00	GRIN1	1604.00
50018.00	O16	M-011073- low density lipoprotein recept	3949.00	LDLR	2901.00
50018.00	O17	M-006195- glutamate receptor, ionotropic	2903.00	GRIN2A	2385.00
50018.00	O18	M-012315- KDEL (Lys-Asp-Glu-Leu) endopl	11014.00	KDELR2	2347.00
50018.00	O19	M-006196- glutamate receptor, ionotropic	2904.00	GRIN2B	2781.00
50018.00	O20	M-007964- transmembrane emp24 protei	11018.00	TMED1	2142.00
50018.00	O21	M-006198- glutamate receptor, ionotropic	2906.00	GRIN2D	1739.00
50018.00	O23	M-006206- 5-hydroxytryptamine (serotoni	170572.00	HTR3C	707.00
50018.00	P02	M-003446- thyroid hormone receptor, alp	7067.00	THRA	1456.00
50018.00	P04	M-006565- transforming growth factor be	7041.00	TGFB1I1	896.00
50018.00	P05	M-004715- toll-like receptor 8	51311.00	TLR8	3352.00
50018.00	P06	M-006690- signal transducer and activator	6778.00	STAT6	1091.00
50018.00	P07	M-010546- tumor necrosis factor (TNF sup	7124.00	TNF	1275.00
50018.00	P08	M-010539- signal transducer and activator	6777.00	STAT5B	888.00
50018.00	P09	M-008094- tumor necrosis factor receptor	4982.00	TNFRSF11B	2400.00
50018.00	P10	M-005169- signal transducer and activator	6776.00	STAT5A	2023.00
50018.00	P11	M-010661- tumor necrosis factor receptor	51330.00	TNFRSF12A	1634.00
50018.00	P12	M-011784- signal transducer and activator	6775.00	STAT4	1640.00
50018.00	P13	M-008096- tumor necrosis factor receptor	8764.00	TNFRSF14	1678.00
50018.00	P14	M-012064- signal transducer and activator	6773.00	STAT2	1335.00
50018.00	P15	M-006449- tumor necrosis factor receptor	8784.00	TNFRSF18	3252.00
50018.00	P16	M-003543- signal transducer and activator	6772.00	STAT1	2324.00
50018.00	P17	M-008098- tumor necrosis factor receptor	55504.00	TNFRSF19	3164.00
50018.00	P18	M-008598- single-minded homolog 2 (Dro	6493.00	SIM2	1479.00
50018.00	P19	M-005197- tumor necrosis factor receptor	7132.00	TNFRSF1A	1368.00
50018.00	P20	M-009791- single-minded homolog 1 (Dro	6492.00	SIM1	1774.00
50018.00	P21	M-003934- tumor necrosis factor receptor	7133.00	TNFRSF1B	828.00
50018.00	P23	M-004449- tumor necrosis factor receptor	8718.00	TNFRSF25	171.00
				mdmdMAD	1889.50
				3xMAD	
				MADc	
50018.00	C22				2686.00
50018.00	D22				2731.00
50018.00	E22				3062.00

50018.00	F22			2343.00		11.99	
					mn		2826.33
					sd		205.33
50018.00	G22						509.00
50018.00	H22						1237.00
50018.00	I22						882.00
50018.00	J22						1942.00
					mn		1142.50
					sd		610.28
							3posSD
							3negSD
							Sum3SD
							MnDiff
							SumovrM
							1minus
50018.00	G03	M-003290-	polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMARTpoo		202.00
50018.00	H03	M-003290-	polo-like kinase 1 (Drosophila)	5347.00	PLK1 SMARTpoo		112.00
50018.00	I03	D-001206-:	siControl non-targeting siRNA #2				1512.00
50018.00	J03	D-001206-:	siControl non-targeting siRNA #2				2498.00
50018.00	K03	D-001600-(	siGLO RISC-free siRNA				4583.00
50018.00	L03	D-001600-(	siGLO RISC-free siRNA				4039.00

abs dev	**robust Z**	**% inf**	**abs dev**	**robust Z**	**% inf**	**abs dev**	**robust Z**		
8.10	4.41	1.71	1591.00	8.49	4.29	1.37	2203.00	11.67	**7.59**
5.60	1.91	0.74	1668.00	5.16	0.96	0.31	2993.00	4.54	0.46
5.13	1.44	0.56	1860.00	5.54	1.34	0.43	2751.00	3.53	0.55
7.28	3.59	1.39	1246.00	8.99	4.79	1.53	2754.00	6.61	2.53
3.85	0.16	0.06	657.00	14.31	**10.11**	3.23	1323.00	9.30	5.22
9.65	**5.96**	2.31	1549.00	2.45	1.75	-0.56	2459.00	7.44	3.36
2.79	0.90	-0.35	1295.00	2.32	1.88	-0.60	2397.00	3.42	0.66
7.12	3.43	1.33	1978.00	6.42	2.22	0.71	3380.00	6.33	2.25
6.91	3.22	1.25	984.00	2.44	1.76	-0.56	1522.00	2.76	1.32
12.87	**9.18**	3.56	947.00	5.70	1.50	0.48	1358.00	4.05	0.03
5.51	1.82	0.71	1176.00	5.27	1.07	0.34	1511.00	6.88	2.80
1.06	2.63	-1.02	1425.00	5.05	0.85	0.27	1887.00	2.70	1.38
2.38	1.31	-0.51	1447.00	2.83	1.37	-0.44	2297.00	3.70	0.38
3.25	0.44	-0.17	674.00	5.34	1.14	0.37	1837.00	4.30	0.22
5.54	1.85	0.72	932.00	3.76	0.44	-0.14	1723.00	4.12	0.04
9.92	**6.23**	2.42	1005.00	4.78	0.58	0.19	2479.00	3.31	0.77
4.23	0.54	0.21	626.00	4.79	0.59	0.19	1282.00	5.15	1.07
7.11	3.42	1.33	1146.00	2.71	1.49	-0.48	2148.00	4.61	0.53
6.38	2.69	1.04	1343.00	3.05	1.15	-0.37	2049.00	5.81	1.73
2.34	1.35	-0.53	921.00	1.09	3.11	-0.99	859.00	7.80	3.72
2.08	1.61	-0.63	978.00	7.46	3.26	1.04	1241.00	1.61	2.47
3.26	0.43	-0.17	1705.00	9.62	5.42	1.73	2075.00	2.31	1.77
0.91	2.78	-1.08	2499.00	8.92	4.72	1.51	3180.00	1.48	2.60
0.81	2.88	-1.12	2061.00	4.90	0.70	0.23	2929.00	0.92	3.16
2.46	1.23	-0.48	1726.00	4.64	0.44	0.14	2823.00	3.08	1.00
3.20	0.49	-0.19	883.00	2.38	1.82	-0.58	1093.00	3.39	0.69
3.11	0.58	-0.23	846.00	7.33	3.13	1.00	1590.00	2.33	1.75
8.92	**5.23**	2.03	830.00	14.70	**10.50**	3.36	1729.00	5.03	0.95
3.19	0.50	-0.20	1790.00	10.28	6.08	1.94	3088.00	5.25	1.17
1.44	2.25	-0.87	1013.00	4.34	0.14	0.05	1874.00	1.07	3.01
4.30	0.61	0.23	1149.00	1.57	2.63	-0.84	1511.00	1.39	2.69
12.82	**9.13**	3.54	3001.00	6.70	2.50	0.80	3351.00	8.92	4.84
4.32	0.63	0.24	1623.00	3.33	0.87	-0.28	1585.00	1.45	2.63
5.87	2.18	0.84	918.00	5.12	0.92	0.30	1422.00	1.05	3.03
2.76	0.93	-0.36	1988.00	1.46	2.74	-0.87	2536.00	3.63	0.45
5.00	1.31	0.51	707.00	2.40	1.80	-0.57	1444.00	0.35	3.73
8.73	5.04	1.96	2380.00	3.82	0.38	-0.12	4925.00	2.94	1.14
6.28	2.59	1.00	2014.00	1.74	2.46	-0.79	4442.00	5.31	1.23
8.84	5.15	2.00	2080.00	2.31	1.89	-0.60	3618.00	2.24	1.84
5.44	1.75	0.68	2010.00	0.65	3.55	-1.13	4133.00	1.48	2.60
2.82	0.87	-0.34	2389.00	8.87	4.67	1.50	2758.00	4.57	0.49
4.55	0.86	0.33	2006.00	13.11	**8.91**	2.85	2410.00	5.60	1.52
2.79	0.90	-0.35	1976.00	6.38	2.18	0.70	2551.00	1.61	2.47
1.47	2.22	-0.86	2165.00	6.47	2.27	0.73	2600.00	2.31	1.77
5.07	1.38	0.53	2373.00	7.67	3.47	1.11	2191.00	3.10	0.98
1.38	2.31	-0.90	1481.00	4.93	0.73	0.23	1667.00	1.08	3.00

2.08	1.61	-0.63	1922.00	1.82	2.38	-0.76	1707.00	1.41	2.67
5.57	1.88	0.73	2009.00	4.68	0.48	0.15	1633.00	2.76	1.32
2.41	1.28	-0.50	1989.00	3.77	0.43	-0.14	2907.00	1.44	2.64
2.87	0.82	-0.32	1524.00	3.41	0.79	-0.25	1491.00	1.07	3.01
6.43	2.74	1.06	1182.00	3.89	0.31	-0.10	1617.00	1.67	2.41
6.39	2.70	1.05	1717.00	2.97	1.23	-0.39	1850.00	2.11	1.97
10.55	**6.86**	2.66	1317.00	3.11	1.09	-0.35	2225.00	4.58	0.50
3.82	0.13	0.05	582.00	4.98	0.78	0.25	1097.00	3.10	0.98
4.93	1.24	0.48	1139.00	2.02	2.18	-0.70	1820.00	1.32	2.76
19.26	**15.57**	6.04	1215.00	3.79	0.41	-0.13	1441.00	9.37	5.29
5.56	1.87	0.72	1217.00	2.96	1.24	-0.40	2147.00	1.30	2.78
8.33	4.64	1.80	1829.00	2.79	1.41	-0.45	2318.00	2.55	1.53
6.47	2.78	1.08	1435.00	5.09	0.89	0.28	2537.00	11.98	**7.90**
5.43	1.74	0.67	1080.00	1.20	3.00	-0.96	2248.00	5.83	1.75
3.38	0.31	-0.12	3834.00	8.45	4.25	1.36	3620.00	4.92	0.84
13.93	**10.24**	3.98	2026.00	7.95	3.75	1.20	3669.00	7.82	3.74
6.97	3.28	1.27	1647.00	4.43	0.23	0.08	1542.00	5.38	1.30
12.09	**8.40**	3.26	935.00	9.63	5.43	1.74	881.00	5.90	1.82
8.01	4.32	1.68	993.00	6.45	2.25	0.72	2128.00	2.91	1.17
10.81	**7.12**	2.76	839.00	9.65	5.45	1.75	1679.00	6.49	2.41
6.77	3.08	1.19	1607.00	5.91	1.71	0.55	1741.00	5.11	1.03
9.14	**5.45**	2.12	642.00	21.18	**16.98**	5.43	1148.00	8.28	4.20
10.88	**7.19**	2.79	1084.00	8.49	4.29	1.37	1377.00	6.75	2.67
7.19	3.50	1.36	988.00	3.64	0.56	-0.18	1747.00	3.32	0.76
6.75	3.06	1.19	2258.00	3.81	0.39	-0.12	3017.00	5.83	1.75
6.49	2.80	1.09	2321.00	3.96	0.24	-0.07	2855.00	3.64	0.44
5.16	1.47	0.57	998.00	4.51	0.31	0.10	1512.00	4.10	0.02
5.70	2.01	0.78	1352.00	5.03	0.83	0.27	1749.00	5.43	1.35
6.55	2.86	1.11	1057.00	4.07	0.13	-0.04	1294.00	5.33	1.25
8.56	4.87	1.89	2140.00	3.79	0.42	-0.13	3113.00	4.66	0.58
12.63	**8.94**	3.47	1728.00	3.88	0.32	-0.10	2438.00	4.96	0.88
8.05	4.36	1.69	1697.00	2.36	1.84	-0.59	2808.00	2.07	2.01
4.15	0.46	0.18	1425.00	2.46	1.74	-0.56	2901.00	4.24	0.16
8.56	4.87	1.89	3800.00	3.63	0.57	-0.18	5060.00	9.11	5.03
1.42	2.27	-0.88	2646.00	3.14	1.06	-0.34	4130.00	1.19	2.89
6.17	2.48	0.96	2273.00	2.60	1.60	-0.51	3209.00	1.34	2.74
5.62	1.93	0.75	2249.00	3.20	1.00	-0.32	3752.00	2.83	1.25
4.17	0.48	0.18	2897.00	3.24	0.96	-0.30	4311.00	3.25	0.83
6.30	2.61	1.01	999.00	2.80	1.40	-0.45	2208.00	1.40	2.68
4.31	0.62	0.24	1307.00	1.84	2.36	-0.75	1978.00	0.35	3.73
7.86	4.17	1.62	1813.00	1.65	2.55	-0.81	3505.00	4.68	0.60
6.60	2.91	1.13	1215.00	4.12	0.08	-0.03	1884.00	5.52	1.44
5.19	1.50	0.58	1734.00	3.46	0.74	-0.24	1233.00	1.87	2.21
3.69	0.00	0.00	1569.00	0.38	3.82	-1.22	2110.00	2.75	1.33
3.55	0.14	-0.06	1616.00	2.85	1.35	-0.43	2911.00	6.15	2.07
3.08	0.61	-0.24	2344.00	1.54	2.66	-0.85	3596.00	3.64	0.44
1.05	2.64	-1.03	1355.00	2.21	1.99	-0.63	1480.00	1.62	2.46

1.18	2.51	-0.98	1280.00	1.48	2.72	-0.87	1411.00	1.42	2.66
5.22	1.53	0.59	2405.00	1.83	2.37	-0.76	3090.00	4.21	0.13
3.06	0.63	-0.24	2298.00	1.00	3.20	-1.02	4185.00	7.29	3.21
8.34	4.65	1.80	2293.00	3.97	0.23	-0.07	3001.00	3.37	0.71
13.20	**9.51**	3.69	2360.00	3.94	0.26	-0.08	4426.00	10.26	**6.18**
5.52	1.83	0.71	1773.00	1.35	2.85	-0.91	2411.00	9.91	**5.83**
3.72	0.03	0.01	3348.00	1.79	2.41	-0.77	5528.00	3.33	0.75
0.29	3.40	-1.32	2775.00	2.34	1.86	-0.59	2365.00	3.13	0.95
0.35	3.34	-1.30	2756.00	5.84	1.64	0.53	2984.00	3.38	0.70
5.97	2.28	0.88	3708.00	11.17	**6.97**	2.23	3307.00	7.38	3.30
4.39	0.70	0.27	2744.00	5.25	1.05	0.34	1515.00	2.38	1.70
2.52	1.17	-0.46	2267.00	3.22	0.98	-0.31	2391.00	5.02	0.94
3.63	0.06	-0.03	2845.00	7.35	3.15	1.01	3004.00	4.33	0.25
1.58	2.11	-0.82	2565.00	1.99	2.21	-0.71	2387.00	2.89	1.19
1.36	2.34	-0.91	1831.00	6.88	2.68	0.86	1815.00	4.19	0.11
3.39	0.30	-0.12	1846.00	8.13	3.93	1.26	1523.00	5.25	1.17
1.98	1.71	-0.66	2965.00	3.84	0.36	-0.11	2379.00	2.10	1.98
3.51	0.18	-0.07	1142.00	5.43	1.23	0.39	1364.00	4.03	0.05
9.95	**6.26**	2.43	3274.00	20.04	**15.84**	5.06	4964.00	11.32	**7.24**
1.48	2.21	-0.86	2147.00	2.19	2.01	-0.64	2472.00	2.87	1.21
0.00	3.69	-1.43	1708.00	3.28	0.92	-0.29	1652.00	2.97	1.11
0.41	3.28	-1.27	2658.00	3.31	0.89	-0.28	2965.00	0.94	3.14
2.18	1.51	-0.59	1188.00	4.12	0.08	-0.02	2047.00	6.55	2.47
1.79	1.90	-0.74	2518.00	1.67	2.53	-0.81	3018.00	4.51	0.43
4.82	1.13	0.44	2236.00	7.78	3.58	1.15	1917.00	3.81	0.27
7.71	4.02	1.56	3443.00	2.12	2.08	-0.66	4122.00	2.67	1.41
2.18	1.51	-0.59	4234.00	3.05	1.15	-0.37	3701.00	2.38	1.70
3.16	0.53	-0.21	4738.00	4.81	0.61	0.20	5120.00	5.31	1.23
9.59	**5.90**	2.29	3140.00	9.24	5.04	1.61	4730.00	10.51	**6.43**
1.21	2.48	-0.96	1993.00	4.32	0.12	0.04	2697.00	1.82	2.26
4.27	0.58	0.22	3504.00	6.08	1.88	0.60	2887.00	3.39	0.69
1.83	1.86	-0.72	1749.00	1.20	3.00	-0.96	2951.00	2.78	1.30
6.76	3.07	1.19	1304.00	5.52	1.32	0.42	2311.00	8.78	4.70
3.42	0.27	-0.10	2559.00	6.57	2.37	0.76	3339.00	8.15	4.07
1.07	2.62	-1.02	1716.00	5.36	1.16	0.37	2607.00	4.53	0.45
14.29	**10.60**	4.11	3638.00	6.05	1.85	0.59	4320.00	9.40	5.32
3.95	0.26	0.10	2141.00	3.27	0.93	-0.30	3207.00	3.18	0.90
1.56	2.13	-0.83	1837.00	8.38	4.18	1.34	2051.00	6.83	2.75
1.93	1.76	-0.69	2027.00	7.89	3.69	1.18	1996.00	3.61	0.47
2.43	1.26	-0.49	1847.00	1.73	2.47	-0.79	4071.00	1.82	2.26
2.07	1.62	-0.63	2532.00	3.59	0.61	-0.19	2693.00	0.97	3.11
4.22	0.53	0.20	1367.00	5.12	0.92	0.30	2208.00	5.25	1.17
2.01	1.68	-0.65	1724.00	2.61	1.59	-0.51	3364.00	0.89	3.19
3.17	0.52	-0.20	1118.00	2.33	1.87	-0.60	1676.00	1.79	2.29
6.67	2.98	1.15	2549.00	5.06	0.86	0.28	4978.00	6.23	2.15
2.40	1.29	-0.50	733.00	2.32	1.88	-0.60	2032.00	1.48	2.60
5.16	1.47	0.57	2285.00	3.19	1.01	-0.32	3447.00	2.32	1.76

3.29	0.40	-0.16	1793.00	1.39	2.81	-0.90	3529.00	2.15	1.93
1.86	1.83	-0.71	3277.00	4.55	0.35	0.11	4414.00	3.24	0.84
2.21	1.48	-0.57	4067.00	6.07	1.87	0.60	4256.00	2.28	1.80
1.20	2.49	-0.97	1321.00	3.26	0.94	-0.30	1820.00	0.82	3.26
3.02	0.67	-0.26	3300.00	6.45	2.25	0.72	2058.00	1.41	2.67
4.84	1.15	0.44	2839.00	8.31	4.11	1.32	2903.00	1.65	2.43
0.64	3.05	-1.18	1026.00	4.29	0.09	0.03	1860.00	0.97	3.11
3.14	0.55	-0.21	1955.00	5.73	1.53	0.49	2509.00	1.47	2.61
2.12	1.57	-0.61	871.00	10.45	6.25	2.00	1284.00	2.02	2.06
2.66	1.03	-0.40	1862.00	1.02	3.18	-1.02	2612.00	0.77	3.31
3.98	0.29	0.11	1499.00	4.60	0.40	0.13	2182.00	1.51	2.57
1.66	2.03	-0.79	3422.00	4.68	0.48	0.15	2417.00	1.16	2.92
7.69	4.00	1.55	3215.00	8.34	4.14	1.32	3890.00	4.65	0.57
1.74	1.95	-0.76	2879.00	5.00	0.80	0.26	3681.00	0.92	3.16
3.96	0.27	0.11	3587.00	7.25	3.05	0.98	3102.00	1.68	2.40
4.69	1.00	0.39	1571.00	22.72	**18.52**	5.92	2624.00	1.94	2.14
3.02	0.67	-0.26	2884.00	6.97	2.77	0.89	3206.00	1.25	2.83
3.24	0.45	-0.18	1131.00	15.21	**11.01**	3.52	1839.00	0.98	3.10
2.44	1.25	-0.49	3375.00	3.94	0.26	-0.08	4118.00	1.46	2.62
0.94	2.75	-1.07	2574.00	1.86	2.34	-0.75	3076.00	0.81	3.27
6.69	3.00	1.16	4043.00	3.76	0.44	-0.14	5191.00	5.43	1.35
5.37	1.68	0.65	3830.00	1.04	3.16	-1.01	5686.00	7.54	3.46
6.51	2.82	1.10	2629.00	0.68	3.52	-1.12	3370.00	2.28	1.80
4.98	1.29	0.50	1227.00	2.69	1.51	-0.48	1803.00	4.27	0.19
1.92	1.77	-0.69	2095.00	1.58	2.62	-0.84	3245.00	3.51	0.57
4.23	0.54	0.21	2294.00	0.70	3.50	-1.12	3130.00	4.12	0.04
6.22	2.53	0.98	2070.00	1.30	2.90	-0.92	3805.00	7.31	3.23
4.77	1.08	0.42	2318.00	1.77	2.43	-0.78	3586.00	3.68	0.40
6.70	3.01	1.17	2994.00	1.00	3.20	-1.02	2987.00	2.38	1.70
3.19	0.50	-0.20	1356.00	0.15	4.05	-1.29	1935.00	1.91	2.17
5.94	2.25	0.87	1755.00	0.23	3.97	-1.27	1906.00	2.52	1.56
8.32	4.63	1.80	1791.00	2.01	2.19	-0.70	2795.00	1.54	2.54
3.38	0.31	-0.12	2750.00	0.91	3.29	-1.05	2759.00	1.09	2.99
5.33	1.64	0.64	1736.00	2.71	1.49	-0.48	2843.00	2.39	1.69
8.57	4.88	1.89	2604.00	3.34	0.86	-0.27	1623.00	12.94	**8.86**
4.95	1.26	0.49	2994.00	0.47	3.73	-1.19	3142.00	2.39	1.69
2.06	1.63	-0.64	2516.00	0.91	3.29	-1.05	4589.00	2.59	1.49
8.45	4.76	1.85	2795.00	1.90	2.30	-0.74	2674.00	2.21	1.87
8.91	**5.22**	2.03	3524.00	2.04	2.16	-0.69	4496.00	3.63	0.45
3.63	0.06	-0.02	2467.00	1.05	3.15	-1.00	3831.00	1.59	2.49
2.55	1.14	-0.44	3179.00	3.08	1.12	-0.36	4406.00	3.02	1.06
4.00	0.31	0.12	2701.00	6.63	2.43	0.78	4142.00	5.96	1.88
1.71	1.98	-0.77	4089.00	7.80	3.60	1.15	3510.00	2.31	1.77
3.74	0.05	0.02	3848.00	4.47	0.27	0.09	4693.00	5.92	1.84
2.95	0.74	-0.29	2248.00	4.09	0.11	-0.03	3024.00	5.36	1.28
3.49	0.20	-0.08	2633.00	0.57	3.63	-1.16	3116.00	3.02	1.06
1.81	1.88	-0.73	2850.00	2.91	1.29	-0.41	3675.00	3.10	0.98

4.81	1.12	0.44	2015.00	3.77	0.43	-0.14	3404.00	6.17	2.09
1.44	2.25	-0.87	3452.00	2.03	2.17	-0.69	3246.00	2.80	1.28
1.85	1.84	-0.72	2454.00	2.12	2.08	-0.66	2776.00	3.24	0.84
4.14	0.45	0.17	3578.00	5.25	1.05	0.34	2823.00	3.51	0.57
4.98	1.29	0.50	1964.00	8.91	4.71	1.51	2700.00	13.37	**9.29**
3.03	0.66	-0.26	1880.00	1.76	2.44	-0.78	3369.00	2.61	1.47
2.83	0.86	-0.34	3284.00	2.95	1.25	-0.40	1948.00	2.82	1.26
3.19	0.50	-0.20	3222.00	2.95	1.25	-0.40	3623.00	3.95	0.13
1.13	2.56	-0.99	3340.00	6.08	1.88	0.60	5889.00	5.13	1.05
0.79	2.90	-1.13	759.00	1.98	2.22	-0.71	992.00	3.13	0.96
5.07	1.38	0.53	4185.00	4.37	0.17	0.06	4047.00	6.33	2.25
8.33	4.64	1.80	5212.00	6.25	2.05	0.66	5037.00	8.81	4.73
3.38	0.31	-0.12	4049.00	0.84	3.36	-1.07	3187.00	1.98	2.10
7.48	3.79	1.47	2741.00	2.96	1.24	-0.40	3659.00	2.95	1.13
2.37	1.32	-0.52	3434.00	12.17	**7.97**	2.55	5036.00	6.61	2.53
1.81	1.88	-0.73	3248.00	7.57	3.37	1.08	3662.00	6.55	2.47
3.65	0.04	-0.02	4096.00	6.47	2.27	0.73	4013.00	3.99	0.09
1.12	2.57	-1.00	2917.00	1.99	2.21	-0.71	4082.00	3.18	0.90
6.90	3.21	1.24	4316.00	5.86	1.66	0.53	3967.00	3.40	0.68
3.51	0.18	-0.07	1888.00	8.79	4.59	1.47	4001.00	5.45	1.37
5.68	1.99	0.77	2705.00	10.02	5.82	1.86	3409.00	7.45	3.37
5.18	1.49	0.58	2604.00	12.79	**8.59**	2.75	2535.00	8.48	4.40
5.53	1.84	0.71	1184.00	13.01	**8.81**	2.82	2198.00	7.60	3.52
5.27	1.58	0.61	2197.00	10.33	6.13	1.96	3528.00	6.58	2.50
5.90	2.21	0.86	3784.00	17.97	**13.77**	4.40	3503.00	8.91	4.83
5.86	2.17	0.84	4162.00	7.14	2.94	0.94	4401.00	5.25	1.17
7.19	3.50	1.36	4310.00	4.83	0.63	0.20	4512.00	4.19	0.11
2.14	1.55	-0.60	1697.00	2.36	1.84	-0.59	2665.00	6.98	2.90
2.36	1.33	-0.52	2168.00	17.44	**13.24**	4.23	2117.00	12.09	**8.01**
6.57	2.88	1.12	4424.00	10.17	5.97	1.91	3614.00	12.18	**8.10**
4.34	0.65	0.25	2228.00	16.43	**12.23**	3.91	4225.00	16.50	**12.42**
4.73	1.04	0.40	2404.00	7.28	3.08	0.99	4094.00	11.09	**7.01**
6.36	2.67	1.04	2580.00	4.65	0.45	0.15	3989.00	5.84	1.76
2.31	1.38	-0.54	2519.00	16.91	**12.71**	4.07	4329.00	6.42	2.34
2.71	0.98	-0.38	3224.00	8.90	4.70	1.50	5303.00	9.15	5.07
2.93	0.76	-0.30	3601.00	4.89	0.69	0.22	3544.00	3.24	0.84
3.67	0.02	-0.01	2068.00	19.63	**15.43**	4.94	1927.00	6.23	2.15
4.31	0.62	0.24	1228.00	11.16	**6.96**	2.23	2178.00	3.58	0.50
4.00	0.31	0.12	1906.00	9.23	5.03	1.61	2328.00	2.88	1.20
7.22	3.53	1.37	3567.00	8.19	3.99	1.28	4191.00	6.37	2.29
2.86	0.83	-0.32	2766.00	8.35	4.15	1.33	4277.00	8.28	4.20
2.28	1.41	-0.55	1328.00	8.51	4.31	1.38	2550.00	2.00	2.08
0.80	2.89	-1.12	1087.00	10.40	6.20	1.98	1918.00	8.55	4.47
1.16	2.53	-0.98	2323.00	2.58	1.62	-0.52	2976.00	2.25	1.83
1.69	2.00	-0.78	895.00	6.48	2.28	0.73	2850.00	8.95	4.87
3.25	0.44	-0.17	2503.00	4.23	0.03	0.01	3272.00	4.74	0.66

3.50	0.19	-0.07	1968.00	3.96	0.24	-0.07	3456.00	2.49	1.59
3.64	0.05	-0.02	2555.00	6.26	2.06	0.66	4281.00	14.06	**9.98**
2.85	0.84	-0.33	1958.00	14.25	**10.05**	3.21	3828.00	5.67	1.59
1.78	1.91	-0.74	4181.00	2.68	1.52	-0.48	4749.00	3.73	0.35
7.52	3.83	1.49	4085.00	5.80	1.60	0.51	6046.00	18.11	**14.03**
7.10	3.41	1.32	3330.00	5.89	1.69	0.54	3047.00	7.12	3.04
5.85	2.16	0.84	3509.00	4.62	0.42	0.13	4790.00	5.37	1.29
1.83	1.86	-0.72	3483.00	1.18	3.02	-0.97	5554.00	2.97	1.11
3.49	0.20	-0.08	2246.00	0.31	3.89	-1.24	3775.00	3.15	0.93
9.69	**6.00**	2.33	2577.00	0.93	3.27	-1.04	2504.00	2.16	1.92
11.59	**7.90**	3.06	3525.00	3.80	0.40	-0.13	2086.00	5.13	1.05
3.95	0.26	0.10	2634.00	3.57	0.63	-0.20	3312.00	4.65	0.57
2.00	1.69	-0.66	2537.00	1.66	2.54	-0.81	3237.00	1.70	2.38
5.88	2.19	0.85	2817.00	4.65	0.45	0.15	3230.00	3.78	0.30
5.80	2.11	0.82	3074.00	3.22	0.98	-0.31	3441.00	4.21	0.13
2.85	0.84	-0.33	2651.00	1.09	3.11	-0.99	2735.00	3.33	0.75
4.73	1.04	0.40	2153.00	1.02	3.18	-1.01	2946.00	1.97	2.11
9.82	**6.13**	2.38	1849.00	8.92	4.72	1.51	2804.00	8.20	4.12
9.84	**6.15**	2.39	2711.00	3.39	0.81	-0.26	4053.00	7.85	3.77
5.30	1.61	0.62	3823.00	2.54	1.66	-0.53	4623.00	5.47	1.39
5.41	1.72	0.66	2295.00	1.39	2.81	-0.90	3072.00	4.26	0.18
3.53	0.16	-0.06	2769.00	0.65	3.55	-1.13	4747.00	3.90	0.18
5.95	2.26	0.88	3386.00	3.10	1.10	-0.35	3942.00	5.18	1.10
3.98	0.29	0.11	2743.00	2.41	1.79	-0.57	3291.00	2.92	1.16
12.19	**8.50**	3.30	2854.00	6.06	1.86	0.60	5080.00	9.25	5.17
2.12	1.57	-0.61	2786.00	2.91	1.29	-0.41	5531.00	6.22	2.14
3.57	0.12	-0.05	3279.00	1.22	2.98	-0.95	3942.00	3.78	0.30
5.12	1.43	0.55	2606.00	3.03	1.17	-0.37	2409.00	2.37	1.71
4.18	0.49	0.19	3216.00	6.75	2.55	0.82	3954.00	5.59	1.51
2.38	1.31	-0.51	5297.00	8.67	4.47	1.43	5367.00	7.29	3.21
0.92	2.77	-1.08	2959.00	5.51	1.31	0.42	3896.00	10.55	**6.47**
4.46	0.77	0.30	1191.00	3.02	1.18	-0.38	2848.00	4.18	0.10
1.34	2.35	-0.91	1582.00	4.24	0.04	0.01	3975.00	7.20	3.12
4.61	0.92	0.36	3582.00	6.39	2.19	0.70	5742.00	10.01	**5.93**
0.81	2.88	-1.12	2052.00	2.19	2.01	-0.64	2974.00	2.69	1.39
1.97	1.72	-0.67	2701.00	2.85	1.35	-0.43	4901.00	6.90	2.82
0.95	2.74	-1.07	1408.00	4.05	0.15	-0.05	3565.00	10.58	**6.50**
1.86	1.83	-0.71	1831.00	1.91	2.29	-0.73	3282.00	7.77	3.69
3.13	0.57	-0.22	2695.00	4.42	0.22	0.07	4015.00	6.25	2.17
1.72	1.97	-0.77	1318.00	3.34	0.86	-0.27	3126.00	3.90	0.18
3.46	0.23	-0.09	1996.00	2.05	2.15	-0.68	2996.00	7.18	3.10
1.86	1.83	-0.71	2689.00	4.13	0.07	-0.02	5204.00	7.59	3.51
0.30	3.39	-1.32	2639.00	0.83	3.37	-1.07	3870.00	11.03	**6.95**
3.57	0.12	-0.05	1510.00	2.19	2.01	-0.64	4489.00	11.96	**7.88**
0.63	3.06	-1.19	1172.00	1.88	2.32	-0.74	2739.00	12.82	**8.74**
2.74	0.95	-0.37	2463.00	6.74	2.54	0.81	5186.00	9.24	5.16
3.63	0.06	-0.02	1291.00	1.86	2.34	-0.75	3297.00	5.34	1.26

3.70	0.01	0.00	3579.00	4.33	0.13	0.04	4407.00	1.36	2.72
1.03	2.66	-1.03	1636.00	4.16	0.04	-0.01	2236.00	1.70	2.38
2.23	1.46	-0.57	1634.00	14.20	**10.00**	3.20	1731.00	6.53	2.45
3.18	0.51	-0.20	3373.00	3.05	1.15	-0.37	3747.00	5.20	1.12
1.95	1.74	-0.68	2370.00	3.63	0.57	-0.18	2659.00	2.52	1.56
6.34	2.65	1.03	3651.00	10.44	6.24	1.99	4789.00	8.71	4.63
1.72	1.97	-0.77	2792.00	8.24	4.04	1.29	3624.00	4.91	0.83
1.90	1.79	-0.70	3064.00	2.64	1.56	-0.50	2607.00	1.27	2.81
3.40	0.29	-0.11	2075.00	17.11	**12.91**	4.13	3233.00	3.74	0.34
0.37	3.32	-1.29	2406.00	1.83	2.37	-0.76	3264.00	2.88	1.20
10.26	**6.57**	2.55	1777.00	20.54	**16.34**	5.23	3780.00	17.46	**13.38**
5.22	1.53	0.59	2260.00	6.42	2.22	0.71	2910.00	9.69	**5.61**
2.00	1.70	-0.66	2442.00	7.13	2.93	0.94	2719.00	2.28	1.80
3.69	0.00	0.00	3172.00	4.89	0.69	0.22	3458.00	4.48	0.40
3.73	0.04	0.01	2929.00	6.25	2.05	0.66	3710.00	4.80	0.72
1.75	1.94	-0.76	3798.00	8.93	4.73	1.51	3568.00	2.47	1.61
2.73	0.96	-0.37	3053.00	6.75	2.55	0.82	2415.00	5.92	1.84
6.44	2.75	1.07	2576.00	11.49	**7.29**	2.33	3316.00	10.28	**6.20**
1.78	1.91	-0.74	1669.00	5.99	1.79	0.57	2705.00	4.47	0.39
4.67	0.98	0.38	990.00	12.42	**8.22**	2.63	1050.00	5.52	1.44
2.88	0.81	-0.31	913.00	3.61	0.59	-0.19	1453.00	5.23	1.15
3.35	0.34	-0.13	761.00	8.15	3.95	1.26	1570.00	3.89	0.19
4.36	0.67	0.26	1032.00	3.20	1.00	-0.32	1738.00	0.92	3.16
1.01	2.68	-1.04	1099.00	3.00	1.20	-0.38	1822.00	4.01	0.07
3.29	0.40	-0.16	1527.00	8.71	4.51	1.44	3353.00	8.05	3.97
5.41	1.72	0.66	1528.00	8.84	4.64	1.48	2366.00	2.66	1.42
4.29	0.60	0.23	3059.00	6.67	2.47	0.79	4193.00	10.40	**6.32**
1.68	2.01	-0.78	2647.00	3.21	0.99	-0.31	2798.00	2.29	1.79
2.33	1.36	-0.53	2409.00	3.99	0.21	-0.07	3529.00	5.58	1.50
1.89	1.80	-0.70	1551.00	2.97	1.23	-0.39	3360.00	6.46	2.38
2.98	0.71	-0.28	2012.00	13.62	**9.42**	3.01	2955.00	9.68	**5.60**
5.54	1.85	0.72	2224.00	31.21	**27.01**	8.63	3516.00	13.82	**9.74**
2.89	0.80	-0.31	5112.00	11.85	**7.65**	2.45	5773.00	4.47	0.39
0.90	2.79	-1.08	2543.00	14.86	**10.66**	3.41	3420.00	3.77	0.31
4.14	0.45	0.17	3505.00	16.29	**12.09**	3.87	3411.00	5.60	1.52
0.54	3.15	-1.22	2700.00	12.48	**8.28**	2.65	3941.00	5.76	1.68
3.80	0.11	0.04	1600.00	26.38	**22.18**	7.09	2348.00	12.65	**8.57**
3.49	0.20	-0.08	1905.00	9.66	5.46	1.75	2191.00	7.80	3.72
7.25	3.56	1.38	1782.00	26.60	**22.40**	7.16	1297.00	26.91	**22.83**
0.58	3.11	-1.21	250.00	35.20	**31.00**	9.91	360.00	15.56	**11.48**
3.69	1.74		2166.50	4.20	2.11		2960.00	4.08	1.81
	5.22				6.34				5.43
	2.58				3.13				2.68
20.96		2815.00	11.19						
18.35		2794.00	13.24		3982.00	19.84	3158.00	11.34	
21.98		3238.00	17.91		4265.00	23.26			

	4147.00	20.91	4769.00	24.14
20.43	3248.50	15.81	4338.67	22.41
1.87	632.96	4.41	398.64	2.27
3.54	669.00	6.43	772.00	0.26
4.28	999.00	4.00	1443.00	1.18
2.38	985.00	0.91	1111.00	0.63
0.88	1612.00	1.36	1418.00	3.88
2.77	1066.25	3.18	1186.00	1.49
1.49	394.45	2.56	314.59	1.64
5.62		13.23		6.81
4.46		7.68		9.31
10.08		20.91		16.12
17.66		12.64		20.92
0.57		1.65		0.77
0.43		-0.65		0.23
0.00	220.00	31.36	234.00	17.09
6.25	160.00	11.88	348.00	4.60
5.29	2142.00	1.82	5323.00	3.98
2.08	1892.00	2.48	4808.00	6.41
9.30	6738.00	16.36	6135.00	15.26
6.83	5856.00	16.21	6477.00	13.03

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-0.31		
-0.21		
3.47		
-0.55		
-0.47		
-0.05		
0.39		
-0.35		
0.84		
1.77		
-0.78		
-0.42		
0.95		
0.92		
-0.03		
-0.33		
-0.25		
0.51		
1.26		
1.64		
1.31		
0.93		
1.80		
0.44		
0.04		
1.08		
2.99	x	tox a,art b,c
3.02		
4.63	y	
2.62		
0.66		
0.88		
1.89		
-0.31		
0.80		
-0.18		
-0.45		
0.86		
1.57		
-0.77		
1.67		
-0.68		
1.82		
0.25		

-0.59
3.72
0.59
-0.13
5.23
1.14
0.48
-0.41
-0.34
-0.72
0.39
0.21
-0.89
-0.11
0.05
-0.28
-0.79
1.54
1.41
0.52
0.07
-0.07
0.41
-0.43
1.93
0.80
-0.11
-0.64
0.56
1.20
2.41
0.04
1.16
2.21
-0.52
1.05
2.42
1.38
0.81
-0.06
1.16
1.31
2.60
2.94
3.26
1.92
0.47

-1.01						
-0.89						
0.91						
0.42						
-0.58						
1.73						
0.31						
-1.05						
-0.12						
-0.45						
4.99	y					
2.09						
-0.67						
0.15						
0.27						
-0.60						
0.69						
2.32	y					
0.15						
0.54						
0.43						
-0.07						
-1.18						
-0.03						
1.48						
-0.53						
2.36						
-0.67						
0.56						
0.89						
2.09	x	toxic a,b				
3.64	y		5.54	31.21	13.82	
0.15			4.42	5.62	4.89	
-0.11			1.25	5.55	2.83	3.21
0.57						
0.63						
3.20	x	toxic b,c				
1.39						
8.52	x	toxic a,b				
4.28	x	toxic a,b				

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev	rZ
50019.00	A02	M-010992- ankyrin 1	286.00	ANK1	1575.00	5.78	0.78	0.25
50019.00	A04	M-012723- SMAD fa	4086.00	SMAD1	2235.00	0.54	4.46	-1.42
50019.00	A05	M-009306- elastin (s	2006.00	ELN	1848.00	2.22	2.78	-0.88
50019.00	A06	M-017725- general t	2961.00	GTF2E2	1841.00	3.97	1.03	-0.33
50019.00	A07	M-014746- enameli	10117.00	ENAM	3170.00	5.58	0.58	0.18
50019.00	A08	M-006531- general t	2960.00	GTF2E1	2003.00	3.10	1.90	-0.61
50019.00	A09	M-019628- envoplak	2125.00	EVPL	4027.00	5.91	0.91	0.29
50019.00	A10	M-012964- general t	2959.00	GTF2B	1509.00	2.92	2.08	-0.66
50019.00	A11	M-021718- filaggrin	2312.00	FLG	1730.00	3.87	1.13	-0.36
50019.00	A12	M-006376- enhance	80314.00	EPC1	2893.00	2.70	2.30	-0.73
50019.00	A13	M-003893- growth a	1647.00	GADD45A	3035.00	3.72	1.28	-0.41
50019.00	A14	M-017581- embryon	8726.00	EED	2421.00	3.51	1.49	-0.47
50019.00	A15	M-003895- growth a	10912.00	GADD45G	3554.00	10.38	5.38	1.71
50019.00	A16	M-020313- CCR4-NC	4848.00	CNOT2	1570.00	4.59	0.41	-0.13
50019.00	A17	M-011667- glial fibri	2670.00	GFAP	2430.00	2.72	2.28	-0.73
50019.00	A18	M-015355- Cbp/p30	163732.00	CITED4	3208.00	5.89	0.89	0.28
50019.00	A19	M-014183- heparan	3339.00	HSPG2	2527.00	4.27	0.73	-0.23
50019.00	A20	M-008060- pro-plat	5473.00	PPBP	2250.00	4.98	0.02	-0.01
50019.00	A21	M-020783- keratin 7	51350.00	KRT76	2417.00	3.89	1.11	-0.35
50019.00	A23	M-019835- keratin 7	9119.00	KRT75	2035.00	5.85	0.85	0.27
50019.00	B02	M-010994- apolipop	335.00	APOA1	2690.00	0.37	4.63	-1.47
50019.00	B04	M-010760- annexin	310.00	ANXA7	5311.00	1.36	3.64	-1.16
50019.00	B05	M-010530- prohibiti	5245.00	PHB	2608.00	2.45	2.55	-0.81
50019.00	B06	M-011202- alpha-fet	174.00	AFP	3361.00	0.77	4.23	-1.34
50019.00	B07	M-019548- suppress	8464.00	SUPT3H	3753.00	0.83	4.17	-1.33
50019.00	B08	M-009605- ATP-bind	215.00	ABCD1	4036.00	3.54	1.46	-0.46
50019.00	B09	M-012144- TATA bo	9015.00	TAF1A	5389.00	2.04	2.96	-0.94
50019.00	B10	M-007315- ATP-bind	368.00	ABCC6	3622.00	2.71	2.29	-0.73
50019.00	B11	M-012146- TATA bo	9013.00	TAF1C	2278.00	2.33	2.67	-0.85
50019.00	B12	M-007312- ATP-bind	8714.00	ABCC3	3108.00	3.12	1.88	-0.60
50019.00	B13	M-012898- ankylosis	56172.00	ANKH	2440.00	1.11	3.89	-1.24
50019.00	B14	M-004225- ATP-bind	1244.00	ABCC2	3261.00	2.09	2.91	-0.93
50019.00	B15	M-003627- adaptor-	163.00	AP2B1	2393.00	2.76	2.24	-0.71
50019.00	B16	M-007308- ATP-bind	4363.00	ABCC1	3469.00	5.13	0.13	0.04
50019.00	B17	M-017533- adaptor-	8546.00	AP3B1	2491.00	2.33	2.67	-0.85
50019.00	B18	M-007305- ATP-bind	22.00	ABCB7	4037.00	1.51	3.49	-1.11
50019.00	B19	M-011574- apolipop	341.00	APOC1	2699.00	3.26	1.74	-0.55
50019.00	B20	M-003868- ATP-bind	5243.00	ABCB1	2462.00	3.05	1.95	-0.62
50019.00	B21	M-011575- apolipop	346.00	APOC4	4030.00	3.08	1.92	-0.61
50019.00	B23	M-010984- apolipop	55937.00	APOM	2332.00	2.19	2.81	-0.89
50019.00	C02	M-012294- claudin 1	10686.00	CLDN16	4023.00	4.45	0.55	-0.18
50019.00	C04	M-017683- tissue fa	7980.00	TFPI2	4048.00	6.05	1.05	0.33
50019.00	C05	M-018002- keratin 7	319101.00	KRT73	4077.00	5.37	0.37	0.12
50019.00	C06	M-019840- eukaryot	2107.00	ETF1	1942.00	4.27	0.73	-0.23
50019.00	C07	M-023057- keratin 1	3858.00	KRT10	3344.00	5.92	0.92	0.29
50019.00	C08	M-004127- metasta	9112.00	MTA1	3749.00	7.68	2.68	0.85

50019.00	C09	M-011062-	keratin 1	3859.00	KRT12	3490.00	8.14	3.14	0.99
50019.00	C10	M-019743-	thrombo	7057.00	THBS1	4728.00	9.60	4.60	1.46
50019.00	C11	M-011709-	keratin 1	3860.00	KRT13	2670.00	3.37	1.63	-0.52
50019.00	C12	M-004833-	protein S	5627.00	PROS1	2164.00	5.82	0.82	0.26
50019.00	C13	M-010602-	keratin 1	3861.00	KRT14	4460.00	2.00	3.00	-0.95
50019.00	C14	M-011061-	Kallmanr	3730.00	KAL1	2646.00	2.31	2.69	-0.86
50019.00	C15	M-011710-	keratin 1	3866.00	KRT15	2556.00	3.21	1.79	-0.57
50019.00	C16	M-011017-	collagen,	1294.00	COL7A1	2405.00	4.45	0.55	-0.18
50019.00	C17	M-017624-	keratin 1	3880.00	KRT19	3399.00	4.50	0.50	-0.16
50019.00	C18	M-003646-	collagen,	1293.00	COL6A3	2755.00	2.47	2.53	-0.80
50019.00	C19	M-013390-	keratin 2	54474.00	KRT20	3094.00	6.79	1.79	0.57
50019.00	C20	M-011013-	collagen,	1285.00	COL4A3	4585.00	5.04	0.04	0.01
50019.00	C21	M-011066-	keratin 2	3849.00	KRT2	1704.00	4.93	0.07	-0.02
50019.00	C23	M-012902-	keratin 3	3850.00	KRT3	4150.00	8.75	3.75	1.19
50019.00	D02	M-004128-	ATP-bind	19.00	ABCA1	2483.00	1.81	3.19	-1.01
50019.00	D04	M-013184-	X-linked	7504.00	XK	4033.00	2.85	2.15	-0.68
50019.00	D05	M-021494-	aquapori	358.00	AQP1	3641.00	7.11	2.11	0.67
50019.00	D06	M-019825-	bestroph	7439.00	BEST1	3145.00	5.41	0.41	0.13
50019.00	D07	M-019263-	aquapori	359.00	AQP2	4320.00	8.15	3.15	1.00
50019.00	D08	M-020820-	STEAP fa	55240.00	STEAP3	4174.00	2.61	2.39	-0.76
50019.00	D09	M-011812-	aquapori	360.00	AQP3	5579.00	10.67	5.67	1.80
50019.00	D10	M-004195-	transient	59341.00	TRPV4	2650.00	4.64	0.36	-0.12
50019.00	D11	M-011578-	aquapori	361.00	AQP4	1188.00	7.15	2.15	0.68
50019.00	D12	M-006514-	transient	80036.00	TRPM3	2639.00	2.69	2.31	-0.73
50019.00	D13	M-004520-	aquapori	362.00	AQP5	2054.00	1.95	3.05	-0.97
50019.00	D14	M-004193-	transient	7226.00	TRPM2	3976.00	3.47	1.53	-0.49
50019.00	D15	M-011579-	aquapori	363.00	AQP6	3462.00	4.88	0.12	-0.04
50019.00	D16	M-006513-	transient	4308.00	TRPM1	5263.00	18.03	13.03	4.13
50019.00	D17	M-008726-	aquapori	364.00	AQP7	3296.00	0.97	4.03	-1.28
50019.00	D18	M-004192-	transient	7225.00	TRPC6	3691.00	1.49	3.51	-1.11
50019.00	D19	M-013185-	ATPase, I	50617.00	ATP6V0A4	3312.00	2.42	2.58	-0.82
50019.00	D20	M-006511-	transient	7224.00	TRPC5	4373.00	4.67	0.34	-0.11
50019.00	D21	M-020206-	calcium c	781.00	CACNA2D1	5053.00	10.17	5.17	1.64
50019.00	D23	M-006132-	cation ch	117155.00	CATSPER2	4262.00	3.10	1.90	-0.60
50019.00	E02	M-003551-	vimentin	7431.00	VIM	1961.00	5.10	0.10	0.03
50019.00	E04	M-012382-	utrophin	7402.00	UTRN	3666.00	7.04	2.04	0.64
50019.00	E05	M-011711-	keratin 4	3851.00	KRT4	2745.00	9.40	4.40	1.39
50019.00	E06	M-018323-	tubulin, g	10426.00	TUBGCP3	2646.00	9.45	4.45	1.41
50019.00	E07	M-011067-	keratin 5	3852.00	KRT5	4597.00	8.20	3.20	1.01
50019.00	E08	M-019841-	myotilin	9499.00	MYOT	5008.00	20.93	15.93	5.05
50019.00	E09	M-012116-	keratin 6	3853.00	KRT6A	5080.00	21.54	16.54	5.24
50019.00	E10	M-019753-	tropomy	7171.00	TPM4	3234.00	9.68	4.68	1.48
50019.00	E11	M-012117-	keratin 6	3854.00	KRT6B	2766.00	13.92	8.92	2.83
50019.00	E12	M-012657-	tropomy	7169.00	TPM2	3505.00	4.19	0.81	-0.26
50019.00	E13	M-013021-	keratin 6	140446.00	KRT6C	3746.00	13.13	8.13	2.58
50019.00	E14	M-017837-	tropomy	7168.00	TPM1	2581.00	6.59	1.59	0.50
50019.00	E15	M-019277-	keratin 7	3855.00	KRT7	5110.00	2.99	2.01	-0.64

50019.00	E16	M-017834- thrombo	7060.00	THBS4	2391.00	5.31	0.31	0.10
50019.00	E17	M-019658- keratin 8	3856.00	KRT8	3734.00	2.46	2.54	-0.81
50019.00	E18	M-019745- thrombo	7058.00	THBS2	4176.00	7.81	2.81	0.89
50019.00	E19	M-011312- keratin 3	3886.00	KRT35	3109.00	2.96	2.04	-0.65
50019.00	E20	M-012654- statherin	6779.00	STATH	3834.00	3.76	1.24	-0.40
50019.00	E21	M-011513- keratin 3	8689.00	KRT36	3894.00	9.42	4.42	1.40
50019.00	E23	M-004254- ligase IV,	3981.00	LIG4	2679.00	3.77	1.23	-0.39
50019.00	F02	M-006509- transient	7222.00	TRPC3	1908.00	4.19	0.81	-0.26
50019.00	F04	M-004191- transient	7220.00	TRPC1	1709.00	10.06	5.06	1.60
50019.00	F05	M-012878- vacuolar	23230.00	VPS13A	3208.00	2.24	2.76	-0.88
50019.00	F06	M-006508- two pore	219931.00	TPCN2	4359.00	10.76	5.76	1.83
50019.00	F07	M-003813- chloride	9635.00	CLCA2	3780.00	11.88	6.88	2.18
50019.00	F08	M-003911- target of	10040.00	TOM1L1	3368.00	5.97	0.97	0.31
50019.00	F09	M-006149- chloride	1180.00	CLCN1	3005.00	4.66	0.34	-0.11
50019.00	F10	M-010342- transloca	1678.00	TIMM8A	5386.00	3.73	1.27	-0.40
50019.00	F11	M-006150- chloride	1181.00	CLCN2	3196.00	7.95	2.95	0.93
50019.00	F12	M-012550- Treacher	6949.00	TCOF1	2131.00	2.44	2.56	-0.81
50019.00	F13	M-006153- chloride	1184.00	CLCN5	3372.00	7.15	2.15	0.68
50019.00	F14	M-012198- T-cell, im	10312.00	TCIRG1	2463.00	7.51	2.51	0.80
50019.00	F15	M-006155- chloride	1186.00	CLCN7	2694.00	7.31	2.31	0.73
50019.00	F16	M-012677- syntaxin	6804.00	STX1A	5760.00	8.40	3.40	1.08
50019.00	F17	M-006156- chloride	1187.00	CLCNKA	3879.00	4.51	0.49	-0.16
50019.00	F18	M-007439- solute ca	6579.00	SLCO1A2	3311.00	5.89	0.89	0.28
50019.00	F19	M-013553- chloride	25932.00	CLIC4	3854.00	6.49	1.49	0.47
50019.00	F20	M-007619- solute ca	11136.00	SLC7A9	4436.00	8.27	3.27	1.04
50019.00	F21	M-020570- chloride	53405.00	CLIC5	2986.00	3.38	1.62	-0.51
50019.00	F23	M-013993- compone	25839.00	COG4	3048.00	8.63	3.63	1.15
50019.00	G02	M-017692- spectrin,	6710.00	SPTB	3635.00	3.88	1.12	-0.36
50019.00	G04	M-017440- smoothe	6525.00	SMTN	2790.00	5.38	0.38	0.12
50019.00	G05	M-005290- lamin B2	84823.00	LMNB2	3234.00	5.41	0.41	0.13
50019.00	G06	M-012600- slit homo	6586.00	SLIT3	4173.00	4.82	0.18	-0.06
50019.00	G07	M-011077- loricrin	4014.00	LOR	2945.00	4.21	0.79	-0.25
50019.00	G08	M-015415- sorbin ar	10174.00	SORBS3	4892.00	5.68	0.68	0.22
50019.00	G09	M-013482- microtub	4130.00	MAP1A	3822.00	2.64	2.36	-0.75
50019.00	G10	M-010498- ribosoma	6193.00	RPS5	1533.00	5.48	0.48	0.15
50019.00	G11	M-010348- microtub	4131.00	MAP1B	5036.00	6.75	1.75	0.55
50019.00	G12	M-013607- ribosoma	6188.00	RPS3	1330.00	4.59	0.41	-0.13
50019.00	G13	M-011563- microtub	9053.00	MAP7	4971.00	10.86	5.86	1.86
50019.00	G14	M-011153- ribosoma	6227.00	RPS21	1385.00	6.50	1.50	0.47
50019.00	G15	M-012488- microtub	4137.00	MAPT	3244.00	7.74	2.74	0.87
50019.00	G16	M-013690- ribosoma	6187.00	RPS2	1615.00	4.58	0.42	-0.13
50019.00	G17	M-003685- matrilin	4148.00	MATN3	4370.00	8.08	3.08	0.97
50019.00	G18	M-011762- radixin	5962.00	RDX	5678.00	5.64	0.64	0.20
50019.00	G19	M-019663- myelin ba	4155.00	MBP	5089.00	5.03	0.03	0.01
50019.00	G20	M-003945- plectin 1,	5339.00	PLEC1	3521.00	4.91	0.09	-0.03
50019.00	G21	M-012179- major int	4284.00	MIP	3925.00	9.94	4.94	1.56
50019.00	G23	M-015424- myelin pr	4359.00	MPZ	4315.00	3.82	1.18	-0.37

50019.00	H02	M-007617-	solute ca	9056.00	SLC7A7	3170.00	10.79	5.79	1.83
50019.00	H04	M-007608-	solute ca	6535.00	SLC6A8	4116.00	22.50	17.50	5.55
50019.00	H05	M-012525-	copine V	27132.00	CPNE7	3572.00	6.55	1.55	0.49
50019.00	H06	M-007604-	solute ca	6532.00	SLC6A4	3251.00	19.59	14.59	4.63
50019.00	H07	M-019914-	cystinosi	1497.00	CTNS	4146.00	11.53	6.53	2.07
50019.00	H08	M-007602-	solute ca	6530.00	SLC6A2	4579.00	8.58	3.58	1.14
50019.00	H09	M-007875-	chemoki	9547.00	CXCL14	6006.00	9.84	4.84	1.53
50019.00	H10	M-007593-	solute ca	6528.00	SLC5A5	2349.00	4.64	0.36	-0.12
50019.00	H11	M-021379-	syntaxin	2054.00	STX2	3814.00	11.20	6.20	1.96
50019.00	H12	M-007590-	solute ca	6524.00	SLC5A2	2904.00	10.40	5.40	1.71
50019.00	H13	M-011029-	electron-	2108.00	ETFA	3403.00	5.52	0.52	0.17
50019.00	H14	M-007589-	solute ca	6523.00	SLC5A1	2758.00	1.20	3.80	-1.21
50019.00	H15	M-010494-	electron-	2109.00	ETFB	5150.00	14.87	9.87	3.13
50019.00	H16	M-007584-	solute ca	8671.00	SLC4A4	3099.00	6.16	1.16	0.37
50019.00	H17	M-011977-	FXYD do	5348.00	FXYD1	4792.00	9.18	4.18	1.33
50019.00	H18	M-007583-	solute ca	6508.00	SLC4A3	2972.00	8.34	3.34	1.06
50019.00	H19	M-006853-	GABA(A)	11345.00	GABARAPL	1665.00	8.23	3.23	1.02
50019.00	H20	M-007579-	solute ca	6521.00	SLC4A1	5055.00	14.72	9.72	3.08
50019.00	H21	M-011669-	gap junct	2701.00	GJA4	4980.00	19.46	14.46	4.58
50019.00	H23	M-019941-	gap junct	10052.00	GJA7	3129.00	6.90	1.90	0.60
50019.00	I02	M-011487-	plakophil	8502.00	PKP4	2093.00	2.10	2.90	-0.92
50019.00	I04	M-019664-	plakophil	11187.00	PKP3	3265.00	4.47	0.53	-0.17
50019.00	I05	M-013557-	mitocho	28998.00	MRPL13	2907.00	3.37	1.63	-0.52
50019.00	I06	M-012692-	plakophil	5318.00	PKP2	1897.00	3.95	1.05	-0.33
50019.00	I07	M-017627-	mitocho	10573.00	MRPL28	2290.00	5.07	0.07	0.02
50019.00	I08	M-012545-	plakophil	5317.00	PKP1	2009.00	3.78	1.22	-0.39
50019.00	I09	M-013512-	mitocho	64983.00	MRPL32	1672.00	4.31	0.69	-0.22
50019.00	I10	M-012888-	nephron	261734.00	NPHP4	1971.00	13.14	8.14	2.58
50019.00	I11	M-013623-	mitocho	64963.00	MRPS11	2013.00	2.53	2.47	-0.78
50019.00	I12	M-011094-	nephron	4867.00	NPHP1	2368.00	6.12	1.12	0.35
50019.00	I13	M-011946-	netrin 1	9423.00	NTN1	1088.00	5.97	0.97	0.31
50019.00	I14	M-019674-	nidogen	4811.00	NID1	2679.00	5.79	0.79	0.25
50019.00	I15	M-020117-	netrin 2-	4917.00	NTN2L	1330.00	1.95	3.05	-0.97
50019.00	I16	M-019900-	NHP2 no	4809.00	NHP2L1	394.00	13.71	8.71	2.76
50019.00	I17	M-031987-	netrin 4	59277.00	NTN4	3886.00	5.89	0.89	0.28
50019.00	I18	M-003917-	neurofib	4771.00	NF2	2311.00	3.29	1.71	-0.54
50019.00	I19	M-005272-	nuclear r	4926.00	NUMA1	2059.00	2.72	2.28	-0.72
50019.00	I20	M-019165-	neurofila	4744.00	NEFH	2775.00	5.23	0.23	0.07
50019.00	I21	M-019228-	pinin, de	5411.00	PNN	2123.00	9.47	4.47	1.42
50019.00	I23	M-011496-	titin-cap	8557.00	TCAP	1145.00	3.06	1.94	-0.62
50019.00	J02	M-006343-	solute ca	55630.00	SLC39A4	3883.00	3.81	1.19	-0.38
50019.00	J04	M-007524-	solute ca	7781.00	SLC30A3	3594.00	11.71	6.71	2.13
50019.00	J05	M-017887-	gap junct	2705.00	GJB1	3208.00	4.40	0.60	-0.19
50019.00	J06	M-007521-	solute ca	56606.00	SLC2A9	3122.00	2.18	2.82	-0.90
50019.00	J07	M-019285-	gap junct	2706.00	GJB2	4004.00	6.32	1.32	0.42
50019.00	J08	M-007520-	solute ca	29988.00	SLC2A8	2977.00	4.74	0.26	-0.08
50019.00	J09	M-019948-	gap junct	2707.00	GJB3	3225.00	4.37	0.63	-0.20

50019.00	J10	M-007518- solute ca	6518.00	SLC2A5	3175.00	16.32	11.32	3.59
50019.00	J11	M-016916- gap junct	127534.00	GJB4	3321.00	16.83	11.83	3.75
50019.00	J12	M-007517- solute ca	6517.00	SLC2A4	2960.00	7.30	2.30	0.73
50019.00	J13	M-017789- gap junct	2709.00	GJB5	1610.00	4.29	0.71	-0.23
50019.00	J14	M-007516- solute ca	6515.00	SLC2A3	3309.00	2.93	2.07	-0.66
50019.00	J15	M-019916- gap junct	10804.00	GJB6	3537.00	8.00	3.00	0.95
50019.00	J16	M-007515- solute ca	6514.00	SLC2A2	3044.00	13.54	8.54	2.71
50019.00	J17	M-011047- hemoglo	3043.00	HBB	4446.00	5.62	0.62	0.20
50019.00	J18	M-007509- solute ca	6513.00	SLC2A1	5022.00	18.26	13.26	4.20
50019.00	J19	M-011115- hemoglo	3047.00	HBG1	4265.00	7.20	2.20	0.70
50019.00	J20	M-007493- solute ca	5172.00	SLC26A4	5263.00	7.49	2.49	0.79
50019.00	J21	M-006210- potassiu	3736.00	KCNA1	5478.00	10.19	5.19	1.64
50019.00	J23	M-006213- potassiu	3738.00	KCNA3	3952.00	5.42	0.42	0.13
50019.00	K02	M-011882- nebulin	4703.00	NEB	3234.00	1.95	3.05	-0.97
50019.00	K04	M-011738- myosin, l	4635.00	MYL4	2877.00	4.45	0.55	-0.18
50019.00	K05	M-012065- tectorin	7007.00	TECTA	5523.00	5.20	0.20	0.06
50019.00	K06	M-011085- myosin b	4607.00	MYBPC3	4579.00	2.58	2.42	-0.77
50019.00	K07	M-011794- ubiquitin	7311.00	UBA52	1115.00	8.25	3.25	1.03
50019.00	K08	M-017264- mitocho	65008.00	MRPL1	3414.00	8.00	3.00	0.95
50019.00	K09	M-012381- Usher sy	7399.00	USH2A	3350.00	9.70	4.70	1.49
50019.00	K10	M-009770- matrix Gl	4256.00	MGP	1500.00	6.53	1.53	0.49
50019.00	K11	M-009288- vinculin	7414.00	VCL	3464.00	4.24	0.76	-0.24
50019.00	K12	M-017382- matrin 3	9782.00	MATR3	3685.00	6.32	1.32	0.42
50019.00	K13	M-011195- actinin, a	87.00	ACTN1	2957.00	4.57	0.43	-0.14
50019.00	K14	M-011328- matrilin	4146.00	MATN1	1952.00	2.56	2.44	-0.77
50019.00	K15	M-011196- actinin, a	88.00	ACTN2	2852.00	16.73	11.73	3.72
50019.00	K16	M-007299- microtub	4133.00	MAP2	2761.00	3.98	1.02	-0.32
50019.00	K17	M-011197- actinin, a	89.00	ACTN3	3488.00	3.56	1.45	-0.46
50019.00	K18	M-016684- lumican	4060.00	LUM	2525.00	2.42	2.58	-0.82
50019.00	K19	M-011988- actinin, a	81.00	ACTN4	2700.00	9.67	4.67	1.48
50019.00	K20	M-004978- lamin A/	4000.00	LMNA	2186.00	8.28	3.28	1.04
50019.00	K21	M-009487- adducin	118.00	ADD1	2037.00	4.03	0.97	-0.31
50019.00	K23	M-008468- adducin	120.00	ADD3	2681.00	5.74	0.74	0.23
50019.00	L02	M-007491- solute ca	1836.00	SLC26A2	4983.00	2.39	2.61	-0.83
50019.00	L04	M-007456- solute ca	6584.00	SLC22A5	3816.00	4.19	0.81	-0.26
50019.00	L05	M-009368- potassiu	8514.00	KCNAB2	4427.00	6.03	1.03	0.33
50019.00	L06	M-007446- solute ca	116085.00	SLC22A12	4161.00	3.85	1.15	-0.37
50019.00	L07	M-008846- potassiu	9196.00	KCNAB3	3961.00	3.28	1.72	-0.55
50019.00	L08	M-007425- solute ca	6505.00	SLC1A1	3197.00	2.03	2.97	-0.94
50019.00	L09	M-006224- potassiu	3750.00	KCND1	4023.00	2.19	2.81	-0.89
50019.00	L10	M-007415- solute ca	26503.00	SLC17A5	3417.00	10.39	5.39	1.71
50019.00	L11	M-006225- potassiu	3751.00	KCND2	2780.00	3.99	1.01	-0.32
50019.00	L12	M-007402- solute ca	6566.00	SLC16A1	2314.00	2.03	2.97	-0.94
50019.00	L13	M-006226- potassiu	3752.00	KCND3	3315.00	4.68	0.32	-0.10
50019.00	L14	M-007397- solute ca	8170.00	SLC14A2	2172.00	3.04	1.96	-0.62
50019.00	L15	M-009044- potassiu	3753.00	KCNE1	2979.00	5.10	0.10	0.03
50019.00	L16	M-007396- solute ca	6563.00	SLC14A1	1816.00	1.27	3.73	-1.19

50019.00	L17	M-017528- potassiu	10008.00	KCNE3	4270.00	10.16	5.16	1.64
50019.00	L18	M-007387- solute ca	9990.00	SLC12A6	2952.00	5.76	0.76	0.24
50019.00	L19	M-006236- potassiu	81033.00	KCNH6	1458.00	7.82	2.82	0.89
50019.00	L20	M-007383- solute ca	6558.00	SLC12A2	2633.00	3.91	1.09	-0.35
50019.00	L21	M-006241- potassiu	3767.00	KCNJ11	3080.00	3.99	1.01	-0.32
50019.00	L23	M-006247- potassiu	3759.00	KCNJ2	2822.00	5.42	0.42	0.13
50019.00	M02	M-011877- lethal gia	3996.00	LLGL1	3654.00	1.86	3.14	-1.00
50019.00	M04	M-012173- laminin,	10319.00	LAMC3	3467.00	3.06	1.94	-0.62
50019.00	M05	M-020372- ARP3 act	57180.00	ACTR3B	4447.00	7.71	2.71	0.86
50019.00	M06	M-012119- laminin,	3918.00	LAMC2	2776.00	3.21	1.79	-0.57
50019.00	M07	M-011586- armadill	421.00	ARVCF	6524.00	14.44	9.44	2.99
50019.00	M08	M-011714- laminin,	3915.00	LAMC1	3555.00	10.86	5.86	1.86
50019.00	M09	M-010948- contacti	79937.00	CNTNAP3	3701.00	9.13	4.13	1.31
50019.00	M10	M-011072- laminin,	3914.00	LAMB3	3889.00	11.08	6.08	1.93
50019.00	M11	M-011607- septin 7	989.00	SEPT7	2844.00	13.36	8.36	2.65
50019.00	M12	M-013310- laminin,	3913.00	LAMB2	2961.00	3.34	1.66	-0.53
50019.00	M13	M-017329- contacti	26047.00	CNTNAP2	3590.00	4.37	0.63	-0.20
50019.00	M14	M-011713- laminin,	3912.00	LAMB1	3336.00	7.49	2.49	0.79
50019.00	M15	M-011614- collagen,	1301.00	COL11A1	2294.00	2.92	2.08	-0.66
50019.00	M16	M-011071- laminin,	3909.00	LAMA3	2883.00	6.59	1.59	0.50
50019.00	M17	M-025907- collagen,	7373.00	COL14A1	2941.00	9.25	4.25	1.35
50019.00	M18	M-012118- laminin,	284217.00	LAMA1	4213.00	10.52	5.52	1.75
50019.00	M19	M-012915- collagen,	80781.00	COL18A1	4198.00	8.58	3.58	1.13
50019.00	M20	M-009853- fibronect	2335.00	FN1	4613.00	15.50	10.50	3.33
50019.00	M21	M-011617- collagen,	1310.00	COL19A1	4659.00	15.69	10.69	3.39
50019.00	M23	M-011619- collagen,	1288.00	COL4A6	3868.00	10.45	5.45	1.73
50019.00	N02	M-007382- solute ca	6557.00	SLC12A1	2429.00	8.52	3.52	1.12
50019.00	N04	M-007381- solute ca	4891.00	SLC11A2	3938.00	8.25	3.25	1.03
50019.00	N05	M-006252- potassiu	3764.00	KCNJ8	1891.00	2.75	2.25	-0.72
50019.00	N06	M-007380- solute ca	6556.00	SLC11A1	2732.00	4.28	0.72	-0.23
50019.00	N07	M-006257- potassiu	56659.00	KCNK13	1917.00	2.61	2.39	-0.76
50019.00	N08	M-007377- solute ca	6555.00	SLC10A2	2344.00	4.56	0.44	-0.14
50019.00	N09	M-006262- potassiu	3777.00	KCNK3	3376.00	5.98	0.98	0.31
50019.00	N10	M-007376- solute ca	6554.00	SLC10A1	2050.00	4.83	0.17	-0.06
50019.00	N11	M-004891- potassiu	51305.00	KCNK9	1858.00	5.33	0.33	0.10
50019.00	N12	M-006507- sodium c	6340.00	SCNN1G	2519.00	3.57	1.43	-0.45
50019.00	N13	M-006271- potassiu	3784.00	KCNQ1	2581.00	1.94	3.06	-0.97
50019.00	N14	M-006505- sodium c	6338.00	SCNN1B	2639.00	3.22	1.78	-0.57
50019.00	N15	M-006272- potassiu	3785.00	KCNQ2	1745.00	2.64	2.36	-0.75
50019.00	N16	M-006504- sodium c	6337.00	SCNN1A	4207.00	5.73	0.73	0.23
50019.00	N17	M-006273- potassiu	3786.00	KCNQ3	3694.00	3.30	1.70	-0.54
50019.00	N18	M-006500- sodium c	6331.00	SCN5A	3276.00	1.40	3.60	-1.14
50019.00	N19	M-006274- potassiu	9132.00	KCNQ4	3410.00	2.84	2.16	-0.68
50019.00	N20	M-006300- sodium c	6329.00	SCN4A	3625.00	3.09	1.91	-0.61
50019.00	N21	M-010698- potassiu	3788.00	KCNS2	5930.00	4.69	0.31	-0.10
50019.00	N23	M-010714- potassiu	57582.00	KCNT1	2889.00	2.08	2.92	-0.93
50019.00	O02	M-011656- fibrillin 2	2201.00	FBN2	1813.00	4.80	0.20	-0.07

50019.00	O04	M-011034-	fibrillin 1	2200.00	FBN1	2917.00	12.10	**7.10**	2.25
50019.00	O05	M-011015-	collagen,	1289.00	COL5A1	1922.00	1.77	3.23	-1.03
50019.00	O06	M-019186-	fibulin 1	2192.00	FBLN1	3357.00	18.05	**13.05**	4.14
50019.00	O07	M-011620-	collagen,	1291.00	COL6A1	2517.00	9.89	4.89	1.55
50019.00	O08	M-013149-	Finkel-Bis	2197.00	FAU	884.00	13.24	**8.24**	2.61
50019.00	O09	M-011621-	collagen,	1292.00	COL6A2	3225.00	10.05	5.05	1.60
50019.00	O10	M-011270-	FAT tumo	2196.00	FAT2	2249.00	15.61	**10.61**	3.36
50019.00	O11	M-012020-	collagen,	1296.00	COL8A2	2614.00	5.81	0.81	0.26
50019.00	O12	M-010513-	FAT tumo	2195.00	FAT	1776.00	4.50	0.50	-0.16
50019.00	O13	M-011018-	cartilage	1311.00	COMP	1401.00	6.42	1.42	0.45
50019.00	O14	M-003662-	erythrocy	2038.00	EPB42	4116.00	7.75	2.75	0.87
50019.00	O15	M-012771-	coronin,	11151.00	CORO1A	1974.00	6.28	1.28	0.41
50019.00	O16	M-019042-	erythrocy	2036.00	EPB41L1	2304.00	8.46	3.46	1.10
50019.00	O17	M-012404-	crumbs h	23418.00	CRB1	2158.00	9.18	4.18	1.32
50019.00	O18	M-003660-	erythrocy	2035.00	EPB41	3272.00	12.35	**7.35**	2.33
50019.00	O19	M-019893-	catenin (	1496.00	CTNNA2	3595.00	13.16	**8.16**	2.59
50019.00	O20	M-011642-	dystroph	1821.00	DRP2	3473.00	9.21	4.21	1.34
50019.00	O21	M-003611-	catenin (	1501.00	CTNND2	3844.00	16.68	**11.68**	3.70
50019.00	O23	M-011809-	dystroph	1756.00	DMD	2419.00	11.53	**6.53**	2.07
50019.00	P02	M-006299-	sodium c	6328.00	SCN3A	2869.00	1.64	3.36	-1.07
50019.00	P04	M-006298-	sodium c	6326.00	SCN2A	2749.00	1.09	3.91	-1.24
50019.00	P05	M-006279-	potassiur	169522.00	KCNV2	2537.00	0.79	4.21	-1.34
50019.00	P06	M-020909-	sodium c	6324.00	SCN1B	2607.00	2.22	2.78	-0.88
50019.00	P07	M-017477-	karyophe	3840.00	KPNA4	2246.00	5.16	0.16	0.05
50019.00	P08	M-006297-	sodium c	6323.00	SCN1A	1513.00	4.43	0.57	-0.18
50019.00	P09	M-017295-	karyophe	23633.00	KPNA6	2849.00	2.91	2.09	-0.66
50019.00	P10	M-013442-	secretory	10067.00	SCAMP3	2158.00	3.20	1.80	-0.57
50019.00	P11	M-006281-	mucolipi	57192.00	MCOLN1	1448.00	2.90	2.10	-0.67
50019.00	P12	M-011958-	secretory	9522.00	SCAMP1	1868.00	4.82	0.18	-0.06
50019.00	P13	M-015371-	mucolipi	55283.00	MCOLN3	1974.00	3.60	1.40	-0.45
50019.00	P14	M-008895-	regulator	6248.00	RSC1A1	1657.00	4.83	0.17	-0.06
50019.00	P15	M-012880-	megalen	23209.00	MLC1	1714.00	4.26	0.74	-0.24
50019.00	P16	M-017729-	polymeri	5284.00	PIGR	1684.00	3.15	1.85	-0.59
50019.00	P17	M-019027-	tumor su	7991.00	TUSC3	3205.00	5.59	0.59	0.18
50019.00	P18	M-012591-	peroxiso	5194.00	PEX13	1513.00	5.88	0.88	0.28
50019.00	P19	M-031875-	N-ethylm	63908.00	NAPB	1162.00	5.08	0.08	0.02
50019.00	P20	M-017194-	NTF2-like	29107.00	NXT1	2468.00	4.13	0.87	-0.28
50019.00	P21	M-004529-	neutroph	4688.00	NCF2	2622.00	3.89	1.11	-0.35
50019.00	P23	M-013078-	nucleopo	4928.00	NUP98	1786.00	4.42	0.58	-0.18
					mdn		5.00	2.13	
					3xMAD			6.39	
					MADc			3.15	
		12.50							
50019.00	C22	10 of 40 are SLC family				4368.00	30.88		2684.00
50019.00	D22					4290.00	34.36		
50019.00	E22					2782.00	25.13		3170.00
50019.00	F22					4389.00	45.20		3633.00

					mn	3957.25	33.89	3162.33
					sd		8.45	
50019.00	G22					2909.00	6.50	
50019.00	H22	784.66	8.45			2528.00	7.79	2186.00
50019.00	I22	474.55	1.75			1256.00	2.95	1225.00
50019.00	J22	778.00	3.60			1746.00	8.08	1191.00
		3787.00	36.34		mn	2109.75	6.33	1534.00
					sd	747.20	2.36	564.90
					3psSD		25.34	
					3ngSD		7.07	
					Sum3SD		32.41	
					MeanDiff		27.57	
					SumovrMn		1.18	
					1minus		-0.18	
50019.00	I03	D-001206-	siControl non-targeti			1983.00	7.92	2205.00
50019.00	J03	D-001206-	siControl non-targeti			2180.00	4.22	2709.00
50019.00	K03	D-001600-	siGLO RISC-free siRN			6484.00	8.54	6429.00
50019.00	L03	D-001600-	siGLO RISC-free siRN			6750.00	7.38	3919.00
50019.00	H03	M-003290-	polo-like	5347.00	PLK1 SMA	204.00	28.43	244.00
50019.00	G03	M-003290-	polo-like	5347.00	PLK1 SMA	288.00	7.29	200.00

Cell Coun	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
2332.00	3.34	1.44	-0.18	2744.00	0.80	4.62	-1.31
2607.00	1.53	0.64	-0.96	3503.00	4.05	1.37	-0.39
2248.00	2.89	1.20	-0.37	2665.00	0.64	4.78	-1.36
2075.00	4.82	2.01	0.46	3375.00	3.32	2.10	-0.60
1827.00	6.19	2.58	1.05	5136.00	4.61	0.81	-0.23
2777.00	2.09	0.87	-0.72	5145.00	2.99	2.43	-0.69
4024.00	9.05	3.77	2.28	3821.00	2.33	3.09	-0.88
1677.00	2.68	1.12	-0.46	2818.00	1.21	4.21	-1.20
937.00	4.38	1.82	0.27	1489.00	2.62	2.80	-0.79
2165.00	8.64	3.60	2.11	3272.00	2.38	3.04	-0.86
1951.00	4.77	1.99	0.44	2960.00	1.89	3.53	-1.00
2971.00	2.42	1.01	-0.58	3020.00	1.49	3.93	-1.11
1889.00	5.61	2.34	0.80	3330.00	4.59	0.83	-0.23
1574.00	4.96	2.06	0.52	2679.00	1.01	4.41	-1.25
1708.00	2.87	1.20	-0.38	2402.00	2.16	3.26	-0.92
2919.00	5.34	2.23	0.69	4303.00	6.79	1.37	0.39
1529.00	2.09	0.87	-0.72	3750.00	1.07	4.35	-1.24
2852.00	2.98	1.24	-0.33	2757.00	3.16	2.26	-0.64
2732.00	3.84	1.60	0.04	2576.00	4.04	1.38	-0.39
2093.00	3.06	1.27	-0.30	2425.00	3.22	2.20	-0.63
2794.00	3.69	1.54	-0.03	3347.00	2.51	2.91	-0.83
2135.00	2.39	1.00	-0.59	4543.00	3.52	1.90	-0.54
2018.00	2.18	0.91	-0.68	3290.00	0.94	4.48	-1.27
2601.00	2.61	1.09	-0.49	3534.00	3.28	2.14	-0.61
2362.00	2.96	1.23	-0.34	4582.00	2.20	3.22	-0.91
1339.00	3.96	1.65	0.09	3992.00	4.48	0.94	-0.27
2680.00	3.28	1.37	-0.20	4718.00	3.52	1.90	-0.54
1956.00	3.53	1.47	-0.10	3350.00	2.24	3.18	-0.90
1489.00	3.96	1.65	0.09	2935.00	1.09	4.33	-1.23
1208.00	4.47	1.86	0.31	2174.00	2.67	2.75	-0.78
1950.00	5.13	2.14	0.59	2631.00	2.24	3.18	-0.90
2101.00	6.33	2.64	1.11	2414.00	2.65	2.77	-0.79
1904.00	3.94	1.64	0.08	3921.00	3.03	2.39	-0.68
1534.00	8.15	3.40	1.90	4215.00	6.50	1.08	0.31
2258.00	4.21	1.75	0.19	2685.00	3.17	2.25	-0.64
2608.00	2.76	1.15	-0.43	3722.00	3.30	2.12	-0.60
1871.00	3.74	1.56	-0.01	3562.00	1.82	3.60	-1.02
2511.00	1.83	0.76	-0.83	2940.00	0.92	4.50	-1.28
3412.00	3.08	1.28	-0.29	3424.00	1.52	3.90	-1.11
2983.00	1.54	0.64	-0.96	3533.00	0.96	4.46	-1.26
3438.00	7.68	3.20	1.69	3987.00	6.70	1.28	0.36
2877.00	4.73	1.97	0.42	3149.00	5.24	0.18	-0.05
3126.00	4.19	1.75	0.19	4154.00	8.93	3.51	1.00
1063.00	5.27	2.20	0.65	1737.00	2.82	2.60	-0.74
1262.00	2.54	1.06	-0.53	2841.00	4.47	0.95	-0.27
2410.00	1.83	0.76	-0.83	4518.00	6.66	1.24	0.35

2068.00	4.64	1.93	0.38	3276.00	11.05	5.63	1.60	
2292.00	3.23	1.35	-0.23	4247.00	10.17	4.75	1.35	
1877.00	4.48	1.86	0.31	2705.00	7.80	2.38	0.67	
1979.00	3.23	1.35	-0.23	1746.00	3.38	2.04	-0.58	
2403.00	2.54	1.06	-0.53	2996.00	4.84	0.58	-0.17	
1776.00	2.25	0.94	-0.65	2161.00	5.88	0.46	0.13	
1605.00	4.11	1.71	0.15	3595.00	6.90	1.48	0.42	
1375.00	2.62	1.09	-0.49	2088.00	4.60	0.82	-0.23	
2183.00	4.03	1.68	0.12	4635.00	8.11	2.69	0.76	
1612.00	3.29	1.37	-0.20	3526.00	7.46	2.04	0.58	
1783.00	2.47	1.03	-0.56	2576.00	15.64	10.22	2.90	
2793.00	2.61	1.09	-0.49	4084.00	6.91	1.49	0.42	
1498.00	5.87	2.45	0.91	1978.00	7.33	1.91	0.54	
2739.00	3.03	1.26	-0.31	3960.00	11.92	6.50	1.84	
2737.00	1.57	0.65	-0.94	2598.00	1.54	3.88	-1.10	
3442.00	2.79	1.16	-0.42	4093.00	2.93	2.49	-0.71	
3149.00	5.68	2.37	0.83	3722.00	4.41	1.01	-0.29	
2292.00	2.36	0.98	-0.60	3712.00	4.45	0.98	-0.28	
3191.00	2.10	0.87	-0.72	5090.00	4.09	1.33	-0.38	
3295.00	3.43	1.43	-0.14	4489.00	5.70	0.28	0.08	
2208.00	4.76	1.98	0.43	4255.00	7.90	2.48	0.70	
1587.00	1.76	0.74	-0.86	2256.00	3.46	1.96	-0.56	
1137.00	6.51	2.71	1.19	665.00	7.07	1.65	0.47	
1653.00	3.45	1.44	-0.13	1995.00	1.35	4.07	-1.15	
2158.00	1.48	0.62	-0.98	2311.00	3.51	1.92	-0.54	
2855.00	9.63	4.01	2.54	4140.00	5.65	0.23	0.07	
1485.00	7.41	3.09	1.58	2988.00	5.22	0.20	-0.06	
3699.00	21.36	8.90	7.60	4852.00	16.24	10.82	3.07	y
1956.00	2.76	1.15	-0.43	2789.00	2.87	2.55	-0.72	
3627.00	5.16	2.15	0.60	5292.00	4.99	0.43	-0.12	
2638.00	2.39	1.00	-0.59	3323.00	3.64	1.78	-0.50	
2922.00	2.57	1.07	-0.51	4127.00	2.69	2.73	-0.77	
4544.00	13.42	5.59	4.17	4523.00	7.23	1.81	0.51	
3234.00	4.98	2.07	0.53	4393.00	7.19	1.77	0.50	
1333.00	0.53	0.22	-1.39	1868.00	4.50	0.92	-0.26	
3254.00	1.78	0.74	-0.85	3292.00	5.38	0.04	-0.01	
2596.00	4.24	1.77	0.21	3522.00	12.75	7.33	2.08	
3079.00	3.44	1.43	-0.14	3133.00	10.57	5.15	1.46	
2826.00	2.05	0.86	-0.74	4004.00	7.37	1.95	0.55	
3570.00	4.76	1.98	0.43	4504.00	14.83	9.41	2.67	y
2538.00	3.19	1.33	-0.24	4425.00	13.38	7.96	2.26	y
2566.00	6.51	2.71	1.19	4564.00	13.32	7.90	2.24	
1948.00	5.49	2.29	0.75	2805.00	11.52	6.10	1.73	
2335.00	1.20	0.50	-1.10	2250.00	3.73	1.69	-0.48	
2581.00	12.32	5.13	3.70	3122.00	7.14	1.72	0.49	y
1494.00	3.08	1.28	-0.29	988.00	8.91	3.49	0.99	
3634.00	3.27	1.36	-0.21	4355.00	3.70	1.72	-0.49	

2455.00	4.36	1.82	0.26	2684.00	8.16	2.74	0.78	
2236.00	1.83	0.76	-0.83	3571.00	3.47	1.95	-0.55	
3139.00	5.00	2.08	0.54	3940.00	5.23	0.19	-0.05	
1250.00	1.52	0.63	-0.97	2410.00	3.65	1.77	-0.50	
2368.00	3.67	1.53	-0.04	3820.00	4.58	0.84	-0.24	
3397.00	10.98	4.58	3.12	3758.00	6.57	1.15	0.33	
1468.00	2.04	0.85	-0.74	1859.00	4.63	0.79	-0.23	
2713.00	2.99	1.24	-0.33	2641.00	5.38	0.04	-0.01	
2225.00	5.21	2.17	0.63	2154.00	13.23	7.81	2.21	
4531.00	1.35	0.56	-1.04	4010.00	8.60	3.18	0.90	
5088.00	5.86	2.44	0.91	4934.00	12.53	7.11	2.01	
3160.00	5.38	2.24	0.70	3389.00	14.72	9.30	2.64	y
3908.00	4.30	1.79	0.23	3995.00	16.02	10.60	3.01	
2807.00	4.20	1.75	0.19	1962.00	8.77	3.35	0.95	
3879.00	2.96	1.24	-0.34	4396.00	9.71	4.29	1.22	
1870.00	2.14	0.89	-0.70	3442.00	9.33	3.91	1.11	
2317.00	1.99	0.83	-0.76	2080.00	6.68	1.26	0.36	
2307.00	2.21	0.92	-0.67	2925.00	5.78	0.36	0.10	
1616.00	2.35	0.98	-0.61	2406.00	2.16	3.26	-0.92	
1599.00	1.06	0.44	-1.16	1766.00	4.81	0.61	-0.17	
2867.00	2.27	0.94	-0.64	3762.00	4.60	0.82	-0.23	
3354.00	3.19	1.33	-0.24	3525.00	5.67	0.25	0.07	
2067.00	1.79	0.75	-0.85	3603.00	12.21	6.79	1.93	
2267.00	2.34	0.97	-0.61	3781.00	9.55	4.13	1.17	
4086.00	6.75	2.81	1.29	4676.00	7.81	2.39	0.68	
2586.00	0.85	0.35	-1.25	2763.00	5.61	0.19	0.05	
2434.00	2.63	1.10	-0.49	3797.00	6.72	1.30	0.37	
4246.00	2.61	1.09	-0.49	4727.00	4.93	0.49	-0.14	
1148.00	2.70	1.13	-0.46	1168.00	2.91	2.51	-0.71	
2667.00	2.36	0.98	-0.60	2025.00	4.15	1.27	-0.36	
3574.00	3.61	1.50	-0.06	2774.00	3.32	2.10	-0.60	
2768.00	2.64	1.10	-0.48	2511.00	4.38	1.04	-0.30	
2328.00	2.62	1.09	-0.49	2129.00	2.91	2.51	-0.71	
1601.00	1.75	0.73	-0.87	2110.00	1.94	3.48	-0.99	
529.00	3.59	1.50	-0.07	765.00	10.20	4.78	1.35	
3069.00	3.55	1.48	-0.09	2612.00	4.13	1.29	-0.37	
699.00	1.14	0.48	-1.13	623.00	1.61	3.81	-1.08	
4162.00	10.62	4.43	2.96	3703.00	12.50	7.08	2.01	y
370.00	7.57	3.15	1.65	375.00	13.07	7.65	2.17	
1561.00	3.46	1.44	-0.13	2731.00	7.98	2.56	0.73	
865.00	1.27	0.53	-1.07	904.00	7.52	2.10	0.60	
2281.00	3.77	1.57	0.01	3076.00	6.11	0.69	0.20	
2367.00	1.35	0.56	-1.04	3515.00	2.22	3.20	-0.91	
3238.00	3.24	1.35	-0.22	3372.00	4.89	0.53	-0.15	
1907.00	1.00	0.42	-1.19	2064.00	2.33	3.09	-0.88	
2382.00	6.63	2.76	1.24	2876.00	4.17	1.25	-0.35	
2267.00	1.59	0.66	-0.94	3658.00	3.85	1.57	-0.44	

3337.00	8.72	3.63	2.14	3290.00	7.51	2.09	0.59		
3275.00	20.34	8.47	7.16	4310.00	14.46	9.04	2.56	y	
3085.00	6.90	2.88	1.36	3527.00	6.35	0.93	0.26		
2344.00	11.86	4.94	3.50	2983.00	10.36	4.94	1.40	y	
4380.00	10.91	4.55	3.09	3925.00	6.11	0.69	0.20	y	
3860.00	4.87	2.03	0.48	4124.00	5.19	0.23	-0.07		
3606.00	2.80	1.17	-0.41	4370.00	3.04	2.38	-0.67		
2499.00	2.80	1.17	-0.41	2681.00	2.72	2.70	-0.77		
2623.00	8.08	3.37	1.87	2833.00	10.98	5.56	1.58		
3416.00	15.69	6.54	5.15	3386.00	11.40	5.98	1.70		
2042.00	3.62	1.51	-0.06	1844.00	2.22	3.20	-0.91		
1800.00	1.72	0.72	-0.88	1808.00	2.38	3.04	-0.86		
3810.00	11.16	4.65	3.19	3724.00	10.29	4.87	1.38	y	
3976.00	5.51	2.30	0.76	3445.00	3.19	2.23	-0.63		
3359.00	4.50	1.87	0.32	3563.00	6.93	1.51	0.43		
2439.00	6.36	2.65	1.12	2522.00	7.18	1.76	0.50		
2101.00	4.62	1.92	0.37	1831.00	8.36	2.94	0.83		
5100.00	7.90	3.29	1.79	5321.00	12.35	6.93	1.96		
4249.00	9.86	4.11	2.64	4955.00	11.93	6.51	1.84	y	
2602.00	2.46	1.02	-0.56	2355.00	3.95	1.47	-0.42		
3433.00	1.92	0.80	-0.79	3504.00	3.05	2.37	-0.67		
3172.00	2.55	1.06	-0.52	3863.00	2.95	2.47	-0.70		
2392.00	4.10	1.71	0.15	2784.00	4.31	1.11	-0.32		
1875.00	2.13	0.89	-0.70	2255.00	4.48	0.94	-0.27		
3275.00	6.72	2.80	1.28	2347.00	5.41	0.01	0.00		
2177.00	8.87	3.69	2.21	1493.00	8.44	3.02	0.86		
2270.00	4.19	1.74	0.19	2161.00	2.13	3.29	-0.93		
2003.00	13.98	5.82	4.41	2532.00	15.21	9.79	2.77	y	
2007.00	2.59	1.08	-0.50	2287.00	4.07	1.35	-0.38		
1732.00	1.79	0.75	-0.85	2700.00	6.56	1.14	0.32		
1530.00	8.95	3.73	2.24	1749.00	9.43	4.01	1.14		
3826.00	16.49	6.87	5.50	3669.00	13.22	7.80	2.21	x	art. A,c
1686.00	6.76	2.82	1.30	1869.00	3.37	2.05	-0.58		
504.00	9.33	3.89	2.40	591.00	12.52	7.10	2.01	x	toxic a,b,c
4649.00	7.29	3.04	1.53	4425.00	10.46	5.04	1.43		
2434.00	4.48	1.87	0.31	2928.00	4.58	0.84	-0.24		
2541.00	6.73	2.80	1.28	2710.00	4.54	0.88	-0.25		
3659.00	6.91	2.88	1.36	2991.00	4.75	0.67	-0.19		
3579.00	14.92	6.22	4.82	2714.00	8.51	3.09	0.88		
1976.00	2.83	1.18	-0.40	2229.00	9.02	3.60	1.02		
3928.00	0.89	0.37	-1.24	3108.00	4.57	0.85	-0.24		
3463.00	4.42	1.84	0.29	3696.00	12.61	7.19	2.04	y	
3293.00	7.44	3.10	1.59	3244.00	8.01	2.59	0.74		
3777.00	0.71	0.30	-1.31	2445.00	6.01	0.59	0.17		
3684.00	3.83	1.59	0.03	4126.00	8.63	3.21	0.91		
3442.00	3.20	1.33	-0.24	2977.00	4.06	1.36	-0.38		
3404.00	3.20	1.33	-0.24	3205.00	7.30	1.88	0.53		

2697.00	10.90	4.54	3.09	2731.00	12.63	7.21	2.04	y
2829.00	11.06	4.61	3.16	3739.00	20.89	15.47	4.39	y
2117.00	6.38	2.66	1.13	2383.00	9.78	4.36	1.24	
1986.00	3.37	1.41	-0.17	1911.00	6.96	1.54	0.44	
2543.00	3.38	1.41	-0.16	2823.00	5.92	0.50	0.14	
2369.00	3.38	1.41	-0.16	2764.00	8.29	2.87	0.81	
2769.00	7.69	3.21	1.70	2827.00	12.27	6.85	1.94	
3563.00	3.90	1.63	0.06	3753.00	6.18	0.76	0.22	
3674.00	10.64	4.43	2.97	4394.00	13.36	7.94	2.25	y
2437.00	2.38	0.99	-0.59	3517.00	8.08	2.66	0.75	
3596.00	2.92	1.22	-0.36	4106.00	6.65	1.23	0.35	
3008.00	2.93	1.22	-0.36	4684.00	6.62	1.20	0.34	
3582.00	5.67	2.36	0.83	4463.00	10.60	5.18	1.47	
2949.00	1.70	0.71	-0.89	2526.00	3.76	1.66	-0.47	
3154.00	3.99	1.66	0.10	2559.00	4.26	1.16	-0.33	
6518.00	5.28	2.20	0.66	5574.00	10.17	4.75	1.35	
5831.00	4.65	1.94	0.39	4038.00	7.70	2.28	0.65	
1398.00	5.87	2.44	0.91	917.00	5.45	0.03	0.01	
5464.00	11.42	4.76	3.31	4847.00	9.78	4.36	1.24	
3510.00	6.07	2.53	1.00	2725.00	5.58	0.16	0.04	
2556.00	3.21	1.34	-0.24	2519.00	2.14	3.28	-0.93	
2640.00	2.12	0.88	-0.71	2490.00	3.57	1.85	-0.52	
2116.00	4.11	1.71	0.15	3452.00	9.82	4.40	1.25	
3814.00	4.75	1.98	0.43	3192.00	2.16	3.26	-0.92	
3547.00	2.65	1.10	-0.48	2009.00	2.04	3.38	-0.96	
4158.00	22.01	9.17	7.88	3182.00	13.48	8.06	2.29	y
2834.00	4.80	2.00	0.45	3329.00	4.36	1.06	-0.30	
3842.00	2.34	0.98	-0.61	2426.00	2.43	2.99	-0.85	
2944.00	2.55	1.06	-0.52	2793.00	2.08	3.34	-0.95	
2659.00	7.86	3.28	1.77	3353.00	9.36	3.94	1.12	
2362.00	6.69	2.79	1.27	2192.00	7.76	2.34	0.66	
2910.00	7.22	3.01	1.49	2610.00	5.75	0.33	0.09	
2345.00	1.32	0.55	-1.05	3226.00	4.37	1.05	-0.30	
3779.00	4.71	1.96	0.41	4154.00	4.33	1.09	-0.31	
3132.00	11.24	4.68	3.23	3512.00	6.55	1.13	0.32	
2775.00	7.06	2.94	1.43	3401.00	9.20	3.78	1.07	
3669.00	11.94	4.97	3.53	4992.00	9.05	3.63	1.03	
3875.00	6.17	2.57	1.04	3186.00	8.73	3.31	0.94	
3496.00	3.12	1.30	-0.28	3801.00	5.50	0.08	0.02	
3471.00	3.28	1.37	-0.20	3522.00	4.86	0.56	-0.16	
3067.00	12.62	5.26	3.83	3370.00	15.79	10.37	2.94	y
2023.00	4.10	1.71	0.15	1887.00	6.41	0.99	0.28	
928.00	0.65	0.27	-1.34	2037.00	5.60	0.18	0.05	
2768.00	4.70	1.96	0.41	2561.00	7.73	2.31	0.65	
1986.00	4.38	1.83	0.27	3109.00	8.17	2.75	0.78	
2250.00	5.69	2.37	0.83	3134.00	10.50	5.08	1.44	
2311.00	5.06	2.11	0.56	2051.00	6.73	1.31	0.37	

4145.00	7.89	3.29	1.78	3460.00	11.91	6.49	1.84	
3101.00	4.45	1.85	0.30	3009.00	10.10	4.68	1.33	
1476.00	1.90	0.79	-0.80	1563.00	7.61	2.19	0.62	
3450.00	7.19	3.00	1.48	2138.00	3.88	1.54	-0.44	
3342.00	1.83	0.76	-0.83	2510.00	6.81	1.39	0.39	
2529.00	3.44	1.43	-0.14	3648.00	7.05	1.63	0.46	
3899.00	3.00	1.25	-0.33	3196.00	2.97	2.45	-0.69	
2041.00	3.18	1.33	-0.25	2449.00	2.78	2.64	-0.75	
4055.00	7.23	3.01	1.50	3915.00	3.14	2.28	-0.65	
2987.00	3.15	1.31	-0.26	1999.00	1.35	4.07	-1.15	
6177.00	9.13	3.80	2.32	3534.00	5.43	0.01	0.00	y
4379.00	7.74	3.23	1.72	3446.00	6.82	1.40	0.40	
3696.00	4.19	1.75	0.19	3848.00	5.95	0.53	0.15	
3292.00	9.96	4.15	2.68	2430.00	7.74	2.32	0.66	
3263.00	11.34	4.72	3.27	1568.00	10.27	4.85	1.37	y
383.00	20.63	8.59	7.28	1422.00	3.66	1.76	-0.50	
3934.00	6.10	2.54	1.01	2321.00	4.01	1.41	-0.40	
3410.00	8.04	3.35	1.85	2158.00	3.94	1.48	-0.42	
2330.00	2.19	0.91	-0.68	1037.00	2.70	2.72	-0.77	
3810.00	6.96	2.90	1.38	2553.00	5.88	0.46	0.13	
4349.00	9.27	3.86	2.38	2302.00	9.69	4.27	1.21	
4744.00	8.03	3.35	1.85	2728.00	5.46	0.04	0.01	
4039.00	4.58	1.91	0.36	3075.00	1.95	3.47	-0.98	
4300.00	9.33	3.89	2.40	3287.00	10.80	5.38	1.53	y
4717.00	7.59	3.16	1.66	4509.00	6.88	1.46	0.41	
3246.00	1.85	0.77	-0.82	3943.00	8.90	3.48	0.99	
2487.00	7.96	3.32	1.82	2774.00	7.82	2.40	0.68	
3496.00	10.58	4.41	2.95	5064.00	15.92	10.50	2.98	debris b,c
3104.00	5.03	2.09	0.55	3258.00	8.32	2.90	0.82	
3734.00	4.87	2.03	0.48	3511.00	2.99	2.43	-0.69	
2162.00	0.69	0.29	-1.32	1555.00	2.57	2.85	-0.81	
2118.00	3.45	1.44	-0.13	2535.00	3.39	2.03	-0.58	
3749.00	5.81	2.42	0.89	2783.00	6.97	1.55	0.44	
2553.00	2.00	0.83	-0.76	2180.00	7.02	1.60	0.45	
1966.00	4.83	2.01	0.46	3021.00	14.86	9.44	2.68	
931.00	1.50	0.63	-0.97	2023.00	2.97	2.45	-0.70	
2910.00	4.64	1.93	0.38	2148.00	1.82	3.60	-1.02	
2555.00	2.04	0.85	-0.74	2187.00	5.35	0.07	-0.02	
1419.00	3.31	1.38	-0.19	1531.00	1.57	3.85	-1.09	
3527.00	3.86	1.61	0.04	1992.00	3.26	2.16	-0.61	
3188.00	6.90	2.88	1.36	1998.00	4.50	0.92	-0.26	
2821.00	4.11	1.71	0.15	1876.00	3.36	2.06	-0.59	
3005.00	7.42	3.09	1.58	1804.00	1.72	3.70	-1.05	
3083.00	4.67	1.95	0.40	2915.00	2.26	3.16	-0.90	
4903.00	6.26	2.61	1.08	4513.00	4.68	0.74	-0.21	
2588.00	2.55	1.06	-0.52	2894.00	1.87	3.55	-1.01	
2073.00	2.03	0.84	-0.75	2461.00	2.32	3.10	-0.88	

3306.00	8.98	3.74	2.26	3182.00	11.25	5.83	1.65	x	debris b,c
3338.00	2.55	1.06	-0.52	2968.00	1.45	3.97	-1.13		
3739.00	8.24	3.43	1.94	3768.00	10.32	4.90	1.39		
3080.00	5.71	2.38	0.85	4352.00	7.61	2.19	0.62		
1189.00	4.79	2.00	0.45	1000.00	9.50	4.08	1.16		
2878.00	5.35	2.23	0.69	2820.00	3.40	2.02	-0.57		
4257.00	9.56	3.98	2.51	2267.00	10.23	4.81	1.36	x	debris b,c
2858.00	2.17	0.90	-0.68	2526.00	4.20	1.22	-0.35		
935.00	2.14	0.89	-0.70	1859.00	1.45	3.97	-1.13		
1394.00	2.30	0.96	-0.63	1101.00	2.91	2.51	-0.71		
4405.00	2.66	1.11	-0.47	2652.00	7.32	1.90	0.54		
3433.00	2.36	0.98	-0.60	1773.00	2.82	2.60	-0.74		
3853.00	2.02	0.84	-0.75	2904.00	5.17	0.25	-0.07		
3796.00	5.74	2.39	0.86	2726.00	6.90	1.48	0.42		
3089.00	3.82	1.59	0.03	3573.00	7.92	2.50	0.71		
3348.00	2.00	0.83	-0.76	4383.00	12.57	7.15	2.03	y	
3290.00	4.44	1.85	0.29	3553.00	4.02	1.40	-0.40		
4859.00	11.32	4.72	3.27	6542.00	15.53	10.11	2.87	y	
2249.00	4.00	1.67	0.11	3032.00	6.63	1.21	0.34		
1647.00	1.76	0.73	-0.86	3190.00	8.46	3.04	0.86		
1626.00	1.54	0.64	-0.96	3506.00	3.22	2.20	-0.62		
1987.00	1.76	0.73	-0.86	3990.00	3.31	2.11	-0.60		
1530.00	2.22	0.93	-0.66	2209.00	3.26	2.16	-0.61		
1755.00	1.65	0.69	-0.91	2312.00	6.19	0.77	0.22		
1449.00	0.76	0.32	-1.29	2018.00	4.71	0.71	-0.20		
1943.00	1.60	0.66	-0.93	3607.00	9.12	3.70	1.05		
3803.00	1.71	0.71	-0.88	3233.00	4.52	0.90	-0.26		
1830.00	3.50	1.46	-0.11	1939.00	10.26	4.84	1.37		
1022.00	0.39	0.16	-1.45	2389.00	9.21	3.79	1.07		
1564.00	0.96	0.40	-1.21	1306.00	2.91	2.51	-0.71		
2074.00	1.74	0.72	-0.87	2068.00	10.49	5.07	1.44		
2802.00	1.61	0.67	-0.93	1986.00	6.90	1.48	0.42		
2353.00	1.66	0.69	-0.91	2500.00	5.00	0.42	-0.12		
2916.00	1.30	0.54	-1.06	3135.00	3.96	1.46	-0.42		
1714.00	1.87	0.78	-0.82	1819.00	7.48	2.06	0.58		
1650.00	5.15	2.15	0.60	1102.00	4.17	1.25	-0.35		
3512.00	2.08	0.87	-0.72	3360.00	2.02	3.40	-0.96		
2528.00	1.54	0.64	-0.96	3604.00	5.77	0.35	0.10		
1237.00	1.13	0.47	-1.13	2049.00	2.20	3.22	-0.91		
2630.50	3.76	1.56		2993.50	5.42	2.38			
		4.69				7.15			
		2.32				3.53			
20.19		3382.00	33.53						
		4249.00	37.89						
23.69		4451.00	33.30						
21.94		4462.00	38.39						

21.94	4136.00	35.78
1.75	512.12	2.74
	1562.00	5.06
2.97	974.00	4.52
3.84	1028.00	4.18
2.27	1126.00	4.97
3.03	1172.50	4.68
0.79	267.18	0.41
5.25		8.22
2.36		1.23
7.60		9.44
18.92		31.09
0.40		0.30
0.60		0.70
1.32	2077.00	7.70
2.99	2741.00	5.62
16.29	7099.00	19.37
8.37	5572.00	10.50
20.90	167.00	4.19
3.50	213.00	8.45

Plate	Well		Gene		GeneID	Cell Coun	% inf	Abs Dev	rZ
50020.00	A02	M-012456-	membrane	9863.00	MAGI2	2419.00	9.84	2.67	0.56
50020.00	A04	M-020014-	AHA1, acti	10598.00	AHSA1	2922.00	4.62	2.55	-0.54
50020.00	A05	M-011572-	apolipopro	336.00	APOA2	3561.00	2.05	5.12	-1.08
50020.00	A06	M-015374-	angiotensi	57085.00	AGTRAP	2856.00	6.90	0.27	-0.06
50020.00	A07	M-010995-	apolipopro	337.00	APOA4	3184.00	2.89	4.28	-0.90
50020.00	A08	M-010987-	amylo-1, 6-	178.00	AGL	2686.00	2.90	4.27	-0.90
50020.00	A09	M-010996-	apolipopro	345.00	APOC3	2690.00	4.68	2.49	-0.52
50020.00	A10	M-010643-	myeloid/ly	10962.00	MLLT11	3723.00	3.49	3.68	-0.77
50020.00	A11	M-007749-	apolipopro	347.00	APOD	3105.00	12.75	5.58	1.18
50020.00	A12	M-026036-	MAM dom	158056.00	MAMDC4	4031.00	4.17	3.00	-0.63
50020.00	A13	M-007811-	apolipopro	350.00	APOH	3262.00	4.84	2.33	-0.49
50020.00	A14	M-006656-	poly (ADP-	142.00	PARP1	3714.00	14.32	7.15	1.51
50020.00	A15	M-017402-	apolipopro	8542.00	APOL1	2106.00	4.32	2.85	-0.60
50020.00	A16	M-008114-	alcohol de	128.00	ADH5	3043.00	3.09	4.08	-0.86
50020.00	A17	M-019496-	bicaudal D	636.00	BICD1	2531.00	6.20	0.97	-0.20
50020.00	A18	M-008113-	alcohol de	127.00	ADH4	3784.00	9.22	2.05	0.43
50020.00	A19	M-014060-	bicaudal D	23299.00	BICD2	3816.00	9.59	2.42	0.51
50020.00	A20	M-008112-	alcohol de	125.00	ADH1B	3116.00	9.18	2.01	0.42
50020.00	A21	M-006121-	calcium ch	773.00	CACNA1A	1485.00	8.42	1.25	0.26
50020.00	A23	M-006123-	calcium ch	775.00	CACNA1C	1927.00	5.45	1.72	-0.36
50020.00	B02	M-009265-	YY1 associ	10138.00	YAF2	2851.00	1.54	5.63	-1.18
50020.00	B04	M-004377-	chromoso	51374.00	C2orf28	1493.00	3.88	3.29	-0.69
50020.00	B05	M-017696-	A kinase (P	158798.00	AKAP14	3126.00	8.93	1.76	0.37
50020.00	B06	M-010963-	bromodom	54014.00	BRWD1	4802.00	5.29	1.88	-0.39
50020.00	B07	M-006467-	aurora kin	54998.00	AURKAIP1	3655.00	1.67	5.50	-1.16
50020.00	B08	M-021229-	chromoso	55321.00	C20orf46	2900.00	2.45	4.72	-0.99
50020.00	B09	M-005087-	aldo-keto r	10327.00	AKR1A1	3503.00	3.88	3.29	-0.69
50020.00	B10	M-017986-	chromoso	55245.00	C20orf44	2655.00	5.88	1.29	-0.27
50020.00	B11	M-004036-	aldo-keto r	231.00	AKR1B1	4679.00	6.07	1.10	-0.23
50020.00	B12	M-017050-	chromoso	25876.00	C20orf28	4089.00	7.73	0.56	0.12
50020.00	B13	M-008731-	aldo-keto r	83592.00	AKR1CL2	2298.00	1.31	5.86	-1.23
50020.00	B14	M-019769-	chromoso	24141.00	C20orf103	3137.00	6.22	0.95	-0.20
50020.00	B15	M-008458-	aminolevul	210.00	ALAD	2300.00	2.09	5.08	-1.07
50020.00	B16	M-012536-	compleme	714.00	C1QC	2848.00	2.91	4.26	-0.89
50020.00	B17	M-008722-	aldehyde d	216.00	ALDH1A1	3679.00	3.26	3.91	-0.82
50020.00	B18	M-011000-	compleme	713.00	C1QB	3261.00	5.00	2.17	-0.46
50020.00	B19	M-009386-	aldehyde d	224.00	ALDH3A2	2667.00	3.64	3.53	-0.74
50020.00	B20	M-013136-	compleme	712.00	C1QA	2242.00	2.19	4.98	-1.05
50020.00	B21	M-008379-	aldehyde d	223.00	ALDH9A1	5257.00	12.67	5.50	1.16
50020.00	B23	M-010990-	aldolase B,	229.00	ALDOB	4302.00	2.02	5.15	-1.08
50020.00	C02	M-013437-	ADAMTS-li	92949.00	ADAMTSL1	4445.00	6.66	0.51	-0.11
50020.00	C04	M-005769-	ADAM met	170692.00	ADAMTS1	3646.00	7.93	0.76	0.16
50020.00	C05	M-006124-	calcium ch	776.00	CACNA1D	4091.00	14.47	7.30	1.54
50020.00	C06	M-005767-	ADAM met	170690.00	ADAMTS1	2338.00	2.01	5.16	-1.08
50020.00	C07	M-006125-	calcium ch	777.00	CACNA1E	3259.00	6.93	0.24	-0.05
50020.00	C08	M-032272-	ADAM met	1596.00	ADAM3B	3552.00	14.16	6.99	1.47

50020.00	C09	M-006126-	calcium cha	778.00	CACNA1F	3891.00	29.68	22.51	4.74
50020.00	C10	M-005118-	ADAM met	8038.00	ADAM12	4219.00	8.70	1.53	0.32
50020.00	C11	M-006128-	calcium cha	8912.00	CACNA1H	3663.00	10.67	3.50	0.74
50020.00	C12	M-017297-	SPC25, ND	57405.00	SPC25	1640.00	2.80	4.37	-0.92
50020.00	C13	M-006129-	calcium cha	8911.00	CACNA1I	3023.00	9.26	2.09	0.44
50020.00	C14	M-009937-	acylphosph	97.00	ACYP1	2115.00	10.17	3.00	0.63
50020.00	C15	M-019771-	CD160 mol	11126.00	CD160	2032.00	6.00	1.17	-0.24
50020.00	C16	M-012077-	ARP3 actin	10096.00	ACTR3	2277.00	13.35	6.18	1.30
50020.00	C17	M-011829-	cadherin 1	1015.00	CDH17	3788.00	9.87	2.70	0.57
50020.00	C18	M-012076-	ARP2 actin	10097.00	ACTR2	2378.00	9.92	2.75	0.58
50020.00	C19	M-006159-	cyclic nucle	1261.00	CNGA3	2525.00	6.77	0.40	-0.08
50020.00	C20	M-012074-	ARP1 actin	10121.00	ACTR1A	2575.00	11.69	4.52	0.95
50020.00	C21	M-006160-	cyclic nucle	1258.00	CNGB1	3190.00	6.02	1.15	-0.24
50020.00	C23	M-004413-	CSE1 chro	1434.00	CSE1L	2615.00	13.88	6.71	1.41
50020.00	D02	M-015184-	cell divisio	79577.00	CDC73	2956.00	2.03	5.14	-1.08
50020.00	D04	M-020160-	chromoso	10712.00	C1orf2	3378.00	2.22	4.95	-1.04
50020.00	D05	M-012697-	aldolase C,	230.00	ALDOC	2835.00	6.77	0.40	-0.08
50020.00	D06	M-016688-	chromoso	84520.00	C14orf142	4010.00	3.49	3.68	-0.77
50020.00	D07	M-013662-	asparagine	29929.00	ALG6	4536.00	6.02	1.15	-0.24
50020.00	D08	M-015700-	chromoso	221150.00	C13orf3	1771.00	2.82	4.35	-0.91
50020.00	D09	M-004283-	alkB, alkyla	8846.00	ALKBH1	2617.00	5.01	2.16	-0.45
50020.00	D10	M-020692-	chromoso	745.00	C11orf9	3066.00	4.76	2.41	-0.51
50020.00	D11	M-012889-	Alstrom sy	7840.00	ALMS1	1672.00	2.27	4.90	-1.03
50020.00	D12	M-018682-	cyclin Y	219771.00	CCNY	4201.00	12.45	5.28	1.11
50020.00	D13	M-004530-	arachidona	240.00	ALOX5	4243.00	6.76	0.41	-0.08
50020.00	D14	M-020058-	cell divisio	8872.00	CDC123	2432.00	10.77	3.60	0.76
50020.00	D15	M-008673-	alkaline ph	248.00	ALPI	3316.00	10.86	3.69	0.78
50020.00	D16	M-016002-	chromoso	118924.00	C10orf4	3708.00	12.06	4.89	1.03
50020.00	D17	M-003454-	alkaline ph	250.00	ALPP	2905.00	4.78	2.39	-0.50
50020.00	D18	M-006826-	BUB3 bud	9184.00	BUB3	2328.00	0.47	6.70	-1.41
50020.00	D19	M-016868-	amyotroph	130540.00	ALS2CR12	3426.00	1.96	5.21	-1.10
50020.00	D20	M-013364-	B-cell trans	54766.00	BTG4	1852.00	2.32	4.85	-1.02
50020.00	D21	M-018351-	amyotroph	65068.00	ALS2CR14	4113.00	5.91	1.26	-0.26
50020.00	D23	M-016582-	amyotroph	65062.00	ALS2CR4	3082.00	3.11	4.06	-0.85
50020.00	E02	M-005073-	acyl-Coenz	8309.00	ACOX2	3585.00	5.52	1.65	-0.35
50020.00	E04	M-010001-	acetyl-Coe	39.00	ACAT2	4080.00	4.26	2.91	-0.61
50020.00	E05	M-016697-	cytochrom	1537.00	CYC1	3566.00	2.50	4.67	-0.98
50020.00	E06	M-008773-	acetyl-Coe	10449.00	ACAA2	4127.00	2.13	5.04	-1.06
50020.00	E07	M-008678-	fatty acid	2168.00	FABP1	2896.00	2.87	4.30	-0.90
50020.00	E08	M-011320-	actin bindi	3983.00	ABLIM1	3390.00	6.40	0.77	-0.16
50020.00	E09	M-008710-	fatty acid	2171.00	FABP5	3787.00	3.20	3.97	-0.84
50020.00	E10	M-006622-	ATP-bindin	6833.00	ABCC8	4130.00	7.99	0.82	0.17
50020.00	E11	M-008851-	fatty acid	2172.00	FABP6	2006.00	4.89	2.28	-0.48
50020.00	E12	M-007314-	ATP-bindin	10057.00	ABCC5	2784.00	6.03	1.14	-0.24
50020.00	E13	M-008706-	fatty acid	2173.00	FABP7	3373.00	4.18	2.99	-0.63
50020.00	E14	M-007301-	ATP-bindin	8647.00	ABCB11	1624.00	6.77	0.40	-0.08
50020.00	E15	M-019189-	ferredoxin	2230.00	FDX1	4483.00	16.55	9.38	1.97

50020.00	E16	M-009533- ATP-bindin	24.00	ABCA4	3339.00	8.39	1.22	0.26
50020.00	E17	M-012368- GABA(A) re	11337.00	GABARAP	3362.00	6.34	0.83	-0.17
50020.00	E18	M-023578- chromosor	89876.00	C3orf15	4123.00	6.65	0.52	-0.11
50020.00	E19	M-018856- gastric intr	2694.00	GIF	4126.00	7.22	0.05	0.01
50020.00	E20	M-009830- arylacetam	13.00	AADAC	4669.00	9.77	2.60	0.55
50020.00	E21	M-020464- golgi assoc	57120.00	GOPC	3683.00	13.01	5.84	1.23
50020.00	E23	M-011114- hemoglobi	3039.00	HBA1	4884.00	4.57	2.60	-0.55
50020.00	F02	M-019135- BTG family	10950.00	BTG3	5102.00	5.64	1.53	-0.32
50020.00	F04	M-016634- basic trans	689.00	BTF3	4729.00	10.83	3.66	0.77
50020.00	F05	M-015280- amyotroph	79800.00	ALS2CR8	3616.00	12.92	5.75	1.21
50020.00	F06	M-010998- biotinidase	686.00	BTD	4346.00	15.07	7.90	1.66
50020.00	F07	M-020296- Alport sync	9949.00	AMMECR1	3059.00	6.34	0.83	-0.17
50020.00	F08	M-012848- Bartter syn	7809.00	BSND	4502.00	30.12	**22.95**	4.83
50020.00	F09	M-013455- amnionless	81693.00	AMN	3078.00	8.74	1.57	0.33
50020.00	F10	M-016749- Bernardine	26580.00	BSCL2	3184.00	13.57	6.40	1.35
50020.00	F11	M-009888- adenosine	270.00	AMPD1	3008.00	14.23	7.06	1.49
50020.00	F12	M-017153- BRI3 bindir	140707.00	BRI3BP	4494.00	5.12	2.05	-0.43
50020.00	F13	M-005783- STAM bind	57559.00	STAMBPL1	2792.00	15.29	8.12	1.71
50020.00	F14	M-012411- BCR downs	26228.00	BRDG1	2413.00	4.52	2.65	-0.56
50020.00	F15	M-020957- ankyrin rep	56311.00	ANKRD7	3023.00	14.19	7.02	1.48
50020.00	F16	M-020297- bromodom	29117.00	BRD7	3751.00	5.52	1.65	-0.35
50020.00	F17	M-006838- anillin, acti	54443.00	ANLN	1504.00	13.30	6.13	1.29
50020.00	F18	M-004937- bromodom	23476.00	BRD4	3211.00	8.16	0.99	0.21
50020.00	F19	M-010985- acidic (leuc	23520.00	ANP32C	5223.00	17.08	**9.91**	2.08
50020.00	F20	M-004936- bromodom	8019.00	BRD3	3958.00	11.42	4.25	0.89
50020.00	F21	M-012472- acidic (leuc	23519.00	ANP32D	3656.00	9.76	2.59	0.55
50020.00	F23	M-005784- alanyl (mei	290.00	ANPEP	5586.00	3.83	3.34	-0.70
50020.00	G02	M-017636- achalasia, a	8086.00	AAAS	5046.00	10.82	3.65	0.77
50020.00	G04	M-011754- phospholai	5350.00	PLN	2888.00	6.68	0.49	-0.10
50020.00	G05	M-006200- hyperpolar	348980.00	HCN1	2783.00	12.15	4.98	1.05
50020.00	G06	M-008627- lipocalin 1	3933.00	LCN1	2376.00	4.38	2.79	-0.59
50020.00	G07	M-006201- hyperpolar	610.00	HCN2	2286.00	10.15	2.98	0.63
50020.00	G08	M-007492- solute carr	1811.00	SLC26A3	3054.00	19.71	**12.54**	2.64
50020.00	G09	M-022353- hyperpolar	57657.00	HCN3	2080.00	13.46	6.29	1.32
50020.00	G10	M-012478- SEC14-like	23541.00	SEC14L2	2665.00	3.90	3.27	-0.69
50020.00	G11	M-006203- hyperpolar	10021.00	HCN4	3540.00	36.38	**29.21**	6.15
50020.00	G12	M-003737- huntingtin	3064.00	HD	3755.00	12.97	5.80	1.22
50020.00	G13	M-019956- high densit	3069.00	HDLBP	4111.00	19.58	**12.41**	2.61
50020.00	G14	M-019889- chromosor	9605.00	C16orf7	3099.00	7.29	0.12	0.03
50020.00	G15	M-006211- potassium	3744.00	KCNA10	2988.00	14.76	7.59	1.60
50020.00	G16	M-004448- tumor neci	8795.00	TNFRSF10E	3318.00	12.33	5.16	1.09
50020.00	G17	M-006212- potassium	3737.00	KCNA2	4143.00	8.62	1.45	0.30
50020.00	G18	M-018667- RAB intera	5877.00	RABIF	4353.00	19.02	**11.85**	2.49
50020.00	G19	M-006214- potassium	3739.00	KCNA4	3417.00	14.19	7.02	1.48
50020.00	G20	M-012255- importin 7	10527.00	IPO7	4535.00	19.63	**12.46**	2.62
50020.00	G21	M-006215- potassium	3741.00	KCNA5	5419.00	6.48	0.69	-0.15
50020.00	G23	M-006216- potassium	3742.00	KCNA6	2387.00	5.45	1.72	-0.36

50020.00	H02	M-008664-	3'(2'), 5'-bi	10380.00	BPNT1	4496.00	5.61	1.57	-0.33
50020.00	H04	M-009597-	bactericida	671.00	BPI	5567.00	7.92	0.75	0.16
50020.00	H05	M-011161-	annexin A1	301.00	ANXA1	3793.00	9.15	1.98	0.42
50020.00	H06	M-008917-	2,3-bispho	669.00	BPGM	3397.00	8.15	0.98	0.21
50020.00	H07	M-010741-	annexin A2	302.00	ANXA2	3094.00	5.98	1.19	-0.25
50020.00	H08	M-004394-	BCL2-relat	666.00	BOK	4447.00	14.71	7.54	1.59
50020.00	H09	M-011210-	annexin A6	309.00	ANXA6	3833.00	3.97	3.20	-0.67
50020.00	H10	M-011815-	BCL2/aden	665.00	BNIP3L	3212.00	7.50	0.33	0.07
50020.00	H11	M-011570-	annexin A8	244.00	ANXA8	3728.00	10.97	3.80	0.80
50020.00	H12	M-011222-	BCL2/aden	662.00	BNIP1	2889.00	13.88	6.71	1.41
50020.00	H13	M-011470-	annexin A9	8416.00	ANXA9	2275.00	4.66	2.51	-0.53
50020.00	H14	M-015872-	centromer	55839.00	CENPN	2535.00	4.06	3.11	-0.65
50020.00	H15	M-012375-	AP1 gamm	11276.00	AP1GBP1	3766.00	11.55	4.38	0.92
50020.00	H16	M-021436-	basic leuci	8548.00	BLZF1	4488.00	10.85	3.68	0.77
50020.00	H17	M-005785-	N-acylami	327.00	APEH	4528.00	18.77	**11.60**	2.44
50020.00	H18	M-004040-	biliverdin r	645.00	BLVRB	3605.00	10.76	3.59	0.76
50020.00	H19	M-010237-	APEX nucle	328.00	APEX1	4653.00	18.01	**10.84**	2.28
50020.00	H20	M-005793-	bleomycin	642.00	BLMH	4503.00	13.99	6.82	1.44
50020.00	H21	M-010212-	ATG12 aut	9140.00	ATG12	4046.00	9.64	2.47	0.52
50020.00	H23	M-004374-	ATG5 auto	9474.00	ATG5	3143.00	9.10	1.93	0.41
50020.00	I02	M-019207-	ADP-ribosy	26286.00	ARFGAP3	4381.00	9.13	1.96	0.41
50020.00	I04	M-013321-	ADP-ribosy	55738.00	ARFGAP1	3263.00	7.32	0.15	0.03
50020.00	I05	M-006217-	potassium	3743.00	KCNA7	3024.00	7.41	0.24	0.05
50020.00	I06	M-005293-	alpha-2-ma	2.00	A2M	3900.00	9.41	2.24	0.47
50020.00	I07	M-006218-	potassium	3745.00	KCNB1	3791.00	10.08	2.91	0.61
50020.00	I08	M-023590-	thioredoxi	114112.00	TXNRD3	4307.00	10.43	3.26	0.69
50020.00	I09	M-006219-	potassium	9312.00	KCNB2	2474.00	5.98	1.19	-0.25
50020.00	I10	M-012728-	metallothi	4504.00	MT3	2105.00	4.28	2.89	-0.61
50020.00	I11	M-006220-	potassium	3746.00	KCNC1	3609.00	10.36	3.19	0.67
50020.00	I12	M-009647-	glutathion	2936.00	GSR	2518.00	10.64	3.47	0.73
50020.00	I13	M-006221-	potassium	3747.00	KCNC2	3321.00	15.87	8.70	1.83
50020.00	I14	M-006470-	apolipopro	348.00	APOE	3039.00	6.48	0.69	-0.14
50020.00	I15	M-006222-	potassium	3748.00	KCNC3	3790.00	10.55	3.38	0.71
50020.00	I16	M-010989-	albumin	213.00	ALB	4209.00	12.38	5.21	1.10
50020.00	I17	M-006223-	potassium	3749.00	KCNC4	5221.00	11.89	4.72	0.99
50020.00	I18	M-007638-	uncoupling	7352.00	UCP3	3532.00	8.41	1.24	0.26
50020.00	I19	M-006227-	potassium	3754.00	KCNF1	3961.00	8.51	1.34	0.28
50020.00	I20	M-005114-	uncoupling	7351.00	UCP2	3472.00	10.71	3.54	0.75
50020.00	I21	M-006228-	potassium	3755.00	KCNG1	2837.00	5.04	2.13	-0.45
50020.00	I23	M-006229-	potassium	26251.00	KCNG2	2383.00	2.31	4.86	-1.02
50020.00	J02	M-012276-	bladder ca	10904.00	BLCAP	3208.00	3.34	3.83	-0.81
50020.00	J04	M-020919-	bridging in	51411.00	BIN2	5519.00	12.77	5.60	1.18
50020.00	J05	M-004375-	apoptosis i	8539.00	API5	4046.00	18.83	**11.66**	2.45
50020.00	J06	M-008246-	bridging in	274.00	BIN1	4024.00	7.98	0.81	0.17
50020.00	J07	M-012963-	lipoprotein	80350.00	LPAL2	3214.00	8.59	1.42	0.30
50020.00	J08	M-004388-	BCL2-inter	638.00	BIK	3874.00	6.74	0.43	-0.09
50020.00	J09	M-009467-	apolipopro	338.00	APOB	2702.00	4.85	2.32	-0.49

50020.00	J10	M-004387-	BH3 intera	637.00	BID	3384.00	11.82	4.65	0.98
50020.00	J11	M-011573-	apolipopro	339.00	APOBEC1	1959.00	4.03	3.14	-0.66
50020.00	J12	M-013985-	tripartite m	25893.00	TRIM58	2759.00	7.07	0.10	-0.02
50020.00	J13	M-017322-	apolipopro	9582.00	APOBEC3B	2556.00	9.55	2.38	0.50
50020.00	J14	M-009998-	folliculin	201163.00	FLCN	3325.00	11.49	4.32	0.91
50020.00	J15	M-032279-	apolipopro	140564.00	APOBEC3D	3155.00	4.88	2.29	-0.48
50020.00	J16	M-011471-	beaded fila	8419.00	BFSP2	3631.00	5.67	1.50	-0.31
50020.00	J17	M-019039-	apolipopro	200316.00	APOBEC3F	2879.00	11.46	4.29	0.90
50020.00	J18	M-019160-	mal, T-cell	7851.00	MALL	3956.00	8.52	1.35	0.28
50020.00	J19	M-011576-	apolipopro	319.00	APOF	2650.00	6.98	0.19	-0.04
50020.00	J20	M-007268-	B-cell CLL/l	607.00	BCL9	3522.00	7.84	0.67	0.14
50020.00	J21	M-006328-	adenine ph	353.00	APRT	3110.00	3.99	3.18	-0.67
50020.00	J23	M-013368-	aprataxin	54840.00	APTX	2458.00	1.95	5.22	-1.10
50020.00	K02	M-007636-	uncoupling	7350.00	UCP1	4332.00	8.49	1.32	0.28
50020.00	K04	M-012554-	transthyret	7276.00	TTR	2134.00	4.17	3.00	-0.63
50020.00	K05	M-006230-	potassium	170850.00	KCNG3	4801.00	13.62	6.45	1.36
50020.00	K06	M-019372-	tocopherol	7274.00	TTPA	4246.00	11.33	4.16	0.88
50020.00	K07	M-006239-	potassium	3758.00	KCNJ1	2783.00	8.77	1.60	0.34
50020.00	K08	M-012066-	target of m	10043.00	TOM1	3785.00	6.74	0.43	-0.09
50020.00	K09	M-006267-	potassium	3778.00	KCNMA1	4687.00	23.30	**16.13**	3.39
50020.00	K10	M-010547-	tumor necr	7126.00	TNFAIP1	3493.00	9.93	2.76	0.58
50020.00	K11	M-006270-	potassium	3782.00	KCNN3	2361.00	12.28	5.11	1.08
50020.00	K12	M-003718-	transmemb	10972.00	TMED10	2534.00	3.04	4.13	-0.87
50020.00	K13	M-006276-	potassium	3787.00	KCNS1	2150.00	10.19	3.02	0.63
50020.00	K14	M-011110-	transcobala	6948.00	TCN2	2953.00	7.11	0.06	-0.01
50020.00	K15	M-006277-	potassium	3790.00	KCNS3	3901.00	11.38	4.21	0.89
50020.00	K16	M-007634-	transporte	6890.00	TAP1	2182.00	11.50	4.33	0.91
50020.00	K17	M-006278-	potassium	27012.00	KCNV1	5013.00	11.03	3.86	0.81
50020.00	K18	M-020044-	synaptotag	6857.00	SYT1	2895.00	6.42	0.75	-0.16
50020.00	K19	M-022909-	thrombosp	80731.00	THSD7B	3563.00	8.45	1.28	0.27
50020.00	K20	M-012362-	synapsin I	6853.00	SYN1	3995.00	12.54	5.37	1.13
50020.00	K21	M-027602-	kinesin fam	23046.00	KIF21B	4657.00	12.11	4.94	1.04
50020.00	K23	M-011305-	karyopheri	3836.00	KPNA1	4061.00	5.15	2.02	-0.42
50020.00	L02	M-003874-	B-cell CLL/l	602.00	BCL3	3726.00	7.73	0.56	0.12
50020.00	L04	M-004384-	BCL2-like 2	599.00	BCL2L2	2187.00	11.84	4.67	0.98
50020.00	L05	M-011214-	aquaporin	343.00	AQP8	5132.00	13.74	6.57	1.38
50020.00	L06	M-004385-	BCL2-like 1	79370.00	BCL2L14	4945.00	13.73	6.56	1.38
50020.00	L07	M-007768-	aquaporin	366.00	AQP9	3414.00	19.71	**12.54**	2.64
50020.00	L08	M-004383-	BCL2-like 1	10018.00	BCL2L11	5722.00	8.04	0.87	0.18
50020.00	L09	M-011580-	ADP-ribosy	375.00	ARF1	2511.00	10.51	3.34	0.70
50020.00	L10	M-004382-	BCL2-like 1	10017.00	BCL2L10	2319.00	11.43	4.26	0.90
50020.00	L11	M-011581-	ADP-ribosy	377.00	ARF3	3869.00	9.51	2.34	0.49
50020.00	L12	M-003458-	BCL2-like 1	598.00	BCL2L1	2871.00	4.46	2.71	-0.57
50020.00	L13	M-011582-	ADP-ribosy	378.00	ARF4	3258.00	8.87	1.70	0.36
50020.00	L14	M-003306-	BCL2-relate	597.00	BCL2A1	5062.00	12.82	5.65	1.19
50020.00	L15	M-011584-	ADP-ribosy	381.00	ARF5	3461.00	4.39	2.78	-0.58
50020.00	L16	M-013030-	BRCA2 and	56647.00	BCCIP	2127.00	2.59	4.58	-0.96

50020.00	L17	M-004008-	ADP-ribosy	382.00	ARF6	2907.00	6.23	0.94	-0.20
50020.00	L18	M-010341-	breast carc	8537.00	BCAS1	3420.00	4.33	2.84	-0.60
50020.00	L19	M-013025-	low density	26119.00	LDLRAP1	5132.00	11.77	4.60	0.97
50020.00	L20	M-020465-	breast canc	9564.00	BCAR1	3706.00	3.99	3.18	-0.67
50020.00	L21	M-003860-	ras homol	387.00	RHOA	4551.00	25.20	**18.03**	3.79
50020.00	L23	M-007794-	Rho family	390.00	RND3	3223.00	1.68	5.49	-1.15
50020.00	M02	M-019369-	steroidoge	6770.00	STAR	2140.00	0.33	6.84	-1.44
50020.00	M04	M-007620-	solute carr	6546.00	SLC8A1	5446.00	12.93	5.76	1.21
50020.00	M05	M-004702-	karyopheri	3838.00	KPNA2	2232.00	2.42	4.75	-1.00
50020.00	M06	M-007486-	solute carr	292.00	SLC25A5	3440.00	2.79	4.38	-0.92
50020.00	M07	M-011306-	karyopheri	3839.00	KPNA3	4475.00	4.74	2.43	-0.51
50020.00	M08	M-007483-	solute carr	9481.00	SLC25A27	4487.00	0.42	6.75	-1.42
50020.00	M09	M-017523-	karyopheri	3837.00	KPNB1	2059.00	3.06	4.11	-0.86
50020.00	M10	M-007480-	solute carr	788.00	SLC25A20	4711.00	1.59	5.58	-1.17
50020.00	M11	M-011308-	transportir	3842.00	TNPO1	2947.00	2.55	4.63	-0.97
50020.00	M12	M-007478-	solute carr	60386.00	SLC25A19	3435.00	14.64	7.47	1.57
50020.00	M13	M-003679-	lipocalin 2	3934.00	LCN2	3004.00	3.70	3.47	-0.73
50020.00	M14	M-007474-	solute carr	10166.00	SLC25A15	2386.00	2.26	4.91	-1.03
50020.00	M15	M-004501-	myeloid ce	4170.00	MCL1	3538.00	4.83	2.34	-0.49
50020.00	M16	M-007472-	solute carr	10165.00	SLC25A13	4089.00	6.14	1.03	-0.22
50020.00	M17	M-008301-	microsoma	4547.00	MTTP	4548.00	8.97	1.80	0.38
50020.00	M18	M-007468-	solute carr	6576.00	SLC25A1	3484.00	4.33	2.84	-0.60
50020.00	M19	M-010562-	neighbor o	10230.00	NBR2	3740.00	2.57	4.60	-0.97
50020.00	M20	M-007423-	solute carr	10560.00	SLC19A2	3741.00	4.04	3.13	-0.66
50020.00	M21	M-005283-	nucleopori	9972.00	NUP153	3812.00	4.28	2.89	-0.61
50020.00	M23	M-013898-	p53-regula	63970.00	P53AIP1	3108.00	1.64	5.53	-1.16
50020.00	N02	M-013346-	Bardet-Bie	55212.00	BBS7	3510.00	5.87	1.30	-0.27
50020.00	N04	M-013649-	Bardet-Bie	585.00	BBS4	4357.00	4.36	2.81	-0.59
50020.00	N05	M-009427-	Rho GTPas	23779.00	ARHGAP8	6114.00	16.60	9.43	1.98
50020.00	N06	M-010080-	Bardet-Bie	583.00	BBS2	5398.00	10.89	3.72	0.78
50020.00	N07	M-013460-	Rho guanir	9639.00	ARHGEF10	3463.00	14.81	7.64	1.61
50020.00	N08	M-019180-	Bardet-Bie	582.00	BBS1	5431.00	14.33	7.16	1.51
50020.00	N09	M-009731-	Rho guanir	22899.00	ARHGEF15	4463.00	8.54	1.37	0.29
50020.00	N10	M-004380-	BCL2 bindi	27113.00	BBC3	2491.00	2.93	4.24	-0.89
50020.00	N11	M-010234-	Rho guanir	27237.00	ARHGEF16	3522.00	5.08	2.09	-0.44
50020.00	N12	M-003308-	BCL2-assoc	581.00	BAX	3448.00	1.68	5.49	-1.15
50020.00	N13	M-020314-	Cdc42 guar	23229.00	ARHGEF9	3870.00	4.81	2.36	-0.50
50020.00	N14	M-019008-	brain abun	10409.00	BASP1	3173.00	5.14	2.03	-0.43
50020.00	N15	M-006374-	ras homol	171177.00	RHOV	4184.00	3.30	3.87	-0.81
50020.00	N16	M-010740-	breast canc	317716.00	RP11-49G1	5898.00	7.51	0.34	0.07
50020.00	N17	M-012408-	ADP-ribosy	26225.00	ARL5A	4338.00	9.77	2.60	0.55
50020.00	N18	M-012395-	BarH-like h	8538.00	BARX2	3469.00	3.95	3.22	-0.68
50020.00	N19	M-020731-	ADP-ribosy	51329.00	ARL6IP4	4372.00	11.09	3.92	0.83
50020.00	N20	M-013301-	B-cell rece	55973.00	BCAP29	4760.00	5.86	1.31	-0.27
50020.00	N21	M-012263-	actin relate	10552.00	ARPC1A	2873.00	7.38	0.21	0.04
50020.00	N23	M-008571-	actin relate	10093.00	ARPC4	4374.00	5.17	2.00	-0.42
50020.00	O02	M-024405-	SEC24 rela	10802.00	SEC24A	3550.00	3.69	3.48	-0.73

50020.00	O04	M-019245-	SEC14-like	266629.00	SEC14L3	2722.00	13.30	6.13	1.29
50020.00	O05	M-010615-	PDZ domai	5174.00	PDZK1	2358.00	2.88	4.29	-0.90
50020.00	O06	M-011386-	SEC14-like	6397.00	SEC14L1	3503.00	3.17	4.00	-0.84
50020.00	O07	M-010553-	phosphopr	8682.00	PEA15	4060.00	5.74	1.43	-0.30
50020.00	O08	M-006502-	sodium cha	6334.00	SCN8A	4629.00	8.64	1.47	0.31
50020.00	O09	M-006288-	polycystic l	5311.00	PKD2	3426.00	4.50	2.68	-0.56
50020.00	O10	M-010055-	RAB9B, me	51209.00	RAB9B	4609.00	8.92	1.75	0.37
50020.00	O11	M-006289-	polycystic l	9033.00	PKD2L1	2699.00	3.33	3.84	-0.81
50020.00	O12	M-008909-	RAB33B, m	83452.00	RAB33B	2382.00	5.67	1.50	-0.32
50020.00	O13	M-006290-	polycystic l	27039.00	PKD2L2	2614.00	6.77	0.40	-0.08
50020.00	O14	M-008206-	RAB33A, m	9363.00	RAB33A	4231.00	2.79	4.38	-0.92
50020.00	O15	M-006291-	polycystic l	10343.00	PKDREJ	4632.00	16.13	8.96	1.88
50020.00	O16	M-010366-	RAB25, me	57111.00	RAB25	4012.00	6.83	0.34	-0.07
50020.00	O17	M-003729-	phospholip	5359.00	PLSCR1	2764.00	5.68	1.49	-0.31
50020.00	O18	M-009789-	RAB23, me	51715.00	RAB23	4762.00	18.50	11.33	2.38
50020.00	O19	M-010255-	phospholip	57048.00	PLSCR3	5701.00	31.07	23.90	5.03
50020.00	O20	M-009450-	RAB21, me	23011.00	RAB21	2857.00	8.61	1.44	0.30
50020.00	O21	M-006474-	RAB17, me	64284.00	RAB17	1716.00	5.54	1.63	-0.34
50020.00	O23	M-008317-	RAB20, me	55647.00	RAB20	2221.00	9.55	2.38	0.50
50020.00	P02	M-013093-	BTG3 asso	54971.00	BANP	1771.00	3.44	3.73	-0.78
50020.00	P04	M-003305-	BCL2-antag	578.00	BAK1	2045.00	17.21	10.04	2.11
50020.00	P05	M-012080-	actin relate	10092.00	ARPC5	4771.00	11.03	3.86	0.81
50020.00	P06	M-012206-	BAI1-assoc	10458.00	BAIAP2	2730.00	1.90	5.27	-1.11
50020.00	P07	M-008578-	arylsulfata	415.00	ARSE	2657.00	1.17	6.00	-1.26
50020.00	P08	M-003871-	BCL2-assoc	573.00	BAG1	2856.00	9.14	1.97	0.41
50020.00	P09	M-009575-	ankyrin rep	51676.00	ASB2	2701.00	2.22	4.95	-1.04
50020.00	P10	M-004366-	beta-2-mic	567.00	B2M	2170.00	2.53	4.64	-0.97
50020.00	P11	M-013268-	asialoglyco	432.00	ASGR1	2119.00	6.09	1.08	-0.23
50020.00	P12	M-013653-	AXIN1 up-r	64651.00	AXUD1	1188.00	6.06	1.11	-0.23
50020.00	P13	M-008840-	argininosu	435.00	ASL	3360.00	10.42	3.25	0.68
50020.00	P14	M-006524-	alpha thala	546.00	ATRX	3838.00	16.36	9.19	1.93
50020.00	P15	M-016255-	asp (abnor	259266.00	ASPM	2946.00	5.13	2.04	-0.43
50020.00	P16	M-022341-	ATPase, Cla	57198.00	ATP8B2	3919.00	9.39	2.22	0.47
50020.00	P17	M-006489-	alveolar so	79058.00	ASPSCR1	4706.00	9.80	2.63	0.55
50020.00	P18	M-012733-	ATP syntha	10476.00	ATP5H	4445.00	8.41	1.24	0.26
50020.00	P19	M-009871-	activating t	1386.00	ATF2	2793.00	11.42	4.25	0.89
50020.00	P20	M-012705-	ATP syntha	509.00	ATP5C1	2501.00	7.76	0.59	0.12
50020.00	P21	M-014542-	activating t	80063.00	ATF7IP2	2919.00	20.45	13.28	2.79
50020.00	P23	M-004082-	ATPase, Ca	488.00	ATP2A2	1638.00	4.21	2.96	-0.62
					mdn	3418.50	7.17	3.21	
					3mad			9.64	
					MADc			4.75	
50020.00	C22		0.94						
50020.00	D22					3171.00	34.56	4700.00	37.47
50020.00	E22					3486.00	31.47	5206.00	31.66
50020.00	F22					4047.00	44.45	5298.00	44.26
						3912.00	42.41		

		mn	3654.00	38.22	5068.00	37.80
50020.00	G22	sd	401.05	6.20	322.00	6.31
50020.00	H22		1667.00	5.04	1053.00	2.56
50020.00	I22		1828.00	5.03	1680.00	7.20
50020.00	J22		2082.00	2.79	1388.00	6.34
			2144.00	3.22	2358.00	7.04
		mn	1930.25	4.02	1619.75	5.79
		sd	222.47	1.19	554.84	2.18
		3psSD		18.60		18.93
		3ngSD		3.56		6.54
		SumSD		22.16		25.47
		DiffMn		34.20		32.01
		SmovrDiff		0.65		0.80
		1minus		0.35		0.20

Cell Coun	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
3212.00	8.09	3.34	1.11	2089.00	10.77	5.64	1.62
1926.00	2.34	2.41	-0.80	2081.00	4.81	0.32	-0.09
3470.00	2.82	1.93	-0.64	2771.00	3.61	1.52	-0.44
2307.00	6.76	2.01	0.67	2855.00	10.86	5.73	1.64
4872.00	2.77	1.98	-0.66	2874.00	3.10	2.03	-0.58
3306.00	1.33	3.42	-1.14	2723.00	4.77	0.36	-0.10
2848.00	1.58	3.17	-1.05	1712.00	1.40	3.73	-1.07
2016.00	2.53	2.22	-0.74	2023.00	4.30	0.83	-0.24
3022.00	7.74	2.99	1.00	2356.00	10.70	5.57	1.60
3067.00	0.95	3.80	-1.27	2712.00	5.20	0.07	0.02
3249.00	3.69	1.06	-0.35	2317.00	5.18	0.05	0.01
3106.00	5.67	0.92	0.30	3351.00	9.16	4.03	1.16
1500.00	4.40	0.35	-0.12	1358.00	10.90	5.77	1.66
2125.00	2.26	2.49	-0.83	1960.00	2.40	2.73	-0.78
2479.00	2.54	2.21	-0.73	3680.00	5.71	0.58	0.17
2839.00	4.93	0.18	0.06	1718.00	3.73	1.40	-0.40
4235.00	7.30	2.55	0.85	3525.00	6.61	1.48	0.42
4156.00	11.12	**6.37**	2.12	3437.00	11.64	6.51	1.87
1179.00	6.87	2.12	0.71	1720.00	6.80	1.67	0.48
1564.00	4.54	0.21	-0.07	1574.00	2.41	2.72	-0.78
2751.00	6.87	2.12	0.71	2037.00	7.90	2.77	0.80
1348.00	6.45	1.70	0.57	883.00	3.51	1.62	-0.47
2420.00	8.60	3.85	1.28	2752.00	14.57	**9.44**	2.71
5427.00	8.59	3.84	1.28	3623.00	4.42	0.71	-0.21
5154.00	13.78	**9.03**	3.00	4082.00	10.56	5.43	1.56
3139.00	5.26	0.51	0.17	1513.00	1.26	3.87	-1.11
3025.00	6.35	1.60	0.53	2309.00	6.41	1.28	0.37
2053.00	11.35	**6.60**	2.20	2121.00	10.00	4.87	1.40
5044.00	17.39	**12.64**	4.20	2705.00	11.35	6.22	1.79
2940.00	11.46	**6.71**	2.23	2897.00	7.01	1.88	0.54
1762.00	4.31	0.44	-0.15	1640.00	1.59	3.54	-1.02
3964.00	12.31	**7.56**	2.51	2629.00	5.21	0.08	0.02
2316.00	3.41	1.34	-0.45	2699.00	5.04	0.09	-0.03
3960.00	6.01	1.26	0.42	2005.00	1.40	3.73	-1.07
4053.00	4.07	0.68	-0.23	3263.00	1.44	3.69	-1.06
3880.00	10.57	5.82	1.93	2575.00	4.85	0.28	-0.08
5247.00	16.26	**11.51**	3.83	3506.00	3.19	1.94	-0.56
2415.00	2.40	2.35	-0.78	1590.00	0.25	4.88	-1.40
4430.00	22.53	**17.78**	5.91	4515.00	7.24	2.11	0.61
3516.00	6.29	1.54	0.51	2626.00	0.46	4.67	-1.34
3288.00	2.34	2.41	-0.80	5351.00	4.60	0.53	-0.15
2914.00	2.47	2.28	-0.76	3374.00	5.22	0.09	0.02
4156.00	5.49	0.74	0.24	3997.00	8.06	2.93	0.84
3564.00	0.84	3.91	-1.30	2176.00	0.92	4.21	-1.21
4099.00	4.42	0.33	-0.11	2405.00	1.95	3.18	-0.91
5160.00	10.33	5.58	1.86	3039.00	4.87	0.26	-0.08

4186.00	8.05	3.30	1.10	2595.00	12.25	**7.12**	2.04	y
4083.00	2.40	2.35	-0.78	2641.00	1.82	3.31	-0.95	
3534.00	5.18	0.43	0.14	2215.00	1.58	3.55	-1.02	
2034.00	2.21	2.54	-0.84	1571.00	2.55	2.58	-0.74	
3644.00	2.09	2.66	-0.89	2705.00	5.40	0.27	0.08	
2259.00	3.94	0.81	-0.27	1048.00	2.96	2.17	-0.62	
3076.00	1.07	3.68	-1.22	1916.00	2.40	2.73	-0.78	
2689.00	4.31	0.44	-0.15	1832.00	3.98	1.15	-0.33	
4243.00	2.90	1.85	-0.62	3263.00	4.63	0.50	-0.14	
3631.00	6.61	1.86	0.62	2052.00	4.63	0.50	-0.14	
3331.00	8.65	3.90	1.30	2722.00	7.90	2.77	0.79	
4377.00	5.03	0.28	0.09	3422.00	5.82	0.69	0.20	
4425.00	4.84	0.09	0.03	2907.00	3.92	1.21	-0.35	
3279.00	7.47	2.72	0.91	2780.00	10.50	5.37	1.54	
2675.00	1.31	3.44	-1.14	3090.00	6.63	1.50	0.43	
3451.00	2.09	2.66	-0.89	2173.00	7.04	1.91	0.55	
2920.00	6.99	2.24	0.74	1957.00	14.97	**9.84**	2.83	
4003.00	3.52	1.23	-0.41	2464.00	6.49	1.36	0.39	
3987.00	2.68	2.07	-0.69	2568.00	15.23	**10.10**	2.90	
1272.00	1.49	3.26	-1.08	776.00	5.03	0.10	-0.03	
2411.00	1.66	3.09	-1.03	1278.00	6.96	1.83	0.53	
2627.00	1.45	3.30	-1.10	1280.00	7.42	2.29	0.66	
2022.00	2.08	2.67	-0.89	1548.00	7.62	2.49	0.72	
3837.00	8.11	3.36	1.12	2332.00	19.25	**14.12**	4.05	
4657.00	4.90	0.15	0.05	2963.00	13.43	**8.30**	2.38	
2533.00	3.47	1.28	-0.42	1703.00	24.02	**18.89**	5.42	
4698.00	6.77	2.02	0.67	2389.00	10.80	5.67	1.63	
3910.00	5.63	0.88	0.29	2366.00	17.96	**12.83**	3.68	
4122.00	3.57	1.18	-0.39	2226.00	3.46	1.67	-0.48	
3089.00	0.91	3.84	-1.28	1791.00	4.41	0.72	-0.21	
4274.00	0.91	3.84	-1.28	2327.00	3.18	1.95	-0.56	
2213.00	1.22	3.53	-1.17	2232.00	11.11	5.98	1.72	
5155.00	6.56	1.81	0.60	3063.00	7.48	2.35	0.67	
3567.00	2.94	1.81	-0.60	3327.00	5.14	0.01	0.00	
3053.00	3.64	1.11	-0.37	4513.00	14.98	**9.85**	2.83	
3254.00	5.75	1.00	0.33	2798.00	2.68	2.45	-0.70	
3188.00	3.11	1.64	-0.55	3003.00	4.26	0.87	-0.25	
3785.00	2.72	2.03	-0.67	2419.00	2.73	2.40	-0.69	
2503.00	5.19	0.44	0.15	1862.00	0.91	4.22	-1.21	
2922.00	4.72	0.03	-0.01	1342.00	3.58	1.55	-0.45	
3567.00	5.64	0.89	0.29	2131.00	0.99	4.14	-1.19	
2830.00	7.14	2.39	0.79	1857.00	2.37	2.76	-0.79	
2071.00	7.92	3.17	1.05	1656.00	3.20	1.93	-0.55	
2254.00	6.26	1.51	0.50	1765.00	3.12	2.01	-0.58	
2551.00	1.45	3.30	-1.10	1970.00	3.15	1.98	-0.57	
1781.00	5.33	0.58	0.19	1528.00	5.17	0.04	0.01	
4008.00	8.36	3.61	1.20	1738.00	6.21	1.08	0.31	

2475.00	4.08	0.67	-0.22	1794.00	5.41	0.28	0.08	
3068.00	4.14	0.61	-0.20	2265.00	3.89	1.24	-0.36	
4354.00	5.47	0.72	0.24	2534.00	4.97	0.16	-0.05	
4936.00	5.11	0.36	0.12	2193.00	7.30	2.17	0.62	
4672.00	6.93	2.18	0.73	2427.00	6.26	1.13	0.32	
3651.00	9.56	4.81	1.60	1850.00	5.84	0.71	0.20	
3541.00	4.01	0.74	-0.25	2710.00	2.18	2.95	-0.85	
4344.00	1.98	2.77	-0.92	4322.00	2.36	2.77	-0.80	
3738.00	3.64	1.11	-0.37	3167.00	4.33	0.80	-0.23	
3738.00	5.35	0.60	0.20	3042.00	7.59	2.46	0.71	
3986.00	3.49	1.26	-0.42	2947.00	5.77	0.64	0.18	
2827.00	5.20	0.45	0.15	2127.00	3.10	2.03	-0.58	
3961.00	10.83	6.08	2.02	2805.00	17.79	12.66	3.63	y
2954.00	1.56	3.19	-1.06	1923.00	4.52	0.61	-0.17	
3557.00	9.00	4.25	1.41	2184.00	8.06	2.93	0.84	
3051.00	6.36	1.61	0.54	1748.00	8.12	2.99	0.86	
3970.00	1.71	3.04	-1.01	2698.00	4.34	0.79	-0.23	
2521.00	2.98	1.78	-0.59	1805.00	3.21	1.92	-0.55	
2060.00	1.55	3.20	-1.06	1408.00	1.99	3.14	-0.90	
2392.00	5.10	0.35	0.12	1840.00	5.22	0.09	0.02	
4336.00	2.84	1.91	-0.64	1947.00	1.85	3.28	-0.94	
1405.00	7.54	2.79	0.93	627.00	3.35	1.78	-0.51	
3717.00	7.53	2.78	0.93	1585.00	4.35	0.78	-0.22	
4719.00	11.93	7.18	2.39	2998.00	8.61	3.48	1.00	y
4205.00	7.66	2.91	0.97	2877.00	6.26	1.13	0.32	
3283.00	9.29	4.54	1.51	1837.00	2.67	2.46	-0.71	
4525.00	1.68	3.07	-1.02	2932.00	0.78	4.35	-1.25	
4661.00	4.44	0.31	-0.10	4158.00	3.08	2.05	-0.59	
2304.00	3.60	1.15	-0.38	2546.00	2.83	2.30	-0.66	
2644.00	3.14	1.61	-0.54	3049.00	2.00	3.13	-0.90	
1591.00	0.38	4.37	-1.45	2526.00	1.03	4.10	-1.18	
1675.00	3.52	1.23	-0.41	1009.00	5.45	0.32	0.09	
3238.00	4.60	0.15	-0.05	3457.00	5.93	0.80	0.23	
1938.00	4.44	0.31	-0.10	1690.00	6.33	1.20	0.34	
2639.00	0.80	3.95	-1.32	2419.00	1.49	3.64	-1.05	
2476.00	10.62	5.87	1.95	1910.00	10.42	5.29	1.52	
2554.00	1.84	2.91	-0.97	3408.00	3.61	1.52	-0.44	
2690.00	1.41	3.34	-1.11	3058.00	8.08	2.95	0.85	
2156.00	2.41	2.34	-0.78	1902.00	1.68	3.45	-0.99	
2078.00	2.45	2.30	-0.76	1581.00	3.86	1.27	-0.37	
3259.00	3.90	0.85	-0.28	3287.00	5.81	0.68	0.20	
3293.00	3.58	1.17	-0.39	3218.00	6.74	1.61	0.46	
4710.00	12.65	7.90	2.63	3652.00	11.69	6.56	1.88	y
3095.00	6.33	1.58	0.53	2663.00	5.93	0.80	0.23	
3086.00	6.68	1.93	0.64	3230.00	9.72	4.59	1.32	
3658.00	10.39	5.64	1.88	3269.00	5.93	0.80	0.23	
1978.00	2.58	2.17	-0.72	2067.00	7.31	2.18	0.62	

2510.00	1.24	3.51	-1.17	2034.00	0.74	4.39	-1.26	
4531.00	4.02	0.73	-0.24	3508.00	5.07	0.06	-0.02	
3102.00	6.16	1.41	0.47	2789.00	5.56	0.43	0.12	
2127.00	1.55	3.20	-1.06	2791.00	2.58	2.55	-0.73	
2734.00	5.71	0.96	0.32	1923.00	4.89	0.24	-0.07	
3375.00	10.34	5.59	1.86	3630.00	7.33	2.20	0.63	
3020.00	2.78	1.97	-0.65	3036.00	5.83	0.70	0.20	
2206.00	2.99	1.76	-0.58	1930.00	3.78	1.35	-0.39	
2931.00	4.67	0.08	-0.03	3091.00	7.99	2.86	0.82	
2420.00	6.41	1.66	0.55	2743.00	9.41	4.28	1.23	
1342.00	4.40	0.35	-0.12	1427.00	4.41	0.72	-0.21	
2050.00	4.83	0.08	0.03	1389.00	0.86	4.27	-1.23	
3293.00	6.01	1.26	0.42	3790.00	7.12	1.99	0.57	
3171.00	4.95	0.20	0.07	3158.00	4.62	0.51	-0.15	
3590.00	8.27	3.52	1.17	2684.00	2.98	2.15	-0.62	
3821.00	15.02	**10.27**	3.42	3688.00	6.89	1.76	0.50	
3373.00	7.71	2.96	0.98	4062.00	8.81	3.68	1.06	
2938.00	12.49	**7.74**	2.57	3646.00	6.83	1.70	0.49	
4591.00	9.08	4.33	1.44	5041.00	7.44	2.31	0.66	
2046.00	1.71	3.04	-1.01	2085.00	1.97	3.16	-0.91	
3187.00	4.49	0.26	-0.09	4098.00	5.10	0.03	-0.01	
2764.00	4.59	0.16	-0.05	3147.00	2.86	2.27	-0.65	
2473.00	3.68	1.07	-0.36	2144.00	1.40	3.73	-1.07	
4324.00	9.53	4.78	1.59	3194.00	7.11	1.98	0.57	
2847.00	4.88	0.13	0.04	2952.00	6.13	1.00	0.29	
3344.00	5.62	0.87	0.29	2826.00	5.10	0.03	-0.01	
1867.00	1.55	3.20	-1.06	2267.00	4.28	0.85	-0.24	
1512.00	4.30	0.45	-0.15	1232.00	0.89	4.24	-1.22	
2472.00	2.14	2.61	-0.87	2384.00	2.64	2.49	-0.71	
2505.00	6.43	1.68	0.56	1920.00	2.92	2.21	-0.64	
2398.00	7.01	2.26	0.75	2637.00	7.17	2.04	0.58	
2152.00	5.72	0.97	0.32	2835.00	1.41	3.72	-1.07	
3143.00	9.07	4.32	1.44	2499.00	5.52	0.39	0.11	
4473.00	9.28	4.53	1.51	3679.00	4.59	0.54	-0.15	
5280.00	17.56	**12.81**	4.26	4163.00	13.60	**8.47**	2.43	y
3157.00	5.96	1.21	0.40	3472.00	6.13	1.00	0.29	
3428.00	4.46	0.29	-0.10	3281.00	3.99	1.14	-0.33	
3986.00	9.28	4.53	1.51	2954.00	3.59	1.54	-0.44	
2943.00	4.08	0.67	-0.22	1898.00	3.21	1.92	-0.55	
3320.00	4.70	0.05	-0.02	2334.00	1.37	3.76	-1.08	
2962.00	1.01	3.74	-1.24	2564.00	2.03	3.10	-0.89	
4232.00	8.96	4.21	1.40	4686.00	11.72	6.59	1.89	
2384.00	12.33	**7.58**	2.52	2798.00	13.44	**8.31**	2.38	y
1993.00	5.22	0.47	0.16	3400.00	5.35	0.22	0.06	
2372.00	9.49	4.74	1.58	2292.00	8.94	3.81	1.09	
1658.00	1.51	3.24	-1.08	2525.00	4.16	0.97	-0.28	
1089.00	2.02	2.73	-0.91	2524.00	2.73	2.40	-0.69	

2841.00	5.70	0.95	0.32	3571.00	10.00	4.87	1.40	
1747.00	1.55	3.20	-1.07	2100.00	2.90	2.23	-0.64	
1668.00	0.60	4.15	-1.38	1775.00	2.42	2.71	-0.78	
1462.00	7.87	3.12	1.04	1640.00	7.93	2.80	0.80	
3453.00	6.89	2.14	0.71	3008.00	11.07	5.94	1.70	
3120.00	2.63	2.12	-0.71	2491.00	2.25	2.88	-0.83	
2500.00	5.48	0.73	0.24	2944.00	3.77	1.36	-0.39	
1888.00	6.78	2.03	0.68	2919.00	12.74	7.61	2.19	
3079.00	7.70	2.95	0.98	3704.00	7.05	1.92	0.55	
1240.00	0.73	4.02	-1.34	2126.00	6.96	1.83	0.53	
2520.00	2.30	2.45	-0.81	2241.00	2.32	2.81	-0.81	
4080.00	4.53	0.22	-0.07	3180.00	1.86	3.27	-0.94	
2738.00	0.44	4.31	-1.43	2253.00	1.86	3.27	-0.94	
3845.00	8.66	3.91	1.30	4375.00	2.56	2.57	-0.74	
1863.00	2.79	1.96	-0.65	1521.00	0.39	4.74	-1.36	
3190.00	7.18	2.43	0.81	3239.00	2.41	2.72	-0.78	
3420.00	8.68	3.93	1.31	3532.00	2.66	2.47	-0.71	
2609.00	4.02	0.73	-0.24	2454.00	1.96	3.17	-0.91	
1753.00	4.11	0.64	-0.21	2175.00	1.84	3.29	-0.95	
3121.00	8.49	3.74	1.24	3361.00	12.82	7.69	2.21	y
1814.00	2.09	2.66	-0.88	2302.00	2.48	2.65	-0.76	
2521.00	6.03	1.28	0.43	2115.00	6.38	1.25	0.36	
1693.00	2.78	1.97	-0.66	1457.00	1.92	3.21	-0.92	
2788.00	5.63	0.88	0.29	2022.00	2.18	2.95	-0.85	
1999.00	0.60	4.15	-1.38	2077.00	0.34	4.79	-1.38	
3148.00	5.27	0.52	0.17	2553.00	3.56	1.57	-0.45	
1502.00	0.53	4.22	-1.40	1702.00	1.94	3.19	-0.92	
4938.00	6.97	2.22	0.74	3785.00	5.31	0.18	0.05	
2798.00	1.36	3.39	-1.13	2679.00	1.72	3.41	-0.98	
4544.00	2.71	2.04	-0.68	3174.00	2.80	2.33	-0.67	
2883.00	3.26	1.49	-0.50	3338.00	2.49	2.64	-0.76	
3378.00	2.69	2.06	-0.68	2827.00	5.16	0.03	0.01	
4977.00	3.88	0.87	-0.29	2771.00	1.66	3.47	-1.00	
2861.00	3.39	1.36	-0.45	2118.00	5.15	0.02	0.00	
2066.00	3.24	1.51	-0.50	2231.00	4.66	0.47	-0.13	
4026.00	3.78	0.97	-0.32	3214.00	6.57	1.44	0.41	
3797.00	5.37	0.62	0.21	3881.00	6.67	1.54	0.44	
1950.00	6.10	1.35	0.45	3956.00	16.81	11.68	3.35	y
3742.00	1.79	2.96	-0.98	5320.00	6.20	1.07	0.31	
1351.00	9.18	4.43	1.47	1329.00	13.24	8.11	2.33	
1818.00	5.06	0.31	0.10	1818.00	10.89	5.76	1.65	
1957.00	8.12	3.37	1.12	1915.00	3.34	1.79	-0.51	
1909.00	3.93	0.82	-0.27	1662.00	2.35	2.78	-0.80	
2347.00	4.22	0.53	-0.18	1991.00	5.12	0.01	0.00	
3277.00	5.16	0.41	0.14	3409.00	10.85	5.72	1.64	
2014.00	4.07	0.68	-0.23	2071.00	6.81	1.68	0.48	
1397.00	1.15	3.60	-1.20	1738.00	1.96	3.17	-0.91	

1744.00	7.97	3.22	1.07	1936.00	8.99	3.86	1.11	
3206.00	3.06	1.69	-0.56	2325.00	4.09	1.04	-0.30	
3272.00	7.24	2.49	0.83	3870.00	10.34	5.21	1.49	
2387.00	5.95	1.20	0.40	2239.00	7.19	2.06	0.59	
2238.00	17.16	**12.41**	4.13	2622.00	24.87	**19.74**	5.67	y
2426.00	2.23	2.52	-0.84	2197.00	4.55	0.58	-0.17	
1398.00	1.65	3.10	-1.03	1925.00	2.75	2.38	-0.68	
4423.00	4.18	0.57	-0.19	4232.00	7.49	2.36	0.68	
1243.00	5.95	1.20	0.40	1736.00	5.36	0.23	0.06	
1935.00	2.89	1.86	-0.62	3636.00	3.77	1.36	-0.39	
3823.00	9.18	4.43	1.47	3971.00	10.27	5.14	1.48	
2614.00	2.56	2.19	-0.73	4026.00	1.86	3.27	-0.94	
929.00	2.48	2.27	-0.76	1428.00	3.08	2.05	-0.59	
1771.00	1.36	3.39	-1.13	2603.00	2.00	3.13	-0.90	
1805.00	3.77	0.98	-0.33	2003.00	5.39	0.26	0.07	
1841.00	4.78	0.03	0.01	1687.00	4.92	0.21	-0.06	
3379.00	4.38	0.37	-0.12	2702.00	7.40	2.27	0.65	
1100.00	3.27	1.48	-0.49	1897.00	1.95	3.18	-0.91	
2345.00	5.12	0.37	0.12	2892.00	6.19	1.06	0.30	
1946.00	7.86	3.11	1.04	3083.00	7.53	2.40	0.69	
2123.00	6.64	1.89	0.63	3315.00	6.24	1.11	0.32	
2338.00	5.73	0.98	0.33	3349.00	7.05	1.92	0.55	
2500.00	8.84	4.09	1.36	3484.00	4.54	0.60	-0.17	
2572.00	5.02	0.27	0.09	3546.00	5.78	0.65	0.19	
2558.00	6.49	1.74	0.58	4120.00	7.79	2.66	0.76	
3105.00	1.48	3.27	-1.09	3429.00	3.24	1.89	-0.54	
2239.00	5.18	0.43	0.14	2539.00	5.67	0.54	0.16	
4041.00	6.81	2.06	0.68	4027.00	3.33	1.80	-0.52	
4441.00	8.62	3.87	1.29	3786.00	7.63	2.50	0.72	
3283.00	11.58	**6.83**	2.27	3967.00	7.41	2.28	0.65	
2646.00	16.82	**12.07**	4.01	3616.00	13.25	**8.12**	2.33	y
2778.00	9.79	5.04	1.68	4492.00	8.42	3.29	0.94	
3149.00	7.65	2.90	0.97	3934.00	4.68	0.45	-0.13	
1865.00	3.06	1.69	-0.56	1900.00	2.26	2.87	-0.82	
2339.00	3.12	1.63	-0.54	3040.00	2.07	3.06	-0.88	
2768.00	5.71	0.96	0.32	2412.00	1.87	3.26	-0.94	
2512.00	3.11	1.64	-0.55	2901.00	1.72	3.41	-0.98	
1568.00	4.66	0.09	-0.03	1977.00	1.42	3.71	-1.07	
1589.00	4.09	0.66	-0.22	3063.00	1.60	3.53	-1.01	
3829.00	4.86	0.11	0.04	4577.00	2.69	2.44	-0.70	
2841.00	8.83	4.08	1.36	4486.00	6.80	1.67	0.48	
2502.00	5.88	1.13	0.37	3521.00	1.11	4.02	-1.16	
2812.00	6.83	2.08	0.69	4564.00	5.63	0.50	0.14	
2918.00	3.26	1.49	-0.50	4375.00	2.42	2.71	-0.78	
2414.00	5.59	0.84	0.28	3264.00	1.16	3.97	-1.14	
4562.00	3.99	0.76	-0.25	2612.00	0.84	4.29	-1.23	
2819.00	7.34	2.59	0.86	2790.00	2.65	2.48	-0.71	

1730.00	9.08	4.33	1.44	1959.00	4.59	0.54	-0.15	
1967.00	4.42	0.33	-0.11	2703.00	7.55	2.42	0.69	
2276.00	5.27	0.52	0.17	3540.00	7.71	2.58	0.74	
2497.00	7.49	2.74	0.91	3317.00	4.37	0.76	-0.22	
2528.00	5.58	0.83	0.28	4629.00	6.96	1.83	0.52	
1872.00	1.71	3.04	-1.01	2925.00	3.86	1.27	-0.36	
1395.00	9.96	5.21	1.73	3347.00	6.81	1.68	0.48	
950.00	1.58	3.17	-1.05	1475.00	0.75	4.38	-1.26	
1354.00	1.92	2.83	-0.94	1564.00	7.10	1.97	0.56	
1834.00	5.13	0.38	0.12	2303.00	2.82	2.31	-0.66	
1765.00	2.55	2.20	-0.73	1700.00	3.35	1.78	-0.51	
2266.00	11.47	**6.72**	2.24	2645.00	13.04	**7.91**	2.27	y
3514.00	3.76	0.99	-0.33	4091.00	5.18	0.05	0.01	
1842.00	4.78	0.03	0.01	2154.00	10.68	5.55	1.59	
3881.00	6.39	1.64	0.55	3976.00	11.47	6.34	1.82	
3934.00	13.32	**8.57**	2.85	3811.00	13.93	**8.80**	2.53	y
2426.00	1.57	3.18	-1.06	2805.00	4.63	0.50	-0.14	
904.00	4.98	0.23	0.08	1936.00	7.08	1.95	0.56	
2705.00	4.21	0.54	-0.18	1690.00	3.02	2.11	-0.61	
2550.00	2.78	1.97	-0.65	1625.00	8.06	2.93	0.84	
1382.00	3.91	0.84	-0.28	2153.00	18.39	**13.26**	3.81	y
2038.00	6.33	1.58	0.53	2282.00	19.02	**13.89**	3.99	
777.00	3.22	1.53	-0.51	2193.00	8.48	3.35	0.96	
1608.00	5.78	1.03	0.34	2121.00	8.77	3.64	1.04	
1876.00	4.37	0.38	-0.13	3089.00	10.75	5.62	1.61	
1969.00	5.18	0.43	0.14	2488.00	9.89	4.76	1.37	
1460.00	3.01	1.74	-0.58	1776.00	4.90	0.23	-0.07	
772.00	2.98	1.77	-0.59	1132.00	12.37	**7.24**	2.08	
512.00	1.56	3.19	-1.06	1028.00	8.95	3.82	1.10	
1082.00	3.33	1.42	-0.47	1946.00	10.23	5.10	1.46	
2166.00	7.39	2.64	0.88	2790.00	16.38	**11.25**	3.23	
1693.00	2.72	2.03	-0.68	2132.00	8.86	3.73	1.07	
2369.00	0.84	3.91	-1.30	3111.00	10.29	5.16	1.48	
2445.00	3.03	1.72	-0.57	2885.00	6.07	0.94	0.27	
2204.00	2.13	2.62	-0.87	4293.00	7.24	2.11	0.61	
1327.00	6.18	1.43	0.48	1782.00	5.84	0.71	0.20	
1228.00	5.13	0.38	0.13	2614.00	5.55	0.42	0.12	
1939.00	9.59	4.84	1.61	2599.00	12.62	**7.49**	2.15	y
2058.00	0.97	3.78	-1.26	2550.00	1.73	3.40	-0.98	
2783.00	4.75	2.03		2597.00	5.13	2.35		
		6.09				7.06		
		3.01				3.48		

3098.00	27.44	3987.00	45.72
		5723.00	55.22
3442.00	20.95		
2847.00	20.55		

3129.00	22.98
298.71	3.87
1834.00	4.69
1299.00	1.23
1396.00	2.36
2122.00	1.79
1662.75	2.52
384.58	1.52
	11.60
	4.56
	16.16
	20.46
	0.79
	0.21

Plate	Well		Gene		GeneID	Cell Coun	% inf	Abs Dev
50021.00	A02	M-032274-	dihydrofolate reduct	1720.00	DHFRP1	3369.00	5.52	1.13
50021.00	A04	M-012090-	DiGeorge syndrome	8214.00	DGCR6	2970.00	5.05	1.60
50021.00	A05	M-011122-	complement compo	721.00	C4B	4091.00	4.82	1.83
50021.00	A06	M-011844-	deafness, autosomal	1687.00	DFNA5	2551.00	9.68	3.03
50021.00	A07	M-011003-	complement compo	729.00	C6	3675.00	3.51	3.14
50021.00	A08	M-005847-	transmembrane prot	28983.00	TMPRSS11	2031.00	7.48	0.83
50021.00	A09	M-019499-	CD1b molecule	910.00	CD1B	1845.00	1.25	5.40
50021.00	A10	M-011638-	desmin	1674.00	DES	2206.00	3.40	3.25
50021.00	A11	M-019500-	CD1c molecule	911.00	CD1C	2013.00	1.29	5.36
50021.00	A12	M-017992-	chromosome 17 ope	23587.00	C17orf81	901.00	2.22	4.43
50021.00	A13	M-020689-	CD24 molecule	934.00	CD24	1264.00	2.61	4.04
50021.00	A14	M-004289-	alkB, alkylation repai	221120.00	ALKBH3	2653.00	9.91	3.26
50021.00	A15	M-020827-	CD244 molecule, nat	51744.00	CD244	2461.00	4.35	2.30
50021.00	A16	M-019970-	secretion regulating	26297.00	SERGEF	3385.00	11.34	4.69
50021.00	A17	M-012799-	CD2-associated prot	23607.00	CD2AP	2392.00	8.40	1.75
50021.00	A18	M-013400-	deleted in esophage	50514.00	DEC1	3406.00	9.19	2.54
50021.00	A19	M-020057-	CD2 (cytoplasmic tai	10421.00	CD2BP2	2517.00	3.58	3.07
50021.00	A20	M-012417-	integrator complex s	26512.00	INTS6	2460.00	5.81	0.84
50021.00	A21	M-011604-	CD37 molecule	951.00	CD37	1584.00	12.31	5.66
50021.00	A23	M-011117-	CD53 molecule	963.00	CD53	2061.00	9.90	3.25
50021.00	B02	M-016308-	Fc fragment of IgG, l	2214.00	FCGR3A	1511.00	9.27	2.62
50021.00	B04	M-008725-	fructose-1,6-bisphos	2203.00	FBP1	2229.00	2.87	3.78
50021.00	B05	M-004447-	diablo homolog (Dro	56616.00	DIABLO	3801.00	4.08	2.57
50021.00	B06	M-017621-	fibulin 5	10516.00	FBLN5	3497.00	2.55	4.11
50021.00	B07	M-012029-	diaphanous homolo	1730.00	DIAPH2	4490.00	6.44	0.21
50021.00	B08	M-020818-	zinc finger and BTB d	51341.00	ZBTB7A	3470.00	5.27	1.38
50021.00	B09	M-018997-	diaphanous homolo	81624.00	DIAPH3	3609.00	7.45	0.80
50021.00	B10	M-011854-	phenylalanyl-tRNA s	2193.00	FARSA	2724.00	2.24	4.41
50021.00	B11	M-021454-	disrupted in renal ca	84925.00	DIRC2	3082.00	7.75	1.10
50021.00	B12	M-009237-	FERM, RhoGEF and	9855.00	FARP2	1253.00	1.52	5.13
50021.00	B13	M-020321-	disrupted in schizop	27185.00	DISC1	3116.00	6.64	0.01
50021.00	B14	M-014206-	Fanconi anemia, co	2188.00	FANCF	3451.00	8.46	1.81
50021.00	B15	M-004907-	serine hydrolase-like	253190.00	SERHL2	3490.00	1.52	5.13
50021.00	B16	M-013991-	Fanconi anemia, co	2178.00	FANCE	3396.00	3.59	3.06
50021.00	B17	M-013639-	dyskeratosis congeni	1736.00	DKC1	5038.00	13.30	6.65
50021.00	B18	M-016376-	Fanconi anemia, co	2177.00	FANCD2	4853.00	22.71	16.06
50021.00	B19	M-013972-	integrator complex s	25896.00	INTS7	2656.00	1.81	4.84
50021.00	B20	M-011033-	Fanconi anemia, co	2176.00	FANCC	3140.00	13.03	6.38
50021.00	B21	M-009833-	Src homology 3 dom	26084.00	SGEF	4130.00	12.83	6.18
50021.00	B23	M-022848-	fumarylacetoacetate	151313.00	FAHD2B	2876.00	4.66	1.99
50021.00	C02	M-012890-	damage-specific DN	1642.00	DDB1	3295.00	3.31	3.34
50021.00	C04	M-013592-	proline/serine-rich c	84722.00	PSRC1	2748.00	2.91	3.74
50021.00	C05	M-004537-	CD59 molecule, com	966.00	CD59	3687.00	13.53	6.88
50021.00	C06	M-016592-	ubiquitin domain co	92181.00	UBTD2	2062.00	3.78	2.87
50021.00	C07	M-017256-	CD63 molecule	967.00	CD63	3760.00	9.87	3.22
50021.00	C08	M-015395-	dynactin 4 (p62)	51164.00	DCTN4	4355.00	4.41	2.24

50021.00	C09	M-011236-	CD68 molecule	968.00	CD68	3059.00	3.60	3.05
50021.00	C10	M-012218-	dynactin 2 (p50)	10540.00	DCTN2	3417.00	7.23	0.58
50021.00	C11	M-012680-	CD83 molecule	9308.00	CD83	2778.00	3.64	3.01
50021.00	C12	M-021491-	decorin	1634.00	DCN	2732.00	8.57	1.92
50021.00	C13	M-012623-	CD84 molecule	8832.00	CD84	2423.00	3.84	2.81
50021.00	C14	M-004269-	DNA cross-link repai	64421.00	DCLRE1C	3307.00	9.74	3.09
50021.00	C15	M-016245-	CD99 molecule	4267.00	CD99	3213.00	4.79	1.86
50021.00	C16	M-015780-	DNA cross-link repai	64858.00	DCLRE1B	3269.00	3.70	2.95
50021.00	C17	M-015478-	congenital dyserythr	146059.00	CDAN1	1618.00	2.23	4.43
50021.00	C18	M-020330-	chromosome 16 ope	56942.00	C16orf61	2411.00	8.50	1.85
50021.00	C19	M-003223-	cell division cycle 16	8881.00	CDC16	1632.00	3.92	2.73
50021.00	C20	M-020985-	DAZ associated prot	9802.00	DAZAP2	3465.00	8.28	1.63
50021.00	C21	M-003225-	cell division cycle 20	991.00	CDC20	1755.00	2.51	4.14
50021.00	C23	M-017290-	cell division cycle 26	246184.00	CDC26	2540.00	2.91	3.74
50021.00	D02	M-019283-	Fanconi anemia, con	2175.00	FANCA	2558.00	0.63	6.02
50021.00	D04	M-020999-	Fas apoptotic inhibit	55179.00	FAIM	4056.00	1.31	5.34
50021.00	D05	M-017959-	taxilin alpha	200081.00	TXLNA	2249.00	0.62	6.03
50021.00	D06	M-009106-	Fas (TNFRSF6) associ	11124.00	FAF1	2875.00	2.37	4.28
50021.00	D07	M-031723-	hypothetical protein	84242.00	DKFZp547D	4043.00	4.70	1.95
50021.00	D08	M-008853-	fatty acid binding pr	2167.00	FABP4	3118.00	1.19	5.46
50021.00	D09	M-018592-	haloacid dehalogena	84064.00	HDHD2	3570.00	2.80	3.85
50021.00	D10	M-010022-	fatty acid binding pr	2170.00	FABP3	2369.00	1.01	5.64
50021.00	D11	M-028371-	hypothetical LOC258	25845.00	LOC25845	2396.00	2.42	4.23
50021.00	D12	M-008419-	fatty acid binding pr	2169.00	FABP2	2223.00	3.87	2.78
50021.00	D13	M-020258-	transmembrane prot	26022.00	TMEM98	3228.00	5.27	1.38
50021.00	D14	M-007896-	coagulation factor XI	2165.00	F13B	2709.00	3.14	3.51
50021.00	D15	M-012723-	SMAD family membe	4086.00	SMAD1	2565.00	2.85	3.80
50021.00	D16	M-010070-	coagulation factor XI	2162.00	F13A1	5709.00	3.92	2.73
50021.00	D17	M-027346-	KIAA1217	56243.00	KIAA1217	4218.00	2.99	3.66
50021.00	D18	M-005053-	F11 receptor	50848.00	F11R	2990.00	4.55	2.10
50021.00	D19	M-006039-	spastic paraplegia 7 (	6687.00	SPG7	2876.00	3.58	3.07
50021.00	D20	M-004218-	enhancer of zeste hc	2146.00	EZH2	2989.00	2.28	4.38
50021.00	D21	M-028612-	chromosome 6 open	79747.00	C6orf103	3882.00	3.12	3.53
50021.00	D23	M-012257-	chromosome 6 open	10591.00	C6orf108	3010.00	2.72	3.93
50021.00	E02	M-021042-	deleted in azoosperr	57054.00	DAZ3	3524.00	5.02	1.63
50021.00	E04	M-021073-	deleted in azoosperr	57055.00	DAZ2	3950.00	8.41	1.76
50021.00	E05	M-003229-	cell division cycle 27	996.00	CDC27	3728.00	9.04	2.39
50021.00	E06	M-015509-	LIM domain only 3 (r	55885.00	LMO3	4779.00	7.78	1.13
50021.00	E07	M-005057-	cell division cycle 42	998.00	CDC42	4724.00	7.77	1.12
50021.00	E08	M-004415-	death-associated pr	1611.00	DAP	5214.00	15.40	8.75
50021.00	E09	M-017551-	CDC42 effector prot	11135.00	CDC42EP1	4470.00	7.58	0.93
50021.00	E10	M-004573-	CD55 molecule, deca	1604.00	CD55	4392.00	8.74	2.09
50021.00	E11	M-003232-	CDC45 cell division c	8318.00	CDC45L	3484.00	7.09	0.44
50021.00	E12	M-004414-	defender against cell	1603.00	DAD1	2856.00	4.24	2.41
50021.00	E13	M-017428-	phosphatidylinositol	128869.00	PIGU	3788.00	8.18	1.53
50021.00	E14	M-016440-	dapper, antagonist o	51339.00	DACT1	3594.00	10.99	4.34
50021.00	E15	M-005289-	NUF2, NDC80 kineto	83540.00	NUF2	1376.00	10.47	3.82

50021.00	E16	M-008522-	disabled homolog 2,	1601.00	DAB2	2712.00	5.64	1.01
50021.00	E17	M-010495-	cell division cycle ass	55038.00	CDCA4	3062.00	6.86	0.21
50021.00	E18	M-008943-	disabled homolog 1 (	1600.00	DAB1	5194.00	17.87	**11.22**
50021.00	E19	M-017348-	cell division cycle ass	83879.00	CDCA7	4289.00	6.02	0.63
50021.00	E20	M-012925-	dishevelled associate	23002.00	DAAM1	5334.00	9.90	3.25
50021.00	E21	M-003823-	cadherin 3, type 1, P	1001.00	CDH3	3925.00	5.76	0.89
50021.00	E23	M-011007-	cyclin-dependent kin	1029.00	CDKN2A	3973.00	2.79	3.86
50021.00	F02	M-004217-	enhancer of zeste hc	2145.00	EZH1	3806.00	11.98	5.33
50021.00	F04	M-017233-	eyes absent homolo	2139.00	EYA2	3421.00	2.37	4.28
50021.00	F05	M-018550-	prenyl (decaprenyl) (	57107.00	PDSS2	4753.00	7.15	0.50
50021.00	F06	M-010512-	ecotropic viral integr	2124.00	EVI2B	4634.00	7.62	0.97
50021.00	F07	M-007821-	complement compo	730.00	C7	1933.00	3.47	3.18
50021.00	F08	M-018389-	transmembrane cha	147138.00	TMC8	2861.00	6.54	0.11
50021.00	F09	M-016140-	limb region 1 homol	64327.00	LMBR1	2970.00	1.38	5.27
50021.00	F10	M-016167-	transmembrane cha	11322.00	TMC6	4174.00	4.65	2.00
50021.00	F11	M-028907-	sterile alpha motif d	219285.00	SAMD9L	4622.00	10.17	3.52
50021.00	F12	M-018291-	Ellis van Creveld syn	132884.00	EVC2	2433.00	1.15	5.50
50021.00	F13	M-011119-	complement compo	731.00	C8A	2607.00	12.28	5.63
50021.00	F14	M-013594-	Ellis van Creveld syn	2121.00	EVC	3718.00	3.82	2.83
50021.00	F15	M-011004-	complement compo	732.00	C8B	3273.00	10.24	3.59
50021.00	F16	M-008894-	ets variant gene 5 (e	2119.00	ETV5	3114.00	3.50	3.15
50021.00	F17	M-017853-	complement compo	735.00	C9	2344.00	12.63	5.98
50021.00	F18	M-003801-	ets variant gene 1	2115.00	ETV1	2819.00	3.51	3.14
50021.00	F19	M-010173-	carbonic anhydrase I	759.00	CA1	4853.00	4.66	1.99
50021.00	F20	M-015367-	intraflagellar transpc	55081.00	IFT57	3712.00	10.72	4.07
50021.00	F21	M-009639-	carbonic anhydrase I	760.00	CA2	3194.00	3.01	3.64
50021.00	F23	M-004939-	chaperone, ABC1 act	56997.00	CABC1	2368.00	3.25	3.40
50021.00	G02	M-008330-	cytochrome P450, fa	1544.00	CYP1A2	4071.00	7.05	0.40
50021.00	G04	M-008329-	cytochrome P450, fa	1583.00	CYP11A1	3849.00	11.95	5.30
50021.00	G05	M-020888-	Cdon homolog (mou	50937.00	CDON	2331.00	6.18	0.47
50021.00	G06	M-013511-	CAP-GLY domain cor	7461.00	CLIP2	3780.00	4.87	1.78
50021.00	G07	M-019791-	cerebellar degenerat	1038.00	CDR1	3981.00	5.17	1.48
50021.00	G08	M-017355-	cytochrome c, soma	54205.00	CYCS	2698.00	2.97	3.68
50021.00	G09	M-022509-	cerebellar degenerat	1039.00	CDR2	2049.00	1.71	4.94
50021.00	G10	M-011021-	cytochrome b-245, b	1536.00	CYBB	2468.00	11.59	4.94
50021.00	G11	M-011238-	corneodesmosin	1041.00	CDSN	3967.00	13.59	6.94
50021.00	G12	M-019621-	cytochrome b5 type	1528.00	CYB5A	2107.00	5.32	1.33
50021.00	G13	M-007853-	angiopoietin-like 7	10218.00	ANGPTL7	1677.00	7.39	0.74
50021.00	G14	M-007879-	chemokine (C-X-C m	6374.00	CXCL5	3076.00	19.67	**13.02**
50021.00	G15	M-019693-	carcinoembryonic ar	1087.00	CEACAM7	2837.00	13.36	6.71
50021.00	G16	M-019553-	cullin 5	8065.00	CUL5	3696.00	11.58	4.93
50021.00	G17	M-009515-	CCAAT/enhancer bin	1053.00	CEBPE	2473.00	3.52	3.13
50021.00	G18	M-016631-	V-set and immunogl	23584.00	VSIG2	4083.00	9.48	2.83
50021.00	G19	M-019449-	cerebral endothelial	51148.00	CEECAM1	3755.00	6.82	0.17
50021.00	G20	M-005840-	cathepsin K	1513.00	CTSK	3661.00	7.65	1.00
50021.00	G21	M-008871-	carboxyl ester lipase	1056.00	CEL	3246.00	5.55	1.10
50021.00	G23	M-003253-	centromere protein	1063.00	CENPF	5116.00	18.88	**12.23**

50021.00	H02	M-020493-	ERO1-like (S. cerevisi	30001.00	ERO1L	3660.00	9.04	2.39
50021.00	H04	M-004878-	endoplasmic reticulu	10595.00	ERN2	6674.00	18.46	**11.81**
50021.00	H05	M-006122-	calcium channel, vol	774.00	CACNA1B	4833.00	28.72	**22.07**
50021.00	H06	M-012670-	enhancer of rudimer	2079.00	ERH	2885.00	9.43	2.78
50021.00	H07	M-006127-	calcium channel, vol	8913.00	CACNA1G	2308.00	7.80	1.15
50021.00	H08	M-019946-	excision repair cross-	2072.00	ERCC4	2806.00	12.22	5.57
50021.00	H09	M-006130-	calcium channel, vol	779.00	CACNA1S	2558.00	7.78	1.13
50021.00	H10	M-011028-	excision repair cross-	2071.00	ERCC3	2336.00	8.35	1.70
50021.00	H11	M-009062-	calcium channel, vol	785.00	CACNB4	3691.00	9.89	3.24
50021.00	H12	M-017905-	epidermal growth fa	2059.00	EPS8	2948.00	3.12	3.53
50021.00	H13	M-011989-	calbindin 1, 28kDa	793.00	CALB1	2815.00	3.62	3.03
50021.00	H14	M-008245-	glutamyl-prolyl-tRN	2058.00	EPRS	3231.00	6.10	0.55
50021.00	H15	M-010410-	dopamine receptor	50632.00	DRD1IP	3472.00	6.16	0.49
50021.00	H16	M-005866-	protease, serine, 33	260429.00	PRSS33	3328.00	6.49	0.16
50021.00	H17	M-019790-	cathelicidin antimicr	820.00	CAMP	3665.00	1.53	5.12
50021.00	H18	M-003809-	ectonucleotide pyro	5167.00	ENPP1	4441.00	3.02	3.63
50021.00	H19	M-019047-	calmodulin binding t	23125.00	CAMTA2	3176.00	1.54	5.11
50021.00	H20	M-009718-	enolase 3 (beta, mus	2027.00	ENO3	3063.00	9.73	3.08
50021.00	H21	M-012210-	CAP, adenylate cycla	10487.00	CAP1	4737.00	4.05	2.60
50021.00	H23	M-012213-	capping protein (acti	830.00	CAPZA2	4279.00	4.72	1.93
50021.00	I02	M-017535-	catenin, beta like 1	56259.00	CTNNBL1	3132.00	0.86	5.79
50021.00	I04	M-012620-	catenin (cadherin-as	8727.00	CTNNAL1	5526.00	26.71	**20.06**
50021.00	I05	M-003254-	centromere protein	64946.00	CENPH	2825.00	3.72	2.93
50021.00	I06	M-010505-	catenin (cadherin-as	1495.00	CTNNA1	3264.00	4.78	1.87
50021.00	I07	M-010209-	centromere protein	55835.00	CENPJ	1992.00	4.07	2.58
50021.00	I08	M-016267-	cytotoxic T-lymphoc	1493.00	CTLA4	3523.00	6.19	0.46
50021.00	I09	M-006841-	centrosomal protein	11064.00	CEP110	3001.00	3.33	3.32
50021.00	I10	M-017236-	cystatin F (leukocyst	8530.00	CST7	4004.00	8.92	2.27
50021.00	I11	M-008938-	carboxylesterase 2 (i	8824.00	CES2	2568.00	2.80	3.85
50021.00	I12	M-009598-	cystatin C (amyloid a	1471.00	CST3	2387.00	5.15	1.50
50021.00	I13	M-015133-	hypothetical gene C	90634.00	CG018	3106.00	7.37	0.72
50021.00	I14	M-011424-	cysteine and glycine-	8048.00	CSRP3	2286.00	4.68	1.97
50021.00	I15	M-011164-	chorionic gonadotro	1082.00	CGB	3518.00	1.05	5.60
50021.00	I16	M-011839-	cysteine and glycine-	1465.00	CSRP1	4438.00	7.08	0.43
50021.00	I17	M-013674-	chorionic gonadotro	93659.00	CGB5	3872.00	1.24	5.41
50021.00	I18	M-011243-	chorionic somatoma	1442.00	CSH1	2278.00	1.32	5.33
50021.00	I19	M-013699-	chorionic gonadotro	94115.00	CGB8	2884.00	1.73	4.92
50021.00	I20	M-017208-	chondrosarcoma ass	158511.00	CSAG1	2368.00	5.79	0.86
50021.00	I21	M-008529-	chromodomain helic	1105.00	CHD1	5060.00	16.52	**9.87**
50021.00	I23	M-031153-	chromodomain helic	80205.00	CHD9	4368.00	7.69	1.04
50021.00	J02	M-009777-	enolase 2 (gamma, n	2026.00	ENO2	5020.00	17.49	**10.84**
50021.00	J04	M-010508-	cortactin	2017.00	CTTN	4708.00	18.18	**11.53**
50021.00	J05	M-011990-	capping protein (acti	832.00	CAPZB	3346.00	8.34	1.69
50021.00	J06	M-011025-	emerin (Emery-Dreif	2010.00	EMD	3065.00	4.86	1.79
50021.00	J07	M-019890-	CART prepropeptide	9607.00	CARTPT	3765.00	9.35	2.70
50021.00	J08	M-016006-	ELAV (embryonic let	1996.00	ELAVL4	2715.00	10.76	4.11
50021.00	J09	M-012413-	CASP8 associated pr	9994.00	CASP8AP2	807.00	7.56	0.91

50021.00	J10	M-019534-	eukaryotic translatio	8661.00	EIF3S10	1156.00	5.80	0.85
50021.00	J11	M-013008-	ELKS/RAB6-interacti	26059.00	ERC2	4006.00	17.30	**10.65**
50021.00	J12	M-020180-	eukaryotic translatio	1967.00	EIF2B1	3989.00	25.72	**19.07**
50021.00	J13	M-006131-	cation channel, sper	117144.00	CATSPER1	3788.00	10.48	3.83
50021.00	J14	M-009822-	enoyl-Coenzyme A, h	1962.00	EHHADH	4154.00	5.22	1.43
50021.00	J15	M-010958-	caveolin 2	858.00	CAV2	2501.00	14.35	7.70
50021.00	J16	M-007245-	eukaryotic translatio	1938.00	EEF2	4278.00	9.21	2.56
50021.00	J17	M-011229-	caveolin 3	859.00	CAV3	2737.00	3.98	2.67
50021.00	J18	M-017199-	eukaryotic translatio	1915.00	EEF1A1	2673.00	3.67	2.98
50021.00	J19	M-019985-	CCAAT/enhancer bin	10153.00	CEBPZ	2961.00	19.59	**12.94**
50021.00	J20	M-011259-	extracellular matrix p	1842.00	ECM2	5779.00	28.62	**21.97**
50021.00	J21	M-011825-	cerebellin 1 precurso	869.00	CBLN1	5040.00	19.44	**12.79**
50021.00	J23	M-004513-	carbonyl reductase 1	873.00	CBR1	3962.00	6.97	0.32
50021.00	K02	M-013585-	cripto, FRL-1, cryptic	55997.00	CFC1	3163.00	6.42	0.23
50021.00	K04	M-012876-	crystallin, gamma S	1427.00	CRYGS	4082.00	10.83	4.18
50021.00	K05	M-019067-	cysteine-rich hydrop	26511.00	CHIC2	4744.00	10.12	3.47
50021.00	K06	M-012336-	crystallin, gamma D	1421.00	CRYGD	3969.00	12.88	6.23
50021.00	K07	M-006133-	CHRNA7 (cholinergic	89832.00	CHRFAM7	3835.00	12.15	5.50
50021.00	K08	M-013470-	crystallin, gamma A	1418.00	CRYGA	4317.00	17.49	**10.84**
50021.00	K09	M-006145-	cholinergic receptor,	1143.00	CHRNB4	3317.00	3.95	2.70
50021.00	K10	M-011019-	crystallin, beta B2	1415.00	CRYBB2	3592.00	23.89	**17.24**
50021.00	K11	M-006148-	cholinergic receptor,	1146.00	CHRNG	3715.00	12.60	5.95
50021.00	K12	M-011629-	crystallin, beta B1	1414.00	CRYBB1	2497.00	2.12	4.53
50021.00	K13	M-010926-	lysosomal trafficking	1130.00	LYST	3882.00	8.19	1.54
50021.00	K14	M-011628-	crystallin, beta A4	1413.00	CRYBA4	3267.00	1.96	4.69
50021.00	K15	M-019857-	cytosolic iron-sulfur	9391.00	CIAO1	4340.00	2.72	3.93
50021.00	K16	M-021059-	cytotoxic and regula	56253.00	CRTAM	3474.00	5.04	1.61
50021.00	K17	M-017367-	NLR family, pyrin do	114548.00	NLRP3	3924.00	4.28	2.37
50021.00	K18	M-011949-	cofactor required fo	9442.00	CRSP8	3672.00	4.93	1.72
50021.00	K19	M-015423-	radical S-adenosyl m	91543.00	RSAD2	3054.00	3.83	2.82
50021.00	K20	M-013220-	cofactor required fo	9439.00	CRSP3	4963.00	3.26	3.39
50021.00	K21	M-015011-	cirrhosis, autosomal	84916.00	CIRH1A	3645.00	1.07	5.58
50021.00	K23	M-017381-	cytokine inducible S	1154.00	CISH	3906.00	1.25	5.40
50021.00	L02	M-012093-	Epstein-Barr virus in	10148.00	EBI3	2147.00	2.38	4.27
50021.00	L04	M-006313-	ELL associated facto	55840.00	EAF2	4554.00	9.46	2.81
50021.00	L05	M-008597-	carbonyl reductase 3	874.00	CBR3	3697.00	8.57	1.92
50021.00	L06	M-003264-	E2F transcription fac	1876.00	E2F6	3911.00	7.11	0.46
50021.00	L07	M-009716-	chromobox homolog	10951.00	CBX1	2384.00	3.65	3.00
50021.00	L08	M-003263-	E2F transcription fac	1875.00	E2F5	3525.00	18.61	**11.96**
50021.00	L09	M-003825-	KRIT1, ankyrin repea	889.00	KRIT1	3206.00	6.58	0.07
50021.00	L10	M-003262-	E2F transcription fac	1874.00	E2F4	2582.00	3.25	3.40
50021.00	L11	M-003204-	cyclin A1	8900.00	CCNA1	3576.00	11.77	5.12
50021.00	L12	M-003261-	E2F transcription fac	1871.00	E2F3	1805.00	6.15	0.50
50021.00	L13	M-003205-	cyclin A2	890.00	CCNA2	1511.00	7.88	1.23
50021.00	L14	M-003260-	E2F transcription fac	1870.00	E2F2	4091.00	10.07	3.42
50021.00	L15	M-003206-	cyclin B1	891.00	CCNB1	1795.00	8.97	2.32
50021.00	L16	M-009707-	ubiquitin-conjugatin	27338.00	UBE2S	4884.00	21.11	**14.46**

50021.00	L17	M-003207-	cyclin B2	9133.00	CCNB2	2164.00	3.65	3.00
50021.00	L18	M-003652-	dysferlin, limb girdle	8291.00	DYSF	2867.00	5.34	1.31
50021.00	L19	M-003208-	cyclin B3	85417.00	CCNB3	3310.00	3.57	3.09
50021.00	L20	M-017455-	dystrobrevin binding	84062.00	DTNBP1	3778.00	10.77	4.12
50021.00	L21	M-003209-	cyclin C	892.00	CCNC	3541.00	6.21	0.44
50021.00	L23	M-003210-	cyclin D1	595.00	CCND1	1504.00	2.39	4.26
50021.00	M02	M-020109-	chromosome 1 open	10485.00	C1orf61	1868.00	3.32	3.33
50021.00	M04	M-017786-	cytokine receptor-lik	51379.00	CRLF3	2179.00	34.70	**28.05**
50021.00	M05	M-023462-	cytoplasmic linker as	23122.00	CLASP2	4437.00	28.94	**22.29**
50021.00	M06	M-007863-	cytokine receptor-lik	9244.00	CRLF1	3612.00	13.48	6.83
50021.00	M07	M-006157-	chloride channel Kb	1188.00	CLCNKB	4353.00	21.14	**14.49**
50021.00	M08	M-017495-	cysteine-rich secreto	167.00	CRISP1	3704.00	10.37	3.72
50021.00	M09	M-021368-	C-type lectin domain	51267.00	CLEC1A	2219.00	8.65	2.00
50021.00	M10	M-013998-	cell cycle progressio	9236.00	CCPG1	2410.00	6.02	0.63
50021.00	M11	M-023690-	pleckstrin homology	64857.00	PLEKHG2	3226.00	11.47	4.82
50021.00	M12	M-010558-	transforming growth	9238.00	TBRG4	2668.00	9.48	2.83
50021.00	M13	M-011805-	chloride intracellular	9022.00	CLIC3	2655.00	3.65	3.00
50021.00	M14	M-015972-	coproporphyrinogen	1371.00	CPOX	3175.00	11.18	4.53
50021.00	M15	M-013944-	CAP-GLY domain co	25999.00	CLIP3	2658.00	11.78	5.13
50021.00	M16	M-013155-	copine V	57699.00	CPNE5	3990.00	17.64	**10.99**
50021.00	M17	M-019282-	ceroid-lipofuscinosis	1201.00	CLN3	3698.00	13.66	7.01
50021.00	M18	M-023553-	carboxypeptidase N,	1370.00	CPN2	4385.00	12.91	6.26
50021.00	M19	M-020163-	ceroid-lipofuscinosis	1203.00	CLN5	4082.00	22.17	**15.52**
50021.00	M20	M-012088-	COX17 cytochrome c	10063.00	COX17	3496.00	10.70	4.05
50021.00	M21	M-020875-	ceroid-lipofuscinosis	54982.00	CLN6	5001.00	11.02	4.37
50021.00	M23	M-013304-	ceroid-lipofuscinosis	2055.00	CLN8	4923.00	17.55	**10.90**
50021.00	N02	M-021367-	dystrobrevin, beta	1838.00	DTNB	2946.00	3.39	3.26
50021.00	N04	M-012303-	destrin (actin depoly	11034.00	DSTN	4730.00	11.08	4.43
50021.00	N05	M-003211-	cyclin D2	894.00	CCND2	3542.00	13.69	7.04
50021.00	N06	M-012493-	dentin sialophospho	1834.00	DSPP	2742.00	12.00	5.35
50021.00	N07	M-003212-	cyclin D3	896.00	CCND3	3263.00	16.89	**10.24**
50021.00	N08	M-004268-	Down syndrome crit	1827.00	DSCR1	2688.00	21.65	**15.00**
50021.00	N09	M-012418-	cyclin D-type binding	23582.00	CCNDBP1	2385.00	12.50	5.85
50021.00	N10	M-020215-	UTP20, small subuni	27340.00	UTP20	2960.00	16.15	9.50
50021.00	N11	M-003213-	cyclin E1	898.00	CCNE1	1795.00	9.14	2.49
50021.00	N12	M-016718-	developmentally reg	129831.00	DRB1	2600.00	12.50	5.85
50021.00	N13	M-003214-	cyclin E2	9134.00	CCNE2	3401.00	12.20	5.55
50021.00	N14	M-008974-	DR1-associated prot	10589.00	DRAP1	2502.00	8.27	1.62
50021.00	N15	M-003215-	cyclin F	899.00	CCNF	3251.00	26.36	**19.71**
50021.00	N16	M-012695-	dedicator of cytokin	1795.00	DOCK3	3366.00	7.07	0.42
50021.00	N17	M-003216-	cyclin G1	900.00	CCNG1	3735.00	9.72	3.07
50021.00	N18	M-015792-	CDK2-associated pro	10263.00	CDK2AP2	2890.00	7.37	0.72
50021.00	N19	M-003217-	cyclin G2	901.00	CCNG2	4435.00	14.48	7.83
50021.00	N20	M-019458-	filamin A interacting	11259.00	FILIP1L	3722.00	6.66	0.01
50021.00	N21	M-003218-	cyclin H	902.00	CCNH	3264.00	14.58	7.93
50021.00	N23	M-003219-	cyclin I	10983.00	CCNI	3870.00	10.00	3.35
50021.00	O02	M-005814-	COP9 constitutive ph	10987.00	COPS5	2296.00	4.01	2.64

50021.00	O04	M-011494-	COP9 constitutive ph	8533.00	COPS3	2182.00	3.53	3.12
50021.00	O05	M-010594-	cleft lip and palate a:	1209.00	CLPTM1	3869.00	10.24	3.59
50021.00	O06	M-013197-	collagen-like tail sub	8292.00	COLQ	3276.00	6.56	0.09
50021.00	O07	M-020393-	calsyntenin 1	22883.00	CLSTN1	2076.00	5.92	0.73
50021.00	O08	M-013006-	collagen, type VIII, al	1295.00	COL8A1	2802.00	11.92	5.27
50021.00	O09	M-019513-	clusterin	1191.00	CLU	2276.00	24.96	**18.31**
50021.00	O10	M-013073-	collagen, type II, alpl	1280.00	COL2A1	3931.00	19.59	**12.94**
50021.00	O11	M-006158-	cyclic nucleotide gat	1259.00	CNGA1	2663.00	13.78	7.13
50021.00	O12	M-011615-	collagen, type XV, al	1306.00	COL15A1	2259.00	6.20	0.45
50021.00	O13	M-006161-	cyclic nucleotide gat	54714.00	CNGB3	4015.00	24.09	**17.44**
50021.00	O14	M-011845-	coagulation factor C	1690.00	COCH	2948.00	18.08	**11.43**
50021.00	O15	M-020830-	cyclin M1	26507.00	CNNM1	1706.00	5.63	1.02
50021.00	O16	M-032257-	hypothetical LOC200	200025.00	LOC20002	3037.00	13.17	6.52
50021.00	O17	M-017176-	cyclin M2	54805.00	CNNM2	3230.00	4.40	2.25
50021.00	O18	M-009725-	contactin associated	8506.00	CNTNAP1	3842.00	12.65	6.00
50021.00	O19	M-019438-	cyclin M3	26505.00	CNNM3	4390.00	7.49	0.84
50021.00	O20	M-012529-	contactin 6	27255.00	CNTN6	3170.00	9.37	2.72
50021.00	O21	M-016411-	CCR4-NOT transcript	246175.00	CNOT6L	3456.00	7.81	1.16
50021.00	O23	M-007858-	contactin 5	53942.00	CNTN5	1500.00	10.87	4.22
50021.00	P02	M-015171-	deoxynucleotidyltra	116092.00	DNTTIP1	2461.00	6.54	0.11
50021.00	P04	M-019392-	DnaJ (Hsp40) homol	55466.00	DNAJA4	2873.00	3.79	2.86
50021.00	P05	M-029590-	cyclin K	8812.00	CCNK	1584.00	2.27	4.38
50021.00	P06	M-012104-	DnaJ (Hsp40) homol	10294.00	DNAJA2	1791.00	3.41	3.24
50021.00	P07	M-008682-	cyclin L1	57018.00	CCNL1	1819.00	9.24	2.59
50021.00	P08	M-016792-	DnaJ (Hsp40) homol	85406.00	DNAJC14	3452.00	5.50	1.15
50021.00	P09	M-003220-	cyclin T1	904.00	CCNT1	2625.00	9.49	2.84
50021.00	P10	M-023757-	dystrophia myotonic	1762.00	DMWD	2349.00	4.73	1.92
50021.00	P11	M-003221-	cyclin T2	905.00	CCNT2	1781.00	6.40	0.25
50021.00	P12	M-008862-	discs, large (Drosoph	9229.00	DLGAP1	928.00	2.05	4.60
50021.00	P13	M-020147-	chaperonin containi	10575.00	CCT4	1626.00	3.01	3.64
50021.00	P14	M-016846-	discs, large homolog	9787.00	DLG7	2465.00	11.60	4.95
50021.00	P15	M-020161-	chaperonin containi	10693.00	CCT6B	2171.00	11.75	5.10
50021.00	P16	M-020066-	deleted in lymphocy	8847.00	DLEU2	3093.00	4.72	1.93
50021.00	P17	M-016196-	CD164 molecule, sial	8763.00	CD164	2010.00	4.88	1.77
50021.00	P18	M-011983-	deleted in lung and e	9940.00	DLEC1	2059.00	5.63	1.02
50021.00	P19	M-012629-	CD1a molecule	909.00	CD1A	2780.00	17.16	**10.51**
50021.00	P20	M-015443-	hypothetical protein	55355.00	DKFZp762E	1914.00	6.11	0.54
50021.00	P21	M-013613-	chorionic gonadotro	114335.00	CGB1	1452.00	1.65	5.00
50021.00	P23	M-013614-	chorionic gonadotro	114336.00	CGB2	2762.00	2.10	4.55
				mdn		3209.50	6.65	3.25
				3MAD				9.74
				MADc				4.80
		%hits	4.38					
50021.00	C22					3270.00	24.10	
50021.00	D22					4484.00	26.47	
50021.00	E22					4643.00	39.87	
50021.00	F22					3705.00	32.42	

		mn	4025.50	30.71
		sd	649.37	7.03
50021.00	G22		1603.00	4.99
50021.00	H22		1578.00	1.65
50021.00	I22		1552.00	0.90
50021.00	J22		1838.00	8.65
		mn	1642.75	4.05
		sd	131.82	3.55
		3psSD		21.10
		3ngSD		10.64
		SumSD		31.74
		DiffMn		26.67
		SmovrDiff		1.19
		1minus		-0.19

rZ	Cell Coun	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	
-0.24	2595.00	3.58	0.63	-0.20	1639.00	4.51	1.84	1.01	
-0.33	2575.00	3.84	0.37	-0.11	2126.00	6.35	3.68	2.02	
-0.38	2227.00	2.47	1.74	-0.55	1958.00	1.99	0.68	-0.38	
0.63	2654.00	8.14	3.93	1.23	1909.00	4.35	1.68	0.92	
-0.65	2110.00	3.60	0.61	-0.19	3147.00	2.70	0.03	0.02	
0.17	1926.00	6.33	2.12	0.67	2462.00	3.82	1.15	0.63	
-1.13	989.00	1.82	2.39	-0.75	1642.00	2.80	0.13	0.07	
-0.68	2051.00	6.68	2.47	0.77	1182.00	1.95	0.72	-0.40	
-1.12	1411.00	5.24	1.03	0.32	1758.00	2.10	0.57	-0.31	
-0.92	940.00	3.19	1.02	-0.32	612.00	3.27	0.60	0.33	
-0.84	661.00	2.12	2.09	-0.66	477.00	3.56	0.89	0.49	
0.68	1841.00	12.93	8.72	2.73	2609.00	10.73	8.06	4.44	y
-0.48	1772.00	1.19	3.02	-0.95	1595.00	1.94	0.73	-0.40	
0.98	2749.00	9.49	5.28	1.66	2160.00	4.91	2.24	1.23	
0.36	912.00	5.37	1.16	0.36	1154.00	4.59	1.92	1.06	
0.53	1398.00	5.72	1.51	0.47	2332.00	2.44	0.23	-0.13	
-0.64	1555.00	2.96	1.25	-0.39	1936.00	3.51	0.84	0.46	
-0.17	2047.00	2.64	1.57	-0.49	2086.00	1.49	1.18	-0.65	
1.18	1277.00	1.80	2.41	-0.76	2284.00	3.06	0.39	0.22	
0.68	1763.00	5.28	1.07	0.33	1696.00	7.19	4.52	2.49	
0.54	2217.00	6.63	2.42	0.76	1413.00	1.98	0.69	-0.38	
-0.79	1941.00	1.24	2.97	-0.93	1763.00	0.34	2.33	-1.28	
-0.54	3501.00	3.14	1.07	-0.33	2009.00	1.05	1.62	-0.90	
-0.86	2388.00	0.54	3.67	-1.15	2899.00	1.45	1.22	-0.67	
-0.05	2571.00	2.29	1.92	-0.60	3499.00	1.26	1.41	-0.78	
-0.29	1464.00	5.40	1.19	0.37	476.00	3.36	0.69	0.38	
0.17	2143.00	6.44	2.23	0.70	3329.00	2.37	0.30	-0.17	
-0.92	1590.00	1.51	2.70	-0.85	1783.00	1.23	1.44	-0.79	
0.23	1848.00	11.31	7.10	2.22	3026.00	6.81	4.14	2.28	y
-1.07	1011.00	0.20	4.01	-1.26	945.00	3.81	1.14	0.63	
0.00	2687.00	1.64	2.57	-0.81	2251.00	0.67	2.00	-1.11	
0.38	2981.00	4.93	0.72	0.23	1940.00	2.47	0.20	-0.11	
-1.07	1862.00	0.81	3.40	-1.07	2100.00	1.86	0.81	-0.45	
-0.64	1752.00	0.91	3.30	-1.03	1197.00	6.35	3.68	2.02	
1.38	2657.00	4.06	0.15	-0.05	4046.00	4.30	1.63	0.90	
3.34	2405.00	11.10	6.89	2.16	3551.00	13.74	11.07	6.10	y
-1.01	2900.00	1.24	2.97	-0.93	2231.00	2.11	0.56	-0.31	
1.33	2051.00	3.36	0.85	-0.27	1892.00	4.18	1.51	0.83	
1.29	3027.00	2.08	2.13	-0.67	2729.00	4.29	1.62	0.89	
-0.42	2314.00	7.35	3.14	0.98	2828.00	3.25	0.58	0.32	
-0.70	3934.00	2.59	1.62	-0.51	3468.00	0.63	2.04	-1.12	
-0.78	1969.00	0.61	3.60	-1.13	1840.00	1.03	1.64	-0.90	
1.43	3214.00	6.35	2.14	0.67	3814.00	4.27	1.60	0.88	
-0.60	1772.00	3.39	0.82	-0.26	1848.00	0.60	2.07	-1.14	
0.67	2523.00	6.18	1.97	0.62	3185.00	2.35	0.32	-0.18	
-0.47	2869.00	2.02	2.19	-0.69	3719.00	0.94	1.73	-0.95	

-0.64	1828.00	1.04	3.17	-0.99	2783.00	0.32	2.35	-1.29
0.12	1910.00	3.19	1.02	-0.32	2305.00	0.43	2.24	-1.23
-0.63	1299.00	3.08	1.13	-0.35	1292.00	0.77	1.90	-1.05
0.40	1788.00	5.20	0.99	0.31	1321.00	1.51	1.16	-0.64
-0.59	2167.00	3.37	0.84	-0.26	1771.00	1.30	1.37	-0.76
0.64	2293.00	7.98	3.77	1.18	3390.00	2.27	0.40	-0.22
-0.39	1955.00	4.04	0.17	-0.05	2118.00	0.99	1.68	-0.93
-0.61	1583.00	2.02	2.19	-0.69	1893.00	1.16	1.51	-0.83
-0.92	1628.00	3.26	0.95	-0.30	1812.00	0.33	2.34	-1.29
0.38	1401.00	6.21	2.00	0.63	2872.00	5.71	3.04	1.67
-0.57	1115.00	3.68	0.53	-0.17	1769.00	1.30	1.37	-0.76
0.34	2490.00	6.14	1.93	0.61	3098.00	5.36	2.69	1.48
-0.86	1110.00	3.78	0.43	-0.13	1627.00	1.41	1.26	-0.69
-0.78	2649.00	6.12	1.91	0.60	2023.00	1.73	0.94	-0.52
-1.25	3416.00	1.55	2.66	-0.83	3817.00	1.28	1.39	-0.77
-1.11	4985.00	2.79	1.42	-0.45	3776.00	0.93	1.74	-0.96
-1.26	2455.00	1.34	2.87	-0.90	2791.00	0.43	2.24	-1.24
-0.89	2661.00	1.62	2.59	-0.81	1818.00	0.55	2.12	-1.17
-0.41	2489.00	4.22	0.01	0.00	2577.00	2.10	0.57	-0.32
-1.14	1587.00	0.38	3.83	-1.20	2607.00	3.26	0.59	0.32
-0.80	2699.00	4.89	0.68	0.21	2899.00	2.90	0.23	0.12
-1.17	1982.00	0.15	4.06	-1.27	1616.00	0.31	2.36	-1.30
-0.88	2279.00	3.64	0.57	-0.18	1966.00	2.44	0.23	-0.13
-0.58	2815.00	2.06	2.15	-0.67	2631.00	2.51	0.16	-0.09
-0.29	3096.00	3.00	1.21	-0.38	2894.00	0.97	1.70	-0.94
-0.73	1901.00	1.63	2.58	-0.81	1954.00	0.77	1.90	-1.05
-0.79	997.00	3.11	1.10	-0.35	1647.00	1.15	1.52	-0.84
-0.57	3593.00	2.64	1.57	-0.49	5438.00	2.19	0.48	-0.27
-0.76	3075.00	3.38	0.83	-0.26	5604.00	4.46	1.79	0.98
-0.44	1898.00	4.79	0.58	0.18	3171.00	3.50	0.83	0.46
-0.64	2333.00	1.03	3.18	-1.00	3436.00	3.58	0.91	0.50
-0.91	2367.00	0.21	4.00	-1.25	2948.00	2.31	0.36	-0.20
-0.74	2910.00	2.06	2.15	-0.67	3524.00	1.33	1.34	-0.74
-0.82	2558.00	0.82	3.39	-1.06	2050.00	3.95	1.28	0.70
-0.34	3986.00	1.35	2.86	-0.90	3165.00	0.60	2.07	-1.14
0.36	3173.00	2.74	1.47	-0.46	3187.00	0.85	1.82	-1.01
0.50	2703.00	7.14	2.93	0.92	3424.00	3.68	1.01	0.55
0.24	3271.00	0.92	3.29	-1.03	5116.00	2.37	0.30	-0.17
0.23	2704.00	1.70	2.51	-0.79	3963.00	1.54	1.13	-0.62
1.82	1783.00	3.14	1.07	-0.34	3577.00	3.16	0.49	0.27
0.19	2837.00	2.26	1.95	-0.61	4630.00	0.60	2.07	-1.14
0.44	2662.00	1.01	3.20	-1.00	3082.00	0.65	2.02	-1.11
0.09	2371.00	2.36	1.85	-0.58	2525.00	2.38	0.29	-0.16
-0.50	1837.00	0.76	3.45	-1.08	2002.00	1.55	1.12	-0.62
0.32	2129.00	1.97	2.24	-0.70	3022.00	2.12	0.55	-0.31
0.90	1982.00	6.41	2.20	0.69	2735.00	3.58	0.91	0.50
0.79	494.00	1.01	3.20	-1.00	1100.00	1.18	1.49	-0.82

-0.21	1625.00	1.05	3.16	-0.99	2181.00	0.50	2.17	-1.19	
0.04	2290.00	3.71	0.50	-0.16	3014.00	1.33	1.34	-0.74	
2.33	3564.00	11.11	6.90	2.16	4054.00	3.63	0.96	0.52	y
-0.13	2943.00	2.11	2.10	-0.66	4376.00	1.94	0.73	-0.40	
0.68	3958.00	3.41	0.80	-0.25	4057.00	1.60	1.07	-0.59	
-0.19	1940.00	2.42	1.79	-0.56	2488.00	0.72	1.95	-1.07	
-0.80	3270.00	1.62	2.59	-0.81	2610.00	1.07	1.60	-0.88	
1.11	2424.00	3.42	0.79	-0.25	4031.00	1.94	0.74	-0.41	
-0.89	2964.00	2.73	1.48	-0.46	2841.00	0.99	1.68	-0.93	
0.10	3956.00	2.63	1.58	-0.50	4005.00	2.75	0.08	0.04	
0.20	3303.00	1.60	2.61	-0.82	3796.00	2.71	0.04	0.02	
-0.66	1101.00	0.36	3.85	-1.21	1557.00	0.06	2.61	-1.44	
-0.02	2266.00	3.05	1.17	-0.37	2708.00	1.26	1.41	-0.78	
-1.10	1894.00	0.69	3.52	-1.10	2171.00	0.92	1.75	-0.96	
-0.42	1476.00	1.15	3.06	-0.96	2783.00	2.12	0.55	-0.30	
0.73	3681.00	6.25	2.04	0.64	3390.00	5.49	2.82	1.55	
-1.15	2153.00	0.65	3.56	-1.12	2041.00	1.13	1.54	-0.85	
1.17	2243.00	13.60	9.39	2.94	1897.00	8.07	5.40	2.97	y
-0.59	2037.00	5.55	1.34	0.42	2735.00	3.84	1.17	0.64	
0.75	2864.00	9.36	5.15	1.61	3565.00	10.01	7.34	4.04	
-0.66	1808.00	2.27	1.94	-0.61	3011.00	0.93	1.74	-0.96	
1.24	1339.00	4.41	0.20	0.06	1838.00	5.06	2.39	1.31	
-0.65	2488.00	1.85	2.36	-0.74	3369.00	2.73	0.06	0.03	
-0.42	3588.00	1.90	2.31	-0.73	4392.00	2.73	0.06	0.03	
0.85	2941.00	5.47	1.26	0.40	4686.00	15.83	13.16	7.25	
-0.76	1516.00	1.98	2.23	-0.70	2858.00	4.69	2.02	1.11	
-0.71	2594.00	3.89	0.32	-0.10	2077.00	4.19	1.52	0.83	
0.08	3239.00	16.21	12.00	3.76	3424.00	0.70	1.97	-1.09	
1.10	3425.00	3.68	0.53	-0.17	3270.00	1.44	1.23	-0.68	
-0.10	1810.00	3.81	0.40	-0.12	1642.00	3.05	0.38	0.20	
-0.37	2162.00	1.20	3.01	-0.94	3257.00	2.95	0.28	0.15	
-0.31	2539.00	0.47	3.74	-1.17	3456.00	0.75	1.92	-1.06	
-0.77	1899.00	1.32	2.89	-0.91	2065.00	1.11	1.56	-0.86	
-1.03	982.00	1.22	2.99	-0.94	1836.00	0.93	1.74	-0.96	
1.03	1158.00	3.97	0.24	-0.07	1891.00	7.24	4.57	2.52	
1.44	2304.00	5.03	0.82	0.26	2977.00	3.33	0.66	0.36	
-0.28	1744.00	1.89	2.32	-0.73	1579.00	2.53	0.14	-0.08	
0.15	1777.00	5.01	0.80	0.25	2221.00	2.48	0.19	-0.11	
2.71	1694.00	7.44	3.23	1.01	2649.00	6.46	3.79	2.08	x
1.40	2066.00	8.13	3.92	1.23	2928.00	5.26	2.59	1.42	
1.03	2593.00	4.94	0.73	0.23	4188.00	4.75	2.08	1.14	
-0.65	1785.00	2.24	1.97	-0.62	2358.00	2.71	0.04	0.02	
0.59	2800.00	4.82	0.61	0.19	2747.00	4.91	2.24	1.23	
0.03	2466.00	2.92	1.29	-0.40	3525.00	2.35	0.32	-0.18	
0.21	2427.00	3.26	0.96	-0.30	2714.00	2.28	0.39	-0.21	
-0.23	2760.00	3.66	0.55	-0.17	2914.00	2.30	0.37	-0.21	
2.55	3761.00	8.61	4.40	1.38	3328.00	7.69	5.02	2.76	y

0.50	2677.00	5.98	1.77	0.55	3014.00	1.53	1.14	-0.63	
2.46	4125.00	3.64	0.57	-0.18	3752.00	2.91	0.24	0.13	
4.59	3066.00	17.87	13.66	4.28	2942.00	9.31	6.64	3.66	y
0.58	1198.00	3.34	0.87	-0.27	1069.00	3.46	0.79	0.43	
0.24	774.00	4.39	0.18	0.06	694.00	3.03	0.36	0.19	
1.16	1667.00	8.04	3.83	1.20	1219.00	2.71	0.04	0.02	
0.23	2106.00	14.34	10.13	3.17	2158.00	4.91	2.24	1.23	
0.35	1929.00	8.76	4.55	1.43	3535.00	6.17	3.50	1.92	
0.67	1778.00	3.04	1.17	-0.37	1940.00	2.11	0.56	-0.31	
-0.74	1763.00	1.53	2.68	-0.84	1781.00	0.84	1.83	-1.01	
-0.63	1787.00	7.11	2.90	0.91	2074.00	1.74	0.93	-0.52	
-0.12	1693.00	6.02	1.81	0.57	1892.00	3.44	0.77	0.42	
-0.10	2663.00	8.37	4.16	1.30	2625.00	3.81	1.14	0.63	
-0.03	1536.00	10.16	5.95	1.86	2212.00	2.03	0.64	-0.35	
-1.07	2167.00	5.49	1.28	0.40	2086.00	2.25	0.42	-0.23	
-0.76	2401.00	2.46	1.75	-0.55	2890.00	1.28	1.39	-0.77	
-1.06	1924.00	3.01	1.20	-0.37	2622.00	2.94	0.27	0.14	
0.64	2186.00	5.35	1.14	0.36	2060.00	1.70	0.97	-0.54	
-0.54	3119.00	8.72	4.51	1.41	3729.00	1.80	0.87	-0.48	
-0.40	2004.00	11.53	7.32	2.29	2366.00	2.79	0.12	0.06	
-1.21	2335.00	0.43	3.78	-1.19	2038.00	0.69	1.98	-1.09	
4.17	5068.00	16.58	12.37	3.87	5400.00	13.67	11.00	6.05	y
-0.61	1885.00	2.60	1.61	-0.50	2742.00	2.41	0.26	-0.15	
-0.39	2171.00	2.99	1.22	-0.38	2601.00	3.23	0.56	0.31	
-0.54	974.00	1.85	2.36	-0.74	1669.00	2.58	0.09	-0.05	
-0.10	2377.00	1.68	2.53	-0.79	2828.00	4.77	2.10	1.16	
-0.69	2304.00	3.04	1.17	-0.37	3369.00	1.81	0.86	-0.48	
0.47	2143.00	2.89	1.32	-0.41	2809.00	3.99	1.32	0.72	
-0.80	1601.00	2.31	1.90	-0.60	1284.00	0.47	2.20	-1.21	
-0.31	1972.00	3.50	0.71	-0.22	1811.00	2.60	0.07	-0.04	
0.15	2375.00	14.27	10.06	3.15	3627.00	12.21	9.54	5.25	y
-0.41	2078.00	3.90	0.31	-0.10	2339.00	9.06	6.39	3.52	
-1.17	2747.00	1.27	2.94	-0.92	4041.00	1.41	1.26	-0.70	
0.09	3879.00	7.40	3.19	1.00	4845.00	7.00	4.33	2.38	
-1.13	2435.00	4.44	0.23	0.07	3919.00	2.09	0.58	-0.32	
-1.11	2294.00	7.59	3.38	1.06	2027.00	2.81	0.14	0.08	
-1.02	2479.00	2.34	1.87	-0.59	3658.00	1.34	1.33	-0.73	
-0.18	2568.00	4.67	0.46	0.14	2682.00	6.38	3.71	2.04	
2.05	3603.00	18.29	14.08	4.41	4917.00	20.77	18.10	9.96	y
0.22	1963.00	6.72	2.51	0.79	2800.00	5.54	2.87	1.58	
2.26	4560.00	18.40	14.19	4.45	3687.00	2.96	0.29	0.16	y
2.40	4379.00	11.94	7.73	2.42	2878.00	3.93	1.26	0.69	y
0.35	2866.00	2.90	1.31	-0.41	2013.00	1.29	1.38	-0.76	
-0.37	1847.00	1.35	2.86	-0.90	2333.00	1.54	1.13	-0.62	
0.56	3534.00	4.05	0.16	-0.05	2562.00	1.91	0.76	-0.42	
0.85	1391.00	2.08	2.13	-0.67	1670.00	1.92	0.75	-0.42	
0.19	832.00	4.33	0.12	0.04	872.00	3.56	0.89	0.49	

-0.18	645.00	5.27	1.06	0.33	797.00	1.88	0.79	-0.44	
2.22	2961.00	7.70	3.49	1.09	3297.00	3.49	0.82	0.45	
3.97	2661.00	18.79	14.58	4.57	2498.00	11.01	8.34	4.59	y
0.80	3448.00	5.42	1.21	0.38	2688.00	3.13	0.46	0.25	
-0.30	2316.00	5.10	0.89	0.28	2782.00	1.33	1.34	-0.74	
1.60	1855.00	6.79	2.58	0.81	998.00	0.80	1.87	-1.03	
0.53	2902.00	4.69	0.48	0.15	2540.00	1.93	0.74	-0.41	
-0.56	2151.00	3.11	1.10	-0.34	1996.00	1.50	1.17	-0.64	
-0.62	1313.00	1.83	2.38	-0.75	1727.00	3.42	0.75	0.41	
2.69	2287.00	13.56	9.35	2.93	2413.00	9.66	6.99	3.85	y
4.57	4045.00	12.44	8.23	2.58	4225.00	10.08	7.41	4.08	y
2.66	3464.00	3.98	0.23	-0.07	3817.00	2.65	0.02	-0.02	
0.07	2731.00	1.35	2.86	-0.90	2955.00	6.57	3.90	2.14	
-0.05	2820.00	3.48	0.73	-0.23	3523.00	1.93	0.74	-0.41	
0.87	2679.00	5.08	0.87	0.27	3783.00	1.27	1.40	-0.77	
0.72	2815.00	1.46	2.75	-0.86	2329.00	0.90	1.77	-0.98	
1.30	3065.00	5.64	1.43	0.45	2678.00	2.20	0.47	-0.26	
1.14	2378.00	5.64	1.43	0.45	2647.00	2.80	0.13	0.07	
2.26	2325.00	3.91	0.30	-0.09	2304.00	3.82	1.15	0.63	
-0.56	2275.00	4.88	0.67	0.21	3142.00	2.32	0.35	-0.19	
3.59	3150.00	18.89	14.68	4.60	3008.00	8.41	5.74	3.16	y
1.24	2358.00	2.16	2.05	-0.64	2731.00	2.27	0.40	-0.22	
-0.94	1732.00	5.25	1.04	0.33	2164.00	2.17	0.50	-0.28	
0.32	2983.00	6.34	2.13	0.67	3076.00	2.37	0.30	-0.17	
-0.98	2705.00	2.96	1.25	-0.39	2468.00	1.78	0.89	-0.49	
-0.82	3337.00	4.91	0.70	0.22	3890.00	1.93	0.74	-0.41	
-0.34	2253.00	3.99	0.22	-0.07	3083.00	2.98	0.31	0.17	
-0.49	2474.00	8.21	4.00	1.25	3067.00	3.72	1.05	0.57	
-0.36	2164.00	2.63	1.58	-0.49	2484.00	2.13	0.54	-0.30	
-0.59	3051.00	10.75	6.54	2.05	3422.00	2.75	0.08	0.04	
-0.71	3573.00	4.70	0.49	0.15	4311.00	4.38	1.71	0.94	
-1.16	2940.00	2.24	1.97	-0.62	2673.00	1.76	0.91	-0.50	
-1.12	2167.00	1.34	2.87	-0.90	2152.00	1.67	1.00	-0.55	
-0.89	2130.00	0.94	3.27	-1.03	1851.00	1.94	0.73	-0.40	
0.59	4614.00	6.09	1.88	0.59	2571.00	1.83	0.84	-0.47	
0.40	3197.00	3.41	0.80	-0.25	2620.00	3.24	0.57	0.31	
0.09	3708.00	3.94	0.27	-0.09	2452.00	1.10	1.57	-0.87	
-0.63	2420.00	2.40	1.81	-0.57	1627.00	1.84	0.83	-0.46	
2.49	4269.00	16.02	11.81	3.70	3423.00	7.54	4.87	2.68	y
-0.01	4232.00	5.98	1.77	0.55	2641.00	2.88	0.21	0.11	
-0.71	2792.00	6.30	2.09	0.66	1859.00	2.42	0.25	-0.14	
1.07	4165.00	6.43	2.22	0.70	2725.00	5.06	2.39	1.32	
-0.10	1321.00	3.33	0.88	-0.28	913.00	1.42	1.25	-0.69	
0.25	1144.00	4.46	0.25	0.08	1145.00	6.29	3.62	1.99	
0.71	4797.00	6.44	2.23	0.70	3700.00	2.86	0.19	0.11	
0.48	2771.00	7.72	3.51	1.10	1733.00	2.71	0.04	0.02	
3.01	3167.00	11.46	7.25	2.27	2936.00	6.81	4.14	2.28	y

-0.62	1721.00	3.02	1.19	-0.37	1584.00	4.92	2.25	1.24	
-0.27	2607.00	8.75	4.54	1.42	1956.00	3.53	0.86	0.47	
-0.64	2326.00	2.36	1.85	-0.58	2381.00	2.06	0.61	-0.34	
0.86	4523.00	10.68	6.47	2.03	3738.00	3.58	0.91	0.50	
-0.09	3322.00	7.22	3.01	0.94	3310.00	3.53	0.86	0.47	
-0.89	1224.00	1.63	2.58	-0.81	1552.00	1.35	1.32	-0.73	
-0.69	1369.00	0.58	3.63	-1.14	1499.00	2.33	0.34	-0.19	
5.84	2195.00	23.87	19.66	6.16	1998.00	18.87	16.20	8.92	y
4.64	3724.00	12.59	8.38	2.63	3129.00	8.92	6.25	3.44	y
1.42	3195.00	9.20	4.99	1.56	2288.00	4.68	2.01	1.10	
3.01	4008.00	9.53	5.32	1.67	2803.00	5.17	2.50	1.38	
0.77	3180.00	3.46	0.75	-0.24	2897.00	0.59	2.08	-1.15	
0.42	3045.00	3.48	0.73	-0.23	1425.00	3.37	0.70	0.38	
-0.13	3167.00	3.88	0.33	-0.10	1606.00	4.17	1.50	0.83	
1.00	3997.00	4.20	0.01	0.00	1709.00	1.81	0.86	-0.47	
0.59	2448.00	6.37	2.16	0.68	1769.00	3.67	1.00	0.55	
-0.62	2088.00	2.20	2.01	-0.63	1808.00	3.65	0.98	0.54	
0.94	3341.00	4.34	0.13	0.04	2385.00	4.91	2.24	1.23	
1.07	3563.00	9.99	5.78	1.81	2525.00	4.67	2.00	1.10	
2.29	3022.00	6.85	2.64	0.83	3018.00	3.11	0.44	0.24	
1.46	3524.00	9.28	5.07	1.59	2585.00	3.87	1.20	0.66	
1.30	3774.00	6.89	2.68	0.84	2563.00	3.16	0.49	0.27	
3.23	2468.00	12.40	8.19	2.57	2326.00	6.23	3.56	1.96	x
0.84	2358.00	9.84	5.63	1.76	2498.00	5.72	3.05	1.68	
0.91	2833.00	6.60	2.39	0.75	2528.00	2.77	0.10	0.05	
2.27	3120.00	11.64	7.43	2.33	3199.00	2.72	0.05	0.03	y
-0.68	1152.00	1.56	2.65	-0.83	2233.00	1.48	1.19	-0.66	
0.92	3809.00	4.20	0.01	0.00	4039.00	4.18	1.51	0.83	
1.47	2790.00	8.57	4.36	1.36	3020.00	4.30	1.63	0.90	
1.11	2792.00	4.66	0.45	0.14	2783.00	1.01	1.66	-0.92	
2.13	3254.00	4.43	0.22	0.07	2896.00	6.22	3.55	1.95	
3.12	2209.00	8.51	4.30	1.35	1412.00	6.87	4.20	2.31	y
1.22	3173.00	10.53	6.32	1.98	1962.00	1.78	0.89	-0.49	
1.98	4535.00	7.19	2.98	0.93	3344.00	1.05	1.62	-0.90	
0.52	1270.00	3.15	1.06	-0.33	1072.00	2.52	0.15	-0.09	
1.22	1408.00	4.62	0.41	0.13	1932.00	1.71	0.96	-0.53	
1.16	3307.00	11.37	7.16	2.24	2769.00	1.95	0.72	-0.40	
0.34	2767.00	5.75	1.54	0.48	1773.00	1.07	1.60	-0.88	
4.10	3143.00	13.01	8.80	2.76	2946.00	3.73	1.06	0.58	y
0.09	2724.00	1.58	2.63	-0.82	1862.00	2.79	0.12	0.07	
0.64	5093.00	7.64	3.43	1.07	3652.00	3.23	0.56	0.31	
0.15	3489.00	10.06	5.85	1.83	3677.00	2.61	0.06	-0.03	
1.63	2519.00	7.90	3.69	1.16	2239.00	1.16	1.51	-0.83	
0.00	2457.00	5.62	1.41	0.44	1866.00	2.63	0.04	-0.03	
1.65	3178.00	10.89	6.68	2.09	3316.00	5.43	2.76	1.52	
0.70	2909.00	11.17	6.96	2.18	3562.00	7.24	4.57	2.52	y
-0.55	1468.00	1.36	2.85	-0.89	1587.00	0.95	1.72	-0.95	

-0.65	2021.00	1.19	3.02	-0.95	1665.00	0.78	1.89	-1.04	
0.75	2969.00	4.75	0.54	0.17	3504.00	2.08	0.59	-0.33	
-0.02	2248.00	2.09	2.12	-0.66	1898.00	0.53	2.14	-1.18	
-0.15	1781.00	6.68	2.47	0.77	1530.00	1.83	0.84	-0.46	
1.10	1660.00	7.77	3.56	1.12	1638.00	1.40	1.27	-0.70	
3.81	1647.00	14.39	**10.18**	3.19	1721.00	5.69	3.02	1.66	x
2.69	3333.00	15.69	**11.48**	3.60	2854.00	5.96	3.29	1.81	y
1.48	1486.00	11.24	**7.03**	2.20	1420.00	2.96	0.29	0.16	
-0.09	1832.00	4.86	0.65	0.20	2110.00	1.75	0.92	-0.51	
3.63	3380.00	25.27	**21.06**	6.60	2904.00	7.09	**4.42**	2.43	y
2.38	1913.00	9.93	5.72	1.79	2442.00	2.87	0.20	0.11	
-0.21	1391.00	6.54	2.33	0.73	1087.00	2.39	0.28	-0.16	
1.36	2078.00	10.92	**6.71**	2.10	1661.00	3.67	1.00	0.55	
-0.47	1819.00	2.69	1.52	-0.48	1621.00	0.86	1.81	-1.00	
1.25	2741.00	6.02	1.81	0.57	3331.00	4.83	2.16	1.19	
0.18	2337.00	2.48	1.73	-0.54	3075.00	2.18	0.49	-0.27	
0.57	3369.00	12.47	**8.26**	2.59	2740.00	2.85	0.18	0.10	
0.24	3630.00	6.78	2.57	0.80	4095.00	1.29	1.38	-0.76	
0.88	952.00	4.52	0.31	0.10	1661.00	1.69	0.98	-0.54	
-0.02	1697.00	6.48	2.27	0.71	1616.00	6.31	3.64	2.00	
-0.60	3051.00	3.41	0.80	-0.25	2021.00	5.10	2.43	1.33	
-0.91	1178.00	2.89	1.32	-0.42	663.00	4.22	1.55	0.85	
-0.68	1467.00	6.27	2.06	0.65	1452.00	2.96	0.29	0.16	
0.54	1863.00	3.11	1.10	-0.34	1248.00	5.85	3.18	1.75	
-0.24	2922.00	6.88	2.67	0.84	2304.00	6.08	3.41	1.87	
0.59	2878.00	3.72	0.49	-0.15	1524.00	4.13	1.46	0.80	
-0.40	3042.00	5.39	1.18	0.37	1481.00	3.71	1.04	0.57	
-0.05	1945.00	6.94	2.73	0.86	994.00	9.05	**6.38**	3.51	
-0.96	901.00	4.77	0.56	0.18	682.00	4.25	1.58	0.87	
-0.76	1376.00	4.51	0.30	0.09	1292.00	6.35	3.68	2.02	
1.03	2295.00	9.02	4.81	1.51	1590.00	5.47	2.80	1.54	
1.06	1978.00	17.54	**13.33**	4.18	2225.00	8.72	**6.05**	3.33	y
-0.40	2747.00	7.97	3.76	1.18	2485.00	3.02	0.35	0.19	
-0.37	1749.00	12.41	**8.20**	2.57	2026.00	7.60	**4.93**	2.71	x
-0.21	1343.00	6.18	1.97	0.62	1158.00	7.17	**4.50**	2.47	
2.19	1934.00	19.49	**15.28**	4.79	1788.00	6.43	**3.76**	2.07	y
-0.11	1117.00	10.92	**6.71**	2.10	1273.00	2.20	0.47	-0.26	
-1.04	1047.00	2.29	1.92	-0.60	1137.00	1.93	0.74	-0.41	
-0.95	1081.00	9.99	5.78	1.81	2711.00	2.25	0.42	-0.23	
	2358.00	4.21	2.16		2493.00	2.67	1.23		
			6.47				3.68		
			3.19				1.82		

2771.00	26.02		2817.00	24.00		
2707.00	23.79		3246.00	22.86	3848.00	15.75
3906.00	27.06					
2645.00	22.31		4419.00	31.52		

3007.25	24.79	3494.00	26.13
601.37	2.15	829.29	4.71
1264.00	4.51	1149.00	2.70
948.00	4.22	1230.00	4.31
1336.00	3.14	1493.00	1.14
1451.00	4.00	1425.00	7.09
1249.75	3.97	1324.25	3.81
215.40	0.59	161.48	2.54
	6.44		14.12
	1.76		7.62
	8.21		21.75
	20.83		22.32
	0.39		0.97
	0.61		0.03

art b,c

art a,c

toxic b,c

art a,c, tox b

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50022.00	A02	M-013209- Wilms tumor upstre	51352.00	WIT1	2936.00	1.74	1.79
50022.00	A04	M-011046- hemoglobin, alpha 2	3040.00	HBA2	3982.00	3.01	0.52
50022.00	A05	M-008632- farnesyl diphosphat	2224.00	FDPS	3022.00	1.26	2.27
50022.00	A06	M-031782- ubiquitin-conjugatin	7325.00	UBE2E2	4683.00	2.54	0.99
50022.00	A07	M-013010- fasciculation and el	9638.00	FEZ1	2723.00	0.59	2.94
50022.00	A08	M-020419- hypoxia-inducible pr	29923.00	HIG2	2650.00	2.34	1.19
50022.00	A09	M-007901- fibrinogen alpha cha	2243.00	FGA	942.00	3.29	0.24
50022.00	A10	M-003899- chromosome 2 open	192137.00	C2orf12	2449.00	1.67	1.86
50022.00	A11	M-007902- fibrinogen beta chai	2244.00	FGB	2422.00	3.43	0.10
50022.00	A12	M-012406- frequently rearrang	23401.00	FRAT2	3512.00	4.30	0.77
50022.00	A13	M-013145- fibroblast growth fa	2257.00	FGF12	1476.00	1.29	2.24
50022.00	A14	M-032286- forkhead box G1C	2292.00	FOXG1C	941.00	1.49	2.04
50022.00	A15	M-006695- fibroblast growth fa	2247.00	FGF2	2260.00	5.80	2.27
50022.00	A16	M-011863- forkhead box E1 (th	2304.00	FOXE1	1922.00	1.51	2.02
50022.00	A17	M-019117- FGFR1 oncogene pa	11116.00	FGFR1OP	2921.00	4.69	1.16
50022.00	A18	M-019348- chromosome 12 ope	51275.00	C12orf47	4024.00	3.65	0.12
50022.00	A19	M-007903- fibrinogen gamma c	2266.00	FGG	3151.00	2.95	0.58
50022.00	A20	M-021179- family with sequenc	54478.00	FAM64A	3495.00	3.18	0.35
50022.00	A21	M-009512- fumarate hydratase	2271.00	FH	2949.00	5.87	2.34
50022.00	A23	M-006905- four and a half LIM	9457.00	FHL5	1787.00	1.29	2.24
50022.00	B02	M-008605- mediator of RNA po	112950.00	MED8	1662.00	4.81	1.28
50022.00	B04	M-013750- Mdm4, transformed	56890.00	MDM1	2841.00	2.92	0.61
50022.00	B05	M-011689- high-mobility group	3148.00	HMGB2	4140.00	5.99	2.46
50022.00	B06	M-016082- MAM domain conta	266727.00	MDGA1	3358.00	1.55	1.98
50022.00	B07	M-019958- high-mobility group	3149.00	HMGB3	3033.00	1.71	1.82
50022.00	B08	M-003506- mediator of DNA da	9656.00	MDC1	2607.00	2.34	1.19
50022.00	B09	M-032258- immunoglobulin hea	3503.00	IGHG4	1330.00	3.99	0.46
50022.00	B10	M-020590- malignant T cell amp	28985.00	MCTS1	1705.00	0.59	2.94
50022.00	B11	M-027162- immunoglobulin hea	3507.00	IGHM	2953.00	4.40	0.87
50022.00	B12	M-020603- mbt domain contain	54799.00	MBTD1	2177.00	1.79	1.74
50022.00	B13	M-032259- immunoglobulin kap	3514.00	IGKC	2586.00	1.20	2.33
50022.00	B14	M-017393- methyl-CpG binding	85509.00	MBD3L1	1747.00	4.01	0.48
50022.00	B15	M-032277- immunoglobulin lam	28831.00	IGLJ3	2559.00	1.33	2.20
50022.00	B16	M-010092- MYC associated fact	4149.00	MAX	2907.00	0.28	3.25
50022.00	B17	M-011876- immunoglobulin lam	3543.00	IGLL1	1610.00	1.43	2.10
50022.00	B18	M-013153- solute carrier family	51151.00	SLC45A2	2007.00	0.85	2.68
50022.00	B19	M-014015- glucose-6-phosphata	57818.00	G6PC2	1877.00	1.60	1.93
50022.00	B20	M-004772- myristoylated alanin	4082.00	MARCKS	2193.00	1.69	1.84
50022.00	B21	M-007929- interleukin 12A (nat	3592.00	IL12A	4809.00	4.66	1.13
50022.00	B23	M-004704- interleukin 13	3596.00	IL13	5039.00	2.38	1.15
50022.00	C02	M-011654- acyl-CoA synthetase	2180.00	ACSL1	3923.00	1.38	2.15
50022.00	C04	M-010965- high-mobility group	27126.00	HMG1L10	4670.00	3.81	0.28
50022.00	C05	M-004427- apoptosis inhibitor	59347.00	FKSG2	3595.00	1.25	2.28
50022.00	C06	M-019647- human immunodefi	3096.00	HIVEP1	3121.00	0.26	3.27
50022.00	C07	M-003892- Friend leukemia viru	2313.00	FLI1	2996.00	2.04	1.49
50022.00	C08	M-011459- histone cluster 1, H4	8362.00	HIST1H4K	3045.00	1.41	2.12

50022.00	C09	M-021085-	transmembrane pro	55076.00	TMEM45A	2630.00	4.75	1.22
50022.00	C10	M-011461-	histone cluster 1, H4	8364.00	HIST1H4C	1299.00	1.85	1.68
50022.00	C11	M-020318-	pleckstrin homology	55200.00	PLEKHG6	2851.00	1.86	1.67
50022.00	C12	M-011463-	histone cluster 1, H4	8366.00	HIST1H4B	2304.00	1.56	1.97
50022.00	C13	M-018145-	transmembrane pro	55219.00	TMEM57	2761.00	3.19	0.34
50022.00	C14	M-011450-	histone cluster 1, H3	8351.00	HIST1H3D	2973.00	1.85	1.68
50022.00	C15	M-020397-	cyclin J	54619.00	CCNJ	3173.00	2.99	0.54
50022.00	C16	M-011481-	HIRA interacting pro	8479.00	HIRIP3	1503.00	6.59	3.06
50022.00	C17	M-020280-	chromosome 1 oper	55765.00	C1orf106	4453.00	7.21	3.68
50022.00	C18	M-005001-	huntingtin interactir	3092.00	HIP1	2458.00	3.54	0.01
50022.00	C19	M-006810-	hypothetical proteir	55277.00	FLJ10986	3435.00	5.76	2.23
50022.00	C20	M-018500-	histidine triad nucle	3094.00	HINT1	4070.00	4.23	0.70
50022.00	C21	M-026895-	FYVE, RhoGEF and P	55785.00	FGD6	2727.00	1.25	2.28
50022.00	C23	M-014393-	SAP30-like	79685.00	SAP30L	2931.00	5.94	2.41
50022.00	D02	M-010183-	monoamine oxidase	4129.00	MAOB	2888.00	3.81	0.28
50022.00	D04	M-008328-	mannosidase, alpha,	4123.00	MAN2C1	4121.00	2.77	0.76
50022.00	D05	M-027180-	integrin-linked kinas	55522.00	ILK-2	4069.00	3.66	0.13
50022.00	D06	M-013417-	mastermind-like 1 (	9794.00	MAML1	2813.00	4.23	0.70
50022.00	D07	M-014334-	leukocyte immunog	79166.00	LILRP2	3198.00	4.07	0.54
50022.00	D08	M-009135-	melanoma antigen f	28986.00	MAGEH1	2465.00	2.56	0.97
50022.00	D09	M-014335-	leukocyte immunog	79168.00	LILRA6	2482.00	2.34	1.19
50022.00	D10	M-006682-	melanoma antigen f	9500.00	MAGED1	2845.00	2.46	1.07
50022.00	D11	M-003976-	insulin-like growth f	10643.00	IGF2BP3	2232.00	2.91	0.62
50022.00	D12	M-017226-	melanoma antigen f	139081.00	MAGEC3	2103.00	4.56	1.03
50022.00	D13	M-009687-	IMP (inosine monop	3614.00	IMPDH1	2355.00	8.03	4.50
50022.00	D14	M-016192-	SMAD family memb	4093.00	SMAD9	1717.00	1.11	2.42
50022.00	D15	M-019614-	interphotoreceptor	3617.00	IMPG1	2071.00	4.35	0.82
50022.00	D16	M-003272-	MAD2 mitotic arrest	10459.00	MAD2L2	2281.00	3.90	0.37
50022.00	D17	M-020890-	interphotoreceptor	50939.00	IMPG2	3605.00	5.30	1.77
50022.00	D18	M-003271-	MAD2 mitotic arrest	4085.00	MAD2L1	1121.00	5.44	1.91
50022.00	D19	M-015214-	inhibitor of growth f	27160.00	INGX	3589.00	5.68	2.15
50022.00	D20	M-006825-	MAD1 mitotic arrest	8379.00	MAD1L1	2520.00	4.17	0.64
50022.00	D21	M-011299-	inositol polyphospha	3631.00	INPP4A	3183.00	7.51	3.98
50022.00	D23	M-020409-	inositol polyphospha	22876.00	INPP5F	2401.00	2.79	0.74
50022.00	E02	M-009852-	3-hydroxyisobutyryl	26275.00	HIBCH	5334.00	0.94	2.59
50022.00	E04	M-020000-	HERV-H LTR-associa	10086.00	HHLA1	2784.00	0.32	3.21
50022.00	E05	M-016207-	gasdermin domain c	79792.00	GSDMDC1	4905.00	0.80	2.73
50022.00	E06	M-021212-	RAB GTPase activati	9910.00	RABGAP1L	3219.00	0.56	2.97
50022.00	E07	M-010289-	acyltransferase like	79888.00	AYTL2	3416.00	1.49	2.04
50022.00	E08	M-007920-	complement factor	3075.00	CFH	3209.00	0.93	2.60
50022.00	E09	M-008447-	microcephaly, prima	79648.00	MCPH1	1771.00	1.13	2.40
50022.00	E10	M-008408-	hairy and enhancer	55502.00	HES6	2903.00	1.38	2.15
50022.00	E11	M-014509-	WD repeat domain	79968.00	WDR76	2655.00	0.87	2.66
50022.00	E12	M-020918-	homocysteine-induc	9709.00	HERPUD1	2132.00	0.28	3.25
50022.00	E13	M-014496-	cyclin N-terminal do	79935.00	CNTD2	2142.00	1.07	2.46
50022.00	E14	M-004106-	NDC80 homolog, kir	10403.00	NDC80	1093.00	1.37	2.16
50022.00	E15	M-014463-	thrombospondin, ty	79875.00	THSD4	2922.00	0.99	2.54

50022.00	E16	M-005100- hematopoietic cell s	10870.00	HCST	3308.00	1.39	2.14
50022.00	E17	M-018626- zinc finger protein 6	79788.00	ZNF665	3384.00	2.54	0.99
50022.00	E18	M-016834- SAP30 binding prote	29115.00	SAP30BP	3083.00	1.56	1.97
50022.00	E19	M-015006- chromosome 9 oper	84904.00	C9orf100	1198.00	1.17	2.36
50022.00	E20	M-016920- LETM1 domain cont	25875.00	LETMD1	4380.00	1.76	1.77
50022.00	E21	M-020676- hypothetical proteir	54848.00	FLJ20184	3450.00	0.61	2.92
50022.00	E23	M-016819- leucine rich repeat c	55631.00	LRRC40	3003.00	1.70	1.83
50022.00	F02	M-012852- mab-21-like 2 (C. ele	10586.00	MAB21L2	3279.00	0.49	3.04
50022.00	F04	M-012125- mab-21-like 1 (C. ele	4081.00	MAB21L1	2552.00	1.72	1.81
50022.00	F05	M-032273- insulin activator fact	3637.00	INSAF	4038.00	3.52	0.01
50022.00	F06	M-012318- leucine-zipper-like tı	8216.00	LZTR1	2399.00	3.04	0.49
50022.00	F07	M-017880- insulin induced gene	3638.00	INSIG1	2829.00	1.98	1.55
50022.00	F08	M-031982- leucine zipper transc	54585.00	LZTFL1	3803.00	1.89	1.64
50022.00	F09	M-021039- insulin induced gene	51141.00	INSIG2	3946.00	6.54	3.01
50022.00	F10	M-011079- lysozyme (renal amy	4069.00	LYZ	1512.00	2.12	1.41
50022.00	F11	M-010584- Fc receptor-like 4	83417.00	FCRL4	2798.00	0.93	2.60
50022.00	F12	M-015814- lymphoblastic leuke	4066.00	LYL1	2178.00	0.60	2.93
50022.00	F13	M-010583- Fc receptor-like 5	83416.00	FCRL5	2317.00	0.95	2.58
50022.00	F14	M-015383- cisplatin resistance-a	51747.00	CROP	1808.00	2.65	0.88
50022.00	F15	M-020007- iroquois homeobox	10265.00	IRX5	3719.00	4.19	0.66
50022.00	F16	M-008637- leukotriene C4 syntl	4056.00	LTC4S	2539.00	0.87	2.66
50022.00	F17	M-011707- ISL1 transcription fa	3670.00	ISL1	3639.00	1.29	2.24
50022.00	F18	M-014144- latent transforming	4054.00	LTBP3	2707.00	1.15	2.38
50022.00	F19	M-008000- integrin, alpha 11	22801.00	ITGA11	3429.00	2.04	1.49
50022.00	F20	M-005935- leukotriene A4 hydr	4048.00	LTA4H	3455.00	3.47	0.06
50022.00	F21	M-032260- integrin, alpha D	3681.00	ITGAD	4351.00	6.76	3.23
50022.00	F23	M-008013- integrin, beta 7	3695.00	ITGB7	3638.00	2.06	1.47
50022.00	G02	M-006628- FUN14 domain cont	65991.00	FUNDC2	3634.00	4.07	0.54
50022.00	G04	M-012055- hemoglobin, zeta	3050.00	HBZ	4432.00	6.95	3.42
50022.00	G05	M-014444- glutamine and serin	79832.00	QSER1	4121.00	2.89	0.64
50022.00	G06	M-012054- hemoglobin, theta 1	3049.00	HBQ1	2470.00	20.12	**16.59**
50022.00	G07	M-016961- RNA binding motif a	84173.00	RBED1	2483.00	5.28	1.75
50022.00	G08	M-011116- hemoglobin, gamma	3048.00	HBG2	2068.00	3.38	0.15
50022.00	G09	M-016231- armadillo repeat coı	79637.00	ARMC7	2289.00	1.05	2.48
50022.00	G10	M-012069- hemoglobin, epsilor	3046.00	HBE1	2554.00	9.83	**6.30**
50022.00	G11	M-015783- rhomboid 5 homolo	79651.00	RHBDF2	2500.00	3.88	0.35
50022.00	G12	M-011048- hemoglobin, delta	3045.00	HBD	1778.00	10.97	**7.44**
50022.00	G13	M-014581- ATH1, acid trehalase	80162.00	ATHL1	2223.00	5.13	1.60
50022.00	G14	M-008817- atonal homolog 8 (D	84913.00	ATOH8	3074.00	5.11	1.58
50022.00	G15	M-018769- zinc finger protein 5	151126.00	ZNF533	3093.00	6.21	2.68
50022.00	G16	M-011490- histone acetyltransf	8520.00	HAT1	3678.00	6.72	3.19
50022.00	G17	M-015711- heat shock transcrip	159119.00	HSFY2	2022.00	14.10	**10.57**
50022.00	G18	M-020779- cell division cycle 37	55664.00	CDC37L1	3355.00	12.73	**9.20**
50022.00	G19	M-016758- zinc finger, DHHC-ty	253832.00	ZDHHC20	3566.00	8.75	5.22
50022.00	G20	M-011560- huntingtin-associate	9001.00	HAP1	3910.00	12.23	**8.70**
50022.00	G21	M-015618- mesoderm inductioı	166968.00	MIER3	2416.00	8.24	4.71
50022.00	G23	M-017037- hypothetical proteir	158677.00	FLJ38564	3365.00	2.44	1.09

50022.00	H02	M-020025- leucine rich repeat c	10234.00	LRRC17	3773.00	2.62	0.91
50022.00	H04	M-018629- low density lipoprot	84918.00	LRP11	1674.00	6.45	2.92
50022.00	H05	M-008014- integrin, beta 8	3696.00	ITGB8	2893.00	3.84	0.31
50022.00	H06	M-018824- low density lipoprot	26020.00	LRP10	2873.00	5.22	1.69
50022.00	H07	M-019854- integrin, beta-like 1	9358.00	ITGBL1	2910.00	2.92	0.61
50022.00	H08	M-012233- lymphoid-restricted	4033.00	LRMP	3690.00	14.09	**10.56**
50022.00	H09	M-003828- integral membrane	9445.00	ITM2B	2486.00	2.70	0.83
50022.00	H10	M-013940- leucine-rich repeats	26018.00	LRIG1	1560.00	1.35	2.18
50022.00	H11	M-019071- G protein-coupled re	160897.00	GPR180	3622.00	4.03	0.50
50022.00	H12	M-004428- leucine-rich repeats	55367.00	LRDD	1762.00	3.41	0.12
50022.00	H13	M-009841- intersectin 2	50618.00	ITSN2	1991.00	2.46	1.07
50022.00	H14	M-012751- LPS-responsive vesic	987.00	LRBA	3715.00	6.57	3.04
50022.00	H15	M-013174- junctophilin 3	57338.00	JPH3	1943.00	3.71	0.18
50022.00	H16	M-009746- leupaxin	9404.00	LPXN	2629.00	9.01	**5.48**
50022.00	H17	M-011514- jerky homolog-like (	8690.00	JRKL	2832.00	4.34	0.81
50022.00	H18	M-013736- lipid phosphate pho	64748.00	LPPR2	2961.00	4.66	1.13
50022.00	H19	M-011708- junction plakoglobir	3728.00	JUP	4913.00	13.05	**9.52**
50022.00	H20	M-020012- LIM domain contain	4026.00	LPP	3411.00	7.53	4.00
50022.00	H21	M-003901- CD82 molecule	3732.00	CD82	3883.00	9.86	**6.33**
50022.00	H23	M-008831- potassium voltage-g	7881.00	KCNAB1	3626.00	5.32	1.79
50022.00	I02	M-008698- heart and neural cre	9464.00	HAND2	4197.00	3.38	0.15
50022.00	I04	M-019999- WD repeat domain (	10238.00	WDR68	3857.00	5.47	1.94
50022.00	I05	M-011272- filamin C, gamma (a	2318.00	FLNC	2985.00	2.41	1.12
50022.00	I06	M-009629- hydroxyacylglutathi	84264.00	HAGHL	3942.00	6.19	2.66
50022.00	I07	M-009243- flavin containing mc	2328.00	FMO3	2120.00	2.50	1.03
50022.00	I08	M-008280- hydroxyacyl-Coenzy	3032.00	HADHB	3011.00	2.29	1.24
50022.00	I09	M-019632- AF4/FMR2 family, m	2334.00	AFF2	4152.00	4.94	1.41
50022.00	I10	M-023893- histocompatibility (r	23526.00	HMHA1	3206.00	2.65	0.88
50022.00	I11	M-012036- frequently rearrange	10023.00	FRAT1	3056.00	1.90	1.63
50022.00	I12	M-010913- H2A histone family,	55506.00	H2AFY2	2064.00	2.23	1.30
50022.00	I13	M-019576- fascin homolog 1, ac	6624.00	FSCN1	2962.00	1.59	1.94
50022.00	I14	M-032256- H19, imprinted mate	283120.00	H19	3760.00	1.46	2.07
50022.00	I15	M-012098- follistatin-like 3 (sec	10272.00	FSTL3	2416.00	7.28	3.75
50022.00	I16	M-011680- glycophorin C (Gerb	2995.00	GYPC	4318.00	2.76	0.77
50022.00	I17	M-016214- ferritin, light polype	2512.00	FTL	3617.00	1.80	1.73
50022.00	I18	M-011678- glycophorin A (MNS	2993.00	GYPA	3713.00	4.87	1.34
50022.00	I19	M-009211- fucosidase, alpha-L-	2519.00	FUCA2	2990.00	1.44	2.09
50022.00	I20	M-019952- guanylate cyclase ac	9626.00	GUCA1C	4874.00	1.31	2.22
50022.00	I21	M-009497- fusion (involved in t	2521.00	FUS	2808.00	3.10	0.43
50022.00	I23	M-008172- fucosyltransferase 3	2525.00	FUT3	3646.00	0.88	2.65
50022.00	J02	M-005107- loss of heterozygosi	4013.00	LOH11CR2A	2178.00	2.80	0.73
50022.00	J04	M-015773- RNA polymerase I tr	94431.00	LOC94431	2466.00	3.20	0.33
50022.00	J05	M-012452- KCNE1-like	23630.00	KCNE1L	3089.00	3.40	0.13
50022.00	J06	M-018365- transmembrane pro	93380.00	TMEM32	3523.00	11.55	**8.02**
50022.00	J07	M-006275- potassium voltage-g	56479.00	KCNQ5	2119.00	5.71	2.18
50022.00	J08	M-017755- hypothetical proteir	90925.00	LOC90925	2001.00	3.85	0.32
50022.00	J09	M-005903- Kell blood group, me	3792.00	KEL	4601.00	3.00	0.53

50022.00	J10	M-016548- coiled-coil domain c	90557.00	CCDC74A	1567.00	1.40	2.13
50022.00	J11	M-012764- keratocan	11081.00	KERA	1681.00	6.48	2.95
50022.00	J12	M-016673- MTERF domain cont	80298.00	MTERFD3	2402.00	5.33	1.80
50022.00	J13	M-020735- leucine rich repeat c	9684.00	LRRC14	2778.00	3.28	0.25
50022.00	J14	M-016114- NADH dehydrogena	56901.00	NDUFA4L2	3193.00	4.42	0.89
50022.00	J15	M-026775- transmembrane pro	23027.00	TMEM41B	3493.00	4.15	0.62
50022.00	J16	M-018664- BAI1-associated pro	55971.00	BAIAP2L1	4203.00	5.04	1.51
50022.00	J17	M-025495- KIAA0265 protein	23008.00	KIAA0265	3823.00	4.58	1.05
50022.00	J18	M-032271- hypothetical proteir	254571.00	LOC254571	2714.00	2.69	0.84
50022.00	J19	M-019141- KIAA0274	9896.00	KIAA0274	4036.00	13.50	9.97
50022.00	J20	M-032270- hypothetical proteir	253039.00	LOC25303S	2339.00	6.71	3.18
50022.00	J21	M-020971- ADAMTS-like 2	9719.00	ADAMTSL2	4426.00	4.36	0.83
50022.00	J23	M-023594- transmembrane anc	23023.00	TMCC1	3846.00	5.62	2.09
50022.00	K02	M-019288- guanylate cyclase ac	2978.00	GUCA1A	2101.00	3.38	0.15
50022.00	K04	M-005286- G-2 and S-phase exp	51512.00	GTSE1	3137.00	2.23	1.30
50022.00	K05	M-003672- interferon, alpha-inc	2537.00	IFI6	2823.00	11.30	7.77
50022.00	K06	M-020031- general transcriptioi	9328.00	GTF3C5	5034.00	5.76	2.23
50022.00	K07	M-026790- chromosome 11 ope	25758.00	C11orf41	3545.00	1.21	2.32
50022.00	K08	M-019620- general transcriptioi	2976.00	GTF3C2	2832.00	2.90	0.63
50022.00	K09	M-015549- glucose 6 phosphata	92579.00	G6PC3	2419.00	1.57	1.96
50022.00	K10	M-028674- general transcriptioi	2968.00	GTF2H4	1312.00	10.67	7.14
50022.00	K11	M-008881- glucosidase, alpha; a	2548.00	GAA	2474.00	4.73	1.20
50022.00	K12	M-011181- glutathione S-transfe	2953.00	GSTT2	1817.00	2.20	1.33
50022.00	K13	M-015239- GRB2-associated bir	139716.00	GAB3	2036.00	6.48	2.95
50022.00	K14	M-011180- glutathione S-transfe	2952.00	GSTT1	3568.00	10.06	6.53
50022.00	K15	M-014715- GABA(A) receptor-as	23710.00	GABARAPL1	3203.00	9.15	5.62
50022.00	K16	M-011179- glutathione S-transfe	2950.00	GSTP1	3796.00	3.27	0.26
50022.00	K17	M-008247- glutamate decarbox	2572.00	GAD2	2752.00	6.14	2.61
50022.00	K18	M-019644- G1 to S phase transi	2935.00	GSPT1	2960.00	1.69	1.84
50022.00	K19	M-003894- growth arrest and D	4616.00	GADD45B	5481.00	12.84	9.31
50022.00	K20	M-032230- GRIP1 associated pr	56850.00	GRIPAP1	3999.00	7.33	3.80
50022.00	K21	M-011665- growth arrest-specif	2619.00	GAS1	4203.00	5.47	1.94
50022.00	K23	M-012037- growth arrest-specif	2620.00	GAS2	4966.00	9.32	5.79
50022.00	L02	M-015971- similar to common s	124220.00	LOC12422C	2302.00	5.30	1.77
50022.00	L04	M-004301- poliovirus receptor-i	81607.00	PVRL4	1269.00	1.73	1.80
50022.00	L05	M-025298- KIAA0960 protein	23249.00	KIAA0960	4039.00	4.63	1.10
50022.00	L06	M-012124- LIM domain only 4	8543.00	LMO4	2291.00	2.05	1.48
50022.00	L07	M-022166- kazrin	23254.00	KIAA1026	3964.00	1.67	1.87
50022.00	L08	M-012123- LIM domain only 2 (	4005.00	LMO2	3172.00	6.90	3.37
50022.00	L09	M-009502- forkhead box J3	22887.00	FOXJ3	2810.00	1.25	2.28
50022.00	L10	M-011721- LIM domain only 1 (	4004.00	LMO1	2801.00	3.78	0.25
50022.00	L11	M-010722- endoplasmic reticulu	57222.00	ERGIC1	3926.00	4.64	1.11
50022.00	L12	M-005270- lamin B1	4001.00	LMNB1	2407.00	6.90	3.37
50022.00	L13	M-022416- ADAMTS-like 3	57188.00	ADAMTSL3	2268.00	5.47	1.94
50022.00	L14	M-009672- lipolysis stimulated l	51599.00	LSR	3663.00	6.74	3.21
50022.00	L15	M-023583- poly (ADP-ribose) pc	54625.00	PARP14	5255.00	11.13	7.60
50022.00	L16	M-009441- lipase, hormone-ser	3991.00	LIPE	1581.00	2.21	1.32

50022.00	L17	M-026434- KIAA1274	27143.00	KIAA1274	3930.00	8.47	4.94
50022.00	L18	M-011999- LIM and senescent c	3987.00	LIMS1	3262.00	1.87	1.66
50022.00	L19	M-019274- KIAA1609	57707.00	KIAA1609	3928.00	4.68	1.15
50022.00	L20	M-016292- lens intrinsic memb	3982.00	LIM2	2614.00	4.48	0.95
50022.00	L21	M-013007- KIAA1622	57718.00	KIAA1622	3335.00	4.95	1.42
50022.00	L23	M-031251- KIAA1683	80726.00	KIAA1683	2893.00	18.36	**14.83**
50022.00	M02	M-006197- glutamate receptor,	2905.00	GRIN2C	3055.00	2.62	0.91
50022.00	M04	M-006189- glutamate receptor,	2897.00	GRIK1	4250.00	3.51	0.02
50022.00	M05	M-017270- growth arrest-specif	10634.00	GAS2L1	3721.00	0.83	2.70
50022.00	M06	M-008982- glutathione peroxid	2876.00	GPX1	2870.00	1.53	2.00
50022.00	M07	M-005280- YEATS domain conta	8089.00	YEATS4	1651.00	0.97	2.56
50022.00	M08	M-012272- G protein pathway s	2873.00	GPS1	2819.00	2.23	1.30
50022.00	M09	M-011492- growth arrest-specif	8522.00	GAS7	3339.00	6.38	2.85
50022.00	M10	M-005529- G protein-coupled r	57720.00	GPR107	2610.00	1.95	1.58
50022.00	M11	M-021155- G protein-coupled r	9737.00	GPRASP1	2605.00	8.29	4.76
50022.00	M12	M-011868- glypican 3	2719.00	GPC3	2991.00	3.98	0.45
50022.00	M13	M-008351- GATA binding protei	2627.00	GATA6	3658.00	7.63	4.10
50022.00	M14	M-011522- glycosylphosphatidy	8733.00	GPAA1	3631.00	7.22	3.69
50022.00	M15	M-018076- opposite strand tra	352954.00	GATS	3072.00	6.61	3.08
50022.00	M16	M-019809- golgi autoantigen, g	2804.00	GOLGB1	3539.00	2.29	1.24
50022.00	M17	M-011039- glucan (1,4-alpha-),	2632.00	GBE1	4536.00	6.72	3.19
50022.00	M18	M-010633- golgi autoantigen, g	9950.00	GOLGA5	4225.00	7.22	3.69
50022.00	M19	M-011120- group-specific comp	2638.00	GC	3118.00	3.14	0.39
50022.00	M20	M-010074- glycine N-methyltra	27232.00	GNMT	3304.00	4.66	1.13
50022.00	M21	M-009212- glutamate-cysteine	2729.00	GCLC	2842.00	3.31	0.22
50022.00	M23	M-012223- glucosidase I	7841.00	GCS1	4466.00	2.02	1.51
50022.00	N02	M-009227- ligase III, DNA, ATP-	3980.00	LIG3	3421.00	3.57	0.04
50022.00	N04	M-008017- leukemia inhibitory	3977.00	LIFR	4971.00	6.54	3.01
50022.00	N05	M-025286- KIAA1856 protein	84629.00	KIAA1856	4011.00	3.74	0.21
50022.00	N06	M-012121- LIM homeobox 1	3975.00	LHX1	4253.00	8.79	5.26
50022.00	N07	M-016026- killer cell immunogl	115653.00	KIR3DL3	3338.00	6.80	3.27
50022.00	N08	M-012714- lipoma HMGIC fusio	10184.00	LHFPL2	3244.00	2.53	1.00
50022.00	N09	M-011300- KiSS-1 metastasis-su	3814.00	KISS1	3567.00	5.75	2.22
50022.00	N10	M-011982- leucine-rich, glioma	9211.00	LGI1	2206.00	6.21	2.68
50022.00	N11	M-019507- Kruppel-like factor	11279.00	KLF8	2451.00	6.57	3.04
50022.00	N12	M-011719- lectin, galactoside-b	3963.00	LGALS7	2082.00	4.18	0.65
50022.00	N13	M-004988- MLF1 interacting pr	79682.00	MLF1IP	2336.00	3.42	0.11
50022.00	N14	M-010606- lectin, galactoside-b	3958.00	LGALS3	3580.00	4.19	0.66
50022.00	N15	M-016300- killer cell lectin-like	10219.00	KLRG1	4018.00	3.93	0.40
50022.00	N16	M-025279- LFNG O-fucosylpept	3955.00	LFNG	3844.00	3.10	0.43
50022.00	N17	M-011307- karyopherin alpha 5	3841.00	KPNA5	4511.00	9.24	**5.71**
50022.00	N18	M-020301- leptin receptor over	23484.00	LEPROTL1	4785.00	5.31	1.78
50022.00	N19	M-017318- RAN binding protein	3843.00	RANBP5	4504.00	10.61	**7.08**
50022.00	N20	M-015164- leukocyte receptor	114823.00	LENG8	3435.00	1.51	2.02
50022.00	N21	M-003846- kringle containing tr	83999.00	KREMEN1	4090.00	8.75	5.22
50022.00	N23	M-003847- kringle containing tr	79412.00	KREMEN2	3035.00	5.01	1.48
50022.00	O02	M-012490- granulysin	10578.00	GNLY	2551.00	2.74	0.79

50022.00	O04	M-006876-	guanine nucleotide I	10399.00	GNB2L1	2248.00	2.40	1.13
50022.00	O05	M-021225-	ganglioside-induced	54332.00	GDAP1	4139.00	8.14	4.61
50022.00	O06	M-008681-	guanine monphosph	8833.00	GMPS	4539.00	11.52	**7.99**
50022.00	O07	M-012041-	growth factor, augm	2671.00	GFER	6155.00	16.65	**13.12**
50022.00	O08	M-003270-	geminin, DNA replic	51053.00	GMNN	4327.00	4.18	0.65
50022.00	O09	M-020589-	tumor necrosis facto	25816.00	TNFAIP8	2956.00	6.66	3.13
50022.00	O10	M-019639-	GPI anchored molec	2765.00	GML	2448.00	1.23	2.30
50022.00	O11	M-011041-	growth hormone 1	2688.00	GH1	3139.00	3.22	0.31
50022.00	O12	M-004032-	glutamate dehydrog	2746.00	GLUD1	3162.00	4.40	0.87
50022.00	O13	M-016102-	zinc finger protein 4	92283.00	ZNF461	4040.00	1.63	1.90
50022.00	O14	M-006464-	glioma tumor suppre	29997.00	GLTSCR2	2076.00	2.07	1.46
50022.00	O15	M-020380-	gap junction protein	57165.00	GJA12	5847.00	14.06	**10.53**
50022.00	O16	M-020751-	glioma tumor suppre	29998.00	GLTSCR1	3577.00	1.96	1.57
50022.00	O17	M-015676-	gap junction protein	2700.00	GJA3	2510.00	4.22	0.69
50022.00	O18	M-012634-	glutaredoxin (thioltr	2745.00	GLRX	1762.00	1.08	2.45
50022.00	O19	M-017368-	gap junction protein	2702.00	GJA5	4306.00	3.81	0.28
50022.00	O20	M-012277-	glyoxalase I	2739.00	GLO1	5099.00	5.63	2.10
50022.00	O21	M-012698-	gap junction protein	2703.00	GJA8	3541.00	0.34	3.19
50022.00	O23	M-019819-	GLI pathogenesis-re	11010.00	GLIPR1	2862.00	6.71	3.18
50022.00	P02	M-010084-	leukocyte receptor c	79143.00	LENG4	3100.00	3.19	0.34
50022.00	P04	M-014332-	leukocyte receptor c	79165.00	LENG1	3400.00	4.50	0.97
50022.00	P05	M-012865-	keratin 1 (epidermo	3848.00	KRT1	2014.00	5.16	1.63
50022.00	P06	M-012461-	leucine zipper, dowr	23641.00	LDOC1	2811.00	4.41	0.88
50022.00	P07	M-017550-	keratin 16 (focal nor	3868.00	KRT16	1944.00	5.56	2.03
50022.00	P08	M-008759-	lactate dehydrogena	3948.00	LDHC	2834.00	10.90	**7.37**
50022.00	P09	M-010603-	keratin 17	3872.00	KRT17	2130.00	7.65	4.12
50022.00	P10	M-009779-	lactate dehydrogena	3945.00	LDHB	3835.00	7.46	3.93
50022.00	P11	M-010604-	keratin 18	3875.00	KRT18	2549.00	1.65	1.88
50022.00	P12	M-008201-	lactate dehydrogena	3939.00	LDHA	2228.00	3.41	0.12
50022.00	P13	M-011068-	keratin 9 (epidermo	3857.00	KRT9	2813.00	11.13	**7.60**
50022.00	P14	M-028861-	KIAA1147	57189.00	KIAA1147	3830.00	4.60	1.07
50022.00	P15	M-011313-	keratin 81	3887.00	KRT81	2030.00	2.17	1.36
50022.00	P16	M-011715-	lysosomal-associate	3920.00	LAMP2	3521.00	5.34	1.81
50022.00	P17	M-011316-	keratin 86	3892.00	KRT86	4123.00	4.83	1.30
50022.00	P18	M-011712-	laminin, alpha 4	3910.00	LAMA4	3583.00	12.98	**9.45**
50022.00	P19	M-010605-	kinectin 1 (kinesin re	3895.00	KTN1	3627.00	5.05	1.52
50022.00	P20	M-011070-	laminin, alpha 2 (me	3908.00	LAMA2	2538.00	3.47	0.06
50022.00	P21	M-006418-	leukocyte-associate	3903.00	LAIR1	2648.00	6.19	2.66
50022.00	P23	M-011318-	leukocyte-associate	3904.00	LAIR2	2146.00	9.97	**6.44**
					mdn	2990.50	3.53	1.81
					3MAD			5.44
					MADc			2.68
		%	3.13					
50022.00	C22					3274.00	17.93	
50022.00	D22			4689.00	25.61	2629.00	16.97	
50022.00	E22					4476.00	12.76	
50022.00	F22							

		mn	3459.67	15.88
		sd	937.39	2.75
50022.00	G22		1171.00	4.78
50022.00	H22		1410.00	2.70
50022.00	I22		1492.00	0.80
50022.00	J22		1805.00	2.99
		mn	1469.50	2.82
		sd	261.86	1.63
		3psSD		8.25
		3ngSD		4.89
		SumSD		13.14
		DiffMn		13.07
		SmovrDiff		1.01
		1minus		-0.01

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
-0.67	1183.00	0.34	3.19	-1.24	2524.00	1.62	2.37	-0.86
-0.19	2060.00	1.89	1.64	-0.64	3271.00	4.89	0.90	0.33
-0.85	2590.00	1.58	1.95	-0.76	2735.00	0.95	3.04	-1.10
-0.37	3044.00	2.27	1.26	-0.49	4870.00	6.57	2.58	0.94
-1.10	3079.00	0.55	2.98	-1.16	2560.00	1.76	2.23	-0.81
-0.44	3086.00	3.50	0.03	-0.01	2557.00	3.32	0.67	-0.24
-0.09	838.00	3.34	0.19	-0.07	2004.00	1.45	2.54	-0.92
-0.69	1718.00	2.62	0.91	-0.35	2726.00	1.47	2.52	-0.91
-0.04	1651.00	6.84	3.31	1.29	1773.00	2.54	1.45	-0.52
0.29	2956.00	4.74	1.21	0.47	2799.00	2.61	1.38	-0.50
-0.84	1557.00	2.18	1.35	-0.52	1787.00	1.06	2.93	-1.06
-0.76	669.00	2.99	0.54	-0.21	1677.00	4.29	0.30	0.11
0.85	1850.00	12.49	8.96	3.49	2309.00	9.18	5.19	1.88
-0.75	1691.00	1.72	1.82	-0.71	2268.00	2.16	1.83	-0.66
0.43	2819.00	3.37	0.16	-0.06	2862.00	4.05	0.06	0.02
0.05	5423.00	8.21	4.68	1.82	4929.00	6.94	2.95	1.07
-0.21	2392.00	3.14	0.39	-0.15	4199.00	1.88	2.11	-0.76
-0.13	4370.00	10.76	7.23	2.82	3654.00	5.56	1.57	0.57
0.87	2735.00	6.11	2.58	1.01	3499.00	4.06	0.07	0.03
-0.84	2034.00	6.93	3.40	1.33	2793.00	1.72	2.27	-0.82
0.48	2793.00	4.19	0.66	0.26	2346.00	5.24	1.25	0.46
-0.23	2735.00	3.33	0.20	-0.08	3216.00	6.84	2.85	1.03
0.92	3038.00	0.86	2.67	-1.04	3689.00	2.44	1.55	-0.56
-0.74	3914.00	1.43	2.10	-0.82	3498.00	4.95	0.96	0.35
-0.68	4662.00	2.57	0.96	-0.37	4102.00	7.83	3.84	1.39
-0.44	3823.00	2.17	1.36	-0.53	2630.00	2.13	1.86	-0.67
0.17	2257.00	2.39	1.14	-0.44	1350.00	3.56	0.43	-0.16
-1.10	3613.00	2.49	1.04	-0.40	1920.00	1.88	2.12	-0.76
0.33	3886.00	3.04	0.49	-0.19	2468.00	2.80	1.19	-0.43
-0.65	3087.00	2.46	1.07	-0.41	3187.00	2.48	1.51	-0.55
-0.87	2068.00	1.74	1.79	-0.70	3652.00	5.18	1.19	0.43
0.18	1285.00	5.60	2.07	0.81	1666.00	7.14	3.15	1.14
-0.82	2908.00	2.37	1.16	-0.45	3528.00	5.81	1.82	0.66
-1.21	3100.00	0.16	3.37	-1.31	2951.00	2.54	1.45	-0.52
-0.78	2891.00	3.94	0.41	0.16	2642.00	2.65	1.34	-0.48
-1.00	3425.00	1.14	2.39	-0.93	3136.00	0.86	3.13	-1.13
-0.72	2252.00	2.40	1.13	-0.44	3531.00	3.65	0.34	-0.12
-0.69	2499.00	6.36	2.83	1.11	3069.00	3.98	0.01	0.00
0.42	2318.00	3.32	0.21	-0.08	3349.00	3.37	0.62	-0.22
-0.43	5228.00	8.89	5.36	2.09	5380.00	5.95	1.96	0.71
-0.80	3354.00	1.58	1.95	-0.76	3694.00	1.73	2.26	-0.82
0.11	4590.00	9.65	6.12	2.39	2919.00	5.62	1.63	0.59
-0.85	5358.00	2.00	1.53	-0.60	2801.00	1.71	2.28	-0.82
-1.22	3726.00	0.27	3.26	-1.27	3549.00	1.13	2.86	-1.04
-0.56	3791.00	1.87	1.66	-0.64	2138.00	3.23	0.76	-0.27
-0.79	4681.00	2.24	1.29	-0.50	1911.00	0.21	3.78	-1.37

0.46	2912.00	3.91	0.38	0.15	2163.00	5.55	1.56	0.57
-0.63	1903.00	2.21	1.32	-0.51	1044.00	1.05	2.94	-1.06
-0.62	2854.00	1.26	2.27	-0.88	2184.00	2.29	1.70	-0.61
-0.73	1998.00	1.80	1.73	-0.67	2451.00	1.35	2.64	-0.96
-0.13	3137.00	2.49	1.04	-0.41	2611.00	6.09	2.10	0.76
-0.63	2581.00	4.92	1.39	0.54	2766.00	1.99	2.00	-0.72
-0.20	3511.00	2.22	1.31	-0.51	2633.00	1.63	2.36	-0.85
1.14	2314.00	3.93	0.40	0.16	1617.00	4.64	0.65	0.24
1.37	2954.00	3.22	0.31	-0.12	390.00	1.54	2.45	-0.89
0.00	2953.00	1.35	2.18	-0.85	2927.00	1.54	2.45	-0.89
0.83	4124.00	3.64	0.11	0.04	3179.00	2.80	1.19	-0.43
0.26	3955.00	1.16	2.37	-0.92	4847.00	4.62	0.63	0.23
-0.85	3032.00	1.72	1.82	-0.71	4159.00	6.18	2.19	0.79
0.90	2209.00	10.96	**7.43**	2.89	2847.00	4.36	0.37	0.13
0.10	2773.00	1.41	2.12	-0.83	3437.00	6.92	2.93	1.06
-0.28	4106.00	1.75	1.78	-0.69	4196.00	2.84	1.15	-0.42
0.05	4832.00	1.86	1.67	-0.65	4040.00	7.08	3.09	1.12
0.26	4264.00	4.17	0.64	0.25	4434.00	13.35	**9.36**	3.39
0.20	4052.00	2.05	1.48	-0.58	3375.00	3.47	0.52	-0.19
-0.36	3440.00	1.37	2.16	-0.84	2197.00	3.28	0.71	-0.26
-0.44	2942.00	1.77	1.76	-0.69	2792.00	4.84	0.85	0.31
-0.40	3746.00	0.45	3.08	-1.20	1792.00	2.96	1.03	-0.37
-0.23	3611.00	1.44	2.09	-0.81	2216.00	2.57	1.42	-0.51
0.39	2938.00	1.74	1.79	-0.70	2745.00	4.52	0.53	0.19
1.68	3610.00	3.99	0.46	0.18	3122.00	13.65	**9.66**	3.50
-0.90	2804.00	0.50	3.03	-1.18	2175.00	2.25	1.74	-0.63
0.30	4402.00	1.00	2.53	-0.98	3069.00	3.65	0.34	-0.12
0.14	3917.00	1.63	1.90	-0.74	2196.00	2.09	1.90	-0.68
0.66	3909.00	3.02	0.51	-0.20	3629.00	5.48	1.49	0.54
0.71	1741.00	1.32	2.21	-0.86	1192.00	5.20	1.21	0.44
0.80	4649.00	1.03	2.50	-0.97	3429.00	4.61	0.62	0.23
0.24	2614.00	1.45	2.08	-0.81	3198.00	6.79	2.80	1.01
1.48	3262.00	2.12	1.41	-0.55	3482.00	6.43	2.44	0.89
-0.27	3446.00	1.57	1.96	-0.76	3983.00	3.19	0.80	-0.29
-0.97	4272.00	3.53	0.00	0.00	6048.00	10.14	**6.15**	2.23
-1.19	2472.00	0.08	3.45	-1.34	1418.00	0.85	3.14	-1.14
-1.02	5641.00	2.93	0.61	-0.23	3478.00	5.18	1.19	0.43
-1.11	3875.00	1.42	2.11	-0.82	2922.00	2.53	1.46	-0.53
-0.76	3331.00	1.59	1.94	-0.75	2201.00	1.86	2.13	-0.77
-0.97	4702.00	3.89	0.36	0.14	2853.00	3.86	0.13	-0.05
-0.89	2808.00	1.14	2.39	-0.93	1458.00	2.13	1.86	-0.67
-0.80	2944.00	1.73	1.80	-0.70	2232.00	5.15	1.16	0.42
-0.99	3737.00	3.21	0.32	-0.12	2502.00	3.48	0.51	-0.18
-1.21	1889.00	0.42	3.11	-1.21	1728.00	2.84	1.15	-0.42
-0.91	1413.00	0.85	2.68	-1.04	1352.00	2.07	1.92	-0.69
-0.80	1067.00	3.28	0.25	-0.10	655.00	1.22	2.77	-1.00
-0.95	3843.00	2.21	1.32	-0.51	2685.00	2.12	1.87	-0.67

-0.80	4083.00	0.96	2.57	-1.00	3341.00	3.41	0.58	-0.21	
-0.37	4293.00	3.52	0.01	0.00	3701.00	9.40	5.41	1.96	
-0.73	3111.00	4.02	0.49	0.19	1883.00	3.98	0.01	0.00	
-0.88	1891.00	0.32	3.21	-1.25	1080.00	0.28	3.71	-1.34	
-0.66	3501.00	2.09	1.44	-0.56	3131.00	5.05	1.06	0.38	
-1.09	3811.00	1.50	2.03	-0.79	3485.00	3.99	0.00	0.00	
-0.68	3745.00	1.74	1.79	-0.70	4258.00	4.58	0.59	0.22	
-1.13	2268.00	3.48	0.05	-0.02	2726.00	2.38	1.61	-0.58	
-0.67	2942.00	3.13	0.40	-0.16	3129.00	3.13	0.86	-0.31	
0.00	3851.00	4.15	0.62	0.24	4272.00	4.99	1.00	0.36	
-0.18	1671.00	6.22	2.69	1.05	1711.00	7.60	3.61	1.31	
-0.58	2169.00	4.24	0.71	0.28	2757.00	3.23	0.76	-0.27	
-0.61	3092.00	2.23	1.30	-0.50	3777.00	4.95	0.96	0.35	
1.12	3714.00	7.51	3.98	1.55	3877.00	4.44	0.45	0.16	
-0.53	2752.00	3.27	0.26	-0.10	1914.00	1.20	2.79	-1.01	
-0.97	2925.00	3.11	0.42	-0.16	2320.00	1.34	2.65	-0.96	
-1.09	3262.00	5.92	2.39	0.93	1947.00	2.00	1.99	-0.72	
-0.96	2332.00	1.29	2.24	-0.87	2012.00	0.50	3.49	-1.26	
-0.33	2375.00	3.16	0.37	-0.14	2050.00	5.37	1.38	0.50	
0.25	3362.00	2.08	1.45	-0.56	2526.00	1.62	2.37	-0.86	
-0.99	3120.00	2.76	0.77	-0.30	1914.00	0.37	3.62	-1.31	
-0.83	4678.00	4.55	1.02	0.40	4122.00	4.66	0.67	0.24	
-0.89	3096.00	3.13	0.40	-0.15	1906.00	1.10	2.89	-1.04	
-0.55	4235.00	7.41	3.88	1.51	4066.00	1.75	2.24	-0.81	
-0.02	4198.00	6.19	2.66	1.04	2240.00	1.65	2.34	-0.85	
1.20	4325.00	5.29	1.76	0.69	4344.00	3.04	0.95	-0.34	
-0.55	3046.00	2.33	1.20	-0.47	4403.00	2.66	1.33	-0.48	
0.20	4015.00	1.49	2.04	-0.79	4352.00	0.90	3.09	-1.12	
1.28	4704.00	3.89	0.36	0.14	3334.00	3.30	0.69	-0.25	
-0.24	3932.00	1.78	1.75	-0.68	3143.00	2.48	1.51	-0.54	
6.19	2364.00	9.01	**5.48**	2.14	3075.00	14.18	**10.19**	3.69	y
0.65	3488.00	5.48	1.95	0.76	2013.00	3.18	0.81	-0.29	
-0.05	4353.00	3.26	0.27	-0.10	3121.00	2.85	1.14	-0.41	
-0.92	1821.00	2.42	1.11	-0.43	2077.00	2.26	1.73	-0.62	
2.35	2267.00	4.19	0.66	0.26	2095.00	2.53	1.46	-0.53	
0.13	2286.00	2.10	1.43	-0.56	2506.00	3.19	0.80	-0.29	
2.77	2132.00	8.68	5.15	2.01	1173.00	3.32	0.67	-0.24	x
0.60	2782.00	7.66	4.13	1.61	2190.00	7.81	3.82	1.38	
0.59	3957.00	5.84	2.31	0.90	3048.00	5.68	1.69	0.61	
1.00	3666.00	2.73	0.80	-0.31	3441.00	2.94	1.05	-0.38	
1.19	5103.00	11.86	**8.33**	3.25	3946.00	6.21	2.22	0.81	
3.94	3404.00	14.16	**10.63**	4.14	2869.00	10.56	**6.57**	2.38	y
3.43	4615.00	16.32	**12.79**	4.98	3430.00	11.55	**7.56**	2.74	y
1.95	5457.00	12.99	**9.46**	3.69	3235.00	4.98	0.99	0.36	
3.24	2950.00	10.41	**6.88**	2.68	2951.00	3.86	0.13	-0.04	y
1.76	2697.00	7.64	4.11	1.60	3174.00	3.72	0.27	-0.10	
-0.41	4165.00	4.75	1.22	0.48	3999.00	3.95	0.04	-0.01	

-0.34	3930.00	4.02	0.49	0.19	3442.00	3.20	0.79	-0.29	
1.09	2167.00	4.52	0.99	0.39	2822.00	8.50	4.51	1.64	
0.12	3479.00	4.40	0.87	0.34	4480.00	6.81	2.82	1.02	
0.63	3226.00	2.67	0.86	-0.34	2731.00	3.30	0.69	-0.25	
-0.23	3151.00	2.51	1.02	-0.40	2597.00	5.62	1.63	0.59	
3.94	3715.00	12.81	9.28	3.62	3119.00	12.99	9.00	3.26	y
-0.31	3617.00	4.37	0.84	0.33	3474.00	9.30	5.31	1.92	
-0.81	2406.00	1.16	2.37	-0.92	2178.00	2.20	1.79	-0.65	
0.19	4664.00	4.61	1.08	0.42	3214.00	7.25	3.26	1.18	
-0.05	1412.00	0.42	3.11	-1.21	1679.00	3.10	0.89	-0.32	
-0.40	1571.00	4.01	0.48	0.19	1595.00	1.82	2.17	-0.79	
1.13	4679.00	4.45	0.92	0.36	3989.00	10.45	6.46	2.34	
0.07	1885.00	2.23	1.30	-0.51	1804.00	2.88	1.11	-0.40	
2.05	3875.00	5.68	2.15	0.84	3318.00	6.54	2.55	0.93	
0.30	3694.00	3.41	0.12	-0.04	3680.00	8.94	4.95	1.79	
0.42	2545.00	2.51	1.02	-0.39	2847.00	6.15	2.16	0.78	
3.55	5577.00	7.84	4.31	1.68	3530.00	12.01	8.02	2.91	y
1.49	3509.00	7.01	3.48	1.36	2756.00	7.58	3.59	1.30	
2.36	3343.00	3.77	0.24	0.09	4017.00	7.37	3.38	1.23	
0.67	6777.00	8.06	4.53	1.77	5876.00	15.81	11.82	4.28	
-0.05	5061.00	3.91	0.38	0.15	4401.00	1.80	2.20	-0.79	
0.72	3192.00	3.10	0.43	-0.17	3735.00	6.16	2.17	0.79	
-0.42	3120.00	6.70	3.17	1.24	2277.00	4.61	0.62	0.23	
0.99	3595.00	5.51	1.98	0.77	3972.00	6.14	2.15	0.78	
-0.38	2866.00	4.78	1.25	0.49	2221.00	2.93	1.06	-0.38	
-0.46	3153.00	5.77	2.24	0.88	2916.00	2.98	1.01	-0.36	
0.53	4428.00	12.04	8.51	3.32	4460.00	9.01	5.02	1.82	
-0.33	2930.00	4.20	0.67	0.26	3324.00	2.29	1.70	-0.62	
-0.61	3309.00	3.14	0.39	-0.15	2308.00	4.51	0.52	0.19	
-0.48	2367.00	3.68	0.15	0.06	1703.00	1.12	2.87	-1.04	
-0.72	2899.00	2.21	1.32	-0.51	1761.00	2.33	1.66	-0.60	
-0.77	3188.00	2.73	0.80	-0.31	3328.00	3.40	0.59	-0.21	
1.40	2321.00	8.40	4.87	1.90	2589.00	7.84	3.85	1.40	
-0.29	3589.00	1.73	1.80	-0.70	2900.00	1.38	2.61	-0.94	
-0.65	3747.00	3.98	0.45	0.18	3503.00	5.45	1.46	0.53	
0.50	4161.00	3.10	0.43	-0.17	2268.00	3.88	0.11	-0.04	
-0.78	3869.00	1.55	1.98	-0.77	3378.00	2.04	1.95	-0.70	
-0.83	5235.00	4.41	0.88	0.35	5039.00	4.90	0.91	0.33	
-0.16	3648.00	4.30	0.77	0.30	3278.00	6.41	2.42	0.88	
-0.99	3626.00	1.93	1.60	-0.62	3856.00	2.13	1.86	-0.67	
-0.27	2487.00	0.80	2.73	-1.06	3815.00	5.58	1.59	0.58	
-0.12	3419.00	2.84	0.69	-0.27	2398.00	6.01	2.02	0.73	
-0.05	2744.00	3.28	0.25	-0.10	3658.00	6.21	2.22	0.80	
2.99	2638.00	4.93	1.40	0.55	3542.00	16.94	12.95	4.69	y
0.81	2734.00	7.72	4.19	1.63	2074.00	10.27	6.28	2.28	
0.12	2002.00	5.09	1.56	0.61	1719.00	2.04	1.95	-0.71	
-0.20	3978.00	4.52	0.99	0.39	4654.00	5.26	1.27	0.46	

-0.79	1378.00	2.83	0.70	-0.27	864.00	6.13	2.14	0.78	
1.10	1546.00	3.43	0.10	-0.04	2425.00	7.13	3.14	1.14	
0.67	1178.00	2.29	1.24	-0.48	2098.00	7.44	3.45	1.25	
-0.09	2114.00	0.61	2.92	-1.13	2955.00	4.87	0.88	0.32	
0.33	2682.00	3.62	0.09	0.04	3602.00	2.83	1.16	-0.42	
0.23	2336.00	5.61	2.08	0.81	4126.00	10.47	**6.48**	2.35	
0.57	2619.00	2.94	0.59	-0.23	3004.00	6.06	2.07	0.75	
0.39	3095.00	2.68	0.85	-0.33	3928.00	4.25	0.26	0.10	
-0.31	1988.00	3.42	0.11	-0.04	3186.00	4.27	0.28	0.10	
3.72	2779.00	20.37	**16.84**	6.56	4290.00	21.33	**17.34**	6.28	y
1.19	1607.00	7.59	4.06	1.58	2190.00	5.25	1.26	0.46	
0.31	2885.00	2.77	0.76	-0.29	4558.00	7.33	3.34	1.21	
0.78	3838.00	5.89	2.36	0.92	5227.00	9.72	**5.73**	2.08	
-0.06	1937.00	6.81	3.28	1.28	1759.00	1.02	2.97	-1.07	
-0.48	2636.00	4.59	1.06	0.41	3332.00	2.19	1.80	-0.65	
2.90	3131.00	6.26	2.73	1.07	4271.00	9.06	5.07	1.84	
0.83	4677.00	3.04	0.49	-0.19	3490.00	2.58	1.41	-0.51	
-0.86	1535.00	3.84	0.31	0.12	1843.00	2.17	1.82	-0.66	
-0.24	2762.00	4.96	1.43	0.56	2460.00	4.88	0.89	0.32	
-0.73	1575.00	1.33	2.20	-0.85	1454.00	0.76	3.23	-1.17	
2.66	1296.00	11.96	**8.43**	3.29	1269.00	10.32	**6.33**	2.30	x
0.45	1901.00	5.94	2.41	0.94	1236.00	5.83	1.84	0.67	
-0.49	1578.00	2.53	1.00	-0.39	1261.00	0.71	3.28	-1.19	
1.10	2631.00	5.44	1.91	0.74	1773.00	8.74	4.75	1.72	
2.44	2905.00	3.86	0.33	0.13	2672.00	2.77	1.22	-0.44	
2.09	2711.00	9.78	**6.25**	2.43	1484.00	2.36	1.63	-0.59	y
-0.10	2649.00	3.06	0.47	-0.18	3147.00	4.42	0.43	0.16	
0.97	1803.00	5.49	1.96	0.77	2387.00	4.11	0.12	0.04	
-0.69	2003.00	3.05	0.48	-0.19	2013.00	1.34	2.65	-0.96	
3.47	3603.00	7.47	3.94	1.54	4826.00	14.28	**10.29**	3.73	y
1.42	2970.00	7.34	3.81	1.49	3365.00	7.19	3.20	1.16	
0.72	3156.00	4.18	0.65	0.26	277.00	1.44	2.55	-0.92	
2.16	3217.00	9.54	**6.01**	2.34	3709.00	5.23	1.24	0.45	y
0.66	3031.00	4.72	1.19	0.46	3707.00	12.19	**8.20**	2.97	
-0.67	946.00	0.11	3.42	-1.33	1045.00	1.91	2.08	-0.75	
0.41	3118.00	5.64	2.11	0.83	3843.00	4.61	0.62	0.22	
-0.55	2508.00	0.44	3.09	-1.20	2172.00	3.55	0.44	-0.16	
-0.69	3406.00	2.29	1.24	-0.48	3719.00	2.88	1.11	-0.40	
1.26	3139.00	8.06	4.53	1.77	3080.00	12.18	**8.19**	2.97	
-0.85	2266.00	2.82	0.71	-0.27	2654.00	3.13	0.86	-0.31	
0.10	2035.00	5.36	1.83	0.71	2193.00	4.88	0.89	0.32	
0.41	2914.00	2.33	1.20	-0.46	3941.00	3.35	0.64	-0.23	
1.26	2390.00	8.79	**5.26**	2.05	1861.00	5.53	1.54	0.56	
0.72	2163.00	2.77	0.76	-0.29	1878.00	5.96	1.97	0.72	
1.20	2916.00	5.59	2.06	0.80	2998.00	5.30	1.31	0.48	
2.83	3497.00	4.06	0.53	0.21	4262.00	7.09	3.10	1.12	
-0.49	1794.00	1.28	2.25	-0.87	1766.00	0.91	3.08	-1.12	

1.84	3103.00	5.16	1.63	0.64	4158.00	5.82	1.83	0.66	
-0.62	2490.00	2.57	0.96	-0.37	3061.00	2.19	1.80	-0.65	
0.43	3212.00	1.12	2.41	-0.94	4033.00	2.48	1.51	-0.55	
0.35	2207.00	1.45	2.08	-0.81	2131.00	2.39	1.60	-0.58	
0.53	2361.00	2.63	0.90	-0.35	3092.00	1.42	2.57	-0.93	
5.53	3190.00	11.03	**7.50**	2.93	2640.00	9.36	5.37	1.95	y
-0.34	3632.00	3.19	0.34	-0.13	3359.00	2.80	1.19	-0.43	
-0.01	4093.00	7.11	3.58	1.40	5467.00	7.94	3.95	1.43	
-1.00	3631.00	6.69	3.16	1.23	4761.00	5.25	1.26	0.46	
-0.74	1920.00	3.13	0.41	-0.16	2961.00	2.40	1.59	-0.58	
-0.95	1340.00	2.09	1.44	-0.56	2291.00	1.22	2.77	-1.00	
-0.48	2894.00	9.54	**6.01**	2.34	3684.00	2.61	1.38	-0.50	
1.06	2973.00	7.50	3.97	1.55	5169.00	9.15	5.16	1.87	
-0.59	2741.00	3.54	0.01	0.01	3806.00	3.21	0.78	-0.28	
1.78	2227.00	14.41	**10.88**	4.24	3031.00	11.84	**7.85**	2.85	y
0.17	3549.00	8.62	5.09	1.99	3954.00	4.10	0.11	0.04	
1.53	3414.00	8.93	**5.40**	2.11	3607.00	6.60	2.61	0.95	
1.37	3784.00	14.14	**10.61**	4.13	3805.00	13.96	**9.97**	3.61	y
1.15	2203.00	4.22	0.69	0.27	3085.00	3.73	0.26	-0.09	
-0.46	3838.00	4.92	1.39	0.54	4331.00	2.68	1.31	-0.47	
1.19	3810.00	10.08	**6.55**	2.55	5410.00	16.12	**12.13**	4.39	y
1.38	4462.00	10.04	**6.51**	2.54	5166.00	3.45	0.54	-0.20	
-0.14	2876.00	4.97	1.44	0.56	3815.00	3.56	0.43	-0.15	
0.42	2635.00	3.57	0.04	0.02	3308.00	0.91	3.08	-1.12	
-0.08	2457.00	6.39	2.86	1.12	2800.00	4.14	0.15	0.06	
-0.56	5189.00	7.82	4.29	1.67	5395.00	2.15	1.84	-0.66	
0.01	3675.00	3.13	0.40	-0.15	4711.00	4.27	0.28	0.10	
1.12	4033.00	4.22	0.69	0.27	4305.00	6.11	2.12	0.77	
0.08	4019.00	1.74	1.79	-0.70	4103.00	6.36	2.37	0.86	
1.96	3593.00	6.12	2.59	1.01	5268.00	17.84	**13.85**	5.02	
1.22	2902.00	5.51	1.98	0.77	3851.00	13.11	**9.12**	3.31	
-0.37	2188.00	1.74	1.79	-0.70	3343.00	4.25	0.26	0.09	
0.83	2801.00	5.96	2.43	0.95	3100.00	7.87	3.88	1.41	
1.00	1084.00	2.40	1.13	-0.44	1954.00	9.37	5.38	1.95	
1.13	3043.00	3.32	0.21	-0.08	2612.00	11.41	**7.42**	2.69	
0.24	2870.00	4.77	1.24	0.49	1980.00	4.24	0.25	0.09	
-0.04	2156.00	1.86	1.67	-0.65	2776.00	12.93	**8.94**	3.24	
0.25	3602.00	1.50	2.03	-0.79	4510.00	10.64	**6.65**	2.41	
0.15	3020.00	3.61	0.08	0.03	3134.00	6.70	2.71	0.98	
-0.16	2944.00	0.82	2.71	-1.06	3612.00	9.14	5.15	1.87	
2.13	3101.00	4.00	0.47	0.18	3853.00	7.89	3.90	1.41	
0.66	3516.00	2.22	1.31	-0.51	3041.00	7.00	3.01	1.09	
2.64	3355.00	2.56	0.97	-0.38	5154.00	17.04	**13.05**	4.73	y
-0.75	1990.00	0.50	3.03	-1.18	3085.00	4.21	0.22	0.08	
1.95	4579.00	3.80	0.27	0.11	2802.00	11.56	**7.57**	2.74	
0.55	3144.00	0.76	2.77	-1.08	2966.00	4.92	0.93	0.34	
-0.29	2292.00	4.71	1.18	0.46	3876.00	6.50	2.51	0.91	

-0.42	2232.00	2.91	0.62	-0.24	3496.00	1.49	2.50	-0.90	
1.72	2979.00	5.27	1.74	0.68	4522.00	10.99	**7.00**	2.54	
2.98	2269.00	4.54	1.01	0.39	3396.00	2.86	1.13	-0.41	
4.89	1155.00	10.56	**7.03**	2.74	1415.00	1.84	2.15	-0.78	x
0.24	2213.00	2.17	1.36	-0.53	4204.00	4.02	0.03	0.01	
1.17	2546.00	4.75	1.22	0.48	3580.00	3.38	0.61	-0.22	
-0.86	2479.00	2.46	1.07	-0.42	2818.00	2.41	1.58	-0.57	
-0.12	1516.00	3.17	0.36	-0.14	2770.00	0.76	3.23	-1.17	
0.32	3196.00	3.35	0.18	-0.07	3480.00	1.58	2.41	-0.87	
-0.71	3539.00	2.68	0.85	-0.33	4591.00	3.20	0.79	-0.28	
-0.54	1206.00	5.56	2.03	0.79	2374.00	1.14	2.85	-1.03	
3.93	4505.00	6.99	3.46	1.35	2708.00	3.14	0.85	-0.31	
-0.59	2979.00	3.02	0.51	-0.20	4011.00	1.97	2.02	-0.73	
0.26	2187.00	5.44	1.91	0.75	2875.00	2.23	1.76	-0.64	
-0.91	827.00	7.26	3.73	1.45	1336.00	1.05	2.94	-1.06	
0.10	2660.00	3.95	0.42	0.16	4295.00	4.68	0.69	0.25	
0.78	4641.00	6.40	2.87	1.12	5158.00	3.33	0.66	-0.24	
-1.19	3495.00	2.09	1.44	-0.56	4387.00	0.59	3.40	-1.23	
1.19	4091.00	6.18	2.65	1.04	3198.00	3.44	0.55	-0.20	
-0.12	1884.00	5.68	2.15	0.84	26.00	26.92	**22.93**	8.31	
0.36	1910.00	9.84	**6.31**	2.46	2507.00	6.14	2.15	0.78	
0.61	2168.00	5.40	1.87	0.73	2243.00	6.46	2.47	0.90	
0.33	2384.00	10.57	**7.04**	2.74	2491.00	6.18	2.19	0.80	
0.76	2448.00	3.59	0.06	0.03	1051.00	7.99	4.00	1.45	
2.75	2898.00	19.08	**15.55**	6.06	1862.00	15.58	**11.59**	4.20	y
1.54	1619.00	6.86	3.33	1.30	1137.00	8.00	4.01	1.46	
1.46	3503.00	6.85	3.32	1.30	2719.00	10.59	**6.60**	2.39	
-0.70	1969.00	1.07	2.46	-0.96	2118.00	2.36	1.63	-0.59	
-0.04	1974.00	5.32	1.79	0.70	527.00	9.30	5.31	1.92	
2.83	2106.00	13.06	**9.53**	3.71	2793.00	13.43	**9.44**	3.42	y
0.40	2227.00	4.31	0.78	0.31	2203.00	3.72	0.27	-0.10	
-0.51	2187.00	5.30	1.77	0.69	1845.00	2.44	1.55	-0.56	
0.68	2650.00	5.70	2.17	0.85	2439.00	3.85	0.14	-0.05	
0.48	3218.00	7.24	3.71	1.45	2427.00	3.67	0.32	-0.12	
3.52	170.00	15.88	**12.35**	4.81	3530.00	7.05	3.06	1.11	y
0.57	2933.00	9.68	**6.15**	2.40	2459.00	2.93	1.06	-0.38	
-0.02	2618.00	6.61	3.08	1.20	1577.00	2.09	1.90	-0.69	
0.99	1985.00	8.61	5.08	1.98	1888.00	4.61	0.62	0.23	
2.40	2409.00	4.48	0.95	0.37	1024.00	0.68	3.31	-1.20	
	2951.50	3.53	1.73		2963.50	3.99	1.87		
			5.20				5.60		
			2.57				2.76		
3126.00	19.61		3611.00	25.20					
4393.00	21.74				4373.00	44.80			
4416.00	16.19		3736.00	24.71					
5078.00	36.24		3568.00	17.52					

4253.25	23.44	3638.33	22.47
815.87	8.83	87.27	4.30
1953.00	2.41	1276.00	1.88
1492.00	2.21	1731.00	5.08
1677.00	2.33	1361.00	2.65
1466.00	2.39	1635.00	6.06
1647.00	2.33	1500.75	3.92
224.59	0.09	216.86	1.97
	26.49		12.90
	0.26		5.92
	26.75		18.83
	21.11		18.56
	1.27		1.01
	-0.27		-0.01

highlighted = image-confirmed

tox a,c

toxic a,b,c

toxic b,c

Plate	Well		Gene		GeneID	Cell Coun	% inf	Abs Dev
50023.00	A02	M-004439-	programmed cell deatl	9141.00	PDCD5	1258.00	2.07	3.25
50023.00	A04	M-004438-	programmed cell deatl	27250.00	PDCD4	2428.00	2.18	3.14
50023.00	A05	M-011726-	Meis homeobox 1	4211.00	MEIS1	2556.00	3.36	1.96
50023.00	A06	M-004436-	programmed cell deatl	11235.00	PDCD10	2859.00	3.67	1.65
50023.00	A07	M-003905-	RAB8A, member RAS o	4218.00	RAB8A	4759.00	5.17	0.15
50023.00	A08	M-017675-	PDGFA associated prot	11333.00	PDAP1	2516.00	1.83	3.49
50023.00	A09	M-005942-	meprin A, beta	4225.00	MEP1B	2606.00	6.37	1.05
50023.00	A10	M-012836-	tudor domain containi	23424.00	TDRD7	2575.00	5.32	0.00
50023.00	A11	M-014164-	mesoderm developme	59274.00	MESDC1	2562.00	3.32	2.00
50023.00	A12	M-012900-	protocadherin LKC	54825.00	PCLKC	3099.00	3.45	1.87
50023.00	A13	M-030446-	mesoderm developme	23184.00	MESDC2	1689.00	4.97	0.35
50023.00	A14	M-013194-	protocadherin 9	5101.00	PCDH9	3382.00	2.10	3.22
50023.00	A15	M-011331-	MFNG O-fucosylpeptid	4242.00	MFNG	2918.00	3.60	1.72
50023.00	A16	M-013372-	protocadherin 18	54510.00	PCDH18	3423.00	3.10	2.22
50023.00	A17	M-009019-	maltase-glucoamylase	8972.00	MGAM	2449.00	2.04	3.28
50023.00	A18	M-012528-	protocadherin 17	27253.00	PCDH17	2362.00	6.65	1.33
50023.00	A19	M-014865-	chromosome 9 open re	84302.00	C9orf125	1489.00	13.57	**8.25**
50023.00	A20	M-008748-	pterin-4 alpha-carbinol	5092.00	PCBD1	1757.00	5.29	0.03
50023.00	A21	M-022312-	RCC1 domain containir	91433.00	RCCD1	3461.00	7.34	2.02
50023.00	A23	M-016541-	F-box protein 31	79791.00	FBXO31	1452.00	2.62	2.70
50023.00	B02	M-012787-	Xg blood group	7499.00	XG	3197.00	0.56	4.76
50023.00	B04	M-013858-	NDRG family member	57447.00	NDRG2	5188.00	7.88	2.56
50023.00	B05	M-004233-	programmed cell deatl	10015.00	PDCD6IP	6308.00	4.71	0.61
50023.00	B06	M-010563-	N-myc downstream re	10397.00	NDRG1	3355.00	2.03	3.29
50023.00	B07	M-007651-	phosphodiesterase 6A,	5145.00	PDE6A	4911.00	6.64	1.32
50023.00	B08	M-010637-	calcium binding and co	10241.00	CALCOCO2	2312.00	3.68	1.64
50023.00	B09	M-007652-	phosphodiesterase 6B,	5158.00	PDE6B	4146.00	4.25	1.07
50023.00	B10	M-018571-	nudE nuclear distributi	81565.00	NDEL1	3414.00	3.05	2.27
50023.00	B11	M-007653-	phosphodiesterase 6C,	5146.00	PDE6C	4115.00	3.43	1.89
50023.00	B12	M-020625-	nudE nuclear distributi	54820.00	NDE1	918.00	1.20	4.12
50023.00	B13	M-009804-	peroxisomal D3,D2-en	10455.00	PECI	2975.00	10.56	5.24
50023.00	B14	M-019865-	natural cytotoxicity trig	9436.00	NCR2	3505.00	1.37	3.95
50023.00	B15	M-004463-	proline, glutamic acid a	27043.00	PELP1	4284.00	5.44	0.12
50023.00	B16	M-018862-	nuclear receptor coact	135112.00	NCOA7	4091.00	2.44	2.88
50023.00	B17	M-005990-	peptidase D	5184.00	PEPD	2572.00	2.61	2.72
50023.00	B18	M-013157-	nuclear receptor coact	57727.00	NCOA5	4258.00	1.67	3.65
50023.00	B19	M-018111-	PERP, TP53 apoptosis e	64065.00	PERP	4571.00	6.80	1.48
50023.00	B20	M-010640-	NCK-associated protei	10787.00	NCKAP1	4019.00	2.61	2.71
50023.00	B21	M-009542-	pescadillo homolog 1,	23481.00	PES1	3602.00	2.14	3.18
50023.00	B23	M-010331-	peroxisome biogenesis	5189.00	PEX1	4043.00	4.45	0.87
50023.00	C02	M-019679-	phosphatidylethanolar	5037.00	PEBP1	3933.00	4.40	0.92
50023.00	C04	M-012795-	PAX interacting (with t	22976.00	PAXIP1	3490.00	0.63	4.69
50023.00	C05	M-013565-	armadillo repeat conta	93436.00	ARMC6	4871.00	4.45	0.87
50023.00	C06	M-011098-	paired box gene 6 (ani	5080.00	PAX6	3615.00	6.20	0.88
50023.00	C07	M-018622-	suppressor of variegati	84787.00	SUV420H2	5753.00	4.47	0.85
50023.00	C08	M-003921-	paired box gene 2	5076.00	PAX2	3119.00	6.09	0.77

50023.00	C09	M-014156-	interferon, alpha 7	3444.00	IFNA7	4403.00	2.98	2.34
50023.00	C10	M-005984-	Parkinson disease (aut	11315.00	PARK7	1991.00	0.90	4.42
50023.00	C11	M-007687-	SPEG complex locus	10290.00	SPEG	3154.00	4.88	0.44
50023.00	C12	M-008053-	progestin and adipoQ r	152559.00	PAQR3	3071.00	5.50	0.18
50023.00	C13	M-015491-	coiled-coil domain con	115106.00	CCDC5	1721.00	4.13	1.19
50023.00	C14	M-018253-	pannexin 1	24145.00	PANX1	4287.00	8.37	3.05
50023.00	C15	M-026322-	phosphatidic acid phos	196051.00	PPAPDC1A	4195.00	3.34	1.98
50023.00	C16	M-003980-	phosphoribosylaminoi	10606.00	PAICS	3820.00	1.86	3.46
50023.00	C17	M-015567-	high-mobility group nu	3150.00	HMGN1	1692.00	1.65	3.67
50023.00	C18	M-010330-	platelet-activating fact	5048.00	PAFAH1B1	2791.00	8.17	2.85
50023.00	C19	M-017567-	high mobility group nu	10473.00	HMGN4	1096.00	4.11	1.21
50023.00	C20	M-011803-	poly(A) binding protein	8106.00	PABPN1	3310.00	3.08	2.24
50023.00	C21	M-020001-	homeobox (H6 family)	3166.00	HMX1	2384.00	1.85	3.47
50023.00	C23	M-003406-	hepatocyte nuclear fac	3172.00	HNF4A	2308.00	1.39	3.93
50023.00	D02	M-006540-	neuroblastoma, suppre	4681.00	NBL1	3875.00	0.54	4.78
50023.00	D04	M-012802-	N-acetyltransferase 6	24142.00	NAT6	3261.00	4.17	1.15
50023.00	D05	M-012622-	peroxisomal biogenesi	8800.00	PEX11A	4931.00	4.99	0.33
50023.00	D06	M-008884-	N-acetyltransferase 1 (	9.00	NAT1	4190.00	5.18	0.14
50023.00	D07	M-019520-	peroxisomal biogenesi	8799.00	PEX11B	2842.00	8.23	2.91
50023.00	D08	M-014387-	NMDA receptor regula	79664.00	NARG2	4385.00	9.24	3.92
50023.00	D09	M-012676-	peroxisomal biogenesi	5195.00	PEX14	3951.00	9.29	3.97
50023.00	D10	M-019254-	NLR family, pyrin doma	338321.00	NLRP9	3222.00	5.46	0.14
50023.00	D11	M-011945-	peroxisomal biogenesi	9409.00	PEX16	2473.00	2.51	2.81
50023.00	D12	M-019472-	NLR family, pyrin doma	126205.00	NLRP8	3905.00	9.53	4.21
50023.00	D13	M-019544-	peroxisomal biogenesi	8504.00	PEX3	3602.00	12.10	**6.78**
50023.00	D14	M-004423-	NLR family, pyrin doma	22861.00	NLRP1	2881.00	5.31	0.01
50023.00	D15	M-012648-	complement factor pro	5199.00	CFP	3716.00	2.88	2.44
50023.00	D16	M-011090-	N-acetylgalactosaminic	4668.00	NAGA	4042.00	4.06	1.26
50023.00	D17	M-013011-	prefoldin subunit 2	5202.00	PFDN2	2389.00	6.15	0.83
50023.00	D18	M-013091-	myosin, light chain 6, a	4637.00	MYL6	3934.00	7.24	1.92
50023.00	D19	M-012003-	profilin 1	5216.00	PFN1	4053.00	13.40	**8.08**
50023.00	D20	M-011739-	myosin, light chain 5, r	4636.00	MYL5	2607.00	2.38	2.94
50023.00	D21	M-008712-	phosphoglycerate mut	5224.00	PGAM2	6338.00	21.68	**16.36**
50023.00	D23	M-017610-	piggyBac transposable	267004.00	PGBD3	4201.00	3.83	1.49
50023.00	E02	M-018580-	chromosome 11 open	83638.00	C11orf68	1591.00	5.85	0.53
50023.00	E04	M-020026-	protein disulfide isome	10130.00	PDIA6	2483.00	7.85	2.53
50023.00	E05	M-008221-	heterogeneous nuclear	3178.00	HNRPA1	4107.00	32.90	**27.58**
50023.00	E06	M-013820-	family with sequence s	55578.00	FAM48A	1980.00	6.11	0.79
50023.00	E07	M-011692-	heterogeneous nuclear	3190.00	HNRPK	2013.00	7.15	1.83
50023.00	E08	M-006287-	purinergic receptor P2	9127.00	P2RXL1	3010.00	1.79	3.53
50023.00	E09	M-017345-	homeobox D3	3232.00	HOXD3	2512.00	6.73	1.41
50023.00	E10	M-006286-	purinergic receptor P2	5026.00	P2RX5	1781.00	3.93	1.39
50023.00	E11	M-009339-	haptoglobin	3240.00	HP	2242.00	11.02	5.70
50023.00	E12	M-020619-	phosphoinositide-3-kir	23533.00	PIK3R5	2219.00	4.10	1.22
50023.00	E13	M-019648-	4-hydroxyphenylpyruv	3242.00	HPD	3709.00	9.68	4.36
50023.00	E14	M-015273-	candidate tumor suppr	124641.00	OVCA2	3068.00	25.55	**20.23**
50023.00	E15	M-008735-	hypoxanthine phosphc	3251.00	HPRT1	4577.00	21.98	**16.66**

50023.00	E16	M-017390-	otoraplin	56914.00	OTOR	3090.00	7.28	1.96
50023.00	E17	M-011054-	Hermansky-Pudlak syn	3257.00	HPS1	3835.00	4.93	0.39
50023.00	E18	M-011942-	otoferlin	9381.00	OTOF	2339.00	6.07	0.75
50023.00	E19	M-017309-	Hermansky-Pudlak syn	84343.00	HPS3	5291.00	7.50	2.18
50023.00	E20	M-016394-	otoancorin	146183.00	OTOA	3964.00	18.11	12.79
50023.00	E21	M-017466-	Hermansky-Pudlak syn	79803.00	HPS6	4719.00	10.17	4.85
50023.00	E23	M-010287-	HRAS-like suppressor	57110.00	HRASLS	4670.00	11.56	6.24
50023.00	F02	M-011088-	myosin, light chain 3, a	4634.00	MYL3	3851.00	3.56	1.76
50023.00	F04	M-011087-	myosin, light chain 2, r	4633.00	MYL2	2975.00	5.61	0.29
50023.00	F05	M-013726-	prostaglandin D2 synth	27306.00	PGDS	4241.00	5.56	0.24
50023.00	F06	M-012816-	c-myc binding protein	26292.00	MYCBP	2743.00	7.18	1.86
50023.00	F07	M-010642-	progesterone receptor	10857.00	PGRMC1	3709.00	12.43	7.11
50023.00	F08	M-011735-	myxovirus (influenza vi	4599.00	MX1	4079.00	8.51	3.19
50023.00	F09	M-009011-	hypoxia-inducible facto	54681.00	PH-4	4597.00	11.77	6.45
50023.00	F10	M-012806-	mutY homolog (E. coli)	4595.00	MUTYH	3069.00	4.92	0.40
50023.00	F11	M-021411-	tetraspanin 32	10077.00	TSPAN32	2656.00	3.43	1.89
50023.00	F12	M-029113-	mucin 3A, cell surface a	4584.00	MUC3A	2547.00	6.12	0.80
50023.00	F13	M-011411-	pleckstrin homology-lil	7262.00	PHLDA2	3299.00	13.25	7.93
50023.00	F14	M-019667-	metaxin 1	4580.00	MTX1	1998.00	5.51	0.19
50023.00	F15	M-020169-	pleckstrin homology-lil	23612.00	PHLDA3	3175.00	5.51	0.19
50023.00	F16	M-009896-	5-methyltetrahydrofola	4548.00	MTR	3763.00	10.44	5.12
50023.00	F17	M-013848-	putative homeodomair	57157.00	PHTF2	4695.00	3.90	1.42
50023.00	F18	M-009577-	methylenetetrahydrofo	4522.00	MTHFD1	2883.00	14.15	8.83
50023.00	F19	M-012245-	phytanoyl-CoA 2-hydro	5264.00	PHYH	4709.00	18.35	13.03
50023.00	F20	M-020677-	mature T-cell prolifera	4515.00	MTCP1	3528.00	6.83	1.51
50023.00	F21	M-008167-	protein inhibitor of act	8554.00	PIAS1	4268.00	9.70	4.38
50023.00	F23	M-009108-	phosphatidylinositol (4	27124.00	PIB5PA	3183.00	3.39	1.93
50023.00	G02	M-008409-	oxysterol binding prote	114884.00	OSBPL10	2945.00	2.17	3.15
50023.00	G04	M-032263-	olfactory receptor, fam	26494.00	OR8G1	3489.00	2.81	2.51
50023.00	G05	M-011873-	HIV-1 Rev binding prot	3267.00	HRB	1856.00	3.99	1.33
50023.00	G06	M-032262-	olfactory receptor, fam	391632.00	OR7E35P	3241.00	4.01	1.31
50023.00	G07	M-011697-	histidine rich calcium b	3270.00	HRC	2870.00	3.17	2.15
50023.00	G08	M-025384-	olfactory receptor, fam	393046.00	OR2A5	3458.00	13.91	8.59
50023.00	G09	M-008216-	harakiri, BCL2 interacti	8739.00	HRK	2388.00	4.73	0.59
50023.00	G10	M-016269-	optineurin	10133.00	OPTN	1189.00	5.55	0.23
50023.00	G11	M-021242-	DCP1 decapping enzym	55802.00	DCP1A	3956.00	4.63	0.69
50023.00	G12	M-014595-	optic atrophy 3 (autos	80207.00	OPA3	2950.00	4.81	0.51
50023.00	G13	M-003408-	p65 protein	55566.00	HSAJ2425	3017.00	16.37	11.05
50023.00	G14	M-009000-	oligodendrocyte transc	167826.00	OLIG3	3133.00	13.18	7.86
50023.00	G15	M-008972-	hydroxy-delta-5-steroi	3283.00	HSD3B1	4580.00	3.86	1.46
50023.00	G16	M-009300-	oral-facial-digital syndr	8481.00	OFD1	3185.00	5.56	0.24
50023.00	G17	M-012542-	hydroxy-delta-5-steroi	3284.00	HSD3B2	3153.00	10.15	4.83
50023.00	G18	M-024101-	odz, odd Oz/ten-m hor	55714.00	ODZ3	3789.00	15.78	10.46
50023.00	G19	M-012343-	heat shock transcriptio	11077.00	HSF2BP	4885.00	10.03	4.71
50023.00	G20	M-010026-	oculocerebrorenal synd	4952.00	OCRL	2857.00	7.25	1.93
50023.00	G21	M-005168-	heat shock 70kDa prot	3303.00	HSPA1A	2967.00	4.89	0.43
50023.00	G23	M-005269-	heat shock 27kDa prot	3315.00	HSPB1	1656.00	1.45	3.87

50023.00	H02	M-013953-	Mdm2, transformed 3	27085.00	MTBP	3928.00	1.68	3.64
50023.00	H04	M-010953-	metallothionein 1L (ge	4500.00	MT1L	4345.00	5.75	0.43
50023.00	H05	M-016285-	phosphoinositide-3-kir	118788.00	PIK3AP1	4580.00	5.52	0.20
50023.00	H06	M-011732-	moesin	4478.00	MSN	3988.00	16.32	**11.00**
50023.00	H07	M-003292-	protein (peptidylprolyl	5301.00	PIN1L	3971.00	18.69	**13.37**
50023.00	H08	M-019665-	mutS homolog 3 (E. co	4437.00	MSH3	2859.00	8.04	2.72
50023.00	H09	M-021326-	myotubularin related p	54545.00	MTMR12	3333.00	2.64	2.68
50023.00	H10	M-021375-	murine retrovirus integ	10335.00	MRVI1	3470.00	3.80	1.52
50023.00	H11	M-018010-	phosphatidylinositol tr	5306.00	PITPNA	2792.00	6.77	1.45
50023.00	H12	M-014172-	paroxysmal nonkinesic	25953.00	PNKD	1573.00	3.37	1.95
50023.00	H13	M-004643-	piwi-like 1 (Drosophila	9271.00	PIWIL1	2274.00	3.12	2.20
50023.00	H14	M-010119-	mercaptopyruvate sulf	4357.00	MPST	1895.00	6.12	0.80
50023.00	H15	M-004642-	piwi-like 2 (Drosophila	55124.00	PIWIL2	2926.00	13.50	**8.18**
50023.00	H16	M-008034-	progestin and adipoQ r	54852.00	PAQR5	3726.00	10.68	5.36
50023.00	H17	M-013923-	PBX/knotted 1 homeol	63876.00	PKNOX2	4927.00	7.65	2.33
50023.00	H18	M-021327-	M-phase phosphoprot	10198.00	MPHOSPH	2914.00	7.45	2.13
50023.00	H19	M-009370-	phospholipase A2, grou	8399.00	PLA2G10	3685.00	8.14	2.82
50023.00	H20	M-020018-	M-phase phosphoprot	10200.00	MPHOSPH	2587.00	3.59	1.73
50023.00	H21	M-008820-	phospholipase A2, grou	8681.00	PLA2G4B	3034.00	2.77	2.55
50023.00	H23	M-009663-	phospholipase A2, grou	8605.00	PLA2G4C	5083.00	4.43	0.89
50023.00	I02	M-011345-	occludin	4950.00	OCLN	4002.00	1.80	3.52
50023.00	I04	M-027177-	obscurin, cytoskeletal	84033.00	OBSCN	2479.00	1.21	4.11
50023.00	I05	M-008830-	heat shock 27kDa prot	8988.00	HSPB3	2984.00	9.75	4.43
50023.00	I06	M-032248-	leptin receptor overlap	54741.00	LEPROT	2096.00	6.35	1.03
50023.00	I07	M-016607-	hsp70-interacting prot	23640.00	HSPBP1	2939.00	2.65	2.67
50023.00	I08	M-012907-	zinc finger protein 423	23090.00	ZNF423	2754.00	4.18	1.14
50023.00	I09	M-018876-	armadillo repeat conta	25852.00	ARMC8	2177.00	6.20	0.88
50023.00	I10	M-014165-	nyctalopin	60506.00	NYX	1344.00	2.31	3.01
50023.00	I11	M-020711-	chromosome 18 open	29090.00	C18orf55	1867.00	7.18	1.86
50023.00	I12	M-004754-	nucleolar and spindle a	51203.00	NUSAP1	3332.00	6.66	1.34
50023.00	I13	M-019649-	heat shock 10kDa prot	3336.00	HSPE1	2918.00	10.66	5.34
50023.00	I14	M-011980-	nucleoporin 214kDa	8021.00	NUP214	2332.00	5.75	0.43
50023.00	I15	M-032275-	succinate dehydrogena	54727.00	HSSUCCDH	2176.00	7.86	2.54
50023.00	I16	M-015902-	numb homolog (Droso	8650.00	NUMB	1602.00	2.75	2.57
50023.00	I17	M-008870-	forkhead box N2	3344.00	FOXN2	1199.00	9.42	4.10
50023.00	I18	M-008719-	nudix (nucleoside diph	318.00	NUDT2	2737.00	10.71	5.39
50023.00	I19	M-011055-	histatin 3	3347.00	HTN3	1662.00	11.19	5.87
50023.00	I20	M-018325-	nuclear distribution ge	10726.00	NUDC	2948.00	14.04	**8.72**
50023.00	I21	M-004899-	phosphatidic acid phos	84513.00	PPAPDC1B	2534.00	16.10	**10.78**
50023.00	I23	M-003267-	HUS1 checkpoint hom	3364.00	HUS1	2185.00	6.22	0.90
50023.00	J02	M-012181-	CD200 molecule	4345.00	CD200	3641.00	5.77	0.45
50023.00	J04	M-008976-	MLX interacting protei	22877.00	MLXIP	3753.00	10.47	5.15
50023.00	J05	M-015328-	phospholipase A2 rece	22925.00	PLA2R1	3636.00	3.33	1.99
50023.00	J06	M-020993-	molybdenum cofactor	55034.00	MOCOS	3572.00	2.88	2.44
50023.00	J07	M-008274-	phospholipase C, beta	5330.00	PLCB2	3053.00	10.55	5.23
50023.00	J08	M-011336-	meningioma (disrupte	4330.00	MN1	4446.00	18.98	**13.66**
50023.00	J09	M-019594-	pleckstrin	5341.00	PLEK	2462.00	9.75	4.43

50023.00	J10	M-012390-	multimerin 1	22915.00	MMRN1	3453.00	7.56	2.24
50023.00	J11	M-020861-	pleckstrin 2	26499.00	PLEK2	3475.00	6.39	1.07
50023.00	J12	M-004145-	matrix metallopeptidas	4323.00	MMP14	2638.00	5.19	0.13
50023.00	J13	M-012753-	pleckstrin homology d	10979.00	PLEKHC1	3408.00	9.15	3.83
50023.00	J14	M-005112-	membrane metallo-en	4311.00	MME	2133.00	3.28	2.04
50023.00	J15	M-003752-	growth arrest and DN	90480.00	GADD45GI	2659.00	7.03	1.71
50023.00	J16	M-015137-	methylmalonic aciduri	326625.00	MMAB	2611.00	12.91	7.59
50023.00	J17	M-015408-	proteolipid protein 1 (	5354.00	PLP1	2542.00	7.55	2.23
50023.00	J18	M-018697-	MARCKS-like 1	65108.00	MARCKSL1	1387.00	5.55	0.23
50023.00	J19	M-031971-	plexin A1	5361.00	PLXNA1	3215.00	8.96	3.64
50023.00	J20	M-016352-	myeloid/lymphoid or n	4298.00	MLLT1	2292.00	1.00	4.32
50023.00	J21	M-025454-	plexin A4, A	57671.00	PLXNA4A	2833.00	7.45	2.13
50023.00	J23	M-010653-	NODAL modulator 1	23420.00	NOMO1	3734.00	11.57	6.25
50023.00	K02	M-014208-	nuclear casein kinase a	64710.00	NUCKS1	4930.00	3.23	2.09
50023.00	K04	M-009314-	nuclear receptor inter	83714.00	NRIP2	2155.00	6.31	0.99
50023.00	K05	M-017519-	HUS1 checkpoint hom	135458.00	HUS1B	1754.00	5.82	0.50
50023.00	K06	M-013496-	neuregulin 2	9542.00	NRG2	3018.00	5.93	0.61
50023.00	K07	M-012448-	SET domain containing	29072.00	SETD2	1216.00	4.69	0.63
50023.00	K08	M-006334-	NAD(P)H dehydrogena	4835.00	NQO2	2780.00	6.22	0.90
50023.00	K09	M-012810-	PRP40 pre-mRNA proc	25766.00	PRPF40B	2864.00	7.58	2.26
50023.00	K10	M-011343-	neuronal pentraxin I	4884.00	NPTX1	1666.00	1.20	4.12
50023.00	K11	M-012763-	Huntingtin interacting	11153.00	HYPE	2037.00	3.49	1.83
50023.00	K12	M-015645-	tumor suppressor canc	10641.00	TUSC4	2161.00	8.24	2.92
50023.00	K13	M-028643-	inhibitor of Bruton aga	25998.00	IBTK	2203.00	6.17	0.85
50023.00	K14	M-015737-	nucleophosmin (nucle	4869.00	NPM1	2136.00	4.73	0.59
50023.00	K15	M-012407-	inducible T-cell co-stim	29851.00	ICOS	2979.00	1.75	3.57
50023.00	K16	M-021200-	nephrosis 2, idiopathic	7827.00	NPHS2	2047.00	6.40	1.08
50023.00	K17	M-005051-	inhibitor of DNA bindi	3397.00	ID1	2794.00	3.08	2.24
50023.00	K18	M-017216-	Niemann-Pick disease,	10577.00	NPC2	1953.00	9.88	4.56
50023.00	K19	M-009864-	inhibitor of DNA bindi	3398.00	ID2	3074.00	1.59	3.73
50023.00	K20	M-008857-	neuronal PAS domain	4862.00	NPAS2	1772.00	10.50	5.18
50023.00	K21	M-005899-	insulin-degrading enzy	3416.00	IDE	2216.00	8.57	3.25
50023.00	K23	M-009357-	isopentenyl-diphospha	3422.00	IDI1	2600.00	7.15	1.83
50023.00	L02	M-012703-	myeloid leukemia fact	8079.00	MLF2	1622.00	6.97	1.65
50023.00	L04	M-012013-	ataxin 3	4287.00	ATXN3	3664.00	5.65	0.33
50023.00	L05	M-005275-	phorbol-12-myristate-	5366.00	PMAIP1	2261.00	6.46	1.14
50023.00	L06	M-016471-	mirror-image polydact	145282.00	MIPOL1	3294.00	8.01	2.69
50023.00	L07	M-008454-	peripheral myelin prot	5375.00	PMP2	2845.00	9.17	3.85
50023.00	L08	M-011335-	macrophage migration	4282.00	MIF	3197.00	11.73	6.41
50023.00	L09	M-010616-	peripheral myelin prot	5376.00	PMP22	3663.00	5.19	0.13
50023.00	L10	M-010189-	microtubule associate	9645.00	MICAL2	1597.00	2.07	3.25
50023.00	L11	M-012722-	paraneoplastic antigen	9240.00	PNMA1	2881.00	1.91	3.41
50023.00	L12	M-016601-	chromosome 18 open	29919.00	C18orf8	3165.00	5.09	0.23
50023.00	L13	M-005164-	polymerase (DNA dire	5423.00	POLB	3037.00	5.17	0.15
50023.00	L14	M-011083-	class II, major histocon	4261.00	CIITA	2791.00	7.60	2.28
50023.00	L15	M-011594-	polymerase (RNA) III (	661.00	POLR3D	3216.00	1.90	3.42
50023.00	L16	M-009403-	monoglyceride lipase	11343.00	MGLL	1847.00	2.82	2.50

50023.00	L17	M-020595-	POM121 membrane gl	25812.00	POM121L1	1846.00	3.14	2.18
50023.00	L18	M-032261-	alkB, alkylation repair	121642.00	ALKBH2	2562.00	4.84	0.48
50023.00	L19	M-012443-	POM (POM121 homol	22932.00	POMZP3	3874.00	1.70	3.62
50023.00	L20	M-015931-	hypothetical protein M	196383.00	MGC7036	3330.00	5.86	0.54
50023.00	L21	M-019821-	POU domain, class 4, t	5458.00	POU4F2	3787.00	9.08	3.76
50023.00	L23	M-019591-	POU domain, class 5, t	5460.00	POU5F1	4703.00	5.12	0.20
50023.00	M02	M-006490-	nitric oxide synthase 3	4846.00	NOS3	2379.00	3.15	2.17
50023.00	M04	M-009496-	nitric oxide synthase 1	4842.00	NOS1	3079.00	5.23	0.09
50023.00	M05	M-012980-	Nipped-B homolog (Dr	25836.00	NIPBL	1449.00	1.93	3.39
50023.00	M06	M-020084-	nucleolar protein 1, 12	4839.00	NOL1	2668.00	2.77	2.55
50023.00	M07	M-011547-	immediate early respo	8870.00	IER3	3437.00	3.52	1.80
50023.00	M08	M-012059-	noggin	9241.00	NOG	3872.00	7.18	1.86
50023.00	M09	M-006465-	interferon, alpha-indu	3429.00	IFI27	1566.00	3.83	1.49
50023.00	M10	M-009835-	natural killer-tumor re	4820.00	NKTR	3638.00	11.60	6.28
50023.00	M11	M-016368-	interferon-induced pro	10561.00	IFI44	3171.00	3.60	1.72
50023.00	M12	M-016047-	natural killer cell grou	4818.00	NKG7	2723.00	4.22	1.10
50023.00	M13	M-019616-	interferon-induced pro	3434.00	IFIT1	2301.00	6.08	0.76
50023.00	M14	M-015988-	interleukin 32	9235.00	IL32	1709.00	1.93	3.39
50023.00	M15	M-012582-	interferon-induced pro	3433.00	IFIT2	2562.00	3.55	1.77
50023.00	M16	M-014037-	chromosome 17 open	64149.00	C17orf75	1876.00	2.67	2.65
50023.00	M17	M-017691-	interferon-induced pro	3437.00	IFIT3	4392.00	8.95	3.63
50023.00	M18	M-020555-	nerve growth factor re	27018.00	NGFRAP1	3424.00	7.01	1.69
50023.00	M19	M-020102-	interferon-induced pro	24138.00	IFIT5	3058.00	2.94	2.38
50023.00	M20	M-015648-	nuclear factor related	4798.00	NFRKB	1728.00	6.37	1.05
50023.00	M21	M-020103-	interferon induced tra	10581.00	IFITM2	3003.00	4.93	0.39
50023.00	M23	M-014116-	interferon induced tra	10410.00	IFITM3	3515.00	1.62	3.70
50023.00	N02	M-008734-	peptidase (mitochond	23203.00	PMPCA	2602.00	6.99	1.67
50023.00	N04	M-009654-	rho/rac guanine nucle	23370.00	ARHGEF18	3153.00	6.22	0.90
50023.00	N05	M-026943-	POU domain, class 6, t	5463.00	POU6F1	3124.00	6.02	0.70
50023.00	N06	M-026203-	olfactory receptor, fam	158131.00	OR1Q1	2309.00	4.20	1.12
50023.00	N07	M-012188-	preferentially express	23532.00	PRAME	2471.00	9.43	4.11
50023.00	N08	M-032254-	v-myc myelocytomato	10408.00	MYCNOS	3513.00	13.04	**7.72**
50023.00	N09	M-019925-	proline-rich protein Bs	5542.00	PRB1	2593.00	1.85	3.47
50023.00	N10	M-010363-	jumonji domain contai	23210.00	JMJD6	2056.00	9.63	4.31
50023.00	N11	M-016647-	peroxisome proliferat	23082.00	PPRC1	3094.00	4.52	0.80
50023.00	N12	M-017157-	pre T-cell antigen rece	171558.00	PTCRA	1595.00	17.68	**12.36**
50023.00	N13	M-019491-	protein regulator of cy	9055.00	PRC1	2554.00	8.26	2.94
50023.00	N14	M-003528-	polypyrimidine tract bi	5725.00	PTBP1	2345.00	2.56	2.76
50023.00	N15	M-015816-	papillary renal cell car	5546.00	PRCC	2510.00	5.42	0.10
50023.00	N16	M-016779-	proline-serine-threoni	9050.00	PSTPIP2	3415.00	12.01	**6.69**
50023.00	N17	M-020712-	PR domain containing	56981.00	PRDM11	2862.00	0.77	4.55
50023.00	N18	M-016239-	proline-serine-threoni	9051.00	PSTPIP1	2639.00	6.37	1.05
50023.00	N19	M-007040-	PR domain containing	59336.00	PRDM13	1302.00	2.15	3.17
50023.00	N20	M-017583-	proteasome (prosome,	5714.00	PSMD8	540.00	4.26	1.06
50023.00	N21	M-024425-	PR domain containing	93166.00	PRDM6	4656.00	6.27	0.95
50023.00	N23	M-020669-	PR domain containing	56978.00	PRDM8	2011.00	3.08	2.24
50023.00	O02	M-012001-	nuclear factor of kappa	4795.00	NFKBIL1	2416.00	6.83	1.51

50023.00	O04	M-004766-	nuclear factor of kappa	4794.00	NFKBIE	2164.00	10.07	4.75
50023.00	O05	M-012712-	interferon, alpha 1	3439.00	IFNA1	2169.00	4.24	1.08
50023.00	O06	M-003915-	neuroepithelial cell tra	10276.00	NET1	2122.00	5.28	0.04
50023.00	O07	M-012713-	interferon gamma rece	3460.00	IFNGR2	2945.00	5.57	0.25
50023.00	O08	M-008327-	nei endonuclease VIII-l	79661.00	NEIL1	2750.00	6.04	0.72
50023.00	O09	M-019615-	interferon-related dev	3475.00	IFRD1	3233.00	6.93	1.61
50023.00	O10	M-020082-	neurofilament, light po	4747.00	NEFL	3246.00	4.04	1.28
50023.00	O11	M-013748-	receptor (chemosenso	64108.00	RTP4	2960.00	3.85	1.47
50023.00	O12	M-019600-	NADH dehydrogenase	4728.00	NDUFS8	3640.00	7.94	2.62
50023.00	O13	M-021110-	insulin-like growth fact	51214.00	IGF2AS	2777.00	2.52	2.80
50023.00	O14	M-019816-	NADH dehydrogenase	4725.00	NDUFS5	2372.00	5.06	0.26
50023.00	O15	M-010601-	insulin-like growth fact	3482.00	IGF2R	2049.00	3.22	2.10
50023.00	O16	M-013861-	NDRG family member	65009.00	NDRG4	2322.00	4.69	0.63
50023.00	O17	M-032276-	immunoglobulin heavy	3502.00	IGHG3	2839.00	2.85	2.47
50023.00	O18	M-013761-	family with sequence s	54537.00	FAM35A	1832.00	7.75	2.43
50023.00	O19	M-016551-	hypothetical protein M	92806.00	MGC16385	3451.00	6.09	0.77
50023.00	O20	M-018569-	hypothetical protein M	348035.00	MGC40069	2859.00	1.43	3.89
50023.00	O21	M-003438-	retinoic acid receptor,	5915.00	RARB	2775.00	1.41	3.91
50023.00	O23	M-008585-	xanthine dehydrogena	7498.00	XDH	2223.00	1.89	3.43
50023.00	P02	M-009621-	proteasome (prosome,	5713.00	PSMD7	1083.00	2.31	3.01
50023.00	P04	M-012006-	proteasome (prosome,	5711.00	PSMD5	2298.00	2.57	2.75
50023.00	P05	M-019692-	serglycin	5552.00	SRGN	2411.00	3.07	2.25
50023.00	P06	M-011365-	proteasome (prosome,	5710.00	PSMD4	2188.00	9.64	4.32
50023.00	P07	M-012129-	proteoglycan 4	10216.00	PRG4	2137.00	3.70	1.62
50023.00	P08	M-006024-	proteasome (prosome,	10213.00	PSMD14	1109.00	3.25	2.07
50023.00	P09	M-007675-	protein kinase, AMP-ac	5564.00	PRKAB1	2197.00	5.10	0.22
50023.00	P10	M-011757-	proteasome (prosome,	5683.00	PSMA2	1249.00	6.41	1.09
50023.00	P11	M-007672-	protein kinase, AMP-ac	5565.00	PRKAB2	2179.00	1.70	3.62
50023.00	P12	M-006018-	presenilin 2 (Alzheimer	5664.00	PSEN2	2228.00	6.82	1.50
50023.00	P13	M-009693-	protein kinase, AMP-ac	51422.00	PRKAG2	3144.00	7.63	2.31
50023.00	P14	M-013688-	pleckstrin homology, S	27128.00	PSCD4	1827.00	4.21	1.11
50023.00	P15	M-017354-	zinc finger, MYND-type	23613.00	ZMYND8	3791.00	8.26	2.94
50023.00	P16	M-020525-	PRP31 pre-mRNA proc	26121.00	PRPF31	1816.00	10.68	5.36
50023.00	P17	M-016416-	protein kinase C, delta	112464.00	PRKCDBP	2434.00	5.09	0.23
50023.00	P18	M-016913-	prospero-related home	5629.00	PROX1	2602.00	4.96	0.36
50023.00	P19	M-019271-	prion protein 2 (dublet	23627.00	PRND	2026.00	3.21	2.11
50023.00	P20	M-010630-	prominin 1	8842.00	PROM1	1360.00	10.00	4.68
50023.00	P21	M-011101-	prion protein (p27-30)	5621.00	PRNP	1411.00	3.76	1.56
50023.00	P23	M-017603-	ATPase family, AAA do	29028.00	ATAD2	1729.00	2.49	2.83
					mdn	2916.00	5.32	2.19
					3MAD			6.57
					MADc			3.24
50023.00	C22	2.81	3574.00	18.91				
50023.00	D22					3813.00	38.42	
50023.00	E22					3668.00	34.79	
50023.00	F22					3223.00	35.93	
					mn	3568.00	36.38	

				sd	307.45	1.86
50023.00	G22				2649.00	8.68
50023.00	H22				2154.00	4.13
50023.00	I22	431.00	81.90			
50023.00	J22				1253.00	3.43
				mn	2018.67	5.42
				sd	707.77	2.85
				3psSD		5.57
				3ngSD		8.55
				SumSD		14.13
				DiffMn		30.96
				SmovrDiff		0.46
				1minus		0.54

rZ	Cell Coun	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	
-1.00	1078.00	4.45	1.42	0.67	1103.00	7.52	3.69	1.56	
-0.97	2650.00	3.25	0.22	0.10	2160.00	4.49	0.66	0.28	
-0.60	1618.00	2.29	0.74	-0.35	2520.00	3.10	0.73	-0.31	
-0.51	2430.00	3.50	0.47	0.22	3370.00	4.96	1.13	0.48	
-0.05	1910.00	2.41	0.62	-0.29	3604.00	3.69	0.14	-0.06	
-1.08	1951.00	4.10	1.07	0.50	2977.00	3.53	0.30	-0.13	
0.33	1833.00	3.55	0.52	0.24	3371.00	10.35	6.52	2.76	
0.00	2017.00	7.19	4.16	1.96	2528.00	7.52	3.69	1.56	
-0.62	1782.00	2.36	0.67	-0.31	2503.00	6.31	2.48	1.05	
-0.57	1700.00	3.71	0.68	0.32	4412.00	12.29	8.46	3.58	
-0.11	1626.00	4.61	1.58	0.75	2865.00	9.91	6.08	2.57	
-0.99	2018.00	1.49	1.54	-0.72	2916.00	4.70	0.87	0.37	
-0.53	1920.00	5.73	2.70	1.27	3539.00	5.20	1.37	0.58	
-0.68	3520.00	3.44	0.41	0.19	4783.00	3.39	0.44	-0.19	
-1.01	1394.00	4.16	1.13	0.53	3123.00	3.94	0.11	0.05	
0.41	1366.00	2.12	0.91	-0.42	3416.00	11.77	7.94	3.36	
2.54	1208.00	8.94	5.91	2.78	1555.00	18.33	14.50	6.13	y
-0.01	966.00	2.80	0.24	-0.11	2236.00	3.04	0.79	-0.33	
0.62	1900.00	4.95	1.92	0.90	3792.00	7.30	3.47	1.47	
-0.83	1280.00	2.27	0.76	-0.36	1749.00	5.15	1.32	0.56	
-1.47	2156.00	0.42	2.61	-1.23	4757.00	1.77	2.06	-0.87	
0.79	2679.00	2.65	0.38	-0.18	5901.00	5.58	1.75	0.74	
-0.19	4328.00	5.45	2.42	1.14	6163.00	5.03	1.20	0.51	
-1.01	2272.00	2.82	0.21	-0.10	4597.00	3.05	0.78	-0.33	
0.41	1768.00	1.02	2.01	-0.94	4860.00	1.77	2.06	-0.87	
-0.51	986.00	2.74	0.29	-0.13	3242.00	3.42	0.41	-0.17	
-0.33	2387.00	2.30	0.73	-0.34	5168.00	1.59	2.24	-0.95	
-0.70	2311.00	1.51	1.52	-0.71	4534.00	4.48	0.65	0.27	
-0.58	2335.00	2.10	0.93	-0.44	4751.00	3.20	0.63	-0.27	
-1.27	986.00	1.32	1.71	-0.80	1171.00	0.43	3.40	-1.44	
1.62	2380.00	5.92	2.89	1.36	3455.00	6.51	2.68	1.13	
-1.22	1559.00	2.05	0.98	-0.46	4140.00	0.85	2.98	-1.26	
0.04	2121.00	1.60	1.43	-0.67	4150.00	2.24	1.59	-0.67	
-0.89	1770.00	1.19	1.84	-0.86	4162.00	2.28	1.55	-0.65	
-0.84	835.00	0.72	2.31	-1.08	3029.00	1.22	2.61	-1.10	
-1.13	2084.00	0.48	2.55	-1.20	5227.00	0.92	2.91	-1.23	
0.46	2352.00	2.04	0.99	-0.46	4903.00	3.20	0.63	-0.27	
-0.83	1841.00	1.74	1.29	-0.60	4185.00	2.41	1.42	-0.60	
-0.98	2552.00	3.17	0.14	0.07	4915.00	1.73	2.10	-0.89	
-0.27	2525.00	2.02	1.01	-0.47	5177.00	2.30	1.53	-0.65	
-0.28	3403.00	1.68	1.36	-0.63	4205.00	3.59	0.24	-0.10	
-1.45	3371.00	1.31	1.72	-0.81	3839.00	0.39	3.44	-1.45	
-0.27	2233.00	2.37	0.66	-0.31	3526.00	1.90	1.93	-0.82	
0.27	2390.00	1.72	1.31	-0.62	2959.00	1.66	2.17	-0.92	
-0.26	2751.00	0.58	2.45	-1.15	3966.00	2.07	1.76	-0.75	
0.24	1987.00	1.86	1.17	-0.55	3397.00	3.77	0.06	-0.03	

-0.72	2043.00	0.59	2.44	-1.15	3718.00	1.80	2.03	-0.86	
-1.36	874.00	0.80	2.23	-1.05	1579.00	0.95	2.88	-1.22	
-0.13	1771.00	0.68	2.35	-1.10	2595.00	1.23	2.60	-1.10	
0.06	2214.00	0.81	2.22	-1.04	2895.00	3.42	0.41	-0.17	
-0.37	996.00	1.51	1.52	-0.71	2373.00	3.75	0.08	-0.03	
0.94	2333.00	2.40	0.63	-0.29	4371.00	4.53	0.70	0.30	
-0.61	1488.00	0.60	2.43	-1.14	4040.00	1.56	2.27	-0.96	
-1.07	1544.00	0.58	2.45	-1.15	3568.00	1.18	2.65	-1.12	
-1.13	1188.00	1.26	1.77	-0.83	2637.00	1.06	2.77	-1.17	
0.88	830.00	2.77	0.26	-0.12	2937.00	4.46	0.63	0.27	
-0.37	531.00	3.20	0.17	0.08	1600.00	3.38	0.46	-0.19	
-0.69	1803.00	0.67	2.36	-1.11	2863.00	4.44	0.61	0.26	
-1.07	1664.00	0.60	2.43	-1.14	3682.00	0.76	3.07	-1.30	
-1.21	1796.00	0.89	2.14	-1.00	3344.00	2.27	1.56	-0.66	
-1.47	2983.00	0.91	2.12	-1.00	3882.00	2.40	1.43	-0.61	
-0.35	2471.00	2.55	0.48	-0.22	3814.00	2.25	1.58	-0.67	
-0.10	3383.00	4.85	1.82	0.86	4952.00	2.71	1.12	-0.48	
-0.04	2642.00	2.65	0.38	-0.18	4869.00	4.79	0.96	0.40	
0.90	1497.00	4.41	1.38	0.65	3169.00	5.84	2.01	0.85	
1.21	2292.00	2.71	0.32	-0.15	3692.00	3.79	0.04	-0.02	
1.23	2098.00	2.34	0.69	-0.32	4181.00	4.52	0.69	0.29	
0.05	1971.00	3.20	0.17	0.08	4143.00	2.73	1.10	-0.47	
-0.87	1476.00	0.75	2.28	-1.07	3063.00	2.35	1.48	-0.63	
1.30	2713.00	5.68	2.65	1.25	4292.00	3.80	0.03	-0.01	
2.09	2339.00	5.43	2.40	1.13	2940.00	3.20	0.63	-0.27	
0.00	2223.00	2.61	0.42	-0.20	3678.00	2.91	0.92	-0.39	
-0.75	1801.00	0.50	2.53	-1.19	4806.00	1.77	2.06	-0.87	
-0.39	2315.00	3.15	0.12	0.06	4193.00	1.50	2.33	-0.98	
0.26	1411.00	4.18	1.15	0.54	3311.00	3.17	0.66	-0.28	
0.59	1984.00	7.61	**4.58**	2.15	4858.00	4.26	0.43	0.18	
2.49	2740.00	5.69	2.66	1.25	5286.00	3.41	0.42	-0.18	
-0.91	1808.00	0.83	2.20	-1.03	3671.00	0.54	3.29	-1.39	
5.05	4844.00	7.54	**4.51**	2.12	6833.00	8.84	**5.01**	2.12	y
-0.46	2713.00	0.88	2.15	-1.01	4718.00	0.72	3.11	-1.31	
0.16	1857.00	3.28	0.25	0.12	2826.00	3.57	0.26	-0.11	
0.78	2268.00	4.45	1.42	0.67	3456.00	2.08	1.75	-0.74	
8.51	3657.00	15.72	**12.69**	5.96	4398.00	12.62	**8.79**	3.72	y
0.25	1765.00	0.28	2.75	-1.29	2532.00	1.78	2.05	-0.87	
0.57	1482.00	1.08	1.95	-0.91	2508.00	3.15	0.68	-0.29	
-1.09	2553.00	0.78	2.25	-1.05	2908.00	1.03	2.80	-1.18	
0.44	1094.00	0.27	2.76	-1.29	2320.00	1.98	1.85	-0.78	
-0.43	1187.00	1.77	1.26	-0.59	1973.00	2.18	1.65	-0.70	
1.76	1536.00	4.62	1.59	0.75	2618.00	3.32	0.51	-0.21	
-0.37	880.00	0.00	3.03	-1.42	2377.00	0.84	2.99	-1.26	
1.35	2721.00	1.40	1.63	-0.77	3122.00	2.31	1.52	-0.64	
6.24	2063.00	2.23	0.80	-0.37	3420.00	6.70	2.87	1.21	
5.14	3621.00	7.68	**4.65**	2.19	4203.00	5.42	1.59	0.67	y

0.61	1849.00	2.16	0.87	-0.41	4230.00	4.63	0.80	0.34	
-0.12	2700.00	2.22	0.81	-0.38	4045.00	2.23	1.61	-0.68	
0.23	616.00	0.16	2.87	-1.34	2515.00	0.99	2.84	-1.20	
0.67	2763.00	1.05	1.98	-0.93	5110.00	3.11	0.72	-0.30	
3.95	2840.00	3.63	0.60	0.28	3970.00	5.44	1.61	0.68	
1.50	3236.00	1.55	1.48	-0.70	5105.00	8.07	4.24	1.79	
1.93	3593.00	1.42	1.61	-0.75	4735.00	4.20	0.37	0.16	
-0.54	2572.00	0.47	2.56	-1.20	4437.00	3.36	0.47	-0.20	
0.09	1460.00	22.67	**19.64**	9.23	3426.00	6.01	2.18	0.92	
0.08	2806.00	2.21	0.82	-0.38	5154.00	4.31	0.48	0.20	
0.58	1728.00	8.10	**5.07**	2.38	3351.00	5.19	1.36	0.58	
2.19	1425.00	5.26	2.23	1.05	3997.00	5.93	2.10	0.89	
0.98	1995.00	2.81	0.22	-0.10	4035.00	4.63	0.80	0.34	
1.99	2644.00	7.26	4.23	1.99	5244.00	7.69	3.86	1.63	
-0.12	1871.00	2.30	0.73	-0.34	4887.00	4.07	0.24	0.10	
-0.58	1929.00	1.40	1.63	-0.76	3313.00	2.32	1.51	-0.64	
0.25	1545.00	6.47	3.44	1.62	3647.00	5.95	2.12	0.90	
2.45	2117.00	6.57	3.54	1.66	3674.00	9.06	**5.23**	2.21	y
0.06	1095.00	8.22	**5.19**	2.44	3044.00	4.57	0.74	0.31	
0.06	2091.00	2.58	0.45	-0.21	3193.00	1.66	2.17	-0.92	
1.58	1338.00	3.74	0.71	0.33	3322.00	3.25	0.58	-0.24	
-0.44	2715.00	5.08	2.05	0.97	5813.00	4.03	0.20	0.08	
2.73	2211.00	5.38	2.35	1.11	3639.00	3.96	0.13	0.05	
4.02	2843.00	3.38	0.35	0.16	5644.00	9.48	**5.65**	2.39	y
0.47	2261.00	2.48	0.55	-0.26	4088.00	3.62	0.21	-0.09	
1.35	3920.00	4.80	1.77	0.83	5989.00	3.51	0.32	-0.14	
-0.59	3337.00	2.49	0.54	-0.25	4524.00	3.76	0.07	-0.03	
-0.97	1898.00	4.22	1.19	0.56	3725.00	2.01	1.82	-0.77	
-0.77	2103.00	4.95	1.92	0.90	3514.00	4.24	0.41	0.17	
-0.41	1150.00	7.57	**4.54**	2.13	2775.00	6.09	2.26	0.96	
-0.40	1881.00	3.56	0.53	0.25	3060.00	4.28	0.45	0.19	
-0.66	1682.00	2.97	0.06	-0.02	2437.00	3.69	0.14	-0.06	
2.65	2003.00	10.43	**7.40**	3.48	3635.00	12.63	**8.80**	3.72	y
-0.18	1047.00	5.83	2.80	1.32	2705.00	3.59	0.24	-0.10	
0.07	390.00	3.08	0.05	0.02	1014.00	5.33	1.50	0.63	
-0.21	2116.00	8.79	**5.76**	2.71	3695.00	6.22	2.39	1.01	
-0.15	1585.00	4.16	1.13	0.53	2859.00	3.95	0.12	0.05	
3.41	2240.00	2.95	0.08	-0.04	2698.00	6.89	3.06	1.30	
2.43	1108.00	8.03	**5.00**	2.35	2200.00	3.45	0.38	-0.16	x
-0.45	2877.00	2.26	0.77	-0.36	3560.00	2.47	1.36	-0.57	
0.07	2617.00	7.87	**4.84**	2.28	3624.00	9.60	**5.77**	2.44	y
1.49	2523.00	4.80	1.77	0.83	3917.00	8.63	**4.80**	2.03	
3.23	3689.00	7.83	**4.80**	2.26	5377.00	8.98	**5.15**	2.18	y
1.45	4010.00	9.98	**6.95**	3.26	4995.00	7.49	3.66	1.55	
0.60	2845.00	7.03	4.00	1.88	3473.00	11.09	**7.26**	3.07	
-0.13	2426.00	0.91	2.12	-1.00	3760.00	1.28	2.55	-1.08	
-1.19	1343.00	1.71	1.32	-0.62	2180.00	0.69	3.14	-1.33	

-1.12	2160.00	0.69	2.34	-1.10	3904.00	4.43	0.60	0.25	
0.14	3175.00	2.30	0.73	-0.34	3582.00	5.19	1.36	0.58	
0.06	3401.00	2.56	0.47	-0.22	3533.00	5.75	1.92	0.81	
3.40	3653.00	7.56	4.53	2.13	3418.00	10.47	6.64	2.81	y
4.12	2854.00	9.85	6.82	3.20	3812.00	12.46	8.63	3.65	y
0.84	3247.00	8.44	5.41	2.54	3450.00	8.03	4.20	1.78	
-0.83	2982.00	1.84	1.19	-0.55	3517.00	2.36	1.47	-0.62	
-0.47	2756.00	1.92	1.11	-0.52	3811.00	1.63	2.20	-0.93	
0.45	2739.00	3.65	0.62	0.29	3287.00	2.59	1.24	-0.53	
-0.60	1552.00	0.64	2.39	-1.12	1541.00	1.82	2.01	-0.85	
-0.68	2364.00	0.59	2.44	-1.14	2566.00	2.81	1.02	-0.43	
0.25	1097.00	0.82	2.21	-1.04	2241.00	1.07	2.76	-1.17	
2.52	3018.00	4.94	1.91	0.90	2647.00	5.36	1.53	0.65	
1.66	3704.00	5.83	2.80	1.32	4311.00	6.84	3.01	1.27	
0.72	3515.00	1.19	1.84	-0.86	4702.00	4.62	0.79	0.33	
0.66	2524.00	4.12	1.09	0.51	3367.00	3.33	0.50	-0.21	
0.87	2917.00	1.92	1.11	-0.52	4060.00	2.98	0.85	-0.36	
-0.53	1666.00	1.44	1.59	-0.74	3913.00	3.71	0.12	-0.05	
-0.79	1769.00	0.17	2.86	-1.34	4551.00	1.76	2.07	-0.88	
-0.27	3983.00	2.08	0.95	-0.44	5569.00	5.98	2.15	0.91	
-1.08	3526.00	1.62	1.41	-0.66	3640.00	3.02	0.81	-0.34	
-1.27	2231.00	1.66	1.37	-0.64	2037.00	5.55	1.72	0.73	
1.37	3362.00	6.60	3.57	1.68	4011.00	10.27	6.44	2.72	
0.32	1711.00	3.86	0.83	0.39	2221.00	2.39	1.44	-0.61	
-0.82	2645.00	1.93	1.10	-0.52	2677.00	2.69	1.14	-0.48	
-0.35	2937.00	3.00	0.03	-0.01	2274.00	2.07	1.76	-0.75	
0.27	3320.00	1.84	1.19	-0.56	1935.00	2.33	1.50	-0.64	
-0.93	1496.00	0.27	2.76	-1.30	1320.00	2.73	1.10	-0.47	
0.57	2134.00	1.87	1.16	-0.54	2187.00	2.01	1.82	-0.77	
0.42	3261.00	3.68	0.65	0.31	3233.00	5.47	1.64	0.70	
1.65	2754.00	4.76	1.73	0.81	3115.00	4.46	0.63	0.27	
0.13	2387.00	2.01	1.02	-0.48	1851.00	2.86	0.97	-0.41	
0.78	2277.00	3.21	0.18	0.08	2138.00	4.21	0.38	0.16	
-0.79	1512.00	0.60	2.43	-1.14	1989.00	4.58	0.75	0.32	
1.27	1307.00	1.22	1.81	-0.85	2252.00	6.88	3.05	1.29	
1.66	2067.00	2.71	0.32	-0.15	3325.00	10.74	6.91	2.92	
1.81	1511.00	4.17	1.14	0.54	1742.00	6.54	2.71	1.15	
2.69	2978.00	5.74	2.71	1.28	3702.00	13.32	9.49	4.01	x
3.33	2601.00	2.81	0.22	-0.10	2785.00	13.54	9.71	4.10	x
0.28	2216.00	1.35	1.68	-0.79	2121.00	5.80	1.97	0.83	
0.14	2853.00	3.08	0.05	0.03	4936.00	6.18	2.35	0.99	
1.59	3843.00	2.89	0.14	-0.06	4989.00	12.97	9.14	3.86	
-0.61	3044.00	1.38	1.65	-0.77	4008.00	2.69	1.14	-0.48	
-0.75	4094.00	4.10	1.07	0.51	4175.00	2.59	1.24	-0.53	
1.61	3932.00	5.93	2.90	1.36	5077.00	7.90	4.07	1.72	
4.22	4831.00	10.35	7.32	3.44	5250.00	12.48	8.65	3.66	y
1.37	3428.00	7.15	4.12	1.94	3766.00	6.00	2.17	0.92	

0.69	2976.00	3.29	0.26	0.13	3811.00	8.29	4.46	1.89	
0.33	3165.00	1.86	1.17	-0.55	3638.00	2.91	0.92	-0.39	
-0.04	3305.00	2.63	0.40	-0.18	4112.00	5.01	1.18	0.50	
1.18	3305.00	2.00	1.03	-0.48	3714.00	4.93	1.10	0.46	
-0.63	1749.00	1.26	1.77	-0.83	2301.00	2.91	0.92	-0.39	
0.53	3225.00	3.69	0.66	0.31	2953.00	3.39	0.44	-0.19	
2.34	3575.00	10.15	**7.12**	3.35	3457.00	7.09	3.26	1.38	y
0.69	2598.00	8.70	**5.67**	2.66	3615.00	6.31	2.48	1.05	
0.07	1693.00	3.07	0.04	0.02	2268.00	3.88	0.05	0.02	
1.12	3917.00	9.85	**6.82**	3.21	4649.00	13.92	**10.09**	4.27	y
-1.33	3272.00	1.99	1.04	-0.49	3305.00	2.97	0.86	-0.37	
0.66	2611.00	2.91	0.12	-0.05	3316.00	4.89	1.06	0.45	
1.93	2669.00	6.26	3.23	1.52	3797.00	5.08	1.25	0.53	
-0.64	3583.00	1.26	1.77	-0.83	4132.00	6.53	2.70	1.14	
0.31	2429.00	2.68	0.35	-0.16	1852.00	10.48	**6.65**	2.81	
0.15	1590.00	0.75	2.28	-1.07	2066.00	1.50	2.33	-0.98	
0.19	3221.00	2.92	0.11	-0.05	2737.00	7.86	4.03	1.70	
-0.19	1315.00	0.61	2.42	-1.14	1524.00	4.07	0.24	0.10	
0.28	2847.00	2.60	0.43	-0.20	2444.00	3.23	0.60	-0.25	
0.70	3483.00	3.22	0.19	0.09	2769.00	9.21	**5.38**	2.27	
-1.27	1251.00	0.16	2.87	-1.35	2073.00	4.44	0.61	0.26	
-0.56	1672.00	3.77	0.74	0.35	2090.00	8.90	**5.07**	2.14	
0.90	1769.00	1.87	1.16	-0.54	2081.00	8.12	4.29	1.81	
0.26	1966.00	4.22	1.19	0.56	3029.00	7.33	3.50	1.48	
-0.18	2414.00	1.49	1.54	-0.72	2450.00	4.86	1.03	0.43	
-1.10	3641.00	1.65	1.38	-0.65	4271.00	6.30	2.47	1.04	
0.33	2651.00	7.51	**4.48**	2.10	2563.00	11.78	**7.95**	3.36	y
-0.69	2341.00	1.54	1.49	-0.70	2610.00	3.87	0.04	0.02	
1.41	1036.00	2.12	0.91	-0.42	1669.00	8.99	**5.16**	2.18	
-1.15	3153.00	4.00	0.97	0.46	2903.00	7.41	3.58	1.51	
1.60	1654.00	12.70	**9.67**	4.54	2839.00	25.54	**21.71**	9.18	y
1.01	2278.00	4.21	1.18	0.56	3254.00	10.97	**7.14**	3.02	
0.57	2860.00	3.53	0.50	0.24	4578.00	8.43	4.60	1.95	
0.51	1352.00	3.03	0.00	0.00	2282.00	5.17	1.34	0.57	
0.10	4881.00	10.35	**7.32**	3.44	4662.00	11.80	**7.97**	3.37	y
0.35	1959.00	4.13	1.10	0.52	1169.00	3.76	0.07	-0.03	
0.83	5049.00	6.10	3.07	1.44	3474.00	3.63	0.20	-0.09	
1.19	4420.00	4.00	0.97	0.46	2670.00	6.70	2.87	1.22	
1.98	3279.00	7.93	**4.90**	2.30	3292.00	6.44	2.61	1.10	
-0.04	4089.00	3.42	0.39	0.19	2935.00	2.56	1.27	-0.54	
-1.00	1399.00	1.36	1.67	-0.78	1071.00	4.01	0.18	0.08	
-1.05	2751.00	3.96	0.93	0.44	2948.00	2.51	1.32	-0.56	
-0.07	2973.00	3.40	0.37	0.17	3159.00	10.45	**6.62**	2.80	
-0.05	3050.00	4.10	1.07	0.50	2311.00	3.46	0.37	-0.16	
0.70	3818.00	9.66	**6.63**	3.12	2692.00	3.90	0.07	0.03	
-1.05	3798.00	2.24	0.79	-0.37	3400.00	1.47	2.36	-1.00	
-0.77	2827.00	1.34	1.69	-0.79	2683.00	3.43	0.40	-0.17	

-0.67	3428.00	4.76	1.73	0.81	3398.00	6.30	2.47	1.04	
-0.15	3321.00	4.94	1.91	0.90	3531.00	6.77	2.94	1.24	
-1.11	3340.00	3.32	0.29	0.14	3365.00	1.99	1.84	-0.78	
0.17	4132.00	3.10	0.07	0.03	4059.00	2.44	1.39	-0.59	
1.16	4100.00	9.49	6.46	3.04	3521.00	8.61	4.78	2.02	y
-0.06	4810.00	3.16	0.13	0.06	5363.00	7.42	3.59	1.52	
-0.67	2639.00	3.75	0.72	0.34	2574.00	3.46	0.37	-0.16	
-0.03	2733.00	4.06	1.03	0.49	2944.00	2.31	1.52	-0.64	
-1.04	2686.00	1.79	1.24	-0.58	1660.00	2.23	1.60	-0.68	
-0.78	2687.00	1.56	1.47	-0.69	2302.00	1.91	1.92	-0.81	
-0.55	2851.00	0.63	2.40	-1.12	4926.00	2.66	1.17	-0.49	
0.58	2343.00	2.39	0.64	-0.30	3967.00	6.71	2.88	1.22	
-0.46	1694.00	1.71	1.32	-0.62	1490.00	3.56	0.27	-0.12	
1.94	4107.00	9.79	6.76	3.18	3482.00	4.71	0.88	0.37	
-0.53	3052.00	1.80	1.23	-0.57	2604.00	2.50	1.33	-0.56	
-0.34	2870.00	1.53	1.50	-0.70	3210.00	1.18	2.65	-1.12	
0.24	2991.00	5.65	2.62	1.23	2723.00	2.39	1.44	-0.61	
-1.04	3505.00	3.11	0.08	0.04	2985.00	0.67	3.16	-1.34	
-0.54	2735.00	4.24	1.21	0.57	2800.00	2.96	0.87	-0.37	
-0.82	1680.00	2.80	0.23	-0.11	1858.00	3.18	0.65	-0.28	
1.12	3741.00	5.29	2.26	1.06	3781.00	2.99	0.84	-0.36	
0.52	4855.00	7.68	4.65	2.19	3946.00	4.76	0.93	0.40	
-0.73	3180.00	3.02	0.01	0.00	3169.00	1.70	2.13	-0.90	
0.32	1561.00	7.50	4.47	2.10	2653.00	3.13	0.70	-0.30	
-0.12	2949.00	3.32	0.29	0.14	3960.00	3.21	0.62	-0.26	
-1.14	3709.00	0.08	2.95	-1.38	4000.00	5.48	1.65	0.70	
0.52	2111.00	3.74	0.71	0.34	3873.00	3.98	0.15	0.06	
0.28	2917.00	7.10	4.07	1.91	4631.00	8.21	4.38	1.85	
0.22	3285.00	7.70	4.67	2.20	5310.00	9.11	5.28	2.23	x
-0.34	2354.00	2.46	0.57	-0.26	3671.00	1.61	2.22	-0.94	
1.27	2563.00	6.24	3.21	1.51	3648.00	6.47	2.64	1.12	
2.38	3561.00	11.18	8.15	3.83	3437.00	4.04	0.21	0.09	y
-1.07	2250.00	2.18	0.85	-0.40	3527.00	3.46	0.37	-0.16	
1.33	2026.00	7.95	4.92	2.31	1940.00	2.22	1.61	-0.68	
-0.24	1927.00	3.17	0.14	0.07	2864.00	2.16	1.67	-0.70	
3.81	1273.00	16.03	13.00	6.11	1786.00	14.50	10.67	4.51	y
0.91	2811.00	14.94	11.91	5.60	3914.00	8.43	4.60	1.95	
-0.85	2315.00	4.32	1.29	0.61	3422.00	1.81	2.02	-0.85	
0.03	2890.00	5.26	2.23	1.05	4278.00	4.53	0.70	0.30	
2.06	3410.00	6.83	3.80	1.79	3370.00	3.38	0.45	-0.19	
-1.40	3464.00	2.54	0.49	-0.23	3128.00	3.39	0.44	-0.19	
0.32	3072.00	5.66	2.63	1.24	4394.00	4.89	1.06	0.45	
-0.98	459.00	2.18	0.85	-0.40	1319.00	3.64	0.19	-0.08	
-0.33	524.00	3.63	0.60	0.28	623.00	2.09	1.74	-0.74	
0.29	3459.00	3.35	0.32	0.15	5053.00	3.46	0.37	-0.15	
-0.69	2441.00	3.32	0.29	0.14	3613.00	2.02	1.81	-0.76	
0.47	3192.00	4.48	1.45	0.68	2353.00	2.04	1.79	-0.76	

1.47	2593.00	13.07	10.04	4.72	1381.00	2.39	1.44	-0.61	
-0.33	2455.00	1.79	1.24	-0.58	2664.00	0.94	2.89	-1.22	
-0.01	2102.00	4.09	1.06	0.50	3052.00	4.75	0.92	0.39	
0.08	2879.00	5.04	2.01	0.94	4159.00	5.22	1.39	0.59	
0.22	2729.00	2.38	0.65	-0.30	2907.00	1.07	2.76	-1.17	
0.50	1401.00	3.07	0.04	0.02	1949.00	1.90	1.93	-0.82	
-0.39	2375.00	1.64	1.39	-0.65	2812.00	3.88	0.05	0.02	
-0.45	2413.00	3.15	0.12	0.06	2309.00	0.82	3.01	-1.27	
0.81	3245.00	8.26	5.23	2.46	3874.00	4.59	0.76	0.32	
-0.86	3078.00	0.94	2.09	-0.98	3087.00	1.20	2.63	-1.11	
-0.08	2355.00	5.82	2.79	1.31	2397.00	4.80	0.97	0.41	
-0.65	1826.00	3.40	0.37	0.17	3134.00	2.46	1.37	-0.58	
-0.19	2470.00	5.22	2.19	1.03	2659.00	2.18	1.65	-0.70	
-0.76	1643.00	1.64	1.39	-0.65	3126.00	2.94	0.89	-0.37	
0.75	1711.00	4.50	1.47	0.69	2737.00	4.97	1.14	0.48	
0.24	3204.00	2.78	0.25	-0.12	3984.00	4.27	0.44	0.19	
-1.20	2978.00	2.35	0.68	-0.32	3551.00	4.31	0.48	0.20	
-1.21	2120.00	1.51	1.52	-0.71	3508.00	5.16	1.33	0.56	
-1.06	1034.00	4.26	1.23	0.58	2683.00	2.27	1.56	-0.66	
-0.93	698.00	0.72	2.31	-1.08	1290.00	0.78	3.05	-1.29	
-0.85	3297.00	2.91	0.12	-0.05	3174.00	3.59	0.24	-0.10	
-0.69	1867.00	0.21	2.82	-1.32	3193.00	1.35	2.48	-1.05	
1.33	1643.00	5.60	2.57	1.21	2457.00	5.49	1.66	0.70	
-0.50	1935.00	4.60	1.57	0.74	3583.00	6.42	2.59	1.10	
-0.64	843.00	0.47	2.56	-1.20	1504.00	4.12	0.29	0.12	
-0.07	2218.00	2.84	0.19	-0.09	3441.00	5.93	2.10	0.89	
0.34	1291.00	3.95	0.92	0.43	1545.00	2.39	1.44	-0.61	
-1.12	1763.00	1.47	1.56	-0.73	2612.00	2.34	1.49	-0.63	
0.46	2195.00	4.28	1.25	0.59	3052.00	6.85	3.02	1.28	
0.72	3567.00	7.49	4.46	2.09	4133.00	8.93	5.10	2.16	y
-0.34	1967.00	3.56	0.53	0.25	2131.00	5.54	1.71	0.72	
0.91	3476.00	3.25	0.22	0.11	4465.00	3.61	0.22	-0.09	
1.66	1605.00	4.17	1.14	0.54	2307.00	6.50	2.67	1.13	
-0.07	2716.00	5.23	2.20	1.03	3313.00	5.64	1.81	0.77	
-0.11	2584.00	4.61	1.58	0.74	3322.00	10.60	6.77	2.86	
-0.65	2627.00	2.51	0.52	-0.24	3056.00	3.86	0.03	0.01	
1.44	1621.00	0.80	2.23	-1.04	2159.00	10.14	6.31	2.67	
-0.48	1697.00	4.77	1.74	0.82	2518.00	6.04	2.21	0.93	
-0.87	1547.00	1.62	1.41	-0.66	2563.00	3.28	0.55	-0.23	
	2354.50	3.03	1.44		3368.50	3.83	1.60		
			4.32				4.79		
			2.13				2.36		
2446.00	20.11		5665.00	34.37					
2661.00	22.85		4830.00	25.20					
3019.00	12.29		4941.00	24.19					
2253.00	19.09		4506.00	27.61					
2594.75	18.58		4985.50	27.84					

328.28	4.49	489.15	4.58
1107.00	0.99	2138.00	4.91
1580.00	0.32	2965.00	6.75
1183.00	1.01	1440.00	6.60
1889.00	2.70	2264.00	5.30
1439.75	1.26	2201.75	5.89
364.30	1.02	624.70	0.92
	13.46		13.75
	3.05		2.76
	16.51		16.51
	17.33		21.95
	0.95		0.75
	0.05		0.25

toxic b

debris a,c
debris b,c

debris a,b

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50024.00	A02	M-003544- signal trans	6774.00	STAT3	4141.00	2.03	2.66
50024.00	A04	M-018709- actin-bindi	137735.00	ABRA	3531.00	2.15	2.54
50024.00	A05	M-008462- prostaglan	9536.00	PTGES	2696.00	1.93	2.76
50024.00	A06	M-017361- signal trans	10254.00	STAM2	1893.00	4.23	0.46
50024.00	A07	M-005207- prothymos	5757.00	PTMA	1448.00	11.26	6.57
50024.00	A08	M-019732- SH3 and cy	6769.00	STAC	2187.00	5.85	1.16
50024.00	A09	M-019928- RNA bindin	5940.00	RBMY1A1	1214.00	5.44	0.75
50024.00	A10	M-017234- suppressio	54879.00	ST7L	2844.00	6.12	1.43
50024.00	A11	M-008289- retinol binc	5950.00	RBP4	1051.00	3.62	1.07
50024.00	A12	M-020119- Sjogren's sy	10534.00	SSSCA1	2054.00	5.31	0.62
50024.00	A13	M-012504- recombinat	11317.00	RBPJL	1032.00	2.23	2.46
50024.00	A14	M-011901- sarcospan (	8082.00	SSPN	499.00	9.02	4.33
50024.00	A15	M-015968- RAB11 fam	80223.00	RAB11FIP1	1801.00	2.94	1.75
50024.00	A16	M-020042- synovial sa	6760.00	SS18	1860.00	10.00	5.31
50024.00	A17	M-012650- recoverin	5957.00	RCVRN	2545.00	8.49	3.80
50024.00	A18	M-015368- serine/argi	23524.00	SRRM2	2360.00	7.37	2.68
50024.00	A19	M-021277- REC8 homo	9985.00	REC8	2077.00	1.83	2.86
50024.00	A20	M-019716- signal reco	6731.00	SRP72	2432.00	2.06	2.63
50024.00	A21	M-013597- RecQ prote	5965.00	RECQL	2802.00	7.03	2.34
50024.00	A23	M-020710- reprimo, TI	56475.00	RPRM	2692.00	6.54	1.85
50024.00	B05	M-021064- signal trans	55250.00	STATIP1	1459.00	0.96	3.73
50024.00	B07	M-019802- stress-indu	10963.00	STIP1	3866.00	3.36	1.33
50024.00	B09	M-015159- serine/thre	114790.00	STK11IP	1118.00	0.18	4.51
50024.00	B11	M-019342- stathmin-li	11075.00	STMN2	1908.00	1.57	3.12
50024.00	B13	M-013600- stathmin-li	50861.00	STMN3	1797.00	1.67	3.02
50024.00	B15	M-016971- stomatin	2040.00	STOM	1407.00	0.78	3.91
50024.00	B17	M-015712- stereocilin	161497.00	STRC	2599.00	1.65	3.04
50024.00	B19	M-008949- sulfotransf	27284.00	SULT1B1	2009.00	1.34	3.35
50024.00	B21	M-009661- sulfotransf	6822.00	SULT2A1	3054.00	4.81	0.12
50024.00	B23	M-016234- suppressor	6829.00	SUPT5H	1956.00	0.31	4.38
50024.00	C02	M-009549- sterol regu	6721.00	SREBF2	3520.00	4.69	0.00
50024.00	C04	M-019726- spectrin, al	6708.00	SPTA1	1934.00	7.29	2.60
50024.00	C05	M-032267- RFNG O-fu	5986.00	RFNG	4189.00	4.06	0.63
50024.00	C06	M-012718- sprouty ho	10251.00	SPRY3	3897.00	4.47	0.23
50024.00	C07	M-017463- chromoson	28984.00	C13orf15	2864.00	5.76	1.07
50024.00	C08	M-005206- sprouty ho	10253.00	SPRY2	3510.00	5.04	0.35
50024.00	C09	M-024506- Rho-guanir	64283.00	RGNEF	3264.00	15.99	11.30
50024.00	C10	M-027339- sprouty ho	10252.00	SPRY1	2125.00	12.89	8.20
50024.00	C11	M-019354- Rh-associat	6005.00	RHAG	2244.00	10.78	6.09
50024.00	C12	M-019983- spindlin 1	10927.00	SPIN1	2708.00	3.73	0.96
50024.00	C13	M-013183- Rh blood gı	6006.00	RHCE	1588.00	4.22	0.47
50024.00	C14	M-016274- Spi-C trans	121599.00	SPIC	1807.00	3.93	0.76
50024.00	C15	M-017229- Rh blood gı	6007.00	RHD	1607.00	3.36	1.33
50024.00	C16	M-019987- S-phase res	10638.00	SPHAR	2301.00	3.35	1.34
50024.00	C17	M-009692- Ras homol	6009.00	RHEB	2155.00	3.67	1.02
50024.00	C18	M-015681- spastic para	23111.00	SPG20	1249.00	3.04	1.65

50024.00	C19	M-008213- Rho GTPas	9743.00	RICS	1163.00	2.92	1.77
50024.00	C20	M-017462- sperm asso	9043.00	SPAG9	701.00	3.99	0.70
50024.00	C21	M-007058- zinc finger	65986.00	ZBTB10	1259.00	1.99	2.70
50024.00	C23	M-005002- RIO kinase	55781.00	RIOK2	2467.00	1.74	2.95
50024.00	D05	M-005161- transformi	6867.00	TACC1	1921.00	3.70	0.99
50024.00	D07	M-012356- transformi	10579.00	TACC2	2442.00	6.76	2.07
50024.00	D09	M-004155- transformi	10460.00	TACC3	1753.00	2.17	2.52
50024.00	D11	M-004568- tumor-asso	4072.00	TACSTD1	1840.00	7.55	2.86
50024.00	D13	M-032253- TAF13 RNA	6884.00	TAF13	1241.00	5.08	0.39
50024.00	D15	M-008930- TAF15 RNA	8148.00	TAF15	1734.00	8.94	4.25
50024.00	D17	M-009341- TAF2 RNA	6873.00	TAF2	1032.00	4.46	0.23
50024.00	D19	M-006878- TAF4 RNA	6874.00	TAF4	1175.00	8.43	3.74
50024.00	D21	M-003714- transgelin	6876.00	TAGLN	1539.00	3.83	0.86
50024.00	D23	M-011468- transgelin	8407.00	TAGLN2	2225.00	3.33	1.36
50024.00	E02	M-012481- sperm asso	9576.00	SPAG6	5996.00	10.06	5.37
50024.00	E04	M-004312- sperm asso	6674.00	SPAG1	1749.00	6.06	1.37
50024.00	E05	M-015969- retinaldeh	6017.00	RLBP1	2531.00	3.67	1.02
50024.00	E06	M-015955- Sp2 transc	6668.00	SP2	3671.00	5.50	0.81
50024.00	E07	M-012270- retinitis pig	6101.00	RP1	1773.00	5.25	0.56
50024.00	E08	M-012143- SRY (sex de	6658.00	SOX3	1973.00	7.81	3.12
50024.00	E09	M-019139- DCN1, defe	54165.00	DCUN1D1	2880.00	6.28	1.59
50024.00	E10	M-014616- sclerosteos	50964.00	SOST	2800.00	7.79	3.10
50024.00	E11	M-015479- retinitis pig	57096.00	RPGRIP1	1156.00	8.22	3.53
50024.00	E12	M-008323- sorbitol de	6652.00	SORD	919.00	7.40	2.71
50024.00	E13	M-015951- RaP2 intera	10900.00	RPIP8	1770.00	6.78	2.09
50024.00	E14	M-008364- superoxide	6647.00	SOD1	2014.00	7.15	2.46
50024.00	E15	M-012164- ribosomal	6134.00	RPL10	645.00	8.68	3.99
50024.00	E16	M-009037- suppressor	122809.00	SOCS4	2399.00	5.00	0.31
50024.00	E17	M-013703- ribosomal	6135.00	RPL11	524.00	11.07	**6.38**
50024.00	E18	M-004299- suppressor	9021.00	SOCS3	1616.00	3.09	1.60
50024.00	E19	M-013601- ribosomal	23521.00	RPL13A	717.00	7.25	2.56
50024.00	E20	M-005240- sterol O-ac	6646.00	SOAT1	1889.00	5.56	0.87
50024.00	E21	M-011146- ribosomal	6161.00	RPL32	589.00	4.75	0.06
50024.00	E23	M-011147- ribosomal	6167.00	RPL37	769.00	2.34	2.35
50024.00	F05	M-017380- suppressio	6767.00	ST13	3024.00	3.11	1.58
50024.00	F07	M-012855- survival of	6607.00	SMN2	751.00	8.66	3.97
50024.00	F09	M-019349- parathymo	5763.00	PTMS	1962.00	4.33	0.36
50024.00	F11	M-018793- pleiotrophi	5764.00	PTN	1310.00	3.89	0.80
50024.00	F13	M-013223- signal-regu	140885.00	SIRPA	1477.00	3.59	1.10
50024.00	F15	M-017788- signal-regu	128646.00	SIRPD	2218.00	6.04	1.35
50024.00	F17	M-012135- protein tyr	5790.00	PTPRCAP	2250.00	2.44	2.25
50024.00	F19	M-010377- 6-pyruvoyl	5805.00	PTS	3406.00	4.99	0.30
50024.00	F21	M-011820- pituitary tu	754.00	PTTG1IP	1900.00	2.53	2.16
50024.00	F23	M-012746- pituitary tu	10744.00	PTTG2	1079.00	2.87	1.82
50024.00	G02	M-012524- sorting nex	27131.00	SNX5	5795.00	10.08	5.39
50024.00	G04	M-012985- SNRPN ups	8926.00	SNURF	2362.00	5.17	0.48
50024.00	G05	M-013478- ribosomal	6168.00	RPL37A	632.00	8.07	3.38

50024.00	G06	M-018536- stannin	8303.00	SNN	1831.00	3.93	0.76
50024.00	G07	M-013611- ribosomal	6125.00	RPL5	710.00	13.10	**8.41**
50024.00	G08	M-016479- Smad nucle	79753.00	SNIP1	1634.00	6.36	1.67
50024.00	G09	M-019738- ribonuclea	11102.00	RPP14	1159.00	4.49	0.20
50024.00	G10	M-011109- synuclein,	6622.00	SNCA	1542.00	3.70	0.99
50024.00	G11	M-013627- ribosomal	6217.00	RPS16	750.00	8.13	3.44
50024.00	G12	M-015399- small nucle	6617.00	SNAPC1	1912.00	5.96	1.27
50024.00	G13	M-003771- ribosomal	6223.00	RPS19	450.00	9.33	4.64
50024.00	G14	M-022719- SMYD fami	10322.00	SMYD5	1907.00	6.50	1.81
50024.00	G15	M-011156- ribosomal	6232.00	RPS27	1345.00	7.21	2.52
50024.00	G16	M-013737- SET and M	64754.00	SMYD3	1704.00	3.87	0.82
50024.00	G17	M-011157- ribosomal	6235.00	RPS29	174.00	41.38	**36.69**
50024.00	G18	M-020291- SET and M	56950.00	SMYD2	1524.00	1.25	3.44
50024.00	G19	M-011138- ribosomal	6191.00	RPS4X	351.00	9.97	5.28
50024.00	G20	M-017273- spermine s	6611.00	SMS	1132.00	3.18	1.51
50024.00	G21	M-011131- ribosomal	6203.00	RPS9	662.00	5.74	1.05
50024.00	G23	M-019972- RCD1 requi	9125.00	RQCD1	1204.00	2.74	1.95
50024.00	H05	M-014110- pituitary tu	26255.00	PTTG3	1513.00	1.98	2.71
50024.00	H07	M-013952- poliovirus	25945.00	PVRL3	917.00	1.74	2.95
50024.00	H09	M-029357- Pvt1 oncog	5820.00	PVT1	2141.00	4.48	0.21
50024.00	H11	M-012594- peroxisom	5824.00	PEX19	883.00	5.32	0.63
50024.00	H13	M-021171- peroxisom	5827.00	PXMP2	1066.00	3.47	1.22
50024.00	H15	M-009569- phosphoryl	5836.00	PYGL	1910.00	8.85	4.16
50024.00	H17	M-009367- phosphoryl	5837.00	PYGM	1139.00	6.85	2.16
50024.00	H19	M-011371- quiescin Q	5768.00	QSCN6	1110.00	5.14	0.45
50024.00	H21	M-010823- RAB10, me	10890.00	RAB10	1982.00	1.01	3.68
50024.00	H23	M-010533- RAB2A, me	5862.00	RAB2A	2399.00	1.96	2.73
50024.00	I02	M-017244- SWI/SNF r	6602.00	SMARCD1	5469.00	2.83	1.86
50024.00	I04	M-010813- SWI/SNF r	6599.00	SMARCC1	4995.00	8.51	3.82
50024.00	I05	M-016120- Ras-relate	58528.00	RRAGD	4098.00	2.73	1.96
50024.00	I06	M-010536- SWI/SNF r	6598.00	SMARCB1	2278.00	2.02	2.67
50024.00	I07	M-019212- Ras suppre	6251.00	RSU1	2681.00	5.22	0.53
50024.00	I08	M-011392- SWI/SNF r	6594.00	SMARCA1	4768.00	9.12	4.43
50024.00	I09	M-012527- rhabdoid t	27156.00	RTDR1	2481.00	5.28	0.59
50024.00	I10	M-012599- slit homolo	6585.00	SLIT1	1632.00	6.92	2.23
50024.00	I11	M-015936- RING1 and	23429.00	RYBP	1901.00	1.16	3.53
50024.00	I12	M-007603- solute carri	6531.00	SLC6A3	1705.00	5.04	0.35
50024.00	I13	M-006292- ryanodine	6261.00	RYR1	1616.00	1.67	3.02
50024.00	I14	M-021089- solute carri	22950.00	SLC4A1AP	2038.00	10.60	5.91
50024.00	I15	M-011766- S100 calciu	6281.00	S100A10	2069.00	3.14	1.55
50024.00	I16	M-007578- solute carri	8501.00	SLC43A1	1590.00	10.94	6.25
50024.00	I17	M-012139- S100 calciu	6283.00	S100A12	1498.00	3.20	1.49
50024.00	I18	M-007485- solute carri	291.00	SLC25A4	1392.00	3.23	1.46
50024.00	I19	M-011768- S100 calciu	6276.00	S100A5	1517.00	2.57	2.12
50024.00	I20	M-007452- solute carri	5002.00	SLC22A18	1940.00	2.27	2.42
50024.00	I21	M-011769- S100 calciu	6278.00	S100A7	2569.00	7.32	2.63
50024.00	I23	M-019361- serum amy	6288.00	SAA1	545.00	3.49	1.20

50024.00	J05	M-019214- RAB22A, m	57403.00	RAB22A	2665.00	7.65	2.96
50024.00	J07	M-010065- RAB31, me	11031.00	RAB31	2621.00	1.87	2.82
50024.00	J09	M-009781- RAB35, me	11021.00	RAB35	2941.00	3.98	0.71
50024.00	J11	M-010822- RAB3D, me	9545.00	RAB3D	848.00	2.83	1.86
50024.00	J13	M-016616- RAB3A inte	5866.00	RAB3IL1	1353.00	6.80	2.11
50024.00	J15	M-008539- RAB4A, me	5867.00	RAB4A	2673.00	8.75	4.06
50024.00	J17	M-004010- RAB5B, me	5869.00	RAB5B	3237.00	8.80	4.11
50024.00	J19	M-032266- RAB9, mem	9366.00	RAB9P1	4589.00	13.69	**9.00**
50024.00	J21	M-019457- Rab9 effec	10244.00	RABEPK	2281.00	3.24	1.45
50024.00	J23	M-020136- Rab accept	10567.00	RABAC1	1315.00	2.59	2.10
50024.00	K02	M-007384- solute carri	6559.00	SLC12A3	5493.00	3.31	1.38
50024.00	K04	M-010535- SKI-like onc	6498.00	SKIL	5054.00	3.96	0.73
50024.00	K05	M-020571- spastic ata	26278.00	SACS	4282.00	7.08	2.39
50024.00	K06	M-003927- v-ski sarco	6497.00	SKI	4622.00	4.95	0.26
50024.00	K07	M-004229- SAM doma	64092.00	SAMSN1	3103.00	2.19	2.50
50024.00	K08	M-013337- signal-regu	55423.00	SIRPG	2499.00	2.76	1.93
50024.00	K09	M-017283- squamous	9092.00	SART1	870.00	6.78	2.09
50024.00	K10	M-012193- signal-regu	10326.00	SIRPB1	1581.00	2.59	2.10
50024.00	K11	M-003703- tetraspani	6302.00	TSPAN31	2478.00	2.18	2.51
50024.00	K12	M-012769- silver hom	6490.00	SILV	1243.00	5.15	0.46
50024.00	K13	M-019217- Shwachma	51119.00	SBDS	3638.00	6.16	1.47
50024.00	K14	M-019717- SCL/TAL1 i	6491.00	STIL	1885.00	4.14	0.55
50024.00	K15	M-011772- ataxin 2	6311.00	ATXN2	2493.00	2.41	2.28
50024.00	K16	M-009503- sucrase-iso	6476.00	SI	756.00	3.70	0.99
50024.00	K17	M-032268- ataxin 8 op	6315.00	ATXN8OS	3260.00	4.60	0.09
50024.00	K18	M-031192- SHC (Src h	25759.00	SHC2	3374.00	2.96	1.73
50024.00	K19	M-003704- secretory c	10066.00	SCAMP2	4218.00	9.06	4.37
50024.00	K20	M-024645- SH3 and m	85358.00	SHANK3	2627.00	7.38	2.69
50024.00	K21	M-012808- SREBF cha	22937.00	SCAP	3500.00	1.57	3.12
50024.00	K23	M-013241- scavenger	51435.00	SCARA3	1509.00	2.32	2.37
50024.00	L05	M-009565- RAB, mem	11020.00	RABL4	3581.00	8.66	3.97
50024.00	L07	M-008836- ras-related	5881.00	RAC3	3874.00	5.94	1.25
50024.00	L09	M-011760- RAD52 ho	5893.00	RAD52	4396.00	11.22	**6.53**
50024.00	L11	M-004592- RAD54-like	8438.00	RAD54L	3627.00	6.78	2.09
50024.00	L13	M-003295- RAD9 hom	5883.00	RAD9A	2080.00	5.82	1.13
50024.00	L15	M-012296- retinoic aci	10742.00	RAI2	1794.00	2.45	2.24
50024.00	L17	M-009266- ralA bindin	10928.00	RALBP1	2508.00	12.80	**8.11**
50024.00	L18	M-010491- X-ray repai	7520.00	XRCC5	3789.00	5.36	0.67
50024.00	L19	M-008248- Ral GEF wit	9649.00	RALGPS1	4889.00	9.82	5.13
50024.00	L20	M-004494- X-ray repai	7518.00	XRCC4	1630.00	5.40	0.71
50024.00	L21	M-020543- denticles	51514.00	DTL	3017.00	3.78	0.91
50024.00	L23	M-006627- RAN bindin	5902.00	RANBP1	3099.00	4.29	0.40
50024.00	M02	M-006657- SH3 and P	9644.00	SH3PXD2A	5222.00	4.27	0.42
50024.00	M04	M-014748- SH3-domai	30011.00	SH3KBP1	4990.00	8.40	3.71
50024.00	M05	M-012087- scavenger	950.00	SCARB2	3807.00	2.97	1.72
50024.00	M06	M-015728- SH3-domai	6457.00	SH3GL3	4814.00	2.93	1.76
50024.00	M07	M-011533- sciellin	8796.00	SCEL	5108.00	2.64	2.05

50024.00	M08	M-019582- SH3-domai	6455.00	SH3GL1	4993.00	7.15	2.46
50024.00	M09	M-012290- secretoglob	10648.00	SCGB1D1	2299.00	2.96	1.73
50024.00	M10	M-015398- SH3-domai	6452.00	SH3BP2	2880.00	4.83	0.14
50024.00	M11	M-015732- secretoglob	117156.00	SCGB3A2	3936.00	3.89	0.80
50024.00	M12	M-019969- SH2 domai	10045.00	SH2D3A	1337.00	2.84	1.85
50024.00	M13	M-012809- sex comb o	22955.00	SCMH1	1510.00	1.85	2.84
50024.00	M14	M-017851- SH2 domai	9047.00	SH2D2A	2805.00	4.53	0.16
50024.00	M15	M-020090- sex comb o	10389.00	SCML2	2725.00	4.26	0.43
50024.00	M16	M-011075- sarcoglyca	6445.00	SGCG	1771.00	1.75	2.94
50024.00	M17	M-006295- sodium cha	6336.00	SCN10A	2576.00	2.10	2.59
50024.00	M18	M-017292- sarcoglyca	6444.00	SGCD	2442.00	3.93	0.76
50024.00	M19	M-006296- sodium cha	11280.00	SCN11A	3143.00	6.05	1.36
50024.00	M20	M-018905- sarcoglyca	6443.00	SGCB	3969.00	6.58	1.89
50024.00	M21	M-006501- sodium cha	6332.00	SCN7A	2915.00	4.36	0.33
50024.00	M23	M-006503- sodium cha	6335.00	SCN9A	1011.00	1.09	3.60
50024.00	N02	M-004361- X-ray repai	7516.00	XRCC2	1305.00	7.89	3.20
50024.00	N04	M-010356- exportin, t	11260.00	XPOT	2926.00	8.00	3.31
50024.00	N05	M-026112- RAN bindin	26953.00	RANBP6	2401.00	4.54	0.15
50024.00	N06	M-003030- exportin 1	7514.00	XPO1	1844.00	7.54	2.85
50024.00	N07	M-012061- RAN bindin	10048.00	RANBP9	2460.00	8.86	4.17
50024.00	N08	M-016040- xeroderma	7508.00	XPC	2955.00	5.99	1.30
50024.00	N09	M-010364- RAP1B, me	5908.00	RAP1B	3823.00	13.08	**8.39**
50024.00	N10	M-009552- X-box bindi	7494.00	XBP1	2137.00	12.17	**7.48**
50024.00	N11	M-009052- RAP2B, me	5912.00	RAP2B	941.00	2.02	2.67
50024.00	N12	M-017323- Wilms tum	9589.00	WTAP	1277.00	10.02	5.33
50024.00	N13	M-031919- Ras associa	65059.00	RAPH1	1250.00	12.16	**7.47**
50024.00	N14	M-003939- wingless-ty	7474.00	WNT5A	909.00	10.45	5.76
50024.00	N15	M-004107- raptor	57521.00	KIAA1303	1422.00	2.67	2.02
50024.00	N16	M-012156- Wolf-Hirsc	7469.00	WHSC2	2396.00	0.63	4.06
50024.00	N17	M-009925- retinoic aci	5918.00	RARRES1	1364.00	1.76	2.93
50024.00	N18	M-009740- Wolfram sy	7466.00	WFS1	1776.00	7.77	3.08
50024.00	N19	M-011374- retinoic aci	5919.00	RARRES2	3158.00	10.51	5.82
50024.00	N20	M-013318- WD repeat	49856.00	WDR8	2891.00	10.45	5.76
50024.00	N21	M-011889- retinoic aci	5920.00	RARRES3	3632.00	5.42	0.73
50024.00	N23	M-008866- RAS p21 pr	10156.00	RASA4	1625.00	2.09	2.60
50024.00	O02	M-012533- sarcoglyca	6442.00	SGCA	1763.00	4.76	0.07
50024.00	O04	M-019712- surfactant,	6440.00	SFTPC	3474.00	6.51	1.82
50024.00	O05	M-011892- SCO cytoch	6341.00	SCO1	3915.00	9.17	4.48
50024.00	O06	M-019276- surfactant,	6439.00	SFTPB	5423.00	18.83	**14.14**
50024.00	O07	M-009398- succinate d	6389.00	SDHA	3284.00	5.57	0.88
50024.00	O08	M-014615- surfactant,	6435.00	SFTPA1	1283.00	4.75	0.06
50024.00	O09	M-006305- succinate d	6392.00	SDHD	2798.00	7.36	2.67
50024.00	O10	M-019838- splicing fac	9169.00	SFRS2IP	1767.00	2.83	1.86
50024.00	O11	M-021125- DEP domai	55635.00	DEPDC1	1963.00	3.31	1.38
50024.00	O12	M-020070- SET domai	9869.00	SETDB1	2667.00	2.44	2.25
50024.00	O13	M-010971- exocyst co	10640.00	EXOC5	2728.00	1.43	3.26
50024.00	O14	M-020244- sestrin 1	27244.00	SESN1	3462.00	2.43	2.26

50024.00	O15	M-012991- SEC31 hom	25956.00	SEC31B	2549.00	1.80	2.89
50024.00	O16	M-016371- serpin pept	5267.00	SERPINA4	1980.00	1.26	3.43
50024.00	O17	M-020441- SERTA dom	29950.00	SERTAD1	3031.00	0.63	4.06
50024.00	O18	M-009576- serpin pept	12.00	SERPINA3	3953.00	2.81	1.88
50024.00	O19	M-004885- sel-1 suppr	6400.00	SEL1L	1767.00	7.53	2.84
50024.00	O20	M-012142- small EDRK	8293.00	SERF1A	1086.00	1.29	3.40
50024.00	O21	M-008078- selectin L (l	6402.00	SELL	4165.00	11.33	**6.64**
50024.00	O23	M-007757- sema doma	10512.00	SEMA3C	2655.00	5.61	0.92
50024.00	P02	M-012867- WD repeat	23335.00	WDR7	1885.00	4.14	0.55
50024.00	P04	M-013085- WD repeat	11180.00	WDR6	1731.00	6.01	1.32
50024.00	P05	M-007767- Ras associa	9770.00	RASSF2	650.00	10.00	5.31
50024.00	P06	M-013383- WD repeat	11091.00	WDR5	1628.00	2.27	2.42
50024.00	P07	M-020496- retina and	30062.00	RAX	1947.00	6.63	1.94
50024.00	P08	M-013491- WD repeat	10785.00	WDR4	1381.00	7.10	2.41
50024.00	P09	M-021117- RB1-inducil	9821.00	RB1CC1	938.00	12.79	**8.10**
50024.00	P10	M-012328- WD repeat	10885.00	WDR3	4423.00	10.83	6.14
50024.00	P11	M-012137- retinoblast	5928.00	RBBP4	2344.00	1.88	2.81
50024.00	P12	M-021319- WD repeat	64743.00	WDR13	970.00	5.46	0.77
50024.00	P13	M-012008- retinoblast	5929.00	RBBP5	1482.00	6.82	2.13
50024.00	P14	M-012972- WD repeat	55759.00	WDR12	1324.00	2.87	1.82
50024.00	P15	M-011375- retinoblast	5931.00	RBBP7	1490.00	4.70	0.01
50024.00	P16	M-012887- bromodom	55717.00	BRWD2	1968.00	10.01	5.32
50024.00	P17	M-011376- retinoblast	5932.00	RBBP8	1073.00	4.66	0.03
50024.00	P18	M-012958- intraflagell	55764.00	IFT122	3153.00	6.25	1.56
50024.00	P19	M-017623- retinoblast	10741.00	RBBP9	1981.00	4.14	0.55
50024.00	P20	M-011984- WD repeat	9948.00	WDR1	1273.00	3.46	1.23
50024.00	P21	M-003298- retinoblast	5933.00	RBL1	1734.00	5.36	0.67
50024.00	P23	M-013725- RNA bindin	27303.00	RBMS3	1028.00	3.50	1.19
				mdn	1976.50	4.69	2.10
				3MAD			6.30
				MADc			3.11
50024.00	C22				1891.00	19.73	
50024.00	D22	4020.00	44.06				
50024.00	E22				2241.00	20.75	
50024.00	F22				3596.00	32.31	
				mn	2576.00	24.26	
				sd	900.51	6.99	
50024.00	G22				1442.00	1.46	
50024.00	H22				1413.00	2.48	
50024.00	I22				1930.00	2.80	
50024.00	J22				1996.00	2.15	
				mn	1695.25	2.22	
				sd	310.57	0.57	
				3psSD		20.97	
				3ngSD		1.72	
				SumSD		22.69	

DiffMn	22.04
SmovrDiff	1.03
1minus	-0.03

50024.00	I03	D-001206-:	siControl non-targeting			4936.00	3.06
50024.00	J03	D-001206-:	siControl non-targeting			1629.00	1.72
50024.00	K03	D-001600-(	siGLO RISC-free siRNA			5809.00	10.78
50024.00	L03	D-001600-(	siGLO RISC-free siRNA			4616.00	10.14
50024.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	79.00	22.79
50024.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	291.00	17.53

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
-0.86	572.00	1.05	0.74	-0.49	920.00	2.28	0.57	-0.30
-0.82	1142.00	0.00	1.79	-1.19	828.00	0.24	2.61	-1.38
-0.89	2265.00	1.02	0.77	-0.51	906.00	1.99	0.86	-0.46
-0.15	2727.00	0.15	1.64	-1.09	821.00	2.07	0.78	-0.41
2.11	1025.00	2.05	0.26	0.17	639.00	4.38	1.53	0.81
0.37	2204.00	1.23	0.57	-0.37	1407.00	3.84	0.99	0.52
0.24	1612.00	0.43	1.36	-0.90	1338.00	3.21	0.36	0.19
0.46	1669.00	1.62	0.17	-0.11	1237.00	3.07	0.22	0.12
-0.35	1742.00	0.23	1.56	-1.04	1072.00	2.80	0.05	-0.03
0.20	1518.00	0.66	1.13	-0.75	1189.00	1.35	1.50	-0.80
-0.79	1247.00	1.04	0.75	-0.50	795.00	4.78	1.93	1.02
1.39	462.00	1.08	0.71	-0.47	210.00	11.91	9.06	4.79
-0.56	1351.00	2.52	0.73	0.49	1382.00	1.09	1.76	-0.93
1.71	1919.00	7.14	5.35	3.56	682.00	4.69	1.84	0.97
1.22	2564.00	6.20	4.41	2.94	1826.00	2.96	0.11	0.06
0.86	3233.00	4.27	2.48	1.65	1303.00	3.15	0.30	0.16
-0.92	1362.00	2.28	0.49	0.33	1027.00	1.95	0.90	-0.48
-0.85	1472.00	2.24	0.45	0.30	1689.00	1.07	1.78	-0.94
0.75	1688.00	3.55	1.76	1.18	2184.00	6.91	4.06	2.15
0.59	1613.00	5.95	4.16	2.77	1185.00	2.95	0.10	0.05
-1.20	2206.00	1.54	0.25	-0.16	1352.00	4.44	1.59	0.84
-0.43	3346.00	1.67	0.12	-0.08	3046.00	4.10	1.25	0.66
-1.45	1697.00	1.18	0.61	-0.41	616.00	3.41	0.56	0.29
-1.00	2378.00	1.01	0.78	-0.52	1569.00	1.27	1.58	-0.83
-0.97	821.00	0.97	0.82	-0.54	1570.00	2.17	0.68	-0.36
-1.26	2062.00	0.29	1.50	-1.00	1497.00	2.34	0.51	-0.27
-0.98	4490.00	2.03	0.24	0.16	1324.00	2.49	0.36	-0.19
-1.08	2212.00	1.85	0.06	0.04	2142.00	6.07	3.22	1.70
0.04	2862.00	5.49	3.70	2.46	3327.00	5.68	2.83	1.50
-1.41	1641.00	0.79	1.00	-0.66	970.00	1.65	1.20	-0.64
0.00	1487.00	0.00	1.79	-1.19	2481.00	0.56	2.29	-1.21
0.84	1739.00	0.00	1.79	-1.19	1283.00	2.34	0.51	-0.27
-0.20	2636.00	0.00	1.79	-1.19	1431.00	2.31	0.54	-0.29
-0.07	2408.00	0.37	1.42	-0.94	1227.00	1.96	0.89	-0.47
0.34	2734.00	0.51	1.28	-0.85	1512.00	0.60	2.25	-1.19
0.11	3970.00	0.60	1.19	-0.79	2577.00	0.66	2.19	-1.16
3.63	3282.00	1.89	0.10	0.07	1609.00	1.62	1.23	-0.65
2.64	2228.00	1.30	0.49	-0.32	1529.00	2.81	0.04	-0.02
1.96	4119.00	2.14	0.35	0.23	1383.00	2.75	0.10	-0.06
-0.31	2072.00	0.24	1.55	-1.03	1291.00	1.01	1.84	-0.98
-0.15	1526.00	0.46	1.33	-0.88	717.00	2.79	0.06	-0.03
-0.25	2497.00	1.52	0.27	-0.18	691.00	3.47	0.62	0.33
-0.43	3967.00	0.73	1.06	-0.70	1655.00	1.63	1.22	-0.65
-0.43	2291.00	0.52	1.27	-0.84	1961.00	2.65	0.20	-0.11
-0.33	3374.00	0.39	1.40	-0.93	1419.00	2.54	0.31	-0.17
-0.53	2003.00	0.20	1.59	-1.06	992.00	1.51	1.34	-0.71

-0.57	1192.00	0.00	1.79	-1.19	1064.00	4.04	1.19	0.63
-0.22	1424.00	0.14	1.65	-1.10	1181.00	1.86	0.99	-0.52
-0.87	1507.00	0.20	1.59	-1.06	1481.00	2.70	0.15	-0.08
-0.95	2632.00	0.15	1.64	-1.09	2647.00	4.34	1.49	0.79
-0.32	3668.00	1.88	0.09	0.06	1432.00	0.35	2.50	-1.32
0.66	2676.00	0.45	1.34	-0.89	1727.00	2.55	0.30	-0.16
-0.81	3337.00	0.27	1.52	-1.01	1881.00	0.43	2.42	-1.28
0.92	4293.00	1.28	0.51	-0.34	2002.00	2.95	0.10	0.05
0.12	1558.00	0.77	1.02	-0.68	1126.00	2.66	0.19	-0.10
1.37	3507.00	1.06	0.74	-0.49	1247.00	2.25	0.60	-0.32
-0.08	2234.00	0.27	1.52	-1.01	1347.00	2.08	0.77	-0.41
1.20	3246.00	3.36	1.57	1.05	918.00	6.54	3.69	1.95
-0.28	3008.00	0.86	0.93	-0.61	1111.00	3.51	0.66	0.35
-0.44	2490.00	1.37	0.42	-0.28	2214.00	4.56	1.71	0.90
1.73	3465.00	2.97	1.18	0.79	3367.00	2.05	0.80	-0.42
0.44	1307.00	2.14	0.35	0.24	1131.00	3.45	0.60	0.32
-0.33	1654.00	2.18	0.39	0.26	788.00	2.28	0.57	-0.30
0.26	2435.00	0.90	0.89	-0.59	1600.00	0.56	2.29	-1.21
0.18	2314.00	1.17	0.62	-0.41	1225.00	1.31	1.54	-0.82
1.00	2865.00	1.71	0.08	-0.05	1018.00	2.16	0.69	-0.37
0.51	4382.00	2.88	1.09	0.72	1693.00	1.77	1.08	-0.57
0.99	4268.00	3.54	1.75	1.17	1767.00	2.60	0.25	-0.13
1.13	2579.00	2.48	0.69	0.46	650.00	3.23	0.38	0.20
0.87	839.00	0.72	1.07	-0.71	372.00	1.34	1.51	-0.80
0.67	1999.00	1.80	0.01	0.01	1049.00	4.00	1.15	0.61
0.79	1265.00	1.90	0.11	0.07	1120.00	4.46	1.61	0.85
1.28	637.00	1.41	0.38	-0.25	387.00	1.55	1.30	-0.69
0.10	2941.00	1.29	0.50	-0.33	2831.00	1.84	1.01	-0.54
2.05	648.00	0.77	1.02	-0.68	491.00	1.22	1.63	-0.86
-0.51	2168.00	0.23	1.56	-1.04	1811.00	0.77	2.08	-1.10
0.82	1159.00	1.73	0.06	-0.04	668.00	0.45	2.40	-1.27
0.28	3497.00	5.06	**3.27**	2.18	1473.00	2.44	0.41	-0.22
0.02	592.00	1.18	0.61	-0.40	574.00	0.35	2.50	-1.32
-0.76	586.00	1.54	0.25	-0.17	777.00	0.39	2.46	-1.30
-0.51	3197.00	3.50	1.71	1.14	2026.00	2.67	0.18	-0.10
1.27	1581.00	0.76	1.03	-0.68	412.00	2.18	0.67	-0.35
-0.12	2372.00	0.72	1.07	-0.71	1889.00	0.90	1.95	-1.03
-0.26	2910.00	1.13	0.66	-0.43	829.00	3.02	0.17	0.09
-0.36	1178.00	1.10	0.69	-0.45	1110.00	0.99	1.86	-0.98
0.43	2956.00	1.52	0.27	-0.18	2140.00	1.17	1.68	-0.89
-0.72	2309.00	2.34	0.55	0.37	1271.00	0.71	2.14	-1.13
0.10	3022.00	1.65	0.14	-0.09	1986.00	1.01	1.84	-0.98
-0.70	2038.00	0.98	0.81	-0.54	1340.00	1.04	1.81	-0.96
-0.59	1578.00	1.01	0.78	-0.51	2168.00	1.52	1.33	-0.70
1.73	2718.00	2.10	0.31	0.21	2356.00	1.06	1.79	-0.95
0.15	1788.00	1.57	0.22	-0.15	1454.00	0.41	2.44	-1.29
1.09	520.00	2.50	0.71	0.47	574.00	0.17	2.68	-1.42

-0.24	1226.00	0.90	0.89	-0.59	1578.00	0.38	2.47	-1.31
2.70	667.00	2.70	0.91	0.61	611.00	0.65	2.20	-1.16
0.54	2150.00	2.47	0.68	0.45	1855.00	0.97	1.88	-1.00
-0.07	1724.00	3.42	1.63	1.09	1321.00	0.61	2.24	-1.19
-0.32	1688.00	0.53	1.26	-0.83	1385.00	1.23	1.62	-0.86
1.11	406.00	3.45	1.66	1.11	509.00	1.77	1.08	-0.57
0.41	1173.00	1.62	0.17	-0.11	1599.00	1.06	1.79	-0.95
1.49	268.00	4.85	**3.06**	2.04	221.00	4.07	1.22	0.65
0.58	2303.00	3.34	1.55	1.04	1452.00	0.96	1.89	-1.00
0.81	2465.00	1.54	0.25	-0.16	1923.00	2.60	0.25	-0.13
-0.26	2017.00	2.13	0.34	0.23	1491.00	1.48	1.37	-0.73
11.80	132.00	8.33	**6.54**	4.36	99.00	12.12	**9.27**	4.90
-1.11	1975.00	4.10	2.31	1.54	2093.00	1.82	1.03	-0.55
1.70	634.00	3.31	1.52	1.02	362.00	8.56	**5.71**	3.02
-0.49	885.00	4.29	2.50	1.67	1115.00	2.69	0.16	-0.09
0.34	821.00	2.80	1.01	0.68	812.00	1.72	1.13	-0.60
-0.63	1640.00	4.39	2.60	1.73	1519.00	3.95	1.10	0.58
-0.87	2700.00	0.33	1.46	-0.97	2410.00	2.45	0.40	-0.21
-0.95	1288.00	0.85	0.94	-0.62	891.00	5.61	2.76	1.46
-0.07	2466.00	2.68	0.89	0.59	1843.00	2.55	0.30	-0.16
0.20	1409.00	2.56	0.77	0.51	1445.00	4.50	1.65	0.87
-0.39	1216.00	2.22	0.43	0.29	768.00	4.82	1.97	1.04
1.34	2420.00	5.79	**4.00**	2.66	1580.00	4.56	1.71	0.90
0.69	1918.00	3.08	1.29	0.86	1319.00	5.38	2.53	1.34
0.14	736.00	2.72	0.93	0.62	431.00	6.03	3.18	1.68
-1.18	2676.00	1.23	0.56	-0.37	1395.00	2.44	0.41	-0.22
-0.88	2615.00	4.93	**3.14**	2.09	2532.00	2.73	0.12	-0.07
-0.60	2991.00	1.97	0.18	0.12	1722.00	4.70	1.85	0.98
1.23	1756.00	5.35	**3.56**	2.37	1675.00	8.78	**5.93**	3.13
-0.63	3463.00	2.14	0.35	0.23	2035.00	5.06	2.21	1.17
-0.86	1308.00	2.45	0.66	0.44	1437.00	5.01	2.16	1.14
0.17	1468.00	0.68	1.11	-0.74	2199.00	10.10	**7.25**	3.83
1.43	2374.00	4.17	2.38	1.59	2286.00	5.12	2.27	1.20
0.19	1127.00	2.57	0.78	0.52	958.00	6.79	**3.94**	2.08
0.72	1067.00	7.69	**5.90**	3.93	1896.00	7.81	**4.96**	2.62
-1.14	2159.00	1.25	0.54	-0.36	1405.00	3.13	0.28	0.15
0.11	607.00	8.40	**6.61**	4.40	807.00	3.22	0.37	0.20
-0.97	900.00	1.44	0.35	-0.23	754.00	4.38	1.53	0.81
1.90	1079.00	9.27	**7.48**	4.98	2273.00	11.31	**8.46**	4.47
-0.50	1276.00	3.29	1.50	1.00	1889.00	5.45	2.60	1.37
2.01	954.00	10.17	**8.38**	5.58	1432.00	4.96	2.11	1.11
-0.48	908.00	2.31	0.52	0.35	881.00	1.82	1.03	-0.55
-0.47	622.00	0.64	1.15	-0.76	861.00	2.67	0.18	-0.10
-0.68	1061.00	1.79	0.00	0.00	1487.00	4.04	1.19	0.63
-0.78	2058.00	1.99	0.20	0.14	1753.00	2.68	0.17	-0.09
0.84	2093.00	5.83	**4.04**	2.69	2276.00	5.71	2.86	1.51
-0.39	807.00	2.97	1.18	0.79	1294.00	3.79	0.94	0.49

0.95	2294.00	1.53	0.26	-0.17	2933.00	4.33	1.48	0.78
-0.91	884.00	0.23	1.56	-1.04	1833.00	0.60	2.25	-1.19
-0.23	1433.00	0.63	1.16	-0.77	1851.00	1.78	1.07	-0.57
-0.60	916.00	1.31	0.48	-0.32	974.00	1.64	1.21	-0.64
0.68	976.00	1.54	0.25	-0.17	855.00	1.99	0.86	-0.46
1.31	1757.00	3.93	2.14	1.42	1830.00	1.75	1.10	-0.58
1.32	1231.00	3.49	1.70	1.14	1782.00	4.99	2.14	1.13
2.89	4179.00	4.91	**3.12**	2.08	3626.00	3.03	0.18	0.10
-0.47	1767.00	3.51	1.72	1.15	2384.00	1.76	1.09	-0.58
-0.68	1560.00	1.35	0.44	-0.29	1910.00	0.63	2.22	-1.18
-0.44	2151.00	1.95	0.16	0.11	2362.00	2.07	0.78	-0.41
-0.24	2591.00	7.49	**5.70**	3.79	1469.00	2.38	0.47	-0.25
0.77	2018.00	5.01	**3.22**	2.14	1586.00	3.34	0.49	0.26
0.08	1455.00	1.44	0.35	-0.23	2371.00	1.73	1.12	-0.59
-0.80	1977.00	2.83	1.04	0.70	2350.00	1.57	1.28	-0.68
-0.62	735.00	4.76	2.97	1.98	1968.00	2.24	0.61	-0.33
0.67	294.00	7.82	**6.03**	4.02	422.00	3.79	0.94	0.50
-0.68	505.00	6.53	**4.74**	3.16	1426.00	3.44	0.59	0.31
-0.81	1677.00	1.91	0.12	0.08	1865.00	2.63	0.22	-0.12
0.15	843.00	2.97	1.18	0.78	962.00	4.05	1.20	0.64
0.47	1699.00	4.18	2.39	1.59	1521.00	2.70	0.15	-0.08
-0.18	453.00	6.84	**5.05**	3.37	682.00	3.52	0.67	0.35
-0.74	1193.00	4.36	2.57	1.71	2133.00	3.28	0.43	0.23
-0.32	453.00	1.99	0.20	0.13	464.00	2.37	0.48	-0.25
-0.03	1114.00	3.14	1.35	0.90	3562.00	6.93	**4.08**	2.16
-0.56	1287.00	2.95	1.16	0.78	1045.00	1.53	1.32	-0.70
1.40	2815.00	3.84	2.05	1.36	2388.00	2.85	0.00	0.00
0.87	2124.00	5.46	**3.67**	2.45	2255.00	3.19	0.34	0.18
-1.00	1412.00	1.98	0.19	0.13	2155.00	0.79	2.06	-1.09
-0.76	1449.00	0.62	1.17	-0.78	1223.00	1.14	1.71	-0.90
1.28	3152.00	4.70	2.91	1.94	3775.00	6.97	**4.12**	2.18
0.40	2068.00	2.66	0.87	0.58	3301.00	2.79	0.06	-0.03
2.10	2776.00	6.77	**4.98**	3.32	4823.00	8.79	**5.94**	3.14
0.67	1899.00	2.95	1.16	0.77	3392.00	4.63	1.78	0.94
0.36	1352.00	2.88	1.09	0.73	1758.00	2.84	0.01	0.00
-0.72	1067.00	1.31	0.48	-0.32	1481.00	2.09	0.76	-0.40
2.61	1028.00	2.04	0.25	0.17	963.00	4.88	2.03	1.07
0.21	1048.00	2.96	1.17	0.78	2292.00	5.50	2.65	1.40
1.65	1675.00	4.30	2.51	1.67	3989.00	3.74	0.89	0.47
0.23	774.00	6.20	**4.41**	2.94	1571.00	4.65	1.80	0.95
-0.29	1832.00	2.13	0.34	0.23	3051.00	5.05	2.20	1.16
-0.13	2497.00	2.28	0.49	0.33	2217.00	2.71	0.14	-0.08
-0.14	2619.00	0.34	1.45	-0.96	2352.00	3.87	1.02	0.54
1.19	1790.00	2.23	0.44	0.30	2056.00	6.32	3.47	1.84
-0.55	1047.00	1.05	0.74	-0.49	1431.00	1.89	0.96	-0.51
-0.57	1381.00	1.23	0.56	-0.37	2313.00	0.69	2.16	-1.14
-0.66	2212.00	1.54	0.25	-0.17	3349.00	2.42	0.43	-0.23

0.79	1861.00	2.36	0.57	0.38	1601.00	1.94	0.91	-0.48
-0.56	787.00	0.76	1.03	-0.68	1390.00	2.30	0.55	-0.29
0.04	2033.00	1.77	0.02	-0.01	2371.00	4.01	1.16	0.61
-0.26	1690.00	2.49	0.70	0.46	2369.00	5.61	2.76	1.46
-0.60	438.00	2.74	0.95	0.63	1240.00	5.08	2.23	1.18
-0.91	1002.00	0.70	1.09	-0.72	1015.00	2.86	0.01	0.00
-0.05	1157.00	1.12	0.67	-0.44	1828.00	4.16	1.31	0.69
-0.14	2118.00	1.56	0.23	-0.15	2745.00	3.68	0.83	0.44
-0.95	877.00	0.23	1.56	-1.04	1068.00	2.43	0.42	-0.22
-0.84	1087.00	0.92	0.87	-0.58	1489.00	5.17	2.32	1.23
-0.24	915.00	1.86	0.07	0.05	2062.00	4.32	1.47	0.77
0.44	2617.00	2.98	1.19	0.79	2698.00	12.90	**10.05**	5.31
0.61	2446.00	2.45	0.66	0.44	3618.00	7.57	**4.72**	2.50
-0.11	1565.00	2.88	1.09	0.72	2289.00	3.41	0.56	0.29
-1.16	1410.00	0.28	1.51	-1.00	1498.00	5.21	2.36	1.24
1.03	1374.00	0.00	1.79	-1.19	1577.00	3.04	0.19	0.10
1.06	1730.00	0.12	1.67	-1.11	3195.00	4.44	1.59	0.84
-0.05	1729.00	1.39	0.40	-0.27	2782.00	2.88	0.03	0.01
0.92	996.00	0.60	1.19	-0.79	2238.00	2.55	0.30	-0.16
1.34	1491.00	1.68	0.11	-0.07	2397.00	4.13	1.28	0.68
0.42	1393.00	2.37	0.58	0.39	2695.00	1.78	1.07	-0.57
2.70	1996.00	1.60	0.19	-0.12	3105.00	3.16	0.31	0.16
2.40	1503.00	1.60	0.19	-0.13	2547.00	6.79	**3.94**	2.08
-0.86	514.00	1.17	0.62	-0.41	906.00	4.86	2.01	1.06
1.71	596.00	0.00	1.79	-1.19	869.00	7.02	**4.17**	2.20
2.40	1066.00	0.84	0.95	-0.63	793.00	6.31	3.46	1.83
1.85	689.00	2.03	0.24	0.16	1901.00	8.78	**5.93**	3.14
-0.65	663.00	0.60	1.19	-0.79	1440.00	3.89	1.04	0.55
-1.31	1751.00	0.57	1.22	-0.81	2591.00	2.32	0.53	-0.28
-0.94	720.00	0.00	1.79	-1.19	1059.00	1.23	1.62	-0.86
0.99	1693.00	0.00	1.79	-1.19	2213.00	1.04	1.81	-0.96
1.87	3042.00	0.56	1.23	-0.82	4264.00	5.82	2.97	1.57
1.85	2024.00	1.09	0.70	-0.47	2546.00	6.52	3.67	1.94
0.24	3281.00	0.55	1.24	-0.82	3572.00	1.76	1.09	-0.58
-0.84	977.00	0.10	1.69	-1.12	1377.00	1.60	1.25	-0.66
0.02	837.00	1.67	0.12	-0.08	847.00	3.07	0.22	0.11
0.58	2549.00	2.04	0.25	0.17	3597.00	4.31	1.46	0.77
1.44	2183.00	4.90	**3.11**	2.07	2649.00	5.74	2.89	1.53
4.55	3052.00	9.11	**7.32**	4.87	3153.00	11.32	**8.47**	4.48
0.28	2106.00	7.22	**5.43**	3.62	2779.00	4.64	1.79	0.95
0.02	1012.00	2.27	0.48	0.32	1014.00	2.96	0.11	0.06
0.86	1249.00	3.12	1.33	0.89	1719.00	6.75	**3.90**	2.06
-0.60	1091.00	3.30	1.51	1.01	1429.00	3.43	0.58	0.30
-0.44	1289.00	3.72	1.93	1.29	1675.00	5.97	3.12	1.65
-0.73	1300.00	1.15	0.64	-0.42	2307.00	4.85	2.00	1.06
-1.05	1397.00	3.79	2.00	1.34	2253.00	2.53	0.32	-0.17
-0.73	1830.00	2.35	0.56	0.37	3035.00	3.92	1.07	0.57

-0.93	1083.00	3.69	1.90	1.27	2066.00	3.58	0.73	0.39
-1.10	729.00	1.78	0.01	0.00	1220.00	1.72	1.13	-0.60
-1.31	1319.00	1.82	0.03	0.02	2008.00	2.34	0.51	-0.27
-0.61	3048.00	1.67	0.12	-0.08	4365.00	3.71	0.86	0.45
0.91	1035.00	2.42	0.63	0.42	1892.00	3.38	0.53	0.28
-1.09	1026.00	2.34	0.55	0.37	999.00	2.30	0.55	-0.29
2.14	2455.00	6.19	4.40	2.93	2397.00	8.26	5.41	2.86
0.30	2379.00	4.16	2.37	1.58	2529.00	9.57	6.72	3.55
-0.18	2190.00	1.19	0.60	-0.40	1559.00	5.77	2.92	1.54
0.42	1627.00	0.55	1.24	-0.82	1512.00	2.78	0.07	-0.04
1.71	451.00	1.55	0.24	-0.16	638.00	8.62	5.77	3.05
-0.78	1307.00	0.31	1.48	-0.99	1028.00	2.82	0.03	-0.02
0.62	1518.00	0.46	1.33	-0.88	1608.00	6.09	3.24	1.71
0.77	964.00	0.31	1.48	-0.98	898.00	5.57	2.72	1.44
2.61	840.00	2.02	0.23	0.16	1565.00	7.16	4.31	2.28
1.97	4385.00	6.55	4.76	3.17	5139.00	9.90	7.05	3.73
-0.91	1531.00	0.00	1.79	-1.19	2794.00	1.79	1.06	-0.56
0.25	403.00	1.49	0.30	-0.20	997.00	4.51	1.66	0.88
0.68	1322.00	2.57	0.78	0.52	1666.00	5.28	2.43	1.28
-0.59	944.00	1.48	0.31	-0.20	1745.00	1.89	0.96	-0.51
0.00	654.00	1.22	0.57	-0.38	2566.00	4.56	1.71	0.90
1.71	1113.00	1.80	0.01	0.01	1819.00	4.73	1.88	0.99
-0.01	1178.00	4.24	2.45	1.64	1585.00	4.61	1.76	0.93
0.50	1555.00	1.61	0.18	-0.12	3221.00	1.21	1.64	-0.87
-0.18	1115.00	1.97	0.18	0.12	854.00	6.32	3.47	1.84
-0.40	1022.00	1.47	0.32	-0.21	1328.00	3.24	0.39	0.20
0.22	2365.00	1.99	0.20	0.13	2341.00	5.55	2.70	1.43
-0.38	1267.00	1.03	0.76	-0.51	532.00	2.63	0.22	-0.12
	1633.50	1.79	1.01		1562.00	2.85	1.28	
			3.04				3.83	
			1.50				1.89	

5405.00	32.36		6603.00	36.33
5878.00	37.84		5178.00	34.26
3215.00	21.37		2777.00	16.89
4195.00	24.32		3508.00	19.47
4673.25	28.97		4516.50	26.74
1203.07	7.52		1716.00	9.97
1590.00	1.57		1627.00	2.70
2229.00	1.70		813.00	2.34
1328.00	3.77		1908.00	2.31
3682.00	2.42		3805.00	2.86
2207.25	2.36		2038.25	2.55
1053.48	1.00		1266.06	0.28
	22.55			29.92
	3.01			0.83
	25.57			30.75

	26.60		24.18
	0.96		1.27
	0.04		-0.27
1247.00	0.56	1648.00	4.61
1242.00	1.93	1552.00	3.03
4363.00	9.70	5436.00	9.77
5403.00	6.11	4728.00	8.78
100.00	2.00	75.00	17.33
153.00	5.23	149.00	0.67

x	toxic a,b,c
y	
x	toxic,b,c
y	
y	

y

y

x debris b,c

y

y

x tox a,b,c
y

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50047.00	A02	M-019509- CD52 mole	1043.00	CD52	1191.00	0.92	1.66
50047.00	A04	M-008680- CDP-diacyl	1040.00	CDS1	3814.00	4.61	2.03
50047.00	A05	M-011191- alpha-1-B	1.00	A1BG	1271.00	1.18	1.40
50047.00	A06	M-010336- cysteine di	1036.00	CDO1	2545.00	2.40	0.18
50047.00	A07	M-010380- arylalkyla	15.00	AANAT	1553.00	2.19	0.39
50047.00	A08	M-012630- cytidine de	978.00	CDA	2111.00	1.42	1.16
50047.00	A09	M-011565- alanyl-tRN	16.00	AARS	3424.00	2.89	0.31
50047.00	A10	M-011233- ectonucleo	955.00	ENTPD6	3054.00	2.36	0.22
50047.00	A11	M-009699- ATP-bindin	20.00	ABCA2	1160.00	2.50	0.08
50047.00	A12	M-010736- ectonucleo	954.00	ENTPD2	1425.00	2.60	0.02
50047.00	A13	M-008795- ATP-bindin	21.00	ABCA3	1474.00	6.31	**3.73**
50047.00	A14	M-004226- sialic acid	946.00	SIGLEC6	1512.00	2.58	0.00
50047.00	A15	M-008263- ATP-bindin	23.00	ABCF1	3341.00	4.37	1.79
50047.00	A16	M-017542- membrane	932.00	MS4A3	3025.00	4.83	2.25
50047.00	A17	M-006105- amiloride-	40.00	ACCN1	684.00	2.19	0.39
50047.00	A18	M-014647- CD1e mole	913.00	CD1E	2642.00	2.01	0.57
50047.00	A19	M-006106- amiloride-	41.00	ACCN2	2773.00	2.52	0.06
50047.00	A20	M-008878- cysteine co	883.00	CCBL1	2591.00	1.58	1.00
50047.00	A21	M-004915- ATP citrate	47.00	ACLY	3612.00	5.51	2.93
50047.00	A23	M-010037- aconitase 1	48.00	ACO1	1653.00	2.00	0.58
50047.00	B02	M-017045- eukaryotic	1968.00	EIF2S3	813.00	1.85	0.74
50047.00	B04	M-015389- eukaryotic	1965.00	EIF2S1	785.00	1.91	0.67
50047.00	B05	M-004567- carcinoem	1048.00	CEACAM5	3238.00	1.33	1.25
50047.00	B06	M-011262- eukaryotic	1964.00	EIF1AX	959.00	0.94	1.64
50047.00	B07	M-010453- CCAAT/en	1052.00	CEBPD	2805.00	2.85	0.27
50047.00	B08	M-026241- multiple E	1955.00	MEGF9	3670.00	2.04	0.54
50047.00	B09	M-010938- carboxyl es	1057.00	CELP	3467.00	4.36	1.78
50047.00	B10	M-010204- multiple E	1954.00	MEGF8	3094.00	2.88	0.30
50047.00	B11	M-011822- centrin, EF	1069.00	CETN2	2639.00	2.58	0.00
50047.00	B12	M-021856- multiple E	1953.00	MEGF6	1062.00	0.75	1.83
50047.00	B13	M-019078- cofilin 2 (m	1073.00	CFL2	2003.00	0.75	1.83
50047.00	B14	M-003680- ligatin	1939.00	LGTN	3223.00	2.61	0.03
50047.00	B15	M-019510- carcinoem	1084.00	CEACAM3	3717.00	5.95	3.37
50047.00	B16	M-017546- eukaryotic	1937.00	EEF1G	3537.00	1.39	1.19
50047.00	B17	M-017056- carcinoem	1088.00	CEACAM8	3778.00	2.14	0.44
50047.00	B18	M-011648- eukaryotic	1936.00	EEF1D	2314.00	1.94	0.64
50047.00	B19	M-019512- carcinoem	1089.00	CEACAM4	2317.00	2.37	0.21
50047.00	B20	M-011848- early B-cell	1879.00	EBF1	2963.00	1.79	0.79
50047.00	B21	M-011239- chondroad	1101.00	CHAD	2986.00	0.67	1.91
50047.00	B23	M-012568- chitinase 3	1116.00	CHI3L1	2161.00	0.97	1.61
50047.00	C02	M-012161- calicin	881.00	CCIN	3459.00	6.45	**3.87**
50047.00	C04	M-003004- Cas-Br-M (	868.00	CBLB	3732.00	3.67	1.09
50047.00	C05	M-009566- aconitase	50.00	ACO2	3521.00	1.68	0.90
50047.00	C06	M-010335- cysteinyl-t	833.00	CARS	2701.00	4.26	1.68
50047.00	C07	M-011566- acrosomal	56.00	ACRV1	2218.00	1.53	1.05
50047.00	C08	M-009423- calpain 6	827.00	CAPN6	4544.00	12.63	**10.05**

50047.00	C09	M-004502- ADAM met	101.00	ADAM8	4676.00	3.46	0.88
50047.00	C10	M-011601- calcium m	819.00	CAMLG	4907.00	3.93	1.35
50047.00	C11	M-008630- adenosine	103.00	ADAR	3113.00	3.02	0.44
50047.00	C12	M-006460- calumenin	813.00	CALU	2883.00	4.09	1.51
50047.00	C13	M-009263- adenosine	104.00	ADARB1	1105.00	1.09	1.49
50047.00	C14	M-019122- calmodulin	810.00	CALML3	3357.00	6.05	3.47
50047.00	C15	M-020743- adenosine	105.00	ADARB2	1996.00	1.40	1.18
50047.00	C16	M-011808- caldesmon	800.00	CALD1	5415.00	6.24	**3.66**
50047.00	C17	M-006819- adenylate	107.00	ADCY1	2533.00	2.45	0.13
50047.00	C18	M-015409- calcitonin-	797.00	CALCB	3248.00	1.82	0.76
50047.00	C19	M-006798- adenylate	108.00	ADCY2	4018.00	4.41	1.83
50047.00	C20	M-011821- S100 calciu	795.00	S100G	3307.00	1.72	0.86
50047.00	C21	M-006799- adenylate	109.00	ADCY3	3579.00	4.78	2.20
50047.00	C23	M-006638- adenylate	111.00	ADCY5	3005.00	5.96	3.38
50047.00	D02	M-011997- epiphycan	1833.00	EPYC	3534.00	0.20	2.38
50047.00	D04	M-021438- TSC22 dom	1831.00	TSC22D3	3755.00	2.37	0.21
50047.00	D05	M-010251- chimerin (	1123.00	CHN1	3599.00	1.39	1.19
50047.00	D06	M-015993- Down synd	1826.00	DSCAM	3587.00	2.90	0.32
50047.00	D07	M-003791- chimerin (	1124.00	CHN2	4254.00	1.43	1.15
50047.00	D08	M-009821- dihydropyr	1809.00	DPYSL3	4342.00	0.90	1.68
50047.00	D09	M-020186- tubulin fol	1155.00	TBCB	4668.00	4.18	1.60
50047.00	D10	M-009519- dihydropyr	1808.00	DPYSL2	2600.00	5.96	3.38
50047.00	D11	M-008170- adaptor-rel	1173.00	AP2M1	2343.00	2.65	0.07
50047.00	D12	M-011641- dermatop	1805.00	DPT	1906.00	0.68	1.90
50047.00	D13	M-011241- adaptor-rel	1174.00	AP1S1	1647.00	0.61	1.97
50047.00	D14	M-010129- dipeptidyl-	1804.00	DPP6	3308.00	5.17	2.59
50047.00	D15	M-011833- adaptor-rel	1175.00	AP2S1	2547.00	1.69	0.89
50047.00	D16	M-011256- DPH2 hom	1802.00	DPH2	2817.00	3.44	0.86
50047.00	D17	M-012569- adaptor-rel	1176.00	AP3S1	3230.00	6.41	**3.83**
50047.00	D18	M-012575- DPH1 hom	1801.00	DPH1	3998.00	1.18	1.40
50047.00	D19	M-012397- Charcot-Le	1178.00	CLC	3006.00	4.16	1.58
50047.00	D20	M-011255- dolichyl-ph	1798.00	DPAGT1	2915.00	2.02	0.56
50047.00	D21	M-003303- chloride ch	1179.00	CLCA1	4820.00	3.86	1.28
50047.00	D23	M-006151- chloride ch	1182.00	CLCN3	3467.00	1.30	1.28
50047.00	E02	M-011600- calbindin 2	794.00	CALB2	3314.00	0.78	1.80
50047.00	E04	M-009471- carbamoyl-	790.00	CAD	2421.00	0.87	1.71
50047.00	E05	M-006636- adenylate	112.00	ADCY6	3619.00	2.21	0.37
50047.00	E06	M-011162- calcium ch	786.00	CACNG1	3227.00	1.58	1.00
50047.00	E07	M-006801- adenylate	113.00	ADCY7	1901.00	0.11	2.47
50047.00	E08	M-008776- calcium ch	784.00	CACNB3	2843.00	0.74	1.84
50047.00	E09	M-006637- adenylate	114.00	ADCY8	2214.00	0.45	2.13
50047.00	E10	M-008741- calcium ch	783.00	CACNB2	4824.00	0.85	1.73
50047.00	E11	M-006802- adenylate	115.00	ADCY9	3066.00	0.82	1.76
50047.00	E12	M-009359- calcium ch	782.00	CACNB1	1501.00	1.20	1.38
50047.00	E13	M-011198- adenylate	116.00	ADCYAP1	2009.00	0.70	1.88
50047.00	E14	M-009336- carbonic a	770.00	CA11	2808.00	1.14	1.44
50047.00	E15	M-019204- adipose dif	123.00	ADFP	2430.00	1.15	1.43

50047.00	E16	M-009012- carbonic ar	767.00	CA8	3677.00	1.82	0.76
50047.00	E17	M-012492- adaptor-rel	160.00	AP2A1	2034.00	1.67	0.91
50047.00	E18	M-008811- carbonic ar	766.00	CA7	3224.00	1.67	0.91
50047.00	E19	M-012812- adaptor-rel	161.00	AP2A2	2092.00	2.82	0.24
50047.00	E20	M-010145- carbonic ar	765.00	CA6	3283.00	3.23	0.65
50047.00	E21	M-011200- adaptor-rel	162.00	AP1B1	4791.00	2.05	0.53
50047.00	E23	M-019183- adaptor-rel	164.00	AP1G1	3076.00	2.73	0.15
50047.00	F02	M-005004- dom-3 hon	1797.00	DOM3Z	3747.00	3.07	0.49
50047.00	F04	M-004007- dynamin 2	1785.00	DNM2	2249.00	2.05	0.53
50047.00	F05	M-006152- chloride ch	1183.00	CLCN4	3924.00	2.19	0.39
50047.00	F06	M-012694- deoxyribon	1776.00	DNASE1L3	2833.00	1.59	0.99
50047.00	F07	M-006154- chloride ch	1185.00	CLCN6	3127.00	8.35	**5.77**
50047.00	F08	M-020181- deoxyribon	1775.00	DNASE1L2	4506.00	6.68	**4.10**
50047.00	F09	M-009530- chloride int	1192.00	CLIC1	2260.00	2.70	0.12
50047.00	F10	M-019918- deoxyribon	1774.00	DNASE1L1	3502.00	5.25	2.67
50047.00	F11	M-012982- chloride int	1193.00	CLIC2	2880.00	5.00	2.42
50047.00	F12	M-009241- dynein, axc	1770.00	DNAH9	3240.00	7.07	**4.49**
50047.00	F13	M-012571- chloride ch	1207.00	CLNS1A	2062.00	2.72	0.14
50047.00	F14	M-010075- dynein, axc	1769.00	DNAH8	2382.00	2.81	0.23
50047.00	F15	M-008267- colipase, pa	1208.00	CLPS	3581.00	7.76	**5.18**
50047.00	F16	M-026431- DNA2 DNA	1763.00	DNA2L	1965.00	3.72	1.14
50047.00	F17	M-004001- clathrin, he	1213.00	CLTC	3270.00	4.95	2.37
50047.00	F18	M-003940- dynamin 1	1759.00	DNM1	4033.00	5.43	2.85
50047.00	F19	M-005812- chymase 1,	1215.00	CMA1	4368.00	9.02	**6.44**
50047.00	F20	M-019798- dentin mat	1758.00	DMP1	3193.00	3.88	1.30
50047.00	F21	M-031937- cyclic nucle	1260.00	CNGA2	3587.00	3.68	1.10
50047.00	F23	M-010695- cyclic nucle	1262.00	CNGA4	2914.00	2.64	0.06
50047.00	G02	M-008961- carbonic ar	763.00	CA5A	2053.00	0.63	1.95
50047.00	G04	M-008775- carbonic ar	762.00	CA4	3062.00	2.81	0.23
50047.00	G05	M-009694- AE binding	165.00	AEBP1	3851.00	2.60	0.02
50047.00	G06	M-008714- carbonic ar	761.00	CA3	2352.00	0.89	1.69
50047.00	G07	M-012157- amino-tern	166.00	AES	3402.00	3.79	1.21
50047.00	G08	M-017688- metallopho	758.00	MPPED1	2752.00	2.11	0.47
50047.00	G09	M-011201- afamin	173.00	AFM	2492.00	2.17	0.41
50047.00	G10	M-020106- transmemb	757.00	TMEM50B	3357.00	4.74	2.16
50047.00	G11	M-011568- alpha-2-HS	197.00	AHSG	2629.00	3.84	1.26
50047.00	G12	M-019913- chromoson	755.00	C21orf2	1831.00	2.13	0.45
50047.00	G13	M-024709- absent in m	202.00	AIM1	1466.00	2.66	0.08
50047.00	G14	M-019789- chromoson	753.00	C18orf1	1878.00	2.66	0.08
50047.00	G15	M-009276- aminolevul	211.00	ALAS1	1862.00	1.34	1.24
50047.00	G16	M-019176- formin-like	752.00	FMNL1	2777.00	2.81	0.23
50047.00	G17	M-008941- ATP-bindin	225.00	ABCD2	3389.00	3.75	1.17
50047.00	G18	M-020190- chromoson	750.00	C16orf3	2990.00	1.04	1.54
50047.00	G19	M-004558- arachidona	239.00	ALOX12	3569.00	5.10	2.52
50047.00	G20	M-012209- diacylglyce	747.00	DAGLA	3887.00	6.05	3.47
50047.00	G21	M-010166- arachidona	241.00	ALOX5AP	3822.00	3.58	1.00
50047.00	G23	M-003808- arachidona	246.00	ALOX15	2849.00	1.19	1.39

50047.00	H02	M-018307- distal-less	1745.00	DLX1	2915.00	3.53	0.95
50047.00	H04	M-008490- dihydrolipo	1737.00	DLAT	2418.00	1.90	0.68
50047.00	H05	M-015851- calponin 1,	1264.00	CNN1	2651.00	2.19	0.39
50047.00	H06	M-011251- deiodinase	1735.00	DIO3	2498.00	1.52	1.06
50047.00	H07	M-019793- calponin 2	1265.00	CNN2	3421.00	2.48	0.10
50047.00	H08	M-011171- deiodinase	1734.00	DIO2	1974.00	7.24	**4.66**
50047.00	H09	M-011612- calponin 3,	1266.00	CNN3	2832.00	4.41	1.83
50047.00	H10	M-011170- deiodinase	1733.00	DIO1	2272.00	2.82	0.24
50047.00	H11	M-018646- 2',3'-cyclic	1267.00	CNP	1716.00	7.58	**5.00**
50047.00	H12	M-006670- deoxyhypu	1725.00	DHPS	2314.00	2.16	0.42
50047.00	H13	M-012906- collagen, ty	1305.00	COL13A1	2116.00	2.74	0.16
50047.00	H14	M-005848- complemer	1675.00	CFD	3153.00	0.98	1.60
50047.00	H15	M-011835- coatomer p	1314.00	COPA	64.00	12.50	**9.92**
50047.00	H16	M-012028- defensin, b	1672.00	DEFB1	2275.00	2.55	0.03
50047.00	H17	M-017940- coatomer p	1315.00	COPB1	714.00	1.54	1.04
50047.00	H18	M-011637- defensin, a	1671.00	DEFA6	2788.00	2.65	0.07
50047.00	H19	M-007531- solute carri	1317.00	SLC31A1	1466.00	2.05	0.53
50047.00	H20	M-013143- defensin, a	1670.00	DEFA5	2583.00	2.01	0.57
50047.00	H21	M-007532- solute carri	1318.00	SLC31A2	2613.00	1.84	0.74
50047.00	H23	M-011625- cytochrom	1327.00	COX4I1	3118.00	2.02	0.56
50047.00	I02	M-012822- chromosom	746.00	C11orf10	2201.00	4.82	2.24
50047.00	I04	M-009356- metallopho	744.00	MPPED2	2183.00	1.65	0.93
50047.00	I05	M-031441- ameloblast	258.00	AMBN	2532.00	3.20	0.62
50047.00	I06	M-008955- zinc finger,	741.00	ZNHIT2	1788.00	1.06	1.52
50047.00	I07	M-009696- alpha-1-mi	259.00	AMBP	2381.00	1.60	0.98
50047.00	I08	M-017507- mitochond	740.00	MRPL49	2777.00	2.45	0.13
50047.00	I09	M-010053- adenosylm	262.00	AMD1	1129.00	2.04	0.54
50047.00	I10	M-020697- chromosom	738.00	C11orf2	2323.00	2.97	0.39
50047.00	I11	M-011205- amelogenir	266.00	AMELY	2924.00	4.72	2.14
50047.00	I12	M-008122- oxidative st	734.00	OSGIN2	3049.00	5.94	3.36
50047.00	I13	M-009880- adenosine	271.00	AMPD2	3217.00	5.75	3.17
50047.00	I14	M-008991- complemer	733.00	C8G	2498.00	8.73	**6.15**
50047.00	I15	M-011569- amphiphys	273.00	AMPH	2903.00	6.48	**3.90**
50047.00	I16	M-005806- calpain 5	726.00	CAPN5	2108.00	3.42	0.84
50047.00	I17	M-012691- amylase, al	276.00	AMY1A	3202.00	6.37	**3.79**
50047.00	I18	M-007818- complemer	725.00	C4BPB	3502.00	6.05	3.47
50047.00	I19	M-016978- amylase, al	279.00	AMY2A	3200.00	13.31	**10.73**
50047.00	I20	M-007817- complemer	722.00	C4BPA	3958.00	6.29	**3.71**
50047.00	I21	M-015880- amylase, al	280.00	AMY2B	2290.00	4.06	1.48
50047.00	I23	M-007487- solute carri	293.00	SLC25A6	2577.00	4.04	1.46
50047.00	J02	M-011636- defensin, a	1669.00	DEFA4	3999.00	2.98	0.40
50047.00	J04	M-012027- defensin, a	1668.00	DEFA3	2186.00	0.46	2.12
50047.00	J05	M-013632- cytochrom	1329.00	COX5B	3423.00	3.83	1.25
50047.00	J06	M-012999- defensin, a	1667.00	DEFA1	2016.00	2.38	0.20
50047.00	J07	M-011836- cytochrom	1337.00	COX6A1	3230.00	1.52	1.06
50047.00	J08	M-011250- DEAH (Asp-	1665.00	DHX15	1630.00	2.27	0.31
50047.00	J09	M-012021- cytochrom	1339.00	COX6A2	1811.00	0.28	2.30

50047.00	J10	M-011842- DEAD (Asp	1662.00	DDX10	2635.00	1.33	1.25
50047.00	J11	M-013148- cytochrom	1340.00	COX6B1	1983.00	2.27	0.31
50047.00	J12	M-009950- DEAH (Asp	1660.00	DHX9	3251.00	7.07	4.49
50047.00	J13	M-013151- cytochrom	1345.00	COX6C	1863.00	0.70	1.88
50047.00	J14	M-012091- Dmx-like 1	1657.00	DMXL1	2880.00	2.05	0.53
50047.00	J15	M-013152- cytochrom	1346.00	COX7A1	3044.00	4.34	1.76
50047.00	J16	M-003774- DEAD (Asp	1655.00	DDX5	2466.00	2.15	0.43
50047.00	J17	M-011626- cytochrom	1347.00	COX7A2	1969.00	0.96	1.62
50047.00	J18	M-006874- DEAD (Asp	1654.00	DDX3X	1408.00	2.34	0.24
50047.00	J19	M-019464- cytochrom	1348.00	COX7AP2	1913.00	1.57	1.01
50047.00	J20	M-011993- DEAD (Asp	1653.00	DDX1	3837.00	3.81	1.23
50047.00	J21	M-011627- cytochrom	1349.00	COX7B	3737.00	2.89	0.31
50047.00	J23	M-013317- cytochrom	1350.00	COX7C	1938.00	1.24	1.34
50047.00	K02	M-011225- compleme	708.00	C1QBP	2668.00	2.02	0.56
50047.00	K04	M-011818- bystin-like	705.00	BYSL	1670.00	1.38	1.20
50047.00	K05	M-027301- annexin A2	303.00	ANXA2P1	2646.00	6.31	3.73
50047.00	K06	M-011597- betacelluli	685.00	BTC	1901.00	8.52	5.94
50047.00	K07	M-010952- annexin A2	305.00	ANXA2P3	3190.00	4.08	1.50
50047.00	K08	M-011817- bone marr	684.00	BST2	1684.00	8.02	5.44
50047.00	K09	M-010381- amine oxid	314.00	AOC2	1513.00	2.45	0.13
50047.00	K10	M-005101- bone marr	683.00	BST1	1611.00	1.99	0.59
50047.00	K11	M-017412- amyloid be	320.00	APBA1	1874.00	2.88	0.30
50047.00	K12	M-013605- zinc finger	678.00	ZFP36L2	2434.00	5.46	2.88
50047.00	K13	M-017413- amyloid be	321.00	APBA2	1674.00	1.08	1.50
50047.00	K14	M-009439- carcinoem	634.00	CEACAM1	2555.00	10.92	8.34
50047.00	K15	M-017423- amyloid be	323.00	APBB2	2090.00	2.44	0.14
50047.00	K16	M-008633- bone gam	632.00	BGLAP	2641.00	2.12	0.46
50047.00	K17	M-011577- shroom fa	357.00	SHROOM2	2220.00	2.97	0.39
50047.00	K18	M-011218- beaded fila	631.00	BFSP1	3369.00	4.57	1.99
50047.00	K19	M-013063- archain 1	372.00	ARCN1	724.00	3.59	1.01
50047.00	K20	M-012567- alpha-2-gly	563.00	AZGP1	3484.00	6.17	3.59
50047.00	K21	M-009454- arginase, t	384.00	ARG2	2292.00	5.45	2.87
50047.00	K23	M-019265- ADP-ribosy	400.00	ARL1	3015.00	4.18	1.60
50047.00	L02	M-012201- D-dopachr	1652.00	DDT	3649.00	0.36	2.22
50047.00	L04	M-015786- dolichyl-di	1650.00	DDOST	3028.00	5.88	3.30
50047.00	L05	M-011819- cytochrom	1351.00	COX8A	1795.00	1.11	1.47
50047.00	L06	M-011113- doublecort	1641.00	DCX	3071.00	3.74	1.16
50047.00	L07	M-005817- carboxype	1359.00	CPA3	3362.00	2.41	0.17
50047.00	L08	M-019622- dCMP dea	1635.00	DCTD	4266.00	9.70	7.12
50047.00	L09	M-004206- claudin 7	1366.00	CLDN7	1413.00	1.63	0.95
50047.00	L10	M-011841- drebrin 1	1627.00	DBN1	1812.00	2.43	0.15
50047.00	L11	M-010266- carnitine p	1375.00	CPT1B	2703.00	2.15	0.43
50047.00	L12	M-013465- deleted in	1620.00	DBC1	2216.00	6.81	4.23
50047.00	L13	M-007860- compleme	1379.00	CR1L	2409.00	4.61	2.03
50047.00	L14	M-011249- deleted in	1618.00	DAZL	3454.00	4.84	2.26
50047.00	L15	M-008754- cellular reti	1381.00	CRABP1	2728.00	2.97	0.39
50047.00	L16	M-009215- cytochrom	1595.00	CYP51A1	1698.00	2.00	0.58

50047.00	L17	M-008385- cellular reti	1382.00	CRABP2	2818.00	3.19	0.61
50047.00	L18	M-009526- cytochrom	1592.00	CYP26A1	1457.00	1.37	1.21
50047.00	L19	M-016212- cysteine-ri	1396.00	CRIP1	2969.00	4.78	2.20
50047.00	L20	M-009269- cytochrom	1591.00	CYP24A1	3542.00	3.19	0.61
50047.00	L21	M-005155- cysteine-ri	1397.00	CRIP2	2881.00	2.64	0.06
50047.00	L23	M-009393- collapsin re	1400.00	CRMP1	3350.00	2.63	0.05
50047.00	M02	M-012410- ancient ubi	550.00	AUP1	3703.00	1.11	1.47
50047.00	M04	M-019495- ATP syntha	539.00	ATP5O	3713.00	7.41	4.83
50047.00	M05	M-009332- arylsulfata	416.00	ARSF	3793.00	3.85	1.27
50047.00	M06	M-021378- ATPase, H+	537.00	ATP6AP1	2359.00	1.65	0.93
50047.00	M07	M-009074- achaete-sc	430.00	ASCL2	2542.00	3.93	1.35
50047.00	M08	M-017618- ATPase, H+	535.00	ATP6V0A1	2899.00	3.24	0.66
50047.00	M09	M-009666- arsA arseni	439.00	ASNA1	2056.00	2.87	0.29
50047.00	M10	M-012916- ATPase, H+	534.00	ATP6V1G2	3047.00	3.31	0.73
50047.00	M11	M-004294- aspartate	444.00	ASPH	2216.00	3.29	0.71
50047.00	M12	M-010907- ATPase, H+	533.00	ATP6V0B	1319.00	1.21	1.37
50047.00	M13	M-021881- astrotactin	460.00	ASTN1	2672.00	2.06	0.52
50047.00	M14	M-011590- ATPase, H+	529.00	ATP6V1E1	1593.00	3.52	0.94
50047.00	M15	M-008915- atonal ho	474.00	ATOH1	2338.00	6.59	4.01
50047.00	M16	M-013139- ATPase, H+	528.00	ATP6V1C1	1929.00	1.92	0.66
50047.00	M17	M-019059- ATX1 antio	475.00	ATOX1	2433.00	9.49	6.91
50047.00	M18	M-017620- ATPase, H+	527.00	ATP6V0C	2082.00	3.36	0.78
50047.00	M19	M-006111- ATPase, Na	476.00	ATP1A1	3038.00	3.13	0.55
50047.00	M20	M-011589- ATPase, H+	526.00	ATP6V1B2	4230.00	10.97	8.39
50047.00	M21	M-004614- ATPase, Na	478.00	ATP1A3	3083.00	5.03	2.45
50047.00	M23	M-006110- ATPase, H+	479.00	ATP12A	2673.00	2.24	0.34
50047.00	N02	M-027298- ADAM met	1587.00	ADAM3A	2457.00	1.47	1.11
50047.00	N04	M-009043- cytochrom	1582.00	CYP8B1	1478.00	1.89	0.69
50047.00	N05	M-019373- C-reactive	1401.00	CRP	2163.00	2.17	0.41
50047.00	N06	M-008792- cytochrom	1581.00	CYP7A1	2743.00	1.75	0.83
50047.00	N07	M-019514- hyaluron	1404.00	HAPLN1	1317.00	0.15	2.43
50047.00	N08	M-008377- cytochrom	1580.00	CYP4B1	1137.00	1.41	1.17
50047.00	N09	M-014151- cryptochro	1408.00	CRY2	2946.00	3.53	0.95
50047.00	N10	M-009147- cytochrom	1579.00	CYP4A11	1559.00	1.15	1.43
50047.00	N11	M-009334- citrate synt	1431.00	CS	3309.00	3.63	1.05
50047.00	N12	M-009684- cytochrom	1577.00	CYP3A5	1949.00	2.46	0.12
50047.00	N13	M-019516- casein alph	1446.00	CSN1S1	2348.00	2.17	0.41
50047.00	N14	M-008169- cytochrom	1576.00	CYP3A4	1420.00	1.90	0.68
50047.00	N15	M-019517- casein bet	1447.00	CSN2	1945.00	1.39	1.19
50047.00	N16	M-008208- cytochrom	1573.00	CYP2J2	3243.00	4.93	2.35
50047.00	N17	M-019940- casein kap	1448.00	CSN3	861.00	1.74	0.84
50047.00	N18	M-011169- cytochrom	1572.00	CYP2F1	3124.00	3.04	0.46
50047.00	N19	M-019794- neurocan	1463.00	NCAN	1477.00	3.93	1.35
50047.00	N20	M-010134- cytochrom	1571.00	CYP2E1	3436.00	6.96	4.38
50047.00	N21	M-011632- chondroiti	1464.00	CSPG4	2980.00	1.85	0.73
50047.00	N23	M-011244- cysteine an	1466.00	CSRP2	3872.00	1.42	1.16
50047.00	O02	M-017590- ATPase, H+	523.00	ATP6V1A	1632.00	0.49	2.09

50047.00	O04	M-019688- ATP syntha	521.00	ATP5I	2965.00	1.62	0.96
50047.00	O05	M-021377- ATPase, Na	480.00	ATP1A4	3420.00	1.02	1.56
50047.00	O06	M-019494- ATP syntha	518.00	ATP5G3	2258.00	0.31	2.27
50047.00	O07	M-008381- ATPase, Na	481.00	ATP1B1	3165.00	1.36	1.22
50047.00	O08	M-019936- ATP syntha	517.00	ATP5G2	1809.00	3.26	0.68
50047.00	O09	M-010235- ATPase, Na	482.00	ATP1B2	2361.00	1.57	1.01
50047.00	O10	M-019935- ATP syntha	516.00	ATP5G1	2491.00	0.52	2.06
50047.00	O11	M-004569- ATPase, Na	483.00	ATP1B3	1216.00	1.15	1.43
50047.00	O12	M-015956- ATP syntha	515.00	ATP5F1	1241.00	0.16	2.42
50047.00	O13	M-006115- ATPase, Ca	490.00	ATP2B1	2241.00	2.86	0.28
50047.00	O14	M-012330- ATP syntha	514.00	ATP5E	2126.00	1.55	1.03
50047.00	O15	M-006116- ATPase, Ca	491.00	ATP2B2	2615.00	1.76	0.82
50047.00	O16	M-017852- ATP syntha	513.00	ATP5D	2902.00	1.62	0.96
50047.00	O17	M-006117- ATPase, Ca	492.00	ATP2B3	3562.00	4.72	2.14
50047.00	O18	M-018615- ATP syntha	506.00	ATP5B	1969.00	0.91	1.67
50047.00	O19	M-006118- ATPase, Ca	493.00	ATP2B4	4345.00	2.03	0.55
50047.00	O20	M-017064- ATP syntha	498.00	ATP5A1	3525.00	4.28	1.70
50047.00	O21	M-006120- ATPase, H+	495.00	ATP4A	3763.00	2.47	0.11
50047.00	O23	M-009118- ATPase, H+	496.00	ATP4B	2869.00	1.53	1.05
50047.00	P02	M-011168- cytochrom	1555.00	CYP2B6	1950.00	0.82	1.76
50047.00	P04	M-010133- cytochrom	1553.00	CYP2A13	1343.00	4.69	2.11
50047.00	P05	M-007469- solute carri	1468.00	SLC25A10	1049.00	1.14	1.44
50047.00	P06	M-008634- cytochrom	1551.00	CYP3A7	1183.00	3.13	0.55
50047.00	P07	M-017398- cystatin SN	1469.00	CST1	701.00	2.14	0.44
50047.00	P08	M-011248- cylicin, bas	1539.00	CYLC2	1648.00	3.58	1.00
50047.00	P09	M-017395- cystatin SA	1470.00	CST2	1066.00	12.01	**9.43**
50047.00	P10	M-024769- cylicin, bas	1538.00	CYLC1	2502.00	6.55	**3.97**
50047.00	P11	M-011633- cystatin S	1472.00	CST4	1922.00	1.20	1.38
50047.00	P12	M-017850- cytochrom	1534.00	CYB561	1184.00	2.20	0.38
50047.00	P13	M-011634- cystatin D	1473.00	CST5	981.00	3.87	1.29
50047.00	P14	M-020184- testis expre	1527.00	TEX28	1764.00	5.27	2.69
50047.00	P15	M-004999- cystatin E/	1474.00	CST6	2648.00	3.40	0.82
50047.00	P16	M-005832- chymotryp	1504.00	CTRB1	2088.00	3.35	0.77
50047.00	P17	M-011245- cleavage st	1477.00	CSTF1	2684.00	3.43	0.85
50047.00	P18	M-019796- chitobiase,	1486.00	CTBS	1689.00	3.73	1.15
50047.00	P19	M-021360- B melanom	574.00	BAGE	4165.00	3.41	0.83
50047.00	P20	M-004342- cancer/tes	1485.00	CTAG1B	1497.00	7.82	**5.24**
50047.00	P21	M-027334- cortistatin	1325.00	CORT	2263.00	6.10	**3.52**
50047.00	P23	M-013001- chorionic s	1443.00	CSH2	3372.00	5.28	2.70
				mdn	2649.50	2.58	1.16
				3MAD			3.49
				MADc			1.72
50047.00	C22				5235.00	32.88	
50047.00	D22				4833.00	31.35	
50047.00	E22				3554.00	21.08	
50047.00	F22				3347.00	18.23	
				mn	4242.25	25.88	

					sd	932.68	7.31
50047.00	G22					1222.00	0.65
50047.00	H22					1327.00	2.41
50047.00	I22					2093.00	2.20
50047.00	J22					2191.00	2.28
					mn	1708.25	1.89
					sd	504.27	0.83
					3psSD		21.94
					3ngSD		2.48
					SumSD		24.42
					DiffMn		23.99
					SmovrDiff		1.02
					1minus		-0.02
50047.00	J03	D-001206-	siControl non-targetin			1882.00	1.28
50047.00	I03	D-001206-	siControl non-targetin			2301.00	1.43
50047.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMA	195.00	1.03
50047.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMA	124.00	0.81
50047.00	K03	D-001600-	siGLO RISC-free siRNA			5873.00	9.50
50047.00	L03	D-001600-	siGLO RISC-free siRNA			5903.00	9.32

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
-0.96	1354.00	1.03	0.52	-0.36	1530.00	6.99	**4.33**	2.06
1.18	1771.00	1.07	0.48	-0.34	3721.00	7.39	**4.73**	2.25
-0.81	1685.00	1.01	0.54	-0.38	1444.00	5.96	3.30	1.57
-0.11	1964.00	1.68	0.13	0.09	2948.00	4.44	1.78	0.85
-0.23	682.00	1.47	0.08	-0.06	998.00	2.81	0.15	0.07
-0.67	1239.00	1.05	0.50	-0.35	1458.00	3.64	0.98	0.46
0.18	1723.00	1.80	0.25	0.17	2969.00	4.38	1.72	0.82
-0.13	1860.00	0.91	0.64	-0.45	2118.00	4.77	2.11	1.00
-0.05	407.00	0.98	0.57	-0.40	465.00	5.81	3.15	1.50
0.01	590.00	1.19	0.36	-0.26	729.00	8.37	**5.71**	2.72
2.17	710.00	6.48	**4.93**	3.46	665.00	10.53	**7.87**	3.75
0.00	931.00	1.07	0.48	-0.34	988.00	6.48	3.82	1.82
1.04	1963.00	0.97	0.58	-0.41	3099.00	2.68	0.02	0.01
1.31	1745.00	0.80	0.75	-0.53	2692.00	1.86	0.80	-0.38
-0.22	523.00	1.15	0.40	-0.28	477.00	8.39	**5.73**	2.73
-0.33	1458.00	1.78	0.23	0.16	2126.00	4.52	1.86	0.88
-0.03	846.00	1.65	0.10	0.07	1936.00	2.01	0.65	-0.31
-0.58	2143.00	0.93	0.62	-0.44	1533.00	5.54	2.88	1.37
1.70	2374.00	2.40	0.85	0.60	2961.00	5.23	2.57	1.23
-0.34	968.00	2.79	1.24	0.87	1140.00	5.26	2.60	1.24
-0.43	518.00	0.39	1.16	-0.82	720.00	2.92	0.26	0.12
-0.39	371.00	0.27	1.28	-0.90	605.00	2.98	0.32	0.15
-0.73	2220.00	0.63	0.92	-0.65	2392.00	1.00	1.66	-0.79
-0.95	928.00	0.32	1.23	-0.86	712.00	2.53	0.13	-0.06
0.16	1029.00	0.19	1.36	-0.95	1998.00	0.35	2.31	-1.10
-0.31	1539.00	0.58	0.97	-0.68	3811.00	1.63	1.03	-0.49
1.03	1650.00	0.61	0.94	-0.66	3949.00	5.01	2.35	1.12
0.17	2191.00	1.41	0.14	-0.10	2471.00	2.39	0.27	-0.13
0.00	1471.00	0.20	1.35	-0.95	1569.00	1.85	0.81	-0.39
-1.06	956.00	0.84	0.71	-0.50	658.00	1.37	1.29	-0.62
-1.06	1262.00	1.66	0.11	0.08	1217.00	1.48	1.18	-0.56
0.02	2256.00	1.15	0.40	-0.28	2766.00	1.99	0.67	-0.32
1.96	2202.00	6.58	**5.03**	3.53	3129.00	6.42	3.76	1.79
-0.69	1837.00	2.78	1.23	0.86	2737.00	1.02	1.64	-0.78
-0.25	1761.00	2.84	1.29	0.90	2892.00	1.14	1.52	-0.72
-0.37	988.00	0.20	1.35	-0.95	1186.00	0.84	1.82	-0.87
-0.12	1038.00	0.19	1.36	-0.95	1817.00	1.54	1.12	-0.53
-0.46	830.00	2.65	1.10	0.77	1635.00	1.41	1.25	-0.60
-1.11	1786.00	0.62	0.93	-0.66	3333.00	0.18	2.48	-1.18
-0.93	2364.00	0.93	0.62	-0.44	1553.00	5.02	2.36	1.12
2.25	2580.00	1.94	0.39	0.27	2929.00	2.83	0.17	0.08
0.64	2884.00	1.63	0.08	0.05	2700.00	3.04	0.38	0.18
-0.52	2754.00	1.45	0.10	-0.07	2110.00	2.27	0.39	-0.18
0.98	1948.00	1.28	0.27	-0.19	2665.00	1.31	1.35	-0.64
-0.61	1087.00	0.00	1.55	-1.09	2685.00	1.68	0.98	-0.47
5.85	3055.00	2.62	1.07	0.75	4256.00	13.56	**10.90**	5.19

0.52	2368.00	3.80	2.25	1.58	4127.00	3.13	0.47	0.22
0.79	3503.00	3.54	1.99	1.39	5107.00	4.17	1.51	0.72
0.26	1987.00	3.57	2.02	1.42	2878.00	2.08	0.58	-0.27
0.88	2277.00	4.79	3.24	2.27	1974.00	5.22	2.56	1.22
-0.87	678.00	0.29	1.26	-0.88	761.00	1.45	1.21	-0.58
2.02	1913.00	2.93	1.38	0.96	2952.00	4.03	1.37	0.65
-0.68	1045.00	1.05	0.50	-0.35	2391.00	3.97	1.31	0.62
2.13	2645.00	3.78	2.23	1.56	4025.00	4.25	1.59	0.76
-0.08	1888.00	0.53	1.02	-0.72	2385.00	1.89	0.77	-0.37
-0.44	2475.00	0.85	0.70	-0.49	2499.00	3.24	0.58	0.28
1.06	1975.00	0.35	1.20	-0.84	3037.00	1.25	1.41	-0.67
-0.50	3150.00	4.63	3.08	2.16	2704.00	4.33	1.67	0.79
1.28	2359.00	1.70	0.15	0.10	2835.00	4.41	1.75	0.83
1.96	2598.00	0.38	1.17	-0.82	2125.00	7.11	4.45	2.12
-1.38	3486.00	0.63	0.92	-0.65	2634.00	1.21	1.45	-0.69
-0.12	3767.00	4.25	2.70	1.89	3155.00	3.39	0.73	0.35
-0.69	2415.00	3.06	1.51	1.06	2003.00	2.10	0.56	-0.27
0.19	1613.00	2.48	0.93	0.65	2615.00	1.57	1.09	-0.52
-0.67	1953.00	2.36	0.81	0.56	3651.00	1.37	1.29	-0.62
-0.98	3078.00	1.04	0.51	-0.36	3791.00	2.03	0.63	-0.30
0.93	2292.00	2.84	1.29	0.90	2834.00	3.95	1.29	0.61
1.97	739.00	6.22	4.67	3.28	2109.00	8.58	5.92	2.82
0.04	1713.00	3.39	1.84	1.29	2217.00	7.44	4.78	2.28
-1.10	1180.00	0.85	0.70	-0.50	1142.00	1.49	1.17	-0.56
-1.15	923.00	0.22	1.33	-0.94	999.00	0.90	1.76	-0.84
1.51	1701.00	2.35	0.80	0.56	2467.00	5.92	3.26	1.55
-0.52	1015.00	0.69	0.86	-0.61	1756.00	2.39	0.27	-0.13
0.50	1258.00	6.84	5.29	3.71	2761.00	4.96	2.30	1.10
2.23	1683.00	5.23	3.68	2.58	2654.00	10.48	7.82	3.72
-0.82	2003.00	2.30	0.75	0.52	2634.00	3.23	0.57	0.27
0.92	1124.00	3.20	1.65	1.16	1665.00	5.35	2.69	1.28
-0.32	1427.00	0.98	0.57	-0.40	3188.00	1.35	1.31	-0.63
0.74	1545.00	1.94	0.39	0.27	4012.00	5.51	2.85	1.36
-0.74	1408.00	1.35	0.20	-0.14	2406.00	4.90	2.24	1.07
-1.04	2397.00	4.21	2.66	1.87	2968.00	9.50	6.84	3.26
-0.99	1628.00	2.64	1.09	0.76	2327.00	3.18	0.52	0.25
-0.21	2118.00	1.56	0.01	0.00	2834.00	6.25	3.59	1.71
-0.58	1950.00	3.59	2.04	1.43	2003.00	6.29	3.63	1.73
-1.44	1204.00	1.00	0.55	-0.39	2021.00	1.78	0.88	-0.42
-1.07	1858.00	2.10	0.55	0.38	3126.00	2.21	0.45	-0.22
-1.24	1139.00	0.70	0.85	-0.60	1975.00	2.38	0.28	-0.13
-1.00	2349.00	3.02	1.47	1.03	3940.00	4.92	2.26	1.08
-1.02	2339.00	2.09	0.54	0.38	2587.00	2.32	0.34	-0.16
-0.80	1125.00	1.51	0.04	-0.03	1462.00	3.69	1.03	0.49
-1.09	1114.00	3.86	2.31	1.62	893.00	1.23	1.43	-0.68
-0.84	1233.00	0.97	0.58	-0.41	1535.00	2.15	0.51	-0.24
-0.83	1647.00	3.46	1.91	1.34	2294.00	4.80	2.14	1.02

-0.44	1511.00	6.49	**4.94**	3.46	3335.00	2.73	0.07	0.03
-0.53	1612.00	5.71	**4.16**	2.92	1578.00	9.82	**7.16**	3.41
-0.53	1359.00	4.49	**2.94**	2.06	2990.00	3.28	0.62	0.29
0.14	1217.00	8.71	**7.16**	5.02	1296.00	5.94	3.28	1.56
0.38	2702.00	3.74	2.19	1.53	4116.00	9.09	**6.43**	3.06
-0.31	2185.00	1.92	0.37	0.26	3281.00	5.39	2.73	1.30
0.09	1970.00	1.73	0.18	0.12	2116.00	4.44	1.78	0.85
0.29	2556.00	1.29	0.26	-0.18	3169.00	3.09	0.43	0.21
-0.31	1579.00	1.14	0.41	-0.29	1852.00	2.65	0.01	-0.01
-0.22	2747.00	0.29	1.26	-0.89	3273.00	2.51	0.15	-0.07
-0.58	2135.00	0.42	1.13	-0.79	2816.00	3.02	0.36	0.17
3.35	2160.00	2.64	1.09	0.76	3141.00	6.49	3.83	1.83
2.38	1851.00	2.49	0.94	0.65	3903.00	5.69	3.03	1.44
0.07	1683.00	1.43	0.12	-0.09	1406.00	3.56	0.90	0.43
1.56	2539.00	0.71	0.84	-0.59	3162.00	5.79	3.13	1.49
1.41	1975.00	2.18	0.63	0.44	1859.00	5.97	3.31	1.58
2.61	2319.00	1.60	0.05	0.03	2109.00	4.84	2.18	1.04
0.08	1153.00	2.60	1.05	0.74	1413.00	4.18	1.52	0.72
0.14	1181.00	1.86	0.31	0.22	978.00	6.34	3.68	1.75
3.01	2035.00	4.52	**2.97**	2.08	2069.00	9.04	**6.38**	3.04
0.66	866.00	1.39	0.16	-0.12	1120.00	2.23	0.43	-0.20
1.38	2713.00	3.43	1.88	1.32	2635.00	5.31	2.65	1.26
1.66	2834.00	2.40	0.85	0.59	4425.00	4.81	2.15	1.03
3.75	3606.00	4.33	2.78	1.95	3901.00	11.05	**8.39**	3.99
0.76	2322.00	0.73	0.82	-0.58	2763.00	2.57	0.09	-0.04
0.64	3315.00	4.59	**3.04**	2.13	3120.00	3.21	0.55	0.26
0.04	2633.00	0.95	0.60	-0.42	2298.00	5.57	2.91	1.39
-1.13	1935.00	0.36	1.19	-0.84	1929.00	1.61	1.05	-0.50
0.13	2368.00	0.63	0.92	-0.65	1802.00	3.00	0.34	0.16
0.01	3341.00	1.77	0.22	0.15	3667.00	5.64	2.98	1.42
-0.98	1268.00	0.24	1.31	-0.92	1639.00	1.71	0.95	-0.45
0.71	2279.00	0.22	1.33	-0.94	2773.00	2.24	0.42	-0.20
-0.27	1332.00	0.53	1.02	-0.72	2335.00	2.83	0.17	0.08
-0.24	2436.00	0.12	1.43	-1.00	2025.00	4.35	1.69	0.80
1.25	1256.00	0.96	0.59	-0.42	1747.00	5.90	3.24	1.54
0.73	1358.00	1.03	0.52	-0.37	1480.00	8.31	**5.65**	2.69
-0.26	1191.00	0.92	0.63	-0.44	1254.00	1.83	0.83	-0.39
0.05	851.00	0.47	1.08	-0.76	1384.00	1.73	0.93	-0.44
0.05	934.00	3.10	1.55	1.09	1558.00	5.91	3.25	1.54
-0.72	822.00	2.43	0.88	0.62	965.00	2.69	0.03	0.02
0.13	1466.00	1.02	0.53	-0.37	1893.00	3.91	1.25	0.59
0.68	1706.00	1.82	0.27	0.19	2586.00	4.72	2.06	0.98
-0.90	1286.00	2.95	1.40	0.98	1748.00	1.72	0.94	-0.45
1.47	2502.00	3.32	1.77	1.24	3803.00	7.57	**4.91**	2.34
2.02	3898.00	4.44	**2.89**	2.03	3804.00	5.26	2.60	1.24
0.59	2300.00	2.26	0.71	0.50	2675.00	2.32	0.34	-0.16
-0.81	1918.00	1.15	0.40	-0.29	2189.00	1.83	0.83	-0.40

0.56	1461.00	1.37	0.18	-0.13	2000.00	3.55	0.89	0.42
-0.39	1672.00	1.50	0.05	-0.04	1873.00	1.66	1.00	-0.48
-0.23	1985.00	1.11	0.44	-0.31	1933.00	1.40	1.26	-0.60
-0.61	1618.00	0.56	0.99	-0.70	1748.00	0.17	2.49	-1.19
-0.05	2142.00	0.23	1.32	-0.93	2458.00	0.81	1.85	-0.88
2.71	1671.00	6.52	**4.97**	3.49	1792.00	10.16	**7.50**	3.57
1.07	2103.00	1.14	0.41	-0.29	2139.00	7.11	**4.45**	2.12
0.14	1247.00	0.48	1.07	-0.75	1077.00	3.34	0.68	0.32
2.91	1261.00	4.76	**3.21**	2.25	985.00	3.45	0.79	0.38
-0.24	1512.00	0.20	1.35	-0.95	2044.00	4.31	1.65	0.78
0.09	1808.00	1.71	0.16	0.11	1429.00	2.94	0.28	0.13
-0.93	1656.00	0.91	0.64	-0.45	1935.00	0.93	1.73	-0.82
5.77	67.00	5.97	**4.42**	3.10	43.00	9.30	**6.64**	3.16
-0.02	973.00	1.44	0.11	-0.08	2564.00	3.16	0.50	0.24
-0.60	339.00	0.59	0.96	-0.68	401.00	0.75	1.91	-0.91
0.04	1843.00	0.76	0.79	-0.56	2252.00	1.42	1.24	-0.59
-0.31	1279.00	0.94	0.61	-0.43	1167.00	3.00	0.34	0.16
-0.33	1439.00	1.60	0.05	0.03	1976.00	2.94	0.28	0.13
-0.43	1071.00	1.21	0.34	-0.24	1412.00	2.41	0.25	-0.12
-0.32	1915.00	1.67	0.12	0.08	3082.00	3.73	1.07	0.51
1.30	1899.00	2.37	0.82	0.57	1912.00	1.15	1.51	-0.72
-0.54	3395.00	2.71	1.16	0.81	2332.00	0.30	2.36	-1.12
0.36	2228.00	1.44	0.11	-0.08	2680.00	1.01	1.65	-0.79
-0.88	1462.00	0.41	1.14	-0.80	1234.00	0.24	2.42	-1.15
-0.57	2528.00	3.68	2.13	1.49	2321.00	0.73	1.93	-0.92
-0.08	2410.00	3.24	1.69	1.18	1486.00	0.74	1.92	-0.92
-0.31	1220.00	2.13	0.58	0.41	1333.00	0.08	2.58	-1.23
0.23	2009.00	3.19	1.64	1.15	1546.00	0.97	1.69	-0.81
1.25	1752.00	1.60	0.05	0.03	1688.00	1.48	1.18	-0.56
1.95	2053.00	1.41	0.14	-0.10	1881.00	0.80	1.86	-0.89
1.84	1996.00	3.26	1.71	1.20	1170.00	1.79	0.87	-0.41
3.58	1676.00	2.63	1.08	0.75	1773.00	1.52	1.14	-0.54
2.27	2550.00	1.65	0.10	0.07	2384.00	2.06	0.60	-0.29
0.49	1935.00	7.08	**5.53**	3.88	1415.00	1.91	0.75	-0.36
2.21	2388.00	3.81	2.26	1.58	2778.00	2.34	0.32	-0.15
2.02	2543.00	1.85	0.30	0.21	3426.00	1.93	0.73	-0.35
6.24	3762.00	7.71	**6.16**	4.32	2758.00	4.50	1.84	0.87
2.16	3270.00	5.38	**3.83**	2.69	2579.00	5.00	2.34	1.11
0.86	3845.00	5.15	**3.60**	2.52	2309.00	5.67	3.01	1.43
0.85	1687.00	1.54	0.01	-0.01	2007.00	3.04	0.38	0.18
0.23	4065.00	7.45	**5.90**	4.14	2660.00	8.31	**5.65**	2.69
-1.23	1394.00	3.44	1.89	1.33	1765.00	2.21	0.45	-0.22
0.73	3727.00	4.29	2.74	1.92	3397.00	5.80	3.14	1.49
-0.11	1942.00	6.28	**4.73**	3.32	1542.00	7.72	**5.06**	2.41
-0.62	2463.00	1.50	0.05	-0.04	2163.00	1.06	1.60	-0.76
-0.18	1212.00	2.31	0.76	0.53	650.00	5.23	2.57	1.22
-1.34	1102.00	0.82	0.73	-0.52	1567.00	5.04	2.38	1.13

-0.73	2858.00	1.71	0.16	0.11	2115.00	2.70	0.04	0.02
-0.18	1001.00	2.40	0.85	0.59	699.00	7.01	**4.35**	2.07
2.61	1929.00	5.86	**4.31**	3.02	1639.00	8.30	**5.64**	2.68
-1.09	1314.00	3.58	2.03	1.42	1788.00	1.62	1.04	-0.50
-0.31	1840.00	2.77	1.22	0.86	2306.00	3.56	0.90	0.43
1.02	3369.00	3.00	1.45	1.01	1817.00	1.54	1.12	-0.53
-0.25	1666.00	3.54	1.99	1.40	870.00	1.72	0.94	-0.45
-0.94	1812.00	5.08	**3.53**	2.47	1341.00	3.13	0.47	0.22
-0.14	880.00	0.57	0.98	-0.69	529.00	6.43	3.77	1.79
-0.59	1044.00	0.67	0.88	-0.62	828.00	5.80	3.14	1.49
0.71	2244.00	5.66	**4.11**	2.88	2015.00	4.47	1.81	0.86
0.18	3428.00	3.62	2.07	1.45	3165.00	2.46	0.20	-0.09
-0.78	2073.00	1.83	0.28	0.20	1743.00	2.12	0.54	-0.26
-0.32	2530.00	0.75	0.80	-0.56	2212.00	4.07	1.41	0.67
-0.70	1690.00	0.30	1.25	-0.88	1120.00	3.21	0.55	0.26
2.17	2849.00	2.32	0.77	0.54	2131.00	5.54	2.88	1.37
3.46	2547.00	2.87	1.32	0.92	747.00	10.17	**7.51**	3.58
0.87	2388.00	1.68	0.13	0.09	2001.00	3.45	0.79	0.37
3.16	2344.00	4.14	2.59	1.81	1095.00	6.67	4.01	1.91
-0.08	1401.00	1.21	0.34	-0.24	982.00	3.87	1.21	0.58
-0.34	1363.00	0.66	0.89	-0.63	876.00	6.85	4.19	1.99
0.18	1887.00	0.69	0.86	-0.61	860.00	3.02	0.36	0.17
1.68	1657.00	0.36	1.19	-0.84	1419.00	2.96	0.30	0.14
-0.87	1532.00	1.04	0.51	-0.36	487.00	7.80	**5.14**	2.45
4.85	3282.00	7.22	**5.67**	3.98	1732.00	9.18	**6.52**	3.10
-0.08	2250.00	0.36	1.19	-0.84	1754.00	4.96	2.30	1.09
-0.27	2617.00	0.00	1.55	-1.09	1797.00	2.06	0.60	-0.29
0.23	1903.00	1.26	0.29	-0.20	2125.00	4.33	1.67	0.79
1.16	3640.00	3.46	1.91	1.34	3178.00	11.33	**8.67**	4.13
0.59	616.00	1.62	0.07	0.05	392.00	7.14	**4.48**	2.13
2.09	2913.00	0.51	1.04	-0.73	2324.00	5.16	2.50	1.19
1.67	2308.00	1.65	0.10	0.07	1202.00	8.15	**5.49**	2.62
0.93	2225.00	2.02	0.47	0.33	2176.00	6.53	3.87	1.84
-1.29	2026.00	0.44	1.11	-0.78	3508.00	1.03	1.63	-0.78
1.92	2391.00	0.63	0.92	-0.65	2138.00	5.66	3.00	1.43
-0.85	2285.00	0.00	1.55	-1.09	1783.00	0.56	2.10	-1.00
0.68	3424.00	2.31	0.76	0.53	2534.00	3.35	0.69	0.33
-0.10	2765.00	0.90	0.65	-0.46	1572.00	2.48	0.18	-0.09
4.14	4714.00	5.03	**3.48**	2.44	4006.00	7.14	**4.48**	2.13
-0.55	2245.00	0.22	1.33	-0.93	1379.00	2.47	0.19	-0.09
-0.09	3287.00	1.40	0.15	-0.11	1398.00	2.65	0.01	-0.01
-0.25	2602.00	1.65	0.10	0.07	1940.00	3.45	0.79	0.38
2.46	1520.00	2.57	1.02	0.71	1175.00	3.57	0.91	0.43
1.18	2900.00	1.55	0.00	0.00	1162.00	2.41	0.25	-0.12
1.31	3327.00	2.89	1.34	0.94	2299.00	2.65	0.01	0.00
0.23	2014.00	1.79	0.24	0.16	1644.00	1.46	1.20	-0.57
-0.33	1866.00	0.86	0.69	-0.49	945.00	0.85	1.81	-0.86

0.36	3039.00	1.35	0.20	-0.14	1707.00	0.59	2.07	-0.99
-0.70	2083.00	0.72	0.83	-0.58	892.00	0.34	2.32	-1.11
1.28	2442.00	2.42	0.87	0.61	1827.00	1.42	1.24	-0.59
0.36	4077.00	2.77	1.22	0.86	3182.00	3.46	0.80	0.38
0.03	3007.00	1.33	0.22	-0.16	2982.00	2.08	0.58	-0.28
0.03	2816.00	1.07	0.48	-0.34	3074.00	1.66	1.00	-0.48
-0.86	2781.00	0.65	0.90	-0.64	2543.00	0.31	2.35	-1.12
2.81	2981.00	2.21	0.66	0.46	3024.00	1.36	1.30	-0.62
0.74	4217.00	3.32	1.77	1.24	2376.00	0.51	2.15	-1.03
-0.54	2549.00	0.71	0.84	-0.59	2175.00	0.41	2.25	-1.07
0.79	3234.00	5.10	**3.55**	2.49	3013.00	2.36	0.30	-0.15
0.39	2983.00	3.69	2.14	1.50	2047.00	0.93	1.73	-0.83
0.17	1395.00	1.29	0.26	-0.18	805.00	0.00	2.66	-1.27
0.43	4584.00	6.72	**5.17**	3.63	1876.00	0.43	2.23	-1.06
0.42	1958.00	2.60	1.05	0.74	800.00	1.38	1.29	-0.61
-0.79	2138.00	0.98	0.57	-0.40	1445.00	0.21	2.45	-1.17
-0.30	1687.00	1.19	0.36	-0.26	1668.00	0.06	2.60	-1.24
0.55	3136.00	3.44	1.89	1.33	2192.00	0.96	1.70	-0.81
2.33	4138.00	8.19	**6.64**	4.66	2299.00	0.91	1.75	-0.83
-0.38	1756.00	1.08	0.47	-0.33	990.00	0.40	2.26	-1.08
4.02	3893.00	14.13	**12.58**	8.83	1144.00	1.49	1.17	-0.56
0.46	3512.00	2.28	0.73	0.51	1734.00	0.06	2.60	-1.24
0.32	3191.00	3.70	2.15	1.51	1801.00	0.67	1.99	-0.95
4.88	3539.00	11.73	**10.18**	7.14	3624.00	5.05	2.39	1.14
1.42	5771.00	11.00	**9.45**	6.63	4212.00	2.47	0.19	-0.09
-0.19	1797.00	4.62	**3.07**	2.15	2727.00	1.36	1.30	-0.62
-0.65	2067.00	3.63	2.08	1.46	2320.00	1.90	0.76	-0.36
-0.40	2181.00	1.19	0.36	-0.25	1022.00	0.59	2.07	-0.99
-0.24	4357.00	1.63	0.08	0.05	2542.00	0.79	1.87	-0.89
-0.48	3987.00	2.98	1.43	1.00	2771.00	2.17	0.49	-0.24
-1.41	1231.00	1.30	0.25	-0.18	1024.00	1.07	1.59	-0.76
-0.68	2895.00	1.55	0.00	0.00	1060.00	0.66	2.00	-0.95
0.55	2971.00	3.10	1.55	1.08	1861.00	1.72	0.94	-0.45
-0.83	2945.00	3.26	1.71	1.20	1297.00	2.78	0.12	0.05
0.61	4614.00	6.52	**4.97**	3.49	1635.00	1.65	1.01	-0.48
-0.07	1537.00	3.32	1.77	1.24	1023.00	5.08	2.42	1.15
-0.24	2612.00	4.59	**3.04**	2.13	1209.00	0.83	1.83	-0.87
-0.39	2396.00	5.09	**3.54**	2.48	1007.00	1.89	0.77	-0.37
-0.69	3226.00	1.83	0.28	0.19	1410.00	2.55	0.11	-0.05
1.37	4097.00	4.81	**3.26**	2.28	3219.00	3.91	1.25	0.60
-0.49	1463.00	0.48	1.07	-0.75	220.00	2.73	0.07	0.03
0.27	4030.00	2.28	0.73	0.51	2547.00	1.81	0.85	-0.41
0.78	1819.00	0.55	1.00	-0.70	1726.00	1.10	1.56	-0.74
2.55	3237.00	4.63	**3.08**	2.16	3788.00	9.45	**6.79**	3.23
-0.43	2498.00	1.40	0.15	-0.11	2789.00	2.15	0.51	-0.24
-0.67	1948.00	1.28	0.27	-0.19	1812.00	3.48	0.82	0.39
-1.21	1700.00	0.41	1.14	-0.80	1327.00	0.68	1.98	-0.94

-0.56	2482.00	0.28	1.27	-0.89	1354.00	1.70	0.96	-0.46
-0.90	2879.00	1.53	0.02	-0.02	2104.00	1.33	1.33	-0.63
-1.32	3330.00	0.45	1.10	-0.77	2027.00	1.38	1.28	-0.61
-0.71	3948.00	0.38	1.17	-0.82	1803.00	3.11	0.45	0.21
0.40	2084.00	3.22	1.67	1.17	1029.00	7.77	5.11	2.44
-0.59	1992.00	0.45	1.10	-0.77	1116.00	0.99	1.67	-0.80
-1.20	3738.00	0.40	1.15	-0.81	1282.00	1.40	1.26	-0.60
-0.83	632.00	0.16	1.39	-0.98	412.00	2.67	0.01	0.00
-1.41	1249.00	0.08	1.47	-1.03	935.00	1.39	1.27	-0.61
0.16	1637.00	1.22	0.33	-0.23	1153.00	1.39	1.27	-0.61
-0.60	3245.00	0.83	0.72	-0.51	1510.00	2.12	0.54	-0.26
-0.48	3051.00	0.07	1.48	-1.04	2027.00	2.02	0.64	-0.30
-0.56	3296.00	0.42	1.13	-0.79	1682.00	1.55	1.11	-0.53
1.24	2835.00	1.02	0.53	-0.37	1270.00	0.87	1.79	-0.86
-0.97	1902.00	0.89	0.66	-0.46	746.00	2.41	0.25	-0.12
-0.32	3759.00	0.56	0.99	-0.70	2072.00	0.63	2.03	-0.97
0.99	3607.00	0.36	1.19	-0.84	1732.00	0.64	2.02	-0.97
-0.06	2515.00	0.40	1.15	-0.81	2041.00	0.69	1.97	-0.94
-0.61	2358.00	1.19	0.36	-0.26	2239.00	5.09	2.43	1.16
-1.02	2224.00	0.36	1.19	-0.84	2147.00	1.77	0.89	-0.42
1.23	1791.00	0.67	0.88	-0.62	1625.00	1.54	1.12	-0.53
-0.83	950.00	0.32	1.23	-0.87	761.00	1.31	1.35	-0.64
0.32	2612.00	0.73	0.82	-0.58	1002.00	2.89	0.23	0.11
-0.25	1106.00	2.08	0.53	0.37	522.00	4.60	1.94	0.92
0.58	2525.00	0.32	1.23	-0.87	1451.00	2.69	0.03	0.01
5.48	1626.00	1.11	0.44	-0.31	622.00	3.22	0.56	0.26
2.31	3386.00	1.42	0.13	-0.10	1553.00	1.55	1.11	-0.53
-0.80	1829.00	0.98	0.57	-0.40	1496.00	3.48	0.82	0.39
-0.22	1449.00	0.28	1.27	-0.90	831.00	1.93	0.73	-0.35
0.75	1740.00	3.45	1.90	1.33	1033.00	1.65	1.01	-0.48
1.57	1870.00	4.65	3.10	2.18	796.00	0.38	2.28	-1.09
0.48	2976.00	0.47	1.08	-0.76	2244.00	1.60	1.06	-0.50
0.45	4045.00	0.42	1.13	-0.80	1432.00	1.40	1.26	-0.60
0.49	3184.00	2.42	0.87	0.61	2638.00	1.06	1.60	-0.76
0.67	1511.00	0.60	0.95	-0.67	1066.00	0.66	2.00	-0.96
0.48	3185.00	2.73	1.18	0.83	2403.00	1.04	1.62	-0.77
3.05	1221.00	1.23	0.32	-0.23	1935.00	3.98	1.32	0.63
2.05	1564.00	0.77	0.78	-0.55	1733.00	1.15	1.51	-0.72
1.57	1014.00	0.59	0.96	-0.67	1546.00	0.45	2.21	-1.05
	1975.00	1.55	0.96		1938.00	2.66	1.42	
			2.89				4.26	
			1.42				2.10	
4480.00	22.55		4041.00	39.50				
2045.00	22.98		4240.00	30.02				
2385.00	33.59		1954.00	31.58				
3017.00	27.64		4430.00	38.40				
2981.75	26.69		3666.25	34.87				

1076.97	5.14	1152.50	4.77
809.00	3.58	976.00	1.43
841.00	0.59	759.00	2.90
2068.00	2.71	1934.00	1.96
1819.00	2.20	1798.00	4.06
1384.25	2.27	1366.75	2.59
653.85	1.26	585.89	1.15
	15.43		14.30
	3.77		3.46
	19.20		17.76
	24.42		32.28
	0.79		0.55
	0.21		0.45
2116.00	2.03	1779.00	5.56
2241.00	1.56	1722.00	0.29
183.00	1.09	148.00	6.76
169.00	4.73	115.00	8.70
6599.00	5.05	5782.00	15.62
5889.00	4.09	5417.00	7.05

x toxic a,b,c

y

y

y

x toxic b,c

y

y

y	
y	
x	toxic a,b,c
y	
x	debris a,b
y	
x	toxic b,c

y

x toxic a,b,c

y

y

y

y

y

y

Plate	Well	Gene		GeneID	Cell Count	% inf
50048.00	A02	M-032506- hypothetical STGC3	474171.00	STGC3	2033.00	0.15
50048.00	A04	M-008337- haptoglobin-related pr	3250.00	HPR	1778.00	0.45
50048.00	A05	M-020178- eukaryotic translation	1973.00	EIF4A1	1138.00	0.44
50048.00	A06	M-004332- hepsin (transmembran	3249.00	HPN	2443.00	0.29
50048.00	A07	M-013758- eukaryotic translation	1974.00	EIF4A2	1690.00	1.36
50048.00	A08	M-008700- hydroxyprostaglandin	3248.00	HPGD	2567.00	2.10
50048.00	A09	M-019474- eukaryotic translation	1981.00	EIF4G1	945.00	2.22
50048.00	A10	M-012911- homeobox D1	3231.00	HOXD1	2906.00	1.45
50048.00	A11	M-011263- eukaryotic translation	1982.00	EIF4G2	954.00	0.52
50048.00	A12	M-017677- homeobox C12	3228.00	HOXC12	1097.00	0.18
50048.00	A13	M-015739- eukaryotic translation	1984.00	EIF5A	990.00	0.00
50048.00	A14	M-012995- homeobox C8	3224.00	HOXC8	1263.00	1.19
50048.00	A15	M-005860- elastase 1, pancreatic	1990.00	ELA1	1179.00	1.44
50048.00	A16	M-017548- homeobox B9	3219.00	HOXB9	2718.00	0.99
50048.00	A17	M-011851- echinoderm microtubu	2009.00	EML1	2332.00	2.32
50048.00	A18	M-017527- homeobox B8	3218.00	HOXB8	524.00	7.82
50048.00	A19	M-010507- epithelial membrane p	2012.00	EMP1	2987.00	2.34
50048.00	A20	M-012892- homeobox B4	3214.00	HOXB4	2293.00	3.62
50048.00	A21	M-016226- epithelial membrane p	2013.00	EMP2	2185.00	6.41
50048.00	A23	M-010595- epithelial membrane p	2014.00	EMP3	2040.00	1.72
50048.00	B02	M-012831- NADH dehydrogenase	4540.00	ND5	1752.00	0.51
50048.00	B04	M-010326- NADH dehydrogenase	4539.00	ND4L	2792.00	0.64
50048.00	B05	M-012560- hemopexin	3263.00	HPX	3638.00	1.02
50048.00	B06	M-012830- NADH dehydrogenase	4538.00	ND4	3348.00	1.31
50048.00	B07	M-009128- ES cell expressed Ras	3266.00	ERAS	2256.00	0.31
50048.00	B08	M-012829- NADH dehydrogenase	4537.00	ND3	1204.00	1.16
50048.00	B09	M-016363- HIV-1 Rev binding prot	3268.00	HRBL	1391.00	0.07
50048.00	B10	M-012828- NADH dehydrogenase	4536.00	ND2	2506.00	2.00
50048.00	B11	M-017685- DnaJ (Hsp40) homolog	3300.00	DNAJB2	2118.00	1.18
50048.00	B12	M-012827- NADH dehydrogenase	4535.00	ND1	1183.00	6.59
50048.00	B13	M-019617- DnaJ (Hsp40) homolog	3301.00	DNAJA1	1901.00	1.26
50048.00	B14	M-011339- mitochondrial translati	4528.00	MTIF2	2666.00	3.38
50048.00	B15	M-019618- immunoglobulin super	3321.00	IGSF3	3050.00	1.34
50048.00	B16	M-012826- cytochrome c oxidase	4513.00	COX2	2297.00	5.88
50048.00	B17	M-026788- heat shock protein 90k	3324.00	HSP90AA2	2902.00	2.24
50048.00	B18	M-012825- cytochrome c oxidase	4512.00	COX1	3573.00	5.91
50048.00	B19	M-012735- DnaJ (Hsp40) homolog	3337.00	DNAJB1	2048.00	1.37
50048.00	B20	M-012824- ATP synthase F0 subur	4509.00	ATP8	1930.00	1.55
50048.00	B21	M-020055- DnaJ (Hsp40) homolog	3338.00	DNAJC4	3964.00	1.77
50048.00	B23	M-009376- N-deacetylase/N-sulfo	3340.00	NDST1	2828.00	2.23
50048.00	C02	M-017429- hippocalcin	3208.00	HPCA	3667.00	1.06
50048.00	C04	M-012891- homeobox A6	3203.00	HOXA6	2712.00	2.88
50048.00	C05	M-004426- endonuclease G	2021.00	ENDOG	2437.00	0.62
50048.00	C06	M-017311- homeobox A3	3200.00	HOXA3	3310.00	4.17
50048.00	C07	M-011852- endosulfine alpha	2029.00	ENSA	2165.00	2.12
50048.00	C08	M-013501- heterogeneous nuclea	3192.00	HNRPU	1563.00	1.73

50048.00	C09	M-003709- solute carrier family 2	2030.00	SLC29A1	1018.00	1.08
50048.00	C10	M-011293- heterogeneous nuclea	3191.00	HNRPL	1531.00	6.40
50048.00	C11	M-003661- erythrocyte membran	2037.00	EPB41L2	1456.00	5.98
50048.00	C12	M-012440- heterogeneous nuclea	3189.00	HNRPH3	2029.00	5.91
50048.00	C13	M-003663- erythrocyte membran	2039.00	EPB49	2931.00	4.44
50048.00	C14	M-013245- heterogeneous nuclea	3188.00	HNRPH2	2748.00	7.97
50048.00	C15	M-011269- fibrillarin	2091.00	FBL	1688.00	1.18
50048.00	C16	M-012107- heterogeneous nuclea	3187.00	HNRPH1	1863.00	1.13
50048.00	C17	M-010511- ecotropic viral integrat	2123.00	EVI2A	2645.00	9.11
50048.00	C18	M-013449- heterogeneous nuclea	3185.00	HNRPF	1293.00	2.09
50048.00	C19	M-003829- fibroblast activation pr	2191.00	FAP	1795.00	1.45
50048.00	C20	M-011869- heterogeneous nuclea	3183.00	HNRPC	1649.00	2.55
50048.00	C21	M-011655- fibulin 2	2199.00	FBLN2	3752.00	1.44
50048.00	C23	M-009472- ficolin (collagen/fibrin	2219.00	FCN1	2619.00	4.05
50048.00	D02	M-012823- ATP synthase F0 subu	4508.00	ATP6	3809.00	0.79
50048.00	D04	M-018440- metallothionein 1E	4493.00	MT1E	2898.00	1.41
50048.00	D05	M-016685- histatin 1	3346.00	HTN1	1956.00	0.56
50048.00	D06	M-011731- microseminoprotein,	4477.00	MSMB	2733.00	1.72
50048.00	D07	M-009272- isoleucyl-tRNA synthet	3376.00	IARS	1328.00	1.05
50048.00	D08	M-011338- musashi homolog 1 (D	4440.00	MSI1	2615.00	0.61
50048.00	D09	M-011998- islet cell autoantigen 1	3382.00	ICA1	1964.00	3.92
50048.00	D10	M-017720- MpV17 mitochondrial	4358.00	MPV17	1767.00	1.87
50048.00	D11	M-011296- intercellular adhesion	3386.00	ICAM4	3076.00	1.95
50048.00	D12	M-014162- Mov10, Moloney leuk	4343.00	MOV10	2866.00	2.09
50048.00	D13	M-008294- isocitrate dehydrogen	3417.00	IDH1	3226.00	7.35
50048.00	D14	M-012642- myelin oligodendrocyt	4340.00	MOG	3216.00	3.11
50048.00	D15	M-004013- isocitrate dehydrogen	3418.00	IDH2	1855.00	0.92
50048.00	D16	M-019476- myelin-associated olig	4336.00	MOBP	2919.00	4.59
50048.00	D17	M-008753- isocitrate dehydrogen	3419.00	IDH3A	2578.00	5.47
50048.00	D18	M-019813- myeloid/lymphoid or	4300.00	MLLT3	3586.00	5.05
50048.00	D19	M-009596- isocitrate dehydrogen	3420.00	IDH3B	2783.00	4.99
50048.00	D20	M-020074- AF4/FMR2 family, mer	4299.00	AFF1	3492.00	6.44
50048.00	D21	M-009361- isocitrate dehydrogen	3421.00	IDH3G	2026.00	4.15
50048.00	D23	M-018788- immunoglobulin J poly	3512.00	IGJ	2463.00	4.55
50048.00	E02	M-013483- heterogeneous nuclea	3182.00	HNRPAB	3863.00	0.34
50048.00	E04	M-011690- heterogeneous nuclea	3181.00	HNRPA2B1	1709.00	1.29
50048.00	E05	M-011271- glypican 4	2239.00	GPC4	3456.00	1.74
50048.00	E06	M-007506- solute carrier family 2	3177.00	SLC29A2	2063.00	0.15
50048.00	E07	M-011861- glypican 5	2262.00	GPC5	1818.00	0.99
50048.00	E08	M-019619- major histocompatibili	3140.00	MR1	824.00	0.61
50048.00	E09	M-007904- fibrinogen-like 1	2267.00	FGL1	2211.00	0.32
50048.00	E10	M-013397- major histocompatibili	3134.00	HLA-F	2037.00	0.20
50048.00	E11	M-015857- four and a half LIM do	2273.00	FHL1	1402.00	0.29
50048.00	E12	M-010514- hepatic leukemia fact	3131.00	HLF	789.00	0.25
50048.00	E13	M-015862- four and a half LIM do	2274.00	FHL2	1422.00	0.28
50048.00	E14	M-013226- major histocompatibili	3127.00	HLA-DRB5	1582.00	0.51
50048.00	E15	M-019805- four and a half LIM do	2275.00	FHL3	2535.00	1.07

50048.00	E16	M-013225- major histocompatibili	3126.00	HLA-DRB4	1930.00	0.21
50048.00	E17	M-009944- FK506 binding protein	2281.00	FKBP1B	1857.00	0.32
50048.00	E18	M-018944- major histocompatibili	3120.00	HLA-DQB2	1611.00	0.12
50048.00	E19	M-017506- flightless I homolog (D	2314.00	FLII	2105.00	0.19
50048.00	E20	M-013829- major histocompatibili	3118.00	HLA-DQA2	2518.00	0.12
50048.00	E21	M-012715- melan-A	2315.00	MLANA	3516.00	0.09
50048.00	E23	M-003666- flotillin 2	2319.00	FLOT2	3055.00	0.33
50048.00	F02	M-019104- muskelin 1, intracellul	4289.00	MKLN1	2490.00	0.84
50048.00	F04	M-008382- microsomal glutathion	4259.00	MGST3	1758.00	4.15
50048.00	F05	M-019613- immunoglobulin super	3547.00	IGSF1	3031.00	0.53
50048.00	F06	M-008856- O-6-methylguanine-D	4255.00	MGMT	2988.00	8.33
50048.00	F07	M-006823- inner centromere prot	3619.00	INCENP	552.00	1.81
50048.00	F08	M-020072- CTAGE family, membe	4253.00	CTAGE5	1657.00	0.91
50048.00	F09	M-010337- indoleamine-pyrrole 2,	3620.00	INDO	2133.00	2.77
50048.00	F10	M-011334- mannosyl (alpha-1,6-)-	4249.00	MGAT5	1761.00	2.27
50048.00	F11	M-012170- intracisternal A particl	3652.00	IPP	1708.00	1.23
50048.00	F12	M-010268- mannosyl (beta-1,4-)-g	4248.00	MGAT3	1779.00	1.57
50048.00	F13	M-022281- iron-responsive eleme	3658.00	IREB2	1776.00	0.68
50048.00	F14	M-011333- mannosyl (alpha-1,6-)-	4247.00	MGAT2	3397.00	1.68
50048.00	F15	M-017742- immunoglobulin super	3671.00	ISLR	2973.00	0.61
50048.00	F16	M-019606- secretoglobin, family 2	4246.00	SCGB2A1	2994.00	3.51
50048.00	F17	M-008516- integrin, alpha 1	3672.00	ITGA1	1565.00	0.38
50048.00	F18	M-011332- mannosyl (alpha-1,3-)-	4245.00	MGAT1	3310.00	1.81
50048.00	F19	M-010096- integrin beta 4 binding	3692.00	ITGB4BP	1990.00	0.20
50048.00	F20	M-012177- antigen p97 (melanom	4241.00	MFI2	3567.00	1.68
50048.00	F21	M-019612- inter-alpha (globulin) i	3697.00	ITIH1	3361.00	7.23
50048.00	F23	M-019610- inter-alpha (globulin) i	3698.00	ITIH2	3492.00	2.12
50048.00	G02	M-010949- major histocompatibili	3116.00	HLA-DPB2	3593.00	0.81
50048.00	G04	M-013548- major histocompatibili	3113.00	HLA-DPA1	3074.00	0.75
50048.00	G05	M-008135- flavin containing mon	2327.00	FMO2	2527.00	2.10
50048.00	G06	M-007922- complement factor H-	3080.00	CFHR2	2753.00	4.94
50048.00	G07	M-016472- folylpolyglutamate syn	2356.00	FPGS	1879.00	1.33
50048.00	G08	M-007921- complement factor H-	3078.00	CFHR1	1361.00	3.01
50048.00	G09	M-011864- FSHD region gene 1	2483.00	FRG1	1237.00	1.21
50048.00	G10	M-019219- NCK-associated protei	3071.00	NCKAP1L	1363.00	4.04
50048.00	G11	M-005268- centromere protein I	2491.00	CENPI	1269.00	1.42
50048.00	G12	M-017444- helicase, lymphoid-spe	3070.00	HELLS	2598.00	5.50
50048.00	G13	M-019635- fucosyltransferase 4 (a	2526.00	FUT4	1888.00	2.33
50048.00	G14	M-008325- histidine decarboxylas	3067.00	HDC	2259.00	3.10
50048.00	G15	M-019636- fucosyltransferase 5 (a	2527.00	FUT5	3292.00	3.49
50048.00	G16	M-017739- hematopoietic cell-spe	3059.00	HCLS1	945.00	1.06
50048.00	G17	M-019806- fucosyltransferase 7 (a	2529.00	FUT7	1203.00	2.58
50048.00	G18	M-009226- holocytochrome c synt	3052.00	HCCS	2437.00	2.83
50048.00	G19	M-007557- solute carrier family 3	2542.00	SLC37A4	1372.00	3.06
50048.00	G20	M-017200- hyaluronan synthase 3	3038.00	HAS3	3184.00	8.64
50048.00	G21	M-011273- G antigen 1	2543.00	GAGE1	3242.00	1.70
50048.00	G23	M-011274- G antigen 2	2574.00	GAGE2	3441.00	2.76

50048.00	H02	M-008026-	microfibrillar-associate	4239.00	MFAP4	2499.00	0.24
50048.00	H04	M-017085-	microfibrillar-associate	4238.00	MFAP3	1848.00	2.44
50048.00	H05	M-012584-	inter-alpha (globulin) i	3699.00	ITIH3	3165.00	1.99
50048.00	H06	M-011727-	microfibrillar-associate	4237.00	MFAP2	1851.00	0.43
50048.00	H07	M-017838-	inter-alpha (globulin) i	3700.00	ITIH4	2166.00	4.71
50048.00	H08	M-020071-	microfibrillar-associate	4236.00	MFAP1	799.00	3.38
50048.00	H09	M-017073-	STT3, subunit of the ol	3703.00	STT3A	3625.00	3.53
50048.00	H10	M-009294-	methyltransferase like	4234.00	METTL1	2993.00	2.27
50048.00	H11	M-006208-	inositol 1,4,5-triphosp	3709.00	ITPR2	2507.00	3.19
50048.00	H12	M-020344-	male-enhanced antige	4201.00	MEA1	2095.00	0.72
50048.00	H13	M-010945-	involucrin	3713.00	IVL	1631.00	1.04
50048.00	H14	M-009461-	malic enzyme 2, NAD(-	4200.00	ME2	2567.00	5.41
50048.00	H15	M-012114-	lysyl-tRNA synthetase	3735.00	KARS	2549.00	1.37
50048.00	H16	M-008439-	malate dehydrogenase	4191.00	MDH2	2815.00	7.21
50048.00	H17	M-006240-	potassium inwardly-re	3766.00	KCNJ10	4081.00	2.25
50048.00	H18	M-009264-	malate dehydrogenase	4190.00	MDH1	2920.00	2.53
50048.00	H19	M-006242-	potassium inwardly-re	3768.00	KCNJ12	3454.00	1.88
50048.00	H20	M-012815-	DnaJ (Hsp40) homolog	4189.00	DNAJB9	2660.00	4.02
50048.00	H21	M-006243-	potassium inwardly-re	3769.00	KCNJ13	3407.00	2.32
50048.00	H23	M-006244-	potassium inwardly-re	3770.00	KCNJ14	3068.00	2.64
50048.00	I02	M-012053-	hyaluronan synthase 2	3037.00	HAS2	2256.00	3.32
50048.00	I04	M-009664-	hyaluronan synthase 1	3036.00	HAS1	1185.00	6.33
50048.00	I05	M-011275-	G antigen 4	2576.00	GAGE4	1985.00	4.89
50048.00	I06	M-013412-	histidyl-tRNA syntheta	3035.00	HARS	1557.00	5.01
50048.00	I07	M-011276-	G antigen 5	2577.00	GAGE5	1756.00	5.92
50048.00	I08	M-009390-	hydroxysteroid (17-be	3028.00	HSD17B10	1819.00	11.16
50048.00	I09	M-011277-	G antigen 6	2578.00	GAGE6	1481.00	5.67
50048.00	I10	M-005893-	hyaluronan binding pr	3026.00	HABP2	1556.00	3.92
50048.00	I11	M-014153-	G antigen 7	2579.00	GAGE7	2194.00	3.83
50048.00	I12	M-012045-	histone cluster 1, H1a	3024.00	HIST1H1A	907.00	5.40
50048.00	I13	M-011280-	UDP-N-acetyl-alpha-D-	2589.00	GALNT1	985.00	5.28
50048.00	I14	M-011684-	H3 histone, family 3A	3020.00	H3F3A	2242.00	2.99
50048.00	I15	M-011865-	UDP-N-acetyl-alpha-D-	2590.00	GALNT2	2592.00	4.90
50048.00	I16	M-013138-	histone cluster 1, H2b	3018.00	HIST1H2BB	2230.00	4.98
50048.00	I17	M-011866-	UDP-N-acetyl-alpha-D-	2591.00	GALNT3	1653.00	6.17
50048.00	I18	M-013137-	histone cluster 1, H2b	3017.00	HIST1H2B	3692.00	7.50
50048.00	I19	M-027288-	glucosidase, alpha; ne	2595.00	GANC	1716.00	1.17
50048.00	I20	M-013147-	histone cluster 1, H2a	3013.00	HIST1H2A	3831.00	3.65
50048.00	I21	M-012100-	leucine rich repeat co	2615.00	LRRC32	2196.00	9.70
50048.00	I23	M-009069-	growth arrest-specific	2621.00	GAS6	3066.00	2.32
50048.00	J02	M-012127-	MyoD family inhibitor	4188.00	MDFI	3321.00	5.45
50048.00	J04	M-017503-	sperm mitochondria-a	4184.00	SMCP	1361.00	5.88
50048.00	J05	M-006245-	potassium inwardly-re	3772.00	KCNJ15	3497.00	13.76
50048.00	J06	M-014136-	muscleblind-like (Dros	4154.00	MBNL1	2913.00	2.68
50048.00	J07	M-006246-	potassium inwardly-re	3773.00	KCNJ16	2188.00	2.06
50048.00	J08	M-012057-	myoglobin	4151.00	MB	3612.00	3.85

50048.00	J09	M-006254- potassium channel, sul	3775.00	KCNK1	2209.00	4.30
50048.00	J10	M-011329- matrilin 2	4147.00	MATN2	1248.00	6.01
50048.00	J11	M-006261- potassium channel, sul	3776.00	KCNK2	2399.00	9.09
50048.00	J12	M-008818- methionine adenosyltr	4144.00	MAT2A	1266.00	3.87
50048.00	J13	M-008428- potassium large condu	3779.00	KCNMB1	2411.00	9.66
50048.00	J14	M-006447- methionyl-tRNA synth	4141.00	MARS	2770.00	8.95
50048.00	J15	M-006268- potassium intermediat	3780.00	KCNN1	2168.00	5.72
50048.00	J16	M-026713- microtubule-associate	4135.00	MAP6	2580.00	3.06
50048.00	J17	M-006269- potassium intermediat	3781.00	KCNN2	3679.00	3.83
50048.00	J18	M-011724- microtubule-associate	4134.00	MAP4	4225.00	4.05
50048.00	J19	M-004461- potassium intermediat	3783.00	KCNN4	3695.00	4.65
50048.00	J20	M-009110- mannosidase, alpha, cl	4122.00	MAN2A2	4552.00	8.11
50048.00	J21	M-018983- killer cell immunoglobu	3805.00	KIR2DL4	2285.00	1.40
50048.00	J23	M-019493- killer cell immunoglobu	3808.00	KIR2DS3	2193.00	1.69
50048.00	K02	M-013146- histone cluster 1, H2ae	3012.00	HIST1H2AE	2310.00	1.30
50048.00	K04	M-012050- histone cluster 1, H1t	3010.00	HIST1H1T	2157.00	3.52
50048.00	K05	M-011282- glioblastoma amplified	2631.00	GBAS	3513.00	3.22
50048.00	K06	M-012049- histone cluster 1, H1b	3009.00	HIST1H1B	3261.00	2.36
50048.00	K07	M-031864- guanylate binding prot	2635.00	GBP3	1850.00	3.41
50048.00	K08	M-012048- histone cluster 1, H1e	3008.00	HIST1H1E	2875.00	0.87
50048.00	K09	M-012038- GTP cyclohydrolase I fe	2644.00	GCHFR	3022.00	1.52
50048.00	K10	M-012046- histone cluster 1, H1d	3007.00	HIST1H1D	2653.00	6.29
50048.00	K11	M-012580- biogenesis of lysosome	2647.00	BLOC1S1	2104.00	1.85
50048.00	K12	M-005892- granzyme M (lymphoc	3004.00	GZMM	1327.00	3.92
50048.00	K13	M-009722- GCN5 general control	2648.00	GCN5L2	2200.00	5.32
50048.00	K14	M-005891- granzyme K (granzyme	3003.00	GZMK	2653.00	3.43
50048.00	K15	M-011284- glucosaminyl (N-acetyl	2650.00	GCNT1	1857.00	1.88
50048.00	K16	M-005890- granzyme H (cathepsin	2999.00	GZMH	3051.00	3.34
50048.00	K17	M-008833- glutamine-fructose-6-	2673.00	GFPT1	4643.00	2.89
50048.00	K18	M-011681- glycophorin E	2996.00	GYPE	2796.00	1.47
50048.00	K19	M-005886- gamma-glutamyltransf	2686.00	GGTL3	3676.00	1.50
50048.00	K20	M-011679- glycophorin B (MNS bl	2994.00	GYPB	4253.00	3.15
50048.00	K21	M-009541- gamma-glutamyltransf	2687.00	GGTLA1	2447.00	1.68
50048.00	K23	M-011670- glutamate-cysteine lig	2730.00	GCLM	2907.00	2.55
50048.00	L02	M-012174- mannosidase, alpha, cl	4121.00	MAN1A1	3084.00	2.66
50048.00	L04	M-011723- mal, T-cell differentiati	4118.00	MAL	3965.00	5.98
50048.00	L05	M-012814- killer cell immunoglobu	3809.00	KIR2DS4	2865.00	3.04
50048.00	L06	M-011327- mago-nashi homolog,	4116.00	MAGOH	3875.00	3.12
50048.00	L07	M-020305- killer cell immunoglobu	3811.00	KIR3DL1	2057.00	1.26
50048.00	L08	M-019089- melanoma antigen fan	4115.00	MAGEB4	4958.00	5.89
50048.00	L09	M-019886- killer cell immunoglobu	3812.00	KIR3DL2	3215.00	2.74
50048.00	L10	M-011326- melanoma antigen fan	4114.00	MAGEB3	3307.00	6.77
50048.00	L11	M-005906- kallikrein 1	3816.00	KLK1	2555.00	4.62
50048.00	L12	M-019094- melanoma antigen fan	4113.00	MAGEB2	2680.00	6.16
50048.00	L13	M-011301- killer cell lectin-like rec	3820.00	KLRB1	2503.00	6.63
50048.00	L14	M-011325- melanoma antigen fan	4112.00	MAGEB1	3661.00	4.62
50048.00	L15	M-021330- killer cell lectin-like rec	3821.00	KLRC1	2142.00	6.82

50048.00	L16	M-010801- melanoma antigen fan	4111.00	MAGEA12	4052.00	2.12
50048.00	L17	M-011302- killer cell lectin-like rec	3822.00	KLRC2	3898.00	3.64
50048.00	L18	M-017280- melanoma antigen fan	4110.00	MAGEA11	4943.00	3.80
50048.00	L19	M-011303- killer cell lectin-like rec	3823.00	KLRC3	3497.00	4.09
50048.00	L20	M-017215- melanoma antigen fan	4109.00	MAGEA10	3074.00	3.48
50048.00	L21	M-020008- keratin associated prot	3846.00	KRTAP5-9	3099.00	1.90
50048.00	L23	M-011309- keratin 31	3881.00	KRT31	2450.00	1.96
50048.00	M02	M-006641- glycogenin 1	2992.00	GYG1	2205.00	0.41
50048.00	M04	M-021488- guanylate cyclase activ	2980.00	GUCA2A	4062.00	0.84
50048.00	M05	M-011287- GLE1 RNA export medi	2733.00	GLE1L	3500.00	2.06
50048.00	M06	M-006732- guanylate cyclase 1, so	2974.00	GUCY1B2	2397.00	0.67
50048.00	M07	M-006183- glycine receptor, beta	2743.00	GLRB	3596.00	2.86
50048.00	M08	M-029875- general transcription fa	2967.00	GTF2H3	2579.00	0.58
50048.00	M09	M-004548- glutaminase	2744.00	GLS	1418.00	3.67
50048.00	M10	M-011178- glutathione S-transfera	2949.00	GSTM5	4116.00	7.80
50048.00	M11	M-009067- glutamate dehydrogen	2747.00	GLUD2	2907.00	1.41
50048.00	M12	M-017188- glutathione S-transfera	2948.00	GSTM4	1457.00	0.34
50048.00	M13	M-008228- glutamate-ammonia lig	2752.00	GLUL	3306.00	2.45
50048.00	M14	M-011177- glutathione S-transfera	2946.00	GSTM2	1859.00	3.66
50048.00	M15	M-009803- GDP-mannose 4,6-deh	2762.00	GMDS	2481.00	2.42
50048.00	M16	M-011289- glutathione S-transfera	2941.00	GSTA4	2433.00	3.82
50048.00	M17	M-008435- guanine nucleotide bir	2768.00	GNA12	3463.00	6.61
50048.00	M18	M-017293- glutathione S-transfera	2940.00	GSTA3	3548.00	4.90
50048.00	M19	M-008349- guanine nucleotide bir	2774.00	GNAL	3330.00	2.43
50048.00	M20	M-017461- glutathione S-transfera	2939.00	GSTA2	4361.00	7.48
50048.00	M21	M-017241- guanine nucleotide bir	2783.00	GNB2	2548.00	4.24
50048.00	M23	M-012700- guanine nucleotide bir	2792.00	GNGT1	1581.00	3.98
50048.00	N02	M-017277- melanoma antigen fan	4108.00	MAGEA9	2901.00	3.65
50048.00	N04	M-017366- melanoma antigen fan	4107.00	MAGEA8	2642.00	1.78
50048.00	N05	M-011310- keratin 32	3882.00	KRT32	3486.00	1.26
50048.00	N06	M-019169- melanoma antigen fan	4105.00	MAGEA6	3211.00	3.80
50048.00	N07	M-011970- keratin 33A	3883.00	KRT33A	2313.00	4.89
50048.00	N08	M-010800- melanoma antigen fan	4104.00	MAGEA5	2684.00	14.61
50048.00	N09	M-011311- keratin 33B	3884.00	KRT33B	3715.00	6.76
50048.00	N10	M-017288- melanoma antigen fan	4103.00	MAGEA4	2453.00	3.22
50048.00	N11	M-013132- keratin 34	3885.00	KRT34	1406.00	6.19
50048.00	N12	M-006350- melanoma antigen fan	4101.00	MAGEA2	2198.00	4.28
50048.00	N13	M-013650- keratin 82	3888.00	KRT82	2191.00	7.76
50048.00	N14	M-006862- melanoma antigen fan	4100.00	MAGEA1	2243.00	1.52
50048.00	N15	M-011314- keratin 83	3889.00	KRT83	3769.00	6.47
50048.00	N16	M-011722- myelin associated glyc	4099.00	MAG	2929.00	3.00
50048.00	N17	M-013651- keratin 84	3890.00	KRT84	3428.00	5.13
50048.00	N18	M-016057- cell cycle associated pr	4076.00	CAPRIN1	2777.00	1.80
50048.00	N19	M-011315- keratin 85	3891.00	KRT85	3928.00	11.86
50048.00	N20	M-019607- lymphocyte antigen 75	4065.00	LY75	2625.00	4.42
50048.00	N21	M-017231- ladinin 1	3898.00	LAD1	2337.00	5.05
50048.00	N23	M-012639- lactalbumin, alpha-	3906.00	LALBA	3338.00	1.32

50048.00	O02	M-009285-	granulin	2896.00	GRN	2926.00	2.73
50048.00	O04	M-007917-	glutamate receptor, io	2894.00	GRID1	2443.00	2.70
50048.00	O05	M-012042-	guanine nucleotide bi	2793.00	GNGT2	1159.00	2.07
50048.00	O06	M-009875-	glutathione peroxidase	2882.00	GPX7	1834.00	3.05
50048.00	O07	M-012043-	guanine nucleotide bi	2794.00	GNL1	2132.00	2.11
50048.00	O08	M-009445-	glutathione peroxidase	2880.00	GPX5	1458.00	1.58
50048.00	O09	M-011672-	golgi autoantigen, golg	2800.00	GOLGA1	2592.00	3.90
50048.00	O10	M-011676-	glutathione peroxidase	2879.00	GPX4	316.00	23.10
50048.00	O11	M-017282-	golgi autoantigen, golg	2801.00	GOLGA2	1605.00	1.25
50048.00	O12	M-006485-	glutathione peroxidase	2878.00	GPX3	1164.00	2.92
50048.00	O13	M-012165-	golgi autoantigen, golg	2802.00	GOLGA3	1573.00	1.84
50048.00	O14	M-031622-	glutamic-pyruvate tra	2875.00	GPT	1897.00	1.16
50048.00	O15	M-012396-	golgi autoantigen, golg	2803.00	GOLGA4	1971.00	1.47
50048.00	O16	M-018825-	glycoprotein M6B	2824.00	GPM6B	2458.00	3.95
50048.00	O17	M-011673-	glutamic-oxaloacetic t	2805.00	GOT1	3339.00	4.76
50048.00	O18	M-010598-	glycoprotein M6A	2823.00	GPM6A	3035.00	3.86
50048.00	O19	M-011674-	glutamic-oxaloacetic t	2806.00	GOT2	1516.00	5.34
50048.00	O20	M-009792-	glycosylphosphatidylin	2822.00	GPLD1	3251.00	1.14
50048.00	O21	M-020171-	glycoprotein 2 (zymog	2813.00	GP2	1521.00	0.66
50048.00	O23	M-004303-	glypican 1	2817.00	GPC1	1296.00	5.09
50048.00	P02	M-010030-	lymphocyte antigen 9	4063.00	LY9	2411.00	8.38
50048.00	P04	M-019608-	lymphocyte antigen 6	4062.00	LY6H	2320.00	3.62
50048.00	P05	M-017237-	laminin, alpha 5	3911.00	LAMA5	717.00	9.34
50048.00	P06	M-012587-	lymphocyte antigen 6	4061.00	LY6E	1402.00	5.78
50048.00	P07	M-013481-	lysosomal-associated	3916.00	LAMP1	1195.00	8.12
50048.00	P08	M-009132-	cytochrome P450, fam	4051.00	CYP4F3	2224.00	4.00
50048.00	P09	M-010519-	LIM and SH3 protein 1	3927.00	LASP1	2552.00	5.02
50048.00	P10	M-011322-	limbic system-associat	4045.00	LSAMP	2456.00	4.93
50048.00	P11	M-011716-	lymphocyte cytosolic p	3936.00	LCP1	1591.00	6.03
50048.00	P12	M-027194-	low density lipoprotei	4038.00	LRP4	1686.00	7.53
50048.00	P13	M-012585-	leukocyte cell-derived	3950.00	LECT2	2501.00	8.00
50048.00	P14	M-011321-	leucine-rich repeats a	4034.00	LRCH4	2151.00	3.39
50048.00	P15	M-019549-	leucine zipper-EF-hand	3954.00	LETM1	2931.00	3.92
50048.00	P16	M-023219-	lactoperoxidase	4025.00	LPO	2401.00	1.00
50048.00	P17	M-008210-	fatty acid desaturase 1	3992.00	FADS1	2094.00	3.06
50048.00	P18	M-008020-	lysyl oxidase-like 2	4017.00	LOXL2	1621.00	4.01
50048.00	P19	M-019812-	lethal giant larvae hom	3993.00	LLGL2	837.00	4.18
50048.00	P20	M-004645-	lysyl oxidase-like 1	4016.00	LOXL1	1226.00	7.67
50048.00	P21	M-008483-	fatty acid desaturase 3	3995.00	FADS3	787.00	2.29
50048.00	P23	M-013079-	LIM domain only 6	4007.00	LMO6	468.00	1.07
					mdn	2437.00	2.69
					3xMAD		
					MADc		
50048.00	C22					4656.00	38.25
50048.00	D22					3935.00	25.85
50048.00	E22		3011.00	8.57			
50048.00	F22		3062.00	16.04			

					mn	4295.50	32.05
					sd	509.82	8.77
50048.00	G22					632.00	0.32
50048.00	H22					903.00	0.66
50048.00	I22					881.00	1.02
50048.00	J22					1359.00	2.80
					mn	943.75	1.20
					sd	302.89	1.10
					3psSD		26.32
					3ngSD		3.31
					SumSD		29.63
					DiffMn		30.85
					SmovrDiff		0.96
					1minus		0.04
50048.00	G03	M-003290-	polo-like kinase 1 (Dro	5347.00	PLK1 SMAF	161.00	2.48
50048.00	H03	M-003290-	polo-like kinase 1 (Dro	5347.00	PLK1 SMAF	145.00	1.38
50048.00	I03	D-001206-:	siControl non-targeting siRNA #2			1154.00	3.73
50048.00	J03	D-001206-:	siControl non-targeting siRNA #2			1803.00	4.05
50048.00	K03	D-001600-(	siGLO RISC-free siRNA			5914.00	9.11
50048.00	L03	D-001600-(	siGLO RISC-free siRNA			5258.00	4.39

Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev
2.54	-1.15	834.00	0.72	1.99	-0.92	2112.00	0.57	2.54
2.24	-1.01	2656.00	1.32	1.39	-0.65	2704.00	0.70	2.41
2.25	-1.02	1499.00	3.54	0.83	0.38	966.00	3.42	0.31
2.40	-1.08	2530.00	0.87	1.84	-0.85	2038.00	0.39	2.72
1.33	-0.60	1946.00	2.77	0.06	0.03	1336.00	1.87	1.24
0.59	-0.26	2548.00	1.14	1.57	-0.73	2001.00	2.65	0.46
0.47	-0.21	2174.00	3.50	0.79	0.36	1233.00	2.03	1.08
1.24	-0.56	3095.00	1.32	1.39	-0.64	2660.00	2.14	0.97
2.17	-0.98	853.00	3.40	0.69	0.32	807.00	4.34	1.23
2.51	-1.13	1159.00	1.29	1.42	-0.66	689.00	0.29	2.82
2.69	-1.21	975.00	2.67	0.04	-0.02	983.00	0.51	2.60
1.50	-0.68	2329.00	0.39	2.32	-1.08	1347.00	2.52	0.59
1.25	-0.56	1306.00	1.45	1.26	-0.58	1605.00	1.12	1.99
1.70	-0.77	2091.00	0.62	2.09	-0.97	2761.00	1.09	2.02
0.37	-0.17	2828.00	3.39	0.68	0.32	1729.00	1.74	1.37
5.13	2.32	1044.00	6.61	3.90	1.81	668.00	7.34	4.23
0.35	-0.16	1966.00	3.00	0.29	0.13	2271.00	2.03	1.08
0.93	0.42	2097.00	5.05	2.34	1.09	2732.00	3.07	0.04
3.72	1.68	2021.00	6.93	4.22	1.95	2062.00	4.66	1.55
0.97	-0.44	1315.00	4.11	1.40	0.65	1959.00	4.39	1.28
2.18	-0.98	2613.00	1.76	0.95	-0.44	1872.00	0.32	2.79
2.05	-0.92	2862.00	5.35	2.64	1.22	2511.00	0.76	2.35
1.67	-0.75	4046.00	1.26	1.45	-0.67	2955.00	2.30	0.81
1.38	-0.62	3237.00	1.51	1.20	-0.56	3023.00	0.86	2.25
2.38	-1.07	3187.00	0.35	2.36	-1.10	1811.00	0.50	2.61
1.53	-0.69	1844.00	0.87	1.84	-0.85	1112.00	0.99	2.12
2.62	-1.18	1815.00	0.17	2.54	-1.18	632.00	2.06	1.05
0.69	-0.31	4508.00	1.00	1.71	-0.79	2269.00	2.60	0.51
1.51	-0.68	3126.00	0.93	1.78	-0.83	1987.00	0.86	2.25
3.90	1.76	1200.00	2.50	0.21	-0.10	875.00	1.26	1.85
1.43	-0.64	1908.00	0.52	2.19	-1.01	2107.00	2.33	0.78
0.69	0.31	2994.00	2.07	0.64	-0.30	2420.00	2.48	0.63
1.35	-0.61	3576.00	1.59	1.12	-0.52	2662.00	4.55	1.44
3.19	1.44	2504.00	2.68	0.03	-0.02	1983.00	6.30	3.19
0.45	-0.20	4349.00	1.13	1.58	-0.73	2685.00	1.83	1.29
3.22	1.45	3286.00	3.07	0.36	0.17	2824.00	4.60	1.49
1.32	-0.60	3246.00	1.79	0.92	-0.43	2039.00	0.74	2.37
1.14	-0.51	2319.00	1.03	1.68	-0.78	2370.00	1.86	1.25
0.92	-0.42	3356.00	0.86	1.85	-0.86	3688.00	4.23	1.12
0.46	-0.21	2041.00	3.63	0.92	0.42	1953.00	1.79	1.32
1.63	-0.73	3308.00	5.26	2.55	1.18	3498.00	1.49	1.62
0.19	0.08	2120.00	2.59	0.12	-0.05	2551.00	2.39	0.72
2.07	-0.94	2967.00	3.37	0.66	0.30	2171.00	4.10	0.99
1.48	0.67	4312.00	5.54	2.83	1.31	2828.00	3.96	0.85
0.57	-0.25	2669.00	5.96	3.25	1.50	1740.00	1.84	1.27
0.96	-0.43	2281.00	1.58	1.13	-0.53	763.00	1.57	1.54

1.61	-0.73	1523.00	3.74	1.03	0.48	639.00	1.88	1.23
3.71	1.68	2325.00	9.38	6.67	3.09	1244.00	8.44	5.33
3.29	1.48	2450.00	6.78	4.07	1.88	1443.00	2.98	0.13
3.22	1.46	1249.00	2.80	0.09	0.04	1554.00	1.42	1.69
1.75	0.79	2490.00	3.94	1.23	0.57	2291.00	2.75	0.36
5.28	2.38	3979.00	7.87	5.16	2.39	3071.00	4.66	1.55
1.51	-0.68	2209.00	1.04	1.67	-0.77	1206.00	1.66	1.45
1.56	-0.71	2275.00	1.54	1.17	-0.54	1787.00	0.78	2.33
6.42	2.90	3355.00	7.78	5.07	2.35	2702.00	6.33	3.22
0.60	-0.27	1783.00	1.18	1.53	-0.71	1379.00	1.09	2.02
1.24	-0.56	2070.00	3.33	0.62	0.29	1639.00	2.32	0.79
0.14	-0.06	1434.00	5.02	2.31	1.07	1632.00	2.21	0.90
1.25	-0.56	3574.00	1.37	1.34	-0.62	5061.00	1.54	1.57
1.36	0.61	2308.00	4.51	1.80	0.83	1410.00	2.48	0.63
1.90	-0.86	2456.00	0.33	2.38	-1.11	3862.00	1.89	1.22
1.28	-0.58	3187.00	0.82	1.89	-0.88	2665.00	5.70	2.59
2.13	-0.96	2248.00	0.58	2.13	-0.99	1581.00	2.09	1.02
0.97	-0.44	4139.00	3.62	0.91	0.42	3250.00	5.63	2.52
1.64	-0.74	2042.00	0.69	2.02	-0.94	1712.00	2.39	0.72
2.08	-0.94	3364.00	1.61	1.10	-0.51	2251.00	0.80	2.31
1.23	0.56	2781.00	2.16	0.55	-0.26	1725.00	3.77	0.66
0.82	-0.37	2361.00	2.16	0.55	-0.26	1337.00	2.84	0.27
0.74	-0.33	2358.00	1.36	1.35	-0.63	1497.00	2.07	1.04
0.60	-0.27	2191.00	2.56	0.15	-0.07	1913.00	4.34	1.23
4.66	2.10	2109.00	2.04	0.67	-0.31	2513.00	4.85	1.74
0.42	0.19	2889.00	1.49	1.22	-0.57	2132.00	4.22	1.11
1.77	-0.80	2342.00	0.21	2.50	-1.16	791.00	1.01	2.10
1.90	0.86	3265.00	1.90	0.81	-0.38	2194.00	1.96	1.15
2.78	1.25	3773.00	0.93	1.78	-0.83	1974.00	3.95	0.84
2.36	1.06	4039.00	2.13	0.58	-0.27	3472.00	3.23	0.12
2.30	1.04	3189.00	1.85	0.86	-0.40	2809.00	5.38	2.27
3.75	1.69	4057.00	6.38	3.67	1.70	3072.00	6.67	3.56
1.46	0.66	2100.00	0.95	1.76	-0.82	2434.00	1.60	1.51
1.86	0.84	1594.00	1.38	1.33	-0.62	2066.00	1.79	1.32
2.35	-1.06	1670.00	1.38	1.33	-0.62	4384.00	0.80	2.31
1.40	-0.63	1722.00	1.28	1.43	-0.66	2429.00	1.28	1.83
0.95	-0.43	3354.00	3.82	1.11	0.51	3363.00	1.67	1.44
2.54	-1.15	2256.00	0.27	2.44	-1.13	2210.00	0.27	2.84
1.70	-0.77	2485.00	0.93	1.78	-0.83	2400.00	0.79	2.32
2.08	-0.94	1270.00	0.08	2.63	-1.22	774.00	0.78	2.33
2.37	-1.07	2866.00	2.34	0.37	-0.17	2251.00	9.24	6.13
2.49	-1.13	2284.00	0.79	1.92	-0.89	1888.00	0.21	2.90
2.40	-1.09	2459.00	1.42	1.29	-0.60	1685.00	0.12	2.99
2.44	-1.10	1068.00	0.09	2.62	-1.21	991.00	0.20	2.91
2.41	-1.09	1106.00	4.52	1.81	0.84	1495.00	1.54	1.57
2.18	-0.99	1285.00	1.09	1.62	-0.75	1367.00	0.66	2.45
1.62	-0.73	2612.00	1.23	1.48	-0.69	2515.00	1.39	1.72

2.48	-1.12	1752.00	0.11	2.60	-1.20	1786.00	0.62	2.49
2.37	-1.07	2515.00	0.80	1.91	-0.89	1645.00	0.91	2.20
2.57	-1.16	1565.00	1.21	1.50	-0.69	1378.00	0.58	2.53
2.50	-1.13	1260.00	1.43	1.28	-0.60	1603.00	0.75	2.36
2.57	-1.16	1333.00	0.83	1.88	-0.87	1050.00	0.48	2.63
2.60	-1.18	3029.00	1.02	1.69	-0.78	3605.00	0.86	2.25
2.36	-1.07	1476.00	0.68	2.03	-0.94	2242.00	2.19	0.92
1.85	-0.83	989.00	0.91	1.80	-0.84	2131.00	2.77	0.34
1.46	0.66	2071.00	2.46	0.25	-0.12	2140.00	5.84	2.73
2.16	-0.98	2821.00	0.50	2.21	-1.03	3132.00	3.03	0.08
5.64	2.55	2862.00	6.36	3.65	1.69	2287.00	14.21	**11.10**
0.88	-0.40	464.00	0.86	1.85	-0.86	476.00	9.66	**6.55**
1.78	-0.81	1994.00	1.86	0.85	-0.40	1439.00	2.92	0.19
0.08	0.03	2442.00	3.15	0.44	0.20	2337.00	8.04	4.93
0.42	-0.19	1759.00	0.17	2.54	-1.18	1781.00	4.94	1.83
1.46	-0.66	1991.00	0.30	2.41	-1.12	1879.00	4.42	1.31
1.12	-0.50	1583.00	0.51	2.20	-1.02	2001.00	7.60	4.49
2.01	-0.91	984.00	0.30	2.41	-1.12	1272.00	1.65	1.46
1.01	-0.46	2220.00	0.50	2.21	-1.03	2097.00	4.34	1.23
2.08	-0.94	2044.00	0.83	1.88	-0.87	1517.00	5.54	2.43
0.82	0.37	2793.00	7.84	**5.13**	2.38	2003.00	12.03	**8.92**
2.31	-1.04	1042.00	0.29	2.42	-1.12	486.00	5.35	2.24
0.88	-0.40	2848.00	0.98	1.73	-0.80	2910.00	5.02	1.91
2.49	-1.12	1940.00	0.72	1.99	-0.92	2025.00	3.01	0.10
1.01	-0.45	2205.00	0.32	2.39	-1.11	3541.00	5.42	2.31
4.54	2.05	3435.00	6.78	4.07	1.89	2711.00	17.15	**14.04**
0.57	-0.26	2668.00	1.46	1.25	-0.58	3251.00	5.41	2.30
1.88	-0.85	1850.00	1.30	1.41	-0.66	2339.00	5.17	2.06
1.94	-0.88	2699.00	1.70	1.01	-0.47	3515.00	7.80	4.69
0.59	-0.27	1710.00	1.52	1.19	-0.55	1995.00	1.50	1.61
2.25	1.02	2753.00	5.16	2.45	1.13	2114.00	15.42	**12.31**
1.36	-0.61	1947.00	0.92	1.79	-0.83	1635.00	4.95	1.84
0.32	0.15	1284.00	0.70	2.01	-0.93	1048.00	8.40	5.29
1.48	-0.67	1751.00	1.66	1.05	-0.49	810.00	3.70	0.59
1.35	0.61	1683.00	2.44	0.27	-0.13	648.00	9.26	**6.15**
1.27	-0.57	1131.00	3.80	1.09	0.50	811.00	5.18	2.07
2.81	1.27	2432.00	2.47	0.24	-0.11	2749.00	9.60	**6.49**
0.36	-0.16	1124.00	2.22	0.49	-0.23	1194.00	3.27	0.16
0.41	0.18	1889.00	1.11	1.60	-0.74	1432.00	6.01	2.90
0.80	0.36	3692.00	1.27	1.44	-0.67	2350.00	5.62	2.51
1.63	-0.74	573.00	1.05	1.66	-0.77	341.00	8.21	5.10
0.11	-0.05	1534.00	4.50	1.79	0.83	640.00	6.41	3.30
0.14	0.06	2546.00	3.69	0.98	0.45	2058.00	6.95	3.84
0.37	0.17	1691.00	2.72	0.01	0.00	1096.00	2.55	0.56
5.95	2.68	4352.00	8.78	**6.07**	2.81	2798.00	7.04	3.93
0.99	-0.45	3962.00	6.81	4.10	1.90	2452.00	3.83	0.72
0.07	0.03	2410.00	1.54	1.17	-0.55	1810.00	1.38	1.73

2.45	-1.11	2304.00	2.43	0.28	-0.13	3474.00	3.89	0.78
0.25	-0.11	1387.00	12.11	**9.40**	4.36	1559.00	6.74	3.63
0.70	-0.32	2508.00	3.07	0.36	0.17	2723.00	4.26	1.15
2.26	-1.02	1390.00	1.51	1.20	-0.56	1707.00	2.05	1.06
2.02	0.91	2750.00	5.82	3.11	1.44	2344.00	9.22	**6.11**
0.69	0.31	509.00	2.16	0.55	-0.26	691.00	17.37	**14.26**
0.84	0.38	3009.00	5.52	2.81	1.30	1788.00	3.30	0.19
0.42	-0.19	2096.00	2.48	0.23	-0.11	1652.00	2.48	0.63
0.50	0.23	2241.00	3.61	0.90	0.42	1970.00	3.50	0.39
1.97	-0.89	1806.00	0.50	2.21	-1.03	2001.00	2.00	1.11
1.65	-0.74	957.00	2.61	0.10	-0.05	1015.00	6.11	3.00
2.72	1.23	3217.00	5.94	3.23	1.49	2724.00	15.86	**12.75**
1.32	-0.59	1450.00	6.28	3.57	1.65	1538.00	4.81	1.70
4.52	2.04	2335.00	6.12	3.41	1.58	1741.00	9.94	**6.83**
0.44	-0.20	2437.00	0.78	1.93	-0.90	2171.00	2.03	1.08
0.16	-0.07	3258.00	2.12	0.59	-0.28	2610.00	3.41	0.30
0.81	-0.36	2441.00	1.27	1.44	-0.67	2838.00	2.78	0.33
1.33	0.60	2952.00	5.76	3.05	1.41	2142.00	5.70	2.59
0.37	-0.17	2228.00	1.35	1.36	-0.63	1851.00	1.08	2.03
0.05	-0.02	2382.00	3.06	0.35	0.16	3228.00	5.14	2.03
0.63	0.29	2591.00	4.09	1.38	0.64	3471.00	2.16	0.95
3.64	1.64	2050.00	8.54	**5.83**	2.70	1753.00	0.68	2.43
2.20	0.99	2015.00	4.12	1.41	0.65	3175.00	1.54	1.57
2.32	1.05	1523.00	0.66	2.05	-0.95	2591.00	0.66	2.45
3.23	1.46	2362.00	2.75	0.04	0.02	3532.00	3.40	0.29
8.47	3.82	2491.00	6.42	3.71	1.72	3340.00	5.48	2.37
2.98	1.35	1957.00	2.55	0.16	-0.07	2555.00	1.41	1.70
1.23	0.56	1791.00	2.18	0.53	-0.25	3105.00	8.37	5.26
1.14	0.51	2183.00	3.30	0.59	0.27	3180.00	3.21	0.10
2.71	1.22	1259.00	7.47	**4.76**	2.20	2360.00	5.21	2.10
2.59	1.17	728.00	3.57	0.86	0.40	1095.00	5.94	2.83
0.30	0.13	1141.00	2.89	0.18	0.08	2183.00	1.92	1.19
2.21	1.00	2965.00	4.42	1.71	0.79	3076.00	8.32	5.21
2.29	1.03	2749.00	5.60	2.89	1.34	3858.00	6.12	3.01
3.48	1.57	953.00	7.45	**4.74**	2.20	1411.00	8.86	**5.75**
4.81	2.17	1920.00	8.13	**5.42**	2.51	3880.00	22.37	**19.26**
1.52	-0.69	809.00	3.46	0.75	0.35	1919.00	3.13	0.02
0.96	0.44	2477.00	6.34	3.63	1.68	3542.00	4.18	1.07
7.01	3.16	1862.00	11.55	**8.84**	4.09	2345.00	21.37	**18.26**
0.37	-0.17	1786.00	3.92	1.21	0.56	4032.00	7.89	4.78
2.76	1.25	1675.00	1.37	1.34	-0.62	2826.00	1.70	1.41
3.19	1.44	812.00	4.31	1.60	0.74	1250.00	3.20	0.09
11.07	4.99	1616.00	5.63	2.92	1.35	2679.00	8.29	5.18
0.01	-0.01	1717.00	1.05	1.66	-0.77	3228.00	1.12	1.99
0.63	-0.29	1683.00	3.39	0.68	0.31	2192.00	1.23	1.88
1.16	0.52	2141.00	1.68	1.03	-0.48	3282.00	1.46	1.65

1.61	0.73	1760.00	2.22	0.49	-0.23	1662.00	1.08	2.03
3.32	1.50	1405.00	2.70	0.01	0.00	1911.00	1.15	1.96
6.40	2.89	1144.00	6.47	3.76	1.74	1941.00	7.78	4.67
1.18	0.53	1126.00	2.66	0.05	-0.02	1446.00	2.28	0.83
6.97	3.15	1574.00	4.45	1.74	0.80	1848.00	2.16	0.95
6.26	2.83	1431.00	5.94	3.23	1.50	1834.00	4.63	1.52
3.03	1.37	1329.00	2.03	0.68	-0.32	2649.00	3.32	0.21
0.37	0.17	1291.00	2.94	0.23	0.11	1772.00	1.75	1.36
1.14	0.52	2641.00	1.97	0.74	-0.34	3864.00	1.79	1.32
1.36	0.61	2196.00	1.28	1.44	-0.67	4417.00	0.77	2.34
1.96	0.89	2819.00	2.13	0.58	-0.27	2944.00	3.29	0.18
5.42	2.44	3165.00	7.87	**5.16**	2.39	4917.00	8.40	5.29
1.29	-0.58	1316.00	2.89	0.18	0.08	1685.00	0.65	2.46
1.00	-0.45	1846.00	1.84	0.87	-0.40	2874.00	0.38	2.73
1.39	-0.63	1766.00	1.53	1.18	-0.55	2101.00	2.95	0.16
0.83	0.38	1435.00	3.76	1.05	0.49	2110.00	4.27	1.16
0.53	0.24	2578.00	3.10	0.39	0.18	4176.00	5.39	2.28
0.33	-0.15	1878.00	4.42	1.71	0.79	3750.00	4.56	1.45
0.72	0.32	1626.00	8.12	**5.41**	2.51	2431.00	6.58	3.47
1.82	-0.82	1840.00	1.74	0.97	-0.45	4208.00	3.75	0.64
1.17	-0.53	1429.00	3.15	0.44	0.20	2828.00	3.57	0.46
3.60	1.63	1677.00	6.68	3.97	1.84	2401.00	5.62	2.51
0.84	-0.38	1646.00	2.98	0.27	0.12	1828.00	3.01	0.10
1.23	0.55	434.00	5.76	3.05	1.41	942.00	4.46	1.35
2.63	1.19	1728.00	9.49	**6.78**	3.14	1747.00	3.49	0.38
0.74	0.33	1513.00	3.50	0.79	0.37	2938.00	8.48	**5.37**
0.81	-0.36	1349.00	2.74	0.03	0.01	1404.00	0.85	2.26
0.65	0.29	1600.00	7.06	4.35	2.02	1498.00	4.21	1.10
0.20	0.09	2999.00	2.47	0.24	-0.11	3650.00	6.27	3.16
1.22	-0.55	2084.00	0.62	2.09	-0.97	3160.00	3.29	0.18
1.19	-0.54	1602.00	1.94	0.77	-0.36	3643.00	4.50	1.39
0.46	0.21	3438.00	6.98	4.27	1.98	4598.00	5.83	2.72
1.01	-0.46	1409.00	2.41	0.30	-0.14	2558.00	3.36	0.25
0.14	-0.07	2779.00	2.45	0.26	-0.12	3635.00	5.53	2.42
0.03	-0.01	3370.00	1.16	1.55	-0.72	2299.00	1.30	1.81
3.29	1.48	2228.00	3.73	1.02	0.47	3381.00	6.45	3.34
0.35	0.16	2165.00	3.14	0.43	0.20	2765.00	6.69	3.58
0.43	0.20	3026.00	6.74	4.03	1.87	3859.00	6.19	3.08
1.43	-0.64	840.00	3.10	0.39	0.18	1706.00	2.34	0.77
3.20	1.44	2799.00	3.61	0.90	0.42	4007.00	2.60	0.51
0.05	0.02	2014.00	7.50	**4.79**	2.22	4150.00	7.23	4.12
4.08	1.84	2436.00	7.92	**5.21**	2.41	3241.00	7.99	4.88
1.93	0.87	628.00	11.94	**9.23**	4.28	1590.00	13.46	**10.35**
3.47	1.56	1949.00	5.85	3.14	1.45	3061.00	9.93	**6.82**
3.94	1.78	1011.00	2.87	0.16	0.07	1506.00	8.57	**5.46**
1.93	0.87	2400.00	7.92	**5.21**	2.41	3399.00	10.53	**7.42**
4.13	1.86	660.00	2.42	0.29	-0.13	1603.00	4.12	1.01

0.57	-0.26	1838.00	2.29	0.42	-0.20	2887.00	5.75	2.64
0.95	0.43	1317.00	2.81	0.10	0.04	3495.00	3.83	0.72
1.11	0.50	2131.00	4.55	1.84	0.85	4154.00	5.83	2.72
1.40	0.63	1421.00	8.94	**6.23**	2.89	3833.00	9.60	**6.49**
0.79	0.36	1685.00	4.69	1.98	0.92	3463.00	4.97	1.86
0.79	-0.35	1133.00	4.41	1.70	0.79	3222.00	4.72	1.61
0.73	-0.33	1966.00	2.24	0.47	-0.22	2582.00	0.70	2.41
2.28	-1.03	1358.00	0.74	1.97	-0.92	2565.00	3.04	0.07
1.85	-0.84	2228.00	3.28	0.57	0.26	5120.00	3.54	0.43
0.63	-0.29	756.00	2.51	0.20	-0.09	3296.00	6.55	3.44
2.02	-0.91	903.00	2.10	0.61	-0.28	2641.00	4.35	1.24
0.17	0.08	2152.00	3.67	0.96	0.44	4289.00	3.96	0.85
2.11	-0.95	1346.00	1.19	1.52	-0.71	2842.00	1.09	2.02
0.98	0.44	431.00	4.18	1.47	0.68	1810.00	1.60	1.51
5.11	2.31	591.00	2.20	0.51	-0.24	2470.00	4.66	1.55
1.28	-0.58	872.00	1.95	0.76	-0.35	2781.00	3.09	0.02
2.35	-1.06	520.00	4.81	2.10	0.97	1547.00	2.91	0.20
0.24	-0.11	1057.00	3.31	0.60	0.28	4288.00	3.54	0.43
0.97	0.44	855.00	7.72	**5.01**	2.32	2289.00	2.27	0.84
0.27	-0.12	1171.00	1.96	0.75	-0.35	2681.00	1.08	2.03
1.13	0.51	819.00	6.11	3.40	1.57	3499.00	4.32	1.21
3.92	1.77	1088.00	6.53	3.82	1.77	2694.00	9.17	**6.06**
2.21	1.00	2490.00	8.67	**5.96**	2.76	5341.00	12.54	**9.43**
0.26	-0.12	1425.00	3.44	0.73	0.34	3649.00	2.80	0.31
4.79	2.16	2861.00	8.39	**5.68**	2.63	3729.00	6.09	2.98
1.55	0.70	919.00	5.33	2.62	1.21	3048.00	2.79	0.32
1.29	0.58	552.00	8.70	**5.99**	2.77	1317.00	6.00	2.89
0.96	0.44	1901.00	1.58	1.13	-0.53	2800.00	3.07	0.04
0.91	-0.41	1054.00	2.56	0.15	-0.07	2672.00	4.98	1.87
1.43	-0.64	1416.00	1.77	0.94	-0.44	4110.00	3.50	0.39
1.11	0.50	2118.00	3.54	0.83	0.38	3776.00	6.25	3.14
2.20	0.99	1764.00	1.53	1.18	-0.55	2791.00	4.62	1.51
11.92	5.38	1211.00	1.98	0.73	-0.34	2266.00	4.55	1.44
4.07	1.84	1443.00	3.40	0.69	0.32	3568.00	5.30	2.19
0.53	0.24	447.00	2.46	0.25	-0.12	1389.00	2.95	0.16
3.50	1.58	951.00	10.41	**7.70**	3.57	2439.00	4.96	1.85
1.59	0.72	910.00	3.85	1.14	0.53	2051.00	3.95	0.84
5.07	2.29	839.00	1.19	1.52	-0.70	2214.00	2.30	0.81
1.17	-0.53	642.00	3.89	1.18	0.55	1599.00	2.50	0.61
3.78	1.71	1466.00	7.23	**4.52**	2.09	3499.00	7.09	3.98
0.31	0.14	1485.00	2.15	0.56	-0.26	2441.00	0.78	2.33
2.44	1.10	1602.00	1.81	0.90	-0.42	3135.00	2.84	0.27
0.89	-0.40	606.00	4.95	2.24	1.04	903.00	2.44	0.67
9.17	4.14	1092.00	4.49	1.78	0.82	2818.00	5.71	2.60
1.73	0.78	1296.00	2.16	0.55	-0.26	2083.00	3.55	0.44
2.36	1.06	1483.00	3.44	0.73	0.34	3136.00	9.82	**6.71**
1.37	-0.62	1619.00	2.29	0.42	-0.20	2810.00	1.60	1.51

0.04	0.02	2472.00	1.09	1.62	-0.75	3414.00	0.12	2.99
0.01	0.01	1982.00	4.89	2.18	1.01	4402.00	0.50	2.61
0.62	-0.28	588.00	4.08	1.37	0.63	1584.00	0.44	2.67
0.36	0.16	1510.00	3.38	0.67	0.31	2365.00	1.78	1.33
0.58	-0.26	1642.00	2.80	0.09	0.04	2482.00	0.56	2.55
1.11	-0.50	733.00	0.95	1.76	-0.81	1907.00	1.21	1.90
1.21	0.54	1307.00	1.68	1.03	-0.48	3278.00	1.43	1.68
20.41	9.21	254.00	18.11	**15.40**	7.14	621.00	4.67	1.56
1.44	-0.65	1111.00	3.60	0.89	0.41	1417.00	1.06	2.05
0.23	0.10	694.00	3.46	0.75	0.35	995.00	0.10	3.01
0.85	-0.38	1366.00	3.15	0.44	0.20	2802.00	1.32	1.79
1.53	-0.69	1106.00	1.18	1.53	-0.71	2874.00	4.45	1.34
1.22	-0.55	701.00	7.70	**4.99**	2.31	1952.00	0.87	2.24
1.26	0.57	1050.00	4.57	1.86	0.86	2001.00	2.45	0.66
2.07	0.94	1150.00	12.44	**9.73**	4.51	2896.00	4.49	1.38
1.17	0.53	1925.00	3.90	1.19	0.55	3519.00	2.56	0.55
2.65	1.20	405.00	4.69	1.98	0.92	1614.00	3.10	0.01
1.55	-0.70	382.00	6.54	3.83	1.78	2183.00	4.90	1.79
2.03	-0.92	1085.00	1.66	1.05	-0.49	1227.00	3.10	0.01
2.40	1.08	750.00	7.73	**5.02**	2.33	1146.00	3.66	0.55
5.69	2.57	13.00	76.92	**74.21**	34.39	2101.00	4.57	1.46
0.93	0.42	1781.00	2.70	0.01	-0.01	2816.00	0.11	3.00
6.65	3.00	308.00	18.51	**15.80**	7.32	934.00	0.75	2.36
3.09	1.39	317.00	7.57	**4.86**	2.25	1112.00	0.63	2.48
5.43	2.45	485.00	9.48	**6.77**	3.14	870.00	0.69	2.42
1.31	0.59	653.00	1.07	1.64	-0.76	1749.00	0.34	2.77
2.33	1.05	992.00	3.43	0.72	0.33	2787.00	1.18	1.93
2.24	1.01	933.00	4.93	2.22	1.03	2024.00	1.43	1.68
3.34	1.51	731.00	2.87	0.16	0.07	2655.00	1.88	1.23
4.84	2.19	696.00	5.89	3.18	1.47	1709.00	4.10	0.99
5.31	2.40	939.00	4.69	1.98	0.91	3044.00	3.84	0.73
0.70	0.32	574.00	4.53	1.82	0.84	2698.00	1.89	1.22
1.23	0.56	789.00	5.70	2.99	1.39	3098.00	5.36	2.25
1.69	-0.76	928.00	4.31	1.60	0.74	1943.00	0.57	2.54
0.37	0.17	956.00	2.41	0.30	-0.14	1839.00	1.20	1.91
1.32	0.60	594.00	3.70	0.99	0.46	1518.00	0.33	2.78
1.49	0.67	346.00	6.36	3.65	1.69	1155.00	4.76	1.65
4.98	2.25	943.00	3.39	0.68	0.32	1793.00	2.29	0.82
0.40	-0.18	287.00	11.15	**8.44**	3.91	355.00	3.66	0.55
1.62	-0.73	743.00	2.56	0.15	-0.07	715.00	5.17	2.06
1.50		1810.50	2.71	1.46		2212.00	3.11	1.77
4.49				4.37				5.30
2.22				2.16				2.62
	3039.00	31.75		4468.00	35.54			
	4674.00	33.50		3452.00	27.93			
				2493.00	27.56		1789.00	9.67
				2397.00	34.04		2740.00	19.78

3856.50	32.63	3202.50	31.27
1156.12	1.24	968.84	4.12
968.00	2.38	444.00	4.28
808.00	1.36	765.00	1.57
489.00	2.45	1108.00	4.24
1573.00	6.36	1788.00	1.23
959.50	3.14	1026.25	2.83
454.89	2.20	575.68	1.66
	3.71		12.36
	6.61		4.97
	10.32		17.33
	29.49		28.44
	0.35		0.61
	0.65		0.39
120.00	11.67	69.00	31.88
63.00	4.76	99.00	21.21
1390.00	2.01	1950.00	0.72
847.00	6.85	1639.00	0.85
4024.00	8.90	6979.00	11.25
5724.00	12.02	5171.00	12.26

rZ
-0.97
-0.92
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0.49
-1.07
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-0.86
-1.00
-0.81
-0.40
-0.20
-0.86
-0.71
-0.30
-0.24
0.55
1.22
-0.49
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-0.91
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-0.62
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-0.59

-0.47	
2.04	y
-0.05	
-0.65	
-0.14	
0.59	y
-0.56	
-0.89	
1.23	y
-0.77	
-0.30	
-0.35	
-0.60	
-0.24	
-0.47	
0.99	
-0.39	
0.96	
-0.27	
-0.88	
0.25	
-0.10	
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0.47	
0.67	
0.42	
-0.80	
-0.44	
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0.04	
0.87	
1.36	
-0.58	
-0.51	
-0.88	
-0.70	
-0.55	
-1.09	
-0.89	
-0.89	
2.34	
-1.11	
-1.14	
-1.11	
-0.60	
-0.94	
-0.66	

-0.95	
-0.84	
-0.97	
-0.90	
-1.01	
-0.86	
-0.35	
-0.13	
1.04	
-0.03	
4.24	y
2.51	
-0.07	
1.89	
0.70	
0.50	
1.71	
-0.56	
0.47	
0.93	
3.41	y
0.86	
0.73	
-0.04	
0.88	
5.37	y
0.88	
0.79	
1.79	
-0.61	
4.71	
0.70	
2.02	
0.23	
2.35	
0.79	
2.48	
0.06	
1.11	
0.96	
1.95	
1.26	
1.47	
-0.21	
1.50	y
0.28	
-0.66	

0.30	
1.39	
0.44	
-0.41	
2.33	
5.45	
0.07	
-0.24	
0.15	
-0.43	
1.15	
4.87	
0.65	
2.61	y
-0.42	
0.11	
-0.13	
0.99	
-0.78	
0.78	
-0.36	
-0.93	
-0.60	
-0.94	
0.11	
0.90	
-0.65	
2.01	
0.04	
0.80	
1.08	
-0.45	
1.99	
1.15	
2.20	y
7.36	y
0.01	
0.41	
6.98	y
1.83	
-0.54	
0.03	
1.98	
-0.76	
-0.72	
-0.63	

-0.78		
-0.75		
1.78		
-0.32		
-0.36		
0.58		
0.08		
-0.52		
-0.51		
-0.90		
0.07		
2.02	y	
-0.94		
-1.04		
-0.06		
0.44		
0.87		
0.55		
1.33		
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-0.04		
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-0.86		
0.42		
1.21		
0.07		
0.53		
1.04		
0.10		
0.92		
-0.69		
1.28		
1.37		
1.18		
-0.29		
-0.20		
1.57		
1.87		
3.96	x	toxic b,c
2.61		
2.09		
2.84	x	debris a,b
0.38		

1.01	
0.28	
1.04	
2.48	y
0.71	
0.61	
-0.92	
-0.03	
0.16	
1.32	
0.47	
0.33	
-0.77	
-0.58	
0.59	
-0.01	
-0.08	
0.17	
-0.32	
-0.78	
0.46	
2.32	
3.61	y
-0.12	
1.14	y
-0.12	
1.10	
-0.02	
0.71	
0.15	
1.20	
0.58	
0.55	
0.84	
-0.06	
0.71	
0.32	
-0.31	
-0.23	
1.52	
-0.89	
-0.10	
-0.26	
0.99	
0.17	
2.57	
-0.58	

-1.15		
-1.00		
-1.02		
-0.51		
-0.97		
-0.73		
-0.64		
0.60	x	toxic a,b,c
-0.79		
-1.15		
-0.69		
0.51		
-0.86		
-0.25		
0.53		
-0.21		
-0.01		
0.68		
-0.01		
0.21		
0.56	x	toxic b
-1.15		
-0.90	x	toxic a,b,c
-0.95		
-0.93	x	toxic a,b,c
-1.06		
-0.74		
-0.64		
-0.47		
0.38		
0.28		
-0.47		
0.86		
-0.97		
-0.73		
-1.06		
0.63		
-0.32		
0.21		
0.79		

Plate	Well	Gene		GeneID	Cell Count	% inf
50049.00	A02	M-009620- polymerase (RNA) II (DI	5432.00	POLR2C	975.00	1.23
50049.00	A04	M-018612- polymerase (DNA direc	5427.00	POLE2	2055.00	9.73
50049.00	A05	M-012832- NADH dehydrogenase s	4541.00	ND6	1867.00	3.05
50049.00	A06	M-020131- polymerase (DNA direc	5425.00	POLD2	1913.00	0.99
50049.00	A07	M-017712- myosin IF	4542.00	MYO1F	3694.00	2.33
50049.00	A08	M-010617- podocalyxin-like	5420.00	PODXL	5862.00	11.82
50049.00	A09	M-004019- mucin 1, cell surface as	4582.00	MUC1	3170.00	4.61
50049.00	A10	M-008737- pancreatic lipase-relate	5408.00	PNLIPRP2	2247.00	5.52
50049.00	A11	M-012643- mucin 2, oligomeric mu	4583.00	MUC2	3366.00	1.52
50049.00	A12	M-019924- exosome component 9	5393.00	EXOSC9	1615.00	0.93
50049.00	A13	M-004577- mucin 4, cell surface as	4585.00	MUC4	2546.00	3.69
50049.00	A14	M-010117- postmeiotic segregatio	5387.00	PMS2L3	2192.00	1.64
50049.00	A15	M-032252- mucin 5AC, oligomeric	4586.00	MUC5AC	3374.00	3.20
50049.00	A16	M-017846- postmeiotic segregatio	5383.00	PMS2L5	2942.00	0.71
50049.00	A17	M-026763- mucin 5B, oligomeric m	4587.00	MUC5B	3225.00	3.50
50049.00	A18	M-012592- postmeiotic segregatio	5380.00	PMS2L2	1705.00	3.75
50049.00	A19	M-026728- mucin 6, oligomeric mu	4588.00	MUC6	2818.00	3.62
50049.00	A20	M-028956- postmeiotic segregatio	5379.00	PMS2L1	1357.00	6.93
50049.00	A21	M-015885- mucin 7, secreted	4589.00	MUC7	1774.00	4.57
50049.00	A23	M-019669- myosin binding protein	4604.00	MYBPC1	2264.00	11.48
50049.00	B02	M-032505- leucine rich repeat cont	474170.00	LRRC37A2	2743.00	2.15
50049.00	B04	M-032026- asthma-associated alte	404744.00	AAA1	1974.00	1.72
50049.00	B05	M-004739- polymerase (RNA) II (DI	5434.00	POLR2E	2172.00	0.55
50049.00	B06	M-014490- adrenomedullin 2	79924.00	ADM2	2925.00	2.50
50049.00	B07	M-004723- polymerase (RNA) II (DI	5435.00	POLR2F	1410.00	1.63
50049.00	B08	M-005907- kallikrein-related peptic	5655.00	KLK10	4335.00	2.28
50049.00	B09	M-012247- polymerase (RNA) II (DI	5437.00	POLR2H	1695.00	0.71
50049.00	B10	M-005917- kallikrein-related peptic	5653.00	KLK6	2243.00	1.74
50049.00	B11	M-012248- polymerase (RNA) II (DI	5438.00	POLR2I	1342.00	2.38
50049.00	B12	M-003696- protease, serine, 8	5652.00	PRSS8	1648.00	3.16
50049.00	B13	M-012249- polymerase (RNA) II (DI	5439.00	POLR2J	1057.00	0.76
50049.00	B14	M-005918- kallikrein-related peptic	5650.00	KLK7	2994.00	4.14
50049.00	B15	M-011979- polymerase (RNA) II (DI	5440.00	POLR2K	2382.00	3.53
50049.00	B16	M-005937- mannan-binding lectin	5648.00	MASP1	2537.00	1.89
50049.00	B17	M-013133- polymerase (RNA) II (DI	5441.00	POLR2L	1441.00	0.42
50049.00	B18	M-006015- protease, serine, 3 (me	5646.00	PRSS3	2726.00	5.72
50049.00	B19	M-012004- polymerase (RNA) mito	5442.00	POLRMT	2252.00	0.67
50049.00	B20	M-010333- proline rich Gla (G-carb	5639.00	PRRG2	809.00	1.24
50049.00	B21	M-004979- peptidylprolyl isomeras	5478.00	PPIA	1640.00	1.04
50049.00	B23	M-004606- peptidylprolyl isomeras	5479.00	PPIB	2102.00	0.95
50049.00	C02	M-011755- phosphomannomutase	5372.00	PMM1	1831.00	0.93
50049.00	C04	M-014745- pro-melanin-concentra	5370.00	PMCHL2	4856.00	1.96
50049.00	C05	M-019814- myosin binding protein	4606.00	MYBPC2	4638.00	2.07
50049.00	C06	M-017145- pro-melanin-concentra	5369.00	PMCHL1	4172.00	1.82
50049.00	C07	M-019896- myosin binding protein	4608.00	MYBPH	3561.00	5.70
50049.00	C08	M-013922- prepronociceptin	5368.00	PNOC	4108.00	2.70

50049.00	C09	M-023017- myosin, heavy chain 10	4628.00	MYH10	3910.00	2.99
50049.00	C10	M-021532- plexin A2	5362.00	PLXNA2	4000.00	2.25
50049.00	C11	M-013075- myosin, light chain 1, al	4632.00	MYL1	3148.00	2.16
50049.00	C12	M-011978- plastin 3 (T isoform)	5358.00	PLS3	2867.00	1.85
50049.00	C13	M-008765- myosin IA	4640.00	MYO1A	2156.00	0.70
50049.00	C14	M-011356- plastin 1 (I isoform)	5357.00	PLS1	3005.00	0.97
50049.00	C15	M-015121- myosin IC	4641.00	MYO1C	3263.00	4.87
50049.00	C16	M-019592- proteolipid protein 2 (c	5355.00	PLP2	3585.00	1.09
50049.00	C17	M-023316- myosin ID	4642.00	MYO1D	4332.00	2.19
50049.00	C18	M-004285- procollagen-lysine, 2-o	5352.00	PLOD2	2678.00	2.50
50049.00	C19	M-019919- myosin IE	4643.00	MYO1E	2344.00	7.59
50049.00	C20	M-003669- FXYD domain containin	5349.00	FXYD3	2059.00	1.89
50049.00	C21	M-023431- myosin VB	4645.00	MYO5B	3113.00	4.27
50049.00	C23	M-022928- myosin VIIB	4648.00	MYO7B	2199.00	0.82
50049.00	D02	M-010332- proline rich Gla (G-carb	5638.00	PRRG1	2820.00	2.70
50049.00	D04	M-012253- peripherin	5630.00	PRPH	2548.00	4.79
50049.00	D05	M-008819- peptidylprolyl isomeras	5480.00	PPIC	3406.00	3.20
50049.00	D06	M-019697- protamine 2	5620.00	PRM2	4038.00	2.92
50049.00	D07	M-017840- periplakin	5493.00	PPL	4408.00	1.93
50049.00	D08	M-019696- protamine 1	5619.00	PRM1	2505.00	1.68
50049.00	D09	M-019691- pancreatic polypeptide	5539.00	PPY	2533.00	2.17
50049.00	D10	M-031716- agrin	375790.00	AGRN	2170.00	0.41
50049.00	D11	M-003693- proline/arginine-rich er	5549.00	PRELP	1742.00	1.15
50049.00	D12	M-019389- putative binding protei	346389.00	7A5	3573.00	2.41
50049.00	D13	M-006006- prolyl endopeptidase	5550.00	PREP	1570.00	1.72
50049.00	D14	M-029709- aldo-keto reductase far	340811.00	AKR1CL1	2922.00	0.21
50049.00	D15	M-017949- proteoglycan 2, bone m	5553.00	PRG2	2486.00	7.16
50049.00	D16	M-007303- ATP-binding cassette, s	340273.00	ABCB5	3108.00	1.29
50049.00	D17	M-012738- proline-rich protein Ha	5554.00	PRH1	3465.00	1.70
50049.00	D18	M-028638- alcohol dehydrogenase	285802.00	ADH5P4	2896.00	4.11
50049.00	D19	M-005081- proline-rich protein Ha	5555.00	PRH2	4709.00	7.79
50049.00	D20	M-005242- abhydrolase domain co	253152.00	ABHD7	4321.00	3.40
50049.00	D21	M-009940- ATP-binding cassette, s	5826.00	ABCD4	4991.00	1.44
50049.00	D23	M-008702- ATP-binding cassette, s	6059.00	ABCE1	1685.00	1.19
50049.00	E02	M-019595- perilipin	5346.00	PLIN	3293.00	1.88
50049.00	E04	M-015748- plasminogen-like B2	5342.00	PLGLB2	2365.00	7.86
50049.00	E05	M-006539- myosin IXA	4649.00	MYO9A	1637.00	7.27
50049.00	E06	M-005064- phospholipase D2	5338.00	PLD2	3148.00	3.34
50049.00	E07	M-015359- NGFI-A binding protein	4664.00	NAB1	1867.00	3.70
50049.00	E08	M-009866- phospholipase C-like 1	5334.00	PLCL1	2669.00	3.00
50049.00	E09	M-027161- nascent polypeptide-as	4666.00	NACA	2468.00	6.44
50049.00	E10	M-004904- prolactin-induced prote	5304.00	PIP	2269.00	3.35
50049.00	E11	M-013452- heterogeneous nuclear	4670.00	HNRPM	3433.00	9.50
50049.00	E12	M-020128- protein (peptidylprolyl	5303.00	PIN4	2070.00	14.64
50049.00	E13	M-017274- nucleosome assembly	4673.00	NAP1L1	1334.00	3.52
50049.00	E14	M-011885- phosphatidylinositol gl	5283.00	PIGH	2794.00	3.08
50049.00	E15	M-012182- nucleosome assembly	4674.00	NAP1L2	1280.00	2.66

50049.00	E16	M-011753-	phosphatidylinositol gl	5281.00	PIGF	2344.00	4.61
50049.00	E17	M-011879-	nucleosome assembly	4675.00	NAP1L3	3638.00	5.06
50049.00	E18	M-017555-	phosphatidylinositol gl	5279.00	PIGC	2202.00	2.18
50049.00	E19	M-012183-	nucleosome assembly	4676.00	NAP1L4	3832.00	5.09
50049.00	E20	M-019923-	serpin peptidase inhibit	5273.00	SERPINB10	2493.00	1.20
50049.00	E21	M-011880-	asparaginyl-tRNA synth	4677.00	NARS	1824.00	3.67
50049.00	E23	M-011740-	nuclear autoantigenic s	4678.00	NASP	2693.00	2.75
50049.00	F02	M-006800-	adenylate cyclase 4	196883.00	ADCY4	2550.00	1.10
50049.00	F04	M-016481-	chromosome 3 open re	165679.00	C3orf57	2626.00	6.32
50049.00	F05	M-004053-	acyl-Coenzyme A oxida	8310.00	ACOX3	3100.00	2.68
50049.00	F06	M-009032-	ATP-binding cassette, s	154664.00	ABCA13	2252.00	2.53
50049.00	F07	M-005757-	ADAM metallopeptidas	8728.00	ADAM19	3964.00	2.60
50049.00	F08	M-018538-	amyotrophic lateral scl	150864.00	ALS2CR13	3204.00	0.66
50049.00	F09	M-010702-	ADAM metallopeptidas	8756.00	ADAM7	2445.00	3.44
50049.00	F10	M-007311-	ATP-binding cassette, s	150000.00	ABCC13	3117.00	3.88
50049.00	F11	M-006107-	amiloride-sensitive cati	9311.00	ACCN3	2454.00	3.22
50049.00	F12	M-015326-	actin-related protein T1	139741.00	ACTRT1	1275.00	6.67
50049.00	F13	M-011938-	adiponectin, C1Q and c	9370.00	ADIPOQ	3216.00	3.48
50049.00	F14	M-008453-	alcohol dehydrogenase	137872.00	ADHFE1	3387.00	7.65
50049.00	F15	M-008615-	ATP-binding cassette, s	9619.00	ABCG1	2644.00	2.19
50049.00	F16	M-024889-	aminoacylase 1-like 2	135293.00	ACY1L2	4367.00	1.83
50049.00	F17	M-007304-	ATP-binding cassette, s	10058.00	ABCB6	3003.00	3.30
50049.00	F18	M-008942-	AHA1, activator of heat	130872.00	AHSA2	5283.00	4.85
50049.00	F19	M-009286-	ATP-binding cassette, s	10061.00	ABCF2	3277.00	11.66
50049.00	F20	M-016849-	islet cell autoantigen 1,	130026.00	ICA1L	3648.00	11.49
50049.00	F21	M-012706-	furry homolog (Drosop	10129.00	FRY	4842.00	11.90
50049.00	F23	M-007313-	ATP-binding cassette, s	10257.00	ABCC4	2318.00	3.45
50049.00	G02	M-019439-	serpin peptidase inhibit	5271.00	SERPINB8	2395.00	0.50
50049.00	G04	M-019066-	peptidase inhibitor 3, s	5266.00	PI3	1409.00	2.70
50049.00	G05	M-015306-	carcinoembryonic antig	4680.00	CEACAM6	1953.00	0.67
50049.00	G06	M-007484-	solute carrier family 25	5250.00	SLC25A3	1828.00	1.70
50049.00	G07	M-011128-	neutrophil cytosolic fac	4689.00	NCF4	2114.00	1.23
50049.00	G08	M-008537-	phosphoglucomutase 5	5239.00	PGM5	2025.00	1.19
50049.00	G09	M-003854-	nucleolin	4691.00	NCL	2055.00	3.31
50049.00	G10	M-013912-	phosphoglucomutase 3	5238.00	PGM3	3116.00	1.54
50049.00	G11	M-011881-	NADH dehydrogenase (	4694.00	NDUFA1	952.00	1.05
50049.00	G12	M-010925-	phosphoglucomutase 1	5236.00	PGM1	3329.00	1.89
50049.00	G13	M-018869-	NADH dehydrogenase (	4695.00	NDUFA2	1974.00	1.06
50049.00	G14	M-008371-	phosphogluconate deh	5226.00	PGD	2919.00	6.34
50049.00	G15	M-012674-	NADH dehydrogenase (	4696.00	NDUFA3	2228.00	3.46
50049.00	G16	M-005992-	progastricsin (pepsinog	5225.00	PGC	2704.00	3.66
50049.00	G17	M-019200-	NADH dehydrogenase (	4697.00	NDUFA4	3097.00	2.94
50049.00	G18	M-005991-	pepsinogen 5, group I (	5222.00	PGA5	2967.00	2.09
50049.00	G19	M-012000-	NADH dehydrogenase (	4698.00	NDUFA5	2045.00	3.42
50049.00	G20	M-015740-	vitrin	5212.00	VIT	3486.00	9.55
50049.00	G21	M-015716-	NADH dehydrogenase (	4700.00	NDUFA6	1579.00	0.57
50049.00	G23	M-012693-	NADH dehydrogenase (	4701.00	NDUFA7	1788.00	1.40

50049.00	H02	M-008523- aminocarboxymuconat	130013.00	ACMSD	2710.00	0.18
50049.00	H04	M-009105- adenylosuccinate synth	122622.00	ADSSL1	3301.00	2.58
50049.00	H05	M-009343- ATP-binding cassette, s	10347.00	ABCA7	3126.00	0.61
50049.00	H06	M-016409- AE binding protein 2	121536.00	AEBP2	2064.00	0.92
50049.00	H07	M-008536- ATP-binding cassette, s	10349.00	ABCA10	3671.00	2.37
50049.00	H08	M-007310- ATP-binding cassette, s	94160.00	ABCC12	2591.00	0.81
50049.00	H09	M-008534- ATP-binding cassette, s	10350.00	ABCA9	2180.00	1.65
50049.00	H10	M-016441- ARP8 actin-related prot	93973.00	ACTR8	1289.00	0.16
50049.00	H11	M-008347- ATP-binding cassette, s	10351.00	ABCA8	2186.00	0.18
50049.00	H12	M-007110- acidic repeat containin	93953.00	ACRC	847.00	0.94
50049.00	H13	M-003626- anterior gradient homo	10551.00	AGR2	1308.00	0.76
50049.00	H14	M-010400- aspartoacylase (amino	91703.00	ACY3	2457.00	0.28
50049.00	H15	M-005781- AFG3 ATPase family ge	10939.00	AFG3L2	1395.00	2.65
50049.00	H16	M-016183- acyl-Coenzyme A bindi	91452.00	ACBD5	1999.00	1.30
50049.00	H17	M-012340- adhesion regulating m	11047.00	ADRM1	2753.00	1.34
50049.00	H18	M-021497- three prime histone m	90459.00	THEX1	3256.00	8.72
50049.00	H19	M-007306- ATP-binding cassette, s	11194.00	ABCB8	2353.00	1.49
50049.00	H20	M-027140- asparagine-linked glyco	85365.00	ALG2	2907.00	0.48
50049.00	H21	M-013395- ataxin 2-like	11273.00	ATXN2L	3131.00	9.36
50049.00	H23	M-020382- actin binding LIM prote	22885.00	ABLIM3	593.00	0.67
50049.00	I02	M-009015- phosphoribosylformylg	5198.00	PFAS	3692.00	2.76
50049.00	I04	M-008059- platelet factor 4 varian	5197.00	PF4V1	1728.00	3.18
50049.00	I05	M-012496- NADH dehydrogenase (	4702.00	NDUFA8	2075.00	3.13
50049.00	I06	M-006544- paternally expressed 3	5178.00	PEG3	2346.00	3.37
50049.00	I07	M-016044- NADH dehydrogenase (	4704.00	NDUFA9	3157.00	5.26
50049.00	I08	M-019151- prodynorphin	5173.00	PDYN	2989.00	7.86
50049.00	I09	M-006752- NADH dehydrogenase (	4705.00	NDUFA10	3104.00	3.32
50049.00	I10	M-008642- phosphate cytidylyltra	5130.00	PCYT1A	1449.00	9.32
50049.00	I11	M-019897- NADH dehydrogenase (	4706.00	NDUFAB1	1548.00	1.87
50049.00	I12	M-005986- proprotein convertase	5126.00	PCSK2	1660.00	4.16
50049.00	I13	M-017848- NADH dehydrogenase (	4707.00	NDUFB1	645.00	7.75
50049.00	I14	M-005987- proprotein convertase	5125.00	PCSK5	2704.00	12.69
50049.00	I15	M-019202- NADH dehydrogenase (	4708.00	NDUFB2	2589.00	3.79
50049.00	I16	M-020122- Purkinje cell protein 4	5121.00	PCP4	1109.00	1.80
50049.00	I17	M-019604- NADH dehydrogenase (	4709.00	NDUFB3	1601.00	3.62
50049.00	I18	M-012172- pericentrin (kendrin)	5116.00	PCNT	1466.00	4.02
50049.00	I19	M-019209- NADH dehydrogenase (	4711.00	NDUFB5	2427.00	3.26
50049.00	I20	M-010000- protein-L-isoaspartate (	5110.00	PCMT1	3480.00	3.10
50049.00	I21	M-017210- NADH dehydrogenase (	4712.00	NDUFB6	1917.00	3.60
50049.00	I23	M-017213- NADH dehydrogenase (	4713.00	NDUFB7	1034.00	2.03
50049.00	J02	M-015856- synapse defective 1, Rh	85360.00	SYDE1	2221.00	3.83
50049.00	J04	M-027138- asparagine-linked glyco	84920.00	ALG10	3833.00	16.05
50049.00	J05	M-014059- ATP/GTP binding protei	23287.00	AGTPBP1	3788.00	3.93
50049.00	J06	M-013589- abhydrolase domain co	84696.00	ABHD1	2566.00	1.71
50049.00	J07	M-007748- acyl-CoA synthetase lo	23305.00	ACSL6	2000.00	7.40
50049.00	J08	M-008549- acyl-CoA synthetase sh	84532.00	ACSS1	1851.00	1.78
50049.00	J09	M-012857- activity-dependent neu	23394.00	ADNP	3343.00	2.60

50049.00	J10	M-013575- acrosin binding protein	84519.00	ACRBP	1380.00	2.03
50049.00	J11	M-007300- ATP-binding cassette, s	23456.00	ABCB10	1648.00	0.85
50049.00	J12	M-014892- actin binding LIM prote	84448.00	ABLIM2	1538.00	15.74
50049.00	J13	M-007307- ATP-binding cassette, s	23457.00	ABCB9	2798.00	5.15
50049.00	J14	M-014886- AKT1 substrate 1 (proli	84335.00	AKT1S1	2116.00	0.95
50049.00	J15	M-008535- ATP-binding cassette, s	23460.00	ABCA6	2238.00	3.57
50049.00	J16	M-008231- acyl-Coenzyme A bindir	84320.00	ACBD6	2088.00	4.41
50049.00	J17	M-004345- ATP-binding cassette, s	23461.00	ABCA5	1955.00	1.43
50049.00	J18	M-017159- leucine rich repeat cont	84230.00	LRRC8C	2974.00	3.46
50049.00	J19	M-009346- adenosine deaminase,	23536.00	ADAT1	3189.00	4.55
50049.00	J20	M-014825- neuroblastoma breakp	84224.00	NBPF3	4081.00	10.32
50049.00	J21	M-010044- acyl-CoA thioesterase	23597.00	ACOT9	1714.00	4.61
50049.00	J23	M-016671- ankyrin repeat and BTB	25841.00	ABTB2	2240.00	1.65
50049.00	K02	M-012243- poly(rC) binding proteir	5093.00	PCBP1	3045.00	4.93
50049.00	K04	M-011348- poly(A)-specific ribonuc	5073.00	PARN	2916.00	0.69
50049.00	K05	M-019898- NADH dehydrogenase (	4714.00	NDUFB8	1936.00	1.70
50049.00	K06	M-007857- contactin 3 (plasmacyt	5067.00	CNTN3	2462.00	0.93
50049.00	K07	M-019899- NADH dehydrogenase (	4715.00	NDUFB9	2798.00	4.22
50049.00	K08	M-008424- peptidylglycine alpha-a	5066.00	PAM	2470.00	5.26
50049.00	K09	M-012675- NADH dehydrogenase (	4716.00	NDUFB10	1716.00	0.82
50049.00	K10	M-019597- paralemmin	5064.00	PALM	2257.00	1.73
50049.00	K11	M-019601- NADH dehydrogenase (	4717.00	NDUFC1	903.00	0.89
50049.00	K12	M-010027- progestagen-associatec	5047.00	PAEP	1219.00	0.41
50049.00	K13	M-015319- NADH dehydrogenase (	4718.00	NDUFC2	1276.00	2.19
50049.00	K14	M-014691- poly(A) binding protein	5042.00	PABPC3	1552.00	1.80
50049.00	K15	M-019815- NADH dehydrogenase (	4722.00	NDUFS3	634.00	1.10
50049.00	K16	M-012696- oxidase (cytochrome c)	5018.00	OXA1L	772.00	0.91
50049.00	K17	M-016266- NADH dehydrogenase (	4723.00	NDUFV1	1895.00	1.37
50049.00	K18	M-006543- ovo-like 1(Drosophila)	5017.00	OVOL1	2509.00	1.91
50049.00	K19	M-019817- NADH dehydrogenase (	4726.00	NDUFS6	1619.00	0.93
50049.00	K20	M-017839- oviductal glycoprotein	5016.00	OVGP1	2536.00	2.88
50049.00	K21	M-016362- NADH dehydrogenase (	4731.00	NDUFV3	1899.00	1.37
50049.00	K23	M-013666- ribosomal protein L10a	4736.00	RPL10A	815.00	0.61
50049.00	L02	M-013535- transmembrane proteir	83935.00	TMEM133	1695.00	1.59
50049.00	L04	M-006809- ADP-dependent glucoki	83440.00	ADPGK	2796.00	6.37
50049.00	L05	M-008407- ATP-binding cassette, s	26154.00	ABCA12	3198.00	2.25
50049.00	L06	M-004525- ADAM metallopeptidas	80332.00	ADAM33	1597.00	2.69
50049.00	L07	M-009258- A kinase (PRKA) anchor	26993.00	AKAP8L	2962.00	9.66
50049.00	L08	M-018395- ARP5 actin-related prot	79913.00	ACTR5	2499.00	3.60
50049.00	L09	M-008501- acyl-Coenzyme A dehyc	27034.00	ACAD8	2176.00	0.41
50049.00	L10	M-021341- agmatine ureohydrolas	79814.00	AGMAT	3196.00	7.98
50049.00	L11	M-004893- kelch-like 20 (Drosophil	27252.00	KLHL20	1360.00	1.99
50049.00	L12	M-014424- acyl-Coenzyme A bindir	79777.00	ACBD4	1730.00	2.95
50049.00	L13	M-020221- neuronal thread proteir	27308.00	RP5-886K2	1094.00	1.28
50049.00	L14	M-007801- adiponectin receptor 2	79602.00	ADIPOR2	1848.00	0.70
50049.00	L15	M-009002- acyl-Coenzyme A dehyc	28976.00	ACAD9	2183.00	2.57
50049.00	L16	M-027141- asparagine-linked glyco	79087.00	ALG12	1703.00	2.06

50049.00	L17	M-008461-	chromosome 9 open re	28989.00	C9orf32	2058.00	3.50
50049.00	L18	M-027136-	asparagine-linked glyco	79053.00	ALG8	2984.00	3.62
50049.00	L19	M-016186-	non-SMC condensin II c	29781.00	NCAPH2	2332.00	2.06
50049.00	L20	M-009458-	acetoacetyl-CoA synthe	65985.00	AACS	1006.00	0.99
50049.00	L21	M-013393-	asparagine-linked glyco	29880.00	ALG5	3830.00	1.10
50049.00	L23	M-013576-	apobec-1 complementa	29974.00	ACF	3781.00	3.09
50049.00	M02	M-008732-	orthodenticle homeobo	5015.00	OTX2	2929.00	1.09
50049.00	M04	M-011124-	orosomucoid 2	5005.00	ORM2	2563.00	1.99
50049.00	M05	M-019466-	neural precursor cell ex	4739.00	NEDD9	3410.00	2.32
50049.00	M06	M-008250-	orosomucoid 1	5004.00	ORM1	1794.00	1.39
50049.00	M07	M-019968-	neurofilament, medium	4741.00	NEFM	2540.00	1.77
50049.00	M08	M-019642-	solute carrier family 22	5003.00	SLC22A18A	882.00	2.38
50049.00	M09	M-012185-	NEL-like 2 (chicken)	4753.00	NELL2	1484.00	0.67
50049.00	M10	M-003287-	origin recognition comp	5001.00	ORC5L	3497.00	3.57
50049.00	M11	M-012058-	sialidase 2 (cytosolic sia	4759.00	NEU2	1433.00	2.02
50049.00	M12	M-003286-	origin recognition comp	5000.00	ORC4L	3795.00	2.71
50049.00	M13	M-008889-	neurogenic differentiat	4761.00	NEUROD2	2516.00	3.34
50049.00	M14	M-003284-	origin recognition comp	4999.00	ORC2L	2411.00	1.62
50049.00	M15	M-009057-	neurogenin 1	4762.00	NEUROG1	891.00	0.79
50049.00	M16	M-003283-	origin recognition comp	4998.00	ORC1L	2707.00	6.10
50049.00	M17	M-020020-	nescient helix loop heli:	4808.00	NHLH2	2631.00	0.72
50049.00	M18	M-012238-	olfactory marker protei	4975.00	OMP	1954.00	1.64
50049.00	M19	M-032018-	Nance-Horan syndrome	4810.00	NHS	3012.00	2.69
50049.00	M20	M-010106-	oligodendrocyte myelin	4974.00	OMG	4255.00	2.91
50049.00	M21	M-020844-	ninjurin 2	4815.00	NINJ2	3000.00	2.27
50049.00	M23	M-020022-	nitrilase 1	4817.00	NIT1	3387.00	0.97
50049.00	N02	M-014237-	adrenocortical dysplasia	65057.00	ACD	1034.00	1.26
50049.00	N04	M-009818-	alanine-glyoxylate amir	64902.00	AGXT2	1371.00	2.19
50049.00	N05	M-007800-	adiponectin receptor 1	51094.00	ADIPOR1	2006.00	0.55
50049.00	N06	M-008696-	alanine-glyoxylate amir	64850.00	AGXT2L1	2230.00	0.54
50049.00	N07	M-021057-	alpha-1,4-N-acetylgluco	51146.00	A4GNT	1969.00	1.22
50049.00	N08	M-010799-	acyl-Coenzyme A bindir	64746.00	ACBD3	1489.00	10.01
50049.00	N09	M-013159-	aminoadipate aminotra	51166.00	AADAT	2859.00	2.20
50049.00	N10	M-009921-	aldehyde dehydrogena:	64577.00	ALDH8A1	3740.00	2.46
50049.00	N11	M-013175-	ABI gene family, memb	51225.00	ABI3	2008.00	1.20
50049.00	N12	M-018058-	ARP6 actin-related prot	64431.00	ACTR6	1771.00	1.64
50049.00	N13	M-021162-	CD320 molecule	51293.00	CD320	1635.00	1.10
50049.00	N14	M-008919-	ATP-binding cassette, s	64137.00	ABCG4	1594.00	2.07
50049.00	N15	M-021120-	androgen-induced 1	51390.00	AIG1	1619.00	0.00
50049.00	N16	M-015921-	HEAT repeat containing	63897.00	HEATR6	3157.00	4.62
50049.00	N17	M-021376-	NCK interacting protein	51517.00	NCKIPSD	1355.00	2.14
50049.00	N18	M-008477-	aminoadipate-semialde	60496.00	AASDHPPT	1393.00	0.65
50049.00	N19	M-006327-	acyl-CoA synthetase lor	51703.00	ACSL5	2029.00	1.28
50049.00	N20	M-013084-	actin filament associate	60312.00	AFAP1	3672.00	3.19
50049.00	N21	M-009278-	amiloride-sensitive cati	51802.00	ACCN5	2731.00	4.17
50049.00	N23	M-013377-	ataxin 2-binding proteir	54715.00	A2BP1	2770.00	3.14
50049.00	O02	M-011974-	osteoglycin	4969.00	OGN	2709.00	2.73

50049.00	O04	M-019921-	osteomodulin	4958.00	OMD	1636.00	0.43
50049.00	O05	M-019118-	neuronatin	4826.00	NNAT	1519.00	0.92
50049.00	O06	M-017319-	outer dense fiber of spe	4957.00	ODF2	1837.00	1.31
50049.00	O07	M-004316-	N-myristoyltransferase	4836.00	NMT1	3193.00	2.32
50049.00	O08	M-011346-	outer dense fiber of spe	4956.00	ODF1	1749.00	0.63
50049.00	O09	M-017771-	nodal homolog (mouse	4838.00	NODAL	1797.00	0.61
50049.00	O10	M-012237-	oncomodulin	4951.00	OCM	1307.00	2.07
50049.00	O11	M-007756-	non-POU domain conta	4841.00	NONO	1538.00	1.89
50049.00	O12	M-024659-	TBC1 domain family, m	4943.00	TBC1D25	843.00	1.78
50049.00	O13	M-019599-	nuclear protein, ataxia-	4863.00	NPAT	875.00	4.23
50049.00	O14	M-008391-	nuclear VCP-like	4931.00	NVL	1593.00	2.39
50049.00	O15	M-012736-	natriuretic peptide pre	4880.00	NPPC	1786.00	3.19
50049.00	O16	M-017547-	nucleoporin 88kDa	4927.00	NUP88	1622.00	3.88
50049.00	O17	M-012647-	neuronal pentraxin II	4885.00	NPTX2	1802.00	3.22
50049.00	O18	M-009401-	N-ethylmaleimide-sens	4905.00	NSF	2098.00	8.20
50049.00	O19	M-012725-	metallothionein 1B	4490.00	MT1B	2738.00	2.19
50049.00	O20	M-005980-	nardilysin (N-arginine d	4898.00	NRD1	1712.00	4.97
50049.00	O21	M-018337-	metallothionein 1X	4501.00	MT1X	1443.00	3.60
50049.00	O23	M-012726-	metallothionein 1F	4494.00	MT1F	2495.00	18.84
50049.00	P02	M-021280-	nuclear fragile X menta	57532.00	NUFIP2	772.00	0.78
50049.00	P04	M-025106-	alanyl-tRNA synthetase	57505.00	AARS2	2063.00	0.68
50049.00	P05	M-018723-	Abelson helper integrat	54806.00	AHI1	1023.00	1.27
50049.00	P06	M-013872-	AD026 protein	57413.00	AD026	2773.00	3.17
50049.00	P07	M-017996-	aftiphilin	54812.00	AFTPH	639.00	2.35
50049.00	P08	M-017580-	MIF4G domain containi	57409.00	MIF4GD	811.00	3.08
50049.00	P09	M-021468-	absent in melanoma 1-	55057.00	AIM1L	3218.00	3.42
50049.00	P10	M-022416-	ADAMTS-like 3	57188.00	ADAMTSL3	652.00	1.99
50049.00	P11	M-008524-	acyl-Coenzyme A oxida	55289.00	ACOXL	1012.00	2.57
50049.00	P12	M-015673-	cancer susceptibility ca	57082.00	CASC5	348.00	2.87
50049.00	P13	M-008641-	ATP-binding cassette, s	55324.00	ABCF3	2332.00	2.36
50049.00	P14	M-021398-	ACN9 homolog (S. cere	57001.00	ACN9	313.00	5.11
50049.00	P15	M-006108-	amiloride-sensitive cati	55515.00	ACCN4	1002.00	3.49
50049.00	P16	M-010928-	chromosome 1 open re	56900.00	C1orf119	905.00	2.76
50049.00	P17	M-020523-	allantoicase	55821.00	ALLC	1859.00	15.12
50049.00	P18	M-009283-	1-acylglycerol-3-phosp	56895.00	AGPAT4	714.00	3.64
50049.00	P19	M-013315-	glycosyltransferase 8 d	55830.00	GLT8D1	762.00	4.59
50049.00	P20	M-008620-	1-acylglycerol-3-phosp	56894.00	AGPAT3	1836.00	3.49
50049.00	P21	M-020824-	actin-related protein 1	55860.00	ACTR10	2183.00	8.47
50049.00	P23	M-027147-	asparagine-linked glyco	56052.00	ALG1	951.00	3.58
					mdn	2254.50	2.38
					3MAD		
					MADc		
50049.00	C22					2743.00	23.88
50049.00	D22					4024.00	27.16
50049.00	E22					2424.00	26.77
50049.00	F22					3128.00	33.38
					mn	3079.75	27.80

					sd	692.18	4.00
50049.00	G22					1179.00	0.93
50049.00	H22					1117.00	0.27
50049.00	I22					1094.00	5.30
50049.00	J22					1839.00	1.63
					mn	1307.25	2.03
					sd	356.31	2.25
					3psSD		11.99
					3ngSD		6.75
					SumSD		18.74
					DiffMn		25.76
					SmovrDiff		0.73
					1minus		0.27
50049.00	G03	M-003290-	polo-like kinase 1 (Dros	5347.00	PLK1 SMAR	166.00	6.63
50049.00	H03	M-003290-	polo-like kinase 1 (Dros	5347.00	PLK1 SMAR	112.00	16.96
50049.00	I03	D-001206-	siControl non-targeting siRNA #2			1903.00	1.58
50049.00	J03	D-001206-	siControl non-targeting siRNA #2			1825.00	4.05
50049.00	K03	D-001600-	siGLO RISC-free siRNA			5140.00	8.89
50049.00	L03	D-001600-	siGLO RISC-free siRNA			4973.00	5.47

Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev
1.15	-0.67	961.00	3.23	0.70	0.34	1088.00	4.04	1.88
7.35	4.25	1692.00	15.25	12.72	6.20	3024.00	12.93	10.77
0.67	0.39	1119.00	4.11	1.58	0.77	2245.00	2.27	0.11
1.39	-0.80	1185.00	0.42	2.11	-1.03	1663.00	2.04	0.12
0.05	-0.03	1320.00	3.56	1.03	0.50	3948.00	2.66	0.50
9.44	5.46	2911.00	7.28	4.75	2.32	3929.00	6.46	4.30
2.23	1.29	1210.00	4.46	1.93	0.94	2462.00	2.40	0.24
3.14	1.81	1487.00	3.36	0.83	0.41	2458.00	2.44	0.28
0.86	-0.50	1253.00	2.87	0.34	0.17	1854.00	1.40	0.76
1.45	-0.84	786.00	4.96	2.43	1.19	1828.00	2.30	0.14
1.31	0.76	492.00	7.52	4.99	2.43	1217.00	5.34	3.18
0.74	-0.43	1406.00	2.35	0.18	-0.09	2499.00	2.00	0.16
0.82	0.47	1412.00	4.89	2.36	1.15	4050.00	1.58	0.58
1.67	-0.96	1592.00	2.58	0.05	0.02	3032.00	0.43	1.73
1.12	0.65	2369.00	7.22	4.69	2.29	2764.00	5.39	3.23
1.37	0.79	630.00	4.60	2.07	1.01	1686.00	1.78	0.38
1.24	0.71	1572.00	2.67	0.14	0.07	3031.00	0.73	1.43
4.55	2.63	939.00	6.82	4.29	2.09	1251.00	2.40	0.24
2.19	1.26	1004.00	4.78	2.25	1.10	1843.00	4.99	2.83
9.10	5.26	1359.00	5.00	2.47	1.21	1755.00	4.73	2.57
0.23	-0.13	1867.00	3.75	1.22	0.60	2744.00	0.66	1.50
0.66	-0.38	1351.00	3.33	0.80	0.39	2687.00	0.45	1.71
1.83	-1.06	2023.00	1.14	1.39	-0.68	2998.00	0.27	1.89
0.12	0.07	1840.00	4.24	1.71	0.83	4022.00	1.19	0.97
0.75	-0.43	499.00	4.21	1.68	0.82	1830.00	0.33	1.83
0.10	-0.06	1851.00	2.54	0.01	0.01	4387.00	0.36	1.80
1.67	-0.97	729.00	6.31	3.78	1.84	2150.00	0.47	1.69
0.64	-0.37	1225.00	3.76	1.23	0.60	2941.00	0.51	1.65
0.00	0.00	888.00	4.84	2.31	1.13	1758.00	1.59	0.57
0.78	0.45	1102.00	3.72	1.19	0.58	2185.00	1.42	0.74
1.62	-0.94	911.00	3.62	1.09	0.53	1183.00	0.17	1.99
1.76	1.02	1537.00	4.03	1.50	0.73	2951.00	1.32	0.84
1.15	0.66	1378.00	3.70	1.17	0.57	3428.00	2.04	0.12
0.49	-0.28	2036.00	2.55	0.02	0.01	3208.00	0.62	1.54
1.96	-1.14	673.00	0.15	2.38	-1.16	2371.00	1.05	1.11
3.34	1.93	1349.00	10.30	7.77	3.79	2739.00	5.81	3.65
1.71	-0.99	1174.00	0.43	2.10	-1.02	2212.00	0.68	1.48
1.14	-0.66	580.00	0.52	2.01	-0.98	1424.00	0.14	2.02
1.34	-0.78	1602.00	0.44	2.09	-1.02	2321.00	1.08	1.08
1.43	-0.83	2731.00	1.94	0.59	-0.29	2631.00	2.24	0.08
1.45	-0.84	1359.00	1.62	0.91	-0.44	2059.00	1.70	0.46
0.42	-0.25	3882.00	1.49	1.04	-0.50	4922.00	1.93	0.23
0.31	-0.18	3201.00	1.03	1.50	-0.73	4390.00	2.87	0.71
0.56	-0.32	1843.00	0.65	1.88	-0.91	3180.00	1.67	0.49
3.32	1.92	1024.00	0.78	1.75	-0.85	3861.00	6.16	4.00
0.32	0.18	715.00	0.28	2.25	-1.10	3210.00	1.90	0.26

0.61	0.35	1466.00	0.48	2.05	-1.00	3920.00	1.79	0.37
0.13	-0.08	1918.00	2.03	0.50	-0.24	4320.00	2.80	0.64
0.22	-0.13	14.00	7.14	**4.61**	2.25	4362.00	3.39	1.23
0.53	-0.31	1549.00	1.48	1.05	-0.51	2925.00	2.56	0.40
1.68	-0.98	1608.00	2.30	0.23	-0.11	2891.00	4.12	1.96
1.41	-0.82	1760.00	0.23	2.30	-1.12	4072.00	1.52	0.64
2.49	1.44	1256.00	0.48	2.05	-1.00	2800.00	3.61	1.45
1.29	-0.75	1592.00	1.07	1.46	-0.71	2954.00	2.47	0.31
0.19	-0.11	2466.00	1.05	1.48	-0.72	4125.00	2.84	0.68
0.12	0.07	1313.00	2.21	0.32	-0.16	1754.00	4.62	2.46
5.21	3.01	1789.00	1.57	0.96	-0.47	2898.00	8.63	**6.47**
0.49	-0.28	1290.00	0.39	2.14	-1.04	3078.00	2.63	0.47
1.89	1.09	2751.00	5.71	3.18	1.55	3712.00	9.40	**7.24**
1.56	-0.90	2369.00	0.13	2.40	-1.17	2238.00	3.57	1.41
0.32	0.18	3030.00	1.91	0.62	-0.30	3562.00	3.00	0.84
2.41	1.39	1765.00	1.42	1.11	-0.54	2176.00	1.65	0.51
0.82	0.47	1877.00	0.53	2.00	-0.97	3274.00	1.56	0.60
0.54	0.31	2258.00	0.84	1.69	-0.82	4782.00	3.05	0.89
0.45	-0.26	2062.00	0.73	1.80	-0.88	4959.00	1.33	0.83
0.70	-0.41	1329.00	0.68	1.85	-0.90	3068.00	1.92	0.24
0.21	-0.12	1645.00	1.16	1.38	-0.67	2764.00	3.40	1.24
1.97	-1.14	1269.00	0.71	1.82	-0.89	1775.00	0.68	1.48
1.23	-0.71	1003.00	0.60	1.93	-0.94	1511.00	2.91	0.75
0.03	0.01	1786.00	1.90	0.63	-0.30	3734.00	5.17	3.01
0.66	-0.38	1603.00	2.00	0.53	-0.26	1735.00	1.56	0.60
2.17	-1.26	1453.00	1.24	1.29	-0.63	3815.00	3.41	1.25
4.78	2.76	1456.00	3.85	1.32	0.64	2296.00	10.19	**8.03**
1.09	-0.63	1985.00	0.71	1.82	-0.89	3785.00	3.65	1.49
0.68	-0.39	1311.00	0.92	1.61	-0.79	3430.00	5.51	**3.35**
1.73	1.00	860.00	4.30	1.77	0.86	2045.00	6.21	**4.05**
5.41	3.13	3022.00	5.03	2.50	1.22	4384.00	7.32	**5.16**
1.02	0.59	2907.00	6.64	4.11	2.00	5328.00	6.02	**3.86**
0.94	-0.54	2504.00	0.40	2.13	-1.04	4134.00	4.72	2.56
1.19	-0.69	1856.00	0.32	2.21	-1.07	1729.00	2.20	0.04
0.50	-0.29	2905.00	0.52	2.01	-0.98	3783.00	0.24	1.92
5.48	3.17	1331.00	3.53	1.00	0.49	1953.00	3.79	1.63
4.89	2.82	1312.00	0.30	2.23	-1.08	2226.00	0.81	1.35
0.96	0.55	1894.00	2.27	0.26	-0.13	3671.00	2.10	0.06
1.32	0.76	947.00	2.53	0.00	0.00	1572.00	1.21	0.95
0.62	0.36	1430.00	1.96	0.57	-0.28	3570.00	1.32	0.84
4.06	2.35	1183.00	1.69	0.84	-0.41	2053.00	0.68	1.48
0.97	0.56	826.00	0.97	1.56	-0.76	1962.00	1.02	1.14
7.12	4.11	1455.00	14.30	**11.77**	5.74	3925.00	10.12	**7.96**
12.26	7.08	1511.00	7.15	**4.62**	2.25	2203.00	4.40	2.24
1.14	0.66	1304.00	1.15	1.38	-0.67	1828.00	0.98	1.18
0.70	0.40	2044.00	3.13	0.60	0.29	3658.00	0.63	1.53
0.28	0.16	451.00	3.55	1.02	0.50	1866.00	1.66	0.50

2.23	1.29	1547.00	3.10	0.57	0.28	2620.00	2.14	0.02
2.68	1.55	2351.00	2.72	0.19	0.09	3678.00	1.14	1.02
0.20	-0.12	1240.00	3.39	0.86	0.42	2899.00	0.83	1.33
2.71	1.56	2164.00	3.19	0.66	0.32	3642.00	1.48	0.68
1.18	-0.68	1747.00	1.26	1.27	-0.62	3161.00	1.74	0.42
1.29	0.75	1422.00	1.13	1.40	-0.68	2374.00	1.05	1.11
0.37	0.21	2567.00	0.66	1.87	-0.91	3315.00	1.42	0.74
1.28	-0.74	1807.00	0.94	1.59	-0.77	2657.00	0.04	2.12
3.94	2.28	2199.00	4.00	1.47	0.72	3374.00	1.42	0.74
0.30	0.17	2387.00	2.68	0.15	0.07	3361.00	1.19	0.97
0.15	0.09	1362.00	0.81	1.72	-0.84	1745.00	1.43	0.73
0.22	0.12	2428.00	2.10	0.43	-0.21	4907.00	1.87	0.29
1.72	-1.00	1373.00	1.46	1.07	-0.52	3009.00	0.43	1.73
1.06	0.61	1734.00	0.35	2.18	-1.06	2737.00	0.88	1.28
1.50	0.87	1523.00	1.58	0.95	-0.46	3223.00	0.93	1.23
0.84	0.48	1042.00	1.82	0.71	-0.34	2279.00	1.10	1.06
4.29	2.48	924.00	1.95	0.58	-0.28	1183.00	1.86	0.30
1.10	0.64	2232.00	5.11	2.58	1.26	4688.00	3.60	1.44
5.27	3.04	1566.00	2.94	0.41	0.20	2723.00	2.20	0.04
0.19	-0.11	1426.00	1.19	1.34	-0.65	2489.00	3.21	1.05
0.55	-0.32	1056.00	1.52	1.01	-0.49	3352.00	0.30	1.86
0.92	0.53	1663.00	1.20	1.33	-0.65	2736.00	4.53	2.37
2.47	1.42	2205.00	3.04	0.51	0.25	4924.00	1.32	0.84
9.28	5.36	1894.00	8.08	**5.55**	2.70	3353.00	11.18	**9.02**
9.11	5.26	1660.00	3.73	1.20	0.59	4051.00	8.69	**6.53**
9.52	5.50	2583.00	9.56	**7.03**	3.43	3851.00	10.18	**8.02**
1.07	0.62	2152.00	1.21	1.32	-0.64	2252.00	3.15	0.99
1.88	-1.09	1642.00	1.58	0.95	-0.46	3168.00	2.71	0.55
0.32	0.18	1089.00	2.39	0.14	-0.07	1446.00	4.77	2.61
1.71	-0.99	1857.00	1.78	0.75	-0.37	2426.00	1.57	0.59
0.68	-0.40	1263.00	1.90	0.63	-0.31	1506.00	2.39	0.23
1.15	-0.67	1553.00	1.29	1.24	-0.60	2362.00	1.52	0.64
1.19	-0.69	1539.00	1.62	0.91	-0.44	1983.00	1.46	0.70
0.93	0.54	1106.00	1.18	1.35	-0.66	1980.00	1.92	0.24
0.84	-0.49	1705.00	3.46	0.93	0.45	3250.00	3.08	0.92
1.33	-0.77	472.00	1.06	1.47	-0.72	1062.00	3.58	1.42
0.49	-0.28	1934.00	5.58	3.05	1.49	2280.00	2.98	0.82
1.32	-0.76	1577.00	0.38	2.15	-1.05	2532.00	1.86	0.30
3.96	2.29	1944.00	6.84	**4.31**	2.10	2796.00	9.30	**7.14**
1.08	0.62	2311.00	1.99	0.54	-0.26	3223.00	1.86	0.30
1.28	0.74	1401.00	2.21	0.32	-0.15	3308.00	3.48	1.32
0.56	0.32	1488.00	2.08	0.45	-0.22	2802.00	2.82	0.66
0.29	-0.17	2047.00	3.42	0.89	0.43	2892.00	2.63	0.47
1.04	0.60	1675.00	2.03	0.50	-0.24	2960.00	7.30	**5.14**
7.17	4.14	3781.00	11.69	**9.16**	4.47	4440.00	13.20	**11.04**
1.81	-1.05	2836.00	0.56	1.97	-0.96	2223.00	2.02	0.14
0.98	-0.57	1530.00	2.35	0.18	-0.09	1454.00	2.54	0.38

2.20	-1.27	2500.00	1.56	0.97	-0.47	3333.00	0.90	1.26
0.20	0.11	2309.00	7.58	**5.05**	2.46	2971.00	3.87	1.71
1.77	-1.03	2880.00	4.72	2.19	1.07	3346.00	0.69	1.47
1.46	-0.85	1408.00	4.19	1.66	0.81	1943.00	1.75	0.41
0.01	-0.01	1984.00	5.39	2.86	1.40	3363.00	2.94	0.78
1.57	-0.91	2294.00	2.75	0.22	0.11	3985.00	0.35	1.81
0.73	-0.42	675.00	3.11	0.58	0.28	1728.00	1.91	0.25
2.22	-1.29	969.00	3.30	0.77	0.38	1749.00	0.46	1.70
2.20	-1.27	1327.00	3.62	1.09	0.53	1625.00	0.55	1.61
1.44	-0.83	594.00	5.05	2.52	1.23	970.00	1.24	0.92
1.62	-0.94	816.00	6.25	3.72	1.81	1159.00	0.69	1.47
2.10	-1.21	1619.00	1.73	0.80	-0.39	2192.00	0.32	1.84
0.27	0.16	1191.00	3.53	1.00	0.49	1068.00	3.28	1.12
1.08	-0.63	814.00	4.42	1.89	0.92	1707.00	4.45	2.29
1.04	-0.60	1641.00	1.10	1.43	-0.70	2862.00	1.22	0.94
6.34	3.66	1970.00	7.67	**5.14**	2.50	3604.00	8.68	**6.52**
0.89	-0.52	1119.00	2.59	0.06	0.03	2197.00	5.14	2.98
1.90	-1.10	2122.00	2.78	0.25	0.12	4617.00	4.68	2.52
6.98	4.03	1545.00	12.10	**9.57**	4.67	2830.00	12.62	**10.46**
1.71	-0.99	277.00	14.08	**11.55**	5.63	628.00	2.87	0.71
0.38	0.22	3386.00	1.74	0.79	-0.38	3567.00	2.41	0.25
0.80	0.46	1367.00	7.39	**4.86**	2.37	1075.00	3.72	1.56
0.75	0.43	1290.00	4.03	1.50	0.73	1551.00	0.71	1.45
0.99	0.57	2427.00	2.88	0.35	0.17	2281.00	1.40	0.76
2.88	1.66	2483.00	8.58	**6.05**	2.95	2865.00	3.18	1.02
5.48	3.17	3366.00	11.47	**8.94**	4.36	3321.00	8.49	**6.33**
0.94	0.54	2312.00	1.82	0.71	-0.35	3940.00	3.45	1.29
6.94	4.01	1621.00	2.90	0.37	0.18	1819.00	1.43	0.73
0.51	-0.29	990.00	2.22	0.31	-0.15	1138.00	1.05	1.11
1.78	1.03	822.00	2.31	0.22	-0.11	1595.00	1.25	0.91
5.37	3.10	691.00	4.92	2.39	1.17	1520.00	2.96	0.80
10.31	5.96	1710.00	13.10	**10.57**	5.15	1827.00	5.47	3.31
1.41	0.81	2491.00	1.89	0.64	-0.31	2819.00	4.26	2.10
0.58	-0.33	709.00	3.81	1.28	0.62	1560.00	7.12	**4.96**
1.24	0.72	1109.00	1.17	1.36	-0.66	2089.00	4.88	2.72
1.64	0.95	903.00	1.55	0.98	-0.48	1654.00	3.63	1.47
0.88	0.50	1530.00	1.18	1.35	-0.66	2436.00	4.06	1.90
0.72	0.42	3162.00	2.66	0.13	0.06	3428.00	4.67	2.51
1.22	0.70	2350.00	2.51	0.02	-0.01	1774.00	2.31	0.15
0.35	-0.20	1179.00	0.85	1.68	-0.82	1347.00	1.78	0.38
1.45	0.83	1647.00	3.95	1.42	0.69	1191.00	0.76	1.40
13.67	7.90	3723.00	29.44	**26.91**	13.12	3203.00	10.93	**8.77**
1.55	0.90	2372.00	4.30	1.77	0.86	2639.00	0.34	1.82
0.67	-0.39	2200.00	4.23	1.70	0.83	1478.00	0.34	1.82
5.02	2.90	1590.00	13.27	**10.74**	5.24	1573.00	4.20	2.04
0.60	-0.35	2186.00	2.79	0.26	0.13	1299.00	2.62	0.46
0.22	0.13	2161.00	3.42	0.89	0.44	1260.00	1.59	0.57

0.35	-0.20	886.00	4.51	1.98	0.97	936.00	0.32	1.84
1.53	-0.89	1693.00	1.89	0.64	-0.31	1175.00	2.13	0.03
13.36	7.72	1451.00	20.06	17.53	8.54	952.00	15.65	13.49
2.77	1.60	1867.00	6.64	4.11	2.00	917.00	3.38	1.22
1.43	-0.83	1420.00	3.87	1.34	0.66	1305.00	0.92	1.24
1.19	0.69	1805.00	5.26	2.73	1.33	975.00	3.08	0.92
2.03	1.17	1384.00	3.11	0.58	0.28	1192.00	9.06	6.90
0.95	-0.55	2385.00	3.02	0.49	0.24	1530.00	1.90	0.26
1.08	0.62	2973.00	3.80	1.27	0.62	1633.00	4.41	2.25
2.17	1.25	2615.00	4.17	1.64	0.80	1878.00	10.86	8.70
7.94	4.59	4220.00	9.05	6.52	3.18	3815.00	8.13	5.97
2.23	1.29	1262.00	5.15	2.62	1.28	1254.00	10.13	7.97
0.73	-0.42	1971.00	2.64	0.11	0.05	1493.00	2.75	0.59
2.55	1.47	1842.00	6.62	4.09	2.00	2386.00	2.47	0.31
1.69	-0.98	2821.00	0.60	1.93	-0.94	2526.00	2.93	0.77
0.68	-0.39	2102.00	2.19	0.34	-0.17	1073.00	0.75	1.41
1.45	-0.84	2447.00	2.90	0.37	0.18	2321.00	1.81	0.35
1.84	1.06	2248.00	6.23	3.70	1.80	2500.00	3.96	1.80
2.88	1.67	2406.00	4.07	1.54	0.75	1812.00	1.05	1.11
1.56	-0.91	1995.00	4.16	1.63	0.80	1148.00	2.96	0.80
0.65	-0.38	2531.00	3.36	0.83	0.40	1789.00	2.01	0.15
1.49	-0.87	1325.00	4.38	1.85	0.90	998.00	4.81	2.65
1.97	-1.14	1014.00	4.64	2.11	1.03	733.00	3.27	1.11
0.19	-0.11	1095.00	4.93	2.40	1.17	1492.00	4.76	2.60
0.58	-0.33	2320.00	3.19	0.66	0.32	2192.00	2.10	0.06
1.28	-0.74	2105.00	3.80	1.27	0.62	1361.00	2.20	0.04
1.47	-0.85	1509.00	3.64	1.11	0.54	597.00	2.51	0.35
1.01	-0.58	2155.00	1.35	1.18	-0.58	1439.00	4.45	2.29
0.47	-0.27	2426.00	3.50	0.97	0.48	2345.00	2.17	0.01
1.45	-0.84	2660.00	6.77	4.24	2.07	2134.00	2.30	0.14
0.50	0.29	4265.00	5.81	3.28	1.60	1254.00	2.95	0.79
1.01	-0.59	2312.00	1.21	1.32	-0.64	1711.00	1.69	0.47
1.77	-1.02	976.00	1.84	0.69	-0.33	675.00	6.96	4.80
0.79	-0.46	1053.00	1.80	0.73	-0.35	1488.00	0.47	1.69
3.99	2.30	3198.00	7.60	5.07	2.47	2176.00	4.46	2.30
0.13	-0.08	3754.00	4.24	1.71	0.83	2460.00	2.89	0.73
0.31	0.18	1798.00	3.34	0.81	0.39	2260.00	2.17	0.01
7.28	4.20	2358.00	8.95	6.42	3.13	1532.00	8.16	6.00
1.22	0.70	2986.00	5.16	2.63	1.28	2140.00	3.83	1.67
1.97	-1.14	2850.00	1.58	0.95	-0.46	1426.00	0.35	1.81
5.60	3.23	3166.00	5.81	3.28	1.60	3365.00	4.87	2.71
0.39	-0.23	2016.00	2.38	0.15	-0.07	1717.00	1.92	0.24
0.57	0.33	1693.00	4.31	1.78	0.87	1684.00	5.88	3.72
1.10	-0.64	1003.00	3.99	1.46	0.71	904.00	1.77	0.39
1.68	-0.97	1917.00	1.36	1.17	-0.57	1122.00	2.67	0.51
0.19	0.11	2311.00	6.97	4.44	2.16	1066.00	5.82	3.66
0.32	-0.19	1601.00	2.25	0.28	-0.14	1277.00	1.49	0.67

1.12	0.64	2802.00	3.35	0.82	0.40	1592.00	2.20	0.04
1.24	0.71	4040.00	7.85	**5.32**	2.59	2594.00	5.63	**3.47**
0.32	-0.19	3264.00	2.51	0.02	-0.01	2783.00	2.87	0.71
1.39	-0.80	1562.00	1.86	0.67	-0.33	1565.00	1.53	0.63
1.28	-0.74	3987.00	1.61	0.92	-0.45	2733.00	1.94	0.22
0.71	0.41	4011.00	1.05	1.48	-0.72	2936.00	4.29	2.13
1.29	-0.75	2039.00	1.81	0.72	-0.35	2218.00	0.86	1.30
0.39	-0.23	2575.00	2.33	0.20	-0.10	1907.00	1.31	0.85
0.06	-0.04	5203.00	2.67	0.14	0.07	2907.00	0.41	1.75
0.99	-0.57	2988.00	2.54	0.01	0.01	2194.00	0.46	1.70
0.61	-0.35	2174.00	2.81	0.28	0.14	2015.00	1.04	1.12
0.00	0.00	874.00	1.83	0.70	-0.34	634.00	3.00	0.84
1.71	-0.99	2410.00	0.12	2.41	-1.17	991.00	0.81	1.35
1.19	0.69	3164.00	2.12	0.41	-0.20	2506.00	1.56	0.60
0.36	-0.21	1933.00	1.19	1.34	-0.65	601.00	0.83	1.33
0.33	0.19	4483.00	1.18	1.35	-0.66	3523.00	1.62	0.54
0.96	0.55	1779.00	2.08	0.45	-0.22	1768.00	0.79	1.37
0.76	-0.44	2729.00	2.49	0.04	-0.02	1505.00	1.33	0.83
1.59	-0.92	2441.00	0.25	2.28	-1.11	1405.00	2.21	0.05
3.72	2.15	2386.00	4.86	2.33	1.14	2405.00	4.70	2.54
1.66	-0.96	2811.00	0.53	2.00	-0.97	1503.00	0.00	2.16
0.74	-0.43	3165.00	1.55	0.98	-0.48	2941.00	0.27	1.89
0.31	0.18	3086.00	0.81	1.72	-0.84	2120.00	1.08	1.08
0.53	0.31	3053.00	6.58	4.05	1.98	2778.00	1.15	1.01
0.11	-0.07	2719.00	0.48	2.05	-1.00	2876.00	1.70	0.46
1.41	-0.81	2245.00	0.58	1.95	-0.95	1980.00	1.62	0.54
1.12	-0.65	797.00	1.63	0.90	-0.44	1414.00	1.91	0.25
0.19	-0.11	1165.00	0.94	1.59	-0.77	926.00	4.43	2.27
1.83	-1.06	2313.00	2.25	0.28	-0.14	1651.00	4.42	2.26
1.84	-1.07	3019.00	2.88	0.35	0.17	1222.00	1.15	1.01
1.16	-0.67	941.00	1.70	0.83	-0.40	824.00	3.16	1.00
7.63	4.41	737.00	8.68	**6.15**	3.00	907.00	4.63	2.47
0.18	-0.10	3535.00	2.43	0.10	-0.05	2227.00	1.21	0.95
0.08	0.04	4093.00	2.69	0.16	0.08	2001.00	1.45	0.71
1.18	-0.69	2495.00	1.08	1.45	-0.70	2169.00	1.43	0.73
0.74	-0.43	1549.00	1.42	1.11	-0.54	1434.00	1.19	0.97
1.28	-0.74	2428.00	2.35	0.18	-0.09	863.00	1.97	0.19
0.31	-0.18	2235.00	0.67	1.86	-0.90	1136.00	2.02	0.14
2.38	-1.38	2416.00	2.07	0.46	-0.22	1126.00	2.66	0.50
2.24	1.30	4455.00	2.13	0.40	-0.19	1919.00	4.53	2.37
0.24	-0.14	2503.00	1.88	0.65	-0.32	1255.00	4.38	2.22
1.73	-1.00	2333.00	1.03	1.50	-0.73	1216.00	2.22	0.06
1.10	-0.64	1990.00	1.46	1.07	-0.52	1165.00	1.63	0.53
0.81	0.46	3906.00	1.66	0.87	-0.42	2787.00	4.27	2.11
1.79	1.04	2686.00	2.20	0.33	-0.16	1875.00	1.49	0.67
0.76	0.44	2174.00	1.75	0.78	-0.38	1606.00	4.92	2.76
0.35	0.20	3300.00	3.94	1.41	0.69	2396.00	3.80	1.64

1.95	-1.13	2604.00	0.31	2.22	-1.08	1560.00	2.24	0.08
1.46	-0.84	2047.00	0.49	2.04	-0.99	964.00	0.00	2.16
1.07	-0.62	1615.00	1.36	1.17	-0.57	1533.00	2.15	0.01
0.06	-0.04	3401.00	0.97	1.56	-0.76	3395.00	2.12	0.04
1.75	-1.01	2102.00	3.62	1.09	0.53	1877.00	0.69	1.47
1.77	-1.02	1661.00	0.36	2.17	-1.06	1503.00	0.80	1.36
0.31	-0.18	2177.00	0.46	2.07	-1.01	836.00	1.32	0.84
0.49	-0.29	2024.00	0.69	1.84	-0.89	1190.00	0.84	1.32
0.60	-0.35	562.00	2.49	0.04	-0.02	463.00	2.16	0.00
1.85	1.07	888.00	0.45	2.08	-1.01	353.00	1.13	1.03
0.01	0.00	2025.00	0.20	2.33	-1.14	1278.00	2.82	0.66
0.81	0.47	3089.00	1.81	0.72	-0.35	1471.00	2.11	0.05
1.50	0.87	1744.00	0.00	2.53	-1.23	838.00	0.84	1.32
0.84	0.48	4376.00	3.82	1.29	0.63	1826.00	1.92	0.24
5.82	3.36	2747.00	1.09	1.44	-0.70	1803.00	5.88	**3.72**
0.19	-0.11	3409.00	1.23	1.30	-0.63	2438.00	1.35	0.81
2.59	1.49	2142.00	0.56	1.97	-0.96	839.00	0.95	1.21
1.22	0.71	1847.00	0.05	2.48	-1.21	1266.00	1.97	0.19
16.46	9.51	1273.00	3.46	0.93	0.45	1706.00	7.21	**5.05**
1.60	-0.93	724.00	0.83	1.70	-0.83	1160.00	0.86	1.30
1.70	-0.99	2207.00	3.72	1.19	0.58	2955.00	1.62	0.54
1.11	-0.64	1968.00	3.15	0.62	0.30	1277.00	2.11	0.05
0.79	0.46	3278.00	3.81	1.28	0.63	3476.00	5.26	3.10
0.03	-0.02	763.00	1.83	0.70	-0.34	589.00	3.57	1.41
0.70	0.40	1006.00	4.08	1.55	0.75	1316.00	3.34	1.18
1.04	0.60	3813.00	7.58	**5.05**	2.46	4399.00	7.66	**5.50**
0.39	-0.22	915.00	5.68	3.15	1.54	839.00	6.44	**4.28**
0.19	0.11	1150.00	2.52	0.01	0.00	1270.00	1.65	0.51
0.49	0.28	458.00	10.92	**8.39**	4.09	596.00	1.68	0.48
0.02	-0.01	3585.00	7.39	**4.86**	2.37	3160.00	4.81	2.65
2.73	1.58	705.00	5.53	3.00	1.46	390.00	5.38	3.22
1.11	0.64	993.00	6.24	3.71	1.81	498.00	1.00	1.16
0.38	0.22	1032.00	1.07	1.46	-0.71	1496.00	1.27	0.89
12.74	7.36	2182.00	13.66	**11.13**	5.42	1814.00	6.34	**4.18**
1.26	0.73	1226.00	2.45	0.08	-0.04	1082.00	2.40	0.24
2.21	1.28	942.00	5.20	2.67	1.30	901.00	3.00	0.84
1.11	0.64	1772.00	4.97	2.44	1.19	2259.00	3.05	0.89
6.09	3.52	1496.00	12.43	**9.90**	4.83	2501.00	10.88	**8.72**
1.20	0.69	445.00	4.94	2.41	1.18	617.00	2.11	0.05
1.17		1768.50	2.53	1.39		2176.00	2.16	1.11
3.51				4.16				3.33
1.73				2.05				1.64
	3747.00	23.59		3257.00	28.12			
	3720.00	27.07		2764.00	24.17			
	2376.00	26.81		2706.00	16.45			
	2210.00	27.78		2901.00	24.13			
	3013.25	26.31		2907.00	23.22			

834.50	1.86	247.24	4.89		
639.00	0.47	1064.00	2.82		
566.00	3.89	1101.00	6.27		
1440.00	0.00			982.00	9.27
1335.00	2.85	1224.00	4.58		
995.00	1.80	1129.67	4.55		
456.22	1.87	83.76	1.72		
	5.58		14.66		
	5.60		5.17		
	11.18		19.84		
	24.51		18.66		
	0.46		1.06		
	0.54		-0.06		
69.00	10.15	115.00	5.22		
69.00	18.84	92.00	2.17		
1180.00	3.47	1669.00	1.92		
1397.00	5.23	1173.00	0.85		
5926.00	9.85	5586.00	8.66		
5520.00	6.76	5763.00	4.23		

rZ		
1.15		
6.56	y	
0.07		
-0.07		
0.31		
2.62	y	
0.15		
0.17		
-0.46		
0.09		
1.94		
-0.09		
-0.35		
-1.05		
1.97		
-0.23		
-0.87		
0.15	x	toxic a,b,c
1.73		
1.57		
-0.91		
-1.04		
-1.15		
-0.59		
-1.11		
-1.09		
-1.03		
-1.00		
-0.34		
-0.45		
-1.21		
-0.51		
-0.07		
-0.93		
-0.67		
2.22	y	
-0.90		
-1.23		
-0.66		
0.05		
-0.28		
-0.14		
0.43		
-0.30		
2.44		
-0.16		

-0.23		
0.39		
0.75		
0.25		
1.19		
-0.39		
0.88		
0.19		
0.41		
1.50		
3.94	x	debris a,b
0.29		
4.41		
0.86		
0.52		
-0.31		
-0.36		
0.55		
-0.50		
-0.14		
0.76		
-0.90		
0.46		
1.84		
-0.37		
0.76		
4.90	y	
0.91		
2.04		
2.47		
3.15	y	
2.36	y	
1.56		
0.03		
-1.17		
0.99		
-0.82		
-0.04		
-0.58		
-0.51		
-0.90		
-0.69		
4.85	y	
1.37	y	
-0.71		
-0.93		
-0.30		

-0.01	
-0.62	
-0.81	
-0.41	
-0.25	
-0.67	
-0.45	
-1.29	
-0.45	
-0.59	
-0.44	
-0.17	
-1.05	
-0.78	
-0.75	
-0.65	
-0.18	
0.88	
0.03	
0.64	
-1.13	
1.45	
-0.51	
5.50	y
3.98	y
4.89	y
0.61	
0.34	
1.59	
-0.36	
0.14	
-0.39	
-0.42	
-0.14	
0.56	
0.87	
0.50	
-0.18	
4.35	y
-0.18	
0.80	
0.40	
0.29	
3.13	
6.73	y
-0.08	
0.24	

-0.77		
1.04		
-0.89		
-0.25		
0.48		
-1.10		
-0.15		
-1.03		
-0.98		
-0.56		
-0.89		
-1.12		
0.68		
1.40		
-0.57		
3.98	y	
1.82		
1.54		
6.37	y	
0.43		
0.16		
0.95		
-0.88		
-0.46		
0.62		
3.86	y	
0.79		
-0.44		
-0.67		
-0.55		
0.49		
2.02	y	
1.28		
3.02		
1.66		
0.90		
1.16		
1.53		
0.09		
-0.23		
-0.85		
5.34	y	
-1.11		
-1.11		
1.24	x	toxic b,c,
0.28		
-0.35		

-1.12		
-0.02		
8.22	y	
0.75		
-0.75		
0.56		
4.21		
-0.16		
1.37		
5.30		
3.64	y	
4.86		
0.36		
0.19		
0.47		
-0.86		
-0.21		
1.10		
-0.67		
0.49		
-0.09		
1.62		
0.68		
1.59		
-0.04		
0.03		
0.22		
1.40		
0.01		
0.09		
0.48		
-0.28		
2.93		
-1.03		
1.40	x	art a,c
0.44		
0.01		
3.66	y	
1.02		
-1.10		
1.66		
-0.14		
2.27		
-0.24		
0.32		
2.23	x	debris a,tox c
-0.41		

0.03		
2.12	x	debris a,c
0.44		
-0.38		
-0.13		
1.30		
-0.79		
-0.51		
-1.06		
-1.04		
-0.68		
0.51		
-0.82		
-0.37		
-0.81		
-0.33		
-0.83		
-0.50		
0.03		
1.55		
-1.31		
-1.15		
-0.65		
-0.61		
-0.28		
-0.33		
-0.15		
1.38		
1.38		
-0.62		
0.61		
1.51	x	toxic a,b,c
-0.57		
-0.43		
-0.44		
-0.59		
-0.11		
-0.08		
0.31		
1.45		
1.36		
0.04		
-0.32		
1.29		
-0.40		
1.68		
1.00		

0.05		
-1.31		
0.00		
-0.02		
-0.89		
-0.83		
-0.51		
-0.80		
0.00		
-0.62		
0.40		
-0.03		
-0.80		
-0.15		
2.27	x	toxic a,b
-0.49		
-0.73		
-0.11		
3.08	x	toxic b,c,
-0.79		
-0.32		
-0.03		
1.89		
0.86		
0.72		
3.35	x	debris a,b
2.61		
-0.31		
-0.29		
1.62		
1.97		
-0.70		
-0.54		
2.55	x	toxic a,c
0.15		
0.51		
0.55		
5.31	y	
-0.03		

Plate	Well	Gene	GeneID	Cell Count	% inf
50050.00	A02	M-018672- splicing factor, arginine/serine-rich	SFRS1	401.00	0.75
50050.00	A04	M-019585- selenoprotein W, 1	SEPW1	1043.00	0.48
50050.00	A05	M-016442- pregnancy specific beta-1-glycopr	PSG1	1544.00	0.39
50050.00	A06	M-012062- selenoprotein P, plasma, 1	SEPP1	1274.00	0.63
50050.00	A07	M-014693- pregnancy specific beta-1-glycopr	PSG2	1236.00	0.32
50050.00	A08	M-019709- semenogelin II	SEMG2	1275.00	1.33
50050.00	A09	M-014137- pregnancy specific beta-1-glycopr	PSG3	1255.00	0.88
50050.00	A10	M-019708- semenogelin I	SEMG1	1223.00	3.35
50050.00	A11	M-019700- pregnancy specific beta-1-glycopr	PSG4	1105.00	0.27
50050.00	A12	M-020455- trafficking protein particle comple	TRAPPC2	1356.00	1.18
50050.00	A13	M-015989- pregnancy specific beta-1-glycopr	PSG5	570.00	0.88
50050.00	A14	M-011387- secreted and transmembrane 1	SECTM1	927.00	0.43
50050.00	A15	M-020127- pregnancy specific beta-1-glycopr	PSG6	941.00	3.08
50050.00	A16	M-012351- SEC13 homolog (S. cerevisiae)	SEC13	810.00	2.96
50050.00	A17	M-019701- pregnancy specific beta-1-glycopr	PSG7	1069.00	1.03
50050.00	A18	M-013504- stromal cell-derived factor 2	SDF2	1093.00	1.56
50050.00	A19	M-017057- pregnancy specific beta-1-glycopr	PSG9	726.00	1.93
50050.00	A20	M-008270- syndecan binding protein (synteni	SDCBP	1960.00	5.26
50050.00	A21	M-019699- pregnancy specific beta-1-glycopr	PSG11	1928.00	3.53
50050.00	A23	M-011758- proteasome (prosome, macropain	PSMA3	1063.00	3.86
50050.00	B02	M-010088- transglutaminase 3 (E polypeptide,	TGM3	1457.00	0.34
50050.00	B04	M-003716- trefoil factor 3 (intestinal)	TFF3	2127.00	1.13
50050.00	B05	M-005151- splicing factor, arginine/serine-rich	SFRS4	1383.00	2.31
50050.00	B06	M-010543- trefoil factor 2 (spasmolytic protei	TFF2	2146.00	0.79
50050.00	B07	M-007279- splicing factor, arginine/serine-rich	SFRS5	967.00	3.41
50050.00	B08	M-003715- trefoil factor 1	TFF1	711.00	1.97
50050.00	B09	M-016067- splicing factor, arginine/serine-rich	SFRS6	1761.00	4.54
50050.00	B10	M-008506- tryptophan 2,3-dioxygenase	TDO2	1411.00	0.71
50050.00	B11	M-007278- splicing factor, arginine/serine-rich	SFRS10	1400.00	0.71
50050.00	B12	M-003780- thymine-DNA glycosylase	TDG	1524.00	0.85
50050.00	B13	M-019736- surfactant, pulmonary-associated	SFTPA2	942.00	0.64
50050.00	B14	M-017784- t-complex-associated-testis-expre	TCTE3	1456.00	1.51
50050.00	B15	M-013002- small glutamine-rich tetratricopept	SGTA	984.00	0.81
50050.00	B16	M-019957- dynein, light chain, Tctex-type 3	DYNLT3	1093.00	1.74
50050.00	B17	M-019584- SH3 domain binding glutamic acid-	SH3BGRL	2540.00	2.80
50050.00	B18	M-015223- tectorin beta	TECTB	1242.00	1.29
50050.00	B19	M-012352- ST3 beta-galactoside alpha-2,3-sial	ST3GAL2	1465.00	0.48
50050.00	B20	M-017977- t-complex 11 (mouse)	TCP11	1443.00	2.01
50050.00	B21	M-020143- ST3 beta-galactoside alpha-2,3-sial	ST3GAL4	1106.00	1.27
50050.00	B23	M-012260- ST3 beta-galactoside alpha-2,3-sial	ST3GAL3	1065.00	0.19
50050.00	C02	M-012653- syndecan 2	SDC2	1250.00	0.24
50050.00	C04	M-010621- syndecan 1	SDC1	967.00	0.83
50050.00	C05	M-017211- proteasome (prosome, macropain	PSMA4	1357.00	1.84
50050.00	C06	M-022618- sarcalumenin	SRL	1613.00	0.56
50050.00	C07	M-011359- proteasome (prosome, macropain	PSMA5	662.00	0.30
50050.00	C08	M-006506- sodium channel, nonvoltage-gated	SCNN1D	1101.00	0.09

50050.00	C09	M-011360-	proteasome (prosome, macropain	PSMA6	474.00	0.00
50050.00	C10	M-017875-	sodium channel, voltage-gated, ty	SCN4B	1122.00	1.69
50050.00	C11	M-004209-	proteasome (prosome, macropain	PSMA7	469.00	0.43
50050.00	C12	M-016088-	sodium channel, voltage-gated, ty	SCN2B	1659.00	0.96
50050.00	C13	M-011361-	proteasome (prosome, macropain	PSMB1	857.00	0.70
50050.00	C14	M-009745-	sterol-C5-desaturase (ERG3 delta-	SC5DL	1053.00	2.09
50050.00	C15	M-010461-	proteasome (prosome, macropain	PSMB2	1036.00	1.16
50050.00	C16	M-021405-	SET binding factor 1	SBF1	1785.00	1.57
50050.00	C17	M-017489-	proteasome (prosome, macropain	PSMB3	555.00	1.44
50050.00	C18	M-011771-	SATB homeobox 1	SATB1	1101.00	0.45
50050.00	C19	M-004522-	proteasome (prosome, macropain	PSMB5	380.00	0.00
50050.00	C20	M-013477-	seryl-tRNA synthetase	SARS	491.00	1.83
50050.00	C21	M-006021-	proteasome (prosome, macropain	PSMB7	1752.00	0.46
50050.00	C23	M-006022-	proteasome (prosome, macropain	PSMB8	1022.00	0.39
50050.00	D02	M-019823-	t-complex 10 (mouse)	TCP10	1139.00	1.32
50050.00	D04	M-011188-	transcobalamin I (vitamin B12 bin	TCN1	1192.00	0.00
50050.00	D05	M-011775-	ST8 alpha-N-acetyl-neuraminide al	ST8SIA1	1091.00	1.37
50050.00	D06	M-011791-	chromosome 2 open reading fram	C2orf3	967.00	0.00
50050.00	D07	M-013435-	superkiller viralicidic activity 2-like	SKIV2L	2097.00	0.52
50050.00	D08	M-022116-	T-box 15	TBX15	1489.00	0.20
50050.00	D09	M-007426-	solute carrier family 1 (glial high af	SLC1A2	1191.00	0.17
50050.00	D10	M-011789-	threonyl-tRNA synthetase	TARS	882.00	0.45
50050.00	D11	M-007427-	solute carrier family 1 (glial high af	SLC1A3	540.00	2.41
50050.00	D12	M-031842-	synaptotagmin V	SYT5	930.00	1.18
50050.00	D13	M-007428-	solute carrier family 1 (glutamate/	SLC1A4	1911.00	0.47
50050.00	D14	M-014054-	synaptotagmin IV	SYT4	1050.00	0.48
50050.00	D15	M-007429-	solute carrier family 1 (neutral ami	SLC1A5	1495.00	0.87
50050.00	D16	M-010623-	synaptophysin-like 1	SYPL1	772.00	1.55
50050.00	D17	M-007430-	solute carrier family 1 (high affinit	SLC1A6	1069.00	1.12
50050.00	D18	M-012655-	synaptophysin	SYP	847.00	0.47
50050.00	D19	M-007431-	solute carrier family 1 (glutamate t	SLC1A7	2771.00	0.54
50050.00	D20	M-011787-	synapsin II	SYN2	2225.00	2.74
50050.00	D21	M-003542-	solute carrier family 3 (activators c	SLC3A2	1396.00	0.93
50050.00	D23	M-007582-	solute carrier family 4, anion excha	SLC4A2	2787.00	3.41
50050.00	E02	M-027199-	sal-like 2 (Drosophila)	SALL2	1116.00	0.36
50050.00	E04	M-005150-	scaffold attachment factor B	SAFB	1697.00	1.12
50050.00	E05	M-019822-	peptide YY	PYY	573.00	0.70
50050.00	E06	M-012747-	serum amyloid A4, constitutive	SAA4	1990.00	0.75
50050.00	E07	M-009578-	proteasome (prosome, macropain	PSMC1	619.00	0.81
50050.00	E08	M-016279-	serum amyloid A2	SAA2	1040.00	0.58
50050.00	E09	M-008180-	proteasome (prosome, macropain	PSMC2	824.00	2.06
50050.00	E10	M-012717-	reticulon 2	RTN2	1276.00	1.41
50050.00	E11	M-008738-	proteasome (prosome, macropain	PSMC3	270.00	2.59
50050.00	E12	M-014138-	reticulon 1	RTN1	1252.00	0.24
50050.00	E13	M-009261-	proteasome (prosome, macropain	PSMC4	325.00	1.85
50050.00	E14	M-015055-	rhotekin	RTKN	990.00	0.81
50050.00	E15	M-009484-	proteasome (prosome, macropain	PSMC5	379.00	0.53

50050.00	E16	M-011891-	ribosome binding protein 1 homol	RRBP1	1323.00	0.30
50050.00	E17	M-009570-	proteasome (prosome, macropain	PSMC6	920.00	3.04
50050.00	E18	M-013679-	ribosomal protein S28	RPS28	560.00	0.54
50050.00	E19	M-011363-	proteasome (prosome, macropain	PSMD1	153.00	1.96
50050.00	E20	M-013722-	ribosomal protein S27a	RPS27A	274.00	4.01
50050.00	E21	M-011364-	proteasome (prosome, macropain	PSMD3	466.00	2.15
50050.00	E23	M-013426-	proteasome (prosome, macropain	PSMD9	943.00	6.68
50050.00	F02	M-019171-	synaptonemal complex protein 1	SYCP1	2274.00	0.22
50050.00	F04	M-020864-	synaptobrevin-like 1	SYBL1	1495.00	0.13
50050.00	F05	M-007591-	solute carrier family 5 (inositol tra	SLC5A3	2288.00	0.48
50050.00	F06	M-012498-	vesicle-associated membrane prot	VAMP2	1022.00	2.05
50050.00	F07	M-007592-	solute carrier family 5 (low affinity	SLC5A4	943.00	0.64
50050.00	F08	M-012497-	vesicle-associated membrane prot	VAMP1	1183.00	1.27
50050.00	F09	M-007597-	solute carrier family 6 (neurotrans	SLC6A1	1409.00	0.50
50050.00	F10	M-017456-	surfeit 6	SURF6	1521.00	0.53
50050.00	F11	M-007606-	solute carrier family 6 (neurotrans	SLC6A6	1607.00	0.81
50050.00	F12	M-012324-	surfeit 5	SURF5	453.00	0.22
50050.00	F13	M-007607-	solute carrier family 6 (neurotrans	SLC6A7	1501.00	0.73
50050.00	F14	M-010622-	surfeit 4	SURF4	974.00	0.92
50050.00	F15	M-007609-	solute carrier family 6 (neurotrans	SLC6A9	713.00	0.56
50050.00	F16	M-017469-	surfeit 2	SURF2	951.00	1.79
50050.00	F17	M-007598-	solute carrier family 6 (neurotrans	SLC6A11	1188.00	0.25
50050.00	F18	M-009488-	sulfotransferase family, cytosolic,	SULT2B1	1180.00	1.69
50050.00	F19	M-007599-	solute carrier family 6 (neurotrans	SLC6A12	2717.00	1.80
50050.00	F20	M-009862-	sulfotransferase family, cytosolic,	SULT1C2	2163.00	2.36
50050.00	F21	M-007600-	solute carrier family 6 (neurotrans	SLC6A13	1422.00	5.49
50050.00	F23	M-007610-	solute carrier family 7 (cationic am	SLC7A1	1516.00	0.20
50050.00	G02	M-013675-	ribosomal protein S26	RPS26	339.00	2.06
50050.00	G04	M-013629-	ribosomal protein S25	RPS25	707.00	0.42
50050.00	G05	M-011366-	proteasome (prosome, macropain	PSMD10	1819.00	0.16
50050.00	G06	M-011155-	ribosomal protein S24	RPS24	309.00	1.94
50050.00	G07	M-011367-	proteasome (prosome, macropain	PSMD11	890.00	0.45
50050.00	G08	M-011154-	ribosomal protein S23	RPS23	187.00	2.67
50050.00	G09	M-011368-	proteasome (prosome, macropain	PSMD12	628.00	1.43
50050.00	G10	M-011137-	ribosomal protein S20	RPS20	469.00	1.28
50050.00	G11	M-011369-	proteasome (prosome, macropain	PSMD13	962.00	1.14
50050.00	G12	M-011890-	ribosomal protein S18	RPS18	429.00	2.33
50050.00	G13	M-011370-	proteasome (prosome, macropain	PSME2	980.00	2.55
50050.00	G14	M-011152-	ribosomal protein S17	RPS17	249.00	0.40
50050.00	G15	M-010619-	prostaglandin F2 receptor negativ	PTGFRN	1152.00	1.74
50050.00	G16	M-013542-	ribosomal protein S15a	RPS15A	226.00	2.65
50050.00	G17	M-017765-	pentraxin-related gene, rapidly ind	PTX3	1238.00	0.48
50050.00	G18	M-011151-	ribosomal protein S15	RPS15	329.00	2.13
50050.00	G19	M-013704-	purine-rich element binding protei	PURB	2639.00	4.05
50050.00	G20	M-013532-	ribosomal protein S14	RPS14	646.00	2.32
50050.00	G21	M-019703-	parvalbumin	PVALB	1488.00	4.10
50050.00	G23	M-019927-	PWP2 periodic tryptophan protein	PWP2	988.00	3.64

50050.00	H02	M-009054-	sulfotransferase family, cytosolic,	SULT1A3	2147.00	1.12
50050.00	H04	M-019626-	syntaxin binding protein 3	STXBP3	872.00	0.23
50050.00	H05	M-004297-	solute carrier family 7 (cationic am	SLC7A2	699.00	2.15
50050.00	H06	M-019713-	syntaxin binding protein 2	STXBP2	826.00	0.85
50050.00	H07	M-007621-	solute carrier family 8 (sodium-cal	SLC8A2	971.00	6.28
50050.00	H08	M-019571-	syntaxin binding protein 1	STXBP1	1277.00	1.02
50050.00	H09	M-007615-	solute carrier family 7 (cationic am	SLC7A4	1018.00	0.20
50050.00	H10	M-017768-	syntaxin 5	STX5	635.00	0.47
50050.00	H11	M-007622-	solute carrier family 8 (sodium-cal	SLC8A3	1414.00	0.78
50050.00	H12	M-016256-	syntaxin 4	STX4	1071.00	0.19
50050.00	H13	M-005277-	solute carrier family 9 (sodium/hy	SLC9A1	923.00	0.22
50050.00	H14	M-015401-	syntaxin 3	STX3	619.00	1.45
50050.00	H15	M-007623-	solute carrier family 9 (sodium/hy	SLC9A2	1136.00	1.23
50050.00	H16	M-019572-	striatin, calmodulin binding protei	STRN	953.00	1.47
50050.00	H17	M-007624-	solute carrier family 9 (sodium/hy	SLC9A3	1256.00	1.04
50050.00	H18	M-009119-	sulfotransferase family, cytosolic,	SULT1A2	2336.00	3.08
50050.00	H19	M-007625-	solute carrier family 9 (sodium/hy	SLC9A5	1747.00	0.80
50050.00	H20	M-011785-	stromal interaction molecule 1	STIM1	1901.00	2.63
50050.00	H21	M-007385-	solute carrier family 12 (potassium	SLC12A4	1205.00	0.00
50050.00	H23	M-007391-	solute carrier family 13 (sodium/s	SLC13A1	2293.00	2.40
50050.00	I02	M-011150-	ribosomal protein S13	RPS13	214.00	0.93
50050.00	I04	M-011149-	ribosomal protein S12	RPS12	709.00	1.69
50050.00	I05	M-009114-	phosphate cytidylyltransferase 2,	PCYT2	2330.00	0.34
50050.00	I06	M-013569-	ribosomal protein S11	RPS11	523.00	0.96
50050.00	I07	M-009587-	phosphorylase, glycogen; brain	PYGB	1533.00	0.65
50050.00	I08	M-011136-	ribosomal protein S10	RPS10	387.00	1.81
50050.00	I09	M-010105-	pregnancy-zone protein	PZP	1734.00	0.40
50050.00	I10	M-011140-	ribosomal protein S8	RPS8	332.00	0.90
50050.00	I11	M-008910-	glutaminyl-tRNA synthetase	QARS	2882.00	0.73
50050.00	I12	M-013700-	ribosomal protein S7	RPS7	246.00	0.81
50050.00	I13	M-009820-	arginyl-tRNA synthetase	RARS	1315.00	0.15
50050.00	I14	M-003024-	ribosomal protein S6	RPS6	240.00	0.83
50050.00	I15	M-018969-	RNA binding motif (RNP1, RRM) pr	RBM3	1771.00	0.23
50050.00	I16	M-013158-	ribosomal protein S4, Y-linked 1	RPS4Y1	1695.00	0.24
50050.00	I17	M-019588-	RNA binding motif protein 4	RBM4	1124.00	1.33
50050.00	I18	M-013603-	ribosomal protein S3A	RPS3A	519.00	0.77
50050.00	I19	M-003300-	retinol binding protein 1, cellular	RBP1	2728.00	3.04
50050.00	I20	M-011765-	ribophorin II	RPN2	1264.00	2.93
50050.00	I21	M-009825-	retinol binding protein 2, cellular	RBP2	2864.00	5.62
50050.00	I23	M-011379-	reticulocalbin 1, EF-hand calcium b	RCN1	676.00	3.99
50050.00	J02	M-006477-	stanniocalcin 1	STC1	1522.00	0.13
50050.00	J04	M-011894-	staufen, RNA binding protein, hom	STAU1	839.00	2.15
50050.00	J05	M-007398-	solute carrier family 15 (oligopepti	SLC15A1	776.00	0.39
50050.00	J06	M-017338-	synovial sarcoma, X breakpoint 5	SSX5	1260.00	0.56
50050.00	J07	M-007399-	solute carrier family 15 (H+/peptid	SLC15A2	2453.00	0.24
50050.00	J08	M-017245-	synovial sarcoma, X breakpoint 2	SSX2	1059.00	0.19
50050.00	J09	M-007405-	solute carrier family 16, member 2	SLC16A2	1768.00	1.36

50050.00	J10	M-015325-	sperm specific antigen 2	SSFA2	1164.00	1.80
50050.00	J11	M-007411-	solute carrier family 17 (sodium ph	SLC17A1	802.00	0.50
50050.00	J12	M-021365-	single-stranded DNA binding prote	SSBP1	596.00	0.34
50050.00	J13	M-007534-	solute carrier family 34 (sodium ph	SLC34A1	1057.00	0.47
50050.00	J14	M-006877-	Sjogren syndrome antigen B (autoa	SSB	1874.00	8.16
50050.00	J15	M-007419-	solute carrier family 18 (vesicular r	SLC18A1	1443.00	2.43
50050.00	J16	M-017733-	TROVE domain family, member 2	TROVE2	885.00	3.16
50050.00	J17	M-007420-	solute carrier family 18 (vesicular r	SLC18A2	1292.00	1.86
50050.00	J18	M-005121-	signal recognition particle 68kDa	SRP68	631.00	0.79
50050.00	J19	M-007421-	solute carrier family 18 (vesicular a	SLC18A3	2990.00	4.65
50050.00	J20	M-005122-	signal recognition particle 54kDa	SRP54	2708.00	2.29
50050.00	J21	M-007422-	solute carrier family 19 (folate tra	SLC19A1	2560.00	6.76
50050.00	J23	M-007432-	solute carrier family 20 (phosphate	SLC20A1	1804.00	9.15
50050.00	K02	M-018903-	ribophorin I	RPN1	1633.00	2.39
50050.00	K04	M-011382-	mitochondrial ribosomal protein S	MRPS12	1971.00	2.99
50050.00	K05	M-011380-	reticulocalbin 2, EF-hand calcium b	RCN2	2056.00	0.34
50050.00	K06	M-017517-	mitochondrial ribosomal protein L	MRPL12	1664.00	0.18
50050.00	K07	M-019070-	regenerating islet-derived 1 alpha	REG1A	1041.00	0.67
50050.00	K08	M-004314-	ribosomal protein, large, P2	RPLP2	530.00	1.70
50050.00	K09	M-012297-	regenerating islet-derived 1 beta (	REG1B	1905.00	0.63
50050.00	K10	M-011135-	ribosomal protein, large, P1	RPLP1	497.00	0.60
50050.00	K11	M-019086-	replication factor C (activator 1) 3,	RFC3	1242.00	1.53
50050.00	K12	M-010864-	ribosomal protein, large, P0	RPLP0	297.00	0.67
50050.00	K13	M-009773-	replication factor C (activator 1) 5,	RFC5	778.00	0.51
50050.00	K14	M-013480-	ribosomal protein L36a	RPL36A	1380.00	2.17
50050.00	K15	M-006553-	ret finger protein-like 1	RFPL1	1323.00	3.02
50050.00	K16	M-011148-	ribosomal protein L39	RPL39	1074.00	0.56
50050.00	K17	M-008472-	regulator of G-protein signalling 1	RGS10	2018.00	1.39
50050.00	K18	M-011133-	ribosomal protein L38	RPL38	602.00	0.33
50050.00	K19	M-010340-	regulator of G-protein signalling 1	RGS13	1188.00	0.17
50050.00	K20	M-013522-	ribosomal protein L36a-like	RPL36AL	1171.00	2.05
50050.00	K21	M-015643-	ribonuclease, RNase A family, 1 (p	RNASE1	1507.00	2.26
50050.00	K23	M-012651-	ribonuclease, RNase A family, 2 (li	RNASE2	768.00	1.30
50050.00	L02	M-019729-	signal recognition particle 19kDa	SRP19	2297.00	1.52
50050.00	L04	M-017767-	signal recognition particle 14kDa (	SRP14	1861.00	1.45
50050.00	L05	M-007433-	solute carrier family 20 (phosphate	SLC20A2	1999.00	0.75
50050.00	L06	M-019731-	signal recognition particle 9kDa	SRP9	2280.00	0.79
50050.00	L07	M-007438-	solute carrier organic anion transp	SLCO2A1	2419.00	1.36
50050.00	L08	M-019727-	sorcin	SRI	1737.00	2.30
50050.00	L09	M-007443-	solute carrier family 22 (organic ca	SLC22A1	3355.00	1.25
50050.00	L10	M-012770-	spectrin, beta, non-erythrocytic 2	SPTBN2	1980.00	0.25
50050.00	L11	M-007454-	solute carrier family 22 (extraneur	SLC22A3	667.00	0.90
50050.00	L12	M-018149-	spectrin, beta, non-erythrocytic 1	SPTBN1	548.00	1.28
50050.00	L13	M-007453-	solute carrier family 22 (organic ca	SLC22A2	996.00	1.41
50050.00	L14	M-009933-	spectrin, alpha, non-erythrocytic 1	SPTAN1	1681.00	1.61
50050.00	L15	M-007455-	solute carrier family 22 (organic ca	SLC22A4	1965.00	3.16
50050.00	L16	M-019976-	small proline-rich protein 3	SPRR3	1081.00	1.94

50050.00	L17	M-019581-	sarcolipin	SLN	2532.00	1.03
50050.00	L18	M-019718-	small proline-rich protein 2B	SPRR2B	3475.00	6.36
50050.00	L19	M-006677-	sphingomyelin phosphodiesterase	SMPD2	1988.00	0.50
50050.00	L20	M-020096-	small proline-rich protein 2A	SPRR2A	4763.00	7.33
50050.00	L21	M-019730-	SMT3 suppressor of mif two 3 hon	SUMO3	2239.00	1.38
50050.00	L23	M-017521-	sialic acid binding Ig-like lectin 1, si	SIGLEC1	1446.00	3.25
50050.00	M02	M-013543-	ribosomal protein L35a	RPL35A	620.00	0.97
50050.00	M04	M-013545-	ribosomal protein L34	RPL34	585.00	1.71
50050.00	M05	M-012652-	ribonuclease, RNase A family, 3 (e	RNASE3	1864.00	3.54
50050.00	M06	M-013587-	ribosomal protein L31	RPL31	524.00	1.53
50050.00	M07	M-021381-	ribonuclease, RNase A family, 4	RNASE4	1887.00	2.38
50050.00	M08	M-012979-	ribosomal protein L29	RPL29	2171.00	2.67
50050.00	M09	M-017075-	ribonuclease, RNase A family, k6	RNASE6	1925.00	0.83
50050.00	M10	M-011145-	ribosomal protein L28	RPL28	1220.00	1.15
50050.00	M11	M-006556-	ring finger protein 2	RNF2	2147.00	5.87
50050.00	M12	M-011159-	ribosomal protein L27a	RPL27A	363.00	6.34
50050.00	M13	M-006558-	ring finger protein 5	RNF5	1003.00	4.29
50050.00	M14	M-013604-	ribosomal protein L30	RPL30	701.00	5.71
50050.00	M15	M-023273-	roundabout, axon guidance recept	ROBO2	2069.00	1.06
50050.00	M16	M-012859-	ribosomal protein L27	RPL27	529.00	1.13
50050.00	M17	M-031918-	retinitis pigmentosa 9 (autosomal	RP9	996.00	4.92
50050.00	M18	M-011132-	ribosomal protein L26	RPL26	758.00	2.24
50050.00	M19	M-015749-	replication protein A1, 70kDa	RPA1	610.00	3.44
50050.00	M20	M-011144-	ribosomal protein L24	RPL24	826.00	2.66
50050.00	M21	M-017058-	replication protein A2, 32kDa	RPA2	816.00	3.31
50050.00	M23	M-003322-	replication protein A3, 14kDa	RPA3	1449.00	8.01
50050.00	N02	M-019725-	small proline-rich protein 1B (corni	SPRR1B	716.00	0.42
50050.00	N04	M-020095-	small proline-rich protein 1A	SPRR1A	432.00	0.69
50050.00	N05	M-011394-	synaptosomal-associated protein,	SNAP25	1869.00	1.34
50050.00	N06	M-012558-	secreted phosphoprotein 1 (osteo	SPP1	2536.00	2.01
50050.00	N07	M-011395-	synuclein, beta	SNCB	2061.00	1.16
50050.00	N08	M-013724-	sparc/osteonectin, cwcv and kazal-	SPOCK1	1811.00	2.87
50050.00	N09	M-019580-	small nuclear RNA activating comp	SNAPC4	1434.00	2.79
50050.00	N10	M-019720-	secreted phosphoprotein 2, 24kDa	SPP2	2753.00	1.71
50050.00	N11	M-011396-	synuclein, gamma (breast cancer-s	SNCG	1362.00	2.20
50050.00	N12	M-004578-	serine peptidase inhibitor, Kunitz t	SPINT1	822.00	2.19
50050.00	N13	M-018811-	small nuclear ribonucleoprotein 7	SNRP70	566.00	1.77
50050.00	N14	M-012759-	serine peptidase inhibitor, Kazal ty	SPINK2	1425.00	3.65
50050.00	N15	M-019435-	small nuclear ribonucleoprotein p	SNRPA	2577.00	1.94
50050.00	N16	M-006039-	spastic paraplegia 7 (pure and com	SPG7	2426.00	1.53
50050.00	N17	M-019577-	small nuclear ribonucleoprotein p	SNRPA1	968.00	2.58
50050.00	N18	M-011397-	sperm associated antigen 4	SPAG4	3662.00	4.59
50050.00	N19	M-017766-	small nuclear ribonucleoprotein p	SNRPB	1127.00	0.71
50050.00	N20	M-017160-	UDP-N-acteylglucosamine pyroph	UAP1	2907.00	5.37
50050.00	N21	M-016910-	small nuclear ribonucleoprotein p	SNRPB2	1261.00	3.49
50050.00	N23	M-019574-	small nuclear ribonucleoprotein p	SNRPC	1014.00	7.79
50050.00	O02	M-013124-	mitochondrial ribosomal protein L	MRPL23	799.00	2.75

50050.00	O04	M-012863-	ribosomal protein L23a	RPL23A	263.00	3.04
50050.00	O05	M-012767-	ribulose-5-phosphate-3-epimerase	RPE	2134.00	0.75
50050.00	O06	M-011143-	ribosomal protein L22	RPL22	1841.00	1.90
50050.00	O07	M-012975-	ribosomal protein L3	RPL3	747.00	2.81
50050.00	O08	M-012910-	ribosomal protein L21	RPL21	794.00	0.50
50050.00	O09	M-012009-	ribosomal protein L3-like	RPL3L	1098.00	0.55
50050.00	O10	M-010865-	ribosomal protein L19	RPL19	623.00	0.32
50050.00	O11	M-008956-	ribosomal protein L4	RPL4	441.00	1.36
50050.00	O12	M-011158-	ribosomal protein L18a	RPL18A	404.00	7.18
50050.00	O13	M-012955-	ribosomal protein L6	RPL6	230.00	1.74
50050.00	O14	M-011142-	ribosomal protein L18	RPL18	412.00	4.85
50050.00	O15	M-013727-	ribosomal protein L7	RPL7	624.00	1.12
50050.00	O16	M-013633-	ribosomal protein L17	RPL17	498.00	1.20
50050.00	O17	M-011134-	ribosomal protein L7a	RPL7A	902.00	3.44
50050.00	O18	M-013718-	ribosomal protein L15	RPL15	1619.00	0.43
50050.00	O19	M-013721-	ribosomal protein L8	RPL8	654.00	2.14
50050.00	O20	M-013714-	ribosomal protein L13	RPL13	1064.00	11.47
50050.00	O21	M-011139-	ribosomal protein L9	RPL9	551.00	1.09
50050.00	O23	M-011141-	ribosomal protein L12	RPL12	218.00	2.75
50050.00	P02	M-017276-	SRY (sex determining region Y)-box	SOX12	637.00	1.57
50050.00	P04	M-017377-	SRY (sex determining region Y)-box	SOX11	1283.00	3.98
50050.00	P05	M-012353-	small nuclear ribonucleoprotein D1	SNRPD1	326.00	2.76
50050.00	P06	M-008203-	SRY (sex determining region Y)-box	SOX5	699.00	1.72
50050.00	P07	M-013617-	small nuclear ribonucleoprotein D2	SNRPD2	628.00	1.75
50050.00	P08	M-012194-	SRY (sex determining region Y)-box	SOX1	1077.00	3.06
50050.00	P09	M-019085-	small nuclear ribonucleoprotein D3	SNRPD3	625.00	3.68
50050.00	P10	M-006037-	small optic lobes homolog (Drosop	SOLH	1260.00	2.94
50050.00	P11	M-019719-	small nuclear ribonucleoprotein po	SNRPE	1376.00	4.58
50050.00	P12	M-012322-	syntrophin, beta 2 (dystrophin-ass	SNTB2	1053.00	2.18
50050.00	P13	M-020039-	regenerating islet-derived-like, par	REGL	808.00	7.05
50050.00	P14	M-017520-	sorting nexin 2	SNX2	1554.00	4.38
50050.00	P15	M-011160-	ribosomal protein L41	RPL41	1298.00	3.39
50050.00	P16	M-017518-	sorting nexin 1	SNX1	1601.00	1.94
50050.00	P17	M-013076-	secretin	SCT	1564.00	1.66
50050.00	P18	M-013125-	syntrophin, beta 1 (dystrophin-ass	SNTB1	3876.00	3.87
50050.00	P19	M-016450-	SMT3 suppressor of mif two 3 hom	SUMO2	2441.00	1.23
50050.00	P20	M-011777-	syntrophin, alpha 1 (dystrophin-as	SNTA1	886.00	3.84
50050.00	P21	M-032463-	gametogenetin binding protein 1	GGNBP1	861.00	2.90
50050.00	P23	M-032420-	FSHD region gene 2 protein	FRG2	563.00	2.84
					1111.00	1.36
				MAD3		
				MADc		
50050.00	C22				2549.00	13.495
50050.00	D22				2788.00	17.001
50050.00	E22				1282.00	12.637
50050.00	F22				1843.00	11.72
				mn	2115.50	13.71

					sd	685.36	2.31
50050.00	G22	550.00		7.2727			
50050.00	H22					538.00	1.3011
50050.00	I22					1058.00	2.6465
50050.00	J22					2124.00	3.3898
					mn	1240.00	2.45
					sd	808.51	1.06
					3psSD		6.93
					3ngSD		3.18
					SumSD		10.10
					DiffMn		11.27
					SmovrDiff		0.90
					1minus		0.10

50050.00	G03	M-003290-	polo-like kinase 1 (Drosophila)	PLK1 SMAR	78.00
50050.00	H03	M-003290-	polo-like kinase 1 (Drosophila)	PLK1 SMAR	68.00
50050.00	I03	D-001206-	siControl non-targeting siRNA #2		1129.00
50050.00	J03	D-001206-	siControl non-targeting siRNA #2		1304.00
50050.00	K03	D-001600-	siGLO RISC-free siRNA		5004.00
50050.00	L03	D-001600-	siGLO RISC-free siRNA		4196.00

Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev
0.61	-0.48	503.00	2.19	0.67	0.51	744.00	4.03	1.90
0.88	-0.69	1910.00	1.88	0.36	0.28	830.00	0.48	1.65
0.97	-0.77	2138.00	2.25	0.73	0.56	1536.00	0.46	1.67
0.73	-0.58	1905.00	2.20	0.68	0.52	1114.00	1.26	0.87
1.04	-0.82	2318.00	2.11	0.59	0.45	1655.00	1.27	0.86
0.03	-0.02	2393.00	2.01	0.49	0.37	1586.00	1.70	0.43
0.48	-0.38	1450.00	2.07	0.55	0.42	1287.00	1.86	0.27
1.99	1.57	1673.00	1.08	0.44	-0.34	933.00	6.00	3.87
1.09	-0.86	2074.00	2.80	1.28	0.98	1461.00	6.37	4.24
0.18	-0.14	1332.00	1.35	0.17	-0.13	527.00	2.09	0.04
0.48	-0.38	1247.00	2.57	1.05	0.80	856.00	0.70	1.43
0.93	-0.73	1644.00	0.85	0.67	-0.52	659.00	1.21	0.92
1.72	1.36	2529.00	3.20	1.68	1.29	1479.00	3.99	1.86
1.60	1.27	1316.00	0.84	0.68	-0.53	761.00	1.97	0.16
0.33	-0.26	1258.00	2.94	1.42	1.09	1423.00	4.64	2.51
0.20	0.15	2308.00	0.82	0.70	-0.54	1012.00	1.78	0.35
0.57	0.45	1477.00	0.54	0.98	-0.75	774.00	1.68	0.45
3.90	3.07	2206.00	6.39	4.87	3.74	2748.00	8.88	6.75
2.17	1.71	2663.00	2.59	1.07	0.82	1867.00	1.66	0.47
2.50	1.97	862.00	0.93	0.59	-0.46	644.00	4.81	2.68
1.02	-0.80	1899.00	0.68	0.84	-0.64	1527.00	0.98	1.15
0.23	-0.18	3213.00	2.99	1.47	1.13	2388.00	2.14	0.01
0.95	0.75	2227.00	1.89	0.37	0.28	1791.00	2.85	0.72
0.57	-0.45	2431.00	0.25	1.27	-0.98	2388.00	0.84	1.29
2.05	1.62	1698.00	1.12	0.40	-0.31	1474.00	1.09	1.04
0.61	0.48	1598.00	0.13	1.39	-1.07	672.00	1.04	1.09
3.18	2.51	2725.00	0.55	0.97	-0.75	1252.00	0.48	1.65
0.65	-0.51	3033.00	1.22	0.30	-0.23	1668.00	2.46	0.33
0.65	-0.51	1541.00	2.92	1.40	1.07	1552.00	2.13	0.00
0.51	-0.40	1387.00	0.58	0.94	-0.73	1243.00	1.37	0.76
0.72	-0.57	1258.00	0.24	1.28	-0.99	1164.00	2.15	0.02
0.15	0.12	1956.00	1.38	0.14	-0.11	1020.00	0.69	1.44
0.55	-0.43	1392.00	0.72	0.80	-0.62	838.00	1.43	0.70
0.38	0.30	1929.00	1.87	0.35	0.26	668.00	9.43	7.30
1.44	1.13	3453.00	2.72	1.20	0.92	2085.00	2.78	0.65
0.07	-0.06	1863.00	2.90	1.38	1.06	1417.00	4.52	2.39
0.88	-0.70	3301.00	1.70	0.18	0.13	2216.00	3.52	1.39
0.65	0.51	1353.00	0.15	1.37	-1.06	2059.00	4.32	2.19
0.09	-0.07	1221.00	0.82	0.70	-0.54	1007.00	2.88	0.75
1.17	-0.92	1305.00	1.23	0.29	-0.23	1736.00	4.21	2.08
1.12	-0.88	1311.00	0.46	1.06	-0.82	1964.00	1.07	1.06
0.53	-0.42	1186.00	1.52	0.00	0.00	827.00	3.39	1.26
0.48	0.38	1672.00	0.90	0.62	-0.48	1654.00	2.78	0.65
0.80	-0.63	2034.00	3.59	2.07	1.59	1914.00	1.57	0.56
1.06	-0.83	1701.00	2.06	0.54	0.41	1567.00	3.70	1.57
1.27	-1.00	3539.00	2.09	0.57	0.44	1860.00	1.29	0.84

1.36	-1.07	937.00	0.64	0.88	-0.68	295.00	7.12	**4.99**
0.33	0.26	3403.00	1.18	0.34	-0.27	1483.00	3.91	1.78
0.93	-0.74	819.00	4.27	2.75	2.11	816.00	4.17	2.04
0.40	-0.31	1382.00	1.16	0.36	-0.28	1438.00	1.60	0.53
0.66	-0.52	850.00	0.82	0.70	-0.54	902.00	4.55	2.42
0.73	0.58	1880.00	2.02	0.50	0.38	1137.00	2.81	0.68
0.20	-0.16	1939.00	0.93	0.59	-0.46	1693.00	5.55	3.42
0.21	0.17	2722.00	4.70	3.18	2.44	2181.00	12.33	**10.20**
0.08	0.06	1167.00	0.69	0.83	-0.64	1011.00	5.93	3.80
0.91	-0.71	1598.00	0.13	1.39	-1.07	1868.00	6.10	3.97
1.36	-1.07	1052.00	1.33	0.19	-0.15	816.00	8.33	**6.20**
0.47	0.37	547.00	1.10	0.42	-0.33	568.00	3.52	1.39
0.90	-0.71	2015.00	2.83	1.31	1.00	1962.00	3.77	1.64
0.97	-0.76	725.00	0.55	0.97	-0.75	1178.00	4.24	2.11
0.04	-0.03	818.00	3.42	1.90	1.46	1156.00	2.42	0.29
1.36	-1.07	1314.00	2.36	0.84	0.64	1194.00	2.76	0.63
0.01	0.01	1153.00	1.47	0.05	-0.04	1117.00	4.12	1.99
1.36	-1.07	2243.00	2.14	0.62	0.47	1460.00	2.26	0.13
0.84	-0.66	2804.00	2.71	1.19	0.91	1824.00	2.30	0.17
1.16	-0.91	2487.00	4.38	2.86	2.20	1913.00	3.29	1.16
1.19	-0.94	2420.00	6.24	4.72	3.62	2441.00	5.24	3.11
0.91	-0.71	2014.00	4.32	2.80	2.15	1084.00	7.38	**5.25**
1.05	0.83	1101.00	5.27	3.75	2.88	1067.00	10.12	**7.99**
0.18	-0.14	823.00	1.58	0.06	0.04	1637.00	5.13	3.00
0.89	-0.70	1728.00	3.01	1.49	1.14	1502.00	4.06	1.93
0.88	-0.70	1324.00	1.59	0.07	0.05	791.00	9.23	**7.10**
0.49	-0.39	2640.00	0.57	0.95	-0.73	1355.00	3.76	1.63
0.19	0.15	1801.00	5.55	4.03	3.10	1435.00	6.97	**4.84**
0.24	-0.19	1717.00	2.33	0.81	0.62	914.00	7.22	**5.09**
0.89	-0.70	1396.00	2.94	1.42	1.09	775.00	6.45	**4.32**
0.82	-0.64	3082.00	2.86	1.34	1.02	2474.00	5.74	3.61
1.38	1.09	2122.00	1.46	0.06	-0.05	1656.00	5.31	3.18
0.43	-0.34	1629.00	1.72	0.20	0.15	1658.00	4.34	2.21
2.05	1.62	1219.00	2.21	0.69	0.53	1473.00	2.10	0.03
1.00	-0.79	1403.00	1.57	0.05	0.03	1667.00	1.56	0.57
0.24	-0.19	1538.00	0.98	0.54	-0.42	461.00	3.47	1.34
0.66	-0.52	976.00	3.59	2.07	1.59	411.00	4.62	2.49
0.61	-0.48	2149.00	0.88	0.64	-0.49	1028.00	1.85	0.28
0.55	-0.43	1261.00	1.74	0.22	0.17	614.00	4.07	1.94
0.78	-0.62	2009.00	3.58	2.06	1.58	872.00	6.54	**4.41**
0.70	0.56	1354.00	2.29	0.77	0.59	593.00	3.20	1.07
0.05	0.04	1610.00	0.99	0.53	-0.41	992.00	3.23	1.10
1.23	0.97	523.00	4.02	2.50	1.92	297.00	3.03	0.90
1.12	-0.88	1081.00	2.13	0.61	0.46	1183.00	7.86	**5.73**
0.49	0.38	120.00	5.00	3.48	2.67	233.00	9.44	**7.31**
0.55	-0.43	1244.00	5.39	3.87	2.97	1430.00	0.84	1.29
0.83	-0.66	425.00	5.65	4.13	3.17	497.00	8.25	**6.12**

1.06	-0.83	1744.00	4.87	3.35	2.58	1848.00	8.50	**6.37**
1.68	1.33	959.00	0.63	0.89	-0.69	625.00	4.64	2.51
0.82	-0.65	849.00	2.36	0.84	0.64	652.00	6.75	**4.62**
0.60	0.47	194.00	8.25	6.73	5.17	113.00	20.35	**18.22**
2.65	2.09	360.00	5.83	4.31	3.31	411.00	14.36	**12.23**
0.79	0.62	461.00	8.24	6.72	5.16	454.00	9.91	**7.78**
5.32	4.20	765.00	3.14	1.62	1.24	1108.00	1.53	0.60
1.14	-0.90	1596.00	0.13	1.39	-1.07	2052.00	0.97	1.16
1.23	-0.97	1728.00	0.17	1.35	-1.04	1775.00	1.97	0.16
0.88	-0.69	2201.00	0.68	0.84	-0.65	2539.00	1.69	0.44
0.69	0.55	1077.00	0.09	1.43	-1.10	1099.00	1.64	0.49
0.72	-0.57	1778.00	2.81	1.29	0.99	1008.00	3.47	1.34
0.09	-0.07	1233.00	3.00	1.48	1.14	945.00	2.75	0.62
0.86	-0.68	1321.00	1.36	0.16	-0.12	922.00	1.84	0.29
0.83	-0.66	1437.00	2.23	0.71	0.54	1150.00	5.83	3.70
0.55	-0.43	1812.00	1.60	0.08	0.06	1688.00	0.41	1.72
1.14	-0.90	304.00	5.26	3.74	2.87	336.00	8.63	**6.50**
0.63	-0.49	1320.00	2.27	0.75	0.58	1373.00	2.62	0.49
0.44	-0.34	1345.00	0.59	0.93	-0.71	951.00	2.21	0.08
0.80	-0.63	802.00	2.37	0.85	0.65	882.00	7.48	**5.35**
0.43	0.34	1080.00	3.06	1.54	1.18	1134.00	4.06	1.93
1.11	-0.87	1296.00	4.78	3.26	2.51	722.00	2.49	0.36
0.33	0.26	3019.00	3.31	1.79	1.38	1333.00	2.55	0.42
0.44	0.35	2245.00	6.41	4.89	3.76	2131.00	3.10	0.97
1.00	0.79	1595.00	5.27	3.75	2.88	1230.00	9.35	**7.22**
4.13	3.25	1977.00	14.32	12.80	9.83	1389.00	7.34	**5.21**
1.16	-0.92	1206.00	4.89	3.37	2.59	2077.00	6.93	**4.80**
0.70	0.56	284.00	1.76	0.24	0.18	408.00	1.23	0.90
0.94	-0.74	687.00	3.06	1.54	1.18	635.00	0.79	1.34
1.20	-0.94	1905.00	0.31	1.21	-0.93	2052.00	1.80	0.33
0.58	0.46	250.00	4.00	2.48	1.90	330.00	1.52	0.61
0.91	-0.72	1137.00	1.67	0.15	0.11	1095.00	0.37	1.76
1.31	1.04	272.00	3.68	2.16	1.66	263.00	3.04	0.91
0.07	0.06	1079.00	2.41	0.89	0.68	789.00	0.51	1.62
0.08	-0.06	612.00	7.68	6.16	4.73	360.00	2.78	0.65
0.22	-0.17	1285.00	2.41	0.89	0.68	1177.00	0.68	1.45
0.97	0.77	175.00	1.71	0.19	0.15	244.00	2.46	0.33
1.19	0.94	1002.00	0.60	0.92	-0.71	975.00	0.72	1.41
0.96	-0.76	616.00	0.32	1.20	-0.92	392.00	2.30	0.17
0.38	0.30	1384.00	0.29	1.23	-0.95	1345.00	0.97	1.16
1.29	1.02	127.00	3.94	2.42	1.86	121.00	4.13	2.00
0.88	-0.69	1919.00	0.78	0.74	-0.57	1043.00	0.67	1.46
0.77	0.61	510.00	1.76	0.24	0.19	560.00	0.00	2.13
2.69	2.13	1248.00	0.64	0.88	-0.68	1186.00	0.84	1.29
0.96	0.76	496.00	1.21	0.31	-0.24	747.00	0.27	1.86
2.74	2.16	2118.00	4.25	2.73	2.10	2259.00	1.42	0.71
2.28	1.80	1435.00	1.67	0.15	0.12	1652.00	0.24	1.89

0.24	-0.19	2853.00	0.67	0.85	-0.66	2873.00	1.32	0.81
1.13	-0.89	1116.00	1.97	0.45	0.34	982.00	3.16	1.03
0.79	0.62	1358.00	1.55	0.03	0.02	703.00	2.56	0.43
0.51	-0.40	958.00	1.57	0.05	0.03	962.00	1.56	0.57
4.92	3.88	797.00	0.50	1.02	-0.78	734.00	2.18	0.05
0.34	-0.27	1368.00	1.75	0.23	0.18	1311.00	0.15	1.98
1.16	-0.92	2022.00	2.97	1.45	1.11	1964.00	8.10	**5.97**
0.89	-0.70	1086.00	0.64	0.88	-0.67	990.00	0.91	1.22
0.58	-0.46	1293.00	3.02	1.50	1.15	1484.00	1.68	0.45
1.17	-0.92	724.00	1.38	0.14	-0.11	1404.00	4.20	2.07
1.14	-0.90	665.00	0.90	0.62	-0.48	1036.00	4.83	2.70
0.09	0.07	843.00	0.95	0.57	-0.44	766.00	3.79	1.66
0.13	-0.10	1075.00	2.05	0.53	0.40	1262.00	3.17	1.04
0.11	0.09	971.00	0.10	1.42	-1.09	1411.00	2.91	0.78
0.33	-0.26	1155.00	1.30	0.22	-0.17	997.00	5.42	3.29
1.72	1.36	2421.00	0.66	0.86	-0.66	3623.00	5.41	3.28
0.56	-0.44	1216.00	0.49	1.03	-0.79	1666.00	2.04	0.09
1.27	1.00	1822.00	0.82	0.70	-0.54	1475.00	4.81	2.68
1.36	-1.07	1234.00	1.78	0.26	0.20	2254.00	2.04	0.09
1.04	0.82	2411.00	0.58	0.94	-0.72	3265.00	6.77	**4.64**
0.43	-0.33	382.00	3.66	2.14	1.65	401.00	0.25	1.88
0.33	0.26	563.00	1.42	0.10	-0.08	815.00	1.47	0.66
1.02	-0.80	2519.00	0.99	0.53	-0.41	2670.00	1.20	0.93
0.40	-0.32	554.00	0.54	0.98	-0.75	688.00	0.58	1.55
0.71	-0.56	1431.00	2.87	1.35	1.03	2388.00	4.61	2.48
0.45	0.35	236.00	5.51	3.99	3.06	406.00	1.72	0.41
0.96	-0.75	1247.00	0.40	1.12	-0.86	1485.00	2.29	0.16
0.46	-0.36	390.00	2.56	1.04	0.80	254.00	0.39	1.74
0.63	-0.50	2061.00	1.70	0.18	0.13	2900.00	2.79	0.66
0.55	-0.43	241.00	1.66	0.14	0.11	259.00	3.86	1.73
1.21	-0.95	346.00	0.87	0.65	-0.50	1745.00	0.74	1.39
0.53	-0.41	398.00	0.25	1.27	-0.98	296.00	1.69	0.44
1.13	-0.89	2685.00	1.56	0.04	0.03	1952.00	1.38	0.75
1.12	-0.89	1060.00	1.32	0.20	-0.16	1658.00	2.29	0.16
0.03	-0.02	862.00	1.51	0.01	-0.01	828.00	1.69	0.44
0.59	-0.46	285.00	0.70	0.82	-0.63	260.00	5.77	3.64
1.68	1.33	2106.00	2.23	0.71	0.54	2226.00	2.83	0.70
1.57	1.24	990.00	2.83	1.31	1.00	775.00	1.55	0.58
4.26	3.36	2616.00	1.99	0.47	0.36	2602.00	5.03	2.90
2.63	2.08	1171.00	0.26	1.26	-0.97	905.00	0.33	1.80
1.23	-0.97	1463.00	0.96	0.56	-0.43	1341.00	1.79	0.34
0.79	0.62	1224.00	2.04	0.52	0.40	1287.00	4.58	2.45
0.97	-0.77	518.00	0.77	0.75	-0.58	921.00	1.52	0.61
0.80	-0.63	1203.00	2.24	0.72	0.55	1470.00	2.38	0.25
1.12	-0.88	1919.00	0.57	0.95	-0.73	3372.00	4.98	2.85
1.17	-0.92	940.00	1.28	0.24	-0.19	953.00	2.73	0.60
0.00	0.00	1149.00	1.39	0.13	-0.10	2321.00	2.20	0.07

0.44	0.35	2335.00	1.58	0.06	0.05	2564.00	1.48	0.65
0.86	-0.68	1053.00	3.23	1.71	1.31	1235.00	4.21	2.08
1.02	-0.81	836.00	2.51	0.99	0.76	842.00	5.34	3.21
0.89	-0.70	1359.00	0.74	0.78	-0.60	1638.00	3.17	1.04
6.80	5.37	1810.00	4.92	3.40	2.61	2208.00	15.63	**13.50**
1.07	0.84	1711.00	2.81	1.29	0.99	1520.00	2.43	0.30
1.80	1.42	729.00	7.96	6.44	4.94	771.00	1.17	0.96
0.50	0.39	1199.00	2.75	1.23	0.94	2394.00	10.32	**8.19**
0.57	-0.45	673.00	4.01	2.49	1.91	758.00	4.49	2.36
3.29	2.59	1702.00	0.41	1.11	-0.85	3628.00	7.17	**5.04**
0.93	0.73	1588.00	1.20	0.32	-0.25	1874.00	1.81	0.32
5.40	4.26	1971.00	4.11	2.59	1.99	1995.00	6.17	4.04
7.79	6.14	2491.00	8.71	7.19	5.52	2493.00	6.98	**4.85**
1.03	0.81	1668.00	1.74	0.22	0.17	1528.00	9.23	**7.10**
1.63	1.29	1218.00	1.48	0.04	-0.03	2314.00	1.04	1.09
1.02	-0.80	1575.00	0.83	0.69	-0.54	2265.00	4.06	1.93
1.18	-0.93	1399.00	0.50	1.02	-0.79	1884.00	3.29	1.16
0.69	-0.54	773.00	0.52	1.00	-0.77	1015.00	6.50	**4.37**
0.34	0.27	158.00	1.90	0.38	0.29	558.00	3.58	1.45
0.73	-0.58	1412.00	3.19	1.67	1.28	1548.00	5.10	2.97
0.76	-0.60	363.00	1.38	0.14	-0.11	540.00	4.26	2.13
0.17	0.13	499.00	1.20	0.32	-0.25	805.00	1.12	1.01
0.69	-0.54	244.00	2.87	1.35	1.03	217.00	5.99	3.86
0.85	-0.67	963.00	0.73	0.79	-0.61	750.00	2.13	0.00
0.81	0.64	682.00	2.20	0.68	0.52	1129.00	6.29	**4.16**
1.66	1.31	972.00	0.51	1.01	-0.77	1339.00	2.39	0.26
0.80	-0.63	507.00	4.54	3.02	2.32	1221.00	5.81	3.68
0.03	0.02	1051.00	1.33	0.19	-0.15	2327.00	1.25	0.88
1.03	-0.81	658.00	1.82	0.30	0.23	811.00	1.36	0.77
1.19	-0.94	1122.00	0.36	1.16	-0.90	1275.00	0.71	1.42
0.69	0.54	681.00	2.06	0.54	0.41	1270.00	3.23	1.10
0.90	0.71	1279.00	0.23	1.29	-0.99	2722.00	0.51	1.62
0.06	-0.04	1438.00	0.35	1.17	-0.90	1582.00	1.45	0.68
0.16	0.13	3554.00	0.59	0.93	-0.72	3072.00	0.33	1.80
0.09	0.07	2335.00	1.11	0.41	-0.31	2122.00	0.24	1.89
0.61	-0.48	1863.00	0.64	0.88	-0.68	2862.00	0.59	1.54
0.57	-0.45	2168.00	0.42	1.10	-0.85	3122.00	0.61	1.52
0.00	0.00	2379.00	1.81	0.29	0.22	3250.00	1.97	0.16
0.94	0.74	1520.00	0.46	1.06	-0.82	2225.00	0.18	1.95
0.11	-0.08	2758.00	0.36	1.16	-0.89	3703.00	0.14	1.99
1.11	-0.87	2117.00	0.28	1.24	-0.95	2493.00	0.56	1.57
0.46	-0.36	909.00	1.21	0.31	-0.24	1066.00	0.75	1.38
0.08	-0.06	713.00	0.42	1.10	-0.85	699.00	1.43	0.70
0.05	0.04	565.00	1.77	0.25	0.19	1177.00	0.17	1.96
0.25	0.19	982.00	0.71	0.81	-0.62	2746.00	0.62	1.51
1.80	1.42	953.00	1.05	0.47	-0.36	2223.00	0.54	1.59
0.58	0.46	681.00	1.03	0.49	-0.38	1193.00	1.51	0.62

0.33	-0.26	1520.00	0.59	0.93	-0.71	2250.00	2.58	0.45
5.00	3.94	3021.00	2.71	1.19	0.92	4378.00	5.73	3.60
0.86	-0.68	1004.00	0.40	1.12	-0.86	2513.00	0.80	1.33
5.97	4.71	2458.00	2.97	1.45	1.11	5250.00	10.00	**7.87**
0.02	0.02	1866.00	2.41	0.89	0.68	2198.00	1.18	0.95
1.89	1.49	2021.00	0.49	1.03	-0.79	1757.00	0.85	1.28
0.39	-0.31	945.00	1.27	0.25	-0.19	821.00	1.83	0.30
0.35	0.28	417.00	0.72	0.80	-0.62	652.00	1.99	0.14
2.18	1.72	1287.00	0.93	0.59	-0.45	2743.00	1.49	0.64
0.17	0.13	340.00	1.18	0.34	-0.27	1177.00	1.61	0.52
1.02	0.81	1459.00	1.65	0.13	0.09	2912.00	7.66	**5.53**
1.31	1.04	2221.00	0.68	0.84	-0.65	2027.00	1.13	1.00
0.53	-0.42	1465.00	0.34	1.18	-0.91	2677.00	0.71	1.42
0.21	-0.17	969.00	0.72	0.80	-0.61	2319.00	0.52	1.61
4.51	3.56	1745.00	0.46	1.06	-0.82	1926.00	3.53	1.40
4.98	3.93	251.00	1.20	0.32	-0.25	399.00	1.25	0.88
2.93	2.31	1217.00	0.41	1.11	-0.85	989.00	0.40	1.73
4.35	3.43	584.00	0.86	0.66	-0.51	788.00	1.14	0.99
0.30	-0.23	2217.00	0.54	0.98	-0.75	3692.00	1.49	0.64
0.23	-0.18	346.00	0.87	0.65	-0.50	773.00	1.29	0.84
3.56	2.81	932.00	0.64	0.88	-0.68	1496.00	1.60	0.53
0.88	0.70	348.00	4.89	3.37	2.58	549.00	1.28	0.86
2.08	1.64	445.00	0.00	1.52	-1.17	695.00	2.30	0.17
1.30	1.03	663.00	0.15	1.37	-1.05	1078.00	0.74	1.39
1.95	1.54	772.00	0.39	1.13	-0.87	873.00	2.18	0.05
6.65	5.24	885.00	0.56	0.96	-0.74	1292.00	2.09	0.04
0.94	-0.74	469.00	0.85	0.67	-0.51	795.00	0.25	1.88
0.67	-0.52	302.00	0.33	1.19	-0.92	870.00	0.69	1.44
0.02	-0.02	1230.00	0.33	1.19	-0.92	2599.00	2.73	0.60
0.65	0.51	1668.00	1.38	0.14	-0.11	3116.00	3.66	1.53
0.20	-0.15	780.00	1.67	0.15	0.11	1258.00	0.79	1.34
1.51	1.19	1671.00	1.44	0.08	-0.07	3069.00	6.97	**4.84**
1.43	1.13	982.00	1.53	0.01	0.00	1454.00	1.51	0.62
0.35	0.27	1375.00	1.09	0.43	-0.33	2724.00	0.99	1.14
0.84	0.67	1207.00	0.75	0.77	-0.60	2333.00	0.30	1.83
0.83	0.66	1200.00	1.00	0.52	-0.40	1520.00	2.30	0.17
0.41	0.32	431.00	1.16	0.36	-0.28	981.00	1.33	0.80
2.29	1.81	643.00	1.56	0.04	0.03	1549.00	0.65	1.48
0.58	0.46	1608.00	0.12	1.40	-1.07	2455.00	3.30	1.17
0.17	0.13	1218.00	0.66	0.86	-0.67	2016.00	0.74	1.39
1.22	0.97	689.00	0.44	1.08	-0.84	1720.00	1.57	0.56
3.23	2.55	1785.00	1.57	0.05	0.04	2417.00	1.57	0.56
0.65	-0.51	522.00	2.11	0.59	0.45	1496.00	2.34	0.21
4.01	3.16	1628.00	1.47	0.05	-0.04	2804.00	5.35	3.22
2.13	1.68	1025.00	0.29	1.23	-0.95	1739.00	2.07	0.06
6.43	5.07	631.00	0.95	0.57	-0.44	560.00	0.89	1.24
1.39	1.10	688.00	0.73	0.79	-0.61	969.00	1.55	0.58

1.68	1.33	243.00	2.06	0.54	0.41	685.00	0.88	1.25
0.61	-0.48	1192.00	0.42	1.10	-0.85	2526.00	0.44	1.69
0.54	0.43	1489.00	1.28	0.24	-0.19	2928.00	5.16	3.03
1.45	1.15	404.00	0.74	0.78	-0.60	720.00	0.42	1.71
0.86	-0.67	412.00	1.21	0.31	-0.24	785.00	0.51	1.62
0.81	-0.64	894.00	0.34	1.18	-0.91	1367.00	0.66	1.47
1.04	-0.82	326.00	0.31	1.21	-0.93	636.00	0.31	1.82
0.00	0.00	483.00	0.21	1.31	-1.01	473.00	0.85	1.28
5.82	4.59	502.00	1.00	0.52	-0.40	431.00	0.70	1.43
0.38	0.30	151.00	3.31	1.79	1.37	287.00	5.92	3.79
3.49	2.76	203.00	0.99	0.53	-0.41	427.00	1.64	0.49
0.24	-0.19	396.00	0.51	1.01	-0.78	750.00	0.27	1.86
0.16	-0.12	253.00	0.40	1.12	-0.87	543.00	3.68	1.55
2.08	1.64	541.00	0.55	0.97	-0.74	1004.00	1.10	1.03
0.93	-0.73	995.00	0.80	0.72	-0.55	1995.00	1.90	0.23
0.78	0.62	360.00	0.28	1.24	-0.96	755.00	3.31	1.18
10.11	7.97	662.00	0.30	1.22	-0.94	1079.00	4.17	2.04
0.27	-0.21	330.00	3.64	2.12	1.62	507.00	0.39	1.74
1.39	1.10	413.00	1.94	0.42	0.32	399.00	1.25	0.88
0.21	0.17	1007.00	6.85	5.33	4.10	952.00	0.21	1.92
2.62	2.06	1129.00	5.67	4.15	3.19	1771.00	1.41	0.72
1.40	1.11	310.00	5.81	4.29	3.29	504.00	0.60	1.53
0.36	0.28	439.00	2.28	0.76	0.58	1338.00	1.64	0.49
0.39	0.31	320.00	15.31	13.79	10.60	792.00	0.51	1.62
1.70	1.34	699.00	4.15	2.63	2.02	1990.00	2.11	0.02
2.32	1.83	406.00	5.42	3.90	2.99	1134.00	0.53	1.60
1.58	1.24	658.00	1.82	0.30	0.23	1137.00	2.99	0.86
3.22	2.54	499.00	1.60	0.08	0.06	1445.00	1.31	0.82
0.82	0.65	295.00	4.75	3.23	2.48	727.00	2.75	0.62
5.69	4.49	563.00	3.91	2.39	1.83	1116.00	4.12	1.99
3.02	2.38	924.00	7.47	5.95	4.57	3093.00	2.97	0.84
2.03	1.60	907.00	3.20	1.68	1.29	1580.00	0.44	1.69
0.58	0.46	1123.00	4.81	3.29	2.52	1966.00	1.83	0.30
0.30	0.24	985.00	4.06	2.54	1.95	2238.00	0.80	1.33
2.51	1.98	702.00	4.84	3.32	2.55	1549.00	0.58	1.55
0.13	-0.10	2146.00	2.28	0.76	0.58	3785.00	1.16	0.97
2.48	1.96	771.00	2.33	0.81	0.62	1107.00	1.17	0.96
1.54	1.22	538.00	1.12	0.40	-0.31	642.00	0.78	1.35
1.48	1.17	361.00	2.49	0.97	0.75	682.00	3.52	1.39
0.86		1217.50	1.52	0.88		1260.00	2.13	1.35
2.57				2.64				4.04
1.27				1.30				1.99
	3645.00	29.33		3693.00	32.12			
	4114.00	33.18		3400.00	48.88			
	1348.00	22.63		2363.00	27.34			
	2755.00	30.67		1830.00	19.34			
	2965.50	28.95		2821.50	31.92			

1216.74	4.51	873.21	12.48
523.00	0.76	1057.00	1.51
937.00	0.75	1252.00	4.31
809.00	0.99	1019.00	1.96
1577.00	1.40	2223.00	4.41
961.50	0.97	1387.75	3.05
445.34	0.30	566.11	1.53
	13.53		37.43
	0.90		4.58
	14.43		42.00
	27.98		28.87
	0.52		1.45
	0.48		-0.45

80.00	13.75	95.00	3.16
98.00	4.08	106.00	7.55
1132.00	1.50	968.00	1.65
1564.00	1.02	1613.00	3.29
4182.00	1.82	5427.00	9.47
4993.00	3.55	5186.00	3.95

rZ		
0.95		
-0.83		
-0.84		
-0.44		
-0.43		
-0.22		
-0.14		
1.94		
2.12		
-0.02		
-0.72		
-0.46		
0.93		
-0.08		
1.26		
-0.18		
-0.23		
3.38	x	toxic a, art b
-0.24		
1.34		
-0.58		
0.00		
0.36		
-0.65		
-0.53		
-0.55		
-0.83		
0.16		
0.00		
-0.38		
0.01		
-0.73		
-0.35		
3.66		
0.32		
1.19		
0.69		
1.10		
0.37		
1.04		
-0.53		
0.63		
0.32		
-0.28		
0.79		
-0.42		

2.50		
0.89		
1.02		
-0.27		
1.21		
0.34		
1.71		
5.12	x	debris a,c
1.91		
1.99		
3.11		
0.70		
0.82		
1.06		
0.14		
0.32		
1.00		
0.06		
0.08		
0.58		
1.56		
2.63	x	toxic a, c
4.01	x	toxic a, b c
1.50		
0.97		
3.56		
0.82		
2.43	x	toxic a,b,c
2.55		
2.17		
1.81		
1.60		
1.11		
-0.02		
-0.29		
0.67		
1.25		
-0.14		
0.97		
2.21		
0.54		
0.55		
0.45		
2.87		
3.67	x	toxic a,b,c
-0.65		
3.07	x	toxic a,b,c

3.19	x	toxic a,b,c
1.26		
2.31		
9.14	x	toxic a,b,c
6.13	x	toxic a,b,c
3.90	x	toxic a,b,c
-0.30		
-0.58		
-0.08		
-0.22		
-0.25		
0.67		
0.31		
-0.15		
1.85		
-0.86		
3.26	x	toxic a,b,c
0.24		
0.04		
2.68		
0.96		
0.18		
0.21		
0.48		
3.62	x	toxic a,b,c
2.61	x	toxic a,b,c
2.41	x	toxic a,b
-0.46		
-0.68		
-0.17		
-0.31		
-0.89		
0.46		
-0.82		
0.32		
-0.73		
0.16		
-0.71		
0.08		
-0.59		
1.00		
-0.73		
-1.07		
-0.65		
-0.94		
-0.36	x	debris a
-0.95		

-0.41
0.51
0.21
-0.29
0.02
-0.99
2.99
-0.61
-0.23
1.04
1.35
0.83
0.52
0.39
1.65
1.64
-0.05
1.34
-0.05
2.32
-0.95
-0.33
-0.47
-0.78
1.24
-0.21
0.08
-0.87
0.33
0.87
-0.70
-0.22
-0.38
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-0.22
1.82
0.35
-0.29
1.45
-0.90
-0.17
1.23
-0.31
0.12
1.43
0.30
0.03

-0.33		
1.04		
1.61		
0.52		
6.77	y	
0.15		
-0.49		
4.10		
1.18		
2.52	y	
-0.16		
2.02	x	tox b,c
2.43	x	tox a, debris b,c
3.56		
-0.55		
0.97		
0.58		
2.19		
0.73		
1.49		
1.07		
-0.51		
1.93		
0.00		
2.08		
0.13		
1.85		
-0.45		
-0.39		
-0.72		
0.55		
-0.81		
-0.34		
-0.91		
-0.95		
-0.77		
-0.77		
-0.08		
-0.98		
-1.00		
-0.79		
-0.69		
-0.35		
-0.99		
-0.76		
-0.80		
-0.31		

0.22
1.81
-0.67
3.95 y
-0.48
-0.64
-0.15
-0.07
-0.32
-0.26
2.77
-0.50
-0.71
-0.81
0.70
-0.44
-0.87
-0.50
-0.32
-0.42
-0.27
-0.43
0.08
-0.70
0.02
-0.02
-0.94
-0.72
0.30
0.76
-0.67
2.43
-0.31
-0.57
-0.92
0.08
-0.41
-0.75
0.58
-0.70
-0.28
-0.28
0.10
1.61
-0.03
-0.62
-0.29

-0.63		
-0.85		
1.52		
-0.86		
-0.82		
-0.74		
-0.91		
-0.65		
-0.72		
1.90		
-0.25		
-0.94		
0.78		
-0.52		
-0.12		
0.59		
1.02		
-0.87		
-0.44		
-0.97		
-0.36	x	toxic a,b,c
-0.77		
-0.25		
-0.82		
-0.01		
-0.81		
0.43		
-0.41		
0.31		
1.00		
0.42	x	toxic a,b
-0.85		
-0.15		
-0.67		
-0.78		
-0.49		
-0.48		
-0.68		
0.69		

Plate	Well	Gene	GeneID		Cell Count	% inf	Abs Dev
50051.00	A02	M-011408- thymosin,	7114.00	TMSB4X	2480.00	2.58	1.01
50051.00	A04	M-019686- leukocyte	7940.00	LST1	3374.00	8.80	5.21
50051.00	A05	M-019637- trichohyali	7062.00	TCHH	2678.00	3.06	0.53
50051.00	A06	M-011761- RD RNA bir	7936.00	RDBP	2866.00	3.94	0.35
50051.00	A07	M-006045- thimet olig	7064.00	THOP1	1182.00	11.84	8.25
50051.00	A08	M-008141- hydroxyste	7923.00	HSD17B8	1408.00	4.26	0.67
50051.00	A09	M-006047- tolloid-like	7093.00	TLL2	629.00	9.70	6.11
50051.00	A10	M-007338- solute carri	7922.00	SLC39A7	1765.00	8.27	4.68
50051.00	A11	M-012949- talin 1	7094.00	TLN1	1662.00	3.67	0.08
50051.00	A12	M-013106- HLA-B asso	7920.00	BAT5	1938.00	4.59	1.00
50051.00	A13	M-010218- translocati	7095.00	TLOC1	1679.00	4.76	1.17
50051.00	A14	M-013701- HLA-B asso	7918.00	BAT4	1994.00	4.01	0.42
50051.00	A15	M-010219- tetraspani	7103.00	TSPAN8	2056.00	6.91	3.32
50051.00	A16	M-005062- HLA-B asso	7917.00	BAT3	1114.00	6.37	2.78
50051.00	A17	M-010624- tetraspani	7105.00	TSPAN6	2102.00	2.05	1.54
50051.00	A18	M-013299- HLA-B asso	7916.00	BAT2	1809.00	2.60	0.99
50051.00	A19	M-010625- tetraspani	7106.00	TSPAN4	606.00	12.38	8.79
50051.00	A20	M-003805- HLA-B asso	7919.00	BAT1	2596.00	2.50	1.09
50051.00	A21	M-005742- G protein-	7107.00	GPR137B	1811.00	5.74	2.15
50051.00	A23	M-008621- transmem	7109.00	TMEM1	2045.00	2.89	0.70
50051.00	B02	M-006599- Fc fragmen	8857.00	FCGBP	1895.00	3.38	0.21
50051.00	B04	M-017561- dolichyl-ph	8818.00	DPM2	2420.00	5.62	2.03
50051.00	B05	M-012228- JTV1 gene	7965.00	JTV1	2934.00	2.59	1.00
50051.00	B06	M-021971- WD repeat	8816.00	WDR22	2993.00	1.77	1.82
50051.00	B07	M-013066- suppressio	7982.00	ST7	2602.00	3.23	0.36
50051.00	B08	M-011536- barrier to a	8815.00	BANF1	1044.00	6.90	3.31
50051.00	B09	M-017526- zinc finger	7988.00	ZNF212	2079.00	2.36	1.23
50051.00	B10	M-008237- succinate-	8803.00	SUCLA2	1468.00	3.61	0.02
50051.00	B11	M-009648- UBX domai	7993.00	UBXD6	1734.00	3.46	0.13
50051.00	B12	M-008677- succinate-	8802.00	SUCLG1	1791.00	2.62	0.97
50051.00	B13	M-019849- MYST histo	7994.00	MYST3	2909.00	1.44	2.15
50051.00	B14	M-008918- succinate-	8801.00	SUCLG2	1712.00	4.44	0.85
50051.00	B15	M-003697- prostate st	8000.00	PSCA	1492.00	3.75	0.16
50051.00	B16	M-011532- fucose-1-p	8790.00	FPGT	2658.00	3.12	0.47
50051.00	B17	M-007475- solute carri	8034.00	SLC25A16	2005.00	2.79	0.80
50051.00	B18	M-011531- matrilin 4	8785.00	MATN4	2425.00	5.48	1.89
50051.00	B19	M-019524- soc-2 supp	8036.00	SHOC2	3701.00	2.92	0.67
50051.00	B20	M-019522- sialic acid	8778.00	SIGLEC5	3352.00	1.85	1.74
50051.00	B21	M-011425- microfibrill	8076.00	MFAP5	2128.00	2.30	1.29
50051.00	B23	M-012281- intraflagell	8100.00	IFT88	3388.00	3.19	0.40
50051.00	C02	M-019467- receptor a	7905.00	REEP5	4518.00	3.63	0.04
50051.00	C04	M-012134- ST8 alpha-	7903.00	ST8SIA4	4885.00	4.28	0.69
50051.00	C05	M-019747- tropomod	7111.00	TMOD1	4946.00	8.63	5.04
50051.00	C06	M-019643- sarcolemm	7871.00	SLMAP	3523.00	3.86	0.27
50051.00	C07	M-027195- thymopoie	7112.00	TMPO	3642.00	3.46	0.13
50051.00	C08	M-007754- sema dom	7869.00	SEMA3B	3255.00	19.75	16.16

50051.00	C09	M-006048- transmemb	7113.00	TMPRSS2	3832.00	3.76	0.17
50051.00	C10	M-016430- interferon-	7866.00	IFRD2	2604.00	4.76	1.17
50051.00	C11	M-019787- troponin T	7140.00	TNNT3	2669.00	4.91	1.32
50051.00	C12	M-006594- ring finger	7844.00	RNF103	1869.00	4.71	1.12
50051.00	C13	M-017809- transition p	7141.00	TNP1	1541.00	7.33	**3.74**
50051.00	C14	M-019880- lysosomal a	7805.00	LAPTM5	2303.00	4.26	0.67
50051.00	C15	M-015315- transition p	7142.00	TNP2	2058.00	6.95	3.36
50051.00	C16	M-021414- dynein, axo	7802.00	DNALI1	2033.00	4.97	1.38
50051.00	C17	M-010125- tryptophan	7166.00	TPH1	2104.00	5.32	1.73
50051.00	C18	M-013027- leucine zipp	7798.00	LUZP1	1527.00	2.75	0.84
50051.00	C19	M-012784- tropomyos	7170.00	TPM3	2250.00	3.64	0.05
50051.00	C20	M-012793- zinc finger,	7789.00	ZXDA	3475.00	4.43	0.84
50051.00	C21	M-006053- tripeptidyl	7174.00	TPP2	2254.00	4.44	0.85
50051.00	C23	M-006054- tryptase, al	7176.00	TPS1	1507.00	7.43	**3.84**
50051.00	D02	M-019523- multiple PD	8777.00	MPDZ	2501.00	0.72	2.87
50051.00	D04	M-011530- N-ethylmal	8775.00	NAPA	381.00	10.24	**6.65**
50051.00	D05	M-012798- D4, zinc an	8110.00	DPF3	2924.00	1.30	2.29
50051.00	D06	M-011529- N-ethylmal	8774.00	NAPG	1349.00	1.85	1.74
50051.00	D07	M-021444- adaptor-rel	8120.00	AP3B2	2632.00	2.01	1.58
50051.00	D08	M-017545- synaptosor	8773.00	SNAP23	1334.00	2.25	1.34
50051.00	D09	M-016060- acidic (leuc	8125.00	ANP32A	2076.00	4.19	0.60
50051.00	D10	M-008102- tumor necr	8771.00	TNFRSF6B	2810.00	2.28	1.31
50051.00	D11	M-012192- ST8 alpha-N	8128.00	ST8SIA2	1123.00	4.01	0.42
50051.00	D12	M-011528- poly(A) bin	8761.00	PABPC4	1691.00	4.44	0.85
50051.00	D13	M-020050- chromoson	8131.00	C16orf35	2445.00	3.93	0.34
50051.00	D14	M-009591- CDP-diacylg	8760.00	CDS2	1160.00	2.16	1.43
50051.00	D15	M-004953- solute carri	8140.00	SLC7A5	1705.00	4.87	1.28
50051.00	D16	M-006342- myomesin	8736.00	MYOM1	2912.00	1.37	2.22
50051.00	D17	M-019894- coilin	8161.00	COIL	1808.00	2.21	1.38
50051.00	D18	M-017399- chromoson	8725.00	C19orf2	2804.00	3.14	0.45
50051.00	D19	M-018282- splicing fac	8175.00	SF3A2	2055.00	3.55	0.04
50051.00	D20	M-011521- sorting nex	8724.00	SNX3	2277.00	2.77	0.82
50051.00	D21	M-008176- elongation	8178.00	ELL	2426.00	2.89	0.70
50051.00	D23	M-020002- zinc finger	8187.00	ZNF239	3170.00	0.69	2.90
50051.00	E02	M-007525- solute carri	7782.00	SLC30A4	4035.00	1.39	2.20
50051.00	E04	M-007523- solute carri	7780.00	SLC30A2	4864.00	9.03	**5.44**
50051.00	E05	M-006055- tryptase alp	7177.00	TPSAB1	1822.00	2.47	1.12
50051.00	E06	M-007522- solute carri	7779.00	SLC30A1	2958.00	6.19	2.60
50051.00	E07	M-019757- cysteine-ric	7180.00	CRISP2	1630.00	2.70	0.89
50051.00	E08	M-012794- zinc finger	7776.00	ZNF236	2437.00	4.06	0.47
50051.00	E09	M-011897- translin	7247.00	TSN	2075.00	5.01	1.42
50051.00	E10	M-021346- zinc finger	7775.00	ZNF232	3275.00	4.40	0.81
50051.00	E11	M-012199- translin-ass	7257.00	TSNAX	3189.00	4.26	0.67
50051.00	E12	M-020111- zinc finger	7773.00	ZNF230	2094.00	4.11	0.52
50051.00	E13	M-012606- testis speci	7258.00	TSPY1	1652.00	3.87	0.28
50051.00	E14	M-023741- zinc finger	7772.00	ZNF229	1229.00	5.70	2.11
50051.00	E15	M-028592- TSPY-like 1	7259.00	TSPYL1	759.00	8.83	**5.24**

50051.00	E16	M-019162- zinc finger	7771.00	ZNF228	2207.00	3.53	0.06
50051.00	E17	M-011412- tissue spec	7264.00	TSTA3	2196.00	4.28	0.69
50051.00	E18	M-018647- zinc finger	7770.00	ZNF227	2003.00	4.34	0.75
50051.00	E19	M-019565- tetratricop	7265.00	TTC1	1598.00	1.75	1.84
50051.00	E20	M-019147- zinc finger	7769.00	ZNF226	1015.00	4.04	0.45
50051.00	E21	M-019566- DnaJ (Hsp4	7266.00	DNAJC7	2182.00	2.15	1.44
50051.00	E23	M-006570- tetratricop	7267.00	TTC3	2131.00	2.02	1.57
50051.00	F02	M-011520- sorting nex	8723.00	SNX4	4526.00	2.54	1.05
50051.00	F04	M-019527- nucleolar p	8715.00	NOL4	3938.00	5.54	1.95
50051.00	F05	M-031779- D4, zinc an	8193.00	DPF1	2449.00	2.53	1.06
50051.00	F06	M-011519- P antigen f	8712.00	PAGE1	3699.00	2.30	1.29
50051.00	F07	M-017791- chromosom	8209.00	C21orf33	4966.00	4.25	0.66
50051.00	F08	M-012619- serpin pept	8710.00	SERPINB7	3124.00	5.63	2.04
50051.00	F09	M-012310- DiGeorge s	8220.00	DGCR14	1163.00	4.73	1.14
50051.00	F10	M-013691- UDP-Gal:be	8708.00	B3GALT1	3725.00	2.63	0.96
50051.00	F11	M-011427- synapsin III	8224.00	SYN3	3528.00	3.97	0.38
50051.00	F12	M-013692- UDP-Gal:be	8707.00	B3GALT2	3064.00	3.79	0.20
50051.00	F13	M-019845- GTP bindin	8225.00	GTPBP6	2777.00	2.88	0.71
50051.00	F14	M-013696- beta-1,3-N-	8706.00	B3GALNT1	3576.00	4.47	0.88
50051.00	F15	M-020040- haloacid de	8226.00	HDHD1A	3041.00	4.24	0.65
50051.00	F16	M-013697- UDP-Gal:be	8705.00	B3GALT4	2822.00	4.04	0.45
50051.00	F17	M-019931- splicing fac	8227.00	SFRS17A	2129.00	1.41	2.18
50051.00	F18	M-011518- UDP-Gal:be	8704.00	B4GALT2	2848.00	2.18	1.41
50051.00	F19	M-006596- zinc finger	8233.00	ZRSR2	4512.00	3.59	0.00
50051.00	F20	M-011517- UDP-Gal:be	8703.00	B4GALT3	5294.00	2.66	0.93
50051.00	F21	M-009065- RNA bindin	8241.00	RBM10	1817.00	1.49	2.10
50051.00	F23	M-010097- jumonji, AT	8242.00	JARID1C	1987.00	3.12	0.47
50051.00	G02	M-020334- zinc finger	7768.00	ZNF225	4503.00	4.31	0.72
50051.00	G04	M-006593- zinc finger	7767.00	ZNF224	6514.00	10.49	6.90
50051.00	G05	M-016741- Tu translati	7284.00	TUFM	2908.00	3.82	0.23
50051.00	G06	M-006592- zinc finger	7766.00	ZNF223	5251.00	3.26	0.33
50051.00	G07	M-021218- tuftelin 1	7286.00	TUFT1	2383.00	7.39	3.80
50051.00	G08	M-004987- zinc finger	7764.00	ZNF217	4115.00	5.59	2.00
50051.00	G09	M-011415- tubby like p	7289.00	TULP3	4248.00	4.80	1.21
50051.00	G10	M-009701- zinc finger,	7763.00	ZFAND5	3224.00	5.24	1.65
50051.00	G11	M-012325- U2 small nu	7307.00	U2AF1	1636.00	4.65	1.06
50051.00	G12	M-020661- zinc finger	7762.00	ZNF215	3798.00	5.69	2.10
50051.00	G13	M-006595- zinc finger	7310.00	ZRSR1	2801.00	5.21	1.62
50051.00	G14	M-020663- zinc finger	7761.00	ZNF214	3638.00	3.11	0.48
50051.00	G15	M-031782- ubiquitin-c	7325.00	UBE2E2	3328.00	3.61	0.02
50051.00	G16	M-009473- zinc finger	7760.00	ZNF213	3864.00	2.82	0.77
50051.00	G17	M-017654- upstream b	7342.00	UBP1	3175.00	2.99	0.60
50051.00	G18	M-019511- zinc finger	7757.00	ZNF208	3629.00	8.65	5.06
50051.00	G19	M-017260- uroplakin 1	7348.00	UPK1B	4507.00	5.46	1.87
50051.00	G20	M-019557- zinc finger	7756.00	ZNF207	2391.00	5.86	2.27
50051.00	G21	M-007538- solute carri	7355.00	SLC35A2	5079.00	5.00	1.41

50051.00	G23	M-019564- UDP-glucos	7358.00	UGDH	1387.00	5.55	1.96
50051.00	H02	M-011516- UDP-Gal:be	8702.00	B4GALT4	4536.00	1.46	2.14
50051.00	H04	M-011515- UDP-N-ace	8693.00	GALNT4	3752.00	2.08	1.51
50051.00	H05	M-006833- structural r	8243.00	SMC1A	2491.00	2.49	1.10
50051.00	H06	M-013689- hyaluronog	8692.00	HYAL2	4138.00	2.90	0.69
50051.00	H07	M-009606- ARD1 hom	8260.00	ARD1A	2139.00	3.60	0.01
50051.00	H08	M-011512- keratin 37	8688.00	KRT37	1361.00	4.92	1.33
50051.00	H09	M-012420- coagulatio	8263.00	F8A1	3140.00	4.08	0.49
50051.00	H10	M-012317- keratin 38	8687.00	KRT38	2837.00	2.64	0.95
50051.00	H11	M-011428- transmem	8269.00	TMEM187	3425.00	2.77	0.82
50051.00	H12	M-019529- splicing fac	8683.00	SFRS9	3307.00	1.81	1.78
50051.00	H13	M-012171- L antigen f	8270.00	LAGE3	3385.00	2.87	0.72
50051.00	H14	M-010552- beclin 1 (cc	8678.00	BECN1	3684.00	5.10	1.51
50051.00	H15	M-007378- solute carri	8273.00	SLC10A3	2945.00	3.02	0.57
50051.00	H16	M-019528- syntaxin 1	8677.00	STX10	2831.00	2.23	1.36
50051.00	H17	M-010820- jumonji, A	8284.00	JARID1D	2001.00	4.80	1.21
50051.00	H18	M-019469- syntaxin 11	8676.00	STX11	3411.00	1.61	1.98
50051.00	H19	M-011429- histone clu	8290.00	HIST3H3	2089.00	3.40	0.19
50051.00	H20	M-019468- syntaxin 1	8675.00	STX16	2776.00	2.27	1.32
50051.00	H21	M-011430- histone clu	8294.00	HIST1H4I	4919.00	6.30	2.71
50051.00	H23	M-011435- histone clu	8334.00	HIST1H2A	2363.00	3.98	0.39
50051.00	I02	M-019556- zinc finger	7755.00	ZNF205	4404.00	3.20	0.39
50051.00	I04	M-006591- zinc finger	7753.00	ZNF202	4161.00	1.25	2.34
50051.00	I05	M-020193- UDP glucur	7364.00	UGT2B7	2325.00	1.51	2.08
50051.00	I06	M-019515- zinc finger	7748.00	ZNF195	3196.00	1.50	2.09
50051.00	I07	M-009737- UDP glucur	7365.00	UGT2B10	3170.00	2.68	0.91
50051.00	I08	M-016171- zinc finger	7746.00	ZNF193	2777.00	3.57	0.02
50051.00	I09	M-020195- UDP glucur	7367.00	UGT2B17	3069.00	3.65	0.06
50051.00	I10	M-020154- zinc finger	7745.00	ZNF192	2533.00	3.51	0.08
50051.00	I11	M-019761- uromoduli	7369.00	UMOD	1848.00	4.44	0.85
50051.00	I12	M-021350- zinc finger	7743.00	ZNF189	1449.00	3.38	0.21
50051.00	I13	M-019784- uroplakin 2	7379.00	UPK2	1969.00	1.47	2.12
50051.00	I14	M-016249- zinc finger	7741.00	ZNF187	1513.00	1.72	1.87
50051.00	I15	M-019707- uroplakin 3	7380.00	UPK3A	2719.00	3.35	0.24
50051.00	I16	M-019519- zinc finger	7739.00	ZNF185	1946.00	2.36	1.23
50051.00	I17	M-014140- ubiquitous	7403.00	UTX	2286.00	3.67	0.08
50051.00	I18	M-012789- zinc finger	7738.00	ZNF184	2772.00	2.34	1.25
50051.00	I19	M-017344- ubiquitous	7404.00	UTY	2103.00	2.43	1.16
50051.00	I20	M-006590- ring finger	7737.00	RNF113A	2124.00	5.70	2.11
50051.00	I21	M-009529- valyl-tRNA	7407.00	VARS	750.00	5.20	1.61
50051.00	I23	M-019763- vasodilator	7408.00	VASP	2256.00	1.60	1.99
50051.00	J02	M-004241- vesicle-ass	8674.00	VAMP4	4004.00	8.47	**4.88**
50051.00	J04	M-004740- tankyrase,	8658.00	TNKS	2842.00	2.96	0.63
50051.00	J05	M-017596- histone clu	8335.00	HIST1H2AB	1946.00	9.10	**5.51**
50051.00	J06	M-011904- DEAD (Asp-	8653.00	DDX3Y	2768.00	3.32	0.27
50051.00	J07	M-011438- histone clu	8338.00	HIST2H2A	2835.00	3.67	0.08
50051.00	J08	M-011510- chordin	8646.00	CHRD	2530.00	5.34	1.75

50051.00	J09	M-017307- histone clu	8339.00	HIST1H2BG	3551.00	4.31	0.72
50051.00	J10	M-006264- potassium	8645.00	KCNK5	3410.00	4.19	0.60
50051.00	J11	M-011441- histone clu	8342.00	HIST1H2BN	2796.00	7.69	**4.10**
50051.00	J12	M-010143- amine oxid	8639.00	AOC3	3566.00	5.47	1.88
50051.00	J13	M-011446- histone clu	8347.00	HIST1H2BC	2081.00	5.19	1.60
50051.00	J14	M-019536- eukaryotic	8637.00	EIF4EBP3	4231.00	1.68	1.91
50051.00	J15	M-011447- histone clu	8348.00	HIST1H2BC	2145.00	2.84	0.75
50051.00	J16	M-019538- Sjogren's sy	8636.00	SSNA1	2696.00	2.74	0.85
50051.00	J17	M-011449- histone clu	8350.00	HIST1H3A	3033.00	2.14	1.45
50051.00	J18	M-019537- RNA termir	8634.00	RTCD1	3899.00	5.67	2.08
50051.00	J19	M-011451- histone clu	8352.00	HIST1H3C	2754.00	3.92	0.33
50051.00	J20	M-009280- hydroxyste	8630.00	HSD17B6	3013.00	3.02	0.57
50051.00	J21	M-011452- histone clu	8353.00	HIST1H3E	2925.00	3.25	0.34
50051.00	J23	M-011453- histone clu	8354.00	HIST1H3I	3143.00	3.44	0.15
50051.00	K02	M-006589- zinc finger	7733.00	ZNF180	5993.00	5.06	1.47
50051.00	K04	M-006588- zinc finger	7732.00	ZNF179	2960.00	6.05	2.46
50051.00	K05	M-008727- valosin-cor	7415.00	VCP	3141.00	2.77	0.82
50051.00	K06	M-019774- zinc finger	7730.00	ZNF177	3179.00	3.81	0.22
50051.00	K07	M-019764- voltage-dep	7416.00	VDAC1	4288.00	3.10	0.49
50051.00	K08	M-021399- zinc finger	7728.00	ZNF175	3243.00	6.94	3.35
50051.00	K09	M-019766- voltage-dep	7417.00	VDAC2	3422.00	3.95	0.36
50051.00	K10	M-011801- zinc finger	7718.00	ZNF165	3352.00	4.45	0.86
50051.00	K11	M-020850- voltage-dep	7419.00	VDAC3	2595.00	2.93	0.66
50051.00	K12	M-011800- zinc finger	7712.00	ZNF157	1323.00	3.78	0.19
50051.00	K13	M-013570- linker for a	7462.00	LAT2	2072.00	4.92	1.33
50051.00	K14	M-006586- zinc finger	7711.00	ZNF155	1930.00	3.73	0.14
50051.00	K15	M-011898- tryptophan	7485.00	WRB	1902.00	2.73	0.86
50051.00	K16	M-023833- zinc finger	7710.00	ZNF154	1233.00	7.62	**4.03**
50051.00	K17	M-012662- splicing fac	7536.00	SF1	2181.00	6.10	2.51
50051.00	K18	M-006585- tripartite m	7706.00	TRIM25	1665.00	6.49	2.90
50051.00	K19	M-010789- zinc finger	7538.00	ZFP36	2390.00	6.99	3.40
50051.00	K20	M-019930- zinc finger	7701.00	ZNF142	1819.00	6.27	2.68
50051.00	K21	M-019375- zinc finger	7542.00	ZFPL1	1889.00	2.70	0.89
50051.00	K23	M-014133- zinc finger	7549.00	ZNF2	2339.00	4.66	1.07
50051.00	L02	M-011504- jerky homc	8629.00	JRK	2029.00	0.94	2.65
50051.00	L04	M-019539- Down synd	8624.00	DSCR2	3122.00	2.21	1.38
50051.00	L05	M-011455- histone clu	8356.00	HIST1H3J	2391.00	1.71	1.88
50051.00	L06	M-012663- acetylserot	8623.00	ASMTL	2044.00	1.52	2.07
50051.00	L07	M-013723- histone clu	8357.00	HIST1H3H	2362.00	1.14	2.45
50051.00	L08	M-011502- neuropepti	8620.00	NPFF	3084.00	2.01	1.58
50051.00	L09	M-006475- histone clu	8358.00	HIST1H3B	3232.00	1.02	2.57
50051.00	L10	M-019218- Ca2+-deper	8618.00	CADPS	2437.00	1.03	2.56
50051.00	L11	M-011456- histone clu	8359.00	HIST1H4A	3230.00	1.83	1.76
50051.00	L12	M-011501- vesicle doc	8615.00	VDP	2560.00	2.03	1.56
50051.00	L13	M-011457- histone clu	8360.00	HIST1H4D	2138.00	1.68	1.91
50051.00	L14	M-012616- stanniocalc	8614.00	STC2	2580.00	5.19	1.60
50051.00	L15	M-011458- histone clu	8361.00	HIST1H4F	2818.00	2.56	1.04

50051.00	L16	M-008311- retinol deh	8608.00	RDH16	3117.00	3.53	0.06
50051.00	L17	M-011460- histone clu	8363.00	HIST1H4J	3563.00	1.35	2.24
50051.00	L18	M-007471- solute carri	8604.00	SLC25A12	2920.00	1.68	1.91
50051.00	L19	M-011462- histone clu	8365.00	HIST1H4H	3425.00	3.21	0.38
50051.00	L20	M-019541- chromosom	8603.00	C4orf8	3173.00	1.80	1.79
50051.00	L21	M-011464- histone clu	8367.00	HIST1H4E	3690.00	4.80	1.21
50051.00	L23	M-011465- histone clu	8368.00	HIST1H4L	3023.00	7.15	3.56
50051.00	M02	M-019773- zinc finger	7700.00	ZNF141	5362.00	1.75	1.84
50051.00	M04	M-021400- zinc finger	7699.00	ZNF140	7308.00	6.60	3.01
50051.00	M05	M-016190- zinc finger	7551.00	ZNF3	6770.00	4.61	1.02
50051.00	M06	M-021278- zinc finger	7697.00	ZNF138	6345.00	6.60	3.01
50051.00	M07	M-008444- zinc finger	7552.00	ZNF711	5569.00	3.66	0.07
50051.00	M08	M-019559- zinc finger	7696.00	ZNF137	5510.00	2.34	1.25
50051.00	M09	M-014124- zinc finger	7554.00	ZNF8	6101.00	1.36	2.23
50051.00	M10	M-019431- zinc finger	7694.00	ZNF135	4199.00	1.19	2.40
50051.00	M11	M-012772- zinc finger	7558.00	ZNF11B	4070.00	2.75	0.84
50051.00	M12	M-019561- zinc finger	7693.00	ZNF134	3398.00	3.83	0.24
50051.00	M13	M-020805- zinc finger	7561.00	ZNF14	4755.00	2.54	1.05
50051.00	M14	M-017702- zinc finger	7692.00	ZNF133	3572.00	3.08	0.51
50051.00	M15	M-012773- zinc finger	7564.00	ZNF16	1005.00	7.76	**4.17**
50051.00	M16	M-019560- zinc finger	7691.00	ZNF132	1591.00	2.26	1.33
50051.00	M17	M-023829- zinc finger	7565.00	ZNF17	5332.00	2.89	0.70
50051.00	M18	M-006582- makorin, ri	7682.00	MKRNP5	3150.00	3.78	0.19
50051.00	M19	M-023022- zinc finger	7566.00	ZNF18	3132.00	1.88	1.71
50051.00	M20	M-006581- makorin, ri	7681.00	MKRN3	3650.00	0.66	2.93
50051.00	M21	M-006575- zinc finger	7567.00	ZNF19	3328.00	2.79	0.80
50051.00	M23	M-006576- zinc finger	7568.00	ZNF20	2795.00	3.61	0.02
50051.00	N02	M-024157- nucleolar p	8602.00	NOL14	2522.00	1.86	1.73
50051.00	N04	M-012615- lymphocyt	8581.00	LY6D	3287.00	4.11	0.52
50051.00	N05	M-011466- histone clu	8369.00	HIST1H4G	3370.00	3.59	0.00
50051.00	N06	M-017405- scavenger	8578.00	SCARF1	2764.00	1.41	2.18
50051.00	N07	M-019056- histone clu	8370.00	HIST2H4A	1601.00	4.12	0.53
50051.00	N08	M-018025- transmem	8577.00	TMEFF1	3630.00	5.40	1.81
50051.00	N09	M-013698- hyaluronog	8372.00	HYAL3	2848.00	2.84	0.75
50051.00	N10	M-015318- ribosomal	8568.00	RRP1	2403.00	1.83	1.76
50051.00	N11	M-007470- solute carri	8402.00	SLC25A11	2775.00	1.55	2.04
50051.00	N12	M-011498- tyrosyl-tRN	8565.00	YARS	1885.00	3.18	0.41
50051.00	N13	M-019055- SRY (sex de	8403.00	SOX14	3169.00	3.82	0.23
50051.00	N14	M-009897- kynurenine	8564.00	KMO	4231.00	2.58	1.01
50051.00	N15	M-017919- speckle-typ	8405.00	SPOP	3334.00	1.23	2.36
50051.00	N16	M-015317- THO compl	8563.00	THOC5	3198.00	3.38	0.21
50051.00	N17	M-004455- ubiquitousl	8409.00	UXT	2258.00	1.06	2.53
50051.00	N18	M-011495- inactivatio	8552.00	INE1	2820.00	1.28	2.31
50051.00	N19	M-004012- early endo	8411.00	EEA1	4592.00	1.59	2.00
50051.00	N20	M-007900- ficolin (coll	8547.00	FCN3	3359.00	0.77	2.82
50051.00	N21	M-019551- syntaxin 7	8417.00	STX7	2143.00	1.26	2.33
50051.00	N23	M-011472- butyrobeta	8424.00	BBOX1	2070.00	2.13	1.46

50051.00	O02	M-020328- zinc finger	7673.00	ZNF222	4841.00	3.51	0.08
50051.00	O04	M-014163- zinc finger	7670.00	ZNF117	3173.00	2.71	0.88
50051.00	O05	M-024670- zinc finger	7569.00	ZNF182	4104.00	6.12	2.53
50051.00	O06	M-019779- zinc finger	7644.00	ZNF91	4301.00	3.16	0.43
50051.00	O07	M-016341- zinc finger	7571.00	ZNF23	3270.00	3.70	0.11
50051.00	O08	M-024032- zinc finger	7643.00	ZNF90	3834.00	4.30	0.71
50051.00	O09	M-021443- zinc finger	7574.00	ZNF26	5047.00	2.66	0.94
50051.00	O10	M-006580- zinc finger	7638.00	ZNF221	4234.00	2.43	1.16
50051.00	O11	M-023811- zinc finger	7576.00	ZNF28	2928.00	4.34	0.75
50051.00	O12	M-019506- zinc finger	7634.00	ZNF80	3249.00	5.05	1.46
50051.00	O13	M-015853- zinc finger	7579.00	ZSCAN20	1715.00	5.25	1.66
50051.00	O14	M-012792- zinc finger	7633.00	ZNF79	3074.00	3.77	0.18
50051.00	O15	M-012775- zinc finger	7580.00	ZNF32	3384.00	4.67	1.08
50051.00	O16	M-016925- zinc finger	7627.00	ZNF75A	3158.00	3.99	0.40
50051.00	O17	M-025422- zinc finger	7586.00	ZKSCAN1	4069.00	3.19	0.40
50051.00	O18	M-012791- zinc finger	7626.00	ZNF75	3368.00	5.11	1.52
50051.00	O19	M-026497- zinc finger	7587.00	ZNF37A	1916.00	9.71	**6.12**
50051.00	O20	M-012790- zinc finger	7621.00	ZNF70	2433.00	4.19	0.60
50051.00	O21	M-021316- zinc finger	7589.00	ZSCAN21	2721.00	4.89	1.30
50051.00	O23	M-012388- zinc finger	7592.00	ZNF41	1795.00	5.68	2.09
50051.00	P02	M-008967- carbohydra	8534.00	CHST1	2031.00	5.32	1.73
50051.00	P04	M-009121- cytochrom	8529.00	CYP4F2	3188.00	4.17	0.58
50051.00	P05	M-011473- zinc finger	8427.00	ZNF282	2720.00	4.56	0.97
50051.00	P06	M-009311- D-aspartat	8528.00	DDO	3107.00	2.48	1.11
50051.00	P07	M-011475- double C2-	8447.00	DOC2B	2808.00	2.17	1.42
50051.00	P08	M-008757- N-deacetyl	8509.00	NDST2	2551.00	7.17	**3.58**
50051.00	P09	M-011476- double C2-	8448.00	DOC2A	3004.00	4.76	1.17
50051.00	P10	M-011489- nipsnap ho	8508.00	NIPSNAP1	2988.00	2.78	0.81
50051.00	P11	M-012403- attractin	8455.00	ATRN	2728.00	5.35	1.76
50051.00	P12	M-011488- poly (ADP-	8505.00	PARG	1174.00	5.79	2.20
50051.00	P13	M-010386- tyrosylprot	8459.00	TPST2	2352.00	1.23	2.36
50051.00	P14	M-011483- PTPRF inte	8496.00	PPFIBP1	2792.00	3.83	0.24
50051.00	P15	M-008839- tyrosylprot	8460.00	TPST1	1646.00	3.52	0.07
50051.00	P16	M-026771- PTPRF inte	8495.00	PPFIBP2	2569.00	1.99	1.60
50051.00	P17	M-012611- TEA domai	8463.00	TEAD2	3511.00	3.82	0.23
50051.00	P18	M-006010- protease, s	8492.00	PRSS12	2761.00	8.55	**4.96**
50051.00	P19	M-011479- sorbin and	8470.00	SORBS2	4035.00	1.36	2.23
50051.00	P20	M-008295- cartilage in	8483.00	CILP	3197.00	1.85	1.74
50051.00	P21	M-011482- RAE1 RNA	8480.00	RAE1	1409.00	1.92	1.67
50051.00	P23	M-021276- semaphori	8482.00	SEMA7A	1938.00	1.24	2.35
					2784.50	3.59	1.19
				MAD3			3.57
				MADc			1.76
50051.00	C22				2099.00	20.39	
50051.00	D22	2242.00	12.89				
50051.00	E22	1694.00	12.63				
50051.00	F22				2827.00	25.82	

					mn	2463.00	23.11
					sd	514.77	3.84
50051.00	G22					939.00	11.93
50051.00	H22					1127.00	3.99
50051.00	I22					554.00	16.25
50051.00	J22					1052.00	11.41
					mn	911.00	10.55
					sd	311.44	6.17
					3psSD		11.52
					3ngSD		18.51
					SumSD		30.03
					DiffMn		12.56
					SmovrDiff		2.39
					1minus		-1.39
50051.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	234.00	27.78
50051.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	157.00	20.38
50051.00	I03	D-001206-:	siControl non-targeting			2373.00	3.58
50051.00	J03	D-001206-:	siControl non-targeting			1649.00	4.85
50051.00	K03	D-001600-(	siGLO RISC-free siRNA			7776.00	6.78
50051.00	L03	D-001600-(	siGLO RISC-free siRNA			4269.00	5.22

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
-0.57	814.00	3.93	1.13	0.73	872.00	1.38	2.26	-1.27
2.96	3258.00	3.47	0.67	0.43	2454.00	6.48	2.84	1.60
-0.30	3554.00	1.07	1.73	1.11	2547.00	1.61	2.03	-1.14
0.20	3669.00	1.94	0.86	0.55	1707.00	2.64	1.00	-0.56
4.68	2615.00	2.72	0.08	0.05	1246.00	2.73	0.91	-0.51
0.38	1238.00	2.18	0.62	0.40	2327.00	2.45	1.19	-0.67
3.47	1021.00	4.60	1.80	1.16	883.00	5.78	2.14	1.20
2.66	3270.00	4.53	1.73	1.11	2268.00	5.51	1.87	1.05
0.05	2174.00	1.75	1.05	0.67	1359.00	1.84	1.80	-1.01
0.57	2560.00	3.24	0.44	0.28	2553.00	3.45	0.19	-0.11
0.67	1997.00	1.45	1.35	0.86	1884.00	2.81	0.83	-0.47
0.24	2214.00	1.85	0.95	0.61	2137.00	4.26	0.62	0.35
1.88	2694.00	3.34	0.54	0.35	1833.00	3.82	0.18	0.10
1.58	1667.00	2.34	0.46	0.30	1287.00	2.95	0.69	-0.39
-0.88	1539.00	2.08	0.72	0.46	1191.00	3.78	0.14	0.08
-0.56	2773.00	1.77	1.03	0.66	1594.00	3.39	0.25	-0.14
4.99	865.00	9.71	6.91	4.43	739.00	4.74	1.10	0.62
-0.62	1860.00	3.49	0.69	0.45	2593.00	2.28	1.36	-0.77
1.22	690.00	4.64	1.84	1.18	1120.00	3.13	0.52	-0.29
-0.40	2052.00	5.46	2.66	1.70	2436.00	4.47	0.83	0.47
-0.12	1729.00	2.95	0.15	0.10	2294.00	0.61	3.03	-1.70
1.15	4072.00	1.72	1.08	0.69	3343.00	2.90	0.74	-0.42
-0.57	4775.00	2.07	0.73	0.47	3765.00	2.71	0.93	-0.52
-1.03	4727.00	5.48	2.68	1.72	3105.00	3.22	0.42	-0.24
-0.21	4582.00	11.59	8.79	5.63	2543.00	6.65	3.01	1.69
1.88	1628.00	4.36	1.56	1.00	949.00	3.27	0.37	-0.21
-0.70	3824.00	1.52	1.28	0.82	1786.00	2.74	0.90	-0.50
0.01	3655.00	2.82	0.02	0.01	1279.00	2.35	1.29	-0.73
-0.07	3774.00	2.38	0.42	0.27	2888.00	2.46	1.18	-0.66
-0.55	2114.00	3.74	0.94	0.60	1105.00	2.17	1.47	-0.83
-1.22	4179.00	3.33	0.53	0.34	3297.00	4.61	0.97	0.54
0.48	3072.00	5.66	2.86	1.84	2018.00	8.28	4.64	2.60
0.09	2331.00	4.33	1.53	0.98	1017.00	2.26	1.38	-0.78
-0.27	4866.00	5.61	2.81	1.80	3305.00	3.48	0.16	-0.09
-0.45	3265.00	6.16	3.36	2.15	1897.00	2.69	0.95	-0.54
1.07	3829.00	5.54	2.74	1.75	2070.00	3.48	0.16	-0.09
-0.38	4284.00	3.03	0.23	0.15	3386.00	1.98	1.66	-0.93
-0.99	3383.00	3.99	1.19	0.76	2590.00	2.28	1.36	-0.77
-0.73	3597.00	3.70	0.90	0.58	2978.00	1.41	2.23	-1.25
-0.23	4912.00	8.39	5.59	3.58	3359.00	4.53	0.89	0.50
0.02	3955.00	4.42	1.62	1.04	3472.00	3.97	0.33	0.19
0.39	2867.00	2.13	0.67	0.43	2095.00	4.63	0.99	0.56
2.86	4065.00	4.82	2.02	1.30	4134.00	10.18	6.54	3.68
0.15	3557.00	3.77	0.97	0.62	2463.00	3.29	0.35	-0.20
-0.07	5181.00	3.17	0.37	0.23	2295.00	2.79	0.85	-0.48
9.17	3210.00	3.24	0.44	0.28	4161.00	5.17	1.53	0.86

0.09	4255.00	1.86	0.94	0.60	3004.00	4.29	0.65	0.37
0.66	3336.00	2.46	0.34	0.22	2543.00	1.85	1.79	-1.01
0.75	3951.00	1.11	1.69	1.08	2550.00	3.76	0.12	0.07
0.63	1900.00	1.79	1.01	0.65	1876.00	4.42	0.78	0.44
2.12	1435.00	5.09	2.29	1.47	1361.00	4.63	0.99	0.56
0.38	3607.00	1.36	1.44	0.92	2340.00	5.85	2.21	1.24
1.91	2126.00	1.22	1.58	1.01	1447.00	9.19	**5.55**	3.12
0.78	2836.00	3.24	0.44	0.28	2300.00	6.30	2.66	1.50
0.98	3469.00	4.18	1.38	0.88	2940.00	5.14	1.50	0.84
-0.48	3735.00	1.07	1.73	1.11	3251.00	6.31	2.67	1.50
0.03	3707.00	1.97	0.83	0.53	4478.00	7.17	3.53	1.98
0.48	4068.00	1.70	1.10	0.71	4441.00	3.33	0.31	-0.17
0.48	1642.00	2.13	0.67	0.43	4204.00	4.33	0.69	0.39
2.18	2050.00	0.83	1.97	1.26	2019.00	2.18	1.46	-0.82
-1.63	2799.00	2.75	0.05	0.03	3146.00	6.04	2.40	1.35
3.77	627.00	22.97	20.17	12.93	568.00	14.09	**10.45**	5.87
-1.30	3652.00	2.00	0.80	0.51	3465.00	1.47	2.17	-1.22
-0.99	2698.00	3.93	1.13	0.72	2635.00	2.47	1.17	-0.66
-0.89	4584.00	4.60	1.80	1.16	2879.00	4.72	1.08	0.61
-0.76	2453.00	2.85	0.05	0.03	2913.00	3.67	0.03	0.02
0.34	4566.00	5.23	2.43	1.56	4937.00	6.02	2.38	1.33
-0.74	4391.00	5.92	3.12	2.00	3601.00	4.33	0.69	0.39
0.24	2759.00	3.99	1.19	0.76	2078.00	1.59	2.05	-1.15
0.48	3615.00	3.82	1.02	0.65	2580.00	2.52	1.12	-0.63
0.19	3237.00	2.78	0.02	0.01	2404.00	1.33	2.31	-1.30
-0.81	2341.00	3.29	0.49	0.31	1026.00	2.05	1.59	-0.90
0.72	2307.00	3.34	0.54	0.34	2313.00	0.26	3.38	-1.90
-1.26	3759.00	2.98	0.18	0.12	2379.00	1.60	2.04	-1.15
-0.78	3310.00	1.54	1.26	0.81	1547.00	1.49	2.15	-1.21
-0.26	4066.00	4.82	2.02	1.30	3041.00	1.97	1.67	-0.94
-0.02	2985.00	7.91	5.11	3.27	3073.00	1.43	2.21	-1.24
-0.47	2642.00	4.43	1.63	1.04	2774.00	1.01	2.63	-1.48
-0.40	2895.00	3.80	1.00	0.64	2987.00	2.24	1.40	-0.79
-1.64	2698.00	1.63	1.17	0.75	5003.00	1.66	1.98	-1.11
-1.25	4194.00	4.08	1.28	0.82	2949.00	4.41	0.77	0.43
3.08	3826.00	4.76	1.96	1.25	2387.00	4.57	0.93	0.52
-0.64	3392.00	2.86	0.06	0.04	2490.00	1.08	2.56	-1.44
1.47	4741.00	8.86	6.06	3.88	2207.00	2.76	0.88	-0.49
-0.51	2305.00	3.64	0.84	0.54	2030.00	1.53	2.11	-1.19
0.27	3055.00	1.80	1.00	0.64	2854.00	1.82	1.82	-1.02
0.81	1675.00	3.46	0.66	0.42	1719.00	1.11	2.53	-1.43
0.46	4814.00	6.19	3.39	2.17	4290.00	2.87	0.77	-0.43
0.38	3867.00	6.26	3.46	2.22	3314.00	4.98	1.34	0.75
0.29	2936.00	6.54	3.74	2.40	1514.00	3.70	0.06	0.03
0.16	1951.00	2.97	0.17	0.11	1746.00	1.72	1.92	-1.08
1.19	1610.00	3.73	0.93	0.59	1662.00	3.85	0.21	0.12
2.97	1017.00	8.65	5.85	3.75	824.00	5.70	2.06	1.16

-0.03	2786.00	1.58	1.22	0.78	2239.00	2.01	1.63	-0.92
0.39	2771.00	3.36	0.56	0.36	2657.00	2.97	0.67	-0.38
0.43	3143.00	4.45	1.65	1.06	3742.00	2.91	0.73	-0.41
-1.04	2469.00	3.12	0.32	0.20	2174.00	3.63	0.01	0.00
0.25	1025.00	3.02	0.22	0.14	1687.00	3.91	0.27	0.15
-0.82	2397.00	1.54	1.26	0.81	3212.00	2.34	1.31	-0.73
-0.89	2236.00	3.00	0.20	0.13	3153.00	5.01	1.37	0.77
-0.60	4227.00	2.08	0.72	0.46	5107.00	4.13	0.49	0.28
1.10	5131.00	11.15	8.35	5.35	4002.00	7.92	**4.28**	2.41
-0.60	3266.00	2.17	0.63	0.40	2806.00	2.60	1.04	-0.58
-0.73	3637.00	3.99	1.19	0.76	2964.00	3.71	0.07	0.04
0.37	5612.00	3.99	1.19	0.76	5021.00	6.51	2.87	1.61
1.16	4572.00	8.07	5.27	3.38	3072.00	4.65	1.01	0.57
0.65	2288.00	1.57	1.23	0.79	1641.00	2.19	1.45	-0.81
-0.54	4805.00	2.98	0.18	0.11	3221.00	4.66	1.02	0.57
0.21	4100.00	2.98	0.18	0.11	3591.00	4.37	0.73	0.41
0.11	3426.00	2.74	0.06	0.04	2755.00	4.76	1.12	0.63
-0.40	2195.00	3.60	0.80	0.51	2261.00	2.52	1.12	-0.63
0.50	2895.00	2.07	0.73	0.47	2460.00	5.37	1.73	0.97
0.37	1753.00	4.62	1.82	1.17	1869.00	3.75	0.11	0.06
0.25	3377.00	4.35	1.55	1.00	2179.00	5.09	1.45	0.82
-1.24	2395.00	1.92	0.88	0.56	2444.00	1.96	1.68	-0.94
-0.80	2637.00	1.63	1.17	0.75	2298.00	2.74	0.90	-0.51
0.00	3853.00	2.08	0.72	0.46	3243.00	3.36	0.28	-0.16
-0.53	2555.00	2.31	0.49	0.31	3565.00	4.46	0.82	0.46
-1.19	2099.00	2.43	0.37	0.24	2751.00	3.89	0.25	0.14
-0.27	1722.00	3.43	0.63	0.40	2810.00	3.24	0.40	-0.23
0.41	2813.00	2.42	0.38	0.25	2265.00	4.06	0.42	0.24
3.91	4810.00	10.89	8.09	5.19	4453.00	10.80	**7.16**	4.02
0.13	2515.00	6.04	3.24	2.08	1711.00	5.73	2.09	1.17
-0.19	3559.00	2.87	0.07	0.04	3145.00	4.26	0.62	0.35
2.15	2186.00	5.76	2.96	1.90	1599.00	12.13	**8.49**	4.77
1.13	3367.00	4.28	1.48	0.95	2298.00	2.61	1.03	-0.58
0.69	4429.00	2.21	0.59	0.38	3080.00	4.22	0.58	0.33
0.94	2775.00	3.71	0.91	0.58	1723.00	4.24	0.60	0.33
0.60	1884.00	2.34	0.46	0.30	1117.00	3.76	0.12	0.07
1.19	3858.00	4.82	2.02	1.30	3393.00	6.07	2.43	1.37
0.92	1871.00	0.91	1.89	1.21	1739.00	5.46	1.82	1.02
-0.27	3360.00	1.22	1.58	1.01	2784.00	4.63	0.99	0.56
0.01	3505.00	2.31	0.49	0.31	3289.00	6.29	2.65	1.49
-0.44	3075.00	1.50	1.30	0.84	3493.00	8.07	**4.43**	2.49
-0.34	3179.00	2.11	0.69	0.44	2659.00	2.56	1.08	-0.61
2.87	3120.00	4.90	2.10	1.35	2566.00	9.08	**5.44**	3.06
1.06	3710.00	2.53	0.27	0.17	3912.00	4.81	1.17	0.65
1.29	1614.00	1.86	0.94	0.60	2236.00	6.98	3.34	1.87
0.80	3710.00	2.59	0.21	0.14	5114.00	5.89	2.25	1.26

1.11	1147.00	1.05	1.75	1.12	1409.00	6.74	3.10	1.74
-1.21	3639.00	0.55	2.25	1.44	4468.00	1.59	2.05	-1.15
-0.86	3984.00	2.81	0.01	0.01	4119.00	1.82	1.82	-1.02
-0.63	2866.00	2.09	0.71	0.45	3115.00	4.04	0.40	0.23
-0.39	3599.00	1.64	1.16	0.74	2836.00	3.77	0.13	0.07
0.01	2823.00	0.53	2.27	1.45	1860.00	2.15	1.49	-0.84
0.76	1665.00	1.50	1.30	0.83	1882.00	2.71	0.93	-0.52
0.28	3844.00	1.07	1.73	1.11	3417.00	1.58	2.06	-1.16
-0.54	2920.00	1.71	1.09	0.70	2318.00	2.63	1.01	-0.57
-0.46	2970.00	0.91	1.89	1.21	3443.00	1.60	2.04	-1.15
-1.01	2989.00	0.64	2.16	1.39	1941.00	3.09	0.55	-0.31
-0.41	3470.00	1.24	1.56	1.00	2715.00	2.58	1.06	-0.60
0.86	3652.00	2.74	0.06	0.04	4036.00	3.59	0.05	-0.03
-0.32	2571.00	1.28	1.52	0.97	1888.00	1.75	1.89	-1.06
-0.77	2124.00	0.19	2.61	1.67	1854.00	2.27	1.37	-0.77
0.69	2289.00	0.52	2.28	1.46	1376.00	1.82	1.82	-1.03
-1.12	3753.00	0.53	2.27	1.45	3594.00	4.84	1.20	0.67
-0.11	2290.00	0.22	2.58	1.65	2142.00	0.89	2.75	-1.55
-0.75	2424.00	0.00	2.80	1.79	2044.00	2.30	1.34	-0.75
1.54	3335.00	3.78	0.98	0.63	3420.00	5.67	2.03	1.14
0.22	2808.00	0.36	2.44	1.57	3066.00	1.34	2.30	-1.29
-0.22	2483.00	4.23	1.43	0.92	2440.00	3.44	0.20	-0.11
-1.33	3572.00	3.00	0.20	0.13	2657.00	1.81	1.83	-1.03
-1.18	2447.00	1.55	1.25	0.80	1792.00	3.24	0.40	-0.23
-1.19	2441.00	3.07	0.27	0.17	2347.00	1.11	2.53	-1.42
-0.52	3231.00	2.26	0.54	0.35	2554.00	1.76	1.88	-1.06
-0.01	2253.00	3.91	1.11	0.71	1551.00	5.09	1.45	0.82
0.03	2694.00	5.68	2.88	1.85	1997.00	2.75	0.89	-0.50
-0.04	3214.00	3.30	0.50	0.32	2132.00	3.38	0.26	-0.15
0.48	2531.00	4.31	1.51	0.97	1590.00	3.65	0.01	0.00
-0.12	1522.00	4.73	1.93	1.24	898.00	4.01	0.37	0.21
-1.20	2177.00	1.56	1.24	0.79	1014.00	3.85	0.21	0.12
-1.06	1689.00	3.67	0.87	0.56	1309.00	3.36	0.28	-0.16
-0.14	3524.00	3.15	0.35	0.22	1927.00	5.14	1.50	0.84
-0.70	2718.00	2.54	0.26	0.17	1860.00	2.37	1.27	-0.72
0.05	2594.00	2.08	0.72	0.46	1495.00	3.08	0.56	-0.32
-0.71	3412.00	3.55	0.75	0.48	2121.00	1.98	1.66	-0.93
-0.66	3182.00	1.82	0.98	0.63	1560.00	3.40	0.24	-0.14
1.20	3983.00	1.78	1.02	0.65	2398.00	5.55	1.91	1.07
0.91	909.00	1.76	1.04	0.67	697.00	4.88	1.24	0.70
-1.13	3522.00	0.97	1.83	1.18	3959.00	4.85	1.21	0.68
2.77	3492.00	3.61	0.81	0.52	3377.00	3.17	0.47	-0.27
-0.36	3778.00	4.53	1.73	1.11	2787.00	2.55	1.09	-0.61
3.12	2560.00	5.86	3.06	1.96	2340.00	2.86	0.78	-0.44
-0.15	2778.00	1.80	1.00	0.64	3180.00	1.57	2.07	-1.16
0.04	2624.00	3.05	0.25	0.16	2120.00	2.26	1.38	-0.77
0.99	2202.00	1.54	1.26	0.81	2283.00	3.77	0.13	0.07

0.41	1718.00	3.03	0.23	0.15	2247.00	2.89	0.75	-0.42
0.34	2194.00	2.69	0.11	0.07	2965.00	3.41	0.23	-0.13
2.33	1516.00	3.50	0.70	0.45	1889.00	4.76	1.12	0.63
1.07	1791.00	4.97	2.17	1.39	2201.00	6.91	3.27	1.84
0.91	2029.00	3.06	0.26	0.16	1550.00	4.97	1.33	0.75
-1.09	2275.00	2.24	0.56	0.36	2118.00	4.86	1.22	0.69
-0.42	910.00	1.54	1.26	0.81	1424.00	4.78	1.14	0.64
-0.48	1352.00	1.63	1.17	0.75	1448.00	4.07	0.43	0.24
-0.82	1410.00	0.99	1.81	1.16	1304.00	4.60	0.96	0.54
1.18	2188.00	4.62	1.82	1.16	2991.00	5.22	1.58	0.89
0.19	1742.00	2.18	0.62	0.40	2805.00	3.07	0.57	-0.32
-0.32	2335.00	3.90	1.10	0.70	2518.00	1.55	2.09	-1.18
-0.19	2423.00	2.44	0.37	0.23	2891.00	3.77	0.13	0.07
-0.09	1386.00	1.23	1.57	1.01	3955.00	5.16	1.52	0.85
0.83	3125.00	4.45	1.65	1.06	3696.00	4.71	1.07	0.60
1.39	1475.00	3.19	0.39	0.25	1911.00	7.59	3.95	2.22
-0.47	1793.00	4.18	1.38	0.89	3002.00	2.66	0.98	-0.55
0.12	2519.00	2.26	0.54	0.34	4172.00	4.51	0.87	0.49
-0.28	3316.00	3.86	1.06	0.68	4398.00	4.84	1.20	0.68
1.90	2049.00	2.59	0.21	0.14	3576.00	4.33	0.69	0.39
0.20	1340.00	0.97	1.83	1.17	2632.00	4.18	0.54	0.30
0.48	2730.00	0.95	1.85	1.18	3832.00	3.58	0.06	-0.04
-0.38	1215.00	0.82	1.98	1.27	2026.00	1.97	1.67	-0.94
0.11	977.00	1.43	1.37	0.88	1475.00	4.07	0.43	0.24
0.76	1425.00	1.82	0.98	0.63	1716.00	3.38	0.26	-0.15
0.08	1538.00	1.69	1.11	0.71	2032.00	6.20	2.56	1.44
-0.49	1213.00	1.24	1.56	1.00	2073.00	3.38	0.26	-0.15
2.29	1545.00	0.45	2.35	1.50	1473.00	5.36	1.72	0.97
1.42	1545.00	1.62	1.18	0.76	2495.00	2.93	0.71	-0.40
1.64	1245.00	0.72	2.08	1.33	2128.00	3.10	0.54	-0.30
1.93	1299.00	0.92	1.88	1.20	2182.00	6.23	2.59	1.46
1.52	1066.00	0.75	2.05	1.31	1512.00	3.90	0.26	0.15
-0.51	1086.00	0.55	2.25	1.44	2742.00	2.01	1.63	-0.92
0.61	2300.00	1.26	1.54	0.99	3479.00	4.57	0.93	0.52
-1.51	1812.00	2.10	0.70	0.45	2458.00	2.97	0.67	-0.38
-0.78	3893.00	6.73	3.93	2.52	5507.00	10.30	6.66	3.74
-1.06	3248.00	0.74	2.06	1.32	4008.00	4.97	1.33	0.74
-1.18	1633.00	1.96	0.84	0.54	2455.00	5.34	1.70	0.95
-1.39	2107.00	2.71	0.09	0.06	2742.00	1.57	2.07	-1.16
-0.90	3841.00	2.21	0.59	0.38	4564.00	5.32	1.68	0.95
-1.46	3525.00	1.50	1.30	0.83	4072.00	3.24	0.40	-0.22
-1.46	2327.00	0.99	1.81	1.16	4075.00	2.58	1.06	-0.60
-1.00	2305.00	2.86	0.06	0.04	3721.00	6.80	3.16	1.78
-0.88	2669.00	3.11	0.31	0.20	2698.00	1.85	1.79	-1.00
-1.08	2077.00	0.67	2.13	1.36	2267.00	1.50	2.14	-1.20
0.91	2143.00	2.29	0.51	0.33	2683.00	7.64	4.00	2.25
-0.59	2643.00	3.03	0.23	0.15	2416.00	2.90	0.74	-0.42

-0.03	2424.00	3.18	0.38	0.24	2875.00	3.23	0.41	-0.23
-1.27	2084.00	0.58	2.22	1.43	2281.00	1.93	1.71	-0.96
-1.09	2748.00	1.64	1.16	0.75	3642.00	1.92	1.72	-0.97
-0.21	2995.00	0.57	2.23	1.43	4548.00	3.69	0.05	0.03
-1.02	1552.00	0.97	1.83	1.18	2497.00	3.28	0.36	-0.20
0.68	2940.00	1.05	1.75	1.12	3661.00	7.46	**3.82**	2.14
2.02	2170.00	2.49	0.31	0.20	2760.00	3.70	0.06	0.03
-1.04	3139.00	1.82	0.98	0.63	3410.00	1.09	2.56	-1.44
1.71	5168.00	6.68	3.88	2.48	5520.00	8.77	**5.13**	2.88
0.58	4012.00	3.29	0.49	0.31	5841.00	7.22	3.58	2.01
1.71	3372.00	9.46	6.66	4.27	3896.00	8.03	**4.39**	2.47
0.04	2918.00	3.26	0.46	0.29	4308.00	5.13	1.49	0.84
-0.71	2465.00	4.18	1.38	0.88	3604.00	4.02	0.38	0.21
-1.27	3644.00	1.54	1.26	0.81	3559.00	3.06	0.58	-0.32
-1.36	2581.00	2.71	0.09	0.06	3528.00	3.00	0.64	-0.36
-0.48	2934.00	5.45	2.65	1.70	3606.00	6.30	2.66	1.49
0.13	2425.00	2.31	0.49	0.31	2719.00	5.48	1.84	1.03
-0.59	2835.00	2.43	0.37	0.23	2942.00	3.03	0.61	-0.35
-0.29	2261.00	4.29	1.49	0.96	2253.00	4.48	0.84	0.47
2.37	347.00	12.68	9.88	6.33	362.00	10.22	**6.58**	3.70
-0.75	785.00	5.99	3.19	2.04	1575.00	4.00	0.36	0.20
-0.40	3094.00	4.27	1.47	0.94	5407.00	3.44	0.20	-0.11
0.11	1579.00	2.41	0.39	0.25	3461.00	2.57	1.07	-0.60
-0.97	1867.00	1.98	0.82	0.52	3824.00	1.94	1.70	-0.96
-1.66	2587.00	2.59	0.21	0.13	3919.00	1.91	1.73	-0.97
-0.45	2286.00	3.24	0.44	0.28	3766.00	1.30	2.34	-1.31
0.01	3727.00	3.57	0.77	0.49	4672.00	7.96	**4.32**	2.43
-0.98	1862.00	6.18	3.38	2.16	2043.00	4.89	1.25	0.70
0.29	4727.00	3.74	0.94	0.61	4397.00	5.69	2.05	1.15
0.00	3545.00	5.44	2.64	1.70	4965.00	7.63	**3.99**	2.24
-1.24	2715.00	5.64	2.84	1.82	3813.00	3.67	0.03	0.02
0.30	1599.00	5.44	2.64	1.69	2317.00	7.04	3.40	1.91
1.03	2831.00	3.46	0.66	0.42	4932.00	5.52	1.88	1.05
-0.42	1888.00	2.75	0.05	0.03	2581.00	4.26	0.62	0.35
-1.00	1964.00	2.75	0.05	0.03	3106.00	3.12	0.52	-0.29
-1.16	2949.00	2.68	0.12	0.08	2883.00	3.40	0.24	-0.14
-0.23	1545.00	3.50	0.70	0.45	1941.00	2.78	0.86	-0.48
0.13	2466.00	2.96	0.16	0.10	2805.00	6.10	2.46	1.38
-0.58	2763.00	3.00	0.20	0.13	2468.00	2.88	0.76	-0.43
-1.34	2007.00	4.63	1.83	1.18	2830.00	3.92	0.28	0.16
-0.12	2260.00	2.08	0.72	0.46	3093.00	4.27	0.63	0.35
-1.43	1067.00	3.37	0.57	0.37	1690.00	2.78	0.86	-0.48
-1.31	2722.00	0.88	1.92	1.23	2691.00	1.15	2.49	-1.40
-1.14	3323.00	1.56	1.24	0.79	3302.00	4.79	1.15	0.64
-1.60	2456.00	2.00	0.80	0.52	2615.00	6.00	2.36	1.33
-1.32	1980.00	2.12	0.68	0.44	2302.00	1.61	2.03	-1.14
-0.83	1481.00	0.54	2.26	1.45	1581.00	1.52	2.12	-1.19

-0.04	2851.00	2.28	0.52	0.33	3871.00	4.21	0.57	0.32
-0.50	1903.00	7.93	5.13	3.29	2193.00	3.33	0.31	-0.18
1.43	2816.00	3.76	0.96	0.62	3783.00	5.34	1.70	0.95
-0.24	2948.00	2.41	0.39	0.25	3386.00	3.84	0.20	0.11
0.06	2827.00	4.53	1.73	1.11	3931.00	1.91	1.73	-0.97
0.40	2647.00	3.36	0.56	0.36	2505.00	1.52	2.12	-1.19
-0.53	3700.00	2.19	0.61	0.39	3526.00	1.87	1.77	-0.99
-0.66	2998.00	1.07	1.73	1.11	3361.00	4.11	0.47	0.26
0.42	1173.00	4.86	2.06	1.32	1799.00	4.17	0.53	0.30
0.83	1691.00	3.08	0.28	0.18	1796.00	0.78	2.86	-1.61
0.94	1177.00	4.76	1.96	1.26	1458.00	1.44	2.20	-1.24
0.10	1805.00	2.05	0.75	0.48	2046.00	3.13	0.51	-0.29
0.61	1775.00	4.62	1.82	1.17	2235.00	1.61	2.03	-1.14
0.23	2637.00	1.90	0.90	0.58	1871.00	2.83	0.81	-0.45
-0.22	2422.00	3.14	0.34	0.22	2194.00	2.83	0.81	-0.46
0.86	3295.00	2.52	0.28	0.18	3097.00	2.68	0.96	-0.54
3.47	561.00	3.03	0.23	0.15	2251.00	5.29	1.65	0.92
0.34	1014.00	1.97	0.83	0.53	777.00	6.18	2.54	1.43
0.74	1694.00	3.42	0.62	0.40	1490.00	2.68	0.96	-0.54
1.19	1138.00	2.64	0.16	0.11	1059.00	3.97	0.33	0.18
0.98	1648.00	6.07	3.27	2.09	1850.00	3.19	0.45	-0.25
0.33	3083.00	1.85	0.95	0.61	3272.00	3.00	0.64	-0.36
0.55	2162.00	1.94	0.86	0.55	2797.00	4.15	0.51	0.28
-0.63	2760.00	1.78	1.02	0.66	4039.00	1.93	1.71	-0.96
-0.80	1593.00	3.08	0.28	0.18	3234.00	1.76	1.88	-1.06
2.03	1914.00	4.44	1.64	1.05	2433.00	6.08	2.44	1.37
0.66	2508.00	1.83	0.97	0.62	2097.00	3.86	0.22	0.12
-0.46	2204.00	2.13	0.67	0.43	3056.00	4.94	1.30	0.73
1.00	1980.00	2.32	0.48	0.31	2377.00	3.87	0.23	0.13
1.25	758.00	5.01	2.21	1.42	873.00	9.05	5.41	3.04
-1.34	1633.00	1.47	1.33	0.85	2350.00	5.96	2.32	1.30
0.14	1972.00	6.54	3.74	2.40	2495.00	3.61	0.03	-0.02
-0.04	2144.00	2.57	0.23	0.15	1979.00	7.23	3.59	2.01
-0.91	2671.00	3.67	0.87	0.56	1913.00	2.61	1.03	-0.58
0.13	2312.00	4.58	1.78	1.14	2674.00	5.12	1.48	0.83
2.81	2568.00	5.84	3.04	1.95	2147.00	7.82	4.18	2.35
-1.26	2985.00	2.48	0.32	0.21	3739.00	5.19	1.55	0.87
-0.99	1954.00	0.61	2.19	1.40	2280.00	2.89	0.75	-0.42
-0.95	1703.00	3.23	0.43	0.28	1374.00	5.39	1.75	0.98
-1.33	2644.00	3.10	0.30	0.19	1782.00	9.15	5.51	3.09
	2639.50	2.80	1.06		2511.50	3.64	1.20	
			3.17				3.61	
			1.56				1.78	
3127.00	10.11		3942.00	25.47				
4028.00	22.72		4327.00	15.51				
1962.00	9.43		3567.00	24.64				
3410.00	14.40		4337.00	22.87				

3131.75	14.16	4043.25	22.12
865.84	6.11	366.91	4.54
892.00	0.34	1113.00	3.77
696.00	0.72	2124.00	2.26
621.00	2.74	810.00	4.32
415.00	2.41	1236.00	4.77
577.33	1.96	1390.00	3.78
145.50	1.08	670.40	1.34
	18.34		13.62
	3.25		4.02
	21.59		17.64
	12.21		18.34
	1.77		0.96
	-0.77		0.04

238.00	23.53	295.00	26.44
188.00	16.49	220.00	21.82
1489.00	4.30	1437.00	3.62
1893.00	1.85	1812.00	4.36
4010.00	4.06	6230.00	10.11
5043.00	3.89	5650.00	8.78

x toxic a,b,c

x art a,b

x	toxic a,b,c

x	toxic a,b,c

y

y

x toxic a,b

y

y

y

y

x toxic a,b,c

x debris a

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50052.00	A02	M-013187- X antigen family, m	9503.00	XAGE1	3145.00	3.78	1.14
50052.00	A04	M-017496- X antigen family, m	9502.00	XAGE2	1550.00	1.94	0.70
50052.00	A05	M-017023- apelin, AGTRL1 liga	8862.00	APLN	2492.00	3.37	0.73
50052.00	A06	M-017670- rabphilin 3A-like (w	9501.00	RPH3AL	2457.00	2.24	0.40
50052.00	A07	M-011545- period homolog 3 (	8863.00	PER3	3112.00	0.96	1.68
50052.00	A08	M-007587- solute carrier family	9498.00	SLC4A8	6178.00	3.98	1.34
50052.00	A09	M-008747- sphingosine-1-phos	8879.00	SGPL1	4439.00	3.76	1.12
50052.00	A10	M-007586- solute carrier family	9497.00	SLC4A7	6026.00	6.06	**3.42**
50052.00	A11	M-009744- zinc finger protein 2	8882.00	ZNF259	2582.00	3.10	0.46
50052.00	A12	M-012320- proteasome (proso	9491.00	PSMF1	1436.00	2.58	0.06
50052.00	A13	M-006401- amyloid beta precu	8883.00	APPBP1	1868.00	3.27	0.63
50052.00	A14	M-009483- phosphatidylglycer	9489.00	PGS1	3920.00	0.59	2.05
50052.00	A15	M-007594- solute carrier family	8884.00	SLC5A6	2634.00	2.35	0.29
50052.00	A16	M-017189- phosphatidylinosito	9488.00	PIGB	3448.00	0.93	1.71
50052.00	A17	M-011549- eukaryotic translati	8894.00	EIF2S2	747.00	2.14	0.50
50052.00	A18	M-011953- phosphatidylinosito	9487.00	PIGL	1610.00	5.96	**3.32**
50052.00	A19	M-018665- BUD31 homolog (S.	8896.00	BUD31	3779.00	2.49	0.15
50052.00	A20	M-009858- carbohydrate sulfot	9486.00	CHST10	5117.00	1.31	1.33
50052.00	A21	M-011551- copine I	8904.00	CPNE1	2001.00	3.10	0.46
50052.00	A23	M-017445- adaptor-related pro	8905.00	AP1S2	3370.00	1.72	0.92
50052.00	B02	M-013864- nucleoporin like 1	9818.00	NUPL1	3088.00	1.46	1.18
50052.00	B04	M-012453- kelch-like ECH-asso	9817.00	KEAP1	2215.00	0.23	2.41
50052.00	B05	M-012344- P antigen family, m	9506.00	PAGE4	3536.00	0.31	2.33
50052.00	B06	M-021052- KIAA0133	9816.00	KIAA0133	4804.00	3.39	0.75
50052.00	B07	M-004747- peptidase (mitocho	9512.00	PMPCB	4097.00	3.27	0.63
50052.00	B08	M-024567- Sfi1 homolog, spind	9814.00	SFI1	3308.00	1.12	1.52
50052.00	B09	M-023581- syntaxin binding pr	9515.00	STXBP5L	2816.00	1.92	0.72
50052.00	B10	M-021022- KIAA0141	9812.00	KIAA0141	3691.00	1.30	1.34
50052.00	B11	M-006674- serine palmitoyltra	9517.00	SPTLC2	5724.00	3.62	0.98
50052.00	B12	M-021020- KIAA0427	9811.00	KIAA0427	3029.00	1.62	1.02
50052.00	B13	M-015983- eukaryotic translati	9521.00	EEF1E1	3960.00	2.73	0.09
50052.00	B14	M-006913- ring finger protein 4	9810.00	RNF40	1995.00	0.75	1.89
50052.00	B15	M-009537- glycoprotein, synap	9524.00	GPSN2	3800.00	0.24	2.40
50052.00	B16	M-021004- KIAA0087 gene pro	9808.00	KIAA0087	4085.00	2.42	0.22
50052.00	B17	M-013119- vacuolar protein so	9525.00	VPS4B	3428.00	3.03	0.39
50052.00	B18	M-021002- sparc/osteonectin,	9806.00	SPOCK2	3860.00	4.74	2.10
50052.00	B19	M-019876- mannose-P-dolichol	9526.00	MPDU1	5902.00	1.66	0.98
50052.00	B20	M-017879- secernin 1	9805.00	SCRN1	3636.00	2.56	0.08
50052.00	B21	M-010909- transmembrane pr	9528.00	TMEM59	4505.00	4.20	1.56
50052.00	B23	M-008887- polymerase (RNA) I	9533.00	POLR1C	2757.00	2.10	0.54
50052.00	C02	M-019873- syntaxin 8	9482.00	STX8	2728.00	1.10	1.54
50052.00	C04	M-006094- Trf (TATA binding p	9477.00	TRFP	3910.00	3.40	0.76
50052.00	C05	M-011552- adaptor-related pro	8906.00	AP1G2	4199.00	2.55	0.09
50052.00	C06	M-005976- napsin A aspartic pe	9476.00	NAPSA	4680.00	0.56	2.08
50052.00	C07	M-013196- adaptor-related pro	8907.00	AP1M1	4889.00	2.86	0.22
50052.00	C08	M-019871- chromosome 1 ope	9473.00	C1orf38	4138.00	1.47	1.17

50052.00	C09	M-006640-	glycogenin 2	8908.00	GYG2	4576.00	2.29	0.35
50052.00	C10	M-019870-	eukaryotic translati	9470.00	EIF4E2	2131.00	0.38	2.26
50052.00	C11	M-008695-	bassoon (presynapt	8927.00	BSN	3901.00	2.59	0.05
50052.00	C12	M-003958-	carbohydrate (chon	9469.00	CHST3	2790.00	2.04	0.60
50052.00	C13	M-012627-	family with sequenc	8933.00	FAM127A	2605.00	2.11	0.53
50052.00	C14	M-009611-	phosphate cytidylyl	9468.00	PCYT1B	2398.00	1.13	1.51
50052.00	C15	M-029452-	far upstream eleme	8939.00	FUBP3	3726.00	4.29	1.65
50052.00	C16	M-016041-	homer homolog 1 (	9456.00	HOMER1	3556.00	2.28	0.36
50052.00	C17	M-016014-	adaptor-related pro	8943.00	AP3D1	3237.00	1.79	0.85
50052.00	C18	M-019867-	homer homolog 2 (	9455.00	HOMER2	3386.00	5.94	3.30
50052.00	C19	M-013127-	histone cluster 1, H	8968.00	HIST1H3F	3103.00	8.19	**5.55**
50052.00	C20	M-005215-	homer homolog 3 (	9454.00	HOMER3	3574.00	4.48	1.84
50052.00	C21	M-013118-	histone cluster 1, H	8970.00	HIST1H2BJ	2522.00	3.29	0.65
50052.00	C23	M-012167-	H1 histone family, r	8971.00	H1FX	4312.00	4.52	1.88
50052.00	D02	M-006487-	translocase of outer	9804.00	TOMM20	2820.00	0.04	2.60
50052.00	D04	M-013418-	mitochondrial ribos	9801.00	MRPL19	4979.00	2.17	0.47
50052.00	D05	M-019877-	zinc finger protein 2	9534.00	ZNF254	5333.00	2.49	0.15
50052.00	D06	M-020977-	KIAA0174	9798.00	KIAA0174	4365.00	1.19	1.45
50052.00	D07	M-016236-	CBF1 interacting co	9541.00	CIR	6058.00	1.14	1.50
50052.00	D08	M-020966-	TatD DNase domain	9797.00	TATDN2	3660.00	0.96	1.68
50052.00	D09	M-011962-	amyloid beta (A4) p	9546.00	APBA3	2900.00	2.83	0.19
50052.00	D10	M-020952-	phytanoyl-CoA 2-hy	9796.00	PHYHIP	4373.00	2.15	0.49
50052.00	D11	M-013608-	ATPase, H+ transpo	9550.00	ATP6V1G1	3985.00	1.43	1.21
50052.00	D12	M-006847-	cytoskeleton associ	9793.00	CKAP5	3009.00	1.83	0.81
50052.00	D13	M-012690-	ATP synthase, H+ tr	9551.00	ATP5J2	4117.00	2.72	0.08
50052.00	D14	M-020913-	BMS1 homolog, rib	9790.00	BMS1	4933.00	3.30	0.66
50052.00	D15	M-019881-	sperm associated a	9552.00	SPAG7	4082.00	1.54	1.10
50052.00	D16	M-020897-	signal peptidase co	9789.00	SPCS2	4779.00	4.37	1.73
50052.00	D17	M-017401-	mitochondrial ribos	9553.00	MRPL33	3509.00	1.20	1.44
50052.00	D18	M-018506-	metastasis suppress	9788.00	MTSS1	5301.00	1.28	1.36
50052.00	D19	M-019882-	chromosome 14 op	9556.00	C14orf2	5640.00	1.72	0.92
50052.00	D20	M-020892-	KIAA0586	9786.00	KIAA0586	3906.00	1.69	0.95
50052.00	D21	M-014368-	chromodomain heli	9557.00	CHD1L	5028.00	4.20	1.56
50052.00	D23	M-013195-	vacuolar protein so	9559.00	VPS26A	4111.00	4.65	2.01
50052.00	E02	M-019433-	integral membrane	9452.00	ITM2A	2618.00	8.06	**5.42**
50052.00	E04	M-019866-	lymphocyte antigen	9450.00	LY86	3535.00	6.79	**4.15**
50052.00	E05	M-006367-	procollagen-proline	8974.00	P4HA2	3162.00	1.39	1.25
50052.00	E06	M-024905-	quaking homolog, K	9444.00	QKI	4052.00	2.64	0.00
50052.00	E07	M-004286-	procollagen-lysine,	8985.00	PLOD3	1209.00	2.98	0.34
50052.00	E08	M-008963-	carbohydrate (N-ac	9435.00	CHST2	6278.00	8.30	**5.66**
50052.00	E09	M-019489-	genethonin 1	8987.00	GENX-3414	2036.00	1.42	1.22
50052.00	E10	M-006265-	potassium channel,	9424.00	KCNK6	3137.00	4.08	1.44
50052.00	E11	M-011559-	ATPase, H+ transpo	8992.00	ATP6V0E1	1832.00	1.20	1.44
50052.00	E12	M-012661-	zinc finger protein 2	9422.00	ZNF264	4363.00	2.91	0.27
50052.00	E13	M-007473-	solute carrier family	9016.00	SLC25A14	2203.00	3.77	1.13
50052.00	E14	M-006904-	cysteine-rich PDZ-bi	9419.00	CRIPT	3512.00	3.39	0.75
50052.00	E15	M-008288-	cholesterol 25-hydr	9023.00	CH25H	3047.00	1.81	0.83

50052.00	E16	M-019861- DEAD (Asp-Glu-Ala-	9416.00	DDX23	5392.00	6.19	**3.55**
50052.00	E17	M-027079- huntingtin interacti	9026.00	HIP1R	3445.00	5.34	2.70
50052.00	E18	M-008211- fatty acid desaturas	9415.00	FADS2	3616.00	2.05	0.59
50052.00	E19	M-006027- rhomboid, veinlet-li	9028.00	RHBDL1	3437.00	4.57	1.93
50052.00	E20	M-021464- chromosome 9 ope	9413.00	C9orf61	2462.00	0.85	1.79
50052.00	E21	M-003717- transmembrane 4 L	9032.00	TM4SF5	3381.00	3.22	0.58
50052.00	E23	M-019490- sema domain, seve	9037.00	SEMA5A	3073.00	3.91	1.27
50052.00	F02	M-013428- DEAH (Asp-Glu-Ala-	9785.00	DHX38	3541.00	1.55	1.09
50052.00	F04	M-013427- sorting nexin 17	9784.00	SNX17	1671.00	4.37	1.73
50052.00	F05	M-004692- hexose-6-phosphat	9563.00	H6PD	3247.00	1.76	0.88
50052.00	F06	M-020891- regulating synaptic	9783.00	RIMS3	3123.00	2.08	0.56
50052.00	F07	M-017321- GTP binding protei	9567.00	GTPBP1	3482.00	2.10	0.54
50052.00	F08	M-020870- family with sequen	9780.00	FAM38A	5514.00	6.13	**3.49**
50052.00	F09	M-004852- growth differentiati	9573.00	GDF3	3663.00	2.76	0.12
50052.00	F10	M-020775- TBC1 domain family	9779.00	TBC1D5	4281.00	2.71	0.07
50052.00	F11	M-020038- SRY (sex determini	9580.00	SOX13	4178.00	1.77	0.87
50052.00	F12	M-024153- KIAA0232 gene pro	9778.00	KIAA0232	2287.00	1.92	0.72
50052.00	F13	M-005904- prolyl endopeptidas	9581.00	PREPL	2423.00	2.64	0.00
50052.00	F14	M-020769- transmembrane 9 s	9777.00	TM9SF4	5050.00	2.69	0.05
50052.00	F15	M-011965- RNA binding motif	9584.00	RBM39	3462.00	2.69	0.05
50052.00	F16	M-020765- KIAA0652	9776.00	KIAA0652	5065.00	3.57	0.93
50052.00	F17	M-020817- MAD2L1 binding pr	9587.00	MAD2L1BP	2354.00	1.91	0.73
50052.00	F18	M-020762- eukaryotic translati	9775.00	EIF4A3	5802.00	4.33	1.69
50052.00	F19	M-019884- immediate early res	9592.00	IER2	4924.00	2.64	0.00
50052.00	F20	M-020722- KIAA0195	9772.00	KIAA0195	3374.00	4.45	1.81
50052.00	F21	M-013414- pleckstrin homolog	9595.00	PSCDBP	4538.00	1.98	0.66
50052.00	F23	M-005212- CSAG family, memb	9598.00	CSAG2	5007.00	2.02	0.62
50052.00	G02	M-010158- zinc finger, RAN-bin	9406.00	ZRANB2	3346.00	0.75	1.89
50052.00	G04	M-009360- stomatin (EPB72)-li	9399.00	STOML1	2135.00	0.70	1.94
50052.00	G05	M-012948- ribosomal protein L	9045.00	RPL14	527.00	1.71	0.93
50052.00	G06	M-019858- immunoglobulin su	9398.00	IGSF2	3787.00	1.64	1.00
50052.00	G07	M-009953- artemin	9048.00	ARTN	3800.00	1.76	0.88
50052.00	G08	M-004317- N-myristoyltransfer	9397.00	NMT2	3073.00	1.92	0.72
50052.00	G09	M-011564- NFS1 nitrogen fixati	9054.00	NFS1	3870.00	2.40	0.24
50052.00	G10	M-011944- heparan sulfate 6-	9394.00	HS6ST1	2581.00	0.93	1.71
50052.00	G11	M-007616- solute carrier family	9057.00	SLC7A6	3212.00	1.21	1.43
50052.00	G12	M-007447- solute carrier family	9390.00	SLC22A13	4629.00	2.31	0.33
50052.00	G13	M-007392- solute carrier family	9058.00	SLC13A2	1863.00	0.97	1.67
50052.00	G14	M-007448- solute carrier family	9389.00	SLC22A14	4248.00	5.13	2.49
50052.00	G15	M-004306- synaptotagmin VII	9066.00	SYT7	3300.00	4.64	2.00
50052.00	G16	M-013309- component of oligo	9382.00	COG1	2837.00	1.52	1.12
50052.00	G17	M-019831- ash2 (absent, small,	9070.00	ASH2L	3366.00	1.40	1.24
50052.00	G18	M-012905- neurexin 2	9379.00	NRXN2	6253.00	4.67	2.03
50052.00	G19	M-017049- claudin 8	9073.00	CLDN8	3212.00	2.68	0.04
50052.00	G20	M-011941- neurexin 1	9378.00	NRXN1	6009.00	4.78	2.14
50052.00	G21	M-015883- claudin 6	9074.00	CLDN6	3887.00	3.47	0.83
50052.00	G23	M-014125- claudin 9	9080.00	CLDN9	2220.00	0.32	2.32

50052.00	H02	M-017672- KIAA0101	9768.00	KIAA0101	4189.00	2.43	0.21
50052.00	H04	M-013431- PHD finger protein	9767.00	PHF16	6269.00	4.40	1.76
50052.00	H05	M-019888- phosphatidylinosito	9600.00	PITPNM1	4048.00	6.77	**4.13**
50052.00	H06	M-020259- KIAA0247	9766.00	KIAA0247	4410.00	1.72	0.92
50052.00	H07	M-009931- guanine deaminase	9615.00	GDA	6735.00	5.40	2.76
50052.00	H08	M-020254- zinc finger, FYVE do	9765.00	ZFYVE16	3657.00	0.82	1.82
50052.00	H09	M-019211- mitochondrial trans	9617.00	MTRF1	4003.00	1.40	1.24
50052.00	H10	M-020292- KIAA0513	9764.00	KIAA0513	3682.00	4.94	2.30
50052.00	H11	M-005915- kallikrein-related pe	9622.00	KLK4	4381.00	5.20	2.56
50052.00	H12	M-013436- ProSAPiP1 protein	9762.00	ProSAPiP1	2802.00	2.28	0.36
50052.00	H13	M-012068- synuclein, alpha int	9627.00	SNCAIP	3563.00	3.17	0.53
50052.00	H14	M-020316- KIAA0152	9761.00	KIAA0152	3382.00	2.60	0.04
50052.00	H15	M-010703- chloride channel, ca	9629.00	CLCA3	3632.00	2.62	0.02
50052.00	H16	M-020339- thymocyte selectio	9760.00	TOX	1460.00	4.38	1.74
50052.00	H17	M-011967- nucleoporin 155kD	9631.00	NUP155	2803.00	1.96	0.68
50052.00	H18	M-010632- FERM and PDZ dom	9758.00	FRMPD4	3242.00	3.08	0.44
50052.00	H19	M-008467- SEC24 related gene	9632.00	SEC24C	3915.00	1.02	1.62
50052.00	H20	M-020406- TBK1 binding protei	9755.00	TBKBP1	2740.00	2.63	0.01
50052.00	H21	M-011968- metallothionein-lik	9633.00	MTL5	4167.00	2.18	0.46
50052.00	H23	M-004235- ISG15 ubiquitin-like	9636.00	ISG15	4617.00	2.49	0.15
50052.00	I02	M-011940- cytochrome c oxida	9377.00	COX5A	4486.00	4.08	1.44
50052.00	I04	M-007459- solute carrier famil	9376.00	SLC22A8	3392.00	1.33	1.31
50052.00	I05	M-019833- PTPN13-like, Y-link	9081.00	PRY	2477.00	0.65	1.99
50052.00	I06	M-010221- transmembrane 9 s	9375.00	TM9SF2	2484.00	2.70	0.06
50052.00	I07	M-011907- basic charge, Y-link	9083.00	BPY2	2232.00	1.57	1.07
50052.00	I08	M-005076- palmitoyl-protein t	9374.00	PPT2	1448.00	4.01	1.37
50052.00	I09	M-006469- variable charge, Y-li	9084.00	VCY	2251.00	4.89	2.25
50052.00	I10	M-011937- neurexin 3	9369.00	NRXN3	4867.00	4.03	1.39
50052.00	I11	M-011909- phosphatidylinosito	9091.00	PIGQ	2919.00	3.87	1.23
50052.00	I12	M-012688- solute carrier famil	9368.00	SLC9A3R1	2677.00	3.81	1.17
50052.00	I13	M-017792- DnaJ (Hsp40) homo	9093.00	DNAJA3	2586.00	1.12	1.52
50052.00	I14	M-011936- klotho	9365.00	KL	4841.00	4.07	1.43
50052.00	I15	M-027340- Fc fragment of IgG,	9103.00	FCGR2C	1416.00	3.67	1.03
50052.00	I16	M-012162- copine VI (neuronal	9362.00	CPNE6	2622.00	1.53	1.11
50052.00	I17	M-013396- regucalcin (senesce	9104.00	RGN	1616.00	2.04	0.60
50052.00	I18	M-003979- lon peptidase 1, mit	9361.00	LONP1	2595.00	3.47	0.83
50052.00	I19	M-019238- ATPase, H+ transpo	9114.00	ATP6V0D1	1169.00	4.96	2.32
50052.00	I20	M-007457- solute carrier famil	9356.00	SLC22A6	2094.00	1.86	0.78
50052.00	I21	M-011911- SEC22 vesicle traffi	9117.00	SEC22C	2613.00	2.03	0.61
50052.00	I23	M-014975- internexin neuronal	9118.00	INA	1999.00	3.45	0.81
50052.00	J02	M-010254- START domain cont	9754.00	STARD8	1702.00	2.76	0.12
50052.00	J04	M-020407- zinc finger and SCA	9753.00	ZSCAN12	4516.00	3.43	0.79
50052.00	J05	M-021364- fasciculation and el	9637.00	FEZ2	3465.00	4.16	1.52
50052.00	J06	M-020417- syntaphilin	9751.00	SNPH	3195.00	1.47	1.17
50052.00	J07	M-020790- zinc finger protein	9640.00	ZNF592	1326.00	9.58	**6.94**
50052.00	J08	M-013598- chromosome 6 ope	9750.00	C6orf32	2541.00	2.75	0.11
50052.00	J09	M-006380- mortality factor 4 li	9643.00	MORF4L2	2146.00	7.32	**4.68**

50052.00	J10	M-020445-	phosphatase and ac	9749.00	PHACTR2	795.00	3.52	0.88
50052.00	J11	M-032246-	Ctr9, Paf1/RNA poly	9646.00	CTR9	1873.00	2.94	0.30
50052.00	J12	M-020501-	KIAA0738 gene proc	9747.00	KIAA0738	1853.00	1.89	0.75
50052.00	J13	M-013457-	GRIP and coiled-coil	9648.00	GCC2	3833.00	2.95	0.31
50052.00	J14	M-020506-	zinc finger protein 5	9745.00	ZNF536	3325.00	12.36	9.72
50052.00	J15	M-019432-	mitochondrial fissio	9650.00	MTFR1	2322.00	2.33	0.31
50052.00	J16	M-021188-	centaurin, beta 1	9744.00	CENTB1	2881.00	1.56	1.08
50052.00	J17	M-027529-	phospholipase C, et	9651.00	PLCH2	3363.00	1.52	1.12
50052.00	J18	M-021253-	intraflagellar transp	9742.00	IFT140	3899.00	2.98	0.34
50052.00	J19	M-020959-	KIAA0372	9652.00	KIAA0372	3095.00	2.42	0.22
50052.00	J20	M-013439-	lysosomal-associate	9741.00	LAPTM4A	2640.00	2.61	0.03
50052.00	J21	M-003863-	heparan sulfate 2-O	9653.00	HS2ST1	3541.00	0.90	1.74
50052.00	J23	M-020210-	tubulin tyrosine liga	9654.00	TTLL4	2567.00	4.64	2.00
50052.00	K02	M-019197-	LIM homeobox 2	9355.00	LHX2	4287.00	1.61	1.03
50052.00	K04	M-012687-	thioredoxin-like 1	9352.00	TXNL1	3305.00	1.33	1.31
50052.00	K05	M-007408-	solute carrier family	9120.00	SLC16A6	3264.00	4.26	1.62
50052.00	K06	M-012019-	cerberus 1, cysteine	9350.00	CER1	3993.00	0.53	2.11
50052.00	K07	M-007407-	solute carrier family	9121.00	SLC16A5	2746.00	2.22	0.42
50052.00	K08	M-013634-	ribosomal protein L	9349.00	RPL23	476.00	3.15	0.51
50052.00	K09	M-007406-	solute carrier family	9122.00	SLC16A4	1866.00	2.14	0.50
50052.00	K10	M-008697-	N-deacetylase/N-su	9348.00	NDST3	3918.00	3.75	1.11
50052.00	K11	M-005126-	solute carrier family	9123.00	SLC16A3	657.00	5.94	3.30
50052.00	K12	M-019851-	elongation factor Tu	9343.00	EFTUD2	986.00	5.17	2.53
50052.00	K13	M-006834-	structural maintena	9126.00	SMC3	1647.00	3.58	0.94
50052.00	K14	M-011935-	synaptosomal-assoc	9342.00	SNAP29	1244.00	1.45	1.19
50052.00	K15	M-012678-	family with sequenc	9130.00	FAM50A	2459.00	1.42	1.22
50052.00	K16	M-011934-	vesicle-associated n	9341.00	VAMP3	1634.00	2.45	0.19
50052.00	K17	M-017645-	rabaptin, RAB GTPa	9135.00	RABEP1	1676.00	3.22	0.58
50052.00	K18	M-010389-	UDP-Gal:betaGlcNA	9334.00	B4GALT5	2385.00	4.99	2.35
50052.00	K19	M-017793-	RRP9, small subunit	9136.00	RRP9	2234.00	3.09	0.45
50052.00	K20	M-009636-	transglutaminase 5	9333.00	TGM5	689.00	3.77	1.13
50052.00	K21	M-019837-	chromosome X ope	9142.00	CXorf1	1846.00	5.96	3.32
50052.00	K23	M-017320-	synaptogyrin 3	9143.00	SYNGR3	3915.00	4.65	2.01
50052.00	L02	M-022793-	SET domain contain	9739.00	SETD1A	2248.00	1.69	0.95
50052.00	L04	M-017658-	CP110 protein	9738.00	CP110	1929.00	1.30	1.34
50052.00	L05	M-021206-	IQ motif containing	9657.00	IQCB1	2931.00	2.05	0.59
50052.00	L06	M-006082-	ubiquitin specific pe	9736.00	USP34	5856.00	3.35	0.71
50052.00	L07	M-006909-	zinc finger protein 5	9658.00	ZNF516	3626.00	1.63	1.01
50052.00	L08	M-006829-	kinetochore associa	9735.00	KNTC1	2206.00	2.40	0.24
50052.00	L09	M-021870-	phosphodiesterase	9659.00	PDE4DIP	2408.00	1.12	1.52
50052.00	L10	M-013447-	squamous cell carci	9733.00	SART3	3222.00	2.89	0.25
50052.00	L11	M-013458-	lipin 2	9663.00	LPIN2	2283.00	2.01	0.63
50052.00	L12	M-017968-	dedicator of cytokir	9732.00	DOCK4	1130.00	5.31	2.67
50052.00	L13	M-019172-	KIAA0430	9665.00	KIAA0430	2446.00	2.37	0.27
50052.00	L14	M-006911-	KIAA0562	9731.00	KIAA0562	2891.00	1.63	1.01
50052.00	L15	M-006910-	zinc finger DAZ inte	9666.00	DZIP3	2288.00	1.62	1.02
50052.00	L16	M-021119-	Vpr (HIV-1) binding	9730.00	VPRBP	1322.00	3.03	0.39

50052.00	L17	M-020373- scaffold attachment	9667.00	SAFB2	4115.00	3.65	1.01
50052.00	L18	M-022242- KIAA0256 gene pro	9728.00	KIAA0256	3685.00	3.85	1.21
50052.00	L19	M-020326- zinc finger protein 4	9668.00	ZNF432	4425.00	3.46	0.82
50052.00	L20	M-021079- RAB11 family intera	9727.00	RAB11FIP3	1699.00	69.69	**67.05**
50052.00	L21	M-013331- eukaryotic translati	9669.00	EIF5B	2404.00	6.82	**4.18**
50052.00	L23	M-020212- importin 13	9670.00	IPO13	3885.00	3.81	1.17
50052.00	M02	M-011933- UDP-Gal:betaGlcNA	9331.00	B4GALT6	2794.00	0.32	2.32
50052.00	M04	M-008740- phosphotriesterase	9317.00	PTER	6024.00	4.13	1.49
50052.00	M05	M-011914- synaptogyrin 2	9144.00	SYNGR2	2904.00	1.52	1.12
50052.00	M06	M-019848- chromosome 5 ope	9315.00	C5orf13	2357.00	0.68	1.96
50052.00	M07	M-011915- synaptogyrin 1	9145.00	SYNGR1	2777.00	0.97	1.67
50052.00	M08	M-011931- zinc finger protein 2	9310.00	ZNF235	2765.00	1.48	1.16
50052.00	M09	M-016835- hepatocyte growth	9146.00	HGS	3290.00	0.85	1.79
50052.00	M10	M-017375- suppressor of cytok	9306.00	SOCS6	4742.00	4.37	1.73
50052.00	M11	M-019106- serologically define	9147.00	SDCCAG1	3085.00	2.50	0.14
50052.00	M12	M-019746- nuclear pore compl	9284.00	NPIP	3363.00	2.29	0.35
50052.00	M13	M-007605- solute carrier family	9152.00	SLC6A5	1955.00	1.38	1.26
50052.00	M14	M-015820- zinc finger and BTB	9278.00	ZBTB22	2702.00	5.40	2.76
50052.00	M15	M-007504- solute carrier family	9153.00	SLC28A2	2665.00	5.67	3.03
50052.00	M16	M-009242- WD repeat domain	9277.00	WDR46	2485.00	1.21	1.43
50052.00	M17	M-007503- solute carrier family	9154.00	SLC28A1	2714.00	2.17	0.47
50052.00	M18	M-017230- B-cell CLL/lymphom	9274.00	BCL7C	2872.00	2.51	0.13
50052.00	M19	M-013179- cytochrome c oxida	9167.00	COX7A2L	2955.00	2.91	0.27
50052.00	M20	M-012719- calcium channel, vo	9254.00	CACNA2D2	164.00	50.61	**47.97**
50052.00	M21	M-011561- myomesin (M-prote	9172.00	MYOM2	3431.00	3.47	0.83
50052.00	M23	M-011918- adaptor-related pro	9179.00	AP4M1	3606.00	9.96	**7.32**
50052.00	N02	M-021050- zinc finger protein 6	9726.00	ZNF646	2277.00	0.61	2.03
50052.00	N04	M-021043- transmembrane pro	9725.00	TMEM63A	2832.00	1.20	1.44
50052.00	N05	M-026920- WSC domain contai	9671.00	WSCD2	2810.00	2.38	0.26
50052.00	N06	M-014126- UTP14, U3 small nu	9724.00	UTP14C	3913.00	4.40	1.76
50052.00	N07	M-020563- syndecan 3	9672.00	SDC3	5000.00	6.46	**3.82**
50052.00	N08	M-020073- sema domain, immu	9723.00	SEMA3E	2073.00	1.93	0.71
50052.00	N09	M-007339- solute carrier family	9673.00	SLC25A44	5090.00	7.09	**4.45**
50052.00	N10	M-032236- G protein regulated	9721.00	GPRIN2	3978.00	6.16	**3.52**
50052.00	N11	M-014187- KIAA0040	9674.00	KIAA0040	2055.00	0.19	2.45
50052.00	N12	M-023028- KIAA0565 gene pro	9720.00	KIAA0565	532.00	6.20	**3.56**
50052.00	N13	M-014188- KIAA0406	9675.00	KIAA0406	3329.00	3.27	0.63
50052.00	N14	M-022626- SEC14-like 5 (S. cere	9717.00	SEC14L5	3050.00	5.02	2.38
50052.00	N15	M-004786- histidine acid phosp	9677.00	HISPPD2A	4901.00	5.43	2.79
50052.00	N16	M-022214- aquarius homolog (	9716.00	AQR	2622.00	3.17	0.53
50052.00	N17	M-020678- PHD finger protein	9678.00	PHF14	2636.00	1.21	1.43
50052.00	N18	M-020927- family with sequen	9715.00	FAM131B	558.00	2.15	0.49
50052.00	N19	M-020690- family with sequen	9679.00	FAM53B	3900.00	3.13	0.49
50052.00	N20	M-020925- USP6 N-terminal lik	9712.00	USP6NL	367.00	28.61	**25.97**
50052.00	N21	M-020708- DEP domain contai	9681.00	DEPDC5	1753.00	1.26	1.39
50052.00	N23	M-004292- jumonji domain con	9682.00	JMJD2A	2182.00	1.33	1.31
50052.00	O02	M-012682- numb homolog (Dr	9253.00	NUMBL	2947.00	3.63	0.99

50052.00	O04	M-008656- dehydrogenase/red	9249.00	DHRS3	6112.00	8.92	**6.28**
50052.00	O05	M-012060- peptidylglycine alph	9182.00	PAMCI	3469.00	2.97	0.33
50052.00	O06	M-011923- glucosaminyl (N-ace	9245.00	GCNT3	4110.00	5.35	2.71
50052.00	O07	M-007464- solute carrier family	9187.00	SLC24A1	2937.00	2.08	0.56
50052.00	O08	M-009640- discs, large (Drosop	9228.00	DLGAP2	2962.00	4.93	2.29
50052.00	O09	M-011919- DEAD (Asp-Glu-Ala-	9188.00	DDX21	3079.00	2.47	0.17
50052.00	O10	M-021382- VAMP (vesicle-asso	9218.00	VAPA	3476.00	2.91	0.27
50052.00	O11	M-012679- zinc finger, BED-typ	9189.00	ZBED1	2545.00	2.59	0.05
50052.00	O12	M-017795- VAMP (vesicle-asso	9217.00	VAPB	3180.00	6.76	**4.12**
50052.00	O13	M-007409- solute carrier family	9194.00	SLC16A7	2934.00	7.43	**4.79**
50052.00	O14	M-020113- leucine rich repeat (	9209.00	LRRFIP2	2829.00	1.98	0.66
50052.00	O15	M-007533- solute carrier family	9197.00	SLC33A1	2195.00	3.55	0.91
50052.00	O16	M-019842- leucine rich repeat (	9208.00	LRRFIP1	4960.00	7.60	**4.96**
50052.00	O17	M-019932- zinc finger, MYM-ty	9202.00	ZMYM4	3395.00	3.95	1.31
50052.00	O18	M-020648- zinc finger, MYM-ty	9205.00	ZMYM5	2269.00	5.24	2.60
50052.00	O19	M-013117- histone cluster 1, H	8969.00	HIST1H2AG	3508.00	3.14	0.50
50052.00	O20	M-016304- zinc finger, MYM-ty	9204.00	ZMYM6	3290.00	3.47	0.83
50052.00	O21	M-010978- thymosin, beta 4, Y-	9087.00	TMSB4Y	2175.00	7.77	**5.13**
50052.00	O23	M-019933- zinc finger, MYM-ty	9203.00	ZMYM3	2341.00	2.90	0.26
50052.00	P02	M-023538- KIAA0226	9711.00	KIAA0226	1738.00	3.86	1.22
50052.00	P04	M-020920- KIAA0355	9710.00	KIAA0355	2539.00	0.79	1.85
50052.00	P05	M-020733- Nedd4 binding prot	9683.00	N4BP1	3603.00	2.22	0.42
50052.00	P06	M-020904- centrosomal protei	9707.00	Cep290	1976.00	0.91	1.73
50052.00	P07	M-021406- clathrin interactor 1	9685.00	CLINT1	1400.00	2.86	0.22
50052.00	P08	M-008451- suppression of tum	9705.00	ST18	2367.00	3.89	1.25
50052.00	P09	M-023447- vestigial like 4 (Dros	9686.00	VGLL4	4066.00	2.61	0.03
50052.00	P10	M-032233- DEAH (Asp-Glu-Ala-	9704.00	DHX34	2113.00	1.89	0.75
50052.00	P11	M-008187- GREB1 protein	9687.00	GREB1	1960.00	3.01	0.37
50052.00	P12	M-023289- KIAA0100	9703.00	KIAA0100	1669.00	3.24	0.60
50052.00	P13	M-020767- nucleoporin 93kDa	9688.00	NUP93	1284.00	2.80	0.16
50052.00	P14	M-020885- centrosomal protei	9702.00	CEP57	1205.00	3.32	0.68
50052.00	P15	M-020787- basic leucine zipper	9689.00	BZW1	2037.00	1.96	0.68
50052.00	P16	M-021331- SAPS domain family	9701.00	SAPS2	1860.00	1.83	0.81
50052.00	P17	M-020859- KIAA0391	9692.00	KIAA0391	2869.00	3.17	0.53
50052.00	P18	M-004104- extra spindle pole b	9700.00	ESPL1	1579.00	1.01	1.63
50052.00	P19	M-010631- tetratricopeptide re	9694.00	TTC35	3232.00	4.55	1.91
50052.00	P20	M-006665- regulating synaptic	9699.00	RIMS2	1252.00	4.79	2.15
50052.00	P21	M-021651- ciliary rootlet coiled	9696.00	CROCC	2164.00	5.13	2.49
50052.00	P23	M-014179- pumilio homolog 1	9698.00	PUM1	1851.00	2.92	0.28
					3117.50	2.64	1.10
							3.31
					MADc		1.63
50052.00	C22				2079.00	16.21	
50052.00	D22				4655.00	16.97	
50052.00	E22				3449.00	14.73	
50052.00	F22				4333.00	17.26	
				mn	3629.00	16.29	

					sd	1152.27	1.13
50052.00	G22					1453.00	2.89
50052.00	H22					1017.00	3.24
50052.00	I22					581.00	5.16
50052.00	J22					1004.00	2.59
					mn	867.33	3.67
					sd	248.06	1.34
					3psSD		3.40
					3ngSD		4.01
					SumSD		7.41
					DiffMn		12.63
					SmovrDiff		0.59
					1minus		0.41
50052.00	G03	M-003290-	polo-like kinase 1 (D	5347.00	PLK1 SMAR	199.00	1.51
50052.00	H03	M-003290-	polo-like kinase 1 (D	5347.00	PLK1 SMAR	5911.00	7.31
50052.00	I03	D-001206-	siControl non-targeting siRNA #			5033.00	4.09
50052.00	J03	D-001206-	siControl non-targeting siRNA #			2408.00	3.24
50052.00	K03	D-001600-	siGLO RISC-free siRNA			5377.00	3.91
50052.00	L03	D-001600-	siGLO RISC-free siRNA			5425.00	3.58

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
0.70	2254.00	0.71	2.50	-1.42	2581.00	1.51	1.53	-0.68
-0.43	1594.00	0.88	2.33	-1.32	2045.00	0.98	2.06	-0.92
0.45	2099.00	0.76	2.45	-1.39	1451.00	1.93	1.11	-0.49
-0.25	1477.00	0.68	2.53	-1.43	859.00	1.05	1.99	-0.88
-1.03	2904.00	1.00	2.21	-1.25	2024.00	1.38	1.66	-0.74
0.82	3407.00	1.82	1.39	-0.79	3928.00	0.71	2.33	-1.03
0.69	2891.00	2.94	0.27	-0.15	3918.00	1.17	1.87	-0.83
2.09	3439.00	2.62	0.59	-0.34	4124.00	1.29	1.75	-0.78
0.28	1602.00	2.31	0.90	-0.51	1436.00	3.83	0.79	0.35
-0.04	545.00	5.32	2.11	1.20	619.00	2.10	0.94	-0.42
0.38	293.00	6.83	**3.62**	2.05	978.00	1.12	1.92	-0.85
-1.26	1326.00	4.00	0.79	0.45	2314.00	0.35	2.69	-1.20
-0.18	1455.00	3.44	0.23	0.13	1557.00	0.64	2.40	-1.06
-1.05	2255.00	4.66	1.45	0.82	2975.00	0.97	2.07	-0.92
-0.31	276.00	4.35	1.14	0.65	436.00	3.44	0.40	0.18
2.03	949.00	2.32	0.89	-0.50	1798.00	0.83	2.21	-0.98
-0.09	1863.00	10.31	**7.10**	4.02	2182.00	1.19	1.85	-0.82
-0.81	4205.00	2.47	0.74	-0.42	4404.00	2.41	0.63	-0.28
0.28	1618.00	3.34	0.13	0.07	1348.00	0.59	2.45	-1.09
-0.56	1615.00	3.22	0.01	0.01	1814.00	0.77	2.27	-1.01
-0.72	2555.00	3.21	0.00	0.00	2650.00	1.28	1.76	-0.78
-1.48	2279.00	3.12	0.09	-0.05	1388.00	1.66	1.38	-0.61
-1.43	2984.00	1.47	1.74	-0.98	2688.00	1.53	1.51	-0.67
0.46	3206.00	2.96	0.25	-0.14	2479.00	3.47	0.43	0.19
0.39	3200.00	5.53	2.32	1.32	2809.00	1.57	1.47	-0.65
-0.93	2346.00	1.53	1.68	-0.95	1764.00	3.23	0.19	0.09
-0.44	1839.00	4.08	0.87	0.49	1569.00	1.72	1.32	-0.59
-0.82	2294.00	2.44	0.77	-0.43	3170.00	0.91	2.13	-0.94
0.60	3945.00	2.86	0.35	-0.19	2863.00	3.14	0.10	0.05
-0.63	3145.00	2.64	0.57	-0.32	1874.00	3.84	0.80	0.36
0.05	2774.00	4.15	0.94	0.53	2054.00	1.95	1.09	-0.48
-1.16	1068.00	4.96	1.75	0.99	1849.00	1.41	1.63	-0.73
-1.47	2433.00	1.19	2.02	-1.14	2477.00	1.98	1.06	-0.47
-0.13	2910.00	4.06	0.85	0.48	3259.00	4.33	1.29	0.57
0.24	1917.00	3.39	0.18	0.10	1198.00	3.42	0.38	0.17
1.28	3772.00	3.08	0.13	-0.08	3031.00	4.45	1.41	0.63
-0.60	4273.00	1.26	1.95	-1.10	4337.00	1.29	1.75	-0.78
-0.05	3208.00	1.75	1.46	-0.83	2034.00	2.06	0.98	-0.43
0.95	4079.00	1.64	1.57	-0.89	3008.00	4.12	1.08	0.48
-0.33	1797.00	2.78	0.43	-0.24	1800.00	4.11	1.07	0.48
-0.94	3163.00	3.16	0.05	-0.03	2878.00	3.96	0.92	0.41
0.47	3550.00	4.59	1.38	0.78	3068.00	0.95	2.09	-0.93
-0.06	3181.00	3.49	0.28	0.16	4459.00	2.53	0.51	-0.22
-1.28	4218.00	3.67	0.46	0.26	3626.00	1.38	1.66	-0.74
0.14	2775.00	2.27	0.94	-0.53	3778.00	2.70	0.34	-0.15
-0.71	1322.00	3.25	0.04	0.03	2600.00	2.00	1.04	-0.46

-0.21	2632.00	2.77	0.44	-0.25	4866.00	2.61	0.43	-0.19	
-1.39	970.00	7.32	**4.11**	2.33	2971.00	1.45	1.59	-0.71	
-0.03	2896.00	3.31	0.10	0.06	3989.00	0.83	2.21	-0.98	
-0.37	1769.00	5.99	2.78	1.58	1763.00	1.02	2.02	-0.90	
-0.32	1537.00	5.34	2.13	1.21	2687.00	1.15	1.89	-0.84	
-0.93	1397.00	9.16	**5.95**	3.38	1761.00	1.42	1.62	-0.72	
1.01	2343.00	8.79	**5.58**	3.17	3686.00	2.25	0.79	-0.35	
-0.22	1918.00	3.18	0.03	-0.02	3333.00	1.08	1.96	-0.87	
-0.52	2608.00	3.53	0.32	0.18	3785.00	0.40	2.64	-1.17	
2.02	2303.00	5.47	2.26	1.28	2776.00	2.70	0.34	-0.15	
3.39	1567.00	3.25	0.04	0.03	2259.00	2.35	0.69	-0.31	
1.12	3093.00	5.21	2.00	1.13	3570.00	1.46	1.58	-0.70	
0.40	2881.00	1.67	1.54	-0.87	3077.00	1.37	1.68	-0.74	
1.15	2942.00	1.63	1.58	-0.89	4585.00	0.24	2.80	-1.24	
-1.59	3392.00	2.45	0.76	-0.43	3600.00	1.81	1.23	-0.55	
-0.29	4087.00	5.73	2.52	1.43	4496.00	2.78	0.26	-0.11	
-0.09	3646.00	3.79	0.58	0.33	4088.00	2.74	0.30	-0.13	
-0.89	1598.00	2.25	0.96	-0.54	3940.00	0.86	2.18	-0.97	
-0.92	3626.00	3.61	0.40	0.23	3796.00	2.63	0.41	-0.18	
-1.03	1605.00	5.23	2.02	1.15	1920.00	4.53	1.49	0.66	
0.11	2312.00	3.72	0.51	0.29	2789.00	3.08	0.04	0.02	
-0.30	1952.00	4.61	1.40	0.79	4488.00	5.17	2.13	0.95	
-0.74	2461.00	5.93	2.72	1.54	2929.00	2.25	0.79	-0.35	
-0.50	1730.00	4.57	1.36	0.77	2207.00	0.95	2.09	-0.93	
0.05	2620.00	5.73	2.52	1.43	2800.00	1.75	1.29	-0.57	
0.41	2578.00	5.28	2.07	1.17	3013.00	4.91	1.87	0.83	
-0.67	2934.00	2.25	0.96	-0.54	3001.00	0.90	2.14	-0.95	
1.06	2278.00	7.46	**4.25**	2.41	3800.00	4.61	1.57	0.70	
-0.88	2134.00	4.59	1.38	0.78	2690.00	1.60	1.44	-0.64	
-0.83	2759.00	4.17	0.96	0.54	4165.00	0.50	2.54	-1.13	
-0.56	3017.00	4.01	0.80	0.45	4625.00	0.93	2.11	-0.94	
-0.58	1752.00	1.14	2.07	-1.17	2474.00	1.33	1.71	-0.76	
0.95	2968.00	5.86	2.65	1.50	4955.00	1.70	1.34	-0.60	
1.23	2032.00	4.48	1.27	0.72	3975.00	2.82	0.22	-0.10	
3.32	3633.00	5.84	2.63	1.49	3881.00	3.84	0.80	0.36	
2.54	3781.00	2.06	1.15	-0.65	2248.00	3.16	0.12	0.05	
-0.76	2410.00	2.57	0.64	-0.36	2104.00	3.33	0.29	0.13	
0.00	2177.00	5.60	2.39	1.36	2935.00	4.19	1.15	0.51	
0.21	891.00	8.19	**4.98**	2.83	688.00	9.74	**6.70**	2.98	x
3.46	5224.00	5.21	2.00	1.13	5523.00	4.13	1.09	0.49	
-0.74	950.00	4.95	1.74	0.99	2316.00	5.05	2.01	0.90	
0.88	1992.00	5.27	2.06	1.17	3082.00	3.24	0.20	0.09	
-0.88	762.00	5.77	2.56	1.45	1281.00	4.92	1.88	0.84	
0.17	2030.00	2.66	0.55	-0.31	3149.00	2.45	0.59	-0.26	
0.69	938.00	3.84	0.63	0.36	733.00	2.86	0.18	-0.08	
0.46	2048.00	1.71	1.50	-0.85	2619.00	7.71	**4.67**	2.08	
-0.51	1475.00	3.12	0.09	-0.05	3228.00	1.61	1.43	-0.63	

2.17	4361.00	2.89	0.32	-0.18	4961.00	5.30	2.26	1.01	
1.65	1412.00	3.47	0.26	0.15	2175.00	5.79	2.75	1.23	
-0.36	2157.00	4.64	1.43	0.81	3046.00	4.40	1.36	0.61	
1.18	1950.00	1.69	1.52	-0.86	2515.00	1.99	1.05	-0.47	
-1.09	1306.00	8.50	5.29	3.00	1616.00	3.03	0.01	0.00	
0.36	2980.00	3.19	0.02	-0.01	3830.00	2.77	0.27	-0.12	
0.77	2647.00	2.80	0.41	-0.23	3016.00	2.98	0.06	-0.02	
-0.67	3943.00	0.99	2.22	-1.26	3448.00	3.07	0.03	0.02	
1.06	2302.00	2.30	0.91	-0.51	2085.00	2.01	1.03	-0.45	
-0.54	2569.00	1.87	1.34	-0.76	3207.00	2.34	0.70	-0.31	
-0.34	1846.00	3.95	0.74	0.42	2578.00	2.83	0.21	-0.09	
-0.33	2272.00	2.86	0.35	-0.20	2505.00	5.55	2.51	1.12	
2.13	4365.00	3.12	0.09	-0.05	3713.00	4.20	1.16	0.52	
0.07	1690.00	3.79	0.58	0.33	1535.00	3.84	0.80	0.36	
0.04	2024.00	2.52	0.69	-0.39	3324.00	3.01	0.03	-0.01	
-0.53	2050.00	2.20	1.01	-0.57	2228.00	1.71	1.33	-0.59	
-0.44	1772.00	1.30	1.91	-1.08	1448.00	4.21	1.17	0.52	
0.00	1248.00	1.84	1.37	-0.77	910.00	4.07	1.03	0.46	
0.03	1688.00	1.78	1.43	-0.81	2081.00	2.50	0.54	-0.24	
0.03	1928.00	1.87	1.34	-0.76	2174.00	2.35	0.69	-0.31	
0.57	2601.00	1.85	1.36	-0.77	2875.00	3.65	0.61	0.27	
-0.45	1713.00	2.80	0.41	-0.23	1076.00	2.97	0.07	-0.03	
1.03	3937.00	4.06	0.85	0.49	4020.00	5.17	2.13	0.95	
0.00	3552.00	2.45	0.76	-0.43	4244.00	3.94	0.90	0.40	
1.10	2725.00	6.94	3.73	2.11	1922.00	4.58	1.54	0.69	
-0.40	3070.00	2.77	0.44	-0.25	1613.00	1.98	1.06	-0.47	
-0.38	3017.00	4.44	1.23	0.70	4112.00	1.97	1.07	-0.47	
-1.16	3578.00	0.95	2.26	-1.28	2703.00	1.04	2.00	-0.89	
-1.19	2214.00	1.04	2.17	-1.23	1814.00	1.10	1.94	-0.86	
-0.57	473.00	3.81	0.60	0.34	462.00	6.28	3.24	1.44	
-0.61	2715.00	1.95	1.26	-0.71	2708.00	1.48	1.56	-0.69	
-0.54	2426.00	0.87	2.34	-1.33	2909.00	2.89	0.15	-0.07	
-0.44	1581.00	1.08	2.13	-1.21	1404.00	1.64	1.40	-0.62	
-0.15	3288.00	2.59	0.62	-0.35	3303.00	5.03	1.99	0.88	
-1.05	1879.00	1.70	1.51	-0.85	1844.00	1.90	1.14	-0.51	
-0.87	1882.00	3.88	0.67	0.38	1914.00	1.99	1.05	-0.47	
-0.20	4892.00	8.91	5.70	3.23	4622.00	5.67	2.63	1.17	
-1.02	2341.00	1.79	1.42	-0.80	1311.00	1.45	1.59	-0.71	
1.52	5139.00	8.81	5.60	3.18	4387.00	9.53	6.49	2.89	y
1.22	4019.00	7.04	3.83	2.17	3635.00	4.13	1.09	0.48	
-0.69	2282.00	4.95	1.74	0.99	1608.00	1.99	1.05	-0.47	
-0.76	1709.00	0.82	2.39	-1.35	1837.00	1.42	1.62	-0.72	
1.24	5070.00	6.71	3.50	1.98	5555.00	6.35	3.31	1.48	
0.02	2223.00	3.73	0.52	0.30	2634.00	5.62	2.58	1.15	
1.31	5722.00	5.77	2.56	1.45	6535.00	5.91	2.87	1.28	
0.51	4224.00	2.98	0.23	-0.13	4539.00	2.45	0.59	-0.26	
-1.42	1667.00	2.22	0.99	-0.56	3617.00	1.27	1.77	-0.78	

-0.13	4104.00	2.95	0.26	-0.15	3962.00	3.61	0.57	0.25	
1.08	5392.00	1.67	1.54	-0.87	4500.00	1.82	1.22	-0.54	
2.53	3810.00	3.39	0.18	0.10	3451.00	2.93	0.11	-0.05	
-0.56	2447.00	2.29	0.92	-0.52	1852.00	4.64	1.60	0.71	
1.69	5758.00	8.48	**5.27**	2.99	5169.00	5.75	2.71	1.20	
-1.11	2855.00	3.29	0.08	0.05	2993.00	4.64	1.60	0.71	
-0.76	3455.00	2.72	0.49	-0.28	2588.00	1.85	1.19	-0.53	
1.41	1986.00	5.19	1.98	1.12	2092.00	3.11	0.07	0.03	
1.57	3002.00	2.53	0.68	-0.38	2379.00	1.43	1.61	-0.71	
-0.22	2499.00	3.16	0.05	-0.03	1329.00	1.96	1.08	-0.48	
0.32	1935.00	4.03	0.82	0.47	2044.00	1.47	1.57	-0.70	
-0.02	995.00	3.52	0.31	0.18	2167.00	1.20	1.84	-0.82	
-0.02	1433.00	87.23	**84.02**	47.63	2442.00	2.54	0.50	-0.22	
1.07	1534.00	2.80	0.41	-0.23	869.00	1.96	1.08	-0.48	
-0.42	1855.00	2.32	0.89	-0.50	1443.00	0.35	2.69	-1.20	
0.27	3500.00	9.26	**6.05**	3.43	2348.00	4.64	1.60	0.71	
-0.99	4305.00	2.79	0.42	-0.24	4386.00	1.57	1.47	-0.65	
-0.01	4135.00	7.71	**4.50**	2.55	2587.00	1.12	1.92	-0.85	
-0.28	4939.00	10.51	**7.30**	4.14	4105.00	2.07	0.97	-0.43	
-0.09	4696.00	3.75	0.54	0.31	5139.00	2.63	0.41	-0.18	
0.88	4609.00	3.08	0.13	-0.07	4185.00	6.12	3.08	1.37	
-0.80	2817.00	2.34	0.87	-0.49	2718.00	6.00	2.96	1.32	
-1.22	1769.00	1.30	1.91	-1.08	1942.00	2.06	0.98	-0.43	
0.03	2738.00	1.53	1.68	-0.95	2141.00	7.19	4.15	1.85	
-0.66	2142.00	2.89	0.32	-0.18	1715.00	7.99	**4.95**	2.20	
0.83	1371.00	8.83	**5.62**	3.18	988.00	12.55	**9.51**	4.23	x
1.37	2278.00	7.46	**4.25**	2.41	2022.00	6.33	3.29	1.46	
0.85	5279.00	7.26	**4.05**	2.29	5926.00	8.34	**5.30**	2.36	y
0.75	2410.00	3.03	0.18	-0.10	2192.00	4.33	1.29	0.58	
0.72	2279.00	2.33	0.88	-0.50	1632.00	6.99	3.95	1.76	
-0.93	1879.00	2.50	0.71	-0.40	1413.00	7.93	**4.89**	2.17	
0.87	5396.00	4.97	1.76	1.00	4259.00	8.99	**5.95**	2.65	
0.63	2147.00	1.44	1.77	-1.00	1186.00	10.62	**7.58**	3.37	
-0.68	3735.00	5.17	1.96	1.11	2182.00	6.05	3.01	1.34	
-0.37	2949.00	4.44	1.23	0.70	1215.00	4.28	1.24	0.55	
0.51	3561.00	2.44	0.77	-0.43	2258.00	4.30	1.26	0.56	
1.42	2963.00	2.16	1.05	-0.59	1423.00	7.80	**4.76**	2.12	
-0.48	2471.00	2.83	0.38	-0.21	2495.00	4.69	1.65	0.73	
-0.37	2957.00	1.86	1.35	-0.76	1883.00	3.08	0.04	0.02	
0.50	3133.00	3.57	0.36	0.21	2074.00	3.66	0.62	0.28	
0.07	2333.00	2.06	1.15	-0.65	1889.00	4.34	1.30	0.58	
0.48	4546.00	3.83	0.62	0.35	3962.00	2.60	0.44	-0.19	
0.93	4482.00	2.32	0.89	-0.50	2975.00	6.29	3.25	1.44	
-0.72	3946.00	3.73	0.52	0.29	2228.00	1.93	1.11	-0.49	
4.24	1034.00	7.54	**4.33**	2.46	832.00	13.46	**10.42**	4.64	x
0.07	2157.00	2.55	0.66	-0.37	1772.00	4.63	1.59	0.71	
2.86	1782.00	6.17	2.96	1.68	1366.00	3.44	0.40	0.18	

0.54	1343.00	2.76	0.46	-0.26	1296.00	2.93	0.11	-0.05	
0.18	1968.00	2.95	0.26	-0.15	1332.00	3.83	0.79	0.35	
-0.46	1368.00	3.07	0.14	-0.08	1164.00	2.58	0.46	-0.20	
0.19	2594.00	1.66	1.55	-0.88	2914.00	1.34	1.70	-0.76	
5.95	2453.00	8.52	**5.31**	3.01	2564.00	8.81	**5.77**	2.57	y
-0.19	1735.00	6.57	3.36	1.91	2257.00	4.52	1.48	0.66	
-0.66	2264.00	3.00	0.21	-0.12	2767.00	1.95	1.09	-0.48	
-0.69	2267.00	3.26	0.05	0.03	1579.00	2.66	0.38	-0.17	
0.20	2614.00	6.50	3.29	1.87	3087.00	3.37	0.33	0.15	
-0.13	1612.00	3.16	0.05	-0.03	2048.00	3.52	0.48	0.21	
-0.02	1420.00	6.41	3.20	1.81	2624.00	1.91	1.13	-0.50	
-1.06	2607.00	2.22	0.99	-0.56	4036.00	1.44	1.60	-0.71	
1.22	1913.00	2.98	0.23	-0.13	2275.00	5.36	2.32	1.03	
-0.63	3557.00	3.23	0.02	0.01	3777.00	2.28	0.76	-0.34	
-0.80	3366.00	2.91	0.30	-0.17	2349.00	3.96	0.92	0.41	
0.99	3235.00	3.09	0.12	-0.07	2674.00	5.46	2.42	1.08	
-1.29	3483.00	3.04	0.17	-0.09	3495.00	1.55	1.49	-0.66	
-0.26	1769.00	6.33	3.12	1.77	1810.00	4.97	1.93	0.86	
0.31	1029.00	3.21	0.00	0.00	772.00	12.69	**9.65**	4.29	
-0.30	2112.00	3.93	0.72	0.41	2029.00	9.46	**6.42**	2.86	
0.68	5105.00	2.92	0.29	-0.16	4408.00	12.34	**9.30**	4.14	
2.02	731.00	4.65	1.44	0.82	522.00	9.20	**6.16**	2.74	x
1.55	635.00	8.03	**4.82**	2.73	734.00	14.85	**11.81**	5.25	x
0.58	1189.00	2.78	0.43	-0.25	1095.00	5.75	2.71	1.21	
-0.73	1665.00	1.32	1.89	-1.07	2074.00	6.94	3.90	1.74	
-0.75	1864.00	2.41	0.80	-0.45	1692.00	5.85	2.81	1.25	
-0.12	2451.00	3.35	0.14	0.08	2107.00	4.94	1.90	0.84	
0.36	2690.00	3.53	0.32	0.18	2034.00	7.82	**4.78**	2.13	
1.44	2092.00	2.92	0.29	-0.17	1868.00	2.68	0.36	-0.16	
0.27	1090.00	2.39	0.82	-0.47	1759.00	3.13	0.09	0.04	
0.69	2157.00	2.32	0.89	-0.50	1677.00	5.01	1.97	0.88	
2.03	2492.00	2.73	0.48	-0.27	1503.00	7.45	4.41	1.96	
1.23	3215.00	3.02	0.19	-0.11	2788.00	3.98	0.94	0.42	
-0.58	2737.00	5.88	2.67	1.52	2373.00	2.53	0.51	-0.23	
-0.82	2292.00	4.19	0.98	0.56	1025.00	3.90	0.86	0.38	
-0.36	1762.00	4.71	1.50	0.85	2269.00	5.11	2.07	0.92	
0.43	6448.00	4.82	1.61	0.92	4915.00	5.05	2.01	0.89	
-0.62	3447.00	4.58	1.37	0.78	2864.00	1.82	1.22	-0.54	
-0.15	2575.00	2.68	0.53	-0.30	1733.00	5.71	2.67	1.19	
-0.93	3025.00	4.03	0.82	0.47	1734.00	3.11	0.07	0.03	
0.15	3494.00	4.58	1.37	0.78	2461.00	2.19	0.85	-0.37	
-0.38	2724.00	4.52	1.31	0.74	1431.00	6.29	3.25	1.45	
1.63	671.00	18.03	**14.82**	8.40	765.00	7.58	4.54	2.02	x
-0.17	2669.00	8.09	**4.88**	2.77	1655.00	6.22	3.18	1.42	
-0.62	2931.00	6.89	**3.68**	2.09	2061.00	3.69	0.65	0.29	
-0.63	2639.00	5.27	2.06	1.17	1512.00	6.22	3.18	1.41	
0.24	1349.00	11.27	**8.06**	4.57	846.00	11.82	**8.78**	3.91	x

0.61	5289.00	8.38	**5.17**	2.93	4720.00	3.92	0.88	0.39	
0.74	4208.00	6.61	3.40	1.93	1802.00	4.72	1.68	0.75	
0.50	4315.00	6.40	3.19	1.81	2792.00	9.99	**6.95**	3.09	
41.03	2812.00	4.80	1.59	0.90	2749.00	5.09	2.05	0.91	
2.56	2495.00	5.29	2.08	1.18	1223.00	4.99	1.95	0.87	
0.71	3173.00	5.58	2.37	1.34	3526.00	4.48	1.44	0.64	
-1.42	3642.00	1.95	1.26	-0.71	4635.00	1.81	1.23	-0.54	
0.91	6710.00	8.60	**5.39**	3.06	5268.00	3.38	0.34	0.15	
-0.69	3784.00	2.72	0.49	-0.28	2106.00	2.61	0.43	-0.19	
-1.20	3204.00	4.56	1.35	0.76	2201.00	1.59	1.45	-0.64	
-1.02	2012.00	1.49	1.72	-0.97	2071.00	1.93	1.11	-0.49	
-0.71	2463.00	2.19	1.02	-0.58	1533.00	1.44	1.60	-0.71	
-1.10	3475.00	3.17	0.04	-0.02	2229.00	0.94	2.10	-0.93	
1.05	4608.00	4.97	1.76	1.00	2993.00	9.09	**6.05**	2.69	
-0.09	2925.00	3.97	0.76	0.43	2249.00	2.09	0.95	-0.42	
-0.22	2324.00	1.33	1.88	-1.06	2221.00	2.39	0.65	-0.29	
-0.77	1605.00	2.62	0.59	-0.34	1447.00	4.98	1.94	0.86	
1.69	2195.00	8.75	**5.54**	3.14	2933.00	7.60	**4.56**	2.03	x
1.85	2201.00	7.18	**3.97**	2.25	1360.00	6.47	3.43	1.53	
-0.88	2353.00	1.91	1.30	-0.73	1161.00	1.81	1.23	-0.55	
-0.29	2712.00	0.26	2.95	-1.67	1280.00	3.83	0.79	0.35	
-0.08	2472.00	4.49	1.28	0.73	1499.00	10.87	**7.83**	3.48	
0.16	2539.00	4.10	0.89	0.50	2385.00	3.14	0.10	0.05	
29.35	4006.00	5.97	2.76	1.56	1459.00	7.13	4.09	1.82	
0.51	2667.00	5.25	2.04	1.16	2176.00	3.58	0.54	0.24	
4.48	3495.00	2.80	0.41	-0.23	2583.00	4.72	1.68	0.75	
-1.24	2906.00	1.10	2.11	-1.19	2304.00	1.35	1.69	-0.75	
-0.88	3311.00	2.11	1.10	-0.62	2079.00	3.99	0.95	0.42	
-0.16	2462.00	2.11	1.10	-0.62	1315.00	3.04	0.00	0.00	
1.07	4504.00	5.26	2.05	1.16	2400.00	6.42	3.38	1.50	
2.34	3952.00	3.24	0.03	0.02	2644.00	6.13	3.09	1.37	
-0.44	2329.00	2.71	0.51	-0.29	1790.00	3.85	0.81	0.36	
2.72	6521.00	7.74	**4.53**	2.57	4428.00	4.27	1.23	0.55	y
2.15	4890.00	6.95	**3.74**	2.12	2294.00	7.45	4.41	1.96	y
-1.50	2059.00	2.33	0.88	-0.50	890.00	6.29	3.25	1.45	
2.18	783.00	6.51	3.30	1.87	485.00	5.36	2.32	1.03	
0.39	3126.00	4.96	1.75	0.99	1875.00	3.68	0.64	0.29	
1.45	2826.00	4.74	1.53	0.87	1772.00	2.26	0.78	-0.35	
1.70	5496.00	5.42	2.21	1.25	3631.00	16.00	**12.96**	5.76	
0.32	2675.00	4.00	0.79	0.45	1188.00	4.12	1.08	0.48	
-0.87	3046.00	2.20	1.01	-0.57	910.00	2.09	0.95	-0.42	
-0.30	425.00	4.94	1.73	0.98	180.00	10.00	**6.96**	3.10	
0.30	2813.00	3.09	0.12	-0.07	1458.00	2.61	0.43	-0.19	
15.89	524.00	9.54	**6.33**	3.59	235.00	11.06	**8.02**	3.57	x
-0.85	2010.00	5.47	2.26	1.28	1058.00	3.59	0.55	0.25	
-0.80	750.00	3.73	0.52	0.30	712.00	2.95	0.09	-0.04	
0.61	3325.00	4.93	1.72	0.98	2815.00	1.24	1.80	-0.80	

3.84	6864.00	11.15	7.94	4.50	4967.00	8.15	5.11	2.28	y
0.20	3427.00	2.51	0.70	-0.40	2349.00	1.58	1.46	-0.65	
1.66	2748.00	1.20	2.01	-1.14	2584.00	1.47	1.57	-0.70	
-0.35	2490.00	3.49	0.28	0.16	2100.00	1.24	1.80	-0.80	
1.40	3908.00	2.71	0.50	-0.28	3660.00	4.78	1.74	0.78	
-0.11	2776.00	1.22	1.99	-1.12	1749.00	1.20	1.84	-0.82	
0.16	2759.00	2.10	1.11	-0.63	1920.00	0.16	2.88	-1.28	
-0.03	3006.00	2.73	0.48	-0.27	1497.00	0.33	2.71	-1.20	
2.52	3017.00	2.82	0.39	-0.22	2833.00	1.45	1.59	-0.71	
2.93	2862.00	4.68	1.47	0.84	2852.00	0.74	2.30	-1.02	
-0.40	3680.00	3.21	0.00	0.00	2640.00	0.34	2.70	-1.20	
0.56	3517.00	4.21	1.00	0.57	1343.00	2.31	0.73	-0.32	
3.03	4791.00	3.53	0.32	0.18	5246.00	2.54	0.50	-0.22	
0.80	3347.00	3.08	0.13	-0.07	2347.00	0.60	2.44	-1.09	
1.59	1713.00	8.76	5.55	3.14	2169.00	4.56	1.52	0.68	
0.30	2717.00	2.94	0.27	-0.15	3718.00	0.89	2.15	-0.96	
0.50	3071.00	4.04	0.83	0.47	3938.00	1.24	1.80	-0.80	
3.14	2612.00	2.34	0.87	-0.49	1695.00	0.35	2.69	-1.19	
0.16	2335.00	2.91	0.30	-0.17	2646.00	0.60	2.44	-1.08	
0.74	2146.00	3.40	0.19	0.11	1115.00	3.41	0.37	0.17	
-1.13	3412.00	3.46	0.25	0.14	1696.00	3.24	0.20	0.09	
-0.26	4579.00	2.18	1.03	-0.58	1887.00	3.87	0.83	0.37	
-1.06	2877.00	0.70	2.51	-1.42	1716.00	2.86	0.18	-0.08	
0.13	2394.00	0.67	2.54	-1.44	766.00	6.53	3.49	1.55	
0.76	2265.00	2.56	0.65	-0.37	1174.00	7.24	4.20	1.87	
-0.02	4909.00	1.32	1.89	-1.07	2499.00	4.36	1.32	0.59	
-0.46	1688.00	3.85	0.64	0.36	1781.00	5.95	2.91	1.30	
0.23	2893.00	1.56	1.65	-0.94	1116.00	6.90	3.86	1.72	
0.36	1734.00	3.23	0.02	0.01	554.00	10.29	7.25	3.22	
0.10	1565.00	1.15	2.06	-1.17	1135.00	3.52	0.48	0.22	
0.42	1395.00	3.15	0.06	-0.03	984.00	5.18	2.14	0.95	
-0.41	1993.00	1.40	1.81	-1.02	2812.00	2.88	0.16	-0.07	
-0.50	2458.00	1.91	1.30	-0.73	1999.00	6.25	3.21	1.43	
0.32	3892.00	1.03	2.18	-1.24	3053.00	2.26	0.78	-0.35	
-1.00	1766.00	0.45	2.76	-1.56	1888.00	2.17	0.87	-0.38	
1.17	5488.00	3.04	0.17	-0.09	5845.00	2.87	0.17	-0.07	
1.32	928.00	1.51	1.70	-0.96	1358.00	2.21	0.83	-0.37	
1.52	3711.00	3.85	0.64	0.37	2706.00	4.14	1.10	0.49	
0.17	2042.00	1.76	1.45	-0.82	2108.00	1.90	1.14	-0.51	
	2562.00	3.21	1.19		2264.00	3.04	1.52		
			3.58				4.56		
			1.76				2.25		
3931.00	22.64						4965.00	8.62	
4116.00	17.47						4920.00	11.24	
			3476.00	18.44					
4530.00	26.65		3215.00	18.91	3396.00	13.22			
4192.33	22.25		3345.50	18.68					

306.71	4.60	184.55	0.33
1331.00	3.68	1422.00	6.05
2130.00	2.35	886.00	4.18
1570.00	4.01	1003.00	2.59
1130.00	5.04	1227.00	5.38
1610.00	3.80	1038.67	4.05
501.20	1.36	173.28	1.40
	13.80		1.00
	4.08		4.19
	17.88		5.19
	18.45		14.63
	0.97		0.35
	0.03		0.65
264.00	10.61	285.00	7.37
6586.00	7.09	4953.00	3.67
4409.00	3.67	5996.00	4.77
2631.00	2.32	1942.00	1.18
5516.00	9.66	5047.00	4.46
5914.00	8.00	5263.00	7.45

toxic a,b,c

toxic a,b,c

toxic a,b,c

toxic a,b,c
toxic a,b,c

toxic a,b,c

toxic a,b,c

debris a,b

toxic a,b,c

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50053.00	A02	M-018891- leucine rich	10233.00	LRRC23	2388.00	3.10	1.06
50053.00	A04	M-020054- Down synd	10231.00	DSCR1L1	1450.00	2.41	0.37
50053.00	A05	M-006909- zinc finger	9658.00	ZNF516	2555.00	2.19	0.15
50053.00	A06	M-017296- coenzyme	10229.00	COQ7	2688.00	6.92	**4.88**
50053.00	A07	M-021095- TSC22 dom	9819.00	TSC22D2	3350.00	1.73	0.31
50053.00	A08	M-017164- syntaxin 6	10228.00	STX6	1340.00	2.39	0.35
50053.00	A09	M-017673- cullin 7	9820.00	CUL7	1107.00	4.97	2.93
50053.00	A10	M-016015- tetracyclin	10227.00	TETRAN	1180.00	2.29	0.25
50053.00	A11	M-010936- armadillo r	9823.00	ARMCX2	2146.00	1.21	0.83
50053.00	A12	M-020045- CD96 mole	10225.00	CD96	2120.00	4.39	2.35
50053.00	A13	M-021122- Rho GTPas	9824.00	ARHGAP11	764.00	8.51	**6.47**
50053.00	A14	M-018335- zinc finger	10224.00	ZNF443	1298.00	3.62	1.58
50053.00	A15	M-020065- spermatog	9825.00	SPATA2	1049.00	5.53	**3.49**
50053.00	A16	M-012072- glycoprotei	10223.00	GPA33	1213.00	1.24	0.80
50053.00	A17	M-021128- KIAA0258	9827.00	KIAA0258	864.00	4.40	2.36
50053.00	A18	M-020003- CTD (carbo	10217.00	CTDSPL	2857.00	6.90	**4.86**
50053.00	A19	M-009885- DnaJ (Hsp4	9829.00	DNAJC6	403.00	10.42	**8.38**
50053.00	A20	M-013112- synovial sa	10214.00	SSX3	749.00	3.47	1.43
50053.00	A21	M-021173- janus kinas	9832.00	JAKMIP2	1238.00	4.77	2.73
50053.00	A23	M-012968- KIAA0125	9834.00	KIAA0125	687.00	2.91	0.87
50053.00	B02	M-017235- guanine nu	10681.00	GNB5	2018.00	2.63	0.59
50053.00	B04	M-013717- UDP-GlcNA	10678.00	B3GNT2	2436.00	2.96	0.92
50053.00	B05	M-010905- heterogene	10236.00	HNRPR	4754.00	9.53	**7.49**
50053.00	B06	M-012275- advillin	10677.00	AVIL	5158.00	4.98	2.94
50053.00	B07	M-007542- solute carri	10237.00	SLC35B1	2726.00	1.61	0.43
50053.00	B08	M-020164- chondroiti	10675.00	CSPG5	2322.00	1.98	0.06
50053.00	B09	M-017162- adaptor-rel	10239.00	AP3S2	2387.00	2.47	0.43
50053.00	B10	M-012302- dynactin 6	10671.00	DCTN6	2640.00	1.63	0.41
50053.00	B11	M-012111- mitochond	10240.00	MRPS31	2805.00	1.75	0.29
50053.00	B12	M-012283- phenylalan	10667.00	FARS2	2957.00	3.58	1.54
50053.00	B13	M-009087- potassium	10242.00	KCNMB2	2182.00	2.52	0.48
50053.00	B14	M-020167- CD226 mol	10666.00	CD226	1779.00	0.84	1.20
50053.00	B15	M-020047- translocase	10245.00	TIMM17B	3472.00	2.71	0.67
50053.00	B16	M-018889- chromoso	10665.00	C6orf10	3963.00	3.71	1.67
50053.00	B17	M-007412- solute carri	10246.00	SLC17A2	2274.00	0.84	1.20
50053.00	B18	M-012748- KH domain	10656.00	KHDRBS3	4139.00	3.58	1.54
50053.00	B19	M-020051- heat-respo	10247.00	HRSP12	4498.00	0.69	1.35
50053.00	B20	M-019237- YKT6 v-SN	10652.00	YKT6	3306.00	1.00	1.04
50053.00	B21	M-010274- glycine-N-a	10249.00	GLYAT	1995.00	1.05	0.99
50053.00	B23	M-020041- serine/argi	10250.00	SRRM1	1941.00	1.60	0.44
50053.00	C02	M-004920- DEAD (Asp-	10212.00	DDX39	3877.00	4.72	2.68
50053.00	C04	M-010636- flotillin 1	10211.00	FLOT1	2673.00	4.30	2.26
50053.00	C05	M-008815- leucine car	9836.00	LCMT2	3324.00	3.76	1.72
50053.00	C06	M-015804- eukaryotic	10209.00	EIF1	4784.00	4.62	2.58
50053.00	C07	M-014001- GINS comp	9837.00	GINS1	4886.00	5.87	**3.83**
50053.00	C08	M-012112- InaD-like (	10207.00	INADL	4014.00	8.74	**6.70**

50053.00	C09	M-021265- KIAA0748	9840.00	KIAA0748	3397.00	3.18	1.14
50053.00	C10	M-017371- epithelial V	10205.00	EVA1	2962.00	1.86	0.18
50053.00	C11	M-006915- zinc finger	9841.00	ZBTB24	3421.00	3.57	1.53
50053.00	C12	M-012132- nuclear tra	10204.00	NUTF2	1354.00	4.14	2.10
50053.00	C13	M-023203- pleckstrin	9842.00	PLEKHM1	3436.00	5.21	**3.17**
50053.00	C14	M-009581- dehydroge	10202.00	DHRS2	2127.00	5.74	**3.70**
50053.00	C15	M-009498- hephaestin	9843.00	HEPH	2812.00	2.56	0.52
50053.00	C16	M-012128- M-phase pl	10199.00	MPHOSPH	2830.00	2.33	0.29
50053.00	C17	M-014180- KIAA0528	9847.00	KIAA0528	3587.00	2.90	0.86
50053.00	C18	M-012133- proteasom	10197.00	PSME3	3527.00	1.76	0.28
50053.00	C19	M-007729- microfibrill	9848.00	MFAP3L	3899.00	1.44	0.60
50053.00	C20	M-026786- protein arg	10196.00	PRMT3	3498.00	2.74	0.70
50053.00	C21	M-021263- KIAA0753	9851.00	KIAA0753	2184.00	5.59	**3.55**
50053.00	C23	M-018914- EPM2A (laf	9852.00	EPM2AIP1	1985.00	8.16	**6.12**
50053.00	D02	M-020087- metaxin 2	10651.00	MTX2	2928.00	2.53	0.49
50053.00	D04	M-020157- slowmo ho	10650.00	SLMO1	3382.00	6.68	**4.64**
50053.00	D05	M-012103- HLA compl	10255.00	HCG9	3446.00	2.41	0.37
50053.00	D06	M-012291- secretoglo	10647.00	SCGB1D2	3196.00	2.00	0.04
50053.00	D07	M-019994- immunoglc	10261.00	IGSF6	3805.00	3.94	1.90
50053.00	D08	M-019483- fibrinogen	10646.00	FSBP	2154.00	2.41	0.37
50053.00	D09	M-017190- splicing fac	10262.00	SF3B4	955.00	5.97	**3.93**
50053.00	D10	M-013114- left-right d	10637.00	LEFTY1	4819.00	2.28	0.24
50053.00	D11	M-010638- stromal an	10274.00	STAG1	3133.00	2.11	0.07
50053.00	D12	M-017969- ATP syntha	10632.00	ATP5L	3339.00	7.01	**4.97**
50053.00	D13	M-012089- Down synd	10281.00	DSCR4	2271.00	3.26	1.22
50053.00	D14	M-017560- podoplanir	10630.00	PDPN	2366.00	4.40	2.36
50053.00	D15	M-012085- BET1 homc	10282.00	BET1	1858.00	3.28	1.24
50053.00	D16	M-010814- thioredoxir	10628.00	TXNIP	3130.00	2.56	0.52
50053.00	D17	M-020024- serologicall	10283.00	SDCCAG10	2663.00	3.57	1.53
50053.00	D18	M-021498- myosin reg	10627.00	MRCL3	2013.00	6.56	**4.52**
50053.00	D19	M-016257- survival mc	10285.00	SMNDC1	3127.00	3.49	1.45
50053.00	D20	M-012220- tripartite m	10626.00	TRIM16	4241.00	7.19	**5.15**
50053.00	D21	M-019996- eukaryotic	10289.00	EIF1B	4374.00	7.54	**5.50**
50053.00	D23	M-012095- macrophag	10296.00	MAEA	3870.00	1.27	0.77
50053.00	E02	M-012131- teashirt far	10194.00	TSHZ1	2866.00	1.81	0.23
50053.00	E04	M-006922- ring finger	10193.00	RNF41	1088.00	2.67	0.63
50053.00	E05	M-026133- RUN and SI	9853.00	RUSC2	1425.00	1.12	0.92
50053.00	E06	M-012079- thioredoxir	10190.00	TXNDC9	1933.00	1.60	0.44
50053.00	E07	M-018353- transmemb	9854.00	TMEM24	2915.00	0.55	1.49
50053.00	E08	M-012078- THO compl	10189.00	THOC4	4461.00	1.68	0.36
50053.00	E09	M-015290- centrosom	9857.00	CEP350	2925.00	2.02	0.02
50053.00	E10	M-017936- RNA bindin	10179.00	RBM7	2920.00	1.34	0.70
50053.00	E11	M-021259- KIAA0649	9858.00	KIAA0649	1827.00	3.01	0.97
50053.00	E12	M-020639- odz, odd O	10178.00	ODZ1	3754.00	1.17	0.87
50053.00	E13	M-021251- leucine-rich	9860.00	LRIG2	1777.00	1.35	0.69
50053.00	E14	M-019989- cornichon	10175.00	CNIH	2262.00	2.34	0.30
50053.00	E15	M-021249- proteasom	9861.00	PSMD6	224.00	5.36	**3.32**

50053.00	E16	M-021347- zinc finger	10172.00	ZNF256	2695.00	1.15	0.89
50053.00	E17	M-021245- KIAA0644 g	9865.00	KIAA0644	2664.00	0.86	1.18
50053.00	E18	M-016313- RNA termir	10171.00	RCL1	3593.00	1.53	0.51
50053.00	E19	M-026772- tripartite m	9866.00	TRIM66	1732.00	0.52	1.52
50053.00	E20	M-009400- dehydroger	10170.00	DHRS9	2620.00	1.07	0.97
50053.00	E21	M-006916- praja 2, RIN	9867.00	PJA2	3190.00	2.16	0.12
50053.00	E23	M-021243- translocase	9868.00	TOMM70A	3410.00	1.96	0.08
50053.00	F02	M-019448- polymerase	10623.00	POLR3C	4680.00	2.59	0.55
50053.00	F04	M-020140- polymerase	10622.00	POLR3G	1501.00	1.27	0.77
50053.00	F05	M-006925- membrane	10299.00	MARCH6	4075.00	1.06	0.98
50053.00	F06	M-019240- polymerase	10621.00	POLR3F	2753.00	2.14	0.10
50053.00	F07	M-012115- katanin p8(	10300.00	KATNB1	3073.00	1.95	0.09
50053.00	F08	M-008511- trans-golgi	10618.00	TGOLN2	632.00	3.48	1.44
50053.00	F09	M-020009- deleted in l	10301.00	DLEU1	3304.00	2.06	0.02
50053.00	F10	M-012202- STAM bind	10617.00	STAMBP	3587.00	1.37	0.67
50053.00	F11	M-020094- small nucle	10302.00	SNAPC5	1374.00	1.24	0.80
50053.00	F12	M-006839- sperm asso	10615.00	SPAG5	3057.00	1.67	0.37
50053.00	F13	M-015637- zinc finger	10308.00	ZNF267	2707.00	0.89	1.15
50053.00	F14	M-012225- hexamethy	10614.00	HEXIM1	1731.00	1.16	0.88
50053.00	F15	M-012163- Down synd	10311.00	DSCR3	2008.00	1.64	0.40
50053.00	F16	M-015639- ER lipid raf	10613.00	ERLIN1	2512.00	0.80	1.24
50053.00	F17	M-020088- reticulon 3	10313.00	RTN3	1849.00	2.22	0.18
50053.00	F18	M-006931- tripartite m	10612.00	TRIM3	2790.00	1.54	0.50
50053.00	F19	M-012159- UDP-Gal:be	10317.00	B3GALT5	3050.00	3.54	1.50
50053.00	F20	M-020149- ST6 (alpha-	10610.00	ST6GALNA(	1924.00	1.30	0.74
50053.00	F21	M-020092- cysteine-ric	10321.00	CRISP3	2250.00	2.09	0.05
50053.00	F23	M-020089- kelch repea	10324.00	KBTBD10	3237.00	3.49	1.45
50053.00	G02	M-016317- small EDRK	10169.00	SERF2	1550.00	2.26	0.22
50053.00	G04	M-004860- carbohydra	10164.00	CHST4	1730.00	3.87	1.83
50053.00	G05	M-007184- KIAA0317	9870.00	KIAA0317	1833.00	2.13	0.09
50053.00	G06	M-010273- membrane	10162.00	MBOAT5	3658.00	4.62	2.58
50053.00	G07	M-008493- SEC24 relat	9871.00	SEC24D	3445.00	1.57	0.47
50053.00	G08	M-013647- ATPase, H+	10159.00	ATP6AP2	2125.00	6.35	**4.31**
50053.00	G09	M-021240- FCH and dc	9873.00	FCHSD2	1449.00	1.52	0.52
50053.00	G10	M-010635- PDZK1 inte	10158.00	PDZK1IP1	2029.00	2.32	0.28
50053.00	G11	M-021236- TOX high m	9878.00	TOX4	1714.00	1.40	0.64
50053.00	G12	M-032198- muscleblin	10150.00	MBNL2	4020.00	1.87	0.17
50053.00	G13	M-021234- DEAD (Asp-	9879.00	DDX46	1763.00	2.38	0.34
50053.00	G14	M-032208- splicing fac	10147.00	SFRS14	2005.00	8.23	**6.19**
50053.00	G15	M-021232- zinc finger	9880.00	ZBTB39	1771.00	1.02	1.02
50053.00	G16	M-020516- family with	10144.00	FAM13A1	3016.00	1.82	0.22
50053.00	G17	M-023465- lupus brain	9881.00	LBA1	3836.00	1.25	0.79
50053.00	G18	M-019986- C-type lecti	10143.00	CLEC3A	3299.00	1.76	0.28
50053.00	G19	M-021230- TBC1 doma	9882.00	TBC1D4	2671.00	1.98	0.06
50053.00	G20	M-012073- chromoson	10141.00	C4orf6	3914.00	4.04	2.00
50053.00	G21	M-017575- POM121 m	9883.00	POM121	1471.00	0.68	1.36
50053.00	G23	M-021228- leucine rich	9884.00	LRRC37A	3910.00	0.84	1.20

50053.00	H02	M-020141- synaptoner	10609.00	SC65	3333.00	0.36	1.68
50053.00	H04	M-019182- poly(A) bin	10605.00	PAIP1	4123.00	0.39	1.65
50053.00	H05	M-012189- Ras-relatec	10325.00	RRAGB	2487.00	0.08	1.96
50053.00	H06	M-007440- solute carri	10599.00	SLCO1B1	3564.00	0.84	1.20
50053.00	H07	M-006926- polycomb g	10336.00	PCGF3	1916.00	0.00	2.04
50053.00	H08	M-006836- structural r	10592.00	SMC2	1134.00	1.68	0.36
50053.00	H09	M-020098- triadin	10345.00	TRDN	2316.00	0.09	1.95
50053.00	H10	M-013631- secretagog	10590.00	SCGN	2144.00	4.01	1.97
50053.00	H11	M-009892- tryptophan	10352.00	WARS2	3266.00	0.28	1.76
50053.00	H12	M-008242- 5,10-methe	10588.00	MTHFS	2151.00	1.02	1.02
50053.00	H13	M-012347- nucleophos	10360.00	NPM3	1988.00	0.15	1.89
50053.00	H14	M-012216- collectin su	10584.00	COLEC10	3512.00	0.46	1.58
50053.00	H15	M-019230- nucleophos	10361.00	NPM2	2777.00	0.90	1.14
50053.00	H16	M-019804- SMA3	10571.00	SMA3	1256.00	0.24	1.80
50053.00	H17	M-012720- calcium bir	10367.00	CBARA1	2178.00	0.37	1.67
50053.00	H18	M-008504- dihydropyr	10570.00	DPYSL4	4488.00	0.29	1.75
50053.00	H19	M-017452- calcium cha	10368.00	CACNG3	3449.00	0.41	1.63
50053.00	H20	M-017191- SLU7 splicir	10569.00	SLU7	1387.00	0.36	1.68
50053.00	H21	M-012160- calcium cha	10369.00	CACNG2	4377.00	0.82	1.22
50053.00	H23	M-021359- butyrophili	10384.00	BTN3A3	2873.00	0.07	1.97
50053.00	I02	M-010094- RNA bindin	10137.00	RBM12	2275.00	0.84	1.20
50053.00	I04	M-005863- elastase 3A	10136.00	ELA3A	2053.00	0.73	1.31
50053.00	I05	M-010361- oxysterol b	9885.00	OSBPL2	2699.00	4.11	2.07
50053.00	I06	M-018679- B-cell recep	10134.00	BCAP31	1596.00	1.94	0.10
50053.00	I07	M-021305- Smg-7 hom	9887.00	SMG7	1705.00	1.88	0.16
50053.00	I08	M-018336- zinc finger	10127.00	ZNF263	2125.00	2.21	0.17
50053.00	I09	M-021226- zinc finger,	9889.00	ZBED4	955.00	2.51	0.47
50053.00	I10	M-019993- dynein, axc	10126.00	DNAL4	2032.00	2.07	0.03
50053.00	I11	M-009911- plasticity re	9890.00	LPPR4	1847.00	1.35	0.69
50053.00	I12	M-012398- ADP-ribosy	10123.00	ARL4C	1765.00	4.02	1.98
50053.00	I13	M-021207- TEL2, telon	9894.00	TELO2	2122.00	1.79	0.25
50053.00	I14	M-006920- tripartite m	10107.00	TRIM10	2238.00	1.16	0.88
50053.00	I15	M-014181- KIAA0329	9895.00	KIAA0329	1315.00	2.43	0.39
50053.00	I16	M-015413- CTD (carbo	10106.00	CTDSP2	2288.00	1.70	0.34
50053.00	I17	M-021222- KIAA0196	9897.00	KIAA0196	2582.00	2.25	0.21
50053.00	I18	M-009708- peptidylprc	10105.00	PPIF	2622.00	0.72	1.32
50053.00	I19	M-021220- ubiquitin a	9898.00	UBAP2L	2935.00	4.05	2.01
50053.00	I20	M-003719- tetraspanir	10103.00	TSPAN1	3752.00	2.00	0.04
50053.00	I21	M-007632- synaptic ve	9899.00	SV2B	1571.00	0.45	1.59
50053.00	I23	M-007631- synaptic ve	9900.00	SV2A	2478.00	2.10	0.06
50053.00	J02	M-007535- solute carri	10568.00	SLC34A2	1137.00	5.80	**3.76**
50053.00	J04	M-012224- olfactomec	10562.00	OLFM4	1995.00	1.25	0.79
50053.00	J05	M-010071- butyrophili	10385.00	BTN2A2	3348.00	2.36	0.32
50053.00	J06	M-007537- solute carri	10559.00	SLC35A1	4217.00	3.41	1.37
50053.00	J07	M-020632- synaptoner	10388.00	SYCP2	4004.00	6.24	**4.20**
50053.00	J08	M-019447- ribonucleas	10557.00	RPP38	2598.00	2.54	0.50
50053.00	J09	M-010350- choline/eth	10390.00	CEPT1	1817.00	2.70	0.66

50053.00	J10	M-015336- ribonucleas	10556.00	RPP30	2014.00	1.09	0.95
50053.00	J11	M-010392- phosphatid	10400.00	PEMT	2575.00	1.20	0.84
50053.00	J12	M-012229- ADP-ribosy	10550.00	ARL6IP5	2464.00	1.58	0.46
50053.00	J13	M-018009- ST3 beta-ga	10402.00	ST3GAL6	1679.00	3.93	1.89
50053.00	J14	M-016357- transmemb	10548.00	TM9SF1	2655.00	4.33	2.29
50053.00	J15	M-005993- plasma glut	10404.00	PGCP	1537.00	2.60	0.56
50053.00	J16	M-012269- hepatitis B	10542.00	HBXIP	2113.00	4.12	2.08
50053.00	J17	M-010564- WAP four-c	10406.00	WFDC2	2864.00	3.49	1.45
50053.00	J18	M-020148- acidic (leuc	10541.00	ANP32B	3082.00	1.95	0.09
50053.00	J19	M-017043- TGF beta-ir	10412.00	TINP1	1989.00	6.03	3.99
50053.00	J20	M-019954- thioredoxir	10539.00	TXNL2	3985.00	1.88	0.16
50053.00	J21	M-020086- acid-induci	10414.00	OA48-18	1167.00	0.86	1.18
50053.00	J23	M-020027- spondin 2,	10417.00	SPON2	3766.00	0.96	1.08
50053.00	K02	M-016336- Ts translati	10102.00	TSFM	2698.00	0.30	1.74
50053.00	K04	M-017266- tetraspanir	10100.00	TSPAN2	2325.00	1.38	0.66
50053.00	K05	M-014175- SLIT-ROBO	9901.00	SRGAP3	2997.00	0.93	1.11
50053.00	K06	M-010735- tetraspanir	10099.00	TSPAN3	3992.00	0.60	1.44
50053.00	K07	M-021216- kelch-like 2	9903.00	KLHL21	3888.00	1.70	0.34
50053.00	K08	M-010634- tetraspanir	10098.00	TSPAN5	1844.00	1.74	0.30
50053.00	K09	M-021123- RNA bindin	9904.00	RBM19	1986.00	0.70	1.34
50053.00	K10	M-020052- uronyl-2-su	10090.00	UST	917.00	1.09	0.95
50053.00	K11	M-022997- RUN and TI	9905.00	RUTBC1	3596.00	2.22	0.18
50053.00	K12	M-006266- potassium	10089.00	KCNK7	4274.00	2.64	0.60
50053.00	K13	M-007548- solute carri	9906.00	SLC35E2	3064.00	2.28	0.24
50053.00	K14	M-012716- polyglutam	10084.00	PQBP1	3211.00	1.74	0.30
50053.00	K15	M-025284- KIAA0415 p	9907.00	tcag7.1310	2520.00	0.44	1.60
50053.00	K16	M-012102- glypican 6	10082.00	GPC6	2441.00	0.25	1.79
50053.00	K17	M-015329- GTPase act	9908.00	G3BP2	3533.00	0.54	1.50
50053.00	K18	M-012096- programme	10081.00	PDCD7	1872.00	0.32	1.72
50053.00	K19	M-006917- DENN/MAI	9909.00	DENND4B	4672.00	3.23	1.19
50053.00	K20	M-013856- chromoson	10069.00	C21orf6	3792.00	0.34	1.70
50053.00	K21	M-014176- transmemb	9911.00	TMCC2	3552.00	1.41	0.63
50053.00	K23	M-009238- KIAA0672 g	9912.00	KIAA0672	3581.00	1.42	0.62
50053.00	L02	M-018228- leprecan-lil	10536.00	LEPREL2	2683.00	2.09	0.05
50053.00	L04	M-003535- ribonucleas	10535.00	RNASEH2A	2757.00	0.98	1.06
50053.00	L05	M-012730- spondin 1,	10418.00	SPON1	2493.00	1.12	0.92
50053.00	L06	M-020114- nebulette	10529.00	NEBL	4280.00	2.06	0.02
50053.00	L07	M-020776- UBA domai	10422.00	UBAC1	1640.00	0.18	1.86
50053.00	L08	M-019143- nucleolar p	10528.00	NOL5A	2444.00	0.61	1.43
50053.00	L09	M-009631- CDP-diacylg	10423.00	CDIPT	3180.00	3.30	1.26
50053.00	L10	M-012256- importin 8	10526.00	IPO8	4202.00	1.24	0.80
50053.00	L11	M-020104- ariadne hor	10425.00	ARIH2	2340.00	2.82	0.78
50053.00	L12	M-016176- calcium ho	10523.00	CHERP	1719.00	1.16	0.88
50053.00	L13	M-008299- SEC24 relat	10427.00	SEC24B	2854.00	1.19	0.85
50053.00	L14	M-020808- deformed e	10522.00	DEAF1	2456.00	0.65	1.39
50053.00	L15	M-020105- craniofacia	10428.00	CFDP1	2322.00	0.13	1.91
50053.00	L16	M-013450- DEAD (Asp-	10521.00	DDX17	1889.00	0.32	1.72

50053.00	L17	M-010704- transmemb	10430.00	TMEM147	1246.00	0.48	1.56
50053.00	L18	M-020153- zinc finger	10520.00	ZNF211	2652.00	0.68	1.36
50053.00	L19	M-020150- translocase	10431.00	TIMM23	2844.00	1.83	0.21
50053.00	L20	M-014733- F-box and	10517.00	FBXW10	1762.00	0.68	1.36
50053.00	L21	M-020144- RNA bindin	10432.00	RBM14	3259.00	0.46	1.58
50053.00	L23	M-012215- CDC42 effe	10435.00	CDC42EP2	3408.00	0.21	1.83
50053.00	M02	M-015414- phenylalan	10056.00	FARSB	1441.00	0.35	1.69
50053.00	M04	M-006402- SUMO1 act	10055.00	SAE1	2115.00	2.74	0.70
50053.00	M05	M-021210- suppressor	9913.00	SUPT7L	3177.00	0.41	1.63
50053.00	M06	M-005248- SUMO1 act	10054.00	SAE2	2101.00	0.71	1.33
50053.00	M07	M-021203- family with	9917.00	FAM20B	2765.00	3.11	1.07
50053.00	M08	M-012056- adaptor-rel	10053.00	AP1M2	2375.00	2.48	0.44
50053.00	M09	M-021198- non-SMC c	9918.00	NCAPD2	1689.00	1.60	0.44
50053.00	M10	M-007414- solute carri	10050.00	SLC17A4	1842.00	2.55	0.51
50053.00	M11	M-026032- KIAA0310	9919.00	KIAA0310	2338.00	1.92	0.12
50053.00	M12	M-013020- DnaJ (Hsp4	10049.00	DNAJB6	2735.00	0.99	1.05
50053.00	M13	M-006918- ring finger	9921.00	RNF10	1991.00	1.21	0.83
50053.00	M14	M-012026- cystatin 8 (	10047.00	CST8	2527.00	1.19	0.85
50053.00	M15	M-006458- IQ motif an	9922.00	IQSEC1	1008.00	1.88	0.16
50053.00	M16	M-019942- chromoson	10046.00	CXorf6	2346.00	0.34	1.70
50053.00	M17	M-006919- zinc finger	9923.00	ZBTB40	1126.00	0.44	1.60
50053.00	M18	M-005996- phosphatid	10026.00	PIGK	1294.00	0.85	1.19
50053.00	M19	M-021190- zinc finger	9925.00	ZBTB5	2922.00	0.55	1.49
50053.00	M20	M-019961- SH2B adap	10019.00	SH2B3	2667.00	1.69	0.35
50053.00	M21	M-021185- lysophosph	9926.00	LPGAT1	3915.00	0.66	1.38
50053.00	M23	M-012961- mitofusin 2	9927.00	MFN2	2936.00	0.92	1.12
50053.00	N02	M-007289- sema dom	10509.00	SEMA4B	1442.00	3.95	1.91
50053.00	N04	M-003708- sema dom	10505.00	SEMA4F	3005.00	7.22	5.18
50053.00	N05	M-019090- EMG1 nucl	10436.00	EMG1	1861.00	3.22	1.18
50053.00	N06	M-013453- sema dom	10500.00	SEMA6C	2700.00	0.96	1.08
50053.00	N07	M-017397- nuclear DN	10438.00	C1D	1948.00	1.23	0.81
50053.00	N08	M-004130- coactivator	10498.00	CARM1	2355.00	3.35	1.31
50053.00	N09	M-012203- olfactomec	10439.00	OLFM1	1914.00	2.19	0.15
50053.00	N10	M-012205- ecto-NOX c	10495.00	ENOX2	1576.00	1.71	0.33
50053.00	N11	M-012739- translocase	10440.00	TIMM17A	1430.00	4.34	2.30
50053.00	N12	M-009726- vesicle ami	10493.00	VAT1	808.00	2.85	0.81
50053.00	N13	M-014177- phosphonc	10443.00	PFAAP5	2549.00	1.61	0.43
50053.00	N14	M-003648- cartilage as	10491.00	CRTAP	2856.00	3.89	1.85
50053.00	N15	M-019424- zer-1 homc	10444.00	ZER1	2751.00	2.76	0.72
50053.00	N16	M-020152- vesicle trar	10490.00	VTI1B	2388.00	2.64	0.60
50053.00	N17	M-018557- microspher	10445.00	MCRS1	1336.00	3.37	1.33
50053.00	N18	M-031268- leucine rich	10489.00	LRRC41	1926.00	2.54	0.50
50053.00	N19	M-010565- leucine rich	10446.00	LRRN2	1879.00	1.70	0.34
50053.00	N20	M-012211- CAP, adeny	10486.00	CAP2	2521.00	3.05	1.01
50053.00	N21	M-020514- family with	10447.00	FAM3C	1732.00	4.33	2.29
50053.00	N23	M-009466- peptidylprc	10450.00	PPIE	997.00	2.91	0.87
50053.00	O02	M-009600- acyl-CoA th	10005.00	ACOT8	2730.00	2.16	0.12

50053.00	O04	M-005975- N-acetylate	10004.00	NAALADL1	3193.00	1.16	0.88
50053.00	O05	M-017674- Josephin do	9929.00	JOSD1	3049.00	2.23	0.19
50053.00	O06	M-005974- N-acetylate	10003.00	NAALAD2	2444.00	2.99	0.95
50053.00	O07	M-021180- helicase wi	9931.00	HELZ	3163.00	2.34	0.30
50053.00	O08	M-008595- potassium	9992.00	KCNE2	1848.00	3.46	1.42
50053.00	O09	M-032027- KIAA0020	9933.00	KIAA0020	3533.00	3.88	1.84
50053.00	O10	M-019452- ROD1 regu	9991.00	ROD1	3504.00	1.31	0.73
50053.00	O11	M-021175- Rho GTPase	9938.00	ARHGAP25	3418.00	3.16	1.12
50053.00	O12	M-012070- heterogene	9987.00	HNRPDL	3697.00	2.41	0.37
50053.00	O13	M-003531- RNA bindin	9939.00	RBM8A	505.00	8.32	**6.28**
50053.00	O14	M-007461- solute carri	9963.00	SLC23A1	2761.00	1.27	0.77
50053.00	O15	M-008572- endonuclea	9941.00	ENDOGL1	2308.00	1.91	0.13
50053.00	O16	M-007462- solute carri	9962.00	SLC23A2	2760.00	0.14	1.90
50053.00	O17	M-022514- heparan su	9951.00	HS3ST4	2782.00	1.73	0.31
50053.00	O18	M-004984- major vault	9961.00	MVP	1459.00	2.40	0.36
50053.00	O19	M-010083- heparan su	9953.00	HS3ST3B1	3149.00	2.45	0.41
50053.00	O20	M-009217- heparan su	9957.00	HS3ST1	3711.00	1.62	0.42
50053.00	O21	M-008530- heparan su	9955.00	HS3ST3A1	1958.00	1.99	0.05
50053.00	O23	M-010031- heparan su	9956.00	HS3ST2	1956.00	1.07	0.97
50053.00	P02	M-009582- Sec23 hom	10484.00	SEC23A	1152.00	4.51	2.47
50053.00	P04	M-009592- Sec23 hom	10483.00	SEC23B	543.00	7.37	**5.33**
50053.00	P05	M-012732- translocase	10452.00	TOMM40	955.00	7.64	**5.60**
50053.00	P06	M-013680- nuclear RN	10482.00	NXF1	521.00	16.70	**14.66**
50053.00	P07	M-012168- HCLS1 asso	10456.00	HAX1	2068.00	8.37	**6.33**
50053.00	P08	M-016219- PCI domair	10480.00	PCID1	479.00	6.89	**4.85**
50053.00	P09	M-011741- glycoprotei	10457.00	GPNMB	1146.00	3.75	1.71
50053.00	P10	M-007626- solute carri	10479.00	SLC9A6	1669.00	3.18	1.14
50053.00	P11	M-010961- C-type lecti	10462.00	CLEC10A	1916.00	4.28	2.24
50053.00	P12	M-007476- solute carri	10478.00	SLC25A17	310.00	15.16	**13.12**
50053.00	P13	M-007530- solute carri	10463.00	SLC30A9	1095.00	6.30	**4.26**
50053.00	P14	M-006929- tripartite m	10475.00	TRIM38	2241.00	1.47	0.57
50053.00	P15	M-020125- chromoson	10464.00	C13orf24	2770.00	7.22	**5.18**
50053.00	P16	M-020630- prefoldin su	10471.00	PFDN6	1735.00	3.11	1.07
50053.00	P17	M-012992- sperm asso	10407.00	SPAG11B	2977.00	6.79	**4.75**
50053.00	P18	M-003864- translocase	10469.00	TIMM44	1297.00	3.08	1.04
50053.00	P19	M-006593- zinc finger	7767.00	ZNF224	2629.00	4.68	2.64
50053.00	P20	M-019123- component	10466.00	COG5	2175.00	1.75	0.29
50053.00	P21	M-012203- olfactomec	10439.00	OLFM1	2328.00	0.52	1.52
50053.00	P23	M-006909- zinc finger	9658.00	ZNF516	3090.00	0.23	1.81
				median	2482.50	2.04	1.05
				3MAD			3.15
				MADc			1.55
50053.00	C22				2704.00	7.99	
50053.00	D22		4245.00	21.96			
50053.00	E22				3304.00	12.02	
50053.00	F22				3239.00	11.30	
				mn	3082.33	10.43	

					sd	329.25	2.15
50053.00	G22					1323.00	1.51
50053.00	H22					1447.00	0.14
50053.00	I22					1237.00	0.81
50053.00	J22					1013.00	0.79
					mn	1232.33	0.58
					sd	217.04	0.38
					3psSD		6.45
					3ngSD		1.14
					SumSD		7.59
					DiffMn		9.86
					SmovrDiff		0.77
					1minus		0.23
50053.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAR	165.00	14.55
50053.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAR	126.00	3.17
50053.00	I03	D-001206-	siControl non-targetin			1219.00	1.23
50053.00	J03	D-001206-	siControl non-targetin			1938.00	1.91
50053.00	K03	D-001600-	siGLO RISC-free siRNA			4995.00	1.64
50053.00	L03	D-001600-	siGLO RISC-free siRNA			6030.00	3.20

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
0.68	2085.00	1.20	0.69	-0.45	2123.00	2.78	0.32	0.20
0.24	985.00	2.03	0.14	0.09	1447.00	1.24	1.22	-0.74
0.10	1822.00	1.87	0.02	-0.02	3004.00	1.20	1.26	-0.77
3.15	2095.00	0.62	1.27	-0.82	2911.00	1.34	1.12	-0.68
-0.20	1306.00	1.45	0.44	-0.28	3401.00	2.29	0.17	-0.10
0.23	1165.00	0.94	0.95	-0.61	2565.00	1.56	0.90	-0.55
1.89	591.00	4.23	2.34	1.51	1059.00	3.31	0.85	0.52
0.16	1257.00	10.02	**8.13**	5.26	2055.00	2.19	0.27	-0.16
-0.53	1155.00	3.90	2.01	1.30	1861.00	2.42	0.04	-0.02
1.51	1424.00	1.97	0.08	0.05	3401.00	2.97	0.51	0.31
4.17	1059.00	1.13	0.76	-0.49	1172.00	6.91	**4.45**	2.72
1.02	1319.00	1.21	0.68	-0.44	1663.00	5.83	**3.37**	2.06
2.25	560.00	3.21	1.32	0.85	2314.00	2.16	0.30	-0.18
-0.52	952.00	3.78	1.89	1.22	1276.00	2.35	0.11	-0.06
1.52	828.00	2.66	0.77	0.49	1133.00	4.59	2.13	1.30
3.13	1897.00	6.80	**4.91**	3.17	2614.00	4.67	2.21	1.35
5.40	1035.00	5.12	**3.23**	2.09	583.00	9.61	**7.15**	4.36
0.92	1323.00	4.16	2.27	1.46	1662.00	3.91	1.45	0.89
1.76	1433.00	4.54	2.65	1.71	1746.00	4.12	1.66	1.02
0.56	479.00	5.64	**3.75**	2.42	437.00	8.47	**6.01**	3.67
0.38	984.00	0.41	1.48	-0.96	1828.00	0.16	2.30	-1.40
0.59	1610.00	0.68	1.21	-0.78	2314.00	0.52	1.94	-1.18
4.83	3469.00	2.83	0.94	0.60	4074.00	2.06	0.40	-0.24
1.90	3525.00	1.70	0.19	-0.12	4435.00	0.59	1.87	-1.14
-0.27	2196.00	1.05	0.84	-0.55	1703.00	0.18	2.28	-1.39
-0.04	1384.00	0.72	1.17	-0.76	1840.00	0.60	1.86	-1.13
0.28	1816.00	0.50	1.39	-0.90	1498.00	1.20	1.26	-0.77
-0.26	1326.00	0.45	1.44	-0.93	1170.00	0.34	2.12	-1.29
-0.19	2761.00	0.58	1.31	-0.85	2950.00	1.39	1.07	-0.65
1.00	1331.00	0.23	1.66	-1.08	2232.00	1.43	1.03	-0.62
0.31	1623.00	0.68	1.21	-0.78	1791.00	0.00	2.46	-1.50
-0.77	2029.00	0.20	1.69	-1.10	1756.00	0.40	2.06	-1.26
0.43	2370.00	1.27	0.62	-0.40	3126.00	3.29	0.83	0.51
1.08	1555.00	3.60	1.71	1.10	2228.00	2.78	0.32	0.20
-0.77	1660.00	1.57	0.32	-0.21	1946.00	0.41	2.05	-1.25
0.99	2819.00	0.60	1.29	-0.83	3821.00	0.29	2.17	-1.32
-0.87	3062.00	1.08	0.81	-0.53	3795.00	4.14	1.68	1.03
-0.67	2523.00	1.27	0.62	-0.40	3741.00	0.80	1.66	-1.01
-0.63	2238.00	0.22	1.67	-1.08	2546.00	0.82	1.64	-1.00
-0.28	1506.00	0.33	1.56	-1.01	1267.00	0.55	1.91	-1.16
1.73	2725.00	3.01	1.12	0.72	3345.00	0.45	2.01	-1.23
1.46	1252.00	2.16	0.27	0.17	2675.00	1.08	1.38	-0.84
1.11	1676.00	2.09	0.20	0.13	2567.00	0.70	1.76	-1.07
1.66	3838.00	1.56	0.33	-0.21	3540.00	0.73	1.73	-1.05
2.47	2168.00	1.38	0.51	-0.33	2304.00	2.08	0.38	-0.23
4.32	1907.00	6.66	**4.77**	3.08	2173.00	1.84	0.62	-0.38

0.74	2122.00	2.03	0.14	0.09	2257.00	1.64	0.82	-0.50
-0.12	1127.00	0.98	0.91	-0.59	1618.00	1.55	0.91	-0.56
0.99	1523.00	4.14	2.25	1.45	1225.00	2.12	0.34	-0.20
1.35	921.00	2.39	0.50	0.32	824.00	2.18	0.28	-0.17
2.04	2714.00	6.26	**4.37**	2.83	3403.00	4.14	1.68	1.03
2.38	1708.00	1.46	0.43	-0.28	1589.00	2.96	0.50	0.31
0.34	1332.00	4.80	2.91	1.88	2096.00	6.82	**4.36**	2.66
0.19	1571.00	1.40	0.49	-0.32	1719.00	7.56	**5.10**	3.12
0.56	1818.00	1.98	0.09	0.06	2211.00	3.89	1.43	0.87
-0.18	1736.00	5.76	**3.87**	2.50	2411.00	3.57	1.11	0.68
-0.39	1788.00	0.78	1.11	-0.72	2143.00	5.46	3.00	1.83
0.46	3087.00	3.98	2.09	1.35	3180.00	2.92	0.46	0.29
2.29	2336.00	4.79	2.90	1.88	2616.00	3.63	1.17	0.72
3.95	1346.00	4.46	2.57	1.66	1423.00	11.03	**8.57**	5.23
0.32	2889.00	4.88	2.99	1.93	3773.00	1.83	0.63	-0.38
2.99	2556.00	5.79	**3.90**	2.52	3677.00	5.14	2.68	1.64
0.24	3198.00	2.50	0.61	0.39	3283.00	1.86	0.60	-0.37
-0.02	2032.00	3.35	1.46	0.94	1670.00	1.98	0.48	-0.29
1.23	1222.00	4.09	2.20	1.42	2683.00	2.46	0.00	0.00
0.24	1438.00	2.92	1.03	0.66	1551.00	2.19	0.27	-0.16
2.53	985.00	3.86	1.97	1.27	908.00	2.20	0.26	-0.16
0.16	2024.00	2.03	0.14	0.09	2579.00	0.81	1.65	-1.00
0.05	1889.00	3.76	1.87	1.21	2065.00	3.39	0.93	0.57
3.20	2426.00	1.36	0.53	-0.34	2823.00	8.18	**5.72**	3.49
0.79	1824.00	4.44	2.55	1.65	2878.00	3.51	1.05	0.64
1.52	2230.00	4.89	3.00	1.94	3615.00	3.90	1.44	0.88
0.80	1157.00	1.56	0.33	-0.22	1808.00	1.55	0.91	-0.55
0.33	1769.00	2.09	0.20	0.13	2378.00	4.42	1.96	1.20
0.99	1460.00	1.64	0.25	-0.16	1948.00	4.00	1.54	0.94
2.91	1361.00	3.01	1.12	0.72	1334.00	1.20	1.26	-0.77
0.93	2456.00	2.85	0.96	0.62	3277.00	2.90	0.44	0.27
3.32	3884.00	2.68	0.79	0.51	3883.00	3.19	0.73	0.45
3.55	3218.00	1.46	0.43	-0.28	4485.00	4.73	2.27	1.39
-0.50	3734.00	0.35	1.54	-1.00	4294.00	1.75	0.71	-0.43
-0.14	3356.00	1.22	0.67	-0.43	3623.00	1.21	1.25	-0.76
0.41	1569.00	2.10	0.21	0.14	1043.00	2.40	0.06	-0.04
-0.59	639.00	8.45	**6.56**	4.24	1132.00	2.03	0.43	-0.26
-0.28	1132.00	7.60	**5.71**	3.69	1373.00	1.31	1.15	-0.70
-0.96	1438.00	3.20	1.31	0.84	1883.00	0.37	2.09	-1.27
-0.23	3302.00	2.36	0.47	0.30	4015.00	0.75	1.71	-1.04
-0.01	785.00	3.57	1.68	1.08	1943.00	0.93	1.53	-0.93
-0.45	1637.00	3.12	1.23	0.79	1720.00	0.76	1.70	-1.04
0.63	1094.00	6.12	**4.23**	2.74	1480.00	1.28	1.18	-0.72
-0.56	1888.00	2.86	0.97	0.63	3245.00	0.09	2.37	-1.44
-0.44	952.00	3.47	1.58	1.02	1498.00	0.87	1.59	-0.97
0.20	1709.00	1.93	0.04	0.03	2411.00	0.75	1.71	-1.04
2.14	131.00	17.56	**15.67**	10.13	91.00	3.30	0.84	0.51

-0.57	1691.00	2.66	0.77	0.50	1699.00	0.94	1.52	-0.92
-0.76	2416.00	2.77	0.88	0.57	2878.00	0.87	1.59	-0.97
-0.33	2165.00	0.97	0.92	-0.60	3291.00	0.85	1.61	-0.98
-0.98	2121.00	1.18	0.71	-0.46	2025.00	0.15	2.31	-1.41
-0.62	2334.00	5.01	3.12	2.02	2381.00	0.13	2.33	-1.42
0.08	2622.00	1.07	0.82	-0.53	3013.00	0.27	2.19	-1.34
-0.05	3266.00	1.71	0.18	-0.11	3708.00	0.19	2.27	-1.38
0.35	3068.00	1.89	0.00	0.00	2546.00	1.10	1.36	-0.83
-0.50	1105.00	4.52	2.63	1.70	1559.00	2.57	0.11	0.07
-0.63	3346.00	1.05	0.84	-0.55	3283.00	0.85	1.61	-0.98
0.07	1580.00	5.19	**3.30**	2.13	2330.00	2.40	0.06	-0.03
-0.05	1763.00	4.08	2.19	1.42	1934.00	0.78	1.68	-1.03
0.93	564.00	14.89	**13.00**	8.40	253.00	7.11	**4.65**	2.84
0.01	1886.00	2.55	0.66	0.42	2635.00	2.16	0.30	-0.18
-0.43	1645.00	3.34	1.45	0.94	1704.00	4.23	1.77	1.08
-0.52	367.00	11.72	**9.83**	6.35	653.00	10.41	**7.95**	4.86
-0.24	1792.00	1.73	0.16	-0.10	1513.00	1.98	0.48	-0.29
-0.74	1302.00	2.07	0.18	0.12	2652.00	1.28	1.18	-0.72
-0.57	1001.00	3.20	1.31	0.84	1457.00	1.17	1.29	-0.79
-0.25	1673.00	3.89	2.00	1.29	2480.00	2.58	0.12	0.08
-0.80	2547.00	3.06	1.17	0.76	2549.00	1.45	1.01	-0.61
0.12	1149.00	2.09	0.20	0.13	1268.00	1.97	0.49	-0.30
-0.32	2475.00	4.77	2.88	1.86	2651.00	2.57	0.11	0.07
0.97	3153.00	3.52	1.63	1.05	3787.00	4.15	1.69	1.03
-0.48	1315.00	5.25	**3.36**	2.17	2000.00	2.75	0.29	0.18
0.03	2726.00	1.76	0.13	-0.08	3335.00	2.19	0.27	-0.16
0.94	3848.00	3.66	1.77	1.15	3519.00	2.53	0.07	0.04
0.14	2416.00	1.57	0.32	-0.21	2561.00	1.48	0.98	-0.59
1.18	1959.00	2.55	0.66	0.43	1696.00	3.24	0.78	0.48
0.06	3158.00	0.76	1.13	-0.73	2549.00	2.82	0.36	0.22
1.66	3850.00	4.78	2.89	1.87	3795.00	7.64	**5.18**	3.16
-0.30	3184.00	1.26	0.63	-0.41	3092.00	1.55	0.91	-0.55
2.78	2169.00	2.77	0.88	0.57	2289.00	2.36	0.10	-0.06
-0.33	1560.00	2.50	0.61	0.39	1704.00	2.88	0.42	0.26
0.18	1687.00	1.42	0.47	-0.30	1934.00	1.45	1.01	-0.62
-0.41	1981.00	2.07	0.18	0.11	2811.00	2.92	0.46	0.28
-0.11	3960.00	2.53	0.64	0.41	3344.00	1.02	1.44	-0.88
0.22	1714.00	2.98	1.09	0.70	1093.00	2.29	0.17	-0.10
3.99	2067.00	4.45	2.56	1.65	1476.00	5.89	**3.43**	2.10
-0.66	1817.00	4.73	2.84	1.84	1522.00	3.48	1.02	0.63
-0.14	2625.00	2.32	0.43	0.28	2399.00	3.96	1.50	0.92
-0.51	2529.00	2.25	0.36	0.23	3146.00	3.40	0.94	0.58
-0.18	1940.00	1.60	0.29	-0.19	1945.00	1.90	0.56	-0.34
-0.03	2880.00	6.91	**5.02**	3.24	2591.00	6.06	**3.60**	2.20
1.29	3724.00	3.09	1.20	0.77	3951.00	2.25	0.21	-0.12
-0.87	2427.00	2.23	0.34	0.22	1785.00	2.47	0.00	0.00
-0.77	3208.00	1.40	0.49	-0.32	3974.00	2.57	0.11	0.07

-1.08	2328.00	1.37	0.52	-0.33	2262.00	3.01	0.55	0.34
-1.06	2193.00	1.78	0.11	-0.07	2364.00	4.65	2.19	1.34
-1.26	2030.00	1.48	0.41	-0.27	1826.00	2.57	0.11	0.07
-0.77	2601.00	1.92	0.03	0.02	2059.00	5.54	3.08	1.88
-1.31	1512.00	1.06	0.83	-0.54	1140.00	3.68	1.22	0.75
-0.23	713.00	2.38	0.49	0.32	754.00	7.03	**4.57**	2.79
-1.26	1842.00	0.81	1.08	-0.70	2034.00	1.77	0.69	-0.42
1.27	745.00	1.88	0.01	-0.01	1248.00	5.85	**3.39**	2.07
-1.13	1812.00	0.72	1.17	-0.76	1801.00	3.50	1.04	0.64
-0.65	1322.00	1.21	0.68	-0.44	1378.00	1.96	0.50	-0.30
-1.22	1206.00	1.24	0.65	-0.42	1480.00	4.59	2.13	1.30
-1.02	1975.00	0.35	1.54	-0.99	2227.00	1.98	0.48	-0.29
-0.73	1537.00	0.33	1.56	-1.01	1426.00	5.89	**3.43**	2.10
-1.16	775.00	0.52	1.37	-0.89	760.00	10.26	**7.80**	4.76
-1.08	1534.00	1.76	0.13	-0.09	1001.00	5.39	2.93	1.79
-1.13	2471.00	1.17	0.72	-0.46	2912.00	2.85	0.39	0.24
-1.05	3152.00	0.67	1.22	-0.79	2836.00	1.27	1.19	-0.72
-1.08	1380.00	1.38	0.51	-0.33	1208.00	7.62	**5.16**	3.15
-0.78	3649.00	1.86	0.03	-0.02	3816.00	2.54	0.08	0.05
-1.27	2616.00	1.11	0.78	-0.51	3442.00	2.76	0.30	0.18
-0.77	2657.00	1.69	0.20	-0.13	3150.00	0.95	1.51	-0.92
-0.84	2251.00	3.51	1.62	1.05	2468.00	2.92	0.46	0.28
1.34	2733.00	2.23	0.34	0.22	2898.00	7.97	**5.51**	3.37
-0.06	2700.00	4.33	2.44	1.58	2485.00	5.27	2.81	1.72
-0.10	1884.00	1.33	0.56	-0.37	1831.00	1.86	0.60	-0.37
0.11	3344.00	1.76	0.13	-0.08	3087.00	2.11	0.35	-0.21
0.31	2510.00	2.87	0.98	0.63	1764.00	2.04	0.42	-0.25
0.02	1693.00	2.01	0.12	0.08	2031.00	0.74	1.72	-1.05
-0.44	2470.00	0.89	1.00	-0.65	2505.00	0.96	1.50	-0.91
1.28	2341.00	1.28	0.61	-0.39	2618.00	1.15	1.31	-0.80
-0.16	1978.00	1.26	0.63	-0.41	2318.00	1.08	1.38	-0.84
-0.56	2470.00	1.74	0.15	-0.10	2557.00	1.56	0.90	-0.54
0.26	1604.00	1.37	0.52	-0.34	1241.00	0.89	1.57	-0.96
-0.21	1732.00	1.44	0.45	-0.29	2522.00	1.51	0.95	-0.58
0.14	2534.00	0.39	1.50	-0.97	2549.00	2.71	0.25	0.15
-0.85	2266.00	0.31	1.58	-1.02	2114.00	2.79	0.33	0.20
1.30	3158.00	2.91	1.02	0.66	3786.00	2.38	0.08	-0.05
-0.02	4402.00	0.32	1.57	-1.02	3784.00	1.51	0.95	-0.58
-1.03	1404.00	0.43	1.46	-0.95	1469.00	2.86	0.40	0.25
0.04	2965.00	1.79	0.10	-0.07	2715.00	1.99	0.47	-0.29
2.43	972.00	1.44	0.45	-0.29	1263.00	2.45	0.01	0.00
-0.50	2001.00	2.40	0.51	0.33	2310.00	1.34	1.12	-0.68
0.21	2607.00	2.19	0.30	0.19	2403.00	1.41	1.05	-0.64
0.89	4120.00	2.72	0.83	0.53	3556.00	1.10	1.36	-0.83
2.71	3301.00	3.85	1.96	1.26	2962.00	1.79	0.67	-0.41
0.32	2107.00	0.57	1.32	-0.85	1744.00	2.47	0.01	0.01
0.43	1803.00	1.28	0.61	-0.40	2117.00	3.12	0.66	0.40

-0.61	1834.00	3.98	2.09	1.35	1574.00	2.03	0.43	-0.26
-0.54	2050.00	0.78	1.11	-0.72	1958.00	1.28	1.18	-0.72
-0.29	2546.00	0.12	1.77	-1.15	1988.00	0.35	2.11	-1.28
1.22	1507.00	1.39	0.50	-0.32	1494.00	5.29	2.83	1.73
1.48	3845.00	4.50	2.61	1.69	3167.00	2.40	0.06	-0.04
0.36	1732.00	0.75	1.14	-0.74	1419.00	2.40	0.06	-0.04
1.34	1911.00	1.47	0.42	-0.28	2700.00	2.85	0.39	0.24
0.94	2326.00	1.59	0.30	-0.19	2388.00	2.43	0.03	-0.02
-0.06	2712.00	1.99	0.10	0.06	3373.00	1.90	0.56	-0.34
2.58	1494.00	1.54	0.35	-0.23	2382.00	0.63	1.83	-1.12
-0.10	3985.00	0.10	1.79	-1.16	3466.00	0.29	2.17	-1.32
-0.76	1087.00	0.55	1.34	-0.87	1028.00	0.68	1.78	-1.08
-0.70	2523.00	1.51	0.38	-0.25	2929.00	2.66	0.20	0.13
-1.12	4376.00	0.87	1.02	-0.66	4321.00	2.11	0.35	-0.21
-0.43	2693.00	1.89	0.00	0.00	3160.00	1.65	0.81	-0.50
-0.71	3281.00	0.82	1.07	-0.69	3291.00	4.44	1.98	1.21
-0.93	3318.00	1.63	0.26	-0.17	3248.00	2.62	0.16	0.10
-0.22	3886.00	3.35	1.46	0.94	4036.00	0.62	1.84	-1.12
-0.19	2249.00	2.49	0.60	0.39	2912.00	4.09	1.63	0.99
-0.86	2086.00	0.43	1.46	-0.94	1775.00	1.24	1.22	-0.74
-0.61	588.00	1.53	0.36	-0.23	1013.00	5.33	2.87	1.75
0.12	2345.00	2.43	0.54	0.35	3316.00	3.02	0.56	0.34
0.39	3491.00	2.38	0.49	0.31	4195.00	4.20	1.74	1.06
0.16	2162.00	0.69	1.20	-0.77	2661.00	0.83	1.63	-1.00
-0.19	2768.00	2.10	0.21	0.13	4498.00	3.56	1.10	0.67
-1.03	2171.00	0.55	1.34	-0.87	2298.00	1.44	1.02	-0.62
-1.15	2558.00	2.89	1.00	0.65	3925.00	3.44	0.98	0.60
-0.97	2947.00	3.22	1.33	0.86	3936.00	2.90	0.44	0.27
-1.11	1320.00	1.44	0.45	-0.29	1926.00	3.74	1.28	0.78
0.77	5418.00	6.37	4.48	2.89	5803.00	6.27	3.81	2.33
-1.09	4164.00	3.60	1.71	1.11	3638.00	4.65	2.19	1.34
-0.41	2858.00	2.17	0.28	0.18	3327.00	3.10	0.64	0.39
-0.39	2699.00	1.78	0.11	-0.07	4156.00	2.09	0.37	-0.22
0.03	1850.00	0.43	1.46	-0.94	1794.00	4.07	1.61	0.98
-0.68	2025.00	3.70	1.81	1.17	1753.00	1.88	0.58	-0.35
-0.59	2345.00	0.68	1.21	-0.78	1602.00	3.75	1.29	0.79
0.01	3812.00	0.94	0.95	-0.61	3648.00	3.89	1.43	0.88
-1.19	1279.00	0.00	1.89	-1.22	1412.00	1.84	0.62	-0.38
-0.92	1761.00	0.28	1.61	-1.04	2051.00	2.05	0.41	-0.25
0.82	3719.00	1.24	0.65	-0.42	3051.00	4.88	2.42	1.48
-0.52	3503.00	1.06	0.83	-0.54	2770.00	2.24	0.22	-0.13
0.51	1470.00	1.97	0.08	0.05	2134.00	2.20	0.26	-0.16
-0.56	1215.00	0.49	1.40	-0.90	1172.00	2.73	0.27	0.17
-0.54	2110.00	0.85	1.04	-0.67	1355.00	2.21	0.25	-0.15
-0.89	2125.00	0.24	1.65	-1.07	1528.00	3.53	1.07	0.66
-1.23	2425.00	0.41	1.48	-0.96	2196.00	4.14	1.68	1.03
-1.11	2516.00	0.40	1.49	-0.97	1907.00	2.78	0.32	0.20

-1.00	1287.00	0.54	1.35	-0.87	1548.00	6.01	**3.55**	2.17
-0.88	2781.00	0.58	1.31	-0.85	2183.00	3.76	1.30	0.79
-0.13	4143.00	1.76	0.13	-0.08	2992.00	3.61	1.15	0.70
-0.87	2813.00	3.73	1.84	1.19	2448.00	6.99	**4.53**	2.76
-1.02	4217.00	1.45	0.44	-0.29	3316.00	2.86	0.40	0.25
-1.18	3713.00	0.51	1.38	-0.89	3081.00	4.93	2.47	1.51
-1.09	2158.00	1.39	0.50	-0.32	2076.00	2.07	0.39	-0.24
0.45	2041.00	1.37	0.52	-0.34	3607.00	3.88	1.42	0.87
-1.05	2832.00	1.06	0.83	-0.54	3162.00	2.18	0.28	-0.17
-0.85	2133.00	0.98	0.91	-0.59	2452.00	1.10	1.36	-0.83
0.69	2642.00	1.74	0.15	-0.10	3050.00	3.87	1.41	0.86
0.29	2999.00	0.30	1.59	-1.03	3064.00	1.86	0.60	-0.36
-0.28	2329.00	0.09	1.80	-1.17	1731.00	2.95	0.49	0.30
0.33	2670.00	2.77	0.88	0.57	2972.00	2.56	0.10	0.06
-0.07	2285.00	1.79	0.10	-0.06	2758.00	1.78	0.68	-0.42
-0.68	2799.00	0.25	1.64	-1.06	2837.00	2.71	0.25	0.16
-0.54	1842.00	0.22	1.67	-1.08	2189.00	1.87	0.59	-0.36
-0.55	3463.00	0.40	1.49	-0.96	3118.00	4.97	2.51	1.53
-0.10	1853.00	0.49	1.40	-0.91	1119.00	5.72	3.26	1.99
-1.09	2137.00	0.56	1.33	-0.86	2519.00	2.70	0.24	0.15
-1.03	1787.00	1.01	0.88	-0.57	1169.00	2.74	0.28	0.17
-0.76	2233.00	0.94	0.95	-0.62	1408.00	4.76	2.30	1.40
-0.96	3712.00	0.38	1.51	-0.98	2678.00	3.10	0.64	0.39
-0.23	3889.00	0.23	1.66	-1.07	3105.00	4.25	1.79	1.09
-0.88	4374.00	0.37	1.52	-0.99	3081.00	3.47	1.01	0.62
-0.72	2749.00	1.13	0.76	-0.49	2311.00	3.72	1.26	0.77
1.23	1218.00	1.40	0.49	-0.32	1699.00	4.59	2.13	1.30
3.34	3145.00	5.60	**3.71**	2.39	4308.00	3.32	0.86	0.53
0.77	2039.00	4.02	2.13	1.38	2737.00	1.06	1.40	-0.85
-0.69	3914.00	2.91	1.02	0.66	4505.00	2.97	0.51	0.32
-0.52	2166.00	0.97	0.92	-0.60	3030.00	5.48	3.02	1.84
0.85	2304.00	2.47	0.58	0.38	3392.00	3.57	1.11	0.68
0.10	2750.00	0.91	0.98	-0.64	2675.00	0.56	1.90	-1.16
-0.21	2104.00	3.71	1.82	1.17	3276.00	2.08	0.38	-0.23
1.48	1239.00	5.49	**3.60**	2.32	2339.00	5.30	2.84	1.74
0.52	980.00	3.16	1.27	0.82	1396.00	1.93	0.53	-0.32
-0.28	2116.00	1.70	0.19	-0.12	3086.00	1.36	1.10	-0.67
1.19	2268.00	3.31	1.42	0.91	3852.00	2.62	0.16	0.10
0.47	2499.00	2.04	0.15	0.10	2693.00	2.23	0.23	-0.14
0.39	1909.00	2.99	1.10	0.71	3152.00	4.60	2.14	1.31
0.86	901.00	5.22	**3.33**	2.15	1024.00	4.00	1.54	0.94
0.33	2488.00	3.22	1.33	0.86	3695.00	2.71	0.25	0.15
-0.21	1679.00	2.03	0.14	0.09	1958.00	2.81	0.35	0.21
0.66	2036.00	4.37	2.48	1.60	3287.00	6.27	**3.81**	2.33
1.48	2903.00	1.89	0.00	0.00	2183.00	2.61	0.15	0.09
0.56	764.00	4.45	2.56	1.65	696.00	7.76	**5.30**	3.24
0.08	3077.00	1.30	0.59	-0.38	2108.00	1.23	1.23	-0.75

-0.57	3718.00	0.54	1.35	-0.88	3293.00	1.49	0.97	-0.59
0.12	2749.00	1.38	0.51	-0.33	4193.00	1.57	0.89	-0.54
0.61	3472.00	1.93	0.04	0.02	4071.00	4.20	1.74	1.06
0.20	2541.00	1.10	0.79	-0.51	3488.00	1.72	0.74	-0.45
0.92	1897.00	2.48	0.59	0.38	2819.00	2.52	0.06	0.04
1.19	2744.00	1.20	0.69	-0.45	3517.00	7.19	**4.73**	2.89
-0.47	5479.00	1.19	0.70	-0.46	5448.00	1.82	0.64	-0.39
0.72	2307.00	1.00	0.89	-0.58	4509.00	2.88	0.42	0.26
0.24	3295.00	0.88	1.01	-0.65	3901.00	2.00	0.46	-0.28
4.05	414.00	8.21	**6.32**	4.09	495.00	3.64	1.18	0.72
-0.50	2815.00	0.75	1.14	-0.74	3758.00	1.22	1.24	-0.75
-0.08	3275.00	0.55	1.34	-0.87	3368.00	1.28	1.18	-0.72
-1.22	1919.00	0.36	1.53	-0.99	3408.00	1.03	1.43	-0.87
-0.20	2511.00	0.84	1.05	-0.68	3918.00	1.45	1.01	-0.61
0.23	966.00	1.86	0.03	-0.02	1745.00	2.06	0.40	-0.24
0.26	2717.00	2.28	0.39	0.25	3953.00	1.34	1.12	-0.68
-0.27	4285.00	1.89	0.00	0.00	3839.00	1.33	1.13	-0.69
-0.03	1989.00	2.51	0.62	0.40	3037.00	2.40	0.06	-0.03
-0.62	2345.00	1.07	0.82	-0.53	1819.00	0.38	2.08	-1.26
1.60	2985.00	4.66	2.77	1.79	1415.00	4.95	2.49	1.52
3.44	1060.00	3.58	1.69	1.09	947.00	2.75	0.29	0.18
3.61	2219.00	5.68	**3.79**	2.45	2316.00	7.08	**4.62**	2.82
9.45	212.00	22.64	**20.75**	13.41	245.00	14.69	**12.23**	7.47
4.08	5266.00	4.50	2.61	1.69	3769.00	4.01	1.55	0.95
3.13	469.00	8.32	**6.43**	4.15	808.00	2.48	0.02	0.01
1.11	1400.00	3.07	1.18	0.76	1175.00	3.49	1.03	0.63
0.73	2730.00	4.07	2.18	1.41	2698.00	2.85	0.39	0.24
1.45	1499.00	3.67	1.78	1.15	2753.00	2.22	0.24	-0.15
8.46	396.00	7.32	**5.43**	3.51	835.00	4.79	2.33	1.42
2.75	1096.00	2.37	0.48	0.31	1295.00	2.78	0.32	0.20
-0.36	1985.00	2.52	0.63	0.41	3595.00	1.17	1.29	-0.79
3.34	2157.00	3.71	1.82	1.17	2566.00	3.04	0.58	0.36
0.69	1112.00	3.33	1.44	0.93	2199.00	4.05	1.59	0.97
3.06	1495.00	6.09	**4.20**	2.71	3294.00	5.56	3.10	1.89
0.68	552.00	10.15	**8.26**	5.33	1603.00	3.24	0.78	0.48
1.70	2257.00	5.58	**3.69**	2.39	4115.00	3.11	0.65	0.40
-0.19	1124.00	5.16	**3.27**	2.11	1348.00	5.79	**3.33**	2.03
-0.98	1016.00	5.02	3.13	2.02	2044.00	1.61	0.85	-0.51
-1.17	1207.00	4.72	2.83	1.83	1521.00	1.64	0.82	-0.50
	2105.50	1.89	1.05		2393.50	2.46	1.11	
			3.14				3.32	
			1.55				1.64	
2600.00	11.73		2704.00	17.53				
3960.00	13.64		4558.00	23.26				
2956.00	13.40		4087.00	13.78				
3996.00	18.97		4308.00	22.15				
3378.00	14.43		3914.25	19.18				

708.05	3.14	829.46	4.37
1537.00	4.03	1230.00	3.25
2162.00	0.28	2240.00	2.72
1507.00	0.86	1380.00	4.28
1339.00	1.49	2047.00	3.96
1669.33	0.88	1889.00	3.65
434.85	0.61	451.25	0.82
	9.42		13.12
	1.82		2.46
	11.25		15.58
	13.56		15.52
	0.83		1.00
	0.17		0.00

156.00	16.03	159.00	18.24
93.00	20.43	153.00	19.61
1612.00	1.74	2108.00	1.71
2736.00	3.03	2010.00	2.74
4864.00	4.73	6181.00	5.19
6060.00	3.94	4479.00	4.89

x	toxic a,b,c
x	debris a,b
x	toxic a,b,c
x	toxic a,b,c
x	debris a

x	debris a
x	toxic a,b,c
x	debris a
x	debris a
x	toxic a,b,c

x	toxic a,b,c
x	toxic a,b,c
x	toxic c
x	debris a,b

y

y

x	toxic a,b,c
x	toxic a, art b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic b
x	toxic b,c

Plate	Well	Gene	GeneID	Cell Count	% inf
50054.00	A02	M-019962- stromal antigen 3	10734.00	STAG3	2670.00	2.13
50054.00	A04	M-012331- butyrophilin, subfamily 2, m	11120.00	BTN2A1	1866.00	1.55
50054.00	A05	M-017715- paraneoplastic antigen MA2	10687.00	PNMA2	2452.00	5.51
50054.00	A06	M-019108- butyrophilin, subfamily 3, m	11119.00	BTN3A1	3056.00	0.88
50054.00	A07	M-019114- fucosyltransferase 9 (alpha (	10690.00	FUT9	2149.00	2.70
50054.00	A08	M-019161- butyrophilin, subfamily 3, m	11118.00	BTN3A2	2183.00	1.24
50054.00	A09	M-019437- trinucleotide repeat contain	10695.00	TNRC5	2180.00	2.52
50054.00	A10	M-019765- elastin microfibril interfacer	11117.00	EMILIN1	1924.00	1.66
50054.00	A11	M-005831- corin, serine peptidase	10699.00	CORIN	1561.00	5.00
50054.00	A12	M-009681- 3-hydroxyisobutyrate dehyd	11112.00	HIBADH	1860.00	2.69
50054.00	A13	M-006087- ubiquitin specific peptidase	10713.00	USP39	888.00	5.63
50054.00	A14	M-005157- katanin p60 (ATPase-contair	11104.00	KATNA1	1538.00	6.05
50054.00	A15	M-026692- polymerase (DNA-directed),	10714.00	POLD3	1216.00	2.47
50054.00	A16	M-012761- arginyltransferase 1	11101.00	ATE1	2566.00	3.55
50054.00	A17	M-010275- LAG1 homolog, ceramide syı	10715.00	LASS1	1122.00	3.21
50054.00	A18	M-006043- protease, serine, 23	11098.00	PRSS23	2189.00	6.85
50054.00	A19	M-020158- adaptor-related protein com	10717.00	AP4B1	1388.00	7.49
50054.00	A20	M-019748- nucleoporin like 2	11097.00	NUPL2	1397.00	4.58
50054.00	A21	M-020192- UDP glucuronosyltransferase	10720.00	UGT2B11	1504.00	5.32
50054.00	A23	M-015180- polymerase (DNA directed),	10721.00	POLQ	1223.00	4.09
50054.00	B02	M-022645- KIAA0953	22979.00	KIAA0953	5400.00	2.52
50054.00	B04	M-009420- 5'-nucleotidase, cytosolic II	22978.00	NT5C2	4445.00	1.57
50054.00	B05	M-012331- butyrophilin, subfamily 2, m	11120.00	BTN2A1	4665.00	3.09
50054.00	B06	M-010571- TPX2, microtubule-associate	22974.00	TPX2	1632.00	2.82
50054.00	B07	M-020467- Down syndrome critical regi	11123.00	DSCR1L2	4773.00	1.49
50054.00	B08	M-015076- double homeobox, 4	22947.00	DUX4	6390.00	7.04
50054.00	B09	M-019741- polymerase (RNA) III (DNA d	11128.00	POLR3A	4270.00	1.66
50054.00	B10	M-003843- dickkopf homolog 1 (Xenopu	22943.00	DKK1	5833.00	1.75
50054.00	B11	M-019710- splicing factor, arginine/serir	11129.00	SFRS16	3801.00	3.26
50054.00	B12	M-012459- SH3 and multiple ankyrin rep	22941.00	SHANK2	3387.00	0.68
50054.00	B13	M-006830- ZW10 interactor	11130.00	ZWINT	3537.00	0.79
50054.00	B14	M-008177- elongation factor, RNA polyr	22936.00	ELL2	4431.00	2.03
50054.00	B15	M-005801- calpain 11	11131.00	CAPN11	4431.00	1.85
50054.00	B16	M-016428- ribose 5-phosphate isomera	22934.00	RPIA	5958.00	1.02
50054.00	B17	M-019744- PWP1 homolog (S. cerevisiae	11137.00	PWP1	4275.00	1.92
50054.00	B18	M-012834- hyaluronan binding protein	22927.00	HABP4	6447.00	4.25
50054.00	B19	M-019705- TBC1 domain family, membe	11138.00	TBC1D8	6183.00	2.36
50054.00	B20	M-015327- nuclear cap binding protein	22916.00	NCBP2	4127.00	3.08
50054.00	B21	M-017668- MYST histone acetyltransfer	11143.00	MYST2	2909.00	1.82
50054.00	B23	M-019760- HRAS-like suppressor 3	11145.00	HRASLS3	2611.00	2.87
50054.00	C02	M-020337- chromosome 9 open reading	11094.00	C9orf7	5443.00	2.41
50054.00	C04	M-019352- chromosome 9 open reading	11092.00	C9orf9	3117.00	3.30
50054.00	C05	M-007388- solute carrier family 12 (pot	10723.00	SLC12A7	4350.00	5.66
50054.00	C06	M-015678- DnaJ (Hsp40) homolog, subf	11080.00	DNAJB4	4740.00	5.36
50054.00	C07	M-021351- stromal antigen 2	10735.00	STAG2	5028.00	5.43
50054.00	C08	M-017170- RER1 retention in endoplasn	11079.00	RER1	3201.00	5.12

50054.00	C09	M-006934-	ret finger protein-like 3	10738.00	RFPL3	6147.00	4.07
50054.00	C10	M-012342-	TRIO and F-actin binding pro	11078.00	TRIOBP	4323.00	4.49
50054.00	C11	M-006935-	ret finger protein-like 2	10739.00	RFPL2	5982.00	4.18
50054.00	C12	M-019695-	tubulin polymerization prom	11076.00	TPPP	3452.00	2.78
50054.00	C13	M-005938-	mannan-binding lectin serin	10747.00	MASP2	3094.00	5.69
50054.00	C14	M-006939-	tripartite motif-containing 3	11074.00	TRIM31	4250.00	6.87
50054.00	C15	M-012279-	cell adhesion molecule with	10752.00	CHL1	4439.00	9.55
50054.00	C16	M-012337-	chromosome 10 open readir	11067.00	C10orf10	5452.00	4.99
50054.00	C17	M-005808-	calpain 9	10753.00	CAPN9	4967.00	1.83
50054.00	C18	M-012359-	U11/U12 snRNP 35K	11066.00	U1SNRNPB	3694.00	3.49
50054.00	C19	M-004311-	TRAF3 interacting protein 2	10758.00	TRAF3IP2	3269.00	2.26
50054.00	C20	M-012355-	SRY (sex determining region	11063.00	SOX30	5731.00	2.76
50054.00	C21	M-013966-	placenta-specific 1	10761.00	PLAC1	3962.00	3.21
50054.00	C23	M-012369-	nucleoporin 50kDa	10762.00	NUP50	4125.00	1.60
50054.00	D02	M-012391-	killer cell lectin-like receptor	22914.00	KLRK1	5129.00	0.92
50054.00	D04	M-012392-	RNA binding protein, autoan	22913.00	RALY	4834.00	4.10
50054.00	D05	M-012339-	glomulin, FKBP associated pı	11146.00	GLMN	5053.00	2.45
50054.00	D06	M-017745-	WD repeat domain 47	22911.00	WDR47	5202.00	4.67
50054.00	D07	M-019762-	HERV-H LTR-associating 3	11147.00	HHLA3	4884.00	3.07
50054.00	D08	M-020327-	myotubularin related proteiı	22909.00	MTMR15	5338.00	3.63
50054.00	D09	M-017669-	HERV-H LTR-associating 2	11148.00	HHLA2	4542.00	3.85
50054.00	D10	M-007280-	SAC1 suppressor of actin mu	22908.00	SACM1L	4377.00	3.84
50054.00	D11	M-012332-	blood vessel epicardial subst	11149.00	BVES	4006.00	8.54
50054.00	D12	M-017196-	DEAH (Asp-Glu-Ala-His) box	22907.00	DHX30	2868.00	5.09
50054.00	D13	M-019758-	WD repeat domain 45	11152.00	WDR45	2487.00	5.03
50054.00	D14	M-020331-	trafficking protein, kinesin bi	22906.00	TRAK1	2160.00	2.13
50054.00	D15	M-016178-	adaptor-related protein com	11154.00	AP4S1	3564.00	3.42
50054.00	D16	M-004743-	strawberry notch homolog 2	22904.00	SBNO2	4870.00	3.33
50054.00	D17	M-026288-	LIM domain binding 3	11155.00	LDB3	5089.00	2.55
50054.00	D18	M-012943-	BTB (POZ) domain containin	22903.00	BTBD3	5460.00	4.40
50054.00	D19	M-019754-	LSM6 homolog, U6 small nu	11157.00	LSM6	4210.00	2.42
50054.00	D20	M-020336-	RUN and FYVE domain conta	22902.00	RUFY3	4838.00	8.62
50054.00	D21	M-017943-	ER lipid raft associated 2	11160.00	ERLIN2	5360.00	7.82
50054.00	D23	M-019683-	chromosome 14 open readir	11161.00	C14orf1	3268.00	1.19
50054.00	E02	M-019096-	dihydrouridine synthase 4-lil	11062.00	DUS4L	3368.00	2.35
50054.00	E04	M-019767-	leukocyte cell derived chem	11061.00	LECT1	3977.00	8.25
50054.00	E05	M-031117-	nestin	10763.00	NES	3494.00	2.80
50054.00	E06	M-012766-	DEAD (Asp-Glu-Ala-Asp) box	11056.00	DDX52	4051.00	5.01
50054.00	E07	M-015677-	HBS1-like (S. cerevisiae)	10767.00	HBS1L	2863.00	4.68
50054.00	E08	M-019723-	zona pellucida binding prote	11055.00	ZPBP	3126.00	3.01
50054.00	E09	M-016091-	cyclic AMP-regulated phospl	10777.00	ARPP-21	3184.00	4.77
50054.00	E10	M-012334-	cleavage and polyadenylatio	11052.00	CPSF6	3899.00	2.33
50054.00	E11	M-015671-	zinc finger protein 271	10778.00	ZNF271	4588.00	5.14
50054.00	E12	M-012335-	nudix (nucleoside diphospha	11051.00	NUDT21	2831.00	5.09
50054.00	E13	M-012750-	zinc finger protein 234	10780.00	ZNF234	3837.00	5.37
50054.00	E14	M-010705-	solute carrier family 35, mer	11046.00	SLC35D2	2363.00	2.16
50054.00	E15	M-021434-	zinc finger protein 266	10781.00	ZNF266	3895.00	2.62

50054.00	E16	M-012360- uroplakin 1A	11045.00	UPK1A	2702.00	4.07
50054.00	E17	M-013359- zinc finger protein 274	10782.00	ZNF274	4329.00	2.70
50054.00	E18	M-006938- midline 2	11043.00	MID2	5521.00	3.22
50054.00	E19	M-007413- solute carrier family 17 (sodi	10786.00	SLC17A3	4604.00	1.78
50054.00	E20	M-012307- UDP-GlcNAc:betaGal beta-1,	11041.00	B3GNT1	3262.00	1.53
50054.00	E21	M-017684- vesicle-associated membran	10791.00	VAMP5	5254.00	1.52
50054.00	E23	M-032003- zinc finger protein 273	10793.00	ZNF273	3847.00	0.55
50054.00	F02	M-008346- arylsulfatase G	22901.00	ARSG	2434.00	3.08
50054.00	F04	M-004454- caspase recruitment domain	22900.00	CARD8	4865.00	1.97
50054.00	F05	M-008874- nudix (nucleoside diphospha	11162.00	NUDT6	2767.00	2.39
50054.00	F06	M-025843- DENN/MADD domain contai	22898.00	DENND3	2206.00	0.95
50054.00	F07	M-008733- nudix (nucleoside diphospha	11164.00	NUDT5	4634.00	3.78
50054.00	F08	M-020351- centrosomal protein 164kDa	22897.00	CEP164	1794.00	0.72
50054.00	F09	M-009801- nudix (nucleoside diphospha	11165.00	NUDT3	3798.00	9.85
50054.00	F10	M-020354- rabphilin 3A homolog (mous	22895.00	RPH3A	4025.00	2.04
50054.00	F11	M-019728- SRY (sex determining region	11166.00	SOX21	4323.00	4.49
50054.00	F12	M-015405- DIS3 mitotic control homolo	22894.00	DIS3	3111.00	2.57
50054.00	F13	M-015209- PC4 and SFRS1 interacting p	11168.00	PSIP1	2925.00	0.38
50054.00	F14	M-020357- bromo adjacent homology d	22893.00	BAHD1	3068.00	3.16
50054.00	F15	M-019780- WD repeat and HMG-box D	11169.00	WDHD1	3780.00	3.78
50054.00	F16	M-020367- zinc finger and BTB domain c	22890.00	ZBTB1	2077.00	2.26
50054.00	F17	M-012785- family with sequence similar	11170.00	FAM107A	3635.00	4.04
50054.00	F18	M-020370- KIAA0907	22889.00	KIAA0907	3065.00	5.97
50054.00	F19	M-016282- serine/threonine kinase rece	11171.00	STRAP	2014.00	1.39
50054.00	F20	M-020390- WD repeat domain 37	22884.00	WDR37	2469.00	3.40
50054.00	F21	M-020470- bromodomain adjacent to zi	11176.00	BAZ2A	3776.00	0.50
50054.00	F23	M-006941- bromodomain adjacent to zi	11177.00	BAZ1A	2813.00	3.24
50054.00	G02	M-017544- stonin 1	11037.00	STON1	4306.00	4.39
50054.00	G04	M-012752- centaurin, alpha 1	11033.00	CENTA1	2250.00	3.07
50054.00	G05	M-032012- zinc finger protein 460	10794.00	ZNF460	3885.00	7.28
50054.00	G06	M-012756- RNA binding protein with m	11030.00	RBPMS	4114.00	7.78
50054.00	G07	M-012660- zinc finger protein 268	10795.00	ZNF268	4166.00	2.76
50054.00	G08	M-019855- leukocyte immunoglobulin-li	11027.00	LILRA2	2453.00	4.57
50054.00	G09	M-009349- methylenetetrahydrofolate	10797.00	MTHFD2	3515.00	5.92
50054.00	G10	M-017686- leukocyte immunoglobulin-li	11026.00	LILRA3	4374.00	3.96
50054.00	G11	M-020030- ribonuclease P 40kDa subun	10799.00	RPP40	3158.00	0.92
50054.00	G12	M-008872- leukocyte immunoglobulin-li	11025.00	LILRB3	3569.00	5.69
50054.00	G13	M-012744- serologically defined colon c	10806.00	SDCCAG8	2523.00	1.03
50054.00	G14	M-019862- leukocyte immunoglobulin-li	11024.00	LILRA1	3194.00	2.16
50054.00	G15	M-016427- serologically defined colon c	10807.00	SDCCAG3	3124.00	3.78
50054.00	G16	M-031769- ventral anterior homeobox 1	11023.00	VAX1	2919.00	2.02
50054.00	G17	M-012743- START domain containing 10	10809.00	STARD10	2616.00	2.94
50054.00	G18	M-019792- tudor and KH domain contai	11022.00	TDRKH	3921.00	4.87
50054.00	G19	M-026087- NADPH oxidase activator 1	10811.00	NOXA1	1965.00	6.82
50054.00	G20	M-010023- lipoic acid synthetase	11019.00	LIAS	2412.00	3.44
50054.00	G21	M-016395- UTP14, U3 small nucleolar ri	10813.00	UTP14A	1368.00	7.75
50054.00	G23	M-012280- complexin 2	10814.00	CPLX2	3295.00	2.00

50054.00	H02	M-020396-	ankyrin repeat domain 6	22881.00	ANKRD6	4738.00	6.50
50054.00	H04	M-021467-	MON1 homolog B (yeast)	22879.00	MON1B	5845.00	5.73
50054.00	H05	M-013990-	zinc finger protein 277 pseu	11179.00	ZNF277P	3975.00	3.47
50054.00	H06	M-010645-	KIAA1012	22878.00	KIAA1012	3628.00	0.50
50054.00	H07	M-019630-	trehalase (brush-border mer	11181.00	TREH	2901.00	1.69
50054.00	H08	M-010644-	pleckstrin homology domain	22874.00	PLEKHA6	3682.00	1.77
50054.00	H09	M-007519-	solute carrier family 2 (facilit	11182.00	SLC2A6	3081.00	3.73
50054.00	H10	M-020416-	DAZ interacting protein 1	22873.00	DZIP1	3686.00	5.59
50054.00	H11	M-015314-	indolethylamine N-methyltra	11185.00	INMT	3000.00	3.77
50054.00	H12	M-014166-	SEC31 homolog A (S. cerevis	22872.00	SEC31A	4594.00	2.85
50054.00	H13	M-019677-	nischarin	11188.00	NISCH	3340.00	1.62
50054.00	H14	M-010278-	neuroligin 1	22871.00	NLGN1	3866.00	3.75
50054.00	H15	M-017833-	trinucleotide repeat contain	11189.00	TNRC4	3128.00	1.25
50054.00	H16	M-020420-	SAPS domain family, membe	22870.00	SAPS1	2436.00	2.30
50054.00	H17	M-012385-	WW domain binding protein	11193.00	WBP4	3893.00	2.59
50054.00	H18	M-020424-	zinc finger protein 510	22869.00	ZNF510	3290.00	3.95
50054.00	H19	M-012370-	SEC23 interacting protein	11196.00	SEC23IP	5015.00	2.87
50054.00	H20	M-020427-	FAST kinase domains 2	22868.00	FASTKD2	3789.00	3.38
50054.00	H21	M-009517-	suppressor of Ty 16 homolo	11198.00	SUPT16H	4095.00	7.77
50054.00	H23	M-019650-	polymerase (DNA directed) i	11201.00	POLI	3344.00	2.63
50054.00	I02	M-012758-	putative nucleic acid binding	11017.00	RY1	2384.00	4.32
50054.00	I04	M-005908-	kallikrein-related peptidase	11012.00	KLK11	2695.00	2.63
50054.00	I05	M-013031-	complexin 1	10815.00	CPLX1	4097.00	10.18
50054.00	I06	M-012311-	coiled-coil domain containin	11007.00	CCDC85B	3549.00	2.28
50054.00	I07	M-010641-	sialidase 3 (membrane sialid	10825.00	NEU3	3290.00	4.01
50054.00	I08	M-007499-	solute carrier family 27 (fatt	11000.00	SLC27A3	2707.00	3.81
50054.00	I09	M-010276-	chromosome 5 open reading	10826.00	C5orf4	2037.00	4.42
50054.00	I10	M-007500-	solute carrier family 27 (fatt	10999.00	SLC27A4	2374.00	2.65
50054.00	I11	M-021041-	chromosome 5 open reading	10827.00	C5orf3	2785.00	3.05
50054.00	I12	M-007501-	solute carrier family 27 (fatt	10998.00	SLC27A5	2285.00	5.73
50054.00	I13	M-024859-	zinc finger protein 275	10838.00	ZNF275	2330.00	3.35
50054.00	I14	M-009658-	ilvB (bacterial acetolactate s	10994.00	ILVBL	2519.00	2.42
50054.00	I15	M-008414-	aldehyde dehydrogenase 1 f	10840.00	ALDH1L1	2702.00	0.93
50054.00	I16	M-008214-	serine dehydratase	10993.00	SDS	2242.00	2.77
50054.00	I17	M-008623-	formiminotransferase cycloc	10841.00	FTCD	3779.00	3.89
50054.00	I18	M-026599-	splicing factor 3b, subunit 2,	10992.00	SF3B2	882.00	4.76
50054.00	I19	M-007663-	phosphodiesterase 10A	10846.00	PDE10A	2914.00	1.00
50054.00	I20	M-007560-	solute carrier family 38, mer	10991.00	SLC38A3	4100.00	1.61
50054.00	I21	M-003815-	protein phosphatase 1, regu	10848.00	PPP1R13L	3092.00	2.62
50054.00	I23	M-020021-	CD3e molecule, epsilon asso	10849.00	CD3EAP	2509.00	1.32
50054.00	J02	M-020433-	connector enhancer of kinas	22866.00	CNKSR2	3595.00	2.92
50054.00	J04	M-020435-	SLIT and NTRK-like family, m	22865.00	SLITRK3	4825.00	2.76
50054.00	J05	M-005919-	kallikrein-related peptidase	11202.00	KLK8	4276.00	4.77
50054.00	J06	M-012950-	R3H domain containing 2	22864.00	R3HDM2	4535.00	3.09
50054.00	J07	M-008449-	proline synthetase co-transc	11212.00	PROSC	2697.00	7.08
50054.00	J08	M-020438-	KIAA0831	22863.00	KIAA0831	3302.00	3.42
50054.00	J09	M-012372-	mitochondrial ribosomal pr	11222.00	MRPL3	3819.00	3.80

50054.00	J10	M-032215-	fibronectin type III domain c	22862.00	FNDC3A	5345.00	7.63
50054.00	J11	M-012366-	UDP-N-acetyl-alpha-D-galact	11226.00	GALNT6	2777.00	4.47
50054.00	J12	M-021339-	carbohydrate (chondroitin)	22856.00	CHSY1	1749.00	6.00
50054.00	J13	M-014197-	UDP-N-acetyl-alpha-D-galact	11227.00	GALNT5	3797.00	4.66
50054.00	J14	M-020443-	netrin G1	22854.00	NTNG1	3007.00	4.19
50054.00	J15	M-016509-	Ras association (RalGDS/AF-	11228.00	RASSF8	2297.00	3.09
50054.00	J16	M-020450-	ankyrin repeat domain 26	22852.00	ANKRD26	3130.00	3.99
50054.00	J17	M-019671-	PRA1 domain family, membe	11230.00	PRAF2	2340.00	4.40
50054.00	J18	M-020456-	zinc finger protein 508	22850.00	ZNF508	2888.00	2.08
50054.00	J19	M-004886-	SEC63 homolog (S. cerevisia	11231.00	SEC63	2849.00	4.67
50054.00	J20	M-020458-	cytoplasmic polyadenylation	22849.00	CPEB3	2623.00	2.55
50054.00	J21	M-019659-	polymerase (DNA directed),	11232.00	POLG2	3523.00	5.39
50054.00	J23	M-017465-	Hermansky-Pudlak syndrom	11234.00	HPS5	3285.00	6.61
50054.00	K02	M-019832-	inner membrane protein, mi	10989.00	IMMT	4420.00	4.52
50054.00	K04	M-005943-	methionyl aminopeptidase 2	10988.00	METAP2	4007.00	2.37
50054.00	K05	M-015322-	heparanase	10855.00	HPSE	3770.00	5.23
50054.00	K06	M-027130-	GCN1 general control of ami	10985.00	GCN1L1	3004.00	1.86
50054.00	K07	M-009292-	cytochrome P450, family 46,	10858.00	CYP46A1	4386.00	2.23
50054.00	K08	M-017017-	COP9 constitutive photomor	10980.00	COPS6	3512.00	2.76
50054.00	K09	M-007488-	solute carrier family 26 (sulf	10861.00	SLC26A1	5392.00	2.52
50054.00	K10	M-019895-	CLP1, cleavage and polyader	10978.00	CLP1	3196.00	2.63
50054.00	K11	M-007458-	solute carrier family 22 (orga	10864.00	SLC22A7	2185.00	3.25
50054.00	K12	M-012306-	chromosome 10 open readir	10974.00	C10orf116	2761.00	6.05
50054.00	K13	M-022856-	AT rich interactive domain 5	10865.00	ARID5A	3319.00	2.65
50054.00	K14	M-012757-	activating signal cointegrato	10973.00	ASCC3	4040.00	4.78
50054.00	K15	M-020059-	HLA complex P5	10866.00	HCP5	2063.00	1.55
50054.00	K16	M-012755-	cytoskeleton-associated pro	10970.00	CKAP4	1811.00	1.66
50054.00	K17	M-012293-	tetraspanin 9	10867.00	TSPAN9	3285.00	1.89
50054.00	K18	M-019834-	EBNA1 binding protein 2	10969.00	EBNA1BP2	1948.00	1.85
50054.00	K19	M-008499-	malic enzyme 3, NADP(+)-de	10873.00	ME3	3531.00	1.44
50054.00	K20	M-009938-	acyl-CoA thioesterase 2	10965.00	ACOT2	3559.00	2.56
50054.00	K21	M-007905-	fibrinogen-like 2	10875.00	FGL2	3253.00	2.12
50054.00	K23	M-012287-	family with sequence similar	10876.00	FAM12A	3065.00	1.31
50054.00	L02	M-006948-	zinc finger protein 507	22847.00	ZNF507	3018.00	2.09
50054.00	L04	M-020466-	vasohibin 1	22846.00	VASH1	2726.00	2.16
50054.00	L05	M-006943-	ring finger protein 24	11237.00	RNF24	3788.00	2.48
50054.00	L06	M-006317-	dolichol kinase	22845.00	DOLK	2213.00	1.76
50054.00	L07	M-008829-	carbonic anhydrase VB, mitc	11238.00	CA5B	2486.00	1.73
50054.00	L08	M-020471-	FERM and PDZ domain conta	22844.00	FRMPD1	1694.00	0.41
50054.00	L09	M-019485-	peptidyl arginine deiminase,	11240.00	PADI2	3403.00	2.32
50054.00	L10	M-020474-	RAB11 family interacting prc	22841.00	RAB11FIP2	2270.00	2.20
50054.00	L11	M-019662-	polyamine-modulated factor	11243.00	PMF1	2500.00	2.88
50054.00	L12	M-009452-	discs, large (Drosophila) hon	22839.00	DLGAP4	2142.00	1.91
50054.00	L13	M-026967-	neurexophilin 4	11247.00	NXPH4	2723.00	3.16
50054.00	L14	M-006947-	ring finger protein 44	22838.00	RNF44	3837.00	5.08
50054.00	L15	M-012780-	neurexophilin 3	11248.00	NXPH3	2416.00	1.03
50054.00	L16	M-020477-	COBL-like 1	22837.00	COBLL1	2738.00	2.92

50054.00	L17	M-027941-	neurexophilin 2	11249.00	NXPH2	1452.00	0.83
50054.00	L18	M-020486-	zinc finger protein 652	22834.00	ZNF652	5014.00	4.59
50054.00	L19	M-019666-	protein kinase C and casein	11252.00	PACSIN2	3718.00	3.36
50054.00	L20	M-020488-	KIAA1009	22832.00	KIAA1009	4016.00	7.59
50054.00	L21	M-019670-	mannosidase, alpha, class 1	11253.00	MAN1B1	3509.00	1.94
50054.00	L23	M-007601-	solute carrier family 6 (amin	11254.00	SLC6A14	2863.00	5.03
50054.00	M02	M-004599-	interferon-induced protein 4	10964.00	IFI44L	1779.00	1.41
50054.00	M04	M-012312-	endoplasmic reticulum prote	10961.00	ERP29	4091.00	5.74
50054.00	M05	M-020170-	complement factor H-relate	10877.00	CFHR4	2240.00	2.41
50054.00	M06	M-019905-	lectin, mannose-binding 2	10960.00	LMAN2	4231.00	5.58
50054.00	M07	M-007906-	complement factor H-relate	10878.00	CFHR3	2692.00	1.71
50054.00	M08	M-008074-	transmembrane emp24 dom	10959.00	TMED2	3038.00	4.11
50054.00	M09	M-020063-	submaxillary gland androge	10879.00	SMR3B	2769.00	4.19
50054.00	M10	M-010811-	amplified in osteosarcoma	10956.00	OS9	2607.00	2.80
50054.00	M11	M-019440-	complement component 1,	10882.00	C1QL1	2218.00	4.24
50054.00	M12	M-016439-	translocase of outer mitoch	10953.00	TOMM34	3261.00	3.07
50054.00	M13	M-020129-	extracellular link domain co	10894.00	XLKD1	2840.00	2.04
50054.00	M14	M-021504-	Sec61 beta subunit	10952.00	SEC61B	2801.00	5.46
50054.00	M15	M-027310-	oculomedin	10896.00	OCLM	4624.00	6.19
50054.00	M16	M-012314-	heterogeneous nuclear ribo	10949.00	HNRPA0	3782.00	2.30
50054.00	M17	M-020155-	Yip1 interacting factor hom	10897.00	YIF1A	4042.00	4.95
50054.00	M18	M-017665-	START domain containing 3	10948.00	STARD3	3240.00	3.58
50054.00	M19	M-012292-	cleavage and polyadenylatio	10898.00	CPSF4	5109.00	4.83
50054.00	M20	M-012309-	adaptor-related protein com	10947.00	AP3M2	2948.00	4.82
50054.00	M21	M-010567-	jumping translocation break	10899.00	JTB	3533.00	5.24
50054.00	M23	M-008576-	dehydrogenase/reductase (	10901.00	DHRS4	3938.00	4.98
50054.00	N02	M-020494-	zinc finger protein 409	22830.00	ZNF409	2124.00	1.08
50054.00	N04	M-008441-	neuroligin 4, Y-linked	22829.00	NLGN4Y	3788.00	4.44
50054.00	N05	M-021437-	calcium binding protein P22	11261.00	CHP	5091.00	5.30
50054.00	N06	M-020498-	RNA binding motif protein 1	22828.00	RBM16	4386.00	1.94
50054.00	N07	M-019074-	peroxisomal membrane prot	11264.00	PXMP4	3221.00	2.39
50054.00	N08	M-012505-	fuse-binding protein-interac	22827.00	SIAHBP1	1430.00	2.94
50054.00	N09	M-004695-	SNF8, ESCRT-II complex subu	11267.00	SNF8	2647.00	2.64
50054.00	N10	M-020627-	DnaJ (Hsp40) homolog, subf	22826.00	DNAJC8	3277.00	3.75
50054.00	N11	M-013471-	DEAD (Asp-Glu-Ala-As) box p	11269.00	DDX19B	2424.00	4.62
50054.00	N12	M-012389-	pleckstrin homology-like do	22822.00	PHLDA1	2939.00	1.84
50054.00	N13	M-012779-	nurim (nuclear envelope me	11270.00	NRM	1653.00	4.17
50054.00	N14	M-019138-	coatomer protein complex,	22820.00	COPG	1220.00	7.13
50054.00	N15	M-012367-	proline rich 4 (lacrimal)	11272.00	PRR4	2559.00	3.87
50054.00	N16	M-020293-	coatomer protein complex,	22818.00	COPZ1	486.00	10.29
50054.00	N17	M-010931-	kelch-like 2, Mayven (Droso	11275.00	KLHL2	2874.00	3.03
50054.00	N18	M-017622-	5'-3' exoribonuclease 2	22803.00	XRN2	2627.00	4.80
50054.00	N19	M-019645-	POU domain, class 6, transc	11281.00	POU6F2	2652.00	2.68
50054.00	N20	M-010706-	chloride channel, calcium ac	22802.00	CLCA4	2459.00	4.39
50054.00	N21	M-012503-	mannosyl (alpha-1,3-)-glyco	11282.00	MGAT4B	2202.00	1.04
50054.00	N23	M-009131-	cytochrome P450, family 4,	11283.00	CYP4F8	3463.00	6.35
50054.00	O02	M-019136-	KDEL (Lys-Asp-Glu-Leu) endo	10945.00	KDELR1	2900.00	3.24

50054.00	O04	M-018988-	chromosome 11 open readir	10944.00	C11orf58	2726.00	2.97
50054.00	O05	M-018883-	myotubularin related proteii	10903.00	MTMR11	2649.00	6.64
50054.00	O06	M-012319-	male-specific lethal 3-like 1 (	10943.00	MSL3L1	2120.00	2.92
50054.00	O07	M-004097-	TRAF-type zinc finger domai	10906.00	TRAFD1	3423.00	4.03
50054.00	O08	M-003695-	protease, serine, 21 (testisin	10942.00	PRSS21	1751.00	4.68
50054.00	O09	M-008361-	thioredoxin-like 4A	10907.00	TXNL4A	2846.00	3.13
50054.00	O10	M-019786-	UDP glucuronosyltransferase	10941.00	UGT2A1	2897.00	2.73
50054.00	O11	M-010277-	patatin-like phospholipase d	10908.00	PNPLA6	3126.00	2.43
50054.00	O12	M-014148-	processing of precursor 1, ril	10940.00	POP1	1989.00	1.76
50054.00	O13	M-012877-	SGT1, suppressor of G2 allel	10910.00	SUGT1	1612.00	3.35
50054.00	O14	M-019022-	EH-domain containing 1	10938.00	EHD1	3609.00	6.21
50054.00	O15	M-012326-	urotensin 2	10911.00	UTS2	3602.00	2.11
50054.00	O16	M-006379-	mortality factor 4 like 1	10933.00	MORF4L1	3156.00	2.85
50054.00	O17	M-018882-	poly(A) polymerase alpha	10914.00	PAPOLA	4565.00	6.31
50054.00	O18	M-012323-	splicing factor, arginine/seri	10929.00	SFRS2B	3821.00	4.66
50054.00	O19	M-017284-	melanoma antigen family D,	10916.00	MAGED2	4977.00	4.44
50054.00	O20	M-003630-	sphingomyelin phosphodiest	10924.00	SMPDL3A	4960.00	8.85
50054.00	O21	M-021357-	butyrophilin-like 3	10917.00	BTNL3	3827.00	3.58
50054.00	O23	M-015831-	COP9 constitutive photomor	10920.00	COPS8	2090.00	2.25
50054.00	P02	M-025439-	laminin, beta 4	22798.00	LAMB4	2703.00	3.00
50054.00	P04	M-019487-	component of oligomeric go	22796.00	COG2	3188.00	6.65
50054.00	P05	M-007442-	solute carrier organic anion	11309.00	SLCO2B1	1396.00	3.72
50054.00	P06	M-010570-	cancer susceptibility candida	22794.00	CASC3	2473.00	3.36
50054.00	P07	M-013407-	vacuolar protein sorting 45 h	11311.00	VPS45	1154.00	2.25
50054.00	P08	M-021390-	synaptopodin	11346.00	SYNPO	1495.00	1.07
50054.00	P09	M-012778-	CD300a molecule	11314.00	CD300A	3741.00	1.92
50054.00	P10	M-006944-	ring finger protein 13	11342.00	RNF13	3124.00	4.77
50054.00	P11	M-017632-	coatomer protein complex, s	11316.00	COPE	3654.00	4.52
50054.00	P12	M-012373-	scrapie responsive protein 1	11341.00	SCRG1	2742.00	2.81
50054.00	P13	M-021485-	XPA binding protein 1, GTPa	11321.00	XAB1	1089.00	2.02
50054.00	P14	M-012782-	exosome component 8	11340.00	EXOSC8	1201.00	1.75
50054.00	P15	M-012393-	DEAD (Asp-Glu-Ala-Asp) box	11325.00	DDX42	2142.00	5.04
50054.00	P16	M-012783-	Opa interacting protein 5	11339.00	OIP5	2750.00	2.55
50054.00	P17	M-012788-	V-set and immunoglobulin d	11326.00	VSIG4	2735.00	2.78
50054.00	P18	M-012380-	U2 small nuclear RNA auxilia	11338.00	U2AF2	1260.00	1.51
50054.00	P19	M-010034-	FK506 binding protein 9, 63	11328.00	FKBP9	3447.00	1.48
50054.00	P20	M-019010-	exocyst complex component	11336.00	EXOC3	1914.00	1.36
50054.00	P21	M-005833-	chymotrypsin C (caldecrin)	11330.00	CTRC	2637.00	1.93
50054.00	P23	M-006478-	tumor suppressor candidate	11334.00	TUSC2	2447.00	1.27
						3195.00	3.08
					MAD3		
					MADc		
50054.00	C22					4287.00	12.20
50054.00	D22					4133.00	15.12
50054.00	E22					3721.00	15.10
50054.00	F22					2943.00	10.91
					mn	3771.00	13.33

						sd	601.49	2.12
50054.00	G22						929.00	4.63
50054.00	H22						1554.00	1.09
50054.00	I22						1643.00	4.87
50054.00	J22			1864.00	7.14			
						mn	1598.50	2.98
						sd	62.93	2.67
						3psSD		6.36
						3ngSD		8.01
						SumSD		14.37
						DiffMn		10.35
						SmovrDiff		1.39
						1minus		-0.39
50054.00	G03	M-003290-	polo-like kinase 1 (Drosophil		5347.00	PLK1 SMAF	265.00	12.45
50054.00	H03	M-003290-	polo-like kinase 1 (Drosophil		5347.00	PLK1 SMAF	414.00	7.73
50054.00	I03	D-001206-	siControl non-targeting siRNA #2				2770.00	2.85
50054.00	J03	D-001206-	siControl non-targeting siRNA #2				3814.00	1.81
50054.00	K03	D-001600-	siGLO RISC-free siRNA				5900.00	5.51
50054.00	L03	D-001600-	siGLO RISC-free siRNA				5136.00	4.50

Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev
0.95	-0.54	3820.00	0.65	2.26	-1.19	3236.00	3.65	1.36
1.53	-0.88	2622.00	1.03	1.88	-0.99	2321.00	2.03	0.27
2.43	1.39	2054.00	2.78	0.13	-0.07	2944.00	3.26	0.97
2.20	-1.26	2100.00	0.76	2.15	-1.13	2803.00	1.50	0.79
0.38	-0.22	2855.00	2.07	0.84	-0.44	3055.00	3.44	1.15
1.84	-1.06	2687.00	1.90	1.01	-0.53	3309.00	2.54	0.25
0.56	-0.32	2793.00	0.90	2.01	-1.06	2386.00	0.84	1.45
1.42	-0.81	2204.00	1.41	1.50	-0.79	1901.00	1.10	1.19
1.92	1.09	1525.00	1.31	1.60	-0.84	2030.00	3.15	0.86
0.39	-0.23	2081.00	1.73	1.18	-0.62	2890.00	1.90	0.39
2.55	1.46	1108.00	1.99	0.92	-0.49	1299.00	3.46	1.17
2.97	1.69	2327.00	1.46	1.45	-0.76	2794.00	1.40	0.89
0.61	-0.35	1629.00	0.74	2.17	-1.14	2609.00	1.95	0.34
0.47	0.26	3281.00	2.22	0.69	-0.36	4077.00	1.79	0.50
0.13	0.07	1237.00	0.65	2.26	-1.19	962.00	5.20	**2.91**
3.77	2.16	2848.00	3.37	0.46	0.24	3108.00	6.21	**3.92**
4.41	2.52	1776.00	4.22	1.31	0.69	2068.00	7.06	**4.77**
1.50	0.86	1662.00	4.33	1.42	0.75	3093.00	1.97	0.32
2.24	1.28	1741.00	3.91	1.00	0.52	3602.00	1.67	0.62
1.01	0.57	1621.00	2.78	0.13	-0.07	2557.00	5.24	**2.95**
0.56	-0.32	4719.00	2.03	0.88	-0.46	4698.00	3.94	1.65
1.51	-0.86	4408.00	0.23	2.68	-1.41	3874.00	1.11	1.18
0.01	0.00	3804.00	0.13	2.78	-1.46	3926.00	1.20	1.09
0.26	-0.15	1625.00	0.49	2.42	-1.27	1384.00	4.70	2.41
1.59	-0.91	4294.00	0.63	2.28	-1.20	3806.00	1.39	0.90
3.96	2.26	4586.00	1.79	1.12	-0.59	5261.00	6.54	**4.25**
1.42	-0.81	2882.00	0.24	2.67	-1.40	4703.00	4.72	2.43
1.33	-0.76	2885.00	0.49	2.42	-1.28	5280.00	4.00	1.71
0.18	0.10	2858.00	0.35	2.56	-1.35	3270.00	2.72	0.43
2.40	-1.38	2359.00	0.47	2.44	-1.29	2508.00	1.52	0.77
2.29	-1.31	2761.00	0.11	2.80	-1.47	3425.00	1.69	0.60
1.05	-0.60	3049.00	0.62	2.29	-1.20	4267.00	1.87	0.42
1.23	-0.71	2698.00	0.78	2.13	-1.12	4356.00	2.66	0.37
2.06	-1.18	3910.00	0.64	2.27	-1.19	5436.00	1.82	0.47
1.16	-0.67	1740.00	0.34	2.57	-1.35	2397.00	2.09	0.20
1.17	0.67	4798.00	1.35	1.56	-0.82	5556.00	4.07	1.78
0.72	-0.41	4905.00	2.47	0.44	-0.23	3189.00	1.16	1.13
0.00	0.00	3126.00	7.61	4.70	2.47	2958.00	4.73	2.44
1.26	-0.72	2648.00	0.49	2.42	-1.27	2359.00	1.65	0.64
0.21	-0.12	1921.00	2.92	0.01	0.00	1521.00	2.17	0.12
0.67	-0.39	5116.00	0.49	2.42	-1.27	4535.00	6.79	**4.50**
0.22	0.13	2436.00	0.57	2.34	-1.23	2581.00	1.55	0.74
2.58	1.47	4007.00	1.07	1.84	-0.97	3032.00	2.47	0.18
2.28	1.30	3293.00	0.79	2.12	-1.12	3321.00	1.66	0.63
2.35	1.34	4137.00	0.10	2.81	-1.48	4344.00	2.90	0.61
2.04	1.17	2424.00	0.58	2.33	-1.23	3202.00	1.25	1.04

0.99	0.56	5286.00	2.06	0.85	-0.45	6051.00	2.30	0.01
1.41	0.80	2996.00	1.74	1.17	-0.62	4401.00	1.59	0.70
1.10	0.63	3025.00	2.08	0.83	-0.44	4793.00	1.82	0.47
0.30	-0.17	2927.00	0.85	2.06	-1.08	2857.00	2.17	0.12
2.61	1.49	1990.00	3.92	1.01	0.53	2305.00	3.77	1.48
3.79	2.17	2402.00	4.75	1.84	0.96	3415.00	2.08	0.21
6.47	3.70	3394.00	4.66	1.75	0.92	4863.00	5.20	2.91
1.91	1.09	4157.00	4.33	1.42	0.74	4783.00	0.98	1.31
1.25	-0.72	3517.00	2.16	0.75	-0.39	3707.00	4.10	1.81
0.41	0.23	2324.00	3.44	0.53	0.28	1603.00	2.31	0.02
0.82	-0.47	2107.00	5.03	2.12	1.11	2778.00	3.49	1.20
0.32	-0.19	5255.00	3.62	0.71	0.37	5262.00	1.50	0.79
0.13	0.07	3143.00	6.46	3.55	1.86	4388.00	3.33	1.04
1.48	-0.85	3519.00	3.50	0.59	0.31	3586.00	0.78	1.51
2.16	-1.24	5275.00	1.52	1.39	-0.73	4560.00	1.03	1.26
1.02	0.58	4418.00	1.86	1.05	-0.56	4071.00	1.92	0.37
0.63	-0.36	4005.00	4.12	1.21	0.63	4308.00	3.44	1.15
1.59	0.91	3924.00	5.99	3.08	1.62	4814.00	3.57	1.28
0.01	-0.01	2395.00	2.17	0.74	-0.39	3315.00	1.12	1.17
0.55	0.31	3598.00	3.22	0.31	0.16	4621.00	1.88	0.41
0.77	0.44	2446.00	3.64	0.73	0.38	3423.00	1.55	0.74
0.76	0.43	3280.00	3.38	0.47	0.25	4196.00	1.60	0.69
5.46	3.12	3014.00	4.94	2.03	1.07	3859.00	2.00	0.29
2.01	1.15	2315.00	8.29	5.38	2.83	2473.00	2.22	0.07
1.95	1.11	1977.00	3.39	0.48	0.25	2858.00	3.36	1.07
0.95	-0.55	1558.00	2.89	0.02	-0.01	1470.00	2.65	0.36
0.34	0.19	3180.00	1.38	1.53	-0.80	3642.00	0.93	1.36
0.25	0.14	3245.00	5.30	2.39	1.26	3501.00	1.40	0.89
0.53	-0.30	3977.00	1.43	1.48	-0.78	3389.00	2.30	0.01
1.32	0.75	3893.00	5.06	2.15	1.13	4768.00	0.94	1.35
0.66	-0.38	3679.00	3.56	0.65	0.34	3911.00	8.08	5.79
5.54	3.17	2694.00	5.23	2.32	1.22	2689.00	2.19	0.10
4.74	2.71	5336.00	2.98	0.07	0.04	3273.00	2.26	0.03
1.89	-1.08	3433.00	2.74	0.17	-0.09	2016.00	1.98	0.31
0.73	-0.42	2532.00	2.92	0.01	0.01	4176.00	3.57	1.28
5.17	2.95	4248.00	11.77	8.86	4.65	3574.00	3.97	1.68
0.28	-0.16	3251.00	4.06	1.15	0.60	4834.00	3.23	0.94
1.93	1.10	3192.00	1.47	1.44	-0.76	4427.00	3.73	1.44
1.60	0.91	2191.00	3.70	0.79	0.41	3288.00	1.03	1.26
0.07	-0.04	2140.00	7.24	4.33	2.28	3745.00	0.40	1.89
1.69	0.97	2577.00	2.68	0.23	-0.12	4903.00	5.67	3.38
0.75	-0.43	3114.00	3.34	0.43	0.22	4666.00	1.35	0.94
2.06	1.18	3408.00	1.20	1.71	-0.90	4551.00	2.31	0.02
2.01	1.15	1338.00	2.77	0.14	-0.08	2345.00	1.58	0.71
2.29	1.31	3289.00	1.79	1.12	-0.59	4457.00	1.82	0.47
0.92	-0.53	1610.00	0.81	2.10	-1.11	2759.00	0.87	1.42
0.46	-0.27	2438.00	2.17	0.74	-0.39	4015.00	2.04	0.25

0.99	0.56	1652.00	1.03	1.88	-0.99	2626.00	0.38	1.91
0.38	-0.22	2155.00	1.58	1.33	-0.70	2251.00	0.76	1.53
0.14	0.08	2880.00	5.07	2.16	1.13	3355.00	1.76	0.53
1.30	-0.75	3712.00	1.48	1.43	-0.75	3040.00	0.72	1.57
1.55	-0.89	2861.00	0.42	2.49	-1.31	3193.00	2.85	0.56
1.56	-0.89	3762.00	2.45	0.46	-0.25	4929.00	2.68	0.39
2.53	-1.45	3999.00	1.80	1.11	-0.58	2880.00	1.63	0.66
0.00	0.00	3286.00	1.55	1.36	-0.71	2939.00	2.62	0.33
1.11	-0.64	5301.00	3.47	0.56	0.29	4190.00	1.43	0.86
0.69	-0.40	1615.00	2.17	0.74	-0.39	2259.00	1.42	0.87
2.13	-1.22	2106.00	5.79	2.88	1.51	2100.00	2.19	0.10
0.70	0.40	4201.00	4.78	1.87	0.98	4852.00	4.29	2.00
2.36	-1.35	618.00	5.83	2.92	1.53	816.00	4.04	1.75
6.77	3.87	3202.00	9.21	6.30	3.31	2907.00	4.20	1.91
1.04	-0.60	2688.00	1.93	0.98	-0.51	4261.00	1.71	0.58
1.41	0.80	3593.00	4.43	1.52	0.80	3125.00	1.22	1.07
0.51	-0.29	2549.00	4.90	1.99	1.05	3660.00	1.34	0.95
2.70	-1.55	3368.00	8.91	6.00	3.15	3101.00	1.32	0.97
0.08	0.04	3478.00	4.14	1.23	0.65	3811.00	2.20	0.09
0.70	0.40	2980.00	5.40	2.49	1.31	4028.00	2.51	0.22
0.82	-0.47	1387.00	2.52	0.39	-0.20	1982.00	4.14	1.85
0.96	0.55	1661.00	5.06	2.15	1.13	1809.00	1.22	1.07
2.89	1.65	2563.00	3.75	0.84	0.44	2883.00	2.43	0.14
1.69	-0.97	2067.00	4.02	1.11	0.58	2565.00	0.78	1.51
0.32	0.18	1929.00	2.80	0.11	-0.06	2930.00	1.43	0.86
2.58	-1.48	4065.00	3.84	0.93	0.49	5741.00	1.31	0.98
0.16	0.09	4520.00	3.65	0.74	0.39	3451.00	0.58	1.71
1.31	0.75	6102.00	1.79	1.12	-0.59	5864.00	0.55	1.74
0.01	-0.01	2860.00	2.03	0.88	-0.46	2968.00	1.38	0.91
4.20	2.40	4255.00	7.85	4.94	2.59	5583.00	4.14	1.85
4.70	2.69	3873.00	4.85	1.94	1.02	3728.00	4.77	2.48
0.32	-0.19	3903.00	2.49	0.42	-0.22	4053.00	1.92	0.37
1.49	0.85	2209.00	9.33	6.42	3.37	3737.00	8.16	5.87
2.84	1.62	3641.00	6.59	3.68	1.93	3919.00	4.06	1.77
0.88	0.50	4121.00	3.23	0.32	0.17	4426.00	2.44	0.15
2.16	-1.24	2158.00	2.13	0.78	-0.41	2318.00	1.98	0.31
2.61	1.49	2704.00	9.17	6.26	3.29	2723.00	4.99	2.70
2.05	-1.17	1847.00	8.28	5.37	2.82	2102.00	2.43	0.14
0.92	-0.53	3063.00	4.67	1.76	0.92	3480.00	2.50	0.21
0.70	0.40	4348.00	3.43	0.52	0.27	3433.00	0.84	1.45
1.06	-0.61	3770.00	2.71	0.20	-0.11	3337.00	1.44	0.85
0.14	-0.08	1788.00	3.19	0.28	0.14	1783.00	2.97	0.68
1.79	1.02	3949.00	2.61	0.30	-0.16	3607.00	2.86	0.57
3.74	2.14	3098.00	6.75	3.84	2.01	2667.00	3.86	1.57
0.36	0.20	3994.00	2.85	0.06	-0.03	2596.00	2.74	0.45
4.67	2.67	3119.00	1.44	1.47	-0.77	1935.00	2.95	0.66
1.08	-0.62	4376.00	3.34	0.43	0.22	3087.00	1.04	1.25

3.42	1.95	5128.00	4.35	1.44	0.75	4579.00	3.21	0.92
2.65	1.51	6441.00	4.32	1.41	0.74	5674.00	6.01	**3.72**
0.39	0.22	3614.00	4.87	1.96	1.03	3591.00	2.70	0.41
2.58	-1.48	2828.00	5.34	2.43	1.28	2058.00	2.19	0.10
1.39	-0.80	2352.00	2.00	0.91	-0.48	2219.00	0.99	1.30
1.31	-0.75	2673.00	4.56	1.65	0.87	3364.00	1.69	0.60
0.65	0.37	3390.00	4.34	1.43	0.75	3955.00	4.85	2.56
2.51	1.43	4277.00	7.25	4.34	2.28	4575.00	3.83	1.54
0.69	0.39	2889.00	4.33	1.42	0.74	2338.00	3.59	1.30
0.23	-0.13	4099.00	5.17	2.26	1.19	4757.00	3.26	0.97
1.46	-0.84	3139.00	5.38	2.47	1.30	2202.00	1.54	0.75
0.67	0.38	4277.00	6.59	3.68	1.93	3721.00	2.15	0.14
1.83	-1.05	4569.00	2.39	0.52	-0.28	3038.00	1.32	0.97
0.78	-0.45	1738.00	2.24	0.67	-0.35	1084.00	2.31	0.02
0.49	-0.28	3126.00	1.44	1.47	-0.77	1932.00	2.38	0.09
0.87	0.50	2696.00	3.12	0.21	0.11	2750.00	2.29	0.00
0.21	-0.12	3938.00	2.72	0.19	-0.10	3256.00	2.58	0.29
0.30	0.17	2860.00	1.08	1.83	-0.96	2707.00	1.00	1.29
4.69	2.68	3921.00	4.54	1.63	0.86	3669.00	2.62	0.33
0.45	-0.26	4259.00	2.49	0.42	-0.22	3419.00	2.87	0.58
1.24	0.71	2545.00	4.13	1.22	0.64	1632.00	1.29	1.00
0.45	-0.26	2734.00	0.51	2.40	-1.26	2224.00	0.58	1.71
7.10	4.06	3539.00	5.85	2.94	1.54	3184.00	1.29	1.00
0.80	-0.46	3696.00	3.06	0.15	0.08	3701.00	2.03	0.26
0.93	0.53	3305.00	2.06	0.85	-0.45	3192.00	1.32	0.97
0.73	0.41	2584.00	2.13	0.78	-0.41	3674.00	2.69	0.40
1.34	0.76	2508.00	1.87	1.04	-0.55	4180.00	2.56	0.27
0.43	-0.25	1999.00	3.25	0.34	0.18	2998.00	3.60	1.31
0.03	-0.02	3381.00	5.68	2.77	1.45	5025.00	4.08	1.79
2.65	1.52	1908.00	1.62	1.29	-0.68	3344.00	1.17	1.12
0.27	0.15	2356.00	5.69	2.78	1.46	3171.00	1.45	0.84
0.66	-0.38	2187.00	4.89	1.98	1.04	2621.00	4.85	2.56
2.15	-1.23	2665.00	2.66	0.25	-0.13	3037.00	1.88	0.41
0.31	-0.18	2530.00	3.87	0.96	0.51	1978.00	0.91	1.38
0.81	0.46	3887.00	5.25	2.34	1.23	3394.00	2.56	0.27
1.68	0.96	654.00	6.42	3.51	1.84	958.00	3.55	1.26
2.08	-1.19	3614.00	3.10	0.19	0.10	3237.00	1.24	1.05
1.47	-0.84	2710.00	4.54	1.63	0.85	3107.00	0.45	1.84
0.46	-0.27	3254.00	4.64	1.73	0.91	1920.00	2.19	0.10
1.76	-1.01	3744.00	3.47	0.56	0.29	2655.00	2.90	0.61
0.16	-0.09	4360.00	3.26	0.35	0.18	2901.00	4.83	2.54
0.32	-0.19	3514.00	2.48	0.43	-0.23	3484.00	1.52	0.77
1.69	0.96	3873.00	2.81	0.10	-0.05	3443.00	1.66	0.63
0.01	0.00	4147.00	2.94	0.03	0.02	4518.00	2.46	0.17
4.00	2.29	1047.00	10.51	7.60	3.99	1678.00	1.67	0.62
0.34	0.19	2898.00	2.38	0.53	-0.28	2803.00	1.32	0.97
0.72	0.41	3304.00	3.90	0.99	0.52	3966.00	2.24	0.05

4.55	2.60	4397.00	7.23	4.32	2.27	4126.00	5.04	2.75
1.39	0.79	1474.00	3.26	0.35	0.18	1580.00	2.59	0.30
2.92	1.67	1119.00	3.22	0.31	0.16	818.00	4.89	2.60
1.58	0.90	2591.00	5.94	3.03	1.59	2173.00	1.93	0.36
1.11	0.63	2283.00	5.12	2.21	1.16	1514.00	1.12	1.17
0.01	0.00	2120.00	2.22	0.69	-0.37	1475.00	1.63	0.66
0.91	0.52	2836.00	4.20	1.29	0.67	2120.00	3.77	1.48
1.32	0.75	1045.00	7.75	4.84	2.54	1148.00	8.62	6.33
1.00	-0.58	1812.00	3.75	0.84	0.44	952.00	5.04	2.75
1.59	0.91	1925.00	2.65	0.26	-0.14	2687.00	1.08	1.21
0.53	-0.30	2121.00	4.48	1.57	0.82	2707.00	2.88	0.59
2.31	1.32	3196.00	2.97	0.06	0.03	3484.00	3.53	1.24
3.53	2.01	3496.00	4.15	1.24	0.65	2805.00	2.42	0.13
1.44	0.82	5349.00	2.34	0.57	-0.30	4318.00	6.90	4.61
0.71	-0.41	3960.00	1.57	1.34	-0.71	3588.00	6.35	4.06
2.15	1.22	3251.00	2.89	0.02	-0.01	3064.00	4.60	2.31
1.22	-0.70	2516.00	1.83	1.08	-0.57	1923.00	1.35	0.94
0.85	-0.49	3912.00	3.17	0.26	0.14	3731.00	4.23	1.94
0.32	-0.18	3853.00	0.70	2.21	-1.16	3559.00	2.64	0.35
0.56	-0.32	3674.00	1.25	1.66	-0.87	3718.00	0.86	1.43
0.45	-0.26	4640.00	2.50	0.41	-0.22	3402.00	1.73	0.56
0.17	0.09	1603.00	1.00	1.91	-1.01	1180.00	2.20	0.09
2.97	1.70	2927.00	4.07	1.16	0.61	1596.00	4.57	2.28
0.43	-0.25	2125.00	0.99	1.92	-1.01	2483.00	2.78	0.49
1.70	0.97	4707.00	2.57	0.34	-0.18	3959.00	4.17	1.88
1.53	-0.88	2944.00	2.89	0.02	-0.01	2307.00	1.73	0.56
1.42	-0.82	2060.00	1.50	1.41	-0.74	1237.00	2.75	0.46
1.19	-0.68	4240.00	0.87	2.04	-1.07	2333.00	3.81	1.52
1.23	-0.71	2005.00	2.19	0.72	-0.38	1735.00	2.77	0.48
1.64	-0.94	3666.00	1.58	1.33	-0.70	2958.00	2.57	0.28
0.52	-0.30	2458.00	0.61	2.30	-1.21	1433.00	3.91	1.62
0.96	-0.55	5067.00	7.70	4.79	2.51	2748.00	4.48	2.19
1.77	-1.02	2827.00	1.77	1.14	-0.60	2795.00	0.61	1.68
0.99	-0.57	4691.00	3.47	0.56	0.30	4690.00	4.69	2.40
0.92	-0.53	3549.00	2.73	0.18	-0.09	3304.00	2.36	0.07
0.60	-0.34	4101.00	2.05	0.86	-0.45	3752.00	3.41	1.12
1.32	-0.76	2860.00	1.47	1.44	-0.76	2298.00	3.09	0.80
1.35	-0.77	3364.00	2.02	0.89	-0.47	2920.00	1.92	0.37
2.67	-1.53	2559.00	3.32	0.41	0.22	2396.00	2.50	0.21
0.76	-0.44	3418.00	2.75	0.16	-0.09	3183.00	0.88	1.41
0.88	-0.50	2502.00	3.16	0.25	0.13	2679.00	0.71	1.58
0.20	-0.12	1405.00	1.71	1.20	-0.63	2893.00	0.76	1.53
1.17	-0.67	1394.00	1.22	1.69	-0.89	1872.00	1.87	0.42
0.08	0.04	2060.00	1.26	1.65	-0.87	2023.00	1.68	0.61
2.00	1.14	3021.00	4.10	1.19	0.63	3413.00	4.25	1.96
2.05	-1.17	2554.00	1.10	1.81	-0.95	2498.00	1.28	1.01
0.16	-0.09	2532.00	1.70	1.21	-0.64	3312.00	1.18	1.11

2.25	-1.29	2262.00	0.40	2.51	-1.32	1275.00	0.78	1.51
1.51	0.86	4755.00	0.76	2.15	-1.13	4626.00	2.53	0.24
0.28	0.16	5181.00	5.23	2.32	1.22	4455.00	1.35	0.94
4.51	2.58	4123.00	10.94	8.03	4.22	4087.00	4.94	2.65
1.14	-0.66	3838.00	3.36	0.45	0.24	3906.00	2.84	0.55
1.95	1.11	3291.00	2.10	0.81	-0.43	3648.00	4.44	2.15
1.67	-0.96	4360.00	1.42	1.49	-0.78	3767.00	1.01	1.28
2.66	1.52	3828.00	1.41	1.50	-0.79	5399.00	1.94	0.35
0.67	-0.39	3218.00	1.34	1.57	-0.83	4450.00	2.36	0.07
2.50	1.43	4319.00	5.56	2.65	1.39	4329.00	2.66	0.37
1.37	-0.79	3576.00	2.32	0.59	-0.31	3924.00	1.89	0.40
1.03	0.59	3461.00	1.47	1.44	-0.76	3482.00	1.41	0.88
1.11	0.63	3829.00	4.36	1.45	0.76	3628.00	1.46	0.83
0.28	-0.16	2628.00	0.88	2.03	-1.07	2933.00	0.65	1.64
1.16	0.66	2048.00	3.91	1.00	0.52	2529.00	1.62	0.67
0.01	-0.01	2134.00	3.37	0.46	0.24	2399.00	1.00	1.29
1.04	-0.60	2183.00	4.76	1.85	0.97	2595.00	1.12	1.17
2.38	1.36	2919.00	6.34	3.43	1.80	2223.00	1.44	0.85
3.11	1.77	3667.00	4.91	2.00	1.05	2864.00	1.92	0.37
0.78	-0.45	3577.00	1.48	1.43	-0.75	2355.00	1.36	0.93
1.87	1.07	3357.00	4.92	2.01	1.05	2533.00	0.79	1.50
0.50	0.28	3792.00	2.24	0.67	-0.35	3670.00	2.64	0.35
1.75	1.00	4947.00	2.83	0.08	-0.04	3837.00	1.46	0.83
1.74	0.99	1593.00	5.34	2.43	1.27	2160.00	2.69	0.40
2.16	1.23	3781.00	2.17	0.74	-0.39	3577.00	2.82	0.53
1.90	1.08	2936.00	3.88	0.97	0.51	2506.00	1.20	1.09
2.00	-1.14	2708.00	2.55	0.36	-0.19	2887.00	2.63	0.34
1.36	0.77	3280.00	2.68	0.23	-0.12	3570.00	4.06	1.77
2.22	1.27	4036.00	4.16	1.25	0.66	4694.00	8.61	6.32
1.14	-0.66	4198.00	3.81	0.90	0.47	4016.00	2.29	0.00
0.69	-0.40	2763.00	0.65	2.26	-1.19	3376.00	1.36	0.93
0.14	-0.08	1714.00	1.87	1.04	-0.55	1519.00	2.17	0.12
0.44	-0.25	2330.00	2.06	0.85	-0.45	2859.00	0.98	1.31
0.67	0.38	3121.00	2.92	0.01	0.00	3372.00	5.93	3.64
1.54	0.88	1302.00	2.38	0.53	-0.28	1759.00	2.62	0.33
1.24	-0.71	1971.00	5.28	2.37	1.24	2479.00	3.95	1.66
1.09	0.62	914.00	6.13	3.22	1.69	1577.00	0.25	2.04
4.05	2.31	552.00	4.89	1.98	1.04	909.00	2.86	0.57
0.79	0.45	2608.00	6.21	3.30	1.73	2703.00	2.55	0.26
7.21	4.12	290.00	10.00	7.09	3.72	404.00	2.48	0.19
0.05	-0.03	1862.00	2.79	0.12	-0.06	2343.00	1.02	1.27
1.72	0.98	1971.00	2.18	0.73	-0.38	2827.00	1.98	0.31
0.40	-0.23	2659.00	1.50	1.41	-0.74	3616.00	1.80	0.49
1.31	0.75	2912.00	4.70	1.79	0.94	2859.00	2.62	0.33
2.04	-1.17	2418.00	2.85	0.06	-0.03	3012.00	0.60	1.69
3.27	1.87	2099.00	6.48	3.57	1.87	3838.00	0.39	1.90
0.16	0.09	3932.00	4.12	1.21	0.63	4672.00	0.47	1.82

0.11	-0.06	4537.00	4.08	1.17	0.61	3861.00	3.89	1.60
3.56	2.04	4202.00	6.54	3.63	1.91	3437.00	6.34	4.05
0.16	-0.09	2337.00	2.91	0.00	0.00	2623.00	5.76	3.47
0.95	0.54	4838.00	4.94	2.03	1.07	4353.00	4.32	2.03
1.60	0.91	3110.00	2.22	0.69	-0.36	2414.00	2.82	0.53
0.05	0.02	4080.00	3.75	0.84	0.44	2930.00	4.61	2.32
0.35	-0.20	3554.00	2.64	0.27	-0.14	3651.00	2.44	0.15
0.65	-0.37	3090.00	3.04	0.13	0.07	2599.00	2.50	0.21
1.32	-0.76	1809.00	2.21	0.70	-0.37	1698.00	1.41	0.88
0.27	0.15	1377.00	3.27	0.36	0.19	1473.00	3.53	1.24
3.13	1.79	2349.00	2.94	0.03	0.01	2833.00	2.75	0.46
0.97	-0.56	2936.00	2.04	0.87	-0.46	1944.00	2.26	0.03
0.23	-0.13	3589.00	1.78	1.13	-0.59	3244.00	1.91	0.38
3.23	1.84	1686.00	3.20	0.29	0.15	2760.00	1.41	0.88
1.58	0.90	2746.00	3.35	0.44	0.23	3041.00	1.32	0.97
1.36	0.78	4182.00	2.46	0.45	-0.24	4802.00	2.98	0.69
5.77	3.30	3986.00	3.21	0.30	0.16	4132.00	3.19	0.90
0.50	0.28	4164.00	2.40	0.51	-0.27	3686.00	1.11	1.18
0.83	-0.48	3108.00	1.48	1.43	-0.75	3281.00	0.79	1.50
0.08	-0.05	3202.00	1.34	1.57	-0.82	2121.00	3.06	0.77
3.57	2.04	2676.00	4.56	1.65	0.87	2234.00	5.46	3.17
0.64	0.37	1304.00	2.84	0.07	-0.04	776.00	4.38	2.09
0.28	0.16	2236.00	3.22	0.31	0.16	1464.00	3.14	0.85
0.83	-0.48	1175.00	2.72	0.19	-0.10	851.00	8.23	5.94
2.01	-1.15	1681.00	3.27	0.36	0.19	981.00	2.75	0.46
1.16	-0.66	3272.00	2.32	0.59	-0.31	2283.00	1.80	0.49
1.69	0.96	3091.00	8.28	5.37	2.82	2605.00	2.73	0.44
1.44	0.82	2135.00	2.90	0.01	0.00	1883.00	2.76	0.47
0.27	-0.16	2327.00	3.09	0.18	0.10	3066.00	2.28	0.01
1.06	-0.61	1299.00	3.85	0.94	0.49	1411.00	4.32	2.03
1.33	-0.76	1543.00	4.15	1.24	0.65	2270.00	3.48	1.19
1.96	1.12	1843.00	8.68	5.77	3.03	2179.00	12.48	10.19
0.53	-0.31	2634.00	5.39	2.48	1.30	2975.00	2.15	0.14
0.30	-0.17	1705.00	6.63	3.72	1.95	2222.00	3.15	0.86
1.57	-0.90	1215.00	6.83	3.92	2.06	1328.00	1.96	0.33
1.60	-0.92	2443.00	5.77	2.86	1.50	3817.00	2.52	0.23
1.72	-0.99	1060.00	6.51	3.60	1.89	1381.00	3.26	0.97
1.15	-0.66	1942.00	3.86	0.95	0.50	2647.00	1.85	0.44
1.81	-1.04	973.00	5.34	2.43	1.28	1810.00	4.20	1.91
1.18		2927.00	2.91	1.29		3065.00	2.29	0.91
3.54				3.86				2.72
1.75				1.90				1.34
				3477.00	15.39		5182.00	25.61
	5310.00	19.68		4595.00	10.01			
	4664.00	13.17						
	5098.00	18.44		4290.00	13.61			
	5024.00	17.09		4120.67	13.00			

329.30	3.46	577.92	2.74
2586.00	1.86	1406.00	5.05
2287.00	0.61	1634.00	0.67
1731.00	4.22	1177.00	1.61
1700.00	1.29	1786.00	3.19
1906.00	2.04	1532.33	1.83
330.32	1.92	316.97	1.27
	10.38		8.22
	5.75		3.82
	16.12		12.04
	15.05		11.18
	1.07		1.08
	-0.07		-0.08
475.00	12.00	368.00	8.70
245.00	20.82	363.00	14.33
2441.00	1.76	3104.00	1.26
3369.00	2.79	3610.00	1.75
6812.00	5.28	5520.00	3.39
5997.00	8.40	5446.00	4.96

rZ		
1.01		
-0.20		
0.72		
-0.59		
0.85		
0.18		
-1.08		
-0.89		
0.64		
-0.29		
0.87		
-0.67		
-0.25		
-0.38		
2.16		
2.92	x	debris a,b
3.55	x	toxic a,b
-0.24		
-0.47		
2.20		
1.23		
-0.88		
-0.82		
1.79		
-0.67		
3.16	y	
1.81		
1.27		
0.32		
-0.58		
-0.45		
-0.31		
0.28		
-0.35		
-0.16		
1.32		
-0.85		
1.82		
-0.48		
-0.09		
3.35		
-0.55		
0.13		
-0.48		
0.45		
-0.78		

0.00		
-0.52		
-0.36		
-0.09		
1.10		
-0.16		
2.17	x	art a,b
-0.98		
1.35		
0.01		
0.89		
-0.59		
0.77		
-1.13		
-0.94		
-0.28		
0.85		
0.95		
-0.88		
-0.31		
-0.56		
-0.52		
-0.22		
-0.05		
0.79		
0.27		
-1.01		
-0.67		
0.01		
-1.01		
4.31		
-0.07		
-0.02		
-0.23		
0.95		
1.25	y	
0.70		
1.07		
-0.94		
-1.41		
2.52		
-0.70		
0.01		
-0.53		
-0.36		
-1.06		
-0.19		

-1.43	
-1.15	
-0.40	
-1.17	
0.41	
0.29	
-0.49	
0.24	
-0.64	
-0.65	
-0.08	
1.49	
1.30	
1.42	y
-0.43	
-0.80	
-0.71	
-0.72	
-0.07	
0.16	
1.37	
-0.80	
0.10	
-1.13	
-0.64	
-0.74	
-1.28	
-1.30	
-0.68	
1.37	y
1.85	
-0.28	
4.37	y
1.31	
0.11	
-0.23	
2.01	debris a,b
0.10	
0.15	
-1.08	
-0.64	
0.51	
0.42	
1.17	x
0.33	
0.49	
-0.94	

0.68		
2.77		
0.30		
-0.08		
-0.97		
-0.45		
1.91		
1.14		
0.97		
0.72		
-0.56		
-0.11		
-0.73		
0.01		
0.06		
0.00		
0.21		
-0.97		
0.24		
0.43		
-0.75		
-1.27		
-0.75		
-0.20		
-0.73		
0.30		
0.20		
0.98		
1.33		
-0.84		
-0.63		
1.90		
-0.31		
-1.03		
0.20		
0.94		
-0.79		
-1.37		
-0.08		
0.45		
1.89		
-0.58		
-0.48		
0.12		
-0.47	x	toxic b,c
-0.73		
-0.04		

2.05	y	
0.22		
1.93		
-0.27		
-0.87		
-0.50		
1.10		
4.72	x	toxic b,c
2.05		
-0.91		
0.44		
0.92		
0.10		
3.43		
3.03		
1.72		
-0.70		
1.45		
0.26		
-1.07		
-0.42		
-0.07		
1.70		
0.36		
1.40		
-0.42		
0.34		
1.13		
0.35		
0.21		
1.20		
1.63		
-1.26		
1.79		
0.05		
0.83		
0.59		
-0.28		
0.16		
-1.05		
-1.18		
-1.14		
-0.32		
-0.46		
1.46		
-0.75		
-0.83		

-1.13		
0.18		
-0.71		
1.97	x	debris a,b
0.41		
1.60		
-0.96		
-0.26		
0.05		
0.27		
-0.30		
-0.66		
-0.62		
-1.23		
-0.50		
-0.96		
-0.88		
-0.64		
-0.28		
-0.70		
-1.12		
0.26		
-0.62		
0.29		
0.39		
-0.82		
0.25		
1.32		
4.70		
0.00		
-0.69		
-0.09		
-0.98		
2.71		
0.24		
1.24		
-1.52		
0.42		
0.19		
0.14	x	toxic a,b,c
-0.95		
-0.23		
-0.37		
0.25		
-1.26		
-1.42		
-1.36		

1.19			
3.02	y		
2.58			
1.51			
0.39			
1.72			
0.11			
0.15			
-0.66			
0.92			
0.34			
-0.02			
-0.29			
-0.66			
-0.73			
0.51			
0.67			
-0.88			
-1.12			
0.57			
2.36	x		debris a,b
1.56			
0.63			
4.42			
0.34			
-0.37			
0.32			
0.35			
-0.01			
1.51			
0.88			
7.59	x		toxic b
-0.11			
0.64			
-0.25			
0.16			
0.72		0.01	
-0.33			
1.42			
2774.00		5.41	

Plate	**Well**	**Gene**		**GeneID**	**Cell Count**	**% inf**	**Abs Dev**
50055.00	A02	M-010280- phospholip	23236.00	PLCB1	3805.00	1.81	0.64
50055.00	A04	M-017868- DnaJ (Hsp4	23234.00	DNAJC9	2837.00	3.07	0.62
50055.00	A05	M-014167- transcriptic	22980.00	TCF25	2753.00	7.63	**5.18**
50055.00	A06	M-022715- exocyst cor	23233.00	EXOC6B	2902.00	2.69	0.24
50055.00	A07	M-018162- KIAA0980 p	22981.00	RP4-691N2	2158.00	2.78	0.33
50055.00	A08	M-026297- TBC1 doma	23232.00	TBC1D12	2391.00	3.09	0.64
50055.00	A09	M-026391- DIP2 disco-	22982.00	DIP2C	2946.00	2.34	0.11
50055.00	A10	M-024222- KIAA0746 p	23231.00	KIAA0746	2236.00	3.22	0.77
50055.00	A11	M-029652- programm	22984.00	PDCD11	2052.00	2.44	0.01
50055.00	A12	M-008544- phospholip	23228.00	PLCL2	2739.00	4.86	2.41
50055.00	A13	M-007633- synaptic ve	22987.00	SV2C	2022.00	1.93	0.52
50055.00	A14	M-017529- nucleopori	23225.00	NUP210	3002.00	2.27	0.18
50055.00	A15	M-023571- myosin, he	22989.00	MYH15	1360.00	4.85	2.40
50055.00	A16	M-019259- spectrin re	23224.00	SYNE2	2420.00	4.21	1.76
50055.00	A17	M-014158- pecanex hc	22990.00	PCNX	2535.00	4.26	1.81
50055.00	A18	M-014081- ribosomal I	23223.00	RRP12	1570.00	4.08	1.63
50055.00	A19	M-028449- KIAA0194 p	22993.00	KIAA0194	2430.00	3.83	1.38
50055.00	A20	M-026663- deltex 4 ho	23220.00	DTX4	2552.00	2.12	0.33
50055.00	A21	M-023335- 5-azacytidi	22994.00	AZI1	2578.00	2.87	0.42
50055.00	A23	M-022241- centrosom	22995.00	CEP152	1787.00	5.37	**2.92**
50055.00	B02	M-014079- TBC1 (tre-2	23216.00	TBC1D1	3198.00	1.50	0.95
50055.00	B04	M-012483- synaptogyr	23546.00	SYNGR4	2358.00	0.85	1.60
50055.00	B05	M-015682- activity-reg	23237.00	ARC	2667.00	0.49	1.96
50055.00	B06	M-019950- ATPase, H+	23545.00	ATP6V0A2	3360.00	0.27	2.18
50055.00	B07	M-019152- KIAA0922	23240.00	KIAA0922	5075.00	3.59	1.14
50055.00	B08	M-008081- seizure rela	23544.00	SEZ6L	2127.00	1.41	1.04
50055.00	B09	M-022015- phosphofu	23241.00	PACS2	3613.00	0.94	1.51
50055.00	B10	M-020616- RNA bindin	23543.00	RBM9	3140.00	0.48	1.97
50055.00	B11	M-021017- cordon-ble	23242.00	COBL	3500.00	2.31	0.14
50055.00	B12	M-007410- solute carri	23539.00	SLC16A8	1882.00	2.76	0.31
50055.00	B13	M-023451- ankyrin rep	23243.00	ANKRD28	3051.00	1.47	0.98
50055.00	B14	M-019949- transportin	23534.00	TNPO3	2276.00	1.01	1.44
50055.00	B15	M-014071- SCC-112 pr	23244.00	SCC-112	2996.00	3.44	0.99
50055.00	B16	M-008032- monocyte t	23531.00	MMD	3675.00	2.23	0.22
50055.00	B17	M-014072- astrotactin	23245.00	ASTN2	3644.00	1.76	0.69
50055.00	B18	M-012811- centaurin, l	23527.00	CENTB2	3898.00	5.05	2.60
50055.00	B19	M-014065- block of pr	23246.00	BOP1	2303.00	1.09	1.36
50055.00	B20	M-012454- calcineurin	23523.00	CABIN1	3878.00	4.54	2.09
50055.00	B21	M-003984- KIAA0556	23247.00	KIAA0556	3079.00	1.01	1.44
50055.00	B23	M-021712- KIAA0460	23248.00	KIAA0460	2673.00	6.17	**3.72**
50055.00	C02	M-014080- F-box prote	23219.00	FBXO28	2884.00	2.91	0.46
50055.00	C04	M-023480- neurobeacl	23218.00	NBEAL2	1945.00	1.75	0.70
50055.00	C05	M-021795- chromosom	22996.00	C1orf34	3582.00	2.85	0.40
50055.00	C06	M-023902- KIAA1086	23217.00	KIAA1086	3593.00	2.78	0.33
50055.00	C07	M-026538- immunoglc	22997.00	IGSF9B	2145.00	3.08	0.63
50055.00	C08	M-014078- BAT2 doma	23215.00	BAT2D1	2956.00	3.59	1.14

50055.00	C09	M-024200- hypothetica	22998.00	DKFZP686A	1689.00	0.53	1.92
50055.00	C10	M-022515- exportin 6	23214.00	XPO6	3646.00	3.54	1.09
50055.00	C11	M-014159- regulating	22999.00	RIMS1	3093.00	2.81	0.36
50055.00	C12	M-006643- sulfatase 1	23213.00	SULF1	2343.00	2.01	0.44
50055.00	C13	M-028430- KIAA0825	23004.00	KIAA0825	2308.00	2.43	0.02
50055.00	C14	M-014077- RRS1 ribos	23212.00	RRS1	1204.00	1.99	0.46
50055.00	C15	M-022225- mitogen ac	23005.00	MAPKBP1	2675.00	5.16	2.71
50055.00	C16	M-023865- chromosom	23211.00	C19orf7	2172.00	2.12	0.33
50055.00	C17	M-010279- phospholip	23007.00	PLCH1	3074.00	1.72	0.73
50055.00	C18	M-018292- synaptotag	23208.00	SYT11	2550.00	2.63	0.18
50055.00	C19	M-017330- golgi autoa	23015.00	GOLGA8A	2228.00	2.92	0.47
50055.00	C20	M-022168- pleckstrin	23207.00	PLEKHM2	3026.00	2.48	0.03
50055.00	C21	M-014160- exosome c	23016.00	EXOSC7	2320.00	1.55	0.90
50055.00	C23	M-017340- Fas apopto	23017.00	FAIM2	3005.00	1.06	1.39
50055.00	D02	M-019563- MYST histo	23522.00	MYST4	5327.00	6.19	**3.74**
50055.00	D04	M-017870- R3H domai	23518.00	R3HDM1	3213.00	1.93	0.52
50055.00	D05	M-021769- ATPase, Cla	23250.00	ATP11A	4319.00	2.64	0.19
50055.00	D06	M-031902- superkiller	23517.00	SKIV2L2	2332.00	3.86	1.41
50055.00	D07	M-022286- KIAA1024	23251.00	KIAA1024	2524.00	2.38	0.07
50055.00	D08	M-007569- solute carri	23516.00	SLC39A14	2196.00	1.23	1.22
50055.00	D09	M-027582- OTU domai	23252.00	OTUD3	3005.00	2.63	0.18
50055.00	D10	M-012976- MORC fam	23515.00	MORC3	3021.00	7.71	**5.26**
50055.00	D11	M-014066- ankyrin rep	23253.00	ANKRD12	2968.00	2.83	0.38
50055.00	D12	M-025937- KIAA0146	23514.00	KIAA0146	2108.00	1.99	0.46
50055.00	D13	M-023376- KIAA0802	23255.00	KIAA0802	2718.00	1.84	0.61
50055.00	D14	M-010500- scribbled h	23513.00	SCRIB	1817.00	1.43	1.02
50055.00	D15	M-010943- sec1 family	23256.00	SCFD1	1955.00	1.18	1.27
50055.00	D16	M-012845- protein O-f	23509.00	POFUT1	2866.00	6.91	**4.46**
50055.00	D17	M-026774- RAB6 intera	23258.00	RAB6IP1	1866.00	3.05	0.60
50055.00	D18	M-021974- tetratricop	23508.00	TTC9	3325.00	3.73	1.28
50055.00	D19	M-025979- DDHD dom	23259.00	DDHD2	3384.00	4.11	1.66
50055.00	D20	M-025099- KIAA0240	23506.00	KIAA0240	2852.00	1.26	1.19
50055.00	D21	M-021559- calmodulin	23261.00	CAMTA1	3903.00	4.89	2.44
50055.00	D23	M-010098- MCF.2 cell	23263.00	MCF2L	3190.00	2.26	0.19
50055.00	E02	M-017221- acyl-CoA sy	23205.00	ACSBG1	3179.00	6.01	**3.56**
50055.00	E04	M-004321- ADP-ribosy	23204.00	ARL6IP1	1139.00	4.21	1.76
50055.00	E05	M-015369- CCR4-NOT	23019.00	CNOT1	1329.00	2.78	0.33
50055.00	E06	M-029912- KIAA0280	23201.00	KIAA0280	2292.00	7.98	**5.53**
50055.00	E07	M-016891- palladin, cy	23022.00	PALLD	2802.00	1.89	0.56
50055.00	E08	M-022627- KIAA0182	23199.00	KIAA0182	2893.00	3.21	0.76
50055.00	E09	M-023265- PDZ domai	23024.00	PDZRN3	2501.00	6.88	**4.43**
50055.00	E10	M-022757- proteasom	23198.00	PSME4	2666.00	5.29	**2.84**
50055.00	E11	M-031249- unc-13 hon	23025.00	UNC13A	3251.00	2.55	0.10
50055.00	E12	M-010649- UBX domai	23197.00	UBXD8	3413.00	2.55	0.10
50055.00	E13	M-021586- myosin XVI	23026.00	MYO16	1940.00	2.37	0.08
50055.00	E14	M-014186- family with	23196.00	FAM120A	2675.00	5.01	2.56
50055.00	E15	M-022399- RNA bindin	23029.00	RBM34	1506.00	5.18	2.73

50055.00	E16	M-009786-	MDN1, mic	23195.00	MDN1	2457.00	2.08	0.37
50055.00	E17	M-004290-	jumonji do	23030.00	JMJD2B	2191.00	4.93	2.48
50055.00	E18	M-009499-	glucosidase	23193.00	GANAB	3858.00	3.91	1.46
50055.00	E19	M-019205-	dopey fami	23033.00	DOPEY1	3206.00	1.62	0.83
50055.00	E20	M-005786-	ATG4 auto	23192.00	ATG4B	2868.00	3.56	1.11
50055.00	E21	M-013911-	sterile alph	23034.00	SAMD4A	3279.00	0.91	1.54
50055.00	E23	M-022586-	PH domain	23035.00	PHLPPL	5158.00	1.59	0.86
50055.00	F02	M-022532-	transmemb	23505.00	TMEM131	5399.00	3.67	1.22
50055.00	F04	M-027090-	RIMS bindi	23504.00	RIMBP2	3961.00	4.62	2.17
50055.00	F05	M-017425-	zinc finger	23264.00	ZC3H7B	2777.00	1.58	0.87
50055.00	F06	M-031136-	zinc finger,	23503.00	ZFYVE26	3881.00	4.17	1.72
50055.00	F07	M-021448-	exocyst co	23265.00	EXOC7	3160.00	5.06	2.61
50055.00	F08	M-008666-	3-hydroxya	23498.00	HAAO	2066.00	3.39	0.94
50055.00	F09	M-026304-	dynamin bi	23268.00	DNMBP	2996.00	2.80	0.35
50055.00	F10	M-009561-	chromobo	23492.00	CBX7	3199.00	6.72	**4.27**
50055.00	F11	M-022224-	MAX gene	23269.00	MGA	2832.00	3.32	0.87
50055.00	F12	M-009492-	TDP-glucos	23483.00	TGDS	2572.00	3.46	1.01
50055.00	F13	M-017980-	TSPY-like 4	23270.00	TSPYL4	2976.00	4.77	2.32
50055.00	F14	M-012509-	Sec61 gam	23480.00	SEC61G	2083.00	7.11	**4.66**
50055.00	F15	M-022091-	calmodulin	23271.00	CAMSAP1L	4162.00	3.05	0.60
50055.00	F16	M-012837-	iron-sulfur	23479.00	ISCU	1526.00	1.11	1.34
50055.00	F17	M-020306-	chromoso	23272.00	C3orf63	1367.00	7.39	**4.94**
50055.00	F18	M-006038-	SEC11 hom	23478.00	SEC11A	3403.00	4.64	2.19
50055.00	F19	M-026004-	KIAA0367	23273.00	KIAA0367	4319.00	4.03	1.58
50055.00	F20	M-003989-	quinolinate	23475.00	QPRT	2861.00	2.06	0.39
50055.00	F21	M-022485-	KIAA0350	23274.00	KIAA0350	3155.00	2.76	0.31
50055.00	F23	M-014064-	protein O-f	23275.00	POFUT2	2912.00	4.29	1.84
50055.00	G02	M-014185-	cytoplasmi	23191.00	CYFIP1	3461.00	3.00	0.55
50055.00	G04	M-014184-	UBX domai	23190.00	UBXD2	2887.00	5.40	**2.95**
50055.00	G05	M-024873-	zinc finger	23036.00	ZNF292	2873.00	4.39	1.94
50055.00	G06	M-012879-	ankyrin rep	23189.00	ANKRD15	2529.00	1.19	1.26
50055.00	G07	M-008056-	PDZ domai	23037.00	PDZD2	3987.00	2.81	0.36
50055.00	G08	M-026522-	pleckstrin	23187.00	PHLDB1	2409.00	1.04	1.41
50055.00	G09	M-016542-	WD and te	23038.00	WDTC1	2183.00	4.81	2.36
50055.00	G10	M-014076-	REST corep	23186.00	RCOR1	3081.00	2.01	0.44
50055.00	G11	M-016571-	exportin 7	23039.00	XPO7	2956.00	2.23	0.22
50055.00	G12	M-008625-	DIP2 disco-	23181.00	DIP2A	3119.00	2.05	0.40
50055.00	G13	M-026971-	MON2 hom	23041.00	MON2	2178.00	1.52	0.93
50055.00	G14	M-023452-	raftlin, lipi	23180.00	RFTN1	2644.00	0.91	1.54
50055.00	G15	M-022519-	pyridoxal-d	23042.00	PDXDC1	2695.00	3.78	1.33
50055.00	G16	M-014087-	centrosom	23177.00	CEP68	3110.00	2.03	0.42
50055.00	G17	M-024204-	furry homo	23045.00	FRYL	3503.00	1.88	0.57
50055.00	G18	M-010647-	septin 8	23176.00	SEPT8	2753.00	2.43	0.02
50055.00	G19	M-026214-	formin bin	23048.00	FNBP1	2996.00	1.77	0.68
50055.00	G20	M-017427-	lipin 1	23175.00	LPIN1	5854.00	2.70	0.25
50055.00	G21	M-014145-	zinc fingers	23051.00	ZHX3	4698.00	3.49	1.04
50055.00	G23	M-026750-	endonucle	23052.00	ENDOD1	3751.00	4.85	2.40

50055.00	H02	M-012508- ethylmalor	23474.00	ETHE1	3440.00	1.92	0.53
50055.00	H04	M-005807- calpain 7	23473.00	CAPN7	2977.00	0.94	1.51
50055.00	H05	M-014549- kelch-like 1	23276.00	KLHL18	2808.00	2.81	0.36
50055.00	H06	M-009547- glycine C-a	23464.00	GCAT	2887.00	2.67	0.22
50055.00	H07	M-010152- KIAA0664	23277.00	KIAA0664	2911.00	1.82	0.63
50055.00	H08	M-005209- isoprenylcy	23463.00	ICMT	1785.00	1.79	0.66
50055.00	H09	M-029990- nucleopori	23279.00	NUP160	1842.00	1.85	0.60
50055.00	H10	M-020061- splicing fac	23451.00	SF3B1	687.00	3.20	0.75
50055.00	H11	M-030156- IQ motif an	440073.00	IQSEC3	2362.00	1.61	0.84
50055.00	H12	M-020085- splicing fac	23450.00	SF3B3	1163.00	2.67	0.22
50055.00	H13	M-006850- KIAA0774	23281.00	KIAA0774	2476.00	1.66	0.79
50055.00	H14	M-010708- solute carri	23446.00	SLC44A1	2991.00	1.17	1.28
50055.00	H15	M-021449- cleavage st	23283.00	CSTF2T	2501.00	1.96	0.49
50055.00	H16	M-007539- solute carri	23443.00	SLC35A3	1846.00	1.35	1.10
50055.00	H17	M-021628- KIAA1107	23285.00	KIAA1107	2919.00	2.02	0.43
50055.00	H18	M-013549- orthopedia	23440.00	OTP	2664.00	4.02	1.57
50055.00	H19	M-014058- WW and C2	23286.00	WWC1	3168.00	2.37	0.08
50055.00	H20	M-009603- ATPase, (Na	23439.00	ATP1B4	2791.00	1.11	1.34
50055.00	H21	M-016993- IQ motif co	23288.00	IQCE	4140.00	3.62	1.17
50055.00	H23	M-024431- KIAA0819 p	23289.00	KIAA0819	2483.00	6.40	**3.95**
50055.00	I02	M-014086- zinc finger,	23174.00	ZCCHC14	3747.00	0.93	1.52
50055.00	I04	M-016146- KIAA0157	23172.00	KIAA0157	2694.00	1.67	0.78
50055.00	I05	M-026438- KIAA0913	23053.00	KIAA0913	1628.00	3.38	0.93
50055.00	I06	M-008514- glycerol-3-p	23171.00	GPD1L	1922.00	1.66	0.79
50055.00	I07	M-008573- nicotinamid	23057.00	NMNAT2	2582.00	0.35	2.10
50055.00	I08	M-014094- tubulin tyro	23170.00	TTLL12	2197.00	2.46	0.01
50055.00	I09	M-014449- clusterin as	23059.00	CLUAP1	2122.00	4.01	1.56
50055.00	I10	M-007546- solute carri	23169.00	SLC35D1	2716.00	4.42	1.97
50055.00	I11	M-022257- zinc finger	23060.00	ZNF609	2366.00	4.31	1.86
50055.00	I12	M-014104- Rtf1, Paf1/	23168.00	RTF1	2126.00	0.71	1.74
50055.00	I13	M-031872- TBC1 doma	23061.00	TBC1D9B	2221.00	3.24	0.79
50055.00	I14	M-025913- KIAA0143 p	23167.00	KIAA0143	2584.00	1.47	0.98
50055.00	I15	M-012908- golgi associ	23062.00	GGA2	1961.00	5.00	2.55
50055.00	I16	M-014103- stabilin 1	23166.00	STAB1	2372.00	0.38	2.07
50055.00	I17	M-026287- wings apar	23063.00	WAPAL	1489.00	1.41	1.04
50055.00	I18	M-010646- nucleopori	23165.00	NUP205	980.00	5.00	2.55
50055.00	I19	M-021420- senataxin	23064.00	SETX	2389.00	5.86	**3.41**
50055.00	I20	M-014102- myosin pho	23164.00	M-RIP	2732.00	1.21	1.24
50055.00	I21	M-014146- KIAA0090	23065.00	KIAA0090	3734.00	5.70	**3.25**
50055.00	I23	M-023448- cullin-asso	23066.00	CAND2	3376.00	0.71	1.74
50055.00	J02	M-013411- histidyl-tRN	23438.00	HARS2	3442.00	0.84	1.61
50055.00	J04	M-005864- elastase 3B	23436.00	ELA3B	3046.00	1.54	0.91
50055.00	J05	M-017845- Smg-6 hom	23293.00	SMG6	2409.00	2.70	0.25
50055.00	J06	M-019492- chromosom	23434.00	C3orf27	1351.00	3.48	1.03
50055.00	J07	M-025085- ankyrin rep	23294.00	ANKS1A	1688.00	4.38	1.93
50055.00	J08	M-021474- adaptor-rel	23431.00	AP4E1	2929.00	4.47	2.02
50055.00	J09	M-022620- mahogunin	23295.00	MGRN1	2486.00	1.37	1.08

50055.00	J10	M-006057- tryptase de	23430.00	TPSD1	3552.00	4.98	2.53
50055.00	J11	M-020304- ATM/ATR-	23300.00	ASCIZ	1453.00	2.00	0.45
50055.00	J12	M-007618- solute carri	23428.00	SLC7A8	3016.00	4.54	2.09
50055.00	J13	M-014061- EH domain	23301.00	EHBP1	2993.00	1.57	0.88
50055.00	J14	M-026981- glutamate	23426.00	GRIP1	2403.00	1.96	0.49
50055.00	J15	M-023005- WSC doma	23302.00	WSCD1	2735.00	1.94	0.51
50055.00	J16	M-008051- transmem	23423.00	TMED3	2397.00	2.42	0.03
50055.00	J17	M-026966- KIAA0286	23306.00	KIAA0286	1545.00	2.01	0.44
50055.00	J18	M-013024- frequenin	23413.00	FREQ	2410.00	2.12	0.33
50055.00	J19	M-029587- FK506 bind	23307.00	FKBP15	2636.00	1.71	0.74
50055.00	J20	M-020053- COMM do	23412.00	COMMD3	2042.00	2.15	0.30
50055.00	J21	M-007812- inducible	23308.00	ICOSLG	1583.00	1.96	0.49
50055.00	J23	M-031246- SIN3 homo	23309.00	SIN3B	2433.00	1.15	1.30
50055.00	K02	M-012881- golgi associ	23163.00	GGA3	3513.00	4.21	1.76
50055.00	K04	M-009381- sorting nex	23161.00	SNX13	4159.00	2.89	0.44
50055.00	K05	M-027025- SET domai	23067.00	SETD1B	2960.00	1.32	1.13
50055.00	K06	M-022651- WD repeat	23160.00	WDR43	2161.00	1.71	0.74
50055.00	K07	M-014142- KIAA0082	23070.00	KIAA0082	2809.00	2.42	0.03
50055.00	K08	M-010024- chloride ch	23155.00	CLCC1	4081.00	2.55	0.10
50055.00	K09	M-026913- KIAA0701	23074.00	KIAA0701	2937.00	2.38	0.07
50055.00	K10	M-012835- neurochon	23154.00	NCDN	3759.00	2.93	0.48
50055.00	K11	M-010323- SWAP-70 p	23075.00	SWAP70	3471.00	2.71	0.26
50055.00	K12	M-015185- capicua ho	23152.00	CIC	3943.00	1.90	0.55
50055.00	K13	M-031402- ribosomal	23076.00	RRP1B	2444.00	2.21	0.24
50055.00	K14	M-024634- death-indu	23151.00	DIP	3347.00	4.57	2.12
50055.00	K15	M-006951- MYC bindi	23077.00	MYCBP2	4295.00	3.66	1.21
50055.00	K16	M-023262- FERM dom	23150.00	FRMD4B	3221.00	2.98	0.53
50055.00	K17	M-021694- KIAA0564	23078.00	RP11-125A	2699.00	4.19	1.74
50055.00	K18	M-014114- FCH domai	23149.00	FCHO1	3595.00	4.14	1.69
50055.00	K19	M-025311- KIAA0241	23080.00	KIAA0241	2506.00	2.87	0.42
50055.00	K20	M-025327- NAC alpha	23148.00	NACAD	1760.00	1.76	0.69
50055.00	K21	M-004293- jumonji do	23081.00	JMJD2C	4218.00	4.39	1.94
50055.00	K23	M-010942- ELKS/RAB6	23085.00	ERC1	2920.00	4.28	1.83
50055.00	L02	M-004827- sirtuin (sile	23410.00	SIRT3	4623.00	2.49	0.04
50055.00	L04	M-012445- sirtuin (sile	23409.00	SIRT4	4090.00	3.37	0.92
50055.00	L05	M-026539- non-SMC c	23310.00	NCAPD3	4251.00	2.52	0.07
50055.00	L06	M-013448- sirtuin (sile	23408.00	SIRT5	3394.00	2.27	0.18
50055.00	L07	M-014049- Dmx-like 2	23312.00	DMXL2	3437.00	6.75	**4.30**
50055.00	L08	M-013104- coactosin-l	23406.00	COTL1	1411.00	9.07	**6.62**
50055.00	L09	M-024630- chromoso	23313.00	C22orf9	2541.00	1.73	0.72
50055.00	L10	M-003483- Dicer1, Dcr	23405.00	DICER1	4002.00	0.97	1.48
50055.00	L11	M-023161- SATB hom	23314.00	SATB2	2119.00	2.12	0.33
50055.00	L12	M-016975- exosome c	23404.00	EXOSC2	3188.00	1.69	0.76
50055.00	L13	M-007628- solute carri	23315.00	SLC9A8	1982.00	1.51	0.94
50055.00	L14	M-023753- F-box prote	23403.00	FBXO46	2452.00	1.06	1.39
50055.00	L15	M-027122- cut-like 2 (	23316.00	CUTL2	2993.00	2.64	0.19
50055.00	L16	M-017869- dullard ho	23399.00	DULLARD	4274.00	3.81	1.36

50055.00	L17	M-010651- DnaJ (Hsp4	23317.00	DNAJC13	3827.00	2.33	0.12
50055.00	L18	M-004742- peptidylprc	23398.00	PPWD1	4782.00	1.07	1.38
50055.00	L19	M-021797- zinc finger,	23318.00	ZCCHC11	4358.00	1.72	0.73
50055.00	L20	M-012853- non-SMC c	23397.00	NCAPH	2936.00	2.18	0.27
50055.00	L21	M-006955- tripartite m	23321.00	TRIM2	4395.00	2.23	0.22
50055.00	L23	M-022557- RPGRIP1-lil	23322.00	RPGRIP1L	4097.00	1.66	0.79
50055.00	M02	M-028871- SCO-spond	23145.00	SSPO	2817.00	1.46	0.99
50055.00	M04	M-014113- zinc finger	23144.00	ZC3H3	3278.00	2.07	0.38
50055.00	M05	M-014134- exophilin 5	23086.00	EXPH5	3028.00	0.76	1.69
50055.00	M06	M-014112- leucine-ricl	23143.00	LRCH1	3120.00	2.66	0.21
50055.00	M07	M-006952- tripartite m	23087.00	TRIM35	3633.00	4.62	2.17
50055.00	M08	M-014118- DCN1, defe	23142.00	DCUN1D4	3081.00	0.45	2.00
50055.00	M09	M-018897- zinc finger	23091.00	ZC3H13	3127.00	1.66	0.79
50055.00	M10	M-031841- zinc finger,	23140.00	ZZEF1	3131.00	5.24	2.79
50055.00	M11	M-023669- signal-indu	23094.00	SIPA1L3	2520.00	5.60	**3.15**
50055.00	M12	M-024612- Nedd4 binc	23138.00	N4BP3	3048.00	3.05	0.60
50055.00	M13	M-024676- IQ motif an	23096.00	IQSEC2	2722.00	3.27	0.82
50055.00	M14	M-014117- structural r	23137.00	SMC5	3567.00	2.55	0.10
50055.00	M15	M-008076- sterile alph	23098.00	SARM1	2479.00	2.34	0.11
50055.00	M16	M-015330- erythrocyte	23136.00	EPB41L3	4338.00	1.24	1.21
50055.00	M17	M-020320- zinc finger	23099.00	ZBTB43	2188.00	1.33	1.12
50055.00	M18	M-023013- jumonji do	23135.00	JMJD3	2530.00	1.50	0.95
50055.00	M19	M-009313- MCF.2 cell	23101.00	MCF2L2	4211.00	3.87	1.42
50055.00	M20	M-004291- PHD finger	23133.00	PHF8	3025.00	1.49	0.96
50055.00	M21	M-014127- TBC1 doma	23102.00	TBC1D2B	3807.00	1.97	0.48
50055.00	M23	M-024404- follistatin-li	23105.00	FSTL4	3994.00	0.48	1.97
50055.00	N02	M-006956- leucyl-tRN	23395.00	LARS2	2227.00	2.60	0.15
50055.00	N04	M-026188- KIAA0368	23392.00	KIAA0368	4996.00	7.39	**4.94**
50055.00	N05	M-026919- KIAA1033	23325.00	KIAA1033	2268.00	0.97	1.48
50055.00	N06	M-014019- zinc finger,	23390.00	ZDHHC17	4430.00	6.19	**3.74**
50055.00	N07	M-014050- SAM and SI	23328.00	SASH1	3152.00	4.44	1.99
50055.00	N08	M-027126- thyroid hor	23389.00	THRAP2	2847.00	3.06	0.61
50055.00	N09	M-026976- KIAA0984	23329.00	KIAA0984	3332.00	2.22	0.23
50055.00	N10	M-014018- NudC doma	23386.00	NUDCD3	4656.00	1.89	0.56
50055.00	N11	M-014051- tetratricop	23331.00	TTC28	2364.00	7.53	**5.08**
50055.00	N12	M-008043- nicastrin	23385.00	NCSTN	2376.00	1.35	1.10
50055.00	N13	M-025317- dpy-19-like	23333.00	DPY19L1	2926.00	2.32	0.13
50055.00	N14	M-024592- SPECC1-like	23384.00	SPECC1L	3222.00	1.96	0.49
50055.00	N15	M-031859- KIAA0467	23334.00	KIAA0467	3334.00	7.80	**5.35**
50055.00	N16	M-031981- KIAA0892	23383.00	KIAA0892	2476.00	1.58	0.87
50055.00	N17	M-012868- desmuslin	23336.00	DMN	2663.00	1.73	0.72
50055.00	N18	M-014023- Smg-5 hom	23381.00	SMG5	4287.00	6.09	**3.64**
50055.00	N19	M-018308- PHD finger	23338.00	PHF15	3407.00	1.70	0.75
50055.00	N20	M-021531- SLIT-ROBO	23380.00	SRGAP2	3511.00	2.25	0.20
50055.00	N21	M-014052- vacuolar pr	23339.00	VPS39	4445.00	4.86	2.41
50055.00	N23	M-014039- spectrin re	23345.00	SYNE1	3405.00	1.53	0.92
50055.00	O02	M-014122- RAD54-like	23132.00	RAD54L2	4831.00	6.29	**3.84**

50055.00	O04	M-023195-	G patch do	23131.00	GPATCH8	2899.00	2.35	0.10
50055.00	O05	M-012903-	mitochond	23107.00	MRPS27	2749.00	2.98	0.53
50055.00	O06	M-026591-	hypothetic	23130.00	KIAA0404	3418.00	3.48	1.03
50055.00	O07	M-023041-	GTPase act	23108.00	GARNL4	4614.00	2.67	0.22
50055.00	O08	M-014121-	plexin D1	23129.00	PLXND1	4215.00	2.47	0.02
50055.00	O09	M-026950-	dendrin	23109.00	DDN	3781.00	3.12	0.67
50055.00	O10	M-014120-	glycosyltra	23127.00	GLT25D2	3542.00	1.21	1.24
50055.00	O11	M-024575-	trinucleoti	23112.00	TNRC6B	4159.00	3.75	1.30
50055.00	O12	M-006953-	pogo trans	23126.00	POGZ	3454.00	1.53	0.92
50055.00	O13	M-019504-	chromoson	11241.00	C10orf1	3995.00	4.73	2.28
50055.00	O14	M-012895-	hypermeth	23119.00	HIC2	3741.00	1.12	1.33
50055.00	O15	M-015406-	tubulin tyr	23093.00	TTLL5	3787.00	2.61	0.16
50055.00	O16	M-022505-	KIAA0220-l	23117.00	LOC23117	2999.00	2.00	0.45
50055.00	O17	M-012371-	ribosomal	11224.00	RPL35	1986.00	1.36	1.09
50055.00	O18	M-021953-	KIAA0423	23116.00	KIAA0423	3952.00	0.94	1.51
50055.00	O19	M-020364-	zinc finger	22891.00	ZNF365	3929.00	1.35	1.10
50055.00	O20	M-021839-	neurofasci	23114.00	NFASC	4379.00	1.12	1.33
50055.00	O21	M-004725-	epsin 2	22905.00	EPN2	4561.00	3.66	1.21
50055.00	O23	M-012924-	WD repeat	23001.00	WDFY3	2840.00	1.73	0.72
50055.00	P02	M-024272-	KIAA0947	23379.00	KIAA0947	1570.00	7.13	**4.68**
50055.00	P04	M-014028-	KIAA0409	23378.00	KIAA0409	2849.00	6.28	**3.83**
50055.00	P05	M-014040-	dedicator	23348.00	DOCK9	3158.00	2.41	0.04
50055.00	P06	M-014027-	KIAA0776	23376.00	KIAA0776	3149.00	1.75	0.70
50055.00	P07	M-026131-	KIAA1045	23349.00	KIAA1045	2636.00	1.18	1.27
50055.00	P08	M-014026-	CREB regul	23373.00	CRTC1	3110.00	5.50	**3.05**
50055.00	P09	M-023607-	U2-associa	23350.00	SR140	2218.00	2.39	0.06
50055.00	P10	M-014031-	pumilio ho	23369.00	PUM2	2976.00	3.83	1.38
50055.00	P11	M-030359-	KIAA0323	23351.00	KIAA0323	1990.00	2.66	0.21
50055.00	P12	M-027187-	La ribonucl	23367.00	LARP1	1327.00	3.01	0.56
50055.00	P13	M-014021-	zinc finger,	23352.00	ZUBR1	1837.00	2.23	0.22
50055.00	P14	M-025319-	KIAA0895	23366.00	KIAA0895	3817.00	2.07	0.38
50055.00	P15	M-025277-	unc-84 ho	23353.00	UNC84A	2971.00	1.88	0.57
50055.00	P16	M-023133-	obscurin-li	23363.00	OBSL1	3546.00	0.39	2.06
50055.00	P17	M-023648-	KIAA0841	23354.00	KIAA0841	1406.00	2.85	0.40
50055.00	P18	M-014030-	pleckstrin	23362.00	PSD3	2329.00	2.58	0.13
50055.00	P19	M-023668-	vacuolar pr	23355.00	VPS8	3682.00	2.06	0.39
50055.00	P20	M-022810-	zinc finger	23361.00	ZNF629	2254.00	0.93	1.52
50055.00	P21	M-014041-	angel hom	23357.00	ANGEL1	3640.00	1.46	0.99
50055.00	P23	M-014029-	formin bin	23360.00	FNBP4	1317.00	2.13	0.32
					mdn	2911.50	2.45	0.93
					3xMAD			2.79
					MADc			1.38
50055.00	C22					2995.00	14.42	
50055.00	D22					4108.00	13.66	
50055.00	E22	2940.00	9.39	3143.00	7.76			
50055.00	F22					3613.00	18.21	
					mn	3572.00	15.43	

					sd	557.63	2.44
50055.00	G22					2026.00	1.97
50055.00	H22					2199.00	1.00
50055.00	I22					1718.00	1.22
50055.00	J22					1767.00	3.11
					mn	1894.67	1.78
					sd	264.70	1.16
					3psSD		7.32
					3ngSD		3.48
					SumSD		10.80
					DiffMn		13.65
					SmovrDiff		0.79
					1minus		0.21
50055.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAR	298.00	5.37
50055.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAR	286.00	9.09
50055.00	I03	D-001206-	siControl non-targeting			2980.00	1.58
50055.00	J03	D-001206-	siControl non-targeting			3096.00	2.42
50055.00	K03	D-001600-	siGLO RISC-free siRNA			5446.00	8.78
50055.00	L03	D-001600-	siGLO RISC-free siRNA			5486.00	4.01

rZ	Cell Count	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ
-0.46	3021.00	1.46	4.06	-0.07	3776.00	2.17	0.35	-0.22
0.45	2335.00	1.84	3.68	0.00	2745.00	1.79	0.73	-0.46
3.76	3198.00	9.38	3.86	1.38	4199.00	12.57	10.05	6.21
0.17	2762.00	1.92	3.60	0.01	2700.00	2.67	0.15	0.09
0.24	2242.00	2.68	2.84	0.15	2943.00	2.00	0.52	-0.32
0.47	2417.00	1.74	3.78	-0.02	2486.00	2.98	0.46	0.28
-0.08	2930.00	0.85	4.67	-0.18	3141.00	1.78	0.74	-0.46
0.56	1728.00	1.97	3.55	0.02	2556.00	1.80	0.72	-0.45
-0.01	1711.00	0.64	4.88	-0.22	2780.00	1.33	1.19	-0.74
1.75	2048.00	4.30	1.22	0.45	2944.00	3.87	1.35	0.83
-0.38	1806.00	1.72	3.80	-0.02	3442.00	2.91	0.39	0.24
-0.13	2849.00	0.98	4.54	-0.16	2542.00	2.01	0.51	-0.32
1.74	921.00	3.15	2.37	0.24	1371.00	6.64	4.12	2.54
1.28	2622.00	1.75	3.77	-0.02	2467.00	2.72	0.20	0.12
1.32	1767.00	4.02	1.50	0.40	2109.00	2.80	0.28	0.17
1.18	1553.00	3.28	2.24	0.26	1820.00	1.70	0.82	-0.51
1.00	2756.00	1.52	4.00	-0.06	2288.00	5.42	2.90	1.79
-0.24	1622.00	5.36	0.16	0.64	2107.00	2.85	0.33	0.20
0.31	1595.00	5.45	0.07	0.66	1570.00	5.73	3.21	1.98
2.12	778.00	7.46	1.94	1.03	1680.00	2.92	0.40	0.24
-0.69	3706.00	1.51	4.01	-0.06	2832.00	2.79	0.27	0.16
-1.16	2379.00	0.59	4.93	-0.23	2872.00	1.25	1.27	-0.78
-1.42	2688.00	0.56	4.96	-0.23	2670.00	2.25	0.27	-0.17
-1.58	3650.00	2.11	3.41	0.05	4025.00	2.31	0.21	-0.13
0.83	5190.00	2.14	3.38	0.05	4754.00	10.37	7.85	4.85
-0.75	2632.00	1.79	3.73	-0.01	2324.00	0.99	1.53	-0.95
-1.09	5137.00	2.22	3.30	0.07	3826.00	2.93	0.41	0.25
-1.43	3496.00	1.03	4.49	-0.15	3625.00	1.93	0.59	-0.37
-0.10	2875.00	3.69	1.83	0.34	2738.00	4.78	2.26	1.40
0.23	2762.00	1.48	4.04	-0.06	3706.00	3.53	1.01	0.62
-0.71	2556.00	1.06	4.46	-0.14	3032.00	2.37	0.15	-0.09
-1.04	1865.00	0.16	5.36	-0.31	2814.00	1.21	1.31	-0.81
0.72	4038.00	3.27	2.25	0.26	2802.00	1.93	0.59	-0.37
-0.16	3542.00	1.10	4.42	-0.13	3445.00	5.02	2.50	1.54
-0.50	3231.00	0.71	4.81	-0.21	2422.00	1.98	0.54	-0.33
1.89	4822.00	1.06	4.46	-0.14	4412.00	1.99	0.53	-0.33
-0.99	3218.00	1.49	4.03	-0.06	2299.00	1.48	1.04	-0.65
1.52	5077.00	4.51	1.01	0.49	4350.00	4.30	1.78	1.10
-1.04	2615.00	0.08	5.44	-0.32	2781.00	0.90	1.62	-1.00
2.70	1380.00	1.59	3.93	-0.04	3133.00	3.89	1.37	0.85
0.34	2715.00	0.41	5.11	-0.26	2570.00	0.31	2.21	-1.37
-0.51	2128.00	2.26	3.26	0.08	2559.00	0.74	1.78	-1.10
0.29	3159.00	0.85	4.67	-0.18	3243.00	2.62	0.10	0.06
0.24	4402.00	2.18	3.34	0.06	4072.00	1.50	1.02	-0.63
0.46	2801.00	3.32	2.20	0.27	2313.00	0.95	1.57	-0.97
0.83	4011.00	4.21	1.31	0.43	2970.00	3.74	1.22	0.75

-1.39	2669.00	1.54	3.98	-0.06	1497.00	0.20	2.32	-1.43
0.79	3714.00	5.71	0.19	0.71	3227.00	2.85	0.33	0.20
0.27	3137.00	1.15	4.37	-0.13	2963.00	1.62	0.90	-0.56
-0.32	3234.00	1.98	3.54	0.03	2999.00	1.23	1.29	-0.80
-0.02	1974.00	1.93	3.60	0.02	2260.00	1.86	0.66	-0.41
-0.33	1692.00	1.54	3.98	-0.06	1769.00	0.79	1.73	-1.07
1.97	3039.00	3.52	2.00	0.31	3259.00	1.41	1.11	-0.69
-0.24	2215.00	3.43	2.09	0.29	2054.00	0.78	1.74	-1.08
-0.52	3578.00	2.46	3.06	0.11	3119.00	0.67	1.85	-1.14
0.13	2094.00	2.91	2.61	0.20	2402.00	1.17	1.35	-0.84
0.34	3006.00	4.22	1.30	0.44	2407.00	3.16	0.64	0.39
0.02	2872.00	2.44	3.08	0.11	3754.00	0.43	2.09	-1.30
-0.65	631.00	2.54	2.98	0.13	1690.00	0.41	2.11	-1.30
-1.00	1969.00	1.78	3.74	-0.01	3956.00	0.68	1.84	-1.14
2.72	4875.00	1.70	3.82	-0.02	5000.00	4.52	2.00	1.23
-0.38	2559.00	2.81	2.71	0.18	3431.00	4.14	1.62	1.00
0.14	2840.00	2.50	3.02	0.12	3312.00	2.11	0.41	-0.25
1.02	3323.00	1.11	4.41	-0.13	2694.00	3.53	1.01	0.62
-0.05	3688.00	1.36	4.16	-0.09	2685.00	0.89	1.63	-1.01
-0.88	3627.00	1.46	4.06	-0.07	3382.00	2.31	0.21	-0.13
0.13	3410.00	1.23	4.29	-0.11	1915.00	2.51	0.01	-0.01
3.82	3550.00	5.21	0.31	0.62	3752.00	4.64	2.12	1.31
0.28	4113.00	2.87	2.65	0.19	3044.00	2.20	0.32	-0.20
-0.33	2095.00	2.67	2.85	0.15	1660.00	2.89	0.37	0.23
-0.44	1894.00	1.43	4.09	-0.08	2065.00	2.03	0.49	-0.30
-0.74	3398.00	2.83	2.69	0.18	2211.00	2.04	0.48	-0.30
-0.92	2551.00	1.33	4.19	-0.09	2136.00	1.69	0.83	-0.52
3.24	3079.00	7.11	1.59	0.96	2494.00	8.50	**5.98**	3.69
0.44	2242.00	4.01	1.51	0.40	1675.00	0.90	1.62	-1.01
0.93	3047.00	1.77	3.75	-0.01	3569.00	1.26	1.26	-0.78
1.20	4791.00	3.26	2.26	0.26	4566.00	4.86	2.34	1.44
-0.86	4294.00	2.12	3.40	0.05	3985.00	1.88	0.64	-0.40
1.77	2978.00	2.42	3.10	0.11	3803.00	3.92	1.40	0.86
-0.14	2394.00	2.59	2.93	0.14	4105.00	3.61	1.09	0.67
2.58	4677.00	3.36	2.16	0.28	4195.00	4.31	1.79	1.11
1.28	2111.00	6.68	1.16	0.88	816.00	3.68	1.16	0.71
0.24	1138.00	3.08	2.44	0.23	1538.00	1.82	0.70	-0.43
4.02	2997.00	1.50	4.02	-0.06	3380.00	5.62	3.10	1.91
-0.40	3635.00	0.83	4.69	-0.18	3786.00	1.06	1.46	-0.91
0.56	2674.00	2.62	2.90	0.14	2833.00	4.45	1.93	1.19
3.21	2972.00	2.22	3.30	0.07	2600.00	2.96	0.44	0.27
2.06	4043.00	2.18	3.34	0.06	3731.00	2.52	0.00	0.00
0.08	4186.00	2.05	3.47	0.04	2551.00	1.65	0.87	-0.54
0.07	3513.00	1.45	4.07	-0.07	3125.00	0.93	1.59	-0.99
-0.06	2866.00	0.24	5.28	-0.29	2329.00	2.15	0.37	-0.23
1.86	3061.00	2.74	2.78	0.17	2576.00	2.41	0.11	-0.07
1.98	2131.00	2.25	3.27	0.08	2483.00	1.33	1.19	-0.74

-0.27	2993.00	0.20	5.32	-0.30	3173.00	1.64	0.88	-0.55
1.80	2164.00	0.05	5.47	-0.33	2209.00	2.67	0.15	0.09
1.06	2811.00	0.25	5.27	-0.29	2700.00	2.15	0.37	-0.23
-0.60	3432.00	0.79	4.73	-0.19	2852.00	1.72	0.80	-0.50
0.80	4274.00	2.74	2.78	0.16	2961.00	1.86	0.66	-0.41
-1.11	3516.00	0.26	5.26	-0.29	3071.00	1.50	1.02	-0.63
-0.62	4368.00	1.10	4.42	-0.14	5010.00	2.59	0.07	0.04
0.88	4918.00	4.86	0.66	0.55	4768.00	0.61	1.91	-1.18
1.58	5221.00	3.43	2.09	0.29	3248.00	2.99	0.47	0.29
-0.63	3568.00	1.49	4.03	-0.06	2403.00	1.62	0.90	-0.56
1.25	3529.00	1.13	4.39	-0.13	3078.00	0.78	1.74	-1.08
1.90	4202.00	2.02	3.50	0.03	2842.00	0.49	2.03	-1.25
0.68	2806.00	2.35	3.17	0.09	1965.00	1.17	1.35	-0.84
0.26	3600.00	2.67	2.85	0.15	3184.00	2.20	0.32	-0.20
3.10	3182.00	8.55	3.03	1.22	3031.00	3.63	1.11	0.68
0.63	2928.00	3.52	2.00	0.31	2529.00	0.99	1.53	-0.95
0.73	2568.00	1.91	3.61	0.01	2220.00	1.49	1.03	-0.64
1.69	3472.00	2.36	3.16	0.10	2763.00	0.47	2.05	-1.27
3.38	1794.00	4.63	0.89	0.51	1472.00	0.88	1.64	-1.01
0.44	3511.00	3.53	1.99	0.31	3052.00	1.25	1.27	-0.79
-0.97	1240.00	3.39	2.13	0.28	1211.00	0.58	1.94	-1.20
3.58	1375.00	2.84	2.68	0.18	1390.00	1.08	1.44	-0.89
1.59	4158.00	2.28	3.24	0.08	3750.00	2.69	0.17	0.10
1.15	3576.00	2.43	3.09	0.11	3092.00	0.91	1.61	-1.00
-0.28	3072.00	3.45	2.07	0.29	2579.00	3.02	0.50	0.31
0.23	2659.00	2.41	3.11	0.10	3770.00	0.93	1.59	-0.99
1.34	2716.00	3.31	2.21	0.27	3974.00	2.74	0.22	0.14
0.40	4781.00	3.70	1.82	0.34	4424.00	2.37	0.15	-0.09
2.14	3503.00	2.14	3.38	0.06	4432.00	4.78	2.26	1.40
1.41	3667.00	2.40	3.12	0.10	3427.00	4.23	1.71	1.05
-0.91	2747.00	2.48	3.04	0.12	2536.00	3.12	0.60	0.37
0.26	4289.00	1.45	4.07	-0.07	4229.00	4.23	1.71	1.06
-1.02	2316.00	2.42	3.10	0.11	2964.00	5.97	**3.45**	2.13
1.71	2996.00	2.37	3.15	0.10	2395.00	1.38	1.14	-0.71
-0.32	3886.00	1.24	4.28	-0.11	2864.00	2.23	0.29	-0.18
-0.16	2770.00	1.26	4.26	-0.10	1926.00	4.26	1.74	1.07
-0.29	3398.00	3.88	1.64	0.37	3148.00	5.21	2.69	1.66
-0.68	2422.00	3.67	1.85	0.34	2746.00	3.46	0.94	0.58
-1.12	1899.00	3.63	1.89	0.33	2246.00	2.85	0.33	0.20
0.97	2237.00	0.89	4.63	-0.17	1990.00	2.16	0.36	-0.22
-0.31	3092.00	1.94	3.58	0.02	2371.00	1.39	1.13	-0.70
-0.41	3855.00	1.63	3.89	-0.04	3484.00	3.36	0.84	0.52
-0.01	2463.00	1.87	3.65	0.01	3248.00	4.31	1.79	1.10
-0.49	3179.00	1.67	3.85	-0.03	3275.00	6.99	**4.47**	2.76
0.18	5366.00	3.43	2.09	0.29	6240.00	5.18	2.66	1.64
0.76	3302.00	1.33	4.19	-0.09	5149.00	6.08	**3.56**	2.20
1.74	3263.00	1.78	3.74	-0.01	4665.00	2.55	0.03	0.02

-0.38	4056.00	1.33	4.19	-0.09	4285.00	0.40	2.12	-1.31
-1.09	3078.00	0.71	4.81	-0.21	3232.00	3.77	1.25	0.77
0.27	3201.00	1.97	3.55	0.02	3313.00	1.96	0.56	-0.35
0.16	2956.00	2.03	3.49	0.03	3811.00	4.22	1.70	1.05
-0.45	2373.00	3.24	2.28	0.26	3598.00	1.97	0.55	-0.34
-0.47	2132.00	2.16	3.36	0.06	1849.00	2.97	0.45	0.28
-0.44	2595.00	0.96	4.56	-0.16	1921.00	2.03	0.49	-0.30
0.55	673.00	7.13	1.61	0.97	671.00	1.64	0.88	-0.55
-0.61	2835.00	2.15	3.37	0.06	1962.00	0.82	1.70	-1.05
0.16	1032.00	3.68	1.84	0.34	1174.00	1.96	0.56	-0.35
-0.57	2514.00	1.63	3.89	-0.04	2036.00	1.62	0.90	-0.56
-0.93	3626.00	1.74	3.78	-0.02	3464.00	2.25	0.27	-0.17
-0.35	2025.00	1.48	4.04	-0.07	1536.00	4.49	1.97	1.22
-0.79	1233.00	1.54	3.98	-0.05	1519.00	3.23	0.71	0.43
-0.31	2322.00	2.89	2.63	0.19	3261.00	2.02	0.50	-0.31
1.14	1823.00	3.68	1.84	0.34	2984.00	5.03	2.51	1.55
-0.06	3474.00	3.83	1.69	0.36	3346.00	1.85	0.67	-0.41
-0.97	2916.00	1.20	4.32	-0.12	3180.00	1.07	1.45	-0.90
0.85	2740.00	4.34	1.18	0.46	3937.00	5.21	2.69	1.66
2.87	1939.00	1.55	3.97	-0.05	3173.00	1.29	1.23	-0.76
-1.10	4063.00	1.40	4.12	-0.08	4350.00	2.99	0.47	0.29
-0.56	1565.00	1.60	3.92	-0.04	2448.00	6.86	**4.34**	2.68
0.68	1546.00	1.03	4.49	-0.15	1915.00	1.62	0.90	-0.56
-0.57	1434.00	2.93	2.59	0.20	2461.00	3.37	0.85	0.52
-1.52	1429.00	1.82	3.70	0.00	2439.00	3.12	0.60	0.37
0.01	1623.00	1.85	3.67	0.00	3356.00	2.38	0.14	-0.09
1.13	1977.00	4.91	0.61	0.56	2232.00	3.32	0.80	0.49
1.43	1621.00	2.96	2.56	0.20	2726.00	2.46	0.06	-0.04
1.35	2442.00	2.54	2.98	0.13	2118.00	3.40	0.88	0.54
-1.26	784.00	3.70	1.82	0.34	1671.00	2.69	0.17	0.10
0.58	1060.00	6.60	1.08	0.87	1966.00	3.61	1.09	0.67
-0.71	2641.00	1.02	4.50	-0.15	3128.00	1.12	1.40	-0.87
1.85	1264.00	5.62	0.10	0.69	2052.00	3.12	0.60	0.37
-1.50	1421.00	1.90	3.62	0.01	2238.00	1.47	1.05	-0.65
-0.75	1085.00	2.40	3.12	0.10	1960.00	1.79	0.73	-0.46
1.85	616.00	12.66	7.14	1.98	889.00	5.62	3.10	1.92
2.48	1260.00	6.11	0.59	0.78	2237.00	2.73	0.21	0.13
-0.90	1989.00	2.46	3.06	0.11	3091.00	2.43	0.09	-0.06
2.36	2520.00	3.81	1.71	0.36	3577.00	4.14	1.62	1.00
-1.26	1186.00	3.54	1.98	0.31	3513.00	1.96	0.56	-0.35
-1.16	4227.00	0.52	5.00	-0.24	4296.00	3.75	1.23	0.76
-0.66	1641.00	0.12	5.40	-0.31	3246.00	2.25	0.27	-0.17
0.18	2602.00	0.92	4.60	-0.17	2540.00	1.57	0.95	-0.59
0.75	1337.00	0.37	5.15	-0.27	1308.00	1.76	0.76	-0.47
1.40	1803.00	2.00	3.52	0.03	1713.00	5.66	3.14	1.94
1.47	2500.00	2.56	2.96	0.13	3260.00	3.74	1.22	0.75
-0.78	2123.00	0.61	4.91	-0.22	2438.00	1.72	0.80	-0.49

1.84	3090.00	2.07	3.45	0.04	3162.00	7.62	**5.10**	3.15
-0.33	1436.00	1.81	3.71	-0.01	1599.00	1.19	1.33	-0.82
1.52	1976.00	2.02	3.50	0.03	3496.00	5.61	3.09	1.90
-0.64	1891.00	1.37	4.15	-0.08	3122.00	1.03	1.50	-0.93
-0.36	1651.00	1.51	4.01	-0.06	2054.00	6.91	**4.39**	2.71
-0.37	1715.00	1.22	4.30	-0.11	2588.00	3.36	0.84	0.52
-0.02	1223.00	1.23	4.29	-0.11	2183.00	1.88	0.64	-0.40
-0.32	683.00	0.88	4.64	-0.18	1980.00	4.60	2.08	1.28
-0.24	723.00	0.83	4.69	-0.18	2240.00	5.63	3.11	1.92
-0.54	2366.00	0.21	5.31	-0.30	3065.00	3.95	1.43	0.88
-0.21	1730.00	1.68	3.84	-0.03	1897.00	4.38	1.86	1.14
-0.35	1327.00	0.38	5.14	-0.27	1471.00	3.40	0.88	0.54
-0.94	1057.00	0.85	4.67	-0.18	3001.00	2.80	0.28	0.17
1.28	3551.00	1.69	3.83	-0.03	4129.00	1.43	1.09	-0.68
0.32	2871.00	2.16	3.36	0.06	3733.00	3.05	0.53	0.33
-0.82	2158.00	1.90	3.62	0.01	2535.00	1.62	0.90	-0.56
-0.53	2179.00	1.01	4.51	-0.15	2108.00	1.76	0.76	-0.47
-0.02	2234.00	4.70	0.82	0.52	4120.00	5.29	2.77	1.71
0.07	2739.00	2.67	2.85	0.15	3859.00	2.38	0.14	-0.09
-0.05	1960.00	1.28	4.24	-0.10	2267.00	1.99	0.54	-0.33
0.35	2062.00	1.45	4.07	-0.07	2970.00	1.11	1.41	-0.87
0.19	1879.00	3.30	2.22	0.27	3069.00	0.42	2.10	-1.30
-0.40	3692.00	1.65	3.87	-0.03	3714.00	1.02	1.50	-0.93
-0.17	1588.00	1.51	4.01	-0.06	1596.00	0.88	1.64	-1.02
1.54	3175.00	4.54	0.98	0.49	2506.00	4.11	1.59	0.98
0.88	2980.00	3.79	1.73	0.36	48.00	62.50	**59.98**	37.05
0.39	1632.00	2.57	2.95	0.13	2797.00	1.14	1.38	-0.85
1.26	2058.00	1.12	4.40	-0.13	2666.00	2.63	0.11	0.06
1.23	2250.00	3.11	2.41	0.23	4475.00	5.32	2.80	1.73
0.31	2778.00	2.99	2.53	0.21	2106.00	0.95	1.57	-0.97
-0.50	1058.00	1.23	4.29	-0.11	1932.00	3.83	1.31	0.81
1.41	2383.00	1.89	3.63	0.01	3284.00	2.53	0.01	0.00
1.33	2100.00	2.19	3.33	0.06	3701.00	1.00	1.52	-0.94
0.03	2809.00	0.89	4.63	-0.17	3671.00	1.85	0.67	-0.41
0.67	3269.00	1.62	3.90	-0.04	4587.00	3.05	0.53	0.33
0.05	3832.00	1.20	4.32	-0.12	4628.00	3.98	1.46	0.90
-0.13	3269.00	2.78	2.74	0.17	3447.00	3.66	1.14	0.70
3.12	2498.00	3.76	1.76	0.35	4331.00	12.72	**10.20**	6.30
4.80	804.00	5.60	0.08	0.69	1297.00	9.10	**6.58**	4.06
-0.52	1784.00	0.62	4.90	-0.22	2421.00	2.52	0.00	0.00
-1.07	2866.00	2.51	3.01	0.12	2810.00	3.52	1.00	0.62
-0.23	1594.00	1.88	3.64	0.01	1767.00	3.28	0.76	0.47
-0.55	3375.00	2.46	3.06	0.11	4198.00	3.14	0.62	0.38
-0.68	1917.00	0.52	5.00	-0.24	1456.00	3.64	1.12	0.69
-1.01	1542.00	0.78	4.74	-0.19	1743.00	2.81	0.29	0.18
0.14	1756.00	0.11	5.41	-0.31	2682.00	2.13	0.39	-0.25
0.99	2759.00	2.07	3.45	0.04	3177.00	3.53	1.01	0.62

-0.09	2512.00	2.03	3.49	0.03	3029.00	4.19	1.67	1.03
-1.00	3621.00	1.55	3.97	-0.05	4516.00	1.62	0.90	-0.56
-0.53	3098.00	0.87	4.65	-0.18	4182.00	1.08	1.44	-0.89
-0.19	2921.00	0.34	5.18	-0.27	3042.00	2.33	0.19	-0.12
-0.16	2998.00	0.40	5.12	-0.26	2543.00	0.63	1.89	-1.17
-0.57	2896.00	1.24	4.28	-0.11	3986.00	3.14	0.62	0.38
-0.72	3370.00	0.89	4.63	-0.17	3051.00	2.06	0.46	-0.28
-0.27	2684.00	3.02	2.50	0.22	4012.00	5.58	3.06	1.89
-1.22	3050.00	1.34	4.18	-0.09	3884.00	1.78	0.74	-0.46
0.15	2855.00	1.37	4.15	-0.09	3820.00	4.74	2.22	1.37
1.58	2098.00	0.86	4.66	-0.18	3949.00	3.14	0.62	0.38
-1.45	1669.00	1.26	4.26	-0.11	2455.00	4.03	1.51	0.93
-0.57	2230.00	0.36	5.16	-0.27	3053.00	5.67	3.15	1.94
2.02	2421.00	0.70	4.82	-0.21	2716.00	9.28	**6.76**	4.17
2.28	2272.00	4.71	0.81	0.52	2188.00	3.29	0.77	0.47
0.44	2595.00	1.00	4.52	-0.15	2586.00	1.39	1.13	-0.70
0.60	2042.00	3.43	2.09	0.29	1741.00	2.07	0.45	-0.28
0.08	1963.00	0.56	4.96	-0.23	2499.00	4.88	2.36	1.46
-0.08	1379.00	0.58	4.94	-0.23	1662.00	2.23	0.29	-0.18
-0.87	2491.00	0.36	5.16	-0.27	2866.00	3.63	1.11	0.68
-0.81	1105.00	0.27	5.25	-0.29	2538.00	2.29	0.23	-0.15
-0.69	1630.00	0.43	5.09	-0.26	2032.00	2.36	0.16	-0.10
1.03	2115.00	1.99	3.53	0.03	2955.00	5.04	2.52	1.56
-0.70	1843.00	0.87	4.65	-0.18	1755.00	1.99	0.53	-0.33
-0.35	1927.00	0.67	4.85	-0.21	1945.00	4.32	1.80	1.11
-1.43	3339.00	0.45	5.07	-0.25	1855.00	3.34	0.82	0.51
0.11	2232.00	0.27	5.25	-0.29	3706.00	1.81	0.71	-0.44
3.58	4847.00	1.44	4.08	-0.07	5225.00	6.53	**4.01**	2.47
-1.07	2031.00	0.15	5.37	-0.31	3347.00	1.46	1.06	-0.65
2.71	3439.00	0.87	4.65	-0.18	4904.00	10.42	**7.90**	4.88
1.45	1700.00	0.88	4.64	-0.17	3074.00	2.67	0.15	0.09
0.44	1515.00	2.71	2.81	0.16	2467.00	6.32	**3.80**	2.35
-0.16	1827.00	0.66	4.86	-0.22	2158.00	7.28	**4.76**	2.94
-0.40	2441.00	0.98	4.54	-0.16	2986.00	2.51	0.01	-0.01
3.69	2445.00	2.82	2.70	0.18	2907.00	6.12	**3.60**	2.22
-0.80	1816.00	3.14	2.38	0.24	1881.00	6.22	**3.70**	2.28
-0.09	2361.00	0.34	5.18	-0.27	3098.00	5.29	2.77	1.71
-0.36	2173.00	0.97	4.55	-0.16	4081.00	4.26	1.74	1.07
3.88	2274.00	4.13	1.39	0.42	3376.00	15.11	**12.59**	7.77
-0.63	777.00	0.77	4.75	-0.19	1869.00	4.65	2.13	1.32
-0.52	1427.00	1.26	4.26	-0.11	2825.00	2.97	0.45	0.28
2.64	2504.00	0.68	4.84	-0.21	4039.00	7.43	**4.91**	3.03
-0.54	3584.00	2.68	2.84	0.15	2752.00	7.01	**4.49**	2.77
-0.14	1840.00	0.27	5.25	-0.29	1913.00	3.76	1.24	0.77
1.75	1942.00	2.32	3.20	0.09	2543.00	2.75	0.23	0.14
-0.67	2227.00	0.45	5.07	-0.25	1523.00	10.83	**8.31**	5.13
2.79	3390.00	0.77	4.75	-0.20	4606.00	2.78	0.26	0.16

-0.07	2036.00	1.82	3.70	0.00	2916.00	3.36	0.84	0.52
0.39	1861.00	1.99	3.53	0.03	2832.00	5.12	2.60	1.60
0.75	3761.00	3.67	1.85	0.33	3904.00	5.61	3.09	1.91
0.16	1929.00	0.73	4.79	-0.20	3816.00	3.62	1.10	0.68
0.01	3339.00	1.41	4.11	-0.08	3429.00	1.22	1.30	-0.80
0.49	3083.00	1.30	4.22	-0.10	2876.00	2.09	0.43	-0.27
-0.89	2220.00	0.59	4.93	-0.23	2813.00	1.88	0.64	-0.39
0.95	2530.00	1.46	4.06	-0.07	4381.00	5.20	2.68	1.66
-0.66	2365.00	1.31	4.21	-0.10	3801.00	1.97	0.55	-0.34
1.66	2985.00	4.32	1.20	0.45	3607.00	4.96	2.44	1.51
-0.96	2494.00	1.96	3.56	0.02	3696.00	3.81	1.29	0.80
0.12	2066.00	0.34	5.18	-0.27	4111.00	2.53	0.01	0.00
-0.32	2134.00	1.22	4.30	-0.11	3180.00	5.69	3.17	1.96
-0.79	1542.00	1.04	4.48	-0.15	1843.00	2.88	0.36	0.22
-1.10	2748.00	0.73	4.79	-0.20	4848.00	1.51	1.01	-0.63
-0.80	3432.00	0.26	5.26	-0.29	3871.00	4.21	1.69	1.04
-0.96	3494.00	1.75	3.77	-0.02	4351.00	2.32	0.20	-0.12
0.88	3049.00	1.05	4.47	-0.14	3857.00	3.86	1.34	0.83
-0.52	2457.00	1.42	4.10	-0.08	3687.00	1.19	1.33	-0.82
3.40	1434.00	2.86	2.66	0.19	1044.00	4.12	1.60	0.99
2.78	1509.00	2.65	2.87	0.15	2412.00	4.77	2.25	1.39
-0.03	1961.00	1.84	3.68	0.00	2417.00	2.32	0.20	-0.13
-0.51	3413.00	5.13	0.39	0.60	2786.00	1.44	1.08	-0.67
-0.92	1441.00	2.64	2.88	0.15	2494.00	1.92	0.60	-0.37
2.21	1741.00	3.56	1.96	0.31	2005.00	0.65	1.87	-1.16
-0.04	1692.00	5.26	0.26	0.62	1358.00	0.66	1.86	-1.15
1.00	2567.00	4.64	0.88	0.51	2033.00	1.03	1.49	-0.92
0.16	1151.00	1.91	3.61	0.01	955.00	3.25	0.73	0.45
0.41	1670.00	1.20	4.32	-0.12	1476.00	2.24	0.28	-0.18
-0.16	1341.00	3.50	2.02	0.30	1422.00	3.23	0.71	0.44
-0.27	2827.00	2.33	3.19	0.09	2334.00	1.67	0.85	-0.53
-0.41	1338.00	0.75	4.77	-0.20	1236.00	1.78	0.74	-0.46
-1.49	2069.00	1.31	4.22	-0.10	2044.00	0.54	1.98	-1.23
0.29	1157.00	1.82	3.71	0.00	466.00	3.86	1.34	0.83
0.09	1523.00	1.05	4.47	-0.14	1597.00	1.50	1.02	-0.63
-0.28	3351.00	2.72	2.80	0.16	2694.00	1.26	1.26	-0.78
-1.10	2128.00	0.61	4.91	-0.22	2214.00	0.77	1.75	-1.08
-0.72	1635.00	0.49	5.03	-0.25	2014.00	0.35	2.17	-1.34
-0.23	1256.00	2.15	3.37	0.06	1549.00	2.20	0.33	-0.20
	2513.00	1.84	3.70		2819.50	2.52	1.09	
		5.52	11.10				3.28	
			5.48				1.62	
2465.00	13.23		4268.00	16.40				
4794.00	14.21		4892.00	21.53				
					3665.00	13.04		
3653.00	15.08		4919.00	15.11				
3637.33	14.17		4693.00	17.68				

1164.58	0.93	368.31	3.39
1426.00	0.70	1859.00	3.17
1917.00	1.20	2727.00	2.49
1031.00	2.72	2596.00	3.78
831.00	1.81	2631.00	4.07
1259.67	1.91	2651.33	3.45
577.98	0.76	67.83	0.84
	2.79		10.18
	2.29		2.51
	5.08		12.70
	12.26		14.23
	0.41		0.89
	0.59		0.11
270.00	5.56	382.00	12.30
192.00	5.21	183.00	7.10
2070.00	1.64	3190.00	2.29
1839.00	1.09	2757.00	3.59
5544.00	1.79	5884.00	4.13
5399.00	1.78	6431.00	7.03

y

x debris a,b

x	debris a
x	toxic a,b,c

debris a.b

y

y

x debris a,b

y

y

Plate	Well	Gene		GeneID	Cell Count	% inf	Abs Dev
50056.00	A02	M-010656- DKFZP564J08	25923.00	DKFZP564J	2172.00	11.14	4.52
50056.00	A04	M-026577- zinc finger, D	25921.00	ZDHHC5	3492.00	8.25	1.63
50056.00	A05	M-009819- tetratricopep	23548.00	TTC33	3015.00	22.16	15.54
50056.00	A06	M-015839- cofactor of B	25920.00	RP13-122B	2568.00	5.37	1.25
50056.00	A07	M-005851- aspartyl amin	23549.00	DNPEP	3241.00	5.62	1.00
50056.00	A08	M-013963- THUMP doma	25917.00	THUMPD3	3866.00	12.73	6.11
50056.00	A09	M-009560- RASD family,	23551.00	RASD2	1400.00	7.29	0.67
50056.00	A10	M-027327- chromosome	25915.00	C3orf60	678.00	19.76	13.14
50056.00	A11	M-012447- hyaluronoglu	23553.00	HYAL4	876.00	14.73	8.11
50056.00	A12	M-031139- rotatin	25914.00	RTTN	3463.00	12.30	5.68
50056.00	A13	M-012466- tetraspanin 1	23554.00	TSPAN12	1956.00	8.79	2.17
50056.00	A14	M-013962- chromosome	25912.00	C1orf43	3881.00	11.31	4.69
50056.00	A15	M-017265- tetraspanin 1	23555.00	TSPAN15	2848.00	9.76	3.14
50056.00	A16	M-027328- deleted in a	25911.00	RP11-529I1	1364.00	15.32	8.70
50056.00	A17	M-012463- phosphatidyli	23556.00	PIGN	2351.00	8.17	1.55
50056.00	A18	M-013960- transmembra	25907.00	TMEM158	3175.00	10.99	4.37
50056.00	A19	M-015835- SNAP-associa	23557.00	SNAPAP	2890.00	13.46	6.84
50056.00	A20	M-020237- chromosome	25906.00	C11orf51	2006.00	5.43	1.19
50056.00	A21	M-012487- WW domain	23559.00	WBP1	2451.00	5.14	1.48
50056.00	A23	M-012467- GTP binding	23560.00	GTPBP4	2147.00	9.32	2.70
50056.00	B02	M-016642- chromosome	26355.00	C3orf28	2131.00	12.91	6.29
50056.00	B04	M-016319- guanine nucle	26354.00	GNL3	2037.00	7.41	0.79
50056.00	B05	M-013957- zinc finger pr	25925.00	ZNF521	1745.00	6.99	0.37
50056.00	B06	M-028212- olfactory rece	26339.00	OR5K1	2858.00	9.94	3.32
50056.00	B07	M-016695- nucleolar pro	25926.00	NOL11	2630.00	4.98	1.64
50056.00	B08	M-029877- olfactory rece	26338.00	OR5L2	2379.00	6.73	0.11
50056.00	B09	M-013958- chromosome	25927.00	C2orf32	1871.00	5.45	1.17
50056.00	B10	M-009671- glyceraldehy	26330.00	GAPDHS	2163.00	5.27	1.35
50056.00	B11	M-013959- sclerostin do	25928.00	SOSTDC1	2272.00	3.87	2.75
50056.00	B12	M-019153- globoside alp	26301.00	GBGT1	3237.00	7.57	0.95
50056.00	B13	M-013954- gem (nuclear	25929.00	GEMIN5	3304.00	2.00	4.62
50056.00	B14	M-013406- UDP-N-acetyl	26290.00	GALNT8	1977.00	5.26	1.36
50056.00	B15	M-013955- nipsnap hom	25934.00	NIPSNAP3	3914.00	8.41	1.79
50056.00	B16	M-013755- ankyrin repea	26287.00	ANKRD2	2869.00	1.01	5.61
50056.00	B17	M-016722- NSL1, MIND	25936.00	NSL1	2744.00	2.48	4.14
50056.00	B18	M-019991- claudin 17	26285.00	CLDN17	3958.00	5.23	1.39
50056.00	B19	M-016083- WW domain	25937.00	WWTR1	4286.00	2.92	3.70
50056.00	B20	M-007261- vacuolar prot	26276.00	VPS33B	4639.00	9.08	2.46
50056.00	B21	M-021927- HEAT repeat	25938.00	HEATR5A	4724.00	4.00	2.62
50056.00	B23	M-013950- SAM domain	25939.00	SAMHD1	3270.00	2.87	3.75
50056.00	C02	M-013968- CCR4-NOT tra	25904.00	CNOT10	4016.00	13.10	6.48
50056.00	C04	M-022077- olfactomedin	25903.00	OLFML2B	3655.00	1.89	4.73
50056.00	C05	M-012800- carbohydrate	23563.00	CHST5	4367.00	6.46	0.16

50056.00	C06	M-009949- methylenetet	25902.00	MTHFD1L	3882.00	4.74	1.88
50056.00	C07	M-009783- dimethylargir	23564.00	DDAH2	4974.00	5.25	1.37
50056.00	C08	M-012989- coiled-coil do	25901.00	CCDC28A	3494.00	1.32	5.30
50056.00	C09	M-012450- zinc finger pr	23567.00	ZNF346	4264.00	1.03	5.59
50056.00	C10	M-012988- hypothetical	25900.00	HOM-TES-1	3345.00	1.38	5.24
50056.00	C11	M-013074- ADP-ribosylat	23568.00	ARL2BP	3545.00	1.33	5.29
50056.00	C12	M-006966- ring finger an	25898.00	RCHY1	2778.00	1.33	5.29
50056.00	C13	M-012471- peptidyl argir	23569.00	PADI4	2070.00	1.01	5.61
50056.00	C14	M-006965- ring finger pr	25897.00	RNF19	2521.00	3.29	3.33
50056.00	C15	M-008528- dimethylargir	23576.00	DDAH1	3307.00	1.27	5.35
50056.00	C16	M-013971- family with se	25895.00	FAM119B	2851.00	0.56	6.06
50056.00	C17	M-020207- PEF protein w	23578.00	PEFLIN	2845.00	1.76	4.86
50056.00	C18	M-022573- pleckstrin hor	25894.00	PLEKHG4	3252.00	1.11	5.51
50056.00	C19	M-013494- CDC42 effect	23580.00	CDC42EP4	3005.00	3.09	3.53
50056.00	C20	M-013984- regeneration	25891.00	DKFZP586H	3156.00	1.87	4.75
50056.00	C21	M-012838- single-strand-	23583.00	SMUG1	3759.00	1.01	5.61
50056.00	C23	M-012510- transmembra	23585.00	TMEM50A	1836.00	1.42	5.20
50056.00	D02	M-007394- solute carrier	26266.00	SLC13A4	2696.00	6.08	0.54
50056.00	D04	M-009637- pallidin homc	26258.00	PLDN	3204.00	7.80	1.18
50056.00	D05	M-022655- family with se	25940.00	FAM98A	4209.00	23.45	**16.83**
50056.00	D06	M-020576- opticin	26254.00	OPTC	3042.00	5.85	0.77
50056.00	D07	M-013951- chromosome	25941.00	C18orf10	3755.00	3.60	3.02
50056.00	D08	M-021374- C-type lectin	26253.00	CLEC4E	3800.00	9.39	2.77
50056.00	D09	M-024236- chromosome	25943.00	C20orf194	4368.00	6.59	0.03
50056.00	D10	M-010911- kelch-like 3 (	26249.00	KLHL3	5105.00	10.66	4.04
50056.00	D11	M-013946- zinc finger pr	25946.00	ZNF385	4012.00	7.63	1.01
50056.00	D12	M-026236- olfactory rece	26248.00	OR2K2	2975.00	1.45	5.17
50056.00	D13	M-025313- kelch repeat	25948.00	KBTBD2	5182.00	8.07	1.45
50056.00	D14	M-027438- olfactory rece	26246.00	OR2L2	3801.00	7.81	1.19
50056.00	D15	M-020239- SYF2 homolo	25949.00	SYF2	2115.00	6.67	0.05
50056.00	D16	M-019978- family with se	26240.00	FAM50B	4693.00	11.34	4.72
50056.00	D17	M-016719- RWD domain	25950.00	RWDD3	4072.00	4.32	2.30
50056.00	D18	M-020580- chromosome	26238.00	C6orf123	6144.00	3.43	3.19
50056.00	D19	M-015028- chromosome	25957.00	C6orf111	5421.00	6.73	0.11
50056.00	D20	M-020583- chromosome	26236.00	C6orf54	4101.00	5.58	1.04
50056.00	D21	M-027345- ankyrin repea	25959.00	ANKRD25	2561.00	1.91	4.71
50056.00	D23	M-008749- nudix (nucleo	25961.00	NUDT13	2411.00	1.00	5.62
50056.00	E02	M-019470- ABI gene fam	25890.00	ABI3BP	5257.00	12.02	5.40
50056.00	E04	M-023781- zinc finger pr	25888.00	ZNF473	3547.00	9.75	3.13
50056.00	E05	M-012511- DEAD (Asp-Gl	23586.00	DDX58	5166.00	9.31	2.69
50056.00	E06	M-017717- WD repeat do	25886.00	WDR51A	4642.00	4.63	1.99
50056.00	E07	M-012839- kelch domain	23588.00	KLHDC2	4178.00	7.23	0.61
50056.00	E08	M-013983- polymerase (	25885.00	POLR1A	2874.00	6.26	0.36
50056.00	E09	M-020614- calcium regul	23589.00	CARHSP1	2912.00	2.44	4.18

50056.00	E10	M-013982- chordin-like 2	25884.00	CHRDL2	2727.00	6.34	0.28
50056.00	E11	M-008464- prenyl (deca	23590.00	PDSS1	2741.00	13.90	7.28
50056.00	E12	M-020236- transmembra	25880.00	TMEM186	1254.00	1.75	4.87
50056.00	E13	M-004376- apoptosis rel	23591.00	APR-2	1979.00	4.04	2.58
50056.00	E14	M-017898- WD repeats a	25879.00	WDSOF1	2483.00	2.09	4.53
50056.00	E15	M-006306- LEM domain	23592.00	LEMD3	1711.00	3.39	3.23
50056.00	E16	M-013988- matrix-remo	25878.00	MXRA5	2635.00	2.47	4.15
50056.00	E17	M-020612- heme binding	23593.00	HEBP2	4346.00	1.06	5.56
50056.00	E18	M-020233- brain protein	25874.00	BRP44	2587.00	1.12	5.50
50056.00	E19	M-003285- origin recogn	23595.00	ORC3L	3080.00	2.11	4.51
50056.00	E20	M-010130- ribosomal pr	25873.00	RPL36	587.00	1.19	5.43
50056.00	E21	M-021371- C-type lectin	23601.00	CLEC5A	1895.00	1.11	5.51
50056.00	E23	M-006959- makorin, ring	23608.00	MKRN1	1856.00	1.40	5.22
50056.00	F02	M-008434- T-cell lympho	26230.00	TIAM2	4059.00	4.31	2.31
50056.00	F04	M-012439- beta-1,3-gluc	26229.00	B3GAT3	3775.00	3.50	3.12
50056.00	F05	M-019278- KIAA1429	25962.00	KIAA1429	4208.00	5.75	0.87
50056.00	F06	M-029608- olfactory rec	26219.00	OR1J4	3526.00	7.03	0.41
50056.00	F07	M-018401- transmembra	25963.00	TMEM87A	3714.00	4.90	1.72
50056.00	F08	M-031855- olfactory rec	26212.00	OR2B6	2814.00	2.24	4.38
50056.00	F09	M-024375- chromosome	25966.00	C21orf25	5001.00	3.46	3.16
50056.00	F10	M-012476- phosphatidyli	26207.00	PITPNC1	4418.00	7.24	0.62
50056.00	F11	M-013947- SH2B adapto	25970.00	SH2B1	5722.00	16.15	**9.53**
50056.00	F12	M-012480- sperm associ	26206.00	SPAG8	3244.00	5.67	0.95
50056.00	F13	M-015937- unc-50 homo	25972.00	UNC50	3981.00	10.17	3.55
50056.00	F14	M-012470- glucocorticoi	26205.00	GMEB2	2675.00	6.13	0.49
50056.00	F15	M-016977- prolyl-tRNA s	25973.00	PARS2	3633.00	6.52	0.10
50056.00	F16	M-030679- olfactory rec	26184.00	OR1F2	3176.00	0.79	5.83
50056.00	F17	M-021789- methylmalon	25974.00	MMACHC	4697.00	6.64	0.02
50056.00	F18	M-021993- chromosome	26175.00	C14orf109	5263.00	17.52	**10.90**
50056.00	F19	M-017872- NECAP endo	25977.00	NECAP1	3473.00	6.39	0.23
50056.00	F20	M-025278- integrator co	26173.00	INTS1	2637.00	4.51	2.11
50056.00	F21	M-004700- chromatin m	25978.00	CHMP2B	3012.00	7.93	1.31
50056.00	F23	M-009732- dehydrogena	25979.00	DHRS7B	1690.00	2.49	4.13
50056.00	G02	M-013987- chromosome	25871.00	C3orf17	2470.00	4.94	1.68
50056.00	G04	M-010655- sulfatase mo	25870.00	SUMF2	4865.00	7.40	0.78
50056.00	G05	M-006960- makorin, ring	23609.00	MKRN2	3781.00	8.94	2.32
50056.00	G06	M-021274- abhydrolase	25864.00	ABHD14A	3868.00	8.20	1.58
50056.00	G07	M-009546- SH3-domain	23616.00	SH3BP1	4235.00	27.93	**21.31**
50056.00	G08	M-005945- ubiquitin spe	25862.00	USP49	3946.00	11.86	5.24
50056.00	G09	M-031995- zinc finger, im	23619.00	ZIM2	3316.00	10.01	3.39
50056.00	G10	M-026195- deafness, aut	25861.00	DFNB31	5049.00	11.19	4.57
50056.00	G11	M-003747- beta-site APP	23621.00	BACE1	1215.00	23.54	**16.92**
50056.00	G12	M-013380- prostate andr	25859.00	PART1	1426.00	8.98	2.36
50056.00	G13	M-020607- RUN and SH3	23623.00	RUSC1	3816.00	13.31	6.69

50056.00	G14	M-020230-	DKFZP586N0	25856.00	DKFZP586N	3726.00	11.76	5.14
50056.00	G15	M-009918-	carbonic anh	23632.00	CA14	1406.00	6.69	0.07
50056.00	G16	M-010497-	breast cancer	25855.00	BRMS1	3552.00	6.81	0.19
50056.00	G17	M-010923-	single-strand	23635.00	SSBP2	3261.00	8.65	2.03
50056.00	G18	M-012981-	WD repeat d	25853.00	WDR40A	2214.00	4.38	2.24
50056.00	G19	M-012803-	RAB GTPase	23637.00	RABGAP1	2813.00	11.84	5.22
50056.00	G20	M-021273-	DKFZP434B0	25851.00	DKFZP434	2689.00	9.48	2.86
50056.00	G21	M-018722-	leucine rich r	23639.00	LRRC6	3810.00	14.46	7.84
50056.00	G23	M-020298-	lymphocyte a	23643.00	LY96	2948.00	10.99	4.37
50056.00	H02	M-023473-	chromosome	26172.00	C3orf41	3212.00	6.38	0.24
50056.00	H04	M-006034-	SUMO1/sent	26168.00	SENP3	2233.00	7.79	1.17
50056.00	H05	M-015233-	chromosome	25980.00	C20orf4	2147.00	8.71	2.09
50056.00	H06	M-013890-	regulator of	26166.00	RGS22	2318.00	9.15	2.53
50056.00	H07	M-021915-	neuroguidin,	25983.00	NGDN	2288.00	8.87	2.25
50056.00	H08	M-013889-	family with s	26165.00	FAM75A7	1757.00	13.09	6.47
50056.00	H09	M-017334-	keratin 23 (hi	25984.00	KRT23	2719.00	12.58	5.96
50056.00	H10	M-013036-	GTP binding	26164.00	GTPBP5	1653.00	8.11	1.49
50056.00	H11	M-013949-	tsukushin	25987.00	TSKU	2770.00	8.01	1.39
50056.00	H12	M-022650-	intraflagellar	26160.00	IFT172	1650.00	4.73	1.89
50056.00	H13	M-023183-	sushi, nidoge	25992.00	SNED1	2492.00	8.75	2.13
50056.00	H14	M-013032-	GTPase, IMA	26157.00	GIMAP2	3035.00	14.14	7.52
50056.00	H15	M-020245-	REX2, RNA ex	25996.00	REXO2	2030.00	7.54	0.92
50056.00	H16	M-022489-	ribosomal L1	26156.00	RSL1D1	2343.00	7.73	1.11
50056.00	H17	M-028643-	inhibitor of B	25998.00	IBTK	2858.00	6.16	0.46
50056.00	H18	M-020539-	nucleolar con	26155.00	NOC2L	1945.00	5.09	1.53
50056.00	H19	M-016723-	TBC1 domain	26000.00	TBC1D10B	2958.00	12.85	6.23
50056.00	H20	M-006970-	zinc finger pr	26152.00	ZNF337	3209.00	5.67	0.95
50056.00	H21	M-006967-	ring finger pr	26001.00	RNF167	3209.00	10.28	3.66
50056.00	H23	M-009446-	monooxygen	26002.00	MOXD1	3253.00	8.52	1.90
50056.00	I02	M-017731-	zinc finger pr	25850.00	ZNF345	5233.00	10.20	3.58
50056.00	I04	M-020227-	DKFZP564O0	25849.00	DKFZP564	5107.00	9.61	2.99
50056.00	I05	M-016635-	enhancer of r	23644.00	EDC4	4225.00	13.44	6.82
50056.00	I06	M-021271-	anaphase pro	25847.00	ANAPC13	5474.00	9.41	2.79
50056.00	I07	M-009659-	phospholipas	23646.00	PLD3	5210.00	11.82	5.20
50056.00	I08	M-013995-	Yip1 domain	25844.00	YIPF3	4070.00	15.06	8.44
50056.00	I09	M-015513-	single strand	23648.00	SSBP3	2522.00	9.04	2.42
50056.00	I10	M-020224-	preimplantati	25843.00	PREI3	2927.00	10.63	4.01
50056.00	I11	M-016027-	polymerase (	23649.00	POLA2	3054.00	12.34	5.72
50056.00	I12	M-020222-	ASF1 anti-sile	25842.00	ASF1A	3629.00	8.79	2.17
50056.00	I13	M-012409-	tripartite mo	23650.00	TRIM29	2151.00	6.09	0.53
50056.00	I14	M-013994-	methyltransf	25840.00	METTL7A	2517.00	11.32	4.70
50056.00	I15	M-031513-	plexin B2	23654.00	PLXNB2	1993.00	8.13	1.51
50056.00	I16	M-020586-	mannosyl (al	25834.00	MGAT4C	2830.00	9.05	2.43
50056.00	I17	M-007612-	solute carrier	23657.00	SLC7A11	3765.00	11.98	5.36

50056.00	I18	M-020218- neuroblaston	25832.00	NBPF14	3230.00	12.07	5.45
50056.00	I19	M-019555- LSM5 homolo	23658.00	LSM5	2060.00	12.57	5.95
50056.00	I20	M-010393- sulfotransfera	25830.00	SULT4A1	2784.00	11.24	4.62
50056.00	I21	M-020348- transmembra	23670.00	TMEM2	3174.00	9.07	2.45
50056.00	I23	M-010654- transmembra	23671.00	TMEFF2	2612.00	11.95	5.33
50056.00	J02	M-017635- N-acetyltrans	26151.00	NAT9	2453.00	2.69	3.93
50056.00	J04	M-013891- RIB43A doma	26150.00	RIBC2	2695.00	4.53	2.09
50056.00	J05	M-019045- golgi reassem	26003.00	GORASP2	2858.00	5.39	1.23
50056.00	J06	M-014109- zinc finger pr	26149.00	ZNF658	3191.00	7.68	1.06
50056.00	J07	M-026690- hypothetical	26005.00	DKFZP586F	2125.00	2.31	4.31
50056.00	J08	M-015742- chromosome	26148.00	C10orf12	2499.00	4.56	2.06
50056.00	J09	M-013939- zinc finger, ZZ	26009.00	ZZZ3	1708.00	2.28	4.34
50056.00	J10	M-026200- PHD finger pr	26147.00	PHF19	2106.00	1.38	5.24
50056.00	J11	M-020248- viral DNA pol	26010.00	LOC26010	2790.00	9.28	2.66
50056.00	J12	M-015848- TNF receptor-	26146.00	TRAF3IP1	3180.00	6.51	0.11
50056.00	J13	M-026701- odz, odd Oz/t	26011.00	ODZ4	4287.00	4.74	1.88
50056.00	J14	M-006969- interferon reg	26145.00	IRF2BP1	3731.00	3.19	3.43
50056.00	J15	M-016760- nasal embryo	26012.00	NELF	3595.00	11.88	5.26
50056.00	J16	M-020535- tubulin tyrosi	26140.00	TTLL3	5038.00	9.37	2.75
50056.00	J17	M-013544- l(3)mbt-like (l	26013.00	L3MBTL	4045.00	3.58	3.04
50056.00	J18	M-020529- zinc finger an	26137.00	ZBTB20	3806.00	5.62	1.00
50056.00	J19	M-017328- RNA polymer	26015.00	RPAP1	2812.00	4.52	2.10
50056.00	J20	M-013026- testis derived	26136.00	TES	4315.00	8.71	2.09
50056.00	J21	M-020251- family with se	26017.00	FAM32A	6196.00	8.46	1.84
50056.00	J23	M-012993- UPF2 regulat	26019.00	UPF2	4066.00	4.35	2.27
50056.00	K02	M-016076- chromosome	25829.00	C22orf5	5348.00	13.26	6.64
50056.00	K04	M-017448- thioredoxin 2	25828.00	TXN2	1944.00	4.37	2.25
50056.00	K05	M-018246- syntaxin 12	23673.00	STX12	3951.00	9.47	2.85
50056.00	K06	M-003802- beta-site APP	25825.00	BACE2	3433.00	6.52	0.10
50056.00	K07	M-020606- small muscle	23676.00	SMPX	4658.00	15.11	8.49
50056.00	K08	M-019102- peroxiredoxir	25824.00	PRDX5	3412.00	5.25	1.37
50056.00	K09	M-008507- potassium vo	23704.00	KCNE4	2587.00	5.30	1.32
50056.00	K10	M-006058- tryptase gam	25823.00	TPSG1	3551.00	6.17	0.45
50056.00	K11	M-016565- cell adhesion	23705.00	CADM1	2380.00	3.45	3.17
50056.00	K12	M-016492- DnaJ (Hsp40)	25822.00	DNAJB5	3034.00	5.34	1.28
50056.00	K13	M-020400- G1 to S phase	23708.00	GSPT2	1934.00	4.60	2.02
50056.00	K14	M-010190- mitochondria	25821.00	MTO1	2192.00	5.98	0.64
50056.00	K15	M-014764- chromosome	23731.00	C9orf5	3233.00	7.08	0.46
50056.00	K16	M-012414- CCR4 carbon	25819.00	CCRN4L	2618.00	8.82	2.20
50056.00	K17	M-026185- chromosome	23732.00	C9orf4	3001.00	6.86	0.24
50056.00	K18	M-005916- kallikrein-rela	25818.00	KLK5	2463.00	4.47	2.15
50056.00	K19	M-003258- EP300 interac	23741.00	EID1	2077.00	3.32	3.30
50056.00	K20	M-013997- family with se	25817.00	FAM19A5	4965.00	21.91	**15.29**
50056.00	K21	M-021248- chromosome	23742.00	C15orf2	2853.00	8.80	2.18

50056.00	K23	M-010395- betaine-hom	23743.00	BHMT2	2030.00	6.90	0.28
50056.00	L02	M-020528- SERPINE1 mR	26135.00	SERBP1	1947.00	2.11	4.51
50056.00	L04	M-021384- transient rece	26133.00	TRPC4AP	2933.00	12.62	6.00
50056.00	L05	M-021366- pentatricope	26024.00	PTCD1	2648.00	3.06	3.56
50056.00	L06	M-026206- GTPase activ	26130.00	GAPVD1	3579.00	13.44	6.82
50056.00	L07	M-022051- pleckstrin ho	26030.00	PLEKHG3	2841.00	9.54	2.92
50056.00	L08	M-013896- KIAA1279	26128.00	KIAA1279	2644.00	11.01	4.39
50056.00	L09	M-009380- oxysterol bin	26031.00	OSBPL3	3356.00	8.49	1.87
50056.00	L10	M-013895- FGFR1 oncog	26127.00	FGFR1OP2	2910.00	11.72	5.10
50056.00	L11	M-023461- sushi domain	26032.00	SUSD5	1615.00	6.19	0.43
50056.00	L12	M-013900- chromosome	26123.00	C10orf61	3485.00	10.04	3.42
50056.00	L13	M-026316- attractin-like	26033.00	ATRNL1	2994.00	13.83	7.21
50056.00	L14	M-016776- enhancer of	26122.00	EPC2	2183.00	13.19	6.57
50056.00	L15	M-027160- phosphoinosi	26034.00	PIP3-E	3106.00	17.32	**10.70**
50056.00	L16	M-013015- WD repeat a	26118.00	WSB1	3169.00	16.03	**9.41**
50056.00	L17	M-022261- glucuronic ac	26035.00	GLCE	3551.00	9.07	2.45
50056.00	L18	M-029428- DKFZP434M1	26117.00	DKFZP434	3799.00	13.14	6.52
50056.00	L19	M-013935- zinc finger pr	26036.00	ZNF451	6021.00	23.07	**16.45**
50056.00	L20	M-030921- tetratricopep	26115.00	TANC2	3075.00	13.33	6.71
50056.00	L21	M-013936- signal-induce	26037.00	SIPA1L1	3765.00	13.89	7.27
50056.00	L23	M-009878- chromodoma	26038.00	CHD5	2213.00	6.91	0.29
50056.00	M02	M-020593- ataxin 10	25814.00	ATXN10	2809.00	4.70	1.92
50056.00	M04	M-017871- sorting and a	25813.00	SAMM50	3920.00	2.73	3.89
50056.00	M05	M-004708- stromal cell-	23753.00	SDF2L1	3864.00	8.57	1.95
50056.00	M06	M-009556- tubulin tyrosi	25809.00	TTLL1	3256.00	5.80	0.82
50056.00	M07	M-007205- peptidylproly	23759.00	PPIL2	2894.00	5.01	1.61
50056.00	M08	M-019752- rhomboid do	25807.00	RHBDD3	1455.00	4.67	1.95
50056.00	M09	M-006459- phosphatidyli	23760.00	PITPNB	2113.00	4.02	2.60
50056.00	M10	M-019596- BMP and acti	25805.00	BAMBI	3393.00	5.04	1.58
50056.00	M11	M-009548- phosphatidyl	23761.00	PISD	3053.00	4.16	2.46
50056.00	M12	M-017025- LSM4 homol	25804.00	LSM4	2270.00	4.98	1.64
50056.00	M13	M-009096- oxysterol bin	23762.00	OSBP2	2215.00	2.48	4.14
50056.00	M14	M-012438- grancalcin, EF	25801.00	GCA	1629.00	5.89	0.73
50056.00	M15	M-010090- fibronectin le	23767.00	FLRT3	2508.00	9.25	2.63
50056.00	M16	M-007572- solute carrier	25800.00	SLC39A6	1559.00	2.76	3.86
50056.00	M17	M-009104- fibronectin le	23768.00	FLRT2	1883.00	4.94	1.68
50056.00	M18	M-006964- zinc finger pr	25799.00	ZNF324	2059.00	13.50	6.88
50056.00	M19	M-010103- fibronectin le	23769.00	FLRT1	1509.00	7.69	1.07
50056.00	M20	M-020217- brain protein	25798.00	BRI3	3401.00	11.79	5.17
50056.00	M21	M-006963- bromodomai	23774.00	BRD1	3579.00	12.18	5.56
50056.00	M23	M-007371- mitochondria	23788.00	MTCH2	1935.00	11.89	5.27
50056.00	N02	M-013899- coiled-coil do	26112.00	CCDC69	2991.00	9.36	2.74
50056.00	N04	M-013908- pygopus hom	26108.00	PYGO1	4222.00	11.01	4.39
50056.00	N05	M-013929- synovial sarc	26039.00	SS18L1	3909.00	17.60	**10.98**

50056.00	N06	M-027968- DKFZP586K1	26106.00	DKFZP586K	4517.00	17.62	**11.00**
50056.00	N07	M-013930- SET binding p	26040.00	SETBP1	3402.00	22.11	**15.49**
50056.00	N08	M-013907- leucine rich r	26103.00	LRRC21	3604.00	8.02	1.40
50056.00	N09	M-023533- UBX domain	26043.00	UBXD7	3081.00	4.51	2.11
50056.00	N10	M-020521- WD repeat d	26100.00	WIPI2	2976.00	6.01	0.61
50056.00	N11	M-006968- zinc finger pr	26046.00	ZNF294	3548.00	23.48	**16.86**
50056.00	N12	M-013910- chromosome	26099.00	C1orf144	2661.00	5.52	1.10
50056.00	N13	M-022625- zinc finger pr	26048.00	ZNF500	3834.00	14.97	8.35
50056.00	N14	M-013017- chromosome	26098.00	C10orf137	3104.00	7.57	0.95
50056.00	N15	M-024510- KIAA0888 prc	26049.00	KIAA0888	2779.00	9.25	2.63
50056.00	N16	M-017681- chromosome	26097.00	C1orf77	2798.00	9.15	2.53
50056.00	N17	M-021578- SLIT and NTR	26050.00	SLITRK5	4246.00	5.77	0.85
50056.00	N18	M-013909- protein tyrosi	26095.00	PTPN20B	3502.00	10.71	4.09
50056.00	N19	M-013931- dynamin 3	26052.00	DNM3	5252.00	22.53	**15.91**
50056.00	N20	M-013016- WD repeat d	26094.00	WDR21A	6457.00	18.32	**11.70**
50056.00	N21	M-006044- SUMO1/sent	26054.00	SENP6	3323.00	8.13	1.51
50056.00	N23	M-004298- RAB11 family	26056.00	RAB11FIP5	2647.00	3.78	2.84
50056.00	O02	M-012474- glutaminyl-pe	25797.00	QPCT	3698.00	13.85	7.23
50056.00	O04	M-020023- 6-phosphoglu	25796.00	PGLS	2400.00	9.54	2.92
50056.00	O05	M-019887- echinoderm r	24139.00	EML2	1760.00	8.30	1.68
50056.00	O06	M-009354- neuronal gua	25791.00	NGEF	1908.00	9.38	2.76
50056.00	O07	M-019966- tuftelin intera	24144.00	TFIP11	2074.00	8.20	1.58
50056.00	O08	M-019578- coiled-coil do	25790.00	CCDC19	1689.00	3.08	3.54
50056.00	O09	M-015596- claudin 15	24146.00	CLDN15	1478.00	4.26	2.36
50056.00	O10	M-012412- transmembra	25789.00	TMEM59L	2737.00	9.86	3.24
50056.00	O11	M-012512- four jointed b	24147.00	FJX1	710.00	2.39	4.23
50056.00	O12	M-015687- KIAA0889 prc	25781.00	KIAA0889	2609.00	9.28	2.66
50056.00	O13	M-012821- PRP6 pre-mR	24148.00	PRPF6	968.00	3.93	2.69
50056.00	O14	M-009959- unc-84 homo	25777.00	UNC84B	2823.00	2.69	3.93
50056.00	O15	M-020601- zinc finger pr	24149.00	ZNF318	1985.00	4.18	2.44
50056.00	O16	M-017047- chibby homol	25776.00	CBY1	1852.00	1.35	5.27
50056.00	O17	M-025036- chromosome	25763.00	CXorf27	2928.00	2.19	4.43
50056.00	O18	M-020281- glutathione S	25774.00	HS322B1A	3768.00	1.06	5.56
50056.00	O19	M-016841- Huntingtin int	25764.00	HYPK	3386.00	3.07	3.55
50056.00	O20	M-009319- TBC1 domain	25771.00	TBC1D22A	1588.00	1.57	5.05
50056.00	O21	M-007465- solute carrier	25769.00	SLC24A2	2593.00	3.70	2.92
50056.00	O23	M-020284- chromosome	25770.00	C22orf31	2241.00	5.53	1.09
50056.00	P02	M-020279- coiled-coil do	26093.00	CCDC9	1013.00	4.64	1.98
50056.00	P04	M-013913- torsin A inter	26092.00	TOR1AIP1	1719.00	4.48	2.14
50056.00	P05	M-013554- ankyrin repea	26057.00	ANKRD17	1234.00	3.32	3.30
50056.00	P06	M-005850- abhydrolase	26090.00	ABHD12	1406.00	2.92	3.70
50056.00	P07	M-013918- trinucleotide	26058.00	TNRC15	1958.00	3.68	2.94
50056.00	P08	M-013694- golgi associat	26088.00	GGA1	1621.00	1.48	5.14
50056.00	P09	M-019772- 2-hydroxyacy	26061.00	HACL1	2103.00	1.38	5.24

50056.00	P10	M-019350-	G-protein sig	26086.00	GPSM1	2111.00	0.95	5.67
50056.00	P11	M-013919-	retinoic acid i	26064.00	RAI14	2359.00	1.14	5.48
50056.00	P12	M-005910-	kallikrein-rela	26085.00	KLK13	3012.00	1.76	4.86
50056.00	P13	M-013920-	LSM14A, SCD	26065.00	LSM14A	978.00	2.05	4.58
50056.00	P14	M-020274-	DKFZP434O0	26083.00	DKFZP434	1747.00	1.43	5.19
50056.00	P15	M-020268-	family with se	26071.00	FAM127B	2656.00	0.98	5.64
50056.00	P16	M-030372-	DKFZP434L1	26082.00	DKFZP434L	2362.00	0.93	5.69
50056.00	P17	M-013009-	polymerase (	26073.00	POLDIP2	3357.00	1.16	5.46
50056.00	P18	M-030267-	DKFZP434B0	26080.00	DKFZP434	2994.00	0.63	5.99
50056.00	P19	M-007320-	ion transport	25947.00	DKFZP434	4226.00	0.99	5.63
50056.00	P20	M-013921-	chromosome	26074.00	C20orf26	2836.00	0.81	5.81
50056.00	P21	M-020324-	peptide YY, 2	23615.00	PYY2	2477.00	1.17	5.45
50056.00	P23	M-013231-	ribosomal pr	51065.00	RPS27L	3250.00	0.43	6.19
						2953.00	6.62	3.08
								9.24
						MADc		4.56
50056.00	C22					1955.00	20.72	
50056.00	D22					1871.00	21.33	
50056.00	E22			1567.00	9.51			
50056.00	F22			2119.00	49.13			
					mn	1913.00	21.02	
					sd	59.40	0.43	
50056.00	G22					936.00	6.52	
50056.00	H22					882.00	5.56	
50056.00	I22			434.00	13.59			
50056.00	J22					1308.00	2.22	
					mn	1095.00	3.89	
					sd	301.23	2.36	
					3psSD		1.29	
					3ngSD		7.08	
					SumSD		8.37	
					DiffMn		17.13	
					SmovrDiff		0.49	
					1minus		0.51	
50056.00	G03	M-003290-	polo-like kina	5347.00	PLK1 SMA	310.00	19.03	
50056.00	H03	M-003290-	polo-like kina	5347.00	PLK1 SMA	136.00	11.77	
50056.00	I03	D-001206-	siControl non-targeting s			4529.00	10.86	
50056.00	J03	D-001206-	siControl non-targeting s			1858.00	6.08	
50056.00	K03	D-001600-	siGLO RISC-free siRNA			4638.00	9.38	
50056.00	L03	D-001600-	siGLO RISC-free siRNA			4347.00	15.39	

rZ	**Cell Count**	**% inf**	**Abs Dev**	**rZ**	**Cell Count**	**% inf**	**Abs Dev**	**rZ**
0.99	1546.00	9.90	4.30	1.08	1035.00	3.19	0.19	0.08
0.36	2050.00	5.90	0.30	0.08	1822.00	1.32	1.68	-0.70
3.41	2101.00	10.00	4.40	1.10	764.00	6.54	3.54	1.48
-0.27	1000.00	3.00	2.60	-0.65	1073.00	0.65	2.35	-0.98
-0.22	1916.00	4.18	1.42	-0.36	1723.00	3.37	0.37	0.15
1.34	2474.00	6.99	1.39	0.35	2420.00	2.02	0.98	-0.41
0.15	1590.00	3.08	2.52	-0.63	573.00	5.76	2.76	1.15
2.88	2629.00	7.57	1.97	0.49	1574.00	5.40	2.40	1.00
1.78	797.00	10.92	5.32	1.33	656.00	3.81	0.81	0.34
1.25	2659.00	3.23	2.37	-0.59	2034.00	1.38	1.62	-0.68
0.48	894.00	9.40	3.80	0.95	1326.00	3.39	0.39	0.16
1.03	2565.00	3.08	2.52	-0.63	2086.00	2.21	0.79	-0.33
0.69	3447.00	6.35	0.75	0.19	1313.00	6.40	3.40	1.42
1.91	1295.00	7.72	2.12	0.53	742.00	7.01	4.01	1.67
0.34	2477.00	2.46	3.14	-0.79	1686.00	1.07	1.93	-0.81
0.96	2162.00	6.20	0.60	0.15	1224.00	5.23	2.23	0.93
1.50	1822.00	5.82	0.22	0.06	1756.00	2.45	0.55	-0.23
-0.26	1047.00	3.92	1.68	-0.42	1709.00	2.81	0.19	-0.08
-0.32	1013.00	2.47	3.13	-0.78	1428.00	1.96	1.04	-0.43
0.59	1053.00	1.42	4.18	-1.05	1222.00	1.31	1.69	-0.71
1.38	1352.00	0.59	5.01	-1.25	1088.00	5.06	2.06	0.86
0.17	2187.00	1.55	4.05	-1.01	1906.00	4.20	1.20	0.50
0.08	2881.00	1.80	3.80	-0.95	1576.00	4.12	1.12	0.47
0.73	2713.00	2.36	3.24	-0.81	3081.00	6.49	3.49	1.46
-0.36	2198.00	0.59	5.01	-1.25	1830.00	3.44	0.44	0.18
0.02	1616.00	4.83	0.77	-0.19	1427.00	3.29	0.29	0.12
-0.26	2631.00	2.43	3.17	-0.79	1732.00	4.04	1.04	0.43
-0.30	1743.00	3.21	2.39	-0.60	1254.00	1.12	1.88	-0.79
-0.60	2463.00	3.09	2.51	-0.63	1190.00	3.95	0.95	0.40
0.21	1826.00	5.20	0.40	-0.10	2545.00	8.88	5.88	2.45
-1.01	2599.00	0.73	4.87	-1.22	2396.00	2.50	0.50	-0.21
-0.30	1128.00	2.39	3.21	-0.80	882.00	1.47	1.53	-0.64
0.39	2164.00	5.04	0.56	-0.14	1552.00	3.87	0.87	0.36
-1.23	2695.00	1.60	4.00	-1.00	1437.00	2.64	0.36	-0.15
-0.91	2073.00	6.27	0.67	0.17	1882.00	2.44	0.56	-0.23
-0.30	3500.00	5.14	0.46	-0.11	2159.00	2.32	0.68	-0.29
-0.81	3422.00	5.20	0.40	-0.10	4308.00	4.64	1.64	0.69
0.54	2457.00	3.05	2.55	-0.64	3892.00	7.37	4.37	1.83
-0.57	2242.00	2.50	3.10	-0.78	3733.00	2.76	0.24	-0.10
-0.82	1837.00	2.29	3.31	-0.83	2091.00	1.05	1.95	-0.81
1.42	2358.00	24.81	19.21	4.81	1662.00	18.89	15.89	6.64
-1.04	3133.00	7.47	1.87	0.47	2294.00	7.50	4.50	1.88
-0.04	2938.00	16.61	11.01	2.76	2412.00	9.25	6.25	2.61

-0.41	2159.00	7.46	1.86	0.47	2673.00	4.75	1.75	0.73
-0.30	2072.00	10.18	4.58	1.15	1695.00	11.03	**8.03**	3.35
-1.16	3272.00	9.69	4.09	1.03	2513.00	5.93	2.93	1.22
-1.23	3648.00	4.17	1.43	-0.36	2954.00	2.17	0.83	-0.35
-1.15	2920.00	5.55	0.05	-0.01	1627.00	4.73	1.73	0.72
-1.16	2564.00	10.84	5.24	1.31	2391.00	6.61	3.61	1.51
-1.16	1270.00	4.25	1.35	-0.34	2041.00	3.18	0.18	0.08
-1.23	1580.00	3.42	2.18	-0.55	2528.00	3.80	0.80	0.33
-0.73	1503.00	6.45	0.85	0.21	1668.00	6.18	3.18	1.33
-1.17	2647.00	7.25	1.65	0.42	2351.00	2.42	0.58	-0.24
-1.33	1503.00	1.33	4.27	-1.07	1288.00	1.79	1.21	-0.51
-1.07	2362.00	2.84	2.76	-0.69	2101.00	0.81	2.19	-0.92
-1.21	1537.00	4.81	0.79	-0.20	2706.00	1.92	1.08	-0.45
-0.77	2182.00	8.34	2.74	0.69	1669.00	6.89	3.89	1.62
-1.04	2566.00	4.56	1.04	-0.26	2164.00	1.89	1.11	-0.46
-1.23	2816.00	3.69	1.91	-0.48	2819.00	1.88	1.12	-0.47
-1.14	2310.00	3.55	2.05	-0.51	1450.00	1.38	1.62	-0.68
-0.12	3759.00	3.91	1.69	-0.42	2676.00	4.63	1.63	0.68
0.26	3712.00	5.50	0.10	-0.03	2990.00	7.12	4.12	1.72
3.69	2527.00	10.72	5.12	1.28	3354.00	21.14	**18.14**	7.57
-0.17	3320.00	2.92	2.68	-0.67	2728.00	4.22	1.22	0.51
-0.66	2715.00	2.14	3.46	-0.87	2607.00	3.87	0.87	0.36
0.61	3766.00	7.25	1.65	0.41	2033.00	4.43	1.43	0.60
-0.01	2409.00	2.37	3.23	-0.81	1862.00	2.58	0.42	-0.18
0.89	3638.00	5.00	0.60	-0.15	2425.00	2.35	0.65	-0.27
0.22	3513.00	4.36	1.24	-0.31	3244.00	4.25	1.25	0.52
-1.13	2629.00	1.94	3.66	-0.92	1158.00	0.95	2.05	-0.86
0.32	4846.00	6.19	0.59	0.15	3297.00	6.79	3.79	1.58
0.26	1911.00	3.40	2.20	-0.55	1467.00	3.41	0.41	0.17
0.01	2124.00	4.76	0.84	-0.21	471.00	1.27	1.73	-0.72
1.04	4244.00	8.29	2.69	0.68	2159.00	8.75	**5.75**	2.40
-0.50	2277.00	1.80	3.80	-0.95	1466.00	1.36	1.64	-0.68
-0.70	4653.00	1.10	4.50	-1.13	2548.00	1.88	1.12	-0.47
0.03	2501.00	1.56	4.04	-1.01	2247.00	1.87	1.13	-0.47
-0.23	3311.00	2.90	2.70	-0.68	2284.00	3.63	0.63	0.26
-1.03	3026.00	3.04	2.56	-0.64	2162.00	1.20	1.80	-0.75
-1.23	2411.00	1.78	3.82	-0.96	1023.00	1.47	1.53	-0.64
1.19	3361.00	4.58	1.02	-0.25	2887.00	2.63	0.37	-0.15
0.69	1265.00	0.79	4.81	-1.20	1167.00	1.63	1.37	-0.57
0.59	2277.00	5.62	0.02	0.01	2875.00	2.96	0.04	-0.02
-0.44	2134.00	2.44	3.16	-0.79	2016.00	0.55	2.45	-1.03
0.13	1613.00	2.98	2.62	-0.66	2826.00	2.65	0.35	-0.15
-0.08	1516.00	2.97	2.63	-0.66	1302.00	3.00	0.00	0.00
-0.92	1351.00	1.55	4.05	-1.01	1294.00	1.39	1.61	-0.67

-0.06	1089.00	4.96	0.64	-0.16	1663.00	3.01	0.01	0.00
1.60	1662.00	4.63	0.97	-0.24	2306.00	3.77	0.77	0.32
-1.07	788.00	0.89	4.71	-1.18	1561.00	3.01	0.01	0.00
-0.57	539.00	3.15	2.45	-0.61	1297.00	2.70	0.30	-0.13
-0.99	939.00	3.19	2.41	-0.60	1774.00	3.78	0.78	0.32
-0.71	1106.00	2.89	2.71	-0.68	1166.00	2.14	0.86	-0.36
-0.91	2444.00	1.80	3.80	-0.95	2490.00	0.96	2.04	-0.85
-1.22	1614.00	3.28	2.32	-0.58	1762.00	4.26	1.26	0.52
-1.21	940.00	0.74	4.86	-1.22	1834.00	2.84	0.16	-0.07
-0.99	2048.00	2.83	2.77	-0.69	2982.00	3.52	0.52	0.22
-1.19	490.00	2.24	3.36	-0.84	751.00	0.80	2.20	-0.92
-1.21	1739.00	2.42	3.18	-0.80	1881.00	2.82	0.18	-0.08
-1.14	1305.00	1.38	4.22	-1.06	1959.00	2.04	0.96	-0.40
-0.51	4191.00	3.36	2.24	-0.56	3562.00	1.57	1.43	-0.60
-0.68	3582.00	3.29	2.31	-0.58	2465.00	1.10	1.90	-0.80
-0.19	2780.00	2.27	3.33	-0.83	3671.00	3.05	0.05	0.02
0.09	3549.00	7.19	1.59	0.40	3222.00	4.62	1.62	0.68
-0.38	2320.00	3.71	1.89	-0.47	2120.00	1.84	1.16	-0.49
-0.96	2650.00	5.92	0.32	0.08	1816.00	1.87	1.13	-0.47
-0.69	3048.00	8.50	2.90	0.73	2327.00	1.59	1.41	-0.59
0.14	2626.00	8.07	2.47	0.62	1763.00	1.93	1.07	-0.45
2.09	3919.00	13.83	**8.23**	2.06	3527.00	6.58	3.58	1.49
-0.21	2046.00	6.11	0.51	0.13	2052.00	1.56	1.44	-0.60
0.78	2955.00	13.40	7.80	1.96	2251.00	7.02	4.02	1.68
-0.11	2686.00	6.07	0.47	0.12	1489.00	0.94	2.06	-0.86
-0.02	2823.00	8.82	3.22	0.81	1901.00	1.32	1.68	-0.70
-1.28	2065.00	5.96	0.36	0.09	1703.00	1.35	1.65	-0.69
0.01	2533.00	4.62	0.98	-0.24	3758.00	4.07	1.07	0.45
2.39	2823.00	14.88	**9.28**	2.33	3634.00	8.15	**5.15**	2.15
-0.05	2943.00	10.26	4.66	1.17	3634.00	6.47	3.47	1.45
-0.46	2345.00	5.88	0.28	0.07	1778.00	2.31	0.69	-0.29
0.29	3126.00	6.05	0.45	0.11	2028.00	5.03	2.03	0.85
-0.91	2183.00	7.47	1.87	0.47	1746.00	3.26	0.26	0.11
-0.37	1454.00	2.54	3.06	-0.76	1593.00	0.06	2.94	-1.23
0.17	4546.00	4.91	0.69	-0.17	3526.00	1.73	1.27	-0.53
0.51	4433.00	5.57	0.03	-0.01	2528.00	1.38	1.62	-0.68
0.35	3756.00	3.99	1.61	-0.40	2587.00	0.89	2.11	-0.88
4.68	3451.00	5.39	0.21	-0.05	1316.00	0.30	2.70	-1.13
1.15	2255.00	6.39	0.79	0.20	1468.00	2.38	0.62	-0.26
0.74	2619.00	3.47	2.13	-0.53	2077.00	2.74	0.26	-0.11
1.00	2572.00	5.83	0.23	0.06	2569.00	1.95	1.05	-0.44
3.71	1201.00	17.57	**11.97**	3.00	517.00	7.74	4.74	1.98
0.52	1421.00	5.42	0.18	-0.04	1028.00	1.36	1.64	-0.68
1.47	3078.00	3.41	2.19	-0.55	1826.00	1.42	1.58	-0.66

1.13	3090.00	4.63	0.97	-0.24	2330.00	0.52	2.48	-1.04
0.01	2714.00	1.40	4.20	-1.05	2146.00	1.17	1.84	-0.77
0.04	2881.00	3.16	2.44	-0.61	3290.00	2.10	0.90	-0.38
0.45	2197.00	2.69	2.91	-0.73	1915.00	1.36	1.64	-0.69
-0.49	2954.00	1.76	3.84	-0.96	3221.00	1.80	1.20	-0.50
1.15	3080.00	2.95	2.65	-0.66	1680.00	1.85	1.15	-0.48
0.63	3812.00	1.99	3.61	-0.90	2357.00	0.68	2.32	-0.97
1.72	4780.00	7.15	1.55	0.39	2738.00	1.17	1.83	-0.77
0.96	2725.00	2.83	2.77	-0.69	2595.00	1.31	1.69	-0.71
-0.05	3724.00	6.74	1.14	0.29	3124.00	2.14	0.86	-0.36
0.26	3170.00	9.05	3.45	0.87	2067.00	2.81	0.19	-0.08
0.46	2312.00	6.31	0.71	0.18	1704.00	1.23	1.77	-0.74
0.55	3160.00	4.91	0.69	-0.17	2340.00	2.39	0.61	-0.25
0.49	1523.00	4.66	0.94	-0.23	816.00	0.49	2.51	-1.05
1.42	3062.00	10.42	4.82	1.21	2395.00	3.84	0.84	0.35
1.31	2748.00	8.12	2.52	0.63	2853.00	3.33	0.33	0.14
0.33	2184.00	10.85	5.25	1.32	2343.00	2.94	0.06	-0.02
0.31	3274.00	6.26	0.66	0.17	1944.00	2.88	0.12	-0.05
-0.41	1510.00	4.64	0.96	-0.24	1029.00	2.04	0.96	-0.40
0.47	3236.00	10.94	5.34	1.34	2424.00	3.75	0.75	0.31
1.65	1568.00	8.67	3.07	0.77	1389.00	4.46	1.46	0.61
0.20	2045.00	4.50	1.10	-0.28	1925.00	3.43	0.43	0.18
0.24	2316.00	6.39	0.79	0.20	1972.00	1.57	1.43	-0.60
-0.10	2994.00	7.58	1.98	0.50	1768.00	2.09	0.91	-0.38
-0.34	2707.00	5.28	0.32	-0.08	2155.00	2.92	0.08	-0.03
1.37	3415.00	15.02	**9.42**	2.36	1173.00	1.19	1.81	-0.76
-0.21	3808.00	10.61	5.01	1.26	2098.00	2.62	0.38	-0.16
0.80	3966.00	20.55	**14.95**	3.75	3149.00	3.94	0.94	0.39
0.42	3353.00	9.84	4.24	1.06	2868.00	3.35	0.35	0.14
0.79	2474.00	14.63	**9.03**	2.26	2598.00	5.12	2.12	0.88
0.66	3006.00	18.83	**13.23**	3.32	2407.00	5.77	2.77	1.16
1.50	3791.00	21.00	**15.40**	3.86	3419.00	14.95	**11.95**	4.99
0.61	3612.00	16.75	**11.15**	2.80	2773.00	4.54	1.54	0.64
1.14	3998.00	16.33	**10.73**	2.69	1887.00	3.60	0.60	0.25
1.85	2872.00	7.45	1.85	0.46	2497.00	3.40	0.40	0.17
0.53	2155.00	11.74	6.14	1.54	2755.00	8.09	**5.09**	2.13
0.88	2784.00	17.57	**11.97**	3.00	2020.00	7.72	4.72	1.97
1.26	1119.00	9.65	4.05	1.02	1497.00	6.48	3.48	1.45
0.48	2276.00	11.95	6.35	1.59	2008.00	5.53	2.53	1.05
-0.12	2386.00	8.30	2.70	0.68	1569.00	3.44	0.44	0.18
1.03	2112.00	11.70	6.10	1.53	1710.00	6.20	3.20	1.34
0.33	2525.00	10.34	4.74	1.19	1029.00	5.25	2.25	0.94
0.53	2788.00	5.92	0.32	0.08	2799.00	6.57	3.57	1.49
1.18	3959.00	9.62	4.02	1.01	1808.00	2.65	0.35	-0.14

1.20	1719.00	5.24	0.36	-0.09	1640.00	10.31	**7.31**	3.05
1.31	3141.00	5.19	0.41	-0.10	1514.00	5.48	2.48	1.04
1.01	4261.00	10.33	4.73	1.19	2866.00	10.89	**7.89**	3.29
0.54	2615.00	5.35	0.25	-0.06	1080.00	5.56	2.56	1.07
1.17	2162.00	2.41	3.19	-0.80	1540.00	6.17	3.17	1.32
-0.86	2209.00	8.01	2.41	0.61	2905.00	3.20	0.20	0.08
-0.46	2546.00	6.09	0.49	0.12	1376.00	0.29	2.71	-1.13
-0.27	4257.00	14.82	**9.22**	2.31	2329.00	5.84	2.84	1.18
0.23	4518.00	9.94	4.34	1.09	2870.00	3.69	0.69	0.29
-0.95	1810.00	4.31	1.29	-0.32	1540.00	1.69	1.31	-0.55
-0.45	2267.00	3.75	1.85	-0.46	2074.00	3.71	0.71	0.30
-0.95	1878.00	4.21	1.39	-0.35	1502.00	3.26	0.26	0.11
-1.15	1949.00	2.36	3.24	-0.81	1406.00	0.85	2.15	-0.90
0.58	1873.00	5.93	0.33	0.08	2081.00	5.38	2.38	0.99
-0.02	2479.00	5.97	0.37	0.09	1893.00	4.91	1.91	0.80
-0.41	2867.00	2.55	3.05	-0.76	1798.00	1.45	1.55	-0.65
-0.75	2360.00	3.56	2.04	-0.51	2386.00	4.74	1.74	0.72
1.15	3505.00	10.01	4.41	1.11	3534.00	13.84	**10.84**	4.52
0.60	3053.00	6.68	1.08	0.27	2574.00	8.43	**5.43**	2.27
-0.67	2456.00	1.75	3.85	-0.96	2144.00	1.59	1.41	-0.59
-0.22	3365.00	9.09	3.49	0.88	2550.00	4.98	1.98	0.83
-0.46	3296.00	4.61	0.99	-0.25	1495.00	1.54	1.46	-0.61
0.46	3789.00	6.49	0.89	0.22	3202.00	4.22	1.22	0.51
0.40	4819.00	4.79	0.81	-0.20	4114.00	5.13	2.13	0.89
-0.50	2861.00	4.96	0.64	-0.16	2119.00	3.30	0.30	0.13
1.46	2545.00	9.98	4.38	1.10	2801.00	4.53	1.53	0.64
-0.49	1734.00	17.13	**11.53**	2.89	758.00	5.94	2.94	1.23
0.62	4082.00	16.78	**11.18**	2.80	2233.00	5.82	2.82	1.18
-0.02	3227.00	7.59	1.99	0.50	2167.00	2.35	0.65	-0.27
1.86	2322.00	17.05	**11.45**	2.87	2174.00	11.22	**8.22**	3.43
-0.30	3086.00	10.14	4.54	1.14	2066.00	9.83	**6.83**	2.85
-0.29	2843.00	10.87	5.27	1.32	947.00	1.58	1.42	-0.59
-0.10	4451.00	12.78	7.18	1.80	2186.00	6.54	3.54	1.48
-0.70	2188.00	4.16	1.44	-0.36	757.00	5.02	2.02	0.84
-0.28	3169.00	10.26	4.66	1.17	1147.00	2.44	0.56	-0.23
-0.44	1437.00	12.80	7.20	1.81	792.00	6.69	3.69	1.54
-0.14	2603.00	9.22	3.62	0.91	1362.00	3.38	0.38	0.16
0.10	3519.00	9.66	4.06	1.02	1751.00	7.37	4.37	1.82
0.48	2097.00	6.44	0.84	0.21	1391.00	7.48	4.48	1.87
0.05	3608.00	9.84	4.24	1.06	1246.00	7.78	4.78	2.00
-0.47	2529.00	6.68	1.08	0.27	922.00	4.12	1.12	0.47
-0.72	3024.00	3.84	1.76	-0.44	1172.00	1.88	1.12	-0.47
3.36	4212.00	11.61	6.01	1.51	1886.00	12.88	**9.88**	4.13
0.48	2499.00	3.92	1.68	-0.42	1297.00	3.32	0.32	0.13

0.06	1512.00	4.89	0.71	-0.18	812.00	5.91	2.91	1.21
-0.99	1702.00	3.53	2.07	-0.52	1557.00	2.83	0.17	-0.07
1.32	4406.00	17.05	**11.45**	2.87	2015.00	8.19	**5.19**	2.17
-0.78	3753.00	4.16	1.44	-0.36	2242.00	0.31	2.69	-1.12
1.50	4083.00	15.33	**9.73**	2.44	3033.00	13.72	**10.72**	4.47
0.64	2234.00	4.48	1.12	-0.28	2610.00	8.24	**5.24**	2.19
0.96	2814.00	13.50	7.90	1.98	2086.00	7.96	**4.96**	2.07
0.41	3471.00	8.70	3.10	0.78	2652.00	5.13	2.13	0.89
1.12	1750.00	10.86	5.26	1.32	1368.00	4.31	1.31	0.55
-0.09	1691.00	5.56	0.04	-0.01	1518.00	3.49	0.49	0.20
0.75	2523.00	11.18	5.58	1.40	1783.00	3.81	0.81	0.34
1.58	1512.00	9.33	3.73	0.93	2076.00	6.36	3.36	1.40
1.44	1576.00	4.12	1.48	-0.37	1584.00	2.90	0.10	-0.04
2.35	1710.00	7.66	2.06	0.52	1679.00	3.81	0.81	0.34
2.07	1458.00	10.22	4.62	1.16	2218.00	3.65	0.65	0.27
0.54	2823.00	6.34	0.74	0.19	1884.00	0.85	2.15	-0.90
1.43	3091.00	9.67	4.07	1.02	2261.00	2.48	0.52	-0.22
3.61	3428.00	12.98	7.38	1.85	3543.00	6.18	3.18	1.33
1.47	3269.00	13.34	7.74	1.94	2585.00	3.98	0.98	0.41
1.60	1326.00	5.13	0.47	-0.12	1784.00	2.91	0.09	-0.04
0.06	1715.00	2.68	2.92	-0.73	982.00	1.02	1.98	-0.83
-0.42	2029.00	7.24	1.64	0.41	1385.00	2.96	0.04	-0.02
-0.85	2329.00	5.93	0.33	0.08	1619.00	0.68	2.32	-0.97
0.43	2770.00	10.04	4.44	1.11	2196.00	4.37	1.37	0.57
-0.18	2384.00	10.86	5.26	1.32	1439.00	2.99	0.01	-0.01
-0.35	1879.00	11.28	5.68	1.43	1802.00	3.00	0.00	0.00
-0.43	1747.00	10.02	4.42	1.11	1344.00	1.49	1.51	-0.63
-0.57	2276.00	11.03	5.43	1.36	1334.00	2.10	0.90	-0.38
-0.35	2932.00	13.95	**8.35**	2.09	2819.00	2.06	0.94	-0.39
-0.54	4046.00	11.15	5.55	1.39	1167.00	0.51	2.49	-1.04
-0.36	2148.00	11.83	6.23	1.56	1530.00	4.84	1.84	0.77
-0.91	2172.00	6.26	0.66	0.17	2220.00	2.12	0.88	-0.37
-0.16	2806.00	10.62	5.02	1.26	1887.00	3.60	0.60	0.25
0.58	3629.00	20.92	**15.32**	3.84	2263.00	5.74	2.74	1.15
-0.85	2710.00	5.68	0.08	0.02	2179.00	0.92	2.08	-0.87
-0.37	3189.00	5.42	0.18	-0.04	1650.00	1.52	1.48	-0.62
1.51	3088.00	15.58	**9.98**	2.50	2219.00	12.84	**9.84**	4.11
0.23	3554.00	9.17	3.57	0.90	2551.00	4.55	1.55	0.65
1.14	4149.00	12.56	6.96	1.74	2352.00	5.99	2.99	1.25
1.22	3040.00	6.25	0.65	0.16	1544.00	3.56	0.56	0.23
1.16	1488.00	8.33	2.73	0.69	1340.00	3.73	0.73	0.30
0.60	2806.00	11.23	5.63	1.41	1493.00	9.04	**6.04**	2.52
0.96	2068.00	11.56	5.96	1.49	1646.00	8.99	**5.99**	2.50
2.41	2791.00	14.80	**9.20**	2.31	1673.00	10.64	**7.64**	3.19

2.41	2319.00	10.00	4.40	1.10	2552.00	12.15	**9.15**	3.82
3.40	2554.00	13.78	**8.18**	2.05	1802.00	14.21	**11.21**	4.68
0.31	3262.00	4.63	0.97	-0.24	1666.00	3.48	0.48	0.20
-0.46	3106.00	3.32	2.28	-0.57	1718.00	4.48	1.48	0.62
-0.13	2966.00	8.80	3.20	0.80	1536.00	3.78	0.78	0.32
3.70	3606.00	23.57	**17.97**	4.50	1452.00	9.50	**6.50**	2.72
-0.24	1360.00	2.72	2.88	-0.72	1225.00	3.27	0.27	0.11
1.83	2773.00	13.27	7.67	1.92	1974.00	6.64	3.64	1.52
0.21	2863.00	8.98	3.38	0.85	2309.00	4.20	1.20	0.50
0.58	2515.00	11.05	5.45	1.37	2809.00	4.81	1.81	0.75
0.56	3656.00	11.16	5.56	1.39	1970.00	5.18	2.18	0.91
-0.19	4018.00	9.58	3.98	1.00	1410.00	1.49	1.51	-0.63
0.90	1725.00	8.93	3.33	0.83	1297.00	2.78	0.22	-0.09
3.49	2690.00	12.49	6.89	1.73	2561.00	6.25	3.25	1.36
2.57	3208.00	11.00	5.40	1.36	3534.00	6.73	3.73	1.56
0.33	1784.00	8.80	3.20	0.80	928.00	2.69	0.31	-0.13
-0.62	1500.00	3.67	1.93	-0.48	718.00	0.42	2.58	-1.08
1.59	2605.00	5.07	0.53	-0.13	3210.00	4.83	1.83	0.76
0.64	1705.00	2.46	3.14	-0.79	1279.00	3.21	0.21	0.09
0.37	1718.00	4.95	0.65	-0.16	1656.00	2.23	0.77	-0.32
0.61	1715.00	6.36	0.76	0.19	3387.00	3.31	0.31	0.13
0.35	2120.00	6.65	1.05	0.26	1946.00	0.87	2.13	-0.89
-0.78	2277.00	3.51	2.09	-0.52	1188.00	0.76	2.24	-0.94
-0.52	2829.00	2.37	3.23	-0.81	1532.00	1.70	1.30	-0.54
0.71	3086.00	5.51	0.09	-0.02	2443.00	2.09	0.91	-0.38
-0.93	1141.00	5.08	0.52	-0.13	1315.00	1.60	1.40	-0.59
0.58	2532.00	5.33	0.27	-0.07	1650.00	4.00	1.00	0.42
-0.59	1378.00	3.48	2.12	-0.53	766.00	1.17	1.83	-0.76
-0.86	3186.00	3.11	2.49	-0.62	2278.00	1.54	1.46	-0.61
-0.53	3015.00	9.05	3.45	0.87	1680.00	1.19	1.81	-0.76
-1.16	3464.00	1.62	3.98	-1.00	1773.00	0.79	2.21	-0.92
-0.97	1697.00	3.71	1.89	-0.47	1352.00	1.11	1.89	-0.79
-1.22	3569.00	0.67	4.93	-1.23	1455.00	1.31	1.69	-0.71
-0.78	2839.00	3.52	2.08	-0.52	1201.00	0.33	2.67	-1.11
-1.11	975.00	0.92	4.68	-1.17	378.00	0.26	2.74	-1.14
-0.64	1678.00	2.80	2.80	-0.70	592.00	0.34	2.66	-1.11
-0.24	1960.00	3.06	2.54	-0.64	1113.00	0.45	2.55	-1.07
-0.43	713.00	11.08	5.48	1.37	732.00	1.78	1.22	-0.51
-0.47	1257.00	4.61	0.99	-0.25	1985.00	3.07	0.07	0.03
-0.72	1691.00	3.08	2.52	-0.63	935.00	0.96	2.04	-0.85
-0.81	2342.00	8.41	2.81	0.71	1246.00	1.20	1.80	-0.75
-0.65	1074.00	3.54	2.06	-0.52	611.00	1.96	1.04	-0.43
-1.13	1779.00	6.80	1.20	0.30	991.00	1.92	1.08	-0.45
-1.15	1027.00	3.99	1.61	-0.40	660.00	0.76	2.24	-0.94

-1.24	451.00	6.21	0.61	0.15	945.00	0.95	2.05	-0.86
-1.20	959.00	7.30	1.70	0.43	615.00	1.14	1.86	-0.78
-1.07	1307.00	2.14	3.46	-0.87	1505.00	0.53	2.47	-1.03
-1.00	877.00	4.45	1.15	-0.29	465.00	1.08	1.92	-0.80
-1.14	2199.00	3.18	2.42	-0.60	757.00	1.19	1.81	-0.76
-1.24	1363.00	3.82	1.78	-0.45	954.00	0.31	2.69	-1.12
-1.25	2655.00	5.88	0.28	0.07	1360.00	0.44	2.56	-1.07
-1.20	1173.00	4.09	1.51	-0.38	1723.00	0.70	2.30	-0.96
-1.31	2091.00	3.25	2.35	-0.59	1272.00	0.31	2.69	-1.12
-1.23	2002.00	3.50	2.10	-0.53	1294.00	0.46	2.54	-1.06
-1.27	2766.00	2.13	3.47	-0.87	786.00	0.76	2.24	-0.93
-1.20	2025.00	2.22	3.38	-0.85	482.00	0.41	2.59	-1.08
-1.36	943.00	0.00	5.60	-1.40	1594.00	0.25	2.75	-1.15
	2508.00	5.60	2.70		1824.00	3.00	1.62	
			8.09				4.85	
			3.99				2.39	
2498.00	36.87				925.00	14.16		
3160.00	23.89		1317.00	26.20				
838.00	23.03		1410.00	22.70				
3153.00	45.13		2608.00	34.16				
2412.25	32.23		1778.33	27.69				
1094.45	10.68		720.02	5.88				
1045.00	1.24		407.00	2.70				
832.00	6.01		481.00	1.04				
180.00	2.78				163.00	11.04		
818.00	2.93		857.00	5.25				
610.00	3.91		669.00	3.15				
372.46	1.82		265.87	2.98				
	32.04			17.63				
	5.47			8.93				
	37.50			26.57				
	28.32			24.54				
	1.32			1.08				
	-0.32			-0.08				
210.00	11.43		323.00	1.55				
147.00	14.97		255.00	5.49				
2876.00	16.17		2289.00	5.64				
2612.00	13.63		1650.00	5.21				
4105.00	14.08		2744.00	7.25				
4692.00	16.97		3459.00	19.20				

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Plate	Well	Gene		GeneID		Cell Coun	% inf	Abs Dev
50057.00	A02	M-013713	proprotein	27344.00	PCSK1N	1734.00	7.90	3.38
50057.00	A04	M-012513	late cornifi	26239.00	LCE2B	2514.00	5.33	0.81
50057.00	A05	M-012819	nuclear pr	26471.00	NUPR1	2378.00	6.39	1.87
50057.00	A06	M-020964	2-deoxyrib	51071.00	DERA	3148.00	7.75	3.23
50057.00	A07	M-030029	olfactory r	26496.00	OR10A3	3417.00	6.88	2.36
50057.00	A08	M-007204	nitric oxide	51070.00	NOSIP	2477.00	4.04	0.48
50057.00	A09	M-012465	nuclear pre	26502.00	NARF	2801.00	9.43	4.91
50057.00	A10	M-017261	mitochond	51069.00	MRPL2	3282.00	4.81	0.29
50057.00	A11	M-013584	fer-1-like 3	26509.00	FER1L3	3710.00	3.21	1.31
50057.00	A12	M-017172	NMD3 hor	51068.00	NMD3	3602.00	5.19	0.67
50057.00	A13	M-018242	fracture ca	26515.00	FXC1	1975.00	2.33	2.19
50057.00	A14	M-020962	tyrosyl-tRN	51067.00	YARS2	819.00	2.81	1.71
50057.00	A15	M-009538	translocase	26517.00	TIMM13	1877.00	2.50	2.02
50057.00	A16	M-020960	chromoson	51066.00	C3orf32	2905.00	2.44	2.08
50057.00	A17	M-008209	translocase	26519.00	TIMM10	2789.00	3.30	1.22
50057.00	A18	M-020197	submaxillar	26952.00	SMR3A	3111.00	11.32	6.80
50057.00	A19	M-009572	translocase	26520.00	TIMM9	2567.00	2.84	1.68
50057.00	A20	M-024450	cat eye syn	27443.00	CECR2	1380.00	1.81	2.71
50057.00	A21	M-008491	translocase	26521.00	TIMM8B	2456.00	2.40	2.12
50057.00	A23	M-004638	eukaryotic	26523.00	EIF2C1	1986.00	1.51	3.01
50057.00	B02	M-014192	Tax1 (hum	30851.00	TAX1BP3	4165.00	7.68	3.16
50057.00	B04	M-014200	cerebellar	30850.00	CDR2L	4075.00	4.49	0.03
50057.00	B05	M-007435	solute carri	28231.00	SLCO4A1	3979.00	8.39	3.87
50057.00	B06	M-005213	cancer/test	30848.00	CTAG2	4609.00	19.42	14.90
50057.00	B07	M-007434	solute carri	28232.00	SLCO3A1	3750.00	1.76	2.76
50057.00	B08	M-016660	EH-domain	30846.00	EHD2	4283.00	5.86	1.34
50057.00	B09	M-021187	solute carri	28234.00	SLCO1B3	3857.00	4.82	0.30
50057.00	B10	M-004728	EH-domain	30845.00	EHD3	5076.00	8.02	3.50
50057.00	B11	M-020554	coiled-coil	28952.00	CCDC22	2011.00	3.38	1.14
50057.00	B12	M-010659	EH-domain	30844.00	EHD4	3073.00	8.46	3.94
50057.00	B13	M-019451	dexametha	28955.00	DEXI	3490.00	3.52	1.00
50057.00	B14	M-020513	deoxynucle	30836.00	DNTTIP2	2423.00	0.45	4.07
50057.00	B15	M-020556	mitogen-ac	28956.00	MAPBPIP	898.00	1.67	2.85
50057.00	B16	M-003468	CD209 mol	30835.00	CD209	4777.00	5.86	1.34
50057.00	B17	M-013492	mitochond	28957.00	MRPS28	2948.00	2.88	1.64
50057.00	B18	M-017359	zinc ribbon	30834.00	ZNRD1	3075.00	1.85	2.67
50057.00	B19	M-020558	coiled-coil	28958.00	CCDC56	3414.00	3.60	0.92
50057.00	B20	M-020511	5', 3'-nucle	30833.00	NT5C	3932.00	8.52	4.00
50057.00	B21	M-016783	transmem	28959.00	TMEM176B	3069.00	0.65	3.87
50057.00	B23	M-021338	decapping	28960.00	DCPS	3718.00	2.61	1.91
50057.00	C02	M-015056	cat eye syn	27440.00	CECR5	3331.00	4.41	0.11
50057.00	C04	M-014747	cat eye syn	27439.00	CECR6	1384.00	5.06	0.54
50057.00	C05	M-012485	tetraspanir	26526.00	TSPAN16	3340.00	10.69	6.17
50057.00	C06	M-008398	echinoder	27436.00	EML4	4261.00	9.04	4.52

50057.00	C07	M-013384	DAZ associa	26528.00	DAZAP1	4043.00	7.89	3.37
50057.00	C08	M-010035	polymerase	27434.00	POLM	4853.00	7.38	2.86
50057.00	C09	M-015205	procollagen	26577.00	PCOLCE2	4005.00	6.29	1.77
50057.00	C10	M-015292	torsin fami	27433.00	TOR2A	3555.00	6.27	1.75
50057.00	C11	M-016553	myeloma o	26579.00	MYEOV	2311.00	7.23	2.71
50057.00	C12	M-017193	methionine	27430.00	MAT2B	3540.00	6.92	2.40
50057.00	C13	M-019904	double hom	26581.00	DUX5	1728.00	4.92	0.40
50057.00	C14	M-018327	RUN and TI	27352.00	RUTBC3	3571.00	5.10	0.58
50057.00	C15	M-021492	gremlin 1,	26585.00	GREM1	3517.00	6.08	1.56
50057.00	C16	M-024576	DNA segme	27351.00	D15Wsu75e	4182.00	7.89	3.37
50057.00	C17	M-017099	cytoskeleto	26586.00	CKAP2	2913.00	5.90	1.38
50057.00	C18	M-014204	malonyl Co	27349.00	MCAT	1339.00	3.51	1.01
50057.00	C19	M-017562	mitochond	26589.00	MRPL46	4034.00	6.02	1.50
50057.00	C20	M-014203	torsin fami	27348.00	TOR1B	4185.00	5.57	1.05
50057.00	C21	M-012484	transducin	26608.00	TBL2	5461.00	10.60	6.08
50057.00	C23	M-016927	elongation	26610.00	ELP4	4666.00	10.65	6.13
50057.00	D02	M-014199	zinc finger	30832.00	ZNF354C	2489.00	0.84	3.68
50057.00	D04	M-008545	CXXC finger	30827.00	CXXC1	1811.00	0.17	4.35
50057.00	D05	M-021389	osteopetro	28962.00	OSTM1	3251.00	4.21	0.31
50057.00	D06	M-013559	Kv channel	30820.00	KCNIP1	3285.00	2.19	2.33
50057.00	D07	M-007502	solute carri	28965.00	SLC27A6	5071.00	3.67	0.85
50057.00	D08	M-017333	Kv channel	30819.00	KCNIP2	3795.00	2.98	1.54
50057.00	D09	M-020568	sorting nex	28966.00	SNX24	4578.00	1.16	3.36
50057.00	D10	M-010573	endogenou	30816.00	ERVWE1	3986.00	3.69	0.83
50057.00	D11	M-007372	solute carri	28968.00	SLC6A16	3488.00	1.43	3.09
50057.00	D12	M-016657	ST6 (alpha-	30815.00	ST6GALNAC6	3316.00	1.96	2.56
50057.00	D13	M-020573	basic leucin	28969.00	BZW2	3547.00	5.10	0.58
50057.00	D14	M-020496	retina and	30062.00	RAX	4527.00	5.21	0.69
50057.00	D15	M-016791	chromosom	28970.00	C11orf54	4058.00	4.63	0.11
50057.00	D16	M-013560	sperm prot	30014.00	SPANXA1	2890.00	3.29	1.23
50057.00	D17	M-014411	chromosom	28971.00	C11orf67	2833.00	7.45	2.93
50057.00	D18	M-014111	T-cell leuke	30012.00	TLX3	3689.00	4.28	0.24
50057.00	D19	M-020577	signal pept	28972.00	SPCS1	4407.00	6.74	2.22
50057.00	D20	M-016786	neurexoph	30010.00	NXPH1	3628.00	3.42	1.10
50057.00	D21	M-013043	mitochond	28973.00	MRPS18B	5271.00	10.43	5.91
50057.00	D23	M-020581	chromosom	28974.00	C19orf53	4362.00	5.91	1.39
50057.00	E02	M-014198	transmemb	27346.00	TMEM97	2708.00	3.25	1.27
50057.00	E04	M-008225	potassium	27345.00	KCNMB4	2419.00	9.30	4.78
50057.00	E05	M-026243	olfactory re	26740.00	OR1J2	2464.00	10.96	6.44
50057.00	E06	M-016782	CGI-96 prot	27341.00	CTA-126B4.3	2230.00	0.76	3.76
50057.00	E07	M-019605	nuclear frag	26747.00	NUFIP1	3678.00	2.77	1.75
50057.00	E08	M-004668	PRP19/PSO	27339.00	PRPF19	2263.00	2.47	2.05
50057.00	E09	M-011278	G antigen	26748.00	GAGE7B	3380.00	2.81	1.71
50057.00	E10	M-020216	eukaryotic	27335.00	EIF3S12	1831.00	3.88	0.64
50057.00	E11	M-012437	G antigen	26749.00	GAGE8	3784.00	6.18	1.66

50057.00	E12	M-013716	golgi phosp	27333.00	GOLPH4	2093.00	5.26	0.74
50057.00	E13	M-020542	SH3 domai	26751.00	SH3YL1	4042.00	4.95	0.43
50057.00	E14	M-013715	zinc finger	27332.00	ZNF638	4166.00	6.24	1.72
50057.00	E15	M-003713	six transme	26872.00	STEAP1	4448.00	6.25	1.73
50057.00	E16	M-014107	trinucleotic	27327.00	TNRC6A	3588.00	10.17	5.65
50057.00	E17	M-025810	5-oxoprolir	26873.00	OPLAH	2279.00	6.01	1.49
50057.00	E18	M-022555	TOX high m	27324.00	TOX3	2941.00	6.46	1.94
50057.00	E19	M-019988	coatomer p	26958.00	COPG2	3983.00	11.75	**7.23**
50057.00	E20	M-009049	basic helix-	27319.00	BHLHB5	3741.00	6.68	2.16
50057.00	E21	M-021457	HMG-box t	26959.00	HBP1	3846.00	6.58	2.06
50057.00	E23	M-019998	cysteine an	26973.00	CHORDC1	4985.00	7.72	3.20
50057.00	F02	M-013089	EGF-contai	30008.00	EFEMP2	2026.00	0.59	3.93
50057.00	F04	M-020491	transportin	30000.00	TNPO2	1327.00	1.21	3.31
50057.00	F05	M-017553	mitochond	28977.00	MRPL42	2933.00	5.35	0.83
50057.00	F06	M-013567	LIM and cy	29995.00	LMCD1	2030.00	3.74	0.78
50057.00	F07	M-018878	transmemb	28978.00	TMEM14A	2751.00	3.89	0.63
50057.00	F08	M-020487	bromodom	29994.00	BAZ2B	1317.00	3.19	1.33
50057.00	F09	M-014740	intraflagell	28981.00	IFT81	3194.00	9.96	5.44
50057.00	F10	M-019011	paired imm	29992.00	PILRA	2871.00	7.00	2.48
50057.00	F11	M-020594	NIN1/RPN1	28987.00	NOB1	3257.00	6.02	1.50
50057.00	F12	M-010028	odorant bir	29991.00	OBP2A	3314.00	3.05	1.47
50057.00	F13	M-019236	asteroid hc	28990.00	ASTE1	3341.00	5.42	0.90
50057.00	F14	M-008879	odorant bir	29989.00	OBP2B	3500.00	7.11	2.59
50057.00	F15	M-015390	COMM dor	28991.00	COMMD5	2333.00	8.92	4.40
50057.00	F16	M-007570	solute carri	29986.00	SLC39A2	2656.00	8.02	3.50
50057.00	F17	M-013863	LRP16 prot	28992.00	LRP16	3277.00	6.16	1.64
50057.00	F18	M-007571	solute carri	29985.00	SLC39A3	3719.00	12.48	**7.96**
50057.00	F19	M-031072	chromoson	29035.00	C16orf72	3990.00	6.34	1.82
50057.00	F20	M-017453	downstrea	29980.00	DONSON	3275.00	15.05	**10.53**
50057.00	F21	M-017637	transmemb	29057.00	TMEM29	3599.00	8.59	4.07
50057.00	F23	M-015123	chromoson	29058.00	C20orf30	3353.00	11.63	**7.11**
50057.00	G02	M-011691	RNA bindin	27316.00	RBMX	2138.00	0.80	3.72
50057.00	G04	M-014202	zinc finger	27309.00	ZNF330	2166.00	1.52	3.00
50057.00	G05	M-016987	zinc finger	26974.00	ZNF285A	3922.00	6.25	1.73
50057.00	G06	M-006406	molybdenu	27304.00	MOCS3	3464.00	4.73	0.21
50057.00	G07	M-012479	SEC22 vesi	26984.00	SEC22A	3577.00	2.82	1.70
50057.00	G08	M-013731	bone morp	27302.00	BMP10	1242.00	4.43	0.09
50057.00	G09	M-013645	adaptor-rel	26985.00	AP3M1	2580.00	2.17	2.35
50057.00	G10	M-013730	APEX nucle	27301.00	APEX2	1739.00	1.67	2.85
50057.00	G11	M-019598	poly(A) bin	26986.00	PABPC1	2888.00	2.49	2.03
50057.00	G12	M-020223	zinc finger	27300.00	ZNF544	3534.00	3.79	0.73
50057.00	G13	M-006971	ring finger	26994.00	RNF11	3192.00	5.98	1.46
50057.00	G14	M-031994	calcitonin g	27297.00	RCP9	2847.00	4.39	0.13
50057.00	G15	M-013879	TruB pseud	26995.00	TRUB2	3417.00	10.86	**6.34**
50057.00	G16	M-020226	chromoson	27296.00	C20orf10	4242.00	5.19	0.67

50057.00	G17	M-012514	fetuin B	26998.00	FETUB	2657.00	7.19	2.67
50057.00	G18	M-020229	PDZ and LI	27295.00	PDLIM3	1805.00	2.99	1.53
50057.00	G19	M-025435	zuotin rela	27000.00	ZRF1	3513.00	4.95	0.43
50057.00	G20	M-009651	dihydrodio	27294.00	DHDH	3146.00	2.99	1.53
50057.00	G21	M-012522	T-cell leuke	27004.00	TCL6	2779.00	5.87	1.35
50057.00	G23	M-013171	fibroblast g	27006.00	FGF22	3691.00	3.77	0.75
50057.00	H02	M-013566	ubiquilin 2	29978.00	UBQLN2	1568.00	3.44	1.08
50057.00	H04	M-020483	schwanno	29970.00	SCHIP1	1889.00	0.69	3.83
50057.00	H05	M-020654	HSPC047 p	29060.00	HSPC047	2370.00	1.31	3.21
50057.00	H06	M-025441	MyoD fami	29969.00	MDFIC	1922.00	0.52	4.00
50057.00	H07	M-020659	HSPC049 p	29062.00	HSPC049	1156.00	0.52	4.00
50057.00	H08	M-010398	phosphose	29968.00	PSAT1	1477.00	1.96	2.56
50057.00	H09	M-028349	zinc finger,	29063.00	ZCCHC4	2536.00	2.52	2.00
50057.00	H10	M-019145	striatin, cal	29966.00	STRN3	2329.00	2.19	2.33
50057.00	H11	M-017719	zinc finger	29066.00	ZC3H7A	2821.00	1.99	2.53
50057.00	H12	M-020451	chromoson	29965.00	C16orf5	2304.00	0.56	3.96
50057.00	H13	M-020671	zinc finger	29068.00	ZBTB44	2507.00	1.83	2.69
50057.00	H14	M-006979	chromoson	29964.00	C6orf49	2409.00	2.95	1.57
50057.00	H15	M-015391	coiled-coil	29070.00	CCDC113	1938.00	4.70	0.18
50057.00	H16	M-013626	FtsJ homol	29960.00	FTSJ2	2719.00	3.31	1.21
50057.00	H17	M-018778	C1GALT1-s	29071.00	C1GALT1C1	1942.00	4.58	0.06
50057.00	H18	M-007325	solute carri	29957.00	SLC25A24	2035.00	3.49	1.03
50057.00	H19	M-017251	mitochond	29074.00	MRPL18	2504.00	4.91	0.39
50057.00	H20	M-010282	LAG1 hom	29956.00	LASS2	2451.00	5.34	0.82
50057.00	H21	M-020673	HSPC072 p	29075.00	HSPC072	2253.00	3.33	1.19
50057.00	H23	M-020684	chromoson	29078.00	C6orf66	2477.00	4.24	0.28
50057.00	I02	M-010136	sphingomy	27293.00	SMPDL3B	2823.00	1.24	3.28
50057.00	I04	M-009476	DIM1 dime	27292.00	DIMT1L	2226.00	2.83	1.69
50057.00	I05	M-019262	nephronop	27031.00	NPHP3	1972.00	1.88	2.64
50057.00	I06	M-018936	chromoson	27291.00	C10orf28	2984.00	4.06	0.47
50057.00	I07	M-010193	NADPH oxi	27035.00	NOX1	3592.00	4.26	0.26
50057.00	I08	M-020235	serine pept	27290.00	SPINK4	1934.00	2.74	1.78
50057.00	I09	M-020546	sialic acid b	27036.00	SIGLEC7	2483.00	7.17	2.65
50057.00	I10	M-012532	testes-spec	27288.00	HNRNPG-T	2259.00	4.43	0.09
50057.00	I11	M-016762	HpaII tiny f	27037.00	HTF9C	3075.00	1.98	2.54
50057.00	I12	M-009614	sushi-repea	27286.00	SRPX2	2868.00	3.49	1.03
50057.00	I13	M-018287	chromoson	27042.00	C1orf107	1148.00	1.92	2.60
50057.00	I14	M-012530	tektin 2 (te	27285.00	TEKT2	1663.00	3.01	1.51
50057.00	I15	M-010657	staphyloco	27044.00	SND1	1834.00	2.29	2.23
50057.00	I16	M-008259	tubulointer	27283.00	TINAG	2661.00	2.67	1.85
50057.00	I17	M-008816	DNA segme	27065.00	D4S234E	1763.00	1.13	3.39
50057.00	I18	M-020240	LSM3 hom	27258.00	LSM3	2708.00	5.32	0.80
50057.00	I19	M-006873	staufen, RN	27067.00	STAU2	2034.00	6.00	1.48
50057.00	I20	M-005124	LSM1 hom	27257.00	LSM1	2092.00	3.92	0.60
50057.00	I21	M-020534	growth hor	27069.00	GHITM	1072.00	2.24	2.28

50057.00	I23	M-020531	dual adapt	27071.00	DAPP1	1392.00	3.30	1.22
50057.00	J02	M-019142	protein-O-	29954.00	POMT2	1970.00	6.09	1.57
50057.00	J04	M-005854	dipeptidyl-	29952.00	DPP7	2545.00	4.79	0.27
50057.00	J05	M-020693	coiled-coil	29080.00	CCDC59	1668.00	7.79	3.27
50057.00	J06	M-020442	PDZ domai	29951.00	PDZRN4	2275.00	5.01	0.49
50057.00	J07	M-020695	methyltran	29081.00	METTL5	2193.00	5.24	0.72
50057.00	J08	M-010197	oxidative s	29948.00	OSGIN1	1790.00	9.94	5.42
50057.00	J09	M-020698	chromatin	29082.00	CHMP4A	2090.00	7.51	2.99
50057.00	J10	M-013637	DNA (cytos	29947.00	DNMT3L	2479.00	8.87	4.35
50057.00	J11	M-020699	GTP-bindin	29083.00	GTPBP8	2033.00	8.51	3.99
50057.00	J12	M-013636	SERTA do	29946.00	SERTAD3	1393.00	12.85	**8.33**
50057.00	J13	M-020702	chromoso	29086.00	C19orf62	1623.00	3.82	0.70
50057.00	J14	M-020437	paraneopla	29944.00	PNMA3	1374.00	6.11	1.59
50057.00	J15	M-020704	thymocyte	29087.00	THYN1	1160.00	6.03	1.51
50057.00	J16	M-008369	peptidyl ar	29943.00	PADI1	2114.00	8.80	4.28
50057.00	J17	M-013052	mitochond	29088.00	MRPL15	1172.00	8.70	4.18
50057.00	J18	M-013641	purine-rich	29942.00	PURG	3611.00	6.40	1.88
50057.00	J19	M-016773	syntaxin bi	29091.00	STXBP6	2457.00	8.14	3.62
50057.00	J20	M-013644	dermatan	29940.00	DSE	2733.00	7.28	2.76
50057.00	J21	M-017259	mitochond	29093.00	MRPL22	1784.00	4.99	0.47
50057.00	J23	M-020714	galectin-rel	29094.00	HSPC159	1451.00	7.72	3.20
50057.00	K02	M-012844	cold shock	27254.00	CSDC2	1698.00	6.95	2.43
50057.00	K04	M-013862	chromoso	27249.00	C2orf25	2065.00	14.19	**9.67**
50057.00	K05	M-006972	vacuolar pr	27072.00	VPS41	2588.00	7.42	2.90
50057.00	K06	M-010658	chromoso	27248.00	C2orf30	2959.00	10.71	6.19
50057.00	K07	M-004716	lysosomal-	27074.00	LAMP3	2326.00	8.00	3.48
50057.00	K08	M-020552	NFU1 iron-	27247.00	NFU1	2747.00	9.79	5.27
50057.00	K09	M-012516	tetraspani	27075.00	TSPAN13	2743.00	11.67	**7.15**
50057.00	K10	M-006974	zinc finger	27246.00	ZNF364	1687.00	10.67	6.15
50057.00	K11	M-010069	LY6/PLAUR	27076.00	LYPD3	2077.00	7.90	3.38
50057.00	K12	M-027522	AT hook, D	27245.00	AHDC1	1633.00	9.25	4.73
50057.00	K13	M-013039	B9 protein	27077.00	EPPB9	1203.00	2.99	1.53
50057.00	K14	M-020247	chromatin	27243.00	CHMP2A	534.00	7.68	3.16
50057.00	K15	M-015920	RNA pseud	27079.00	RPUSD2	3967.00	10.34	5.82
50057.00	K16	M-010940	Bardet-Bie	27241.00	BBS9	2734.00	5.49	0.97
50057.00	K17	M-012896	beta-1,3-gl	27087.00	B3GAT1	2576.00	2.80	1.73
50057.00	K18	M-020250	signaling t	27240.00	SIT1	2796.00	8.94	4.42
50057.00	K19	M-012517	ubiquinol-c	27089.00	UQCRQ	1267.00	2.60	1.92
50057.00	K20	M-015129	G patch do	27238.00	GPKOW	2136.00	3.14	1.38
50057.00	K21	M-017327	ST6 (alpha-	27090.00	ST6GALNAC4	2461.00	32.59	**28.07**
50057.00	K23	M-012518	calcium ch	27091.00	CACNG5	2443.00	3.64	0.88
50057.00	L02	M-016079	neuron der	29937.00	NENF	2711.00	2.58	1.94
50057.00	L04	M-013648	sorting nex	29934.00	SNX12	1375.00	1.45	3.07
50057.00	L05	M-017035	ORM1-like	29095.00	ORMDL2	1731.00	1.16	3.36
50057.00	L06	M-020430	loss of hete	29931.00	LOH3CR2A	2439.00	5.62	1.10

50057.00	L07	M-020717	cornichon h	29097.00	CNIH4	2816.00	3.62	0.90
50057.00	L08	M-006473	translocase	29928.00	TIMM22	2094.00	1.38	3.14
50057.00	L09	M-020497	RAN guanin	29098.00	RANGNRF	2363.00	3.30	1.22
50057.00	L10	M-021503	Sec61 alpha	29927.00	SEC61A1	1296.00	2.16	2.36
50057.00	L11	M-020724	COMM dom	29099.00	COMMD9	696.00	3.88	0.64
50057.00	L12	M-013667	GDP-mann	29926.00	GMPPA	1400.00	3.29	1.23
50057.00	L13	M-020727	HSPC171 p	29100.00	HSPC171	3092.00	4.04	0.48
50057.00	L14	M-008947	GDP-mann	29925.00	GMPPB	1812.00	1.88	2.64
50057.00	L15	M-020740	SSU72 RNA	29101.00	SSU72	1159.00	1.55	2.97
50057.00	L16	M-004724	epsin 1	29924.00	EPN1	3286.00	5.57	1.05
50057.00	L17	M-016996	ribonucleas	29102.00	RNASEN	2815.00	3.23	1.29
50057.00	L18	M-013673	sorting nex	29916.00	SNX11	4262.00	4.34	0.18
50057.00	L19	M-020286	DnaJ (Hsp4	29103.00	DNAJC15	3139.00	5.29	0.77
50057.00	L20	M-020412	UbiA preny	29914.00	UBIAD1	3948.00	5.45	0.93
50057.00	L21	M-008565	N-6 adenin	29104.00	N6AMT1	3056.00	1.90	2.62
50057.00	L23	M-020289	chromosom	29105.00	C16orf80	3011.00	1.03	3.49
50057.00	M02	M-020256	ADP-ribosy	27236.00	ARFIP1	1214.00	9.80	5.28
50057.00	M04	M-018361	coenzyme (	27235.00	COQ2	2454.00	12.43	**7.91**
50057.00	M05	M-012519	calcium cha	27092.00	CACNG4	1565.00	3.19	1.33
50057.00	M06	M-010391	sulfotransf	27233.00	SULT1C4	2306.00	13.14	**8.62**
50057.00	M07	M-008880	potassium	27094.00	KCNMB3	1987.00	7.40	2.88
50057.00	M08	M-006747	integrin be	27231.00	ITGB1BP3	1695.00	6.31	1.79
50057.00	M09	M-017649	trafficking p	27095.00	TRAPPC3	1533.00	11.81	**7.29**
50057.00	M10	M-015404	stress-asso	27230.00	SERP1	1560.00	5.00	0.48
50057.00	M11	M-017042	clusterin-lik	27098.00	CLUL1	1852.00	6.97	2.45
50057.00	M12	M-013092	vacuolar pr	27183.00	VPS4A	1621.00	7.09	2.57
50057.00	M13	M-012841	nasophary	27099.00	NAG8	2733.00	11.12	**6.60**
50057.00	M14	M-012843	sialic acid b	27181.00	SIGLEC8	791.00	18.46	**13.94**
50057.00	M15	M-012521	calcyclin bi	27101.00	CACYBP	2152.00	8.36	3.84
50057.00	M16	M-012842	sialic acid b	27180.00	SIGLEC9	2794.00	14.85	**10.33**
50057.00	M17	M-013874	arrestin do	27106.00	ARRDC2	2241.00	4.55	0.03
50057.00	M18	M-007564	solute carri	27173.00	SLC39A1	1840.00	6.47	1.95
50057.00	M19	M-020524	zinc finger a	27107.00	ZBTB11	2261.00	11.85	**7.33**
50057.00	M20	M-017650	PRELI doma	27166.00	PRELID1	3433.00	12.21	**7.69**
50057.00	M21	M-020544	ATP syntha	27109.00	ATP5S	3384.00	19.36	**14.84**
50057.00	M23	M-015232	syndecan b	27111.00	SDCBP2	1532.00	6.07	1.55
50057.00	N02	M-020408	hook homo	29911.00	HOOK2	2503.00	3.04	1.48
50057.00	N04	M-017488	sorting nex	29907.00	SNX15	3006.00	3.63	0.89
50057.00	N05	M-020746	chromosom	29113.00	C6orf15	2424.00	2.85	1.67
50057.00	N06	M-013672	ST8 alpha-N	29906.00	ST8SIA5	3245.00	4.56	0.04
50057.00	N07	M-020295	transgelin 3	29114.00	TAGLN3	2854.00	4.84	0.32
50057.00	N08	M-020402	coiled-coil d	29903.00	CCDC106	2985.00	3.72	0.80
50057.00	N09	M-006976	myosin reg	29116.00	MYLIP	2072.00	4.58	0.06
50057.00	N10	M-020401	chromosom	29902.00	C12orf24	1732.00	1.21	3.31
50057.00	N11	M-013708	DEAD (Asp-	29118.00	DDX25	4315.00	9.18	4.66

50057.00	N12	M-020398	SAC3 doma	29901.00	SAC3D1	2389.00	1.21	3.31
50057.00	N13	M-009055	testes-spec	29122.00	TSP50	2991.00	7.29	2.77
50057.00	N14	M-019480	transforme	29896.00	TRA2A	2423.00	5.16	0.64
50057.00	N15	M-027299	ankyrin rep	29123.00	ANKRD11	2959.00	3.55	0.97
50057.00	N16	M-017964	fast skeleta	29895.00	MYLPF	1629.00	7.67	3.15
50057.00	N17	M-017203	lectin, gala	29124.00	LGALS13	3061.00	8.33	3.81
50057.00	N18	M-020395	cleavage an	29894.00	CPSF1	2650.00	5.02	0.50
50057.00	N19	M-015836	CD274 mol	29126.00	CD274	3079.00	6.37	1.85
50057.00	N20	M-018726	PSMC3 inte	29893.00	PSMC3IP	4216.00	8.70	4.18
50057.00	N21	M-008650	Rac GTPase	29127.00	RACGAP1	2355.00	8.66	4.14
50057.00	N23	M-020356	tropomodu	29765.00	TMOD4	981.00	5.50	0.98
50057.00	O02	M-012500	glutaminas	27165.00	GLS2	1039.00	3.27	1.25
50057.00	O04	M-008297	N-acylsphin	27163.00	ASAHL	1527.00	3.41	1.11
50057.00	O05	M-020550	transmemb	27112.00	TMEM28	1277.00	2.90	1.62
50057.00	O06	M-004639	eukaryotic	27161.00	EIF2C2	1713.00	3.79	0.73
50057.00	O07	M-020522	dickkopf-lik	27120.00	DKKL1	1616.00	1.92	2.60
50057.00	O08	M-010196	NADPH dep	27158.00	NDOR1	1944.00	4.48	0.04
50057.00	O09	M-020520	dickkopf ho	27121.00	DKK4	1094.00	5.30	0.78
50057.00	O10	M-025088	bromodom	27154.00	BRPF3	2492.00	6.66	2.14
50057.00	O11	M-018352	dickkopf ho	27122.00	DKK3	1567.00	2.74	1.78
50057.00	O12	M-013868	zinc finger	27153.00	ZNF777	1168.00	3.94	0.58
50057.00	O13	M-020278	dickkopf ho	27123.00	DKK2	1264.00	1.42	3.10
50057.00	O14	M-031873	inturned pl	27152.00	INTU	1679.00	1.91	2.61
50057.00	O15	M-015461	structural r	27127.00	8888888888888970.00	1601.00	1.87	2.65
50057.00	O16	M-013870	C3 and PZP	27151.00	CPAMD8	2014.00	1.59	2.93
50057.00	O17	M-012523	inversin	27130.00	INVS	2532.00	2.33	2.19
50057.00	O18	M-025359	DENN/MAD	27147.00	DENND2A	3855.00	2.15	2.37
50057.00	O19	M-009660	tight juncti	27134.00	TJP3	2661.00	0.79	3.73
50057.00	O20	M-024219	KIAA1276 p	27146.00	KIAA1276	1531.00	1.11	3.41
50057.00	O21	M-012526	MORC fam	27136.00	MORC1	1588.00	2.33	2.19
50057.00	O23	M-013875	filamin A in	27145.00	FILIP1	1362.00	0.73	3.79
50057.00	P02	M-018823	RNA bindin	29890.00	RBM15B	1427.00	5.40	0.88
50057.00	P04	M-020392	guanine nu	29889.00	GNL2	1650.00	4.24	0.28
50057.00	P05	M-017656	tropomodu	29766.00	TMOD3	2219.00	3.92	0.60
50057.00	P06	M-020389	striatin, cal	29888.00	STRN4	1834.00	2.29	2.23
50057.00	P07	M-020360	tropomodu	29767.00	TMOD2	1147.00	2.62	1.90
50057.00	P08	M-017559	sorting nex	29887.00	SNX10	1658.00	6.33	1.81
50057.00	P09	M-031949	POM121-lik	29774.00	DKFZP434P211	2300.00	3.83	0.69
50057.00	P10	M-014196	sorting nex	29886.00	SNX8	2111.00	1.42	3.10
50057.00	P11	M-016078	parvin, beta	29780.00	PARVB	2011.00	3.43	1.09
50057.00	P12	M-008048	NPC1 (Nien	29881.00	NPC1L1	2415.00	1.61	2.91
50057.00	P13	M-008783	cytochrome	29785.00	CYP2S1	2083.00	1.44	3.08
50057.00	P14	M-020377	transcriptio	29842.00	TFCP2L1	1351.00	0.74	3.78
50057.00	P15	M-015680	GTP-bindin	29789.00	GTPBP9	1765.00	1.42	3.10
50057.00	P16	M-020375	grainyhead	29841.00	GRHL1	2574.00	1.28	3.24

50057.00	P17	M-010899	ubiquinol-c	29796.00	UCRC	3514.00	1.05	3.47
50057.00	P18	M-006978	replication	29803.00	REPIN1	4102.00	1.46	3.06
50057.00	P19	M-020366	chromosom	29798.00	C2orf27	2096.00	0.38	4.14
50057.00	P20	M-014194	zinc finger,	29801.00	ZDHHC8	2572.00	1.13	3.39
50057.00	P21	M-020369	yippee-like	29799.00	YPEL1	1282.00	1.72	2.80
50057.00	P23	M-014193	zinc finger,	29800.00	ZDHHC1	788.00	1.27	3.25
						2503.50	4.52	2.07
					MAD3			6.20
					MADc			3.06
50057.00	C22					4429.00	39.78	
50057.00	D22					4333.00	41.36	
50057.00	E22					3609.00	43.61	
50057.00	F22					4027.00	48.62	
					mn	4099.50	43.34	
					sd	369.21	3.85	
50057.00	G22					1067.00	1.31	
50057.00	H22					501.00	1.40	
50057.00	I22					185.00	2.70	
50057.00	J22					388.00	1.55	
					mn	358.00	1.88	
					sd	160.12	0.71	
					3psSD		11.56	
					3ngSD		2.14	
					SumSD		13.71	
					DiffMn		41.46	
					SmovrDiff		0.33	
					1minus		0.67	
50057.00	G03	M-003290	polo-like ki	5347.00	PLK1 SMARTpool	261.00	6.51	
50057.00	H03	M-003290	polo-like ki	5347.00	PLK1 SMARTpool	143.00	0.70	
50057.00	I03	D-001206-	siControl non-targeting			2443.00	2.09	
50057.00	J03	D-001206-	siControl non-targeting			2974.00	10.22	
50057.00	K03	D-001600-	siGLO RISC-free siRNA			3599.00	9.98	
50057.00	L03	D-001600-	siGLO RISC-free siRNA			2854.00	5.64	

rZ	Cell Coun	% inf	Abs Dev	rZ	Cell Count	% inf	Abs Dev	rZ	
1.10	1954.00	6.35	3.84	2.05	2259.00	1.02	1.79	-0.75	
0.26	886.00	0.79	1.72	-0.92	1732.00	0.46	2.35	-0.98	
0.61	891.00	3.14	0.63	0.34	1764.00	0.57	2.24	-0.94	
1.06	1181.00	5.76	3.25	1.74	3064.00	1.53	1.28	-0.53	
0.77	1457.00	5.01	2.50	1.34	3547.00	2.48	0.33	-0.14	
-0.16	1819.00	4.23	1.72	0.92	1487.00	0.61	2.20	-0.92	
1.60	1614.00	9.36	6.85	3.66	1703.00	0.53	2.28	-0.96	
0.10	889.00	2.47	0.04	-0.02	2626.00	1.14	1.67	-0.70	
-0.43	846.00	1.65	0.86	-0.46	1773.00	1.30	1.51	-0.63	
0.22	1822.00	2.91	0.40	0.21	2838.00	0.74	2.07	-0.87	
-0.72	1332.00	2.55	0.04	0.02	2781.00	0.93	1.88	-0.78	
-0.56	948.00	4.01	1.50	0.80	1049.00	0.57	2.24	-0.94	
-0.66	1249.00	1.44	1.07	-0.57	1176.00	0.60	2.21	-0.93	
-0.68	2257.00	4.34	1.83	0.98	2146.00	1.35	1.46	-0.61	
-0.40	878.00	2.16	0.35	-0.19	1759.00	0.91	1.90	-0.80	
2.22	1132.00	10.25	7.74	4.14	2076.00	3.95	1.14	0.48	y
-0.55	929.00	5.81	3.30	1.77	2729.00	1.54	1.27	-0.53	
-0.89	1319.00	1.74	0.77	-0.41	3005.00	0.57	2.24	-0.94	
-0.69	1048.00	0.19	2.32	-1.24	1752.00	2.00	0.81	-0.34	
-0.98	1089.00	1.93	0.58	-0.31	2003.00	0.60	2.21	-0.93	
1.03	2791.00	8.06	5.55	2.97	3084.00	1.46	1.35	-0.57	
-0.01	1892.00	7.14	4.63	2.47	2929.00	0.61	2.20	-0.92	
1.27	2282.00	4.82	2.31	1.24	2963.00	0.88	1.93	-0.81	
4.87	3310.00	11.12	8.61	4.61	4361.00	3.42	0.61	0.25	y
-0.90	2407.00	2.49	0.02	-0.01	2557.00	0.90	1.91	-0.80	
0.44	2398.00	5.09	2.58	1.38	2626.00	0.61	2.20	-0.92	
0.10	2987.00	3.11	0.60	0.32	3114.00	0.90	1.91	-0.80	
1.14	2319.00	2.50	0.01	-0.01	2688.00	1.82	0.99	-0.41	
-0.37	1825.00	1.86	0.65	-0.35	3225.00	2.51	0.30	-0.12	
1.29	2957.00	5.41	2.90	1.55	3566.00	5.33	2.52	1.06	
-0.33	2883.00	1.66	0.85	-0.45	3862.00	1.32	1.49	-0.62	
-1.33	1613.00	4.40	1.89	1.01	2001.00	1.00	1.81	-0.76	
-0.93	1181.00	1.27	1.24	-0.66	950.00	2.11	0.70	-0.29	
0.44	1483.00	1.75	0.76	-0.41	2437.00	1.19	1.62	-0.68	
-0.54	1410.00	0.64	1.87	-1.00	3367.00	2.38	0.43	-0.18	
-0.87	2258.00	1.06	1.45	-0.77	2811.00	1.28	1.53	-0.64	
-0.30	3873.00	1.94	0.57	-0.31	4822.00	1.29	1.52	-0.64	
1.31	3691.00	5.99	3.48	1.86	4505.00	13.56	10.75	4.51	
-1.26	3571.00	0.36	2.15	-1.15	4081.00	2.92	0.11	0.05	
-0.63	2940.00	1.70	0.81	-0.43	4019.00	4.21	1.40	0.59	
-0.04	2448.00	5.11	2.60	1.39	3061.00	1.21	1.60	-0.67	
0.18	1317.00	3.57	1.06	0.57	1911.00	0.37	2.44	-1.02	
2.02	3292.00	20.26	17.75	9.50	4170.00	3.77	0.96	0.40	y
1.48	3084.00	12.32	9.81	5.25	3906.00	1.61	1.20	-0.50	

1.10	2330.00	6.31	3.80	2.03	3371.00	0.47	2.34	-0.98	
0.93	3035.00	6.00	3.49	1.87	2604.00	0.31	2.50	-1.05	
0.58	1999.00	5.60	3.09	1.65	3947.00	1.32	1.49	-0.62	
0.57	2504.00	7.79	5.28	2.82	2815.00	0.85	1.96	-0.82	
0.88	1421.00	5.07	2.56	1.37	2727.00	1.39	1.42	-0.59	
0.78	3527.00	7.32	4.81	2.57	3424.00	1.52	1.29	-0.54	
0.13	1311.00	0.99	1.52	-0.81	1069.00	0.37	2.44	-1.02	
0.19	3299.00	5.33	2.82	1.51	1970.00	0.46	2.35	-0.99	
0.51	1749.00	2.23	0.28	-0.15	2232.00	1.93	0.88	-0.37	
1.10	1979.00	2.22	0.29	-0.15	2429.00	1.19	1.62	-0.68	
0.45	1500.00	2.53	0.02	0.01	2279.00	1.27	1.54	-0.64	
-0.33	1709.00	2.57	0.06	0.03	2318.00	0.65	2.16	-0.91	
0.49	2609.00	1.69	0.82	-0.44	3674.00	1.52	1.29	-0.54	
0.34	3895.00	4.18	1.67	0.90	3296.00	1.15	1.66	-0.69	
1.99	3939.00	3.25	0.74	0.40	4774.00	1.21	1.60	-0.67	
2.00	2900.00	4.83	2.32	1.24	2183.00	1.88	0.93	-0.39	
-1.20	2159.00	3.71	1.20	0.64	2125.00	0.28	2.53	-1.06	
-1.42	1938.00	5.31	2.80	1.50	2087.00	1.01	1.80	-0.76	
-0.10	2549.00	15.54	13.03	6.97	2579.00	3.41	0.60	0.25	
-0.76	2417.00	11.96	9.45	5.05	2575.00	0.85	1.96	-0.82	
-0.28	3640.00	7.83	5.32	2.85	3130.00	2.36	0.45	-0.19	
-0.50	1968.00	1.93	0.58	-0.31	2962.00	1.82	0.99	-0.41	
-1.10	2942.00	5.64	3.13	1.68	4041.00	2.05	0.76	-0.32	
-0.27	3018.00	6.63	4.12	2.20	4547.00	1.89	0.92	-0.38	
-1.01	3064.00	3.39	0.88	0.47	3388.00	1.51	1.30	-0.55	
-0.84	2572.00	3.11	0.60	0.32	3938.00	3.38	0.57	0.24	
0.19	2861.00	4.37	1.86	0.99	2559.00	0.66	2.15	-0.90	
0.23	2651.00	2.72	0.21	0.11	3607.00	2.25	0.56	-0.24	
0.04	2545.00	0.98	1.53	-0.82	3235.00	2.57	0.24	-0.10	
-0.40	1354.00	0.81	1.70	-0.91	2412.00	2.11	0.70	-0.29	
0.96	1433.00	1.26	1.25	-0.67	2644.00	3.03	0.22	0.09	
-0.08	1477.00	1.08	1.43	-0.76	3989.00	3.86	1.05	0.44	
0.73	3168.00	3.38	0.87	0.46	4311.00	5.01	2.20	0.92	
-0.36	2080.00	1.30	1.21	-0.65	3686.00	5.43	2.62	1.10	
1.93	2755.00	3.70	1.19	0.64	3995.00	3.28	0.47	0.20	
0.46	2540.00	0.16	2.35	-1.26	3927.00	3.72	0.91	0.38	
-0.42	4445.00	6.86	4.35	2.33	3070.00	4.40	1.59	0.67	
1.56	2609.00	6.78	4.27	2.29	1589.00	8.37	5.56	2.33	y
2.10	2259.00	10.27	7.76	4.15	2468.00	8.79	5.98	2.51	y
-1.23	1774.00	0.62	1.89	-1.01	1712.00	0.88	1.93	-0.81	
-0.57	2576.00	0.27	2.24	-1.20	2639.00	0.64	2.17	-0.91	
-0.67	1732.00	1.67	0.84	-0.45	2080.00	1.15	1.66	-0.69	
-0.56	3304.00	3.75	1.24	0.66	3595.00	4.06	1.25	0.52	
-0.21	1962.00	1.12	1.39	-0.74	1415.00	1.98	0.83	-0.35	
0.54	2035.00	2.26	0.25	-0.13	5337.00	8.38	5.57	2.33	

0.24	2803.00	1.57	0.94	-0.50	2101.00	2.28	0.53	-0.22	
0.14	3147.00	1.49	1.02	-0.54	3130.00	3.13	0.32	0.14	
0.56	3123.00	0.96	1.55	-0.83	4509.00	6.14	3.33	1.40	
0.57	2048.00	0.34	2.17	-1.16	3362.00	3.63	0.82	0.34	
1.85	2281.00	0.66	1.85	-0.99	2927.00	5.19	2.38	1.00	
0.49	1812.00	0.88	1.63	-0.87	2745.00	2.73	0.08	-0.03	
0.63	2193.00	1.32	1.19	-0.64	3680.00	10.46	7.65	3.21	
2.36	3621.00	1.41	1.10	-0.59	3527.00	7.29	4.48	1.88	
0.71	2716.00	0.77	1.74	-0.93	3550.00	4.87	2.06	0.87	
0.67	1893.00	0.58	1.93	-1.03	2122.00	5.09	2.28	0.96	
1.05	3075.00	0.07	2.44	-1.31	3938.00	4.06	1.25	0.53	
-1.28	1877.00	1.86	0.65	-0.35	3204.00	2.09	0.72	-0.30	
-1.08	1185.00	2.03	0.48	-0.26	1801.00	2.50	0.31	-0.13	
0.27	2574.00	8.66	6.15	3.29	1582.00	8.60	5.79	2.43	y
-0.25	1696.00	1.89	0.62	-0.33	1827.00	3.23	0.42	0.18	
-0.21	1141.00	2.02	0.49	-0.26	2078.00	3.42	0.61	0.25	
-0.44	5109.00	13.43	10.92	5.84	1162.00	2.58	0.23	-0.10	
1.78	2857.00	8.89	6.38	3.41	3269.00	12.70	9.89	4.14	y
0.81	1918.00	2.50	0.01	0.00	3028.00	4.26	1.45	0.61	
0.49	3016.00	2.09	0.42	-0.23	3921.00	2.81	0.00	0.00	
-0.48	2113.00	4.35	1.84	0.99	2371.00	2.70	0.11	-0.05	
0.29	2976.00	5.24	2.73	1.46	2857.00	4.48	1.67	0.70	
0.85	2851.00	3.86	1.35	0.72	2894.00	3.84	1.03	0.43	
1.44	2087.00	3.11	0.60	0.32	1790.00	2.18	0.63	-0.26	
1.14	1652.00	1.33	1.18	-0.63	2285.00	2.58	0.23	-0.09	
0.54	2958.00	1.08	1.43	-0.76	3307.00	6.68	3.87	1.62	
2.60	2635.00	2.77	0.26	0.14	2910.00	5.12	2.31	0.97	
0.59	2884.00	1.66	0.85	-0.45	3067.00	3.23	0.42	0.18	
3.44	2179.00	1.97	0.54	-0.29	1627.00	5.96	3.15	1.32	
1.33	1985.00	1.91	0.60	-0.32	2545.00	2.28	0.53	-0.22	
2.32	2884.00	2.60	0.09	0.05	3493.00	6.07	3.26	1.37	
-1.22	2026.00	1.28	1.23	-0.66	1672.00	1.61	1.20	-0.50	
-0.98	2328.00	1.29	1.22	-0.65	1801.00	2.28	0.53	-0.22	
0.56	2464.00	2.80	0.29	0.15	2305.00	5.77	2.96	1.24	
0.07	2342.00	1.24	1.27	-0.68	2431.00	6.13	3.32	1.39	
-0.55	2396.00	0.33	2.18	-1.16	3259.00	0.74	2.07	-0.87	
-0.03	845.00	0.59	1.92	-1.03	921.00	3.37	0.56	0.23	
-0.77	1993.00	0.65	1.86	-0.99	1753.00	2.68	0.13	-0.05	
-0.93	919.00	0.54	1.97	-1.05	1441.00	2.43	0.38	-0.16	
-0.66	2813.00	0.18	2.33	-1.25	3641.00	1.46	1.35	-0.57	
-0.24	2173.00	1.52	0.99	-0.53	2902.00	2.41	0.40	-0.17	
0.48	2390.00	3.89	1.38	0.74	2245.00	3.52	0.71	0.30	
-0.04	1538.00	1.50	1.01	-0.54	2229.00	2.11	0.70	-0.29	
2.07	2846.00	4.67	2.16	1.16	3472.00	6.83	4.02	1.68	
0.22	2352.00	1.83	0.68	-0.37	4066.00	1.52	1.29	-0.54	

0.87	1884.00	0.58	1.93	-1.03	1899.00	1.69	1.12	-0.47	
-0.50	1506.00	1.66	0.85	-0.46	2730.00	1.25	1.56	-0.65	
0.14	1774.00	1.18	1.33	-0.71	1644.00	1.03	1.78	-0.74	
-0.50	2361.00	1.31	1.20	-0.64	1324.00	1.51	1.30	-0.54	
0.44	2114.00	1.14	1.37	-0.74	2435.00	2.18	0.63	-0.26	
-0.25	1728.00	0.46	2.05	-1.10	2432.00	1.23	1.58	-0.66	
-0.35	3537.00	1.50	1.01	-0.54	1724.00	2.78	0.03	-0.01	
-1.25	1925.00	2.44	0.07	-0.04	2293.00	4.06	1.25	0.52	
-1.05	1698.00	3.53	1.02	0.55	1646.00	7.78	**4.97**	2.08	
-1.31	2125.00	2.73	0.22	0.12	1960.00	4.64	1.83	0.77	
-1.31	2586.00	1.16	1.35	-0.72	3792.00	5.41	2.60	1.09	
-0.84	1672.00	2.33	0.18	-0.10	1608.00	3.11	0.30	0.13	
-0.65	3473.00	3.40	0.89	0.47	3821.00	6.20	3.39	1.42	
-0.76	2455.00	2.81	0.30	0.16	2374.00	3.37	0.56	0.24	
-0.83	2236.00	3.76	1.25	0.67	3776.00	11.36	**8.55**	3.58	
-1.29	1543.00	2.46	0.05	-0.03	2867.00	3.10	0.29	0.12	
-0.88	2033.00	1.72	0.79	-0.42	2340.00	5.17	2.36	0.99	
-0.51	1557.00	1.61	0.90	-0.48	2232.00	3.94	1.13	0.48	
0.06	1714.00	0.88	1.63	-0.88	2194.00	4.56	1.75	0.73	
-0.40	1892.00	1.59	0.92	-0.50	2494.00	6.17	3.36	1.41	
0.02	1681.00	2.68	0.17	0.09	1696.00	4.19	1.38	0.58	
-0.34	2309.00	2.99	0.48	0.26	2128.00	10.76	**7.95**	3.33	
0.13	1969.00	3.45	0.94	0.50	2471.00	4.90	2.09	0.87	
0.27	1772.00	2.71	0.20	0.11	2558.00	5.94	3.13	1.31	
-0.39	1722.00	1.05	1.46	-0.78	2912.00	4.40	1.59	0.66	
-0.09	3091.00	3.11	0.60	0.32	3021.00	3.94	1.13	0.47	
-1.07	2628.00	3.23	0.72	0.39	1806.00	0.55	2.26	-0.94	
-0.55	1959.00	5.82	3.31	1.77	1867.00	2.62	0.19	-0.08	
-0.86	2163.00	3.24	0.73	0.39	2527.00	1.31	1.50	-0.63	
-0.15	2393.00	5.52	3.01	1.61	2001.00	2.70	0.11	-0.05	
-0.09	1968.00	2.29	0.22	-0.12	1886.00	3.76	0.95	0.40	
-0.58	1713.00	2.80	0.29	0.16	1489.00	1.07	1.74	-0.73	
0.87	1642.00	8.34	5.83	3.12	1599.00	9.63	**6.82**	2.86	x
-0.03	1542.00	5.38	2.87	1.54	1847.00	1.57	1.24	-0.52	
-0.83	1903.00	3.52	1.01	0.54	1948.00	2.16	0.65	-0.27	
-0.34	2184.00	3.94	1.43	0.76	1788.00	1.90	0.91	-0.38	
-0.85	736.00	2.04	0.47	-0.25	879.00	1.14	1.67	-0.70	
-0.50	1459.00	0.75	1.76	-0.94	723.00	0.69	2.12	-0.89	
-0.73	2474.00	2.10	0.41	-0.22	2673.00	1.95	0.86	-0.36	
-0.61	2843.00	3.06	0.55	0.29	2310.00	3.16	0.35	0.15	
-1.11	1577.00	2.85	0.34	0.18	1119.00	1.34	1.47	-0.62	
0.26	2241.00	1.47	1.04	-0.56	1796.00	3.29	0.48	0.20	
0.48	1230.00	3.25	0.74	0.40	1170.00	6.32	3.51	1.47	
-0.20	1765.00	3.23	0.72	0.38	1852.00	4.05	1.24	0.52	
-0.75	1862.00	2.20	0.31	-0.17	1680.00	8.93	**6.12**	2.56	

-0.40	1740.00	1.26	1.25	-0.67	915.00	7.43	4.62	1.94	
0.51	2773.00	1.44	1.07	-0.57	3196.00	1.00	1.81	-0.76	
0.09	2490.00	0.76	1.75	-0.94	1844.00	2.71	0.10	-0.04	
1.07	2003.00	2.15	0.36	-0.19	1617.00	1.30	1.51	-0.63	
0.16	2610.00	1.30	1.21	-0.65	2517.00	0.99	1.82	-0.76	
0.24	2841.00	1.58	0.93	-0.50	1605.00	0.62	2.19	-0.92	
1.77	1422.00	0.77	1.74	-0.93	888.00	2.36	0.45	-0.19	
0.98	2035.00	0.79	1.72	-0.92	1687.00	1.36	1.45	-0.61	
1.42	1310.00	0.61	1.90	-1.02	1436.00	2.23	0.58	-0.24	
1.30	1717.00	1.16	1.35	-0.72	1236.00	1.54	1.27	-0.53	
2.72	908.00	1.21	1.30	-0.70	1345.00	1.86	0.95	-0.40	
-0.23	1781.00	0.56	1.95	-1.04	1815.00	1.54	1.27	-0.53	
0.52	1752.00	2.85	0.34	0.18	2369.00	6.16	3.35	1.41	
0.49	1844.00	1.95	0.56	-0.30	3060.00	5.82	3.01	1.26	
1.40	1444.00	2.29	0.22	-0.12	2524.00	5.43	2.62	1.10	
1.37	1669.00	0.84	1.67	-0.89	2351.00	1.83	0.98	-0.41	
0.61	1870.00	1.60	0.91	-0.49	3002.00	5.73	2.92	1.22	
1.18	1879.00	0.59	1.92	-1.03	2578.00	9.74	**6.93**	2.90	
0.90	2055.00	2.19	0.32	-0.17	3361.00	5.44	2.63	1.10	
0.15	2632.00	1.67	0.84	-0.45	2881.00	5.62	2.81	1.18	
1.05	1325.00	0.91	1.60	-0.86	1880.00	5.32	2.51	1.05	
0.79	1788.00	6.54	4.03	2.16	2402.00	6.54	3.73	1.56	
3.16	1881.00	9.78	7.27	3.89	2700.00	8.15	**5.34**	2.24	y
0.95	1914.00	5.02	2.51	1.34	2152.00	3.07	0.26	0.11	
2.02	3356.00	6.97	4.46	2.39	3949.00	7.34	4.53	1.90	y
1.14	2332.00	2.49	0.02	-0.01	2308.00	2.64	0.17	-0.07	
1.72	3052.00	2.62	0.11	0.06	1712.00	5.32	2.51	1.05	
2.34	2554.00	3.76	1.25	0.67	2036.00	3.63	0.82	0.35	
2.01	1275.00	4.94	2.43	1.30	1146.00	5.93	3.12	1.31	
1.10	1959.00	1.68	0.83	-0.44	1826.00	4.22	1.41	0.59	
1.54	732.00	2.46	0.05	-0.03	1278.00	4.30	1.49	0.63	
-0.50	1810.00	0.61	1.90	-1.02	1697.00	1.94	0.87	-0.36	
1.03	1205.00	1.00	1.51	-0.81	636.00	4.40	1.59	0.67	
1.90	3794.00	3.85	1.34	0.72	2452.00	12.60	**9.79**	4.10	
0.32	2969.00	3.33	0.82	0.44	1307.00	2.91	0.10	0.04	
-0.56	1693.00	0.89	1.62	-0.87	1487.00	1.61	1.20	-0.50	
1.44	2545.00	2.32	0.19	-0.10	2427.00	4.86	2.05	0.86	
-0.63	712.00	0.42	2.09	-1.12	1144.00	4.98	2.17	0.91	
-0.45	1618.00	1.30	1.21	-0.65	2286.00	9.67	**6.86**	2.87	
9.17	2261.00	5.57	3.06	1.64	1456.00	24.79	**21.98**	9.21	y
-0.29	991.00	1.11	1.40	-0.75	2232.00	4.30	1.49	0.63	
-0.63	2421.00	0.87	1.64	-0.88	3237.00	6.49	3.68	1.54	
-1.00	2135.00	1.41	1.10	-0.59	758.00	2.90	0.09	0.04	
-1.10	2419.00	0.54	1.97	-1.06	1627.00	3.81	1.00	0.42	
0.36	2141.00	0.98	1.53	-0.82	1605.00	4.80	1.99	0.83	

-0.29	3407.00	0.97	1.54	-0.83	2597.00	6.70	3.89	1.63	
-1.03	1383.00	0.65	1.86	-1.00	1790.00	3.41	0.60	0.25	
-0.40	1554.00	0.32	2.19	-1.17	1198.00	1.17	1.64	-0.69	
-0.77	1565.00	1.02	1.49	-0.80	825.00	6.67	3.86	1.62	
-0.21	992.00	1.01	1.50	-0.80	583.00	3.09	0.28	0.12	
-0.40	1068.00	3.75	1.24	0.66	963.00	3.53	0.72	0.30	
-0.16	2299.00	1.35	1.16	-0.62	2329.00	8.72	5.91	2.48	
-0.86	1361.00	1.62	0.89	-0.48	1451.00	6.27	3.46	1.45	
-0.97	1588.00	2.64	0.13	0.07	1205.00	8.71	5.90	2.47	
0.34	1465.00	1.50	1.01	-0.54	2217.00	5.32	2.51	1.05	
-0.42	1485.00	1.89	0.62	-0.33	1475.00	2.51	0.30	-0.13	
-0.06	2568.00	3.35	0.84	0.45	2265.00	3.80	0.99	0.41	
0.25	2177.00	6.52	4.01	2.15	1900.00	4.26	1.45	0.61	
0.30	2598.00	4.70	2.19	1.17	2512.00	12.22	9.41	3.94	
-0.86	1555.00	3.02	0.51	0.27	1520.00	2.89	0.08	0.04	
-1.14	1341.00	3.06	0.55	0.29	1871.00	4.17	1.36	0.57	
1.73	1873.00	7.37	4.86	2.60	1636.00	2.81	0.00	0.00	
2.58	2790.00	7.78	5.27	2.82	1805.00	1.94	0.87	-0.36	y
-0.43	2302.00	2.74	0.23	0.12	864.00	0.69	2.12	-0.89	
2.82	2373.00	6.19	3.68	1.97	1415.00	0.57	2.24	-0.94	
0.94	2883.00	6.56	4.05	2.16	1813.00	1.65	1.16	-0.48	
0.59	1889.00	5.24	2.73	1.46	1127.00	0.53	2.28	-0.95	
2.38	1435.00	6.97	4.46	2.39	562.00	1.96	0.85	-0.36	x
0.16	1123.00	4.72	2.21	1.18	633.00	0.63	2.18	-0.91	
0.80	1512.00	4.37	1.86	0.99	495.00	2.02	0.79	-0.33	
0.84	996.00	2.81	0.30	0.16	877.00	0.91	1.90	-0.79	
2.16	2681.00	6.15	3.64	1.95	1368.00	3.07	0.26	0.11	
4.56	1083.00	3.79	1.28	0.68	579.00	3.28	0.47	0.20	
1.26	2134.00	6.56	4.05	2.17	2092.00	5.21	2.40	1.01	
3.38	1374.00	5.97	3.46	1.85	1240.00	4.76	1.95	0.82	
0.01	1656.00	1.51	1.00	-0.54	1342.00	6.18	3.37	1.41	
0.64	2494.00	2.49	0.02	-0.01	1014.00	5.03	2.22	0.93	
2.40	2220.00	7.12	4.61	2.46	1007.00	5.16	2.35	0.99	y
2.51	2022.00	2.28	0.24	-0.13	2045.00	7.68	4.87	2.04	x
4.85	2403.00	4.79	2.28	1.22	2955.00	12.49	9.68	4.05	y
0.51	724.00	1.66	0.85	-0.46	918.00	1.31	1.50	-0.63	
-0.49	2371.00	2.40	0.11	-0.06	1824.00	0.49	2.32	-0.97	
-0.29	1962.00	3.62	1.11	0.59	1776.00	0.23	2.58	-1.08	
-0.55	3033.00	2.44	0.07	-0.04	1650.00	0.42	2.39	-1.00	
0.01	2127.00	4.89	2.38	1.27	1451.00	1.17	1.64	-0.69	
0.10	1289.00	1.78	0.73	-0.39	1337.00	1.12	1.69	-0.71	
-0.26	1580.00	2.03	0.48	-0.26	1709.00	0.41	2.40	-1.01	
0.02	2020.00	5.15	2.64	1.41	1354.00	0.37	2.44	-1.02	
-1.08	1429.00	2.87	0.36	0.19	978.00	0.51	2.30	-0.96	
1.52	1882.00	5.63	3.12	1.67	1582.00	1.20	1.61	-0.67	

-1.08	2114.00	2.32	0.19	-0.10	2255.00	0.93	1.88	-0.79	
0.90	1544.00	5.57	3.06	1.64	1645.00	4.98	2.17	0.91	
0.21	1258.00	4.61	2.10	1.12	1371.00	2.41	0.40	-0.17	
-0.32	2816.00	2.63	0.12	0.06	1805.00	0.83	1.98	-0.83	
1.03	1390.00	6.76	4.25	2.28	1272.00	6.37	3.56	1.49	
1.25	1858.00	3.12	0.61	0.33	1504.00	3.52	0.71	0.30	
0.16	3011.00	3.85	1.34	0.72	1748.00	3.26	0.45	0.19	
0.60	3100.00	3.74	1.23	0.66	1369.00	0.80	2.01	-0.84	
1.37	3516.00	4.10	1.59	0.85	2119.00	4.96	2.15	0.90	
1.35	1165.00	2.32	0.19	-0.10	960.00	1.56	1.25	-0.52	
0.32	1659.00	2.89	0.38	0.20	1594.00	8.97	**6.16**	2.58	
-0.41	1375.00	0.65	1.86	-0.99	1238.00	5.41	2.60	1.09	
-0.36	1923.00	1.82	0.69	-0.37	915.00	3.28	0.47	0.20	
-0.53	1876.00	2.35	0.16	-0.09	1556.00	4.88	2.07	0.87	
-0.24	1476.00	1.08	1.43	-0.76	2071.00	7.10	4.29	1.80	
-0.85	1936.00	1.03	1.48	-0.79	1049.00	5.43	2.62	1.10	
-0.01	2084.00	1.30	1.21	-0.65	973.00	4.42	1.61	0.67	
0.26	1148.00	1.22	1.29	-0.69	474.00	9.28	**6.47**	2.71	
0.70	1994.00	3.46	0.95	0.51	934.00	5.57	2.76	1.16	
-0.58	1188.00	5.05	2.54	1.36	1466.00	4.30	1.49	0.62	
-0.19	629.00	0.79	1.72	-0.92	792.00	10.48	**7.67**	3.21	
-1.01	2056.00	2.97	0.46	0.24	2038.00	6.58	3.77	1.58	
-0.85	1819.00	2.80	0.29	0.16	2283.00	4.03	1.22	0.51	
-0.87	2819.00	7.73	5.22	2.79	2565.00	8.42	**5.61**	2.35	x
-0.96	3072.00	4.82	2.31	1.23	2060.00	5.39	2.58	1.08	
-0.72	3103.00	3.90	1.39	0.74	3176.00	9.13	**6.32**	2.65	
-0.77	2654.00	3.47	0.96	0.51	4368.00	7.55	4.74	1.99	
-1.22	2340.00	1.28	1.23	-0.66	2541.00	2.72	0.09	-0.04	
-1.11	2140.00	3.74	1.23	0.66	2401.00	9.37	**6.56**	2.75	
-0.72	1021.00	1.08	1.43	-0.77	2142.00	9.29	**6.48**	2.72	
-1.24	2270.00	2.33	0.18	-0.09	1865.00	3.81	1.00	0.42	
0.29	1679.00	6.02	3.51	1.88	1529.00	1.57	1.24	-0.52	
-0.09	1247.00	4.73	2.22	1.19	867.00	1.96	0.85	-0.36	
-0.20	822.00	3.65	1.14	0.61	1900.00	4.58	1.77	0.74	
-0.73	1439.00	3.27	0.76	0.40	1788.00	2.18	0.63	-0.26	
-0.62	1814.00	6.67	4.16	2.23	1188.00	0.93	1.88	-0.79	
0.59	1215.00	4.53	2.02	1.08	1472.00	6.45	3.64	1.53	
-0.23	1018.00	5.50	2.99	1.60	1361.00	2.35	0.46	-0.19	
-1.01	2130.00	4.37	1.86	0.99	1878.00	1.44	1.37	-0.57	
-0.36	1268.00	3.63	1.12	0.60	926.00	3.02	0.21	0.09	
-0.95	1285.00	5.68	3.17	1.70	1578.00	1.20	1.61	-0.67	
-1.01	1985.00	2.52	0.01	0.00	867.00	0.69	2.12	-0.89	
-1.24	1661.00	2.11	0.40	-0.22	535.00	2.06	0.75	-0.32	
-1.01	229.00	3.06	0.55	0.29	1366.00	4.98	2.17	0.91	
-1.06	1767.00	5.15	2.64	1.41	1478.00	2.17	0.64	-0.27	

-1.13	2034.00	2.31	0.20	-0.11	2175.00	6.11	3.30	1.39
-1.00	1879.00	1.38	1.13	-0.60	987.00	3.75	0.94	0.39
-1.35	666.00	2.55	0.04	0.02	579.00	3.11	0.30	0.13
-1.11	1612.00	2.42	0.09	-0.05	1564.00	6.52	3.71	1.56
-0.92	1034.00	1.35	1.16	-0.62	503.00	5.17	2.36	0.99
-1.06	693.00	0.72	1.79	-0.96	679.00	2.80	0.01	0.00
	1968.50	2.51	1.26		2083.50	2.81	1.61	
			3.79				4.84	
			1.87				2.39	
2886.00	19.23						2049.00	12.40
			2460.00	26.10	2187.00	9.51		
			2249.00	31.13	1682.00	11.53		
2529.00	17.91		3113.00	28.69				
2707.50	18.57		2607.33	28.64				
252.44	0.93		450.45	2.51				
482.00	0.83		526.00	3.42				
760.00	1.05		582.00	2.58				
609.00	1.48		169.00	3.55				
799.00	0.88		565.00	3.19				
722.67	1.14		438.67	3.10				
100.35	0.31		233.69	0.49				
	2.80			7.54				
	0.93			1.47				
	3.73			9.02				
	17.44			25.53				
	0.21			0.35				
	0.79			0.65				
259.00	1.16		160.00	3.75				
136.00	3.68		153.00	2.61				
1863.00	6.82		2088.00	1.87				
1206.00	1.24		1938.00	0.88				
3219.00	10.41		3745.00	7.93				
3998.00	2.18		3621.00	8.51				

art b

debris b

debris b,c

debris a,b

Plate	Well		Gene		GeneID	Cell Coun	% inf	Abs Dev
50058.00	A02	M-021104-	claudin 18	51208.00	CLDN18	2623.00	4.96	0.03
50058.00	A04	M-017708-	coiled-coil doma	51204.00	CCDC44	2866.00	9.39	4.40
50058.00	A05	M-020518-	stomatin (EPB72	30968.00	STOML2	2127.00	6.91	1.92
50058.00	A06	M-016299-	DEAD (Asp-Glu-A	51202.00	DDX47	2428.00	4.82	0.17
50058.00	A07	M-005911-	kallikrein-relatec	43847.00	KLK14	1278.00	2.03	2.96
50058.00	A08	M-018402-	zinc finger, DHH	51201.00	ZDHHC2	1212.00	12.95	**7.96**
50058.00	A09	M-005909-	kallikrein-relatec	43849.00	KLK12	2182.00	4.08	0.91
50058.00	A10	M-005818-	carboxypeptidas	51200.00	CPA4	1958.00	10.78	5.79
50058.00	A11	M-013945-	zinc finger protei	49854.00	ZNF295	2594.00	15.92	**10.93**
50058.00	A12	M-019133-	ninein (GSK3B in	51199.00	NIN	1478.00	6.50	1.51
50058.00	A13	M-010660-	zinc finger protei	49855.00	ZNF291	1877.00	12.47	**7.48**
50058.00	A14	M-004201-	phospholipase C,	51196.00	PLCE1	1029.00	6.22	1.23
50058.00	A15	M-010574-	cornulin	49860.00	CRNN	1269.00	6.54	1.55
50058.00	A16	M-015397-	importin 11	51194.00	IPO11	2466.00	7.54	2.55
50058.00	A17	M-015771-	G0/G1switch 2	50486.00	G0S2	4409.00	7.76	2.77
50058.00	A18	M-006984-	zinc finger protei	51193.00	ZNF639	1877.00	12.52	**7.53**
50058.00	A19	M-013059-	CD207 molecule,	50489.00	CD207	2265.00	10.77	5.78
50058.00	A20	M-021092-	synovial sarcoma	51188.00	SS18L2	881.00	15.10	**10.11**
50058.00	A21	M-010194-	NADPH oxidase	50507.00	NOX4	2064.00	14.58	**9.59**
50058.00	A23	M-013866-	NADPH oxidase	50508.00	NOX3	1929.00	9.95	4.96
50058.00	B02	M-005898-	endogenous retr	51354.00	HUMRTVL	1266.00	2.76	2.23
50058.00	B04	M-021068-	zinc finger protei	51157.00	ZNF580	1643.00	4.32	0.67
50058.00	B05	M-021107-	diferentiation-re	51212.00	LOC51212	2077.00	8.14	3.15
50058.00	B06	M-018403-	hypothetical pro	51240.00	LOC51240	1275.00	1.33	3.66
50058.00	B07	M-021108-	leucine zipper pr	51213.00	LUZP4	1730.00	4.10	0.89
50058.00	B08	M-021005-	ubiquitin-fold m	51569.00	UFM1	3587.00	6.13	1.14
50058.00	B09	M-021112-	glutaredoxin 5 h	51218.00	GLRX5	4471.00	10.56	5.57
50058.00	B10	M-013326-	armadillo repeat	51566.00	ARMCX3	2855.00	8.48	3.49
50058.00	B11	M-021114-	zinc finger protei	51222.00	ZNF219	2405.00	9.40	4.41
50058.00	B12	M-007975-	interleukin 23, al	51561.00	IL23A	1329.00	2.63	2.36
50058.00	B13	M-021116-	coatomer protei	51226.00	COPZ2	624.00	2.24	2.75
50058.00	B14	M-021096-	5'-nucleotidase c	51559.00	NT5DC3	3213.00	4.86	0.13
50058.00	B15	M-013176-	phosphatidylinos	51227.00	PIGP	2660.00	3.31	1.68
50058.00	B16	M-021130-	peroxisomal biog	51555.00	PEX5L	3449.00	5.04	0.05
50058.00	B17	M-017247-	glycolipid transfe	51228.00	GLTP	2962.00	3.61	1.38
50058.00	B18	M-009934-	RAB14, member	51552.00	RAB14	3513.00	3.05	1.94
50058.00	B19	M-015234-	PHD finger prote	51230.00	PHF20	3262.00	3.80	1.19
50058.00	B20	M-013306-	sirtuin (silent ma	51548.00	SIRT6	2634.00	2.92	2.07
50058.00	B21	M-008492-	cysteine rich tra	51232.00	CRIM1	3281.00	3.54	1.45
50058.00	B23	M-021124-	hypothetical pro	51233.00	LOC51233	3527.00	2.69	2.30
50058.00	C02	M-013170-	chromosome 15	51187.00	C15orf15	2468.00	2.59	2.40
50058.00	C04	M-021090-	WW domain bin	51186.00	WBP5	1664.00	2.76	2.23
50058.00	C05	M-016025-	synaptonemal c	50511.00	SYCP3	3276.00	5.16	0.17

50058.00	C06	M-021086-	cereblon	51185.00	CRBN	4953.00	6.76	1.77
50058.00	C07	M-020755-	podocalyxin-like	50512.00	PODXL2	5640.00	10.07	5.08
50058.00	C08	M-016860-	ATP binding dom	51184.00	ATPBD1C	4005.00	4.04	0.95
50058.00	C09	M-008882-	carbohydrate (ch	50515.00	CHST11	5036.00	10.15	5.16
50058.00	C10	M-021084-	heat shock 70kD	51182.00	HSPA14	3932.00	4.71	0.29
50058.00	C11	M-007968-	interleukin 20	50604.00	IL20	4751.00	5.83	0.84
50058.00	C12	M-009893-	hydroxyacid oxid	51179.00	HAO2	3994.00	14.57	**9.58**
50058.00	C13	M-013069-	UDP-N-acetyl-alp	50614.00	GALNT9	4167.00	9.94	4.95
50058.00	C14	M-016800-	pleckstrin homol	51177.00	PLEKHO1	3077.00	6.43	1.44
50058.00	C15	M-017817-	differentially exp	50619.00	DEF6	3943.00	8.12	3.13
50058.00	C16	M-021076-	N-acetylglucosar	51172.00	NAGPA	4212.00	6.48	1.49
50058.00	C17	M-018079-	CUB and zona pe	50624.00	CUZD1	4198.00	8.91	3.92
50058.00	C18	M-015668-	EGF-like-domain,	51162.00	EGFL7	3102.00	8.38	3.39
50058.00	C19	M-020756-	gem (nuclear org	50628.00	GEMIN4	3011.00	2.86	2.13
50058.00	C20	M-017937-	chromosome 3 c	51161.00	C3orf18	4496.00	21.24	**16.25**
50058.00	C21	M-021560-	solute carrier far	50651.00	SLC45A1	4210.00	11.07	**6.08**
50058.00	C23	M-010040-	neurogenin 3	50674.00	NEUROG3	3416.00	6.65	1.66
50058.00	D02	M-007774-	sirtuin (silent ma	51547.00	SIRT7	4690.00	5.99	1.00
50058.00	D04	M-021158-	zinc finger protei	51545.00	ZNF581	2934.00	3.78	1.21
50058.00	D05	M-021126-	transmembrane	51234.00	TMEM85	4261.00	2.02	2.97
50058.00	D06	M-021174-	vacuolar protein	51542.00	VPS54	3942.00	3.15	1.84
50058.00	D07	M-014264-	chromosome 8 c	51236.00	C8orf30A	5123.00	6.11	1.12
50058.00	D08	M-017175-	selenocysteine ly	51540.00	SCLY	4112.00	5.47	0.48
50058.00	D09	M-004433-	hypothetical pro	51237.00	MGC2950€	5655.00	4.92	0.07
50058.00	D10	M-016869-	zinc finger, CCHC	51538.00	ZCCHC17	4506.00	7.19	2.20
50058.00	D11	M-019465-	ankyrin repeat d	51239.00	ANKRD39	3480.00	12.90	**7.91**
50058.00	D12	M-021196-	mitochondrial pr	51537.00	MTP18	3677.00	7.61	2.62
50058.00	D13	M-021166-	chromosome 14	51241.00	C14orf112	1838.00	1.14	3.85
50058.00	D14	M-021306-	periphilin 1	51535.00	PPHLN1	3247.00	5.88	0.89
50058.00	D15	M-019087-	chromosome 3 c	51244.00	C3orf19	4552.00	5.87	0.88
50058.00	D16	M-016969-	Vps20-associate	51534.00	VTA1	3708.00	5.31	0.32
50058.00	D17	M-004446-	scotin	51246.00	SCOTIN	2621.00	1.49	3.50
50058.00	D18	M-019179-	PHD finger prote	51533.00	PHF7	3951.00	4.61	0.38
50058.00	D19	M-015376-	poly(A) binding p	51247.00	PAIP2	3075.00	3.61	1.38
50058.00	D20	M-014262-	chromosome 9 c	51531.00	C9orf156	3703.00	14.99	**10.00**
50058.00	D21	M-021134-	PDZ domain cont	51248.00	PDZD11	5312.00	9.49	4.50
50058.00	D23	M-021136-	transmembrane	51249.00	TMEM69	4108.00	7.89	2.90
50058.00	E02	M-006486-	vacuolar protein	51160.00	VPS28	4066.00	2.31	2.68
50058.00	E04	M-021065-	hematological ar	51155.00	HN1	3738.00	5.75	0.76
50058.00	E05	M-013062-	WD repeat doma	50717.00	WDR42A	3630.00	6.25	1.26
50058.00	E06	M-021065-	hematological ar	51155.00	HN1	3449.00	8.06	3.07
50058.00	E07	M-006263-	potassium chanr	50801.00	KCNK4	4614.00	5.37	0.38
50058.00	E08	M-013121-	mRNA turnover 4	51154.00	MRTO4	2844.00	3.41	1.58
50058.00	E09	M-015392-	myelin expressio	50804.00	MYEF2	3230.00	7.59	2.60

50058.00	E10	M-015303-	stromal cell deri	51150.00	SDF4	2612.00	6.16	1.17
50058.00	E11	M-031961-	development an	50807.00	DDEF1	1761.00	4.60	0.39
50058.00	E12	M-021060-	hypothetical LO	51149.00	LOC51149	2371.00	6.62	1.63
50058.00	E13	M-020867-	heterochromati	50809.00	HP1BP3	2519.00	4.25	0.74
50058.00	E14	M-021045-	dynein, cytoplas	51143.00	DYNC1LI1	2209.00	4.16	0.83
50058.00	E15	M-017093-	hepatoma-deriv	50810.00	HDGFRP3	3978.00	18.48	13.49
50058.00	E16	M-019120-	coiled-coil-helix-	51142.00	CHCHD2	2749.00	3.56	1.43
50058.00	E17	M-020873-	COP9 constitutiv	50813.00	COPS7A	2941.00	10.07	5.08
50058.00	E18	M-021037-	COP9 constitutiv	51138.00	COPS4	2488.00	3.70	1.29
50058.00	E19	M-013110-	villin-like	50853.00	VILL	3617.00	4.70	0.29
50058.00	E20	M-010205-	PTD016 protein	51136.00	LOC51136	3768.00	5.60	0.61
50058.00	E21	M-020876-	chromosome 6 c	50854.00	C6orf48	4177.00	5.41	0.42
50058.00	E23	M-013859-	par-6 partitionin	50855.00	PARD6A	2261.00	3.32	1.67
50058.00	F02	M-016879-	zinc finger, C3HC	51530.00	ZC3HC1	3412.00	5.66	0.67
50058.00	F04	M-016876-	chromosome 14	51528.00	C14orf100	2433.00	12.82	7.83
50058.00	F05	M-021137-	chromosome 6 c	51250.00	C6orf203	3047.00	3.48	1.51
50058.00	F06	M-020252-	chromosome 14	51527.00	C14orf129	2037.00	14.09	9.10
50058.00	F07	M-018884-	hypothetical pro	51252.00	LOC51252	2455.00	4.89	0.10
50058.00	F08	M-015649-	chromosome 20	51526.00	C20orf111	1545.00	3.50	1.49
50058.00	F09	M-017460-	mitochondrial ri	51253.00	MRPL37	2478.00	6.50	1.51
50058.00	F10	M-020266-	transmembrane	51524.00	TMEM138	2412.00	5.93	0.94
50058.00	F11	M-006985-	hypothetical pro	51255.00	LOC51255	1890.00	4.92	0.07
50058.00	F12	M-018807-	CXXC finger 5	51523.00	CXXC5	1627.00	1.97	3.02
50058.00	F13	M-021140-	TBC1 domain fa	51256.00	TBC1D7	1814.00	6.67	1.68
50058.00	F14	M-020269-	transmembrane	51522.00	TMEM14C	1929.00	3.78	1.21
50058.00	F15	M-006986-	membrane-asso	51257.00	MARCH2	1735.00	3.11	1.88
50058.00	F16	M-010171-	leucyl-tRNA synt	51520.00	LARS	1382.00	2.75	2.24
50058.00	F17	M-013563-	mitochondrial ri	51258.00	MRPL51	2616.00	3.33	1.66
50058.00	F18	M-004697-	chromatin modif	51510.00	CHMP5	3504.00	1.40	3.59
50058.00	F19	M-017173-	HSPC244	51259.00	MGC1337	2785.00	6.00	1.01
50058.00	F20	M-020569-	chromosome 20	51507.00	C20orf43	2842.00	2.99	2.00
50058.00	F21	M-018898-	chromosome X c	51260.00	CXorf26	3960.00	6.89	1.90
50058.00	F23	M-013181-	mitochondrial ri	51263.00	MRPL30	2922.00	0.89	4.10
50058.00	G02	M-021034-	coiled-coil doma	51134.00	CCDC41	3926.00	1.38	3.61
50058.00	G04	M-021032-	potassium chan	51133.00	KCTD3	3479.00	3.28	1.71
50058.00	G05	M-021372-	C-type lectin do	50856.00	CLEC4A	5852.00	4.97	0.02
50058.00	G06	M-006982-	ring finger protei	51132.00	RNF12	4255.00	4.94	0.05
50058.00	G07	M-020879-	sparc/osteonecti	50859.00	SPOCK3	5312.00	2.97	2.02
50058.00	G08	M-021310-	PHD finger prote	51131.00	PHF11	3176.00	3.31	1.68
50058.00	G09	M-006980-	ring finger protei	50862.00	RNF141	3543.00	5.56	0.57
50058.00	G10	M-017457-	ankyrin repeat a	51130.00	ASB3	3744.00	1.26	3.73
50058.00	G11	M-013115-	heme binding pr	50865.00	HEBP1	4134.00	3.27	1.72
50058.00	G12	M-021029-	SAR1 gene homo	51128.00	SAR1B	3528.00	4.39	0.60
50058.00	G13	M-007664-	phosphodiestera	50940.00	PDE11A	3677.00	3.40	1.59

50058.00	G14	M-006981-	tripartite motif-c	51127.00	TRIM17	3167.00	2.75	2.24
50058.00	G15	M-031945-	SH3 and multiple	50944.00	SHANK1	4820.00	4.05	0.94
50058.00	G16	M-008944-	N-acetyltransfer:	51126.00	NAT5	3520.00	2.53	2.46
50058.00	G17	M-007854-	transmembrane	50999.00	TMED5	3402.00	5.53	0.54
50058.00	G18	M-021027-	golgi autoantiger	51125.00	GOLGA7	4652.00	5.55	0.56
50058.00	G19	M-007544-	solute carrier far	51000.00	SLC35B3	5017.00	3.27	1.72
50058.00	G20	M-018948-	immediate early	51124.00	IER3IP1	4097.00	3.00	1.99
50058.00	G21	M-016763-	MTERF domain c	51001.00	MTERFD1	4269.00	3.09	1.90
50058.00	G23	M-031944-	TP53RK binding	51002.00	TPRKB	2296.00	1.70	3.29
50058.00	H02	M-020623-	ubiquitin-fold mc	51506.00	UFC1	2944.00	1.22	3.77
50058.00	H04	M-020786-	hypothetical pro	51504.00	HSPC152	1867.00	1.45	3.54
50058.00	H05	M-013182-	mitochondrial rit	51264.00	MRPL27	1733.00	1.15	3.84
50058.00	H06	M-020788-	hypothetical pro	51503.00	HSPC148	1961.00	0.61	4.38
50058.00	H07	M-010199-	pipecolic acid ox	51268.00	PIPOX	2371.00	5.44	0.45
50058.00	H08	M-016862-	chromosome 11	51501.00	C11orf73	2640.00	1.48	3.51
50058.00	H09	M-013860-	transcription fac	51270.00	TFDP3	4132.00	4.55	0.44
50058.00	H10	M-020809-	TP53 regulated ii	51499.00	TRIAP1	2875.00	0.87	4.12
50058.00	H11	M-018850-	blocked early in	51272.00	BET1L	4306.00	7.69	2.70
50058.00	H12	M-020811-	TH1-like (Drosop	51497.00	TH1L	1883.00	1.54	3.45
50058.00	H13	M-021144-	zinc finger protei	51276.00	ZNF571	3478.00	4.43	0.56
50058.00	H14	M-008272-	CTD (carboxy-ter	51496.00	CTDSPL2	2376.00	10.19	5.20
50058.00	H15	M-013467-	immediate early	51278.00	IER5	2206.00	3.08	1.91
50058.00	H16	M-010664-	protein tyrosine	51495.00	PTPLAD1	3708.00	6.12	1.13
50058.00	H17	M-007816-	complement con	51279.00	C1RL	2697.00	4.56	0.43
50058.00	H18	M-017647-	chromosome 22	51493.00	C22orf28	4452.00	13.90	**8.91**
50058.00	H19	M-013191-	golgi phosphopr	51280.00	GOLPH2	5096.00	17.03	**12.04**
50058.00	H20	M-016096-	hypothetical pro	51491.00	HSPC111	2993.00	4.88	0.11
50058.00	H21	M-020835-	ankyrin repeat ai	51281.00	ANKMY1	3254.00	4.55	0.44
50058.00	H23	M-013192-	SCAN domain co	51282.00	SCAND1	2879.00	4.03	0.96
50058.00	I02	M-021025-	zinc finger protei	51123.00	ZNF706	3380.00	3.93	1.06
50058.00	I04	M-021024-	COMM domain c	51122.00	COMMD2	3012.00	7.47	2.48
50058.00	I05	M-027282-	mediator of RNA	51003.00	MED31	3813.00	5.14	0.15
50058.00	I06	M-012864-	ribosomal protei	51121.00	RPL26L1	2228.00	6.10	1.11
50058.00	I07	M-009942-	coenzyme Q6 ho	51004.00	COQ6	3618.00	7.88	2.89
50058.00	I08	M-021018-	UTP11-like, U3 si	51118.00	UTP11L	2225.00	4.49	0.50
50058.00	I09	M-009449-	solute carrier far	51006.00	SLC35C2	2781.00	7.23	2.24
50058.00	I10	M-021015-	coenzyme Q4 ho	51117.00	COQ4	3623.00	7.65	2.66
50058.00	I11	M-031954-	activating signal	51008.00	ASCC1	3166.00	8.97	3.98
50058.00	I12	M-013140-	mitochondrial rit	51116.00	MRPS2	2262.00	3.01	1.98
50058.00	I13	M-010576-	Der1-like domair	51009.00	DERL2	948.00	3.59	1.40
50058.00	I14	M-021013-	family with sequ	51115.00	FAM82B	1524.00	7.55	2.56
50058.00	I15	M-031955-	exosome compo	51010.00	EXOSC3	3037.00	4.87	0.12
50058.00	I16	M-021011-	zinc finger, DHH(	51114.00	ZDHHC9	2188.00	9.32	4.33
50058.00	I17	M-020893-	slowmo homolog	51012.00	SLMO2	2123.00	5.18	0.19

50058.00	I18	M-016861-	tetratricopeptide	51112.00	TTC15	2969.00	10.61	5.62
50058.00	I19	M-013122-	exosome compo	51013.00	EXOSC1	1756.00	4.44	0.55
50058.00	I20	M-013366-	suppressor of va	51111.00	SUV420H1	2724.00	4.59	0.40
50058.00	I21	M-007855-	transmembrane	51014.00	TMED7	2572.00	1.75	3.24
50058.00	I23	M-020895-	isochorismatase	51015.00	ISOC1	1747.00	0.40	4.59
50058.00	J02	M-010900-	chromosome 9 c	51490.00	C9orf114	1971.00	2.64	2.35
50058.00	J04	M-013295-	variable charge,	51481.00	VCX3A	2442.00	2.33	2.66
50058.00	J05	M-009634-	RAS-like, family	51285.00	RASL12	3944.00	4.21	0.78
50058.00	J06	M-006631-	variable charge,	51480.00	VCX2	3073.00	6.57	1.58
50058.00	J07	M-019006-	cell cycle exit an	51286.00	CEND1	3328.00	2.43	2.56
50058.00	J08	M-013161-	ankyrin repeat a	51479.00	ANKFY1	2797.00	16.30	**11.31**
50058.00	J09	M-021148-	coiled-coil-helix-	51287.00	CHCHD8	3053.00	6.09	1.10
50058.00	J10	M-009669-	myo-inositol 1-p	51477.00	ISYNA1	1968.00	4.32	0.67
50058.00	J11	M-021151-	ERGIC and golgi	51290.00	ERGIC2	2208.00	4.76	0.23
50058.00	J12	M-013284-	calcium binding	51475.00	CABP2	2525.00	3.29	1.70
50058.00	J13	M-021160-	GEM interacting	51291.00	GMIP	2914.00	6.18	1.19
50058.00	J14	M-010663-	LIM domain and	51474.00	LIMA1	3040.00	6.55	1.56
50058.00	J15	M-010826-	ECSIT homolog (	51295.00	ECSIT	1498.00	3.14	1.85
50058.00	J16	M-020868-	doublecortin do	51473.00	DCDC2	2226.00	2.61	2.38
50058.00	J17	M-007400-	solute carrier fa	51296.00	SLC15A3	2619.00	7.03	2.04
50058.00	J18	M-013269-	N-acetyltransfer	51471.00	NAT8B	3111.00	4.73	0.26
50058.00	J19	M-008613-	palate, lung and	51297.00	PLUNC	2675.00	6.13	1.14
50058.00	J20	M-020911-	Scm-like with fo	51460.00	SFMBT1	3249.00	9.73	4.74
50058.00	J21	M-019203-	neuritin 1	51299.00	NRN1	3888.00	4.37	0.62
50058.00	J23	M-021164-	chromosome 3 c	51300.00	C3orf1	3251.00	5.66	0.67
50058.00	K02	M-021008-	lactamase, beta	51110.00	LACTB2	2289.00	3.06	1.93
50058.00	K04	M-003629-	retinol dehydrog	51109.00	RDH11	2010.00	8.66	3.67
50058.00	K05	M-017638-	chromosome 14	51016.00	C14orf122	2958.00	4.29	0.70
50058.00	K06	M-015394-	methyltransfera	51108.00	METTL9	2316.00	10.36	5.37
50058.00	K07	M-017639-	ribosomal RNA p	51018.00	RRP15	2401.00	5.58	0.59
50058.00	K08	M-007810-	anterior pharynx	51107.00	APH1A	3795.00	11.41	**6.42**
50058.00	K09	M-020900-	coiled-coil doma	51019.00	CCDC53	3375.00	7.05	2.06
50058.00	K10	M-027322-	PHD finger prote	51105.00	PHF20L1	3165.00	10.11	5.12
50058.00	K11	M-009960-	HD domain cont	51020.00	HDDC2	3265.00	8.94	3.95
50058.00	K12	M-005809-	family with sequ	51104.00	FAM108B1	2519.00	2.86	2.13
50058.00	K13	M-013130-	mitochondrial ri	51021.00	MRPS16	3182.00	13.20	**8.21**
50058.00	K14	M-021003-	NADH dehydrog	51103.00	NDUFAF1	2377.00	2.02	2.97
50058.00	K15	M-013131-	mitochondrial ri	51023.00	MRPS18C	2502.00	2.44	2.55
50058.00	K16	M-021000-	chromosome 8 c	51101.00	C8orf70	2281.00	4.47	0.52
50058.00	K17	M-020907-	fission 1 (mitoch	51024.00	FIS1	2880.00	4.41	0.58
50058.00	K18	M-017086-	SH3-domain GR	51100.00	SH3GLB1	4129.00	7.34	2.35
50058.00	K19	M-015261-	mitochondria-as	51025.00	Magmas	4042.00	7.84	2.85
50058.00	K20	M-020994-	intraflagellar tra	51098.00	IFT52	4253.00	11.95	**6.96**
50058.00	K21	M-015393-	golgi transport 1	51026.00	GOLT1B	2893.00	7.71	2.72

50058.00	K23	M-020910-	bolA homolog 1	51027.00	BOLA1	2571.00	4.47	0.52
50058.00	L02	M-020938-	Rh family, C glyc	51458.00	RHCG	4002.00	4.50	0.49
50058.00	L04	M-010198-	prenylcysteine o	51449.00	PCYOX1	3514.00	5.86	0.87
50058.00	L05	M-021167-	glucosaminyl (N-	51301.00	GCNT4	2591.00	10.00	5.01
50058.00	L06	M-006991-	ring finger protei	51444.00	RNF138	3390.00	4.63	0.36
50058.00	L07	M-008432-	cytochrome P45	51302.00	CYP39A1	2992.00	8.22	3.23
50058.00	L08	M-017939-	vestigial like 1 (D	51442.00	VGLL1	2744.00	4.41	0.58
50058.00	L09	M-008687-	zinc finger, DHH	51304.00	ZDHHC3	1698.00	4.95	0.04
50058.00	L10	M-021009-	YTH domain fam	51441.00	YTHDF2	2546.00	2.47	2.52
50058.00	L11	M-020738-	chromosome 5 c	51306.00	C5orf5	1658.00	5.49	0.50
50058.00	L12	M-017416-	hippocalcin like	51440.00	HPCAL4	1939.00	4.54	0.45
50058.00	L13	M-021256-	family with sequ	51307.00	FAM53C	3205.00	8.71	3.72
50058.00	L14	M-021014-	family with sequ	51439.00	FAM8A1	1845.00	5.75	0.76
50058.00	L15	M-021201-	receptor accessc	51308.00	REEP2	3292.00	5.41	0.42
50058.00	L16	M-006683-	melanoma antig	51438.00	MAGEC2	3844.00	7.52	2.53
50058.00	L17	M-013198-	armadillo repeat	51309.00	ARMCX1	4371.00	11.33	**6.34**
50058.00	L18	M-018234-	chromosome 1 c	51430.00	C1orf9	5158.00	10.06	5.07
50058.00	L19	M-007451-	solute carrier far	51310.00	SLC22A17	4102.00	8.92	3.93
50058.00	L20	M-010394-	DEAD (Asp-Glu-A	51428.00	DDX41	4098.00	3.00	1.99
50058.00	L21	M-007369-	solute carrier far	51312.00	SLC25A37	4081.00	5.37	0.38
50058.00	L23	M-018921-	chromosome 4 c	51313.00	C4orf18	2751.00	2.76	2.23
50058.00	M02	M-020992-	saccharopine de	51097.00	SCCPDH	3309.00	5.02	0.03
50058.00	M04	M-020991-	UTP18, small sub	51096.00	UTP18	2447.00	2.25	2.74
50058.00	M05	M-004701-	vacuolar protein	51028.00	VPS36	2196.00	1.82	3.17
50058.00	M06	M-016851-	chromosome 1 c	51093.00	C1orf66	2817.00	3.83	1.16
50058.00	M07	M-020915-	chromosome 1 c	51029.00	C1orf121	3899.00	7.46	2.47
50058.00	M08	M-020988-	SID1 transmemb	51092.00	SIDT2	2893.00	4.53	0.46
50058.00	M09	M-020922-	family with sequ	51030.00	FAM18B	3531.00	4.47	0.52
50058.00	M10	M-015559-	Sep (O-phospho	51091.00	SEPSECS	2563.00	5.35	0.36
50058.00	M11	M-019341-	glyoxalase doma	51031.00	GLOD4	3756.00	2.34	2.65
50058.00	M12	M-010932-	plasma membra	51090.00	PLLP	2281.00	1.32	3.67
50058.00	M13	M-005862-	elastase 2B	51032.00	ELA2B	3053.00	2.00	2.99
50058.00	M14	M-010933-	kelch-like 5 (Dro	51088.00	KLHL5	1523.00	2.69	2.30
50058.00	M15	M-008652-	SAPK substrate p	51035.00	LOC51035	1954.00	3.28	1.71
50058.00	M16	M-020983-	Y box binding pr	51087.00	YBX2	3506.00	2.25	2.74
50058.00	M17	M-017089-	zinc finger protei	51042.00	ZNF593	1919.00	1.04	3.95
50058.00	M18	M-008730-	crystallin, lambd	51084.00	CRYL1	1869.00	1.77	3.22
50058.00	M19	M-020935-	ST8 alpha-N-ace	51046.00	ST8SIA3	3540.00	3.90	1.09
50058.00	M20	M-004139-	galanin	51083.00	GAL	4530.00	2.74	2.25
50058.00	M21	M-013135-	peptidase inhibit	51050.00	PI15	3748.00	3.01	1.98
50058.00	M23	M-020941-	pleckstrin homol	51054.00	PLEKHA9	3023.00	0.93	4.06
50058.00	N02	M-019229-	zinc finger protei	51427.00	ZNF588	2573.00	5.83	0.84
50058.00	N04	M-021038-	polymerase (DN	51426.00	POLK	2106.00	2.99	2.00
50058.00	N05	M-020345-	lysine-rich coiled	51315.00	KRCC1	3719.00	16.56	**11.57**

50058.00	N06	M-013232-	angiomotin like	51421.00	AMOTL2	2046.00	3.86	1.13
50058.00	N07	M-020311-	placenta-specific	51316.00	PLAC8	3951.00	11.24	6.25
50058.00	N08	M-009829-	HemK methyltra	51409.00	HEMK1	3790.00	10.34	5.35
50058.00	N09	M-013206-	mitochondrial ri	51318.00	MRPL35	3188.00	11.86	6.87
50058.00	N10	M-013853-	nucleolar protei	51406.00	NOL7	2398.00	3.96	1.03
50058.00	N11	M-020548-	arginine/serine-	51319.00	RSRC1	4774.00	20.00	15.01
50058.00	N12	M-031953-	heat shock trans	51402.00	HSFX1	3863.00	18.30	13.31
50058.00	N13	M-006989-	ring finger and K	51320.00	RKHD2	2825.00	7.58	2.59
50058.00	N14	M-020929-	trafficking protei	51399.00	TRAPPC4	2627.00	6.28	1.29
	N15	M-010207-	archaemetzincin	51321.00	AMZ2	4370.00	11.88	6.89
50058.00	N16	M-020211-	chromosome 19	51398.00	C19orf56	2353.00	13.81	8.82
50058.00	N17	M-013325-	WW domain con	51322.00	WAC	2335.00	9.94	4.95
50058.00	N18	M-015756-	COMM domain	51397.00	COMMD1	2412.00	11.86	6.87
50058.00	N19	M-013476-	spastic paraplegi	51324.00	SPG21	3513.00	10.76	5.77
50058.00	N20	M-020946-	RWD domain co	51389.00	RWDD1	3580.00	6.65	1.66
50058.00	N21	M-020667-	ADP-ribosylation	51326.00	ARL17P1	2420.00	3.35	1.64
50058.00	N23	M-020729-	erythroid associa	51327.00	ERAF	820.00	0.73	4.26
50058.00	O02	M-020979-	polymerase (RN	51082.00	POLR1D	1603.00	4.55	0.44
50058.00	O04	M-013580-	mitochondrial ri	51081.00	MRPS7	912.00	2.74	2.25
50058.00	O05	M-020947-	hypothetical pro	51057.00	LOC51057	2746.00	13.00	8.01
50058.00	O06	M-016921-	NADH dehydrog	51079.00	NDUFA13	2412.00	5.22	0.23
50058.00	O07	M-020950-	zinc finger protei	51058.00	ZNF691	2838.00	9.16	4.17
50058.00	O08	M-021461-	THAP domain co	51078.00	THAP4	2724.00	10.32	5.33
50058.00	O09	M-020955-	family with sequ	51059.00	FAM135B	1936.00	6.82	1.83
50058.00	O10	M-020976-	FCF1 small subu	51077.00	FCF1	1544.00	3.37	1.62
50058.00	O11	M-009913-	thioredoxin dom	51060.00	TXNDC12	2592.00	11.73	6.74
50058.00	O12	M-020974-	cutC copper tran	51076.00	CUTC	1615.00	4.64	0.35
50058.00	O13	M-016755-	thioredoxin dom	51061.00	TXNDC11	1942.00	5.25	0.26
50058.00	O14	M-020968-	thioredoxin dom	51075.00	TXNDC14	2216.00	15.52	10.53
50058.00	O15	M-016818-	family with sequ	51063.00	FAM26B	1878.00	7.08	2.09
50058.00	O16	M-008475-	APAF1 interactin	51074.00	APIP	2261.00	6.06	1.07
50058.00	O17	M-020713-	HSPC157 protei	29092.00	HSPC157	1650.00	1.52	3.47
50058.00	O18	M-017470-	mitochondrial ri	51073.00	MRPL4	1823.00	1.37	3.62
50058.00	O19	M-020958-	similar to hypot	313156.00	RGD13107	3889.00	3.09	1.90
50058.00	O20	M-016087-	mediator of cell	51072.00	MEMO1	3421.00	4.97	0.02
50058.00	O21	M-013709-	formin homolog	29109.00	FHOD1	3862.00	5.52	0.53
50058.00	O23	M-020940-	prolactin releasi	51052.00	PRLH	1986.00	1.81	3.18
50058.00	P02	M-020446-	nuclear import 7	51388.00	NIP7	1173.00	3.75	1.24
50058.00	P04	M-020949-	eukaryotic transl	51386.00	EIF3S6IP	1558.00	8.67	3.68
50058.00	P05	M-020903-	spectrin, beta, n	51332.00	SPTBN5	1862.00	10.85	5.86
50058.00	P06	M-013216-	sorting nexin 7	51375.00	SNX7	1042.00	3.55	1.44
50058.00	P07	M-006990-	zinc finger protei	51333.00	ZNF771	1155.00	6.67	1.68
50058.00	P08	M-013215-	mitochondrial ri	51373.00	MRPS17	1425.00	10.39	5.40
50058.00	P09	M-020347-	proline rich 16	51334.00	PRR16	1171.00	6.66	1.67

50058.00	P10	M-021053-	coiled-coil doma	51372.00	CCDC72	2247.00	16.73	11.74
50058.00	P11	M-020257-	neugrin, neurite	51335.00	NGRN	545.00	2.39	2.60
50058.00	P12	M-016844-	proteasome mat	51371.00	POMP	840.00	8.93	3.94
50058.00	P13	M-017214-	membrane-span	51338.00	MS4A4A	2047.00	9.97	4.98
50058.00	P14	M-010662-	testis expressed	51368.00	TEX264	1736.00	5.30	0.31
50058.00	P15	M-019013-	crooked neck pre	51340.00	CRNKL1	1541.00	12.98	7.99
50058.00	P16	M-016449-	processing of pre	51367.00	POP5	2382.00	4.87	0.12
50058.00	P17	M-020833-	zinc finger protei	51351.00	ZNF117	1461.00	1.92	3.07
50058.00	P18	M-008411-	phospholipase A	51365.00	PLA1A	2330.00	4.89	0.10
50058.00	P19	M-016845-	hook homolog 1	51361.00	HOOK1	3103.00	2.90	2.09
50058.00	P20	M-021401-	zinc finger, MYN	51364.00	ZMYND10	2048.00	2.15	2.84
50058.00	P21	M-013213-	cell division cycle	51362.00	CDC40	1659.00	3.13	1.86
50058.00	P23	M-003960-	B cell RAG associ	51363.00	GALNAC4S	1203.00	2.66	2.33
						2843.00	4.99	2.00
					MAD3			6.00
					MADc			2.96
50058.00	C22					3439.00	42.95	
50058.00	D22					3985.00	35.38	
50058.00	E22					3005.00	30.32	
50058.00	F22			2151.00	18.13			
					mn	3476.33	36.22	
					sd	491.07	6.36	
50058.00	G22					254.00	5.91	
50058.00	H22					519.00	1.73	
50058.00	I22					69.00	5.80	
50058.00	J22					708.00	2.12	
					mn	432.00	3.22	
					sd	328.26	2.24	
					3psSD		19.07	
					3ngSD		6.73	
					SumSD		25.80	
					DiffMn		33.00	
					SmovrDiff		0.78	
					1minus		0.22	

50058.00	G03	M-003290-	polo-like kinase	5347.00	PLK1 SMA	284.00	1.06
50058.00	H03	M-003290-	polo-like kinase	5347.00	PLK1 SMA	309.00	2.59
50058.00	I03	D-001206-	siControl non-targeting siRN			3506.00	6.93
50058.00	J03	D-001206-	siControl non-targeting siRN			2191.00	7.90
50058.00	K03	D-001600-	siGLO RISC-free siRNA			4274.00	20.61
50058.00	L03	D-001600-	siGLO RISC-free siRNA			2964.00	6.34

rZ	**Cell Coun**	**% inf**	**Abs Dev**	**rZ**	**Cell Count**	**% inf**	**Abs Dev**	**rZ**	
-0.01	1871.00	0.96	1.00	-0.62	1981.00	7.32	2.65	0.74	
1.48	2339.00	1.75	0.21	-0.13	1864.00	8.48	3.81	1.06	
0.65	1725.00	2.84	0.88	0.55	1942.00	8.08	3.41	0.95	
-0.06	1208.00	1.16	0.80	-0.50	1537.00	5.20	0.53	0.15	
-1.00	1010.00	2.97	1.01	0.63	1411.00	5.81	1.14	0.32	
2.69	1078.00	5.66	3.70	2.31	2004.00	13.72	9.05	2.52	y
-0.31	2075.00	2.36	0.40	0.25	1834.00	5.07	0.40	0.11	
1.95	2373.00	5.10	3.14	1.96	2197.00	9.56	4.89	1.36	
3.69	1912.00	6.49	4.53	2.83	1797.00	12.30	7.63	2.12	y
0.51	727.00	3.16	1.20	0.75	1789.00	15.60	10.93	3.04	
2.53	1178.00	3.06	1.10	0.68	1963.00	9.22	4.55	1.27	
0.41	733.00	3.00	1.04	0.65	1478.00	6.43	1.76	0.49	
0.52	583.00	3.43	1.47	0.92	1247.00	5.85	1.18	0.33	
0.86	1838.00	2.99	1.03	0.64	1553.00	8.56	3.89	1.08	
0.93	2359.00	3.90	1.94	1.21	2097.00	5.20	0.53	0.15	
2.54	1184.00	7.26	5.30	3.31	1413.00	10.05	5.38	1.50	x
1.95	1123.00	5.43	3.47	2.17	2232.00	12.41	7.74	2.15	y
3.41	801.00	13.36	11.40	7.12	1652.00	9.38	4.71	1.31	x
3.24	867.00	4.61	2.65	1.66	1289.00	14.28	9.61	2.67	y
1.68	1124.00	3.91	1.95	1.22	2335.00	6.98	2.31	0.64	
-0.75	1956.00	0.66	1.30	-0.81	2158.00	4.12	0.55	-0.15	
-0.23	904.00	0.55	1.41	-0.88	1802.00	5.99	1.32	0.37	
1.06	1513.00	0.53	1.43	-0.89	2904.00	8.30	3.63	1.01	
-1.24	1927.00	0.42	1.54	-0.96	1641.00	2.32	2.35	-0.66	
-0.30	1132.00	0.09	1.87	-1.17	1765.00	2.72	1.95	-0.54	
0.38	2357.00	0.42	1.54	-0.96	4050.00	6.54	1.87	0.52	
1.88	2654.00	0.98	0.98	-0.61	3644.00	7.08	2.41	0.67	
1.18	1233.00	0.57	1.39	-0.87	2318.00	4.79	0.12	0.03	
1.49	2007.00	1.05	0.91	-0.57	2968.00	3.94	0.73	-0.20	
-0.80	1870.00	0.64	1.32	-0.82	2397.00	2.00	2.67	-0.74	
-0.93	886.00	0.11	1.85	-1.15	1017.00	1.87	2.80	-0.78	
-0.05	2351.00	0.09	1.87	-1.17	4756.00	4.23	0.44	-0.12	
-0.57	1107.00	0.27	1.69	-1.05	3210.00	0.81	3.86	-1.08	
0.02	2930.00	0.85	1.11	-0.69	2013.00	0.75	3.92	-1.09	
-0.47	2075.00	0.92	1.04	-0.65	3159.00	4.72	0.05	0.01	
-0.66	3538.00	1.19	0.77	-0.48	4415.00	2.42	2.25	-0.63	
-0.40	2636.00	1.52	0.44	-0.28	3260.00	2.98	1.69	-0.47	
-0.70	1739.00	0.46	1.50	-0.94	4154.00	3.25	1.42	-0.40	
-0.49	4547.00	0.55	1.41	-0.88	4960.00	4.98	0.31	0.09	
-0.78	1802.00	0.55	1.41	-0.88	3138.00	3.35	1.32	-0.37	
-0.81	1637.00	0.61	1.35	-0.84	2852.00	1.93	2.74	-0.76	
-0.75	1301.00	0.61	1.35	-0.84	1776.00	1.80	2.87	-0.80	
0.06	2945.00	2.61	0.65	0.41	2567.00	2.92	1.75	-0.49	

0.60	3222.00	2.39	0.43	0.27	4923.00	3.64	1.03	-0.29	
1.72	1897.00	0.79	1.17	-0.73	5045.00	3.19	1.48	-0.41	
-0.32	2038.00	0.39	1.57	-0.98	3367.00	2.52	2.15	-0.60	
1.74	2350.00	3.91	1.95	1.22	3533.00	2.77	1.90	-0.53	
-0.10	1809.00	2.82	0.86	0.54	2597.00	0.54	4.13	-1.15	
0.28	1693.00	0.59	1.37	-0.85	4975.00	1.87	2.80	-0.78	
3.24	907.00	3.64	1.68	1.05	2411.00	4.40	0.27	-0.08	
1.67	2148.00	4.66	2.70	1.68	4549.00	2.62	2.05	-0.57	
0.49	1482.00	1.89	0.07	-0.04	2924.00	4.41	0.26	-0.07	
1.06	1656.00	4.11	2.15	1.34	4771.00	3.48	1.19	-0.33	
0.50	2179.00	5.46	**3.50**	2.19	3452.00	1.30	3.37	-0.94	
1.32	1777.00	5.23	**3.27**	2.04	3545.00	3.27	1.40	-0.39	
1.14	1122.00	4.81	2.85	1.78	2832.00	2.22	2.45	-0.68	
-0.72	1555.00	1.48	0.48	-0.30	4044.00	2.57	2.10	-0.58	
5.49	1904.00	7.25	**5.29**	3.30	4396.00	6.39	1.72	0.48	y
2.05	1858.00	5.44	**3.48**	2.17	5081.00	6.20	1.53	0.43	y
0.56	2486.00	1.57	0.39	-0.24	2850.00	1.89	2.78	-0.77	
0.34	3033.00	2.67	0.71	0.44	4998.00	4.64	0.03	-0.01	
-0.41	1918.00	5.58	**3.62**	2.26	3977.00	3.85	0.82	-0.23	
-1.01	3077.00	0.49	1.47	-0.92	4041.00	1.29	3.38	-0.94	
-0.63	2003.00	2.20	0.24	0.15	3241.00	1.36	3.31	-0.92	
0.38	2056.00	2.09	0.13	0.08	4572.00	3.39	1.28	-0.36	
0.16	2262.00	1.95	0.01	-0.01	2950.00	0.31	4.36	-1.22	
-0.03	2743.00	1.46	0.50	-0.31	2627.00	0.30	4.37	-1.22	
0.74	2554.00	1.41	0.55	-0.34	3674.00	1.77	2.90	-0.81	
2.67	1727.00	4.00	2.04	1.27	3092.00	3.91	0.76	-0.21	
0.89	2587.00	5.10	3.14	1.96	3113.00	2.47	2.20	-0.61	
-1.30	966.00	1.55	0.41	-0.25	622.00	0.80	3.87	-1.08	
0.30	2260.00	2.57	0.61	0.38	1901.00	1.89	2.78	-0.77	
0.29	3597.00	4.48	2.52	1.57	3604.00	1.11	3.56	-0.99	
0.11	2487.00	2.57	0.61	0.38	2485.00	1.45	3.22	-0.90	
-1.19	2626.00	1.64	0.32	-0.20	2272.00	0.40	4.27	-1.19	
-0.13	4082.00	3.58	1.62	1.01	3981.00	1.93	2.74	-0.76	
-0.47	3565.00	2.44	0.48	0.30	4294.00	1.37	3.30	-0.92	
3.38	2873.00	7.83	**5.87**	3.67	3381.00	3.82	0.85	-0.24	y
1.52	3309.00	4.17	2.21	1.38	3543.00	3.53	1.14	-0.32	
0.98	4337.00	8.37	**6.41**	4.00	3758.00	2.24	2.43	-0.68	
-0.91	2446.00	0.70	1.26	-0.79	3190.00	2.73	1.94	-0.54	
0.26	2312.00	2.77	0.81	0.50	2147.00	1.54	3.13	-0.87	
0.43	2736.00	1.06	0.90	-0.56	2800.00	5.18	0.51	0.14	
1.04	2570.00	2.26	0.30	0.19	4069.00	7.10	2.43	0.68	
0.13	3335.00	3.78	1.82	1.14	3854.00	3.58	1.09	-0.30	
-0.54	1501.00	2.93	0.97	0.61	2160.00	3.19	1.48	-0.41	
0.88	1645.00	3.65	1.69	1.05	2740.00	6.53	1.86	0.52	

0.40	1767.00	2.49	0.53	0.33	3371.00	5.67	1.00	0.28	
-0.13	1724.00	3.94	1.98	1.24	2669.00	3.52	1.15	-0.32	
0.55	1276.00	2.59	0.63	0.39	2215.00	2.93	1.74	-0.48	
-0.25	2507.00	3.11	1.15	0.72	3072.00	3.58	1.09	-0.30	
-0.28	1369.00	3.07	1.11	0.69	2410.00	3.40	1.27	-0.35	
4.56	1635.00	8.44	**6.48**	4.05	2628.00	7.08	2.41	0.67	y
-0.48	1781.00	2.47	0.51	0.32	3281.00	3.14	1.53	-0.43	
1.71	1885.00	8.28	**6.32**	3.94	3884.00	6.44	1.77	0.49	
-0.44	800.00	6.63	**4.67**	2.91	3521.00	1.45	3.22	-0.90	
-0.10	2509.00	6.74	**4.78**	2.98	4444.00	7.25	2.58	0.72	
0.20	1827.00	3.67	1.71	1.07	3871.00	3.88	0.80	-0.22	
0.14	2220.00	5.09	3.13	1.95	3781.00	10.37	5.70	1.59	
-0.57	1945.00	3.55	1.59	0.99	3315.00	3.74	0.93	-0.26	
0.22	3633.00	2.39	0.43	0.27	2438.00	0.78	3.89	-1.08	
2.65	1664.00	9.44	**7.48**	4.67	1825.00	1.70	2.97	-0.83	y
-0.51	1605.00	2.49	0.53	0.33	2091.00	1.05	3.62	-1.01	
3.07	629.00	2.38	0.42	0.27	1579.00	3.55	1.12	-0.31	
-0.04	930.00	0.43	1.53	-0.96	1666.00	0.42	4.25	-1.18	
-0.51	459.00	1.09	0.87	-0.54	955.00	0.10	4.57	-1.27	
0.51	1125.00	3.20	1.24	0.77	2079.00	2.41	2.27	-0.63	
0.32	1034.00	4.16	2.20	1.37	2811.00	3.17	1.50	-0.42	
-0.03	1019.00	4.91	2.95	1.84	2189.00	2.19	2.48	-0.69	
-1.02	1016.00	2.95	0.99	0.62	1297.00	0.23	4.44	-1.24	
0.57	1295.00	5.48	**3.52**	2.20	1691.00	1.54	3.13	-0.87	
-0.41	1180.00	3.31	1.35	0.84	1562.00	1.47	3.20	-0.89	
-0.64	931.00	3.22	1.26	0.79	1204.00	2.08	2.59	-0.72	
-0.76	942.00	3.61	1.65	1.03	1867.00	0.54	4.13	-1.15	
-0.56	1059.00	3.59	1.63	1.02	1853.00	2.75	1.92	-0.53	
-1.22	1526.00	3.08	1.12	0.70	3959.00	2.90	1.77	-0.49	
0.34	1357.00	11.50	**9.54**	5.95	3121.00	10.19	5.52	1.54	
-0.68	1392.00	7.47	**5.51**	3.44	2447.00	6.82	2.15	0.60	
0.64	1527.00	18.34	**16.38**	10.23	3823.00	21.63	**16.96**	4.72	y
-1.39	2080.00	7.21	**5.25**	3.28	2289.00	4.24	0.43	-0.12	
-1.22	3849.00	0.88	1.08	-0.67	3244.00	5.64	0.97	0.27	
-0.58	2553.00	1.14	0.82	-0.51	2991.00	9.43	4.76	1.32	
-0.01	3707.00	1.97	0.01	0.01	3151.00	5.87	1.20	0.33	
-0.02	3258.00	1.17	0.79	-0.50	2928.00	6.15	1.48	0.41	
-0.68	2644.00	0.61	1.35	-0.85	3345.00	7.12	2.45	0.68	
-0.57	1253.00	0.48	1.48	-0.92	3082.00	17.46	**12.79**	3.56	
0.19	2396.00	2.25	0.29	0.18	3216.00	10.04	5.37	1.50	
-1.26	1527.00	0.39	1.57	-0.98	3474.00	3.14	1.53	-0.43	
-0.58	2266.00	1.24	0.72	-0.45	2973.00	8.31	3.64	1.01	
-0.20	2082.00	0.58	1.38	-0.86	3378.00	7.19	2.52	0.70	
-0.54	3212.00	0.78	1.18	-0.74	2886.00	4.75	0.08	0.02	

-0.76	1810.00	1.05	0.91	-0.57	1967.00	3.56	1.11	-0.31
-0.32	3714.00	2.77	0.81	0.51	4380.00	8.13	3.46	0.96
-0.83	2189.00	1.51	0.45	-0.28	3892.00	7.09	2.42	0.67
0.18	1466.00	2.80	0.84	0.52	1968.00	11.43	6.76	1.88
0.19	2153.00	2.23	0.27	0.17	4600.00	6.93	2.26	0.63
-0.58	2509.00	2.27	0.31	0.19	3284.00	2.86	1.81	-0.50
-0.67	3442.00	1.10	0.86	-0.53	3658.00	4.70	0.03	0.01
-0.64	2674.00	3.07	1.11	0.69	5149.00	6.41	1.74	0.48
-1.11	1434.00	1.19	0.77	-0.48	3756.00	3.91	0.76	-0.21
-1.28	2800.00	1.29	0.67	-0.42	2729.00	13.56	**8.89**	2.47
-1.20	2321.00	0.47	1.49	-0.93	2141.00	4.25	0.42	-0.12
-1.30	1476.00	0.47	1.49	-0.93	1299.00	6.70	2.03	0.56
-1.48	1393.00	0.65	1.31	-0.82	1868.00	5.94	1.27	0.35
0.15	1441.00	1.11	0.85	-0.53	1414.00	8.56	3.89	1.08
-1.19	1741.00	0.40	1.56	-0.97	2376.00	4.84	0.17	0.05
-0.15	2944.00	0.82	1.14	-0.71	3017.00	4.11	0.56	-0.16
-1.39	1542.00	0.97	0.99	-0.62	1525.00	3.41	1.26	-0.35
0.91	3456.00	1.79	0.17	-0.10	2800.00	8.57	3.90	1.09
-1.17	1771.00	0.45	1.51	-0.94	1324.00	3.02	1.65	-0.46
-0.19	2522.00	1.39	0.57	-0.36	2113.00	4.59	0.08	-0.02
1.75	941.00	1.28	0.68	-0.43	1948.00	9.03	4.36	1.21
-0.65	1919.00	0.36	1.60	-1.00	3230.00	4.18	0.49	-0.14
0.38	2450.00	0.45	1.51	-0.94	2333.00	2.14	2.53	-0.70
-0.15	2740.00	1.24	0.72	-0.45	1946.00	2.31	2.36	-0.66
3.01	2900.00	1.31	0.65	-0.41	4212.00	6.29	1.62	0.45
4.07	4136.00	3.24	1.28	0.80	3710.00	5.85	1.18	0.33
-0.04	1766.00	0.62	1.34	-0.83	2176.00	0.46	4.21	-1.17
-0.15	3062.00	0.36	1.60	-1.00	3858.00	1.97	2.70	-0.75
-0.33	2691.00	0.37	1.59	-0.99	4231.00	1.28	3.39	-0.95
-0.36	2400.00	1.46	0.50	-0.31	2218.00	3.43	1.24	-0.35
0.84	1193.00	2.43	0.47	0.29	1830.00	1.97	2.70	-0.75
0.05	2088.00	1.44	0.52	-0.33	3429.00	1.72	2.95	-0.82
0.38	1890.00	5.40	**3.44**	2.15	1951.00	1.44	3.23	-0.90
0.97	2889.00	1.83	0.13	-0.08	2624.00	2.17	2.50	-0.70
-0.17	1096.00	0.64	1.32	-0.82	1011.00	3.07	1.60	-0.45
0.75	1520.00	0.53	1.43	-0.90	2337.00	2.10	2.57	-0.72
0.90	2824.00	1.59	0.37	-0.23	2918.00	2.23	2.44	-0.68
1.34	2420.00	1.82	0.14	-0.09	3795.00	1.42	3.25	-0.90
-0.67	1130.00	2.48	0.52	0.32	1391.00	0.93	3.74	-1.04
-0.48	828.00	1.09	0.87	-0.55	515.00	0.78	3.89	-1.08
0.86	1705.00	1.11	0.85	-0.53	1781.00	1.74	2.93	-0.82
-0.04	2891.00	1.87	0.09	-0.06	3499.00	6.72	2.05	0.57
1.46	2024.00	2.87	0.91	0.57	2363.00	2.45	2.22	-0.62
0.06	2533.00	1.26	0.70	-0.43	3050.00	3.38	1.29	-0.36

1.90	2585.00	0.81	1.15	-0.72	2991.00	1.81	2.86	-0.80	
-0.19	2136.00	0.98	0.98	-0.61	2847.00	1.97	2.70	-0.75	
-0.14	3167.00	0.98	0.98	-0.61	3699.00	3.22	1.45	-0.41	
-1.10	2357.00	0.72	1.24	-0.77	2758.00	5.48	0.81	0.22	
-1.55	2175.00	0.28	1.68	-1.05	3162.00	1.49	3.18	-0.89	
-0.80	3113.00	5.17	3.21	2.01	5634.00	4.72	0.05	0.01	
-0.90	1543.00	2.33	0.37	0.23	2227.00	3.19	1.48	-0.41	
-0.27	2488.00	4.10	2.14	1.34	2982.00	3.22	1.45	-0.40	
0.53	1901.00	2.95	0.99	0.62	1894.00	3.01	1.66	-0.46	
-0.87	1931.00	2.18	0.22	0.13	2345.00	1.58	3.09	-0.86	
3.82	1727.00	16.10	**14.14**	8.83	1766.00	7.98	3.31	0.92	y
0.37	3009.00	7.71	**5.75**	3.59	2666.00	4.50	0.17	-0.05	
-0.23	1963.00	2.75	0.79	0.49	1894.00	1.11	3.56	-0.99	
-0.08	1826.00	1.59	0.37	-0.23	1836.00	1.47	3.20	-0.89	
-0.58	1688.00	3.26	1.30	0.81	2252.00	1.02	3.65	-1.02	
0.40	2277.00	7.38	**5.42**	3.38	2132.00	5.49	0.82	0.23	
0.52	1415.00	3.82	1.86	1.16	2326.00	4.64	0.03	-0.01	
-0.63	629.00	6.20	**4.24**	2.65	923.00	1.73	2.94	-0.82	
-0.81	2743.00	3.97	2.01	1.26	2939.00	2.89	1.78	-0.50	
0.69	1632.00	1.29	0.67	-0.42	1937.00	5.27	0.60	0.17	
-0.09	2376.00	3.45	1.49	0.93	2614.00	3.75	0.92	-0.26	
0.38	2102.00	2.66	0.70	0.44	2740.00	8.87	4.20	1.17	
1.60	2244.00	2.58	0.62	0.39	2592.00	4.32	0.35	-0.10	
-0.21	1330.00	2.03	0.07	0.04	3109.00	2.80	1.87	-0.52	
0.22	2658.00	4.29	2.33	1.45	2889.00	7.23	2.56	0.71	
-0.65	2578.00	1.12	0.84	-0.52	3560.00	14.33	**9.66**	2.69	
1.24	1153.00	1.73	0.23	-0.14	1336.00	10.11	5.44	1.51	
-0.24	2567.00	0.35	1.61	-1.00	3003.00	10.19	5.52	1.54	
1.81	2463.00	2.72	0.76	0.47	1757.00	13.89	**9.22**	2.57	
0.20	1742.00	1.84	0.12	-0.08	2480.00	12.98	**8.31**	2.31	
2.17	2505.00	2.52	0.56	0.35	2369.00	18.83	**14.16**	3.94	y
0.70	2372.00	0.97	0.99	-0.62	2654.00	12.74	**8.07**	2.24	
1.73	2878.00	3.30	1.34	0.84	2390.00	16.03	**11.36**	3.16	
1.33	1580.00	0.76	1.20	-0.75	2743.00	20.16	**15.49**	4.31	
-0.72	1600.00	0.69	1.27	-0.79	1688.00	7.11	2.44	0.68	
2.77	2658.00	6.81	**4.85**	3.03	2312.00	20.59	**15.92**	4.43	y
-1.01	967.00	0.93	1.03	-0.64	1031.00	7.47	2.80	0.78	
-0.86	1095.00	2.28	0.32	0.20	2137.00	7.96	3.29	0.91	
-0.18	2562.00	2.07	0.11	0.07	1151.00	10.08	5.41	1.50	
-0.20	1841.00	1.14	0.82	-0.51	1692.00	14.24	**9.57**	2.66	
0.79	1966.00	2.03	0.07	0.05	2843.00	15.48	**10.81**	3.01	
0.96	2245.00	3.79	1.83	1.14	1971.00	15.37	**10.70**	2.98	
2.35	2121.00	3.35	1.39	0.87	2496.00	20.31	**15.64**	4.35	x
0.92	1726.00	2.32	0.36	0.22	1473.00	15.82	**11.15**	3.10	

-0.18	1202.00	1.25	0.71	-0.44	1437.00	11.83	7.16	1.99	
-0.17	3629.00	2.89	0.93	0.58	5073.00	5.95	1.28	0.36	
0.29	2955.00	3.93	1.97	1.23	3694.00	6.93	2.26	0.63	
1.69	2326.00	1.46	0.50	-0.31	2132.00	7.83	3.16	0.88	
-0.12	2655.00	0.68	1.28	-0.80	3303.00	6.60	1.93	0.54	
1.09	1778.00	1.46	0.50	-0.31	1811.00	3.48	1.19	-0.33	
-0.20	1736.00	1.67	0.29	-0.18	2793.00	2.76	1.91	-0.53	
-0.02	1068.00	1.59	0.37	-0.23	1251.00	4.00	0.67	-0.19	
-0.85	1138.00	1.85	0.11	-0.07	3362.00	2.97	1.70	-0.47	
0.17	685.00	2.48	0.52	0.33	1805.00	5.71	1.04	0.29	
-0.15	569.00	1.58	0.38	-0.24	2309.00	3.55	1.12	-0.31	
1.25	1222.00	1.96	0.00	0.00	1743.00	4.13	0.54	-0.15	
0.25	1015.00	2.17	0.21	0.13	1607.00	1.87	2.80	-0.78	
0.14	1422.00	1.48	0.48	-0.30	2157.00	3.15	1.52	-0.42	
0.85	1486.00	1.82	0.14	-0.09	2313.00	1.86	2.81	-0.78	
2.14	2275.00	4.40	2.44	1.52	3763.00	7.76	3.09	0.86	
1.71	2250.00	1.96	0.00	0.00	3847.00	1.98	2.69	-0.75	
1.33	1855.00	1.78	0.18	-0.11	2770.00	3.68	0.99	-0.28	
-0.67	1678.00	2.86	0.90	0.56	4491.00	2.63	2.04	-0.57	
0.13	1510.00	0.66	1.30	-0.81	2064.00	1.60	3.07	-0.86	
-0.75	964.00	1.66	0.30	-0.19	1835.00	0.65	4.02	-1.12	
0.01	1266.00	0.71	1.25	-0.78	2632.00	1.41	3.26	-0.91	
-0.93	1478.00	1.89	0.07	-0.04	1284.00	0.55	4.12	-1.15	
-1.07	1874.00	1.33	0.63	-0.39	1726.00	3.07	1.60	-0.45	
-0.39	2638.00	1.71	0.25	-0.16	2422.00	3.72	0.95	-0.27	
0.83	3208.00	4.77	2.81	1.75	3298.00	2.52	2.15	-0.60	
-0.16	2021.00	5.64	**3.68**	2.30	2581.00	6.08	1.41	0.39	
-0.18	2300.00	3.22	1.26	0.79	3521.00	5.06	0.39	0.11	
0.12	1491.00	4.36	2.40	1.50	1986.00	4.78	0.11	0.03	
-0.90	2285.00	4.73	2.77	1.73	2302.00	2.74	1.93	-0.54	
-1.24	1774.00	3.33	1.37	0.85	2280.00	6.36	1.69	0.47	
-1.01	1637.00	2.81	0.85	0.53	2703.00	6.84	2.17	0.60	
-0.78	1435.00	3.34	1.38	0.86	1643.00	7.30	2.63	0.73	
-0.58	1902.00	2.47	0.51	0.32	1312.00	1.45	3.22	-0.90	
-0.93	1713.00	1.81	0.15	-0.09	2628.00	2.02	2.65	-0.74	
-1.34	1096.00	1.37	0.59	-0.37	2219.00	3.65	1.02	-0.28	
-1.09	1684.00	3.15	1.19	0.74	1397.00	4.01	0.66	-0.18	
-0.37	2559.00	5.35	**3.39**	2.12	3268.00	9.00	4.33	1.20	
-0.76	3083.00	2.34	0.38	0.23	3915.00	5.95	1.28	0.36	
-0.67	2384.00	2.27	0.31	0.19	3069.00	6.68	2.01	0.56	
-1.38	1037.00	2.41	0.45	0.28	1439.00	4.86	0.19	0.05	
0.28	1548.00	0.84	1.12	-0.70	4446.00	4.14	0.53	-0.15	
-0.68	1660.00	1.33	0.63	-0.40	1869.00	3.37	1.30	-0.36	
3.91	3022.00	4.27	2.31	1.44	4317.00	12.88	**8.21**	2.28	y

-0.38	2031.00	0.49	1.47	-0.92	1706.00	4.04	0.63	-0.17	
2.11	998.00	1.60	0.36	-0.22	2002.00	5.39	0.72	0.20	
1.81	1437.00	0.63	1.33	-0.83	3024.00	5.42	0.75	0.21	
2.32	1216.00	2.47	0.51	0.32	1765.00	5.61	0.94	0.26	
-0.35	1409.00	0.71	1.25	-0.78	2274.00	5.85	1.18	0.33	
5.07	1251.00	0.96	1.00	-0.62	3462.00	13.58	**8.91**	2.48	y
4.50	1920.00	2.76	0.80	0.50	2996.00	16.52	**11.85**	3.30	y
0.87	836.00	0.12	1.84	-1.15	2886.00	6.31	1.64	0.45	
0.43	1499.00	0.27	1.69	-1.06	4117.00	14.57	**9.90**	2.76	
2.33	1965.00	1.12	0.84	-0.52	4413.00	21.39	**16.72**	4.65	x
2.98	1687.00	1.72	0.24	-0.15	4196.00	31.65	**26.98**	7.51	y
1.67	1906.00	2.94	0.98	0.61	1607.00	12.07	**7.40**	2.06	
2.32	2103.00	2.23	0.27	0.17	1956.00	11.91	7.24	2.02	
1.95	2150.00	0.65	1.31	-0.82	2607.00	21.17	**16.50**	4.59	
0.56	2285.00	0.61	1.35	-0.84	2289.00	11.01	6.34	1.76	
-0.56	745.00	0.13	1.83	-1.14	1667.00	12.78	**8.11**	2.26	
-1.44	363.00	0.28	1.68	-1.05	588.00	15.31	**10.64**	2.96	
-0.15	2151.00	1.72	0.24	-0.15	2012.00	3.73	0.94	-0.26	
-0.76	1932.00	1.55	0.41	-0.25	1117.00	6.09	1.42	0.39	
2.71	3740.00	5.72	**3.76**	2.35	1634.00	6.43	1.76	0.49	y
0.08	2504.00	1.00	0.96	-0.60	2358.00	4.20	0.47	-0.13	
1.41	1513.00	1.72	0.24	-0.15	2646.00	6.24	1.57	0.44	
1.80	1291.00	1.16	0.80	-0.50	2419.00	7.98	3.31	0.92	
0.62	1921.00	0.57	1.39	-0.87	1307.00	8.11	3.44	0.96	
-0.55	1376.00	0.58	1.38	-0.86	1133.00	7.94	3.27	0.91	
2.28	1574.00	0.51	1.45	-0.91	2100.00	4.76	0.09	0.02	
-0.12	1514.00	0.73	1.23	-0.77	2927.00	8.51	3.84	1.07	
0.09	1813.00	2.81	0.85	0.53	1984.00	5.09	0.42	0.12	
3.56	1906.00	1.68	0.28	-0.18	3522.00	17.55	**12.88**	3.58	y
0.71	2027.00	1.53	0.43	-0.27	3681.00	9.02	4.35	1.21	
0.36	2083.00	2.26	0.30	0.19	2628.00	6.66	1.99	0.55	
-1.18	1277.00	0.47	1.49	-0.93	1600.00	5.19	0.52	0.14	
-1.22	1765.00	0.91	1.05	-0.66	1350.00	5.04	0.37	0.10	
-0.65	2267.00	1.01	0.95	-0.59	2604.00	3.11	1.56	-0.43	
-0.01	1949.00	2.26	0.30	0.19	2131.00	6.80	2.13	0.59	
0.18	2092.00	0.91	1.05	-0.66	3147.00	4.99	0.32	0.09	
-1.08	957.00	1.25	0.71	-0.44	1525.00	5.57	0.90	0.25	
-0.42	538.00	6.88	**4.92**	3.07	1331.00	2.18	2.49	-0.69	
1.24	1283.00	4.29	2.33	1.45	1974.00	7.29	2.62	0.73	
1.98	1307.00	4.13	2.17	1.36	3420.00	4.30	0.37	-0.10	
-0.49	1221.00	4.10	2.14	1.33	1552.00	6.06	1.39	0.39	
0.57	777.00	0.90	1.06	-0.66	2848.00	7.20	2.53	0.70	
1.82	985.00	2.54	0.58	0.36	2196.00	7.42	2.75	0.77	
0.56	884.00	2.49	0.53	0.33	1558.00	3.15	1.52	-0.43	

3.97	2231.00	2.06	0.10	0.06	3586.00	11.52	6.85	1.91	
-0.88	1340.00	0.82	1.14	-0.71	3201.00	7.09	2.42	0.67	
1.33	1089.00	1.84	0.12	-0.08	1147.00	16.39	**11.72**	3.26	
1.68	1719.00	0.87	1.09	-0.68	3538.00	10.77	6.10	1.70	
0.10	2283.00	3.02	1.06	0.66	2018.00	12.34	**7.67**	2.13	
2.70	1292.00	4.80	2.84	1.77	2132.00	15.95	**11.28**	3.14	y
-0.04	3094.00	0.90	1.06	-0.66	2812.00	7.79	3.12	0.87	
-1.04	2336.00	1.97	0.01	0.01	1884.00	8.97	4.30	1.20	
-0.03	2148.00	1.68	0.28	-0.18	1432.00	8.59	3.92	1.09	
-0.71	4009.00	4.81	2.85	1.78	2633.00	19.22	**14.55**	4.05	
-0.96	1905.00	1.47	0.49	-0.31	2359.00	16.02	**11.35**	3.16	
-0.63	2031.00	0.89	1.07	-0.67	1055.00	11.19	6.52	1.81	
-0.79	1587.00	0.76	1.20	-0.75	855.00	13.57	**8.90**	2.48	
	1887.50	1.96	1.08		2490.50	4.67	2.43		
			3.25				7.28		
			1.60				3.59		

1489.00	33.98	2622.00	31.27
3231.00	37.08	2478.00	21.27
1827.00	30.98	3189.00	48.42
1736.00	39.80	2785.00	46.79
2070.75	35.46	2768.50	36.94
786.57	3.82	307.11	12.99
167.00	2.99	509.00	1.57
588.00	0.85	429.00	0.93
178.00	2.25	307.00	2.28
545.00	4.59	512.00	0.98
437.00	2.56	416.00	1.40
225.33	1.89	103.12	0.77
	11.46		38.98
	5.66		2.30
	17.12		41.27
	32.90		35.54
	0.52		1.16
	0.48		-0.16

174.00	2.30	194.00	5.15
215.00	0.47	284.00	15.49
1864.00	2.47	2071.00	1.59
1790.00	7.43	2584.00	5.92
3245.00	1.94	4899.00	25.19
4162.00	6.32	5638.00	11.90

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debris a

Plate	Well	Gene			GeneID	Cell Coun	% inf	Abs Dev	rZ
50059.00	A02	M-013768-	coiled-coil	54482.00	CCDC76	2509.00	2.35	2.68	-0.57
50059.00	A04	M-025373-	chondroitir	54480.00	CSGlcA-T	3020.00	6.46	1.43	0.31
50059.00	A05	M-017972-	family witl	51571.00	FAM49B	1350.00	2.22	2.81	-0.60
50059.00	A06	M-016930-	toll interac	54472.00	TOLLIP	1060.00	1.42	3.61	-0.77
50059.00	A07	M-009233-	membrane	51573.00	MIR16	2616.00	1.80	3.23	-0.69
50059.00	A08	M-015938-	Smith-Mag	54471.00	SMCR7L	1994.00	3.16	1.87	-0.40
50059.00	A09	M-020996-	La ribonucl	51574.00	LARP7	2794.00	2.29	2.74	-0.58
50059.00	A10	M-013756-	armadillo r	54470.00	ARMCX6	3996.00	6.46	1.43	0.31
50059.00	A11	M-015235-	ESF1, nucle	51575.00	ESF1	2967.00	5.19	0.16	0.04
50059.00	A12	M-009477-	zinc finger,	54469.00	ZFAND6	3114.00	6.01	0.98	0.21
50059.00	A13	M-008552-	antizyme ir	51582.00	AZIN1	1837.00	3.38	1.65	-0.35
50059.00	A14	M-021181-	hypothetic	54468.00	FLJ20323	2199.00	4.59	0.44	-0.09
50059.00	A15	M-015381-	PCF11, clea	51585.00	PCF11	1070.00	2.43	2.60	-0.55
50059.00	A16	M-028950-	ankyrin rep	54467.00	ANKIB1	2922.00	2.40	2.63	-0.56
50059.00	A17	M-017015-	PC2 (positi	51586.00	PCQAP	3524.00	10.27	5.24	1.12
50059.00	A18	M-021182-	spindlin far	54466.00	SPIN2A	2793.00	4.62	0.41	-0.09
50059.00	A19	M-019234-	ARS2 prote	51593.00	ARS2	1314.00	3.73	1.30	-0.28
50059.00	A20	M-021193-	Ewing's tur	54465.00	ETAA1	1756.00	4.61	0.42	-0.09
50059.00	A21	M-020986-	neuroblast	51594.00	NAG	1402.00	9.34	4.31	0.92
50059.00	A23	M-020978-	cutA divale	51596.00	CUTA	1922.00	12.54	7.51	1.60
50059.00	B02	M-020715-	glutamine-	54870.00	QRICH1	2613.00	0.65	4.38	-0.93
50059.00	B04	M-013370-	EPS8-like 1	54869.00	EPS8L1	2579.00	0.78	4.25	-0.91
50059.00	B05	M-015713-	DiGeorge s	54487.00	DGCR8	4028.00	0.60	4.43	-0.95
50059.00	B06	M-007329-	transmemt	54868.00	TMEM104	4158.00	2.43	2.60	-0.55
50059.00	B07	M-015187-	UDP glucur	54490.00	UGT2B28	4143.00	3.69	1.34	-0.28
50059.00	B08	M-017177-	hypothetic	54867.00	FLJ20254	3854.00	1.45	3.58	-0.76
50059.00	B09	M-020519-	family witl	54491.00	FAM105A	4419.00	0.79	4.24	-0.90
50059.00	B10	M-013014-	G patch do	54865.00	GPATCH4	3917.00	0.87	4.16	-0.89
50059.00	B11	M-020517-	chromosor	54494.00	C11orf71	2626.00	1.33	3.70	-0.79
50059.00	B12	M-020707-	chromosor	54863.00	C9orf167	3738.00	0.67	4.36	-0.93
50059.00	B13	M-020944-	thioredoxir	54495.00	TXNDC10	3845.00	1.59	3.44	-0.73
50059.00	B14	M-015744-	coiled-coil	54862.00	CC2D1A	4163.00	1.39	3.64	-0.78
50059.00	B15	M-010160-	protein arg	54496.00	PRMT7	3872.00	0.34	4.69	-1.00
50059.00	B16	M-013369-	membrane	54860.00	MS4A12	3945.00	3.47	1.56	-0.33
50059.00	B17	M-022657-	HEAT repea	54497.00	HEATR5B	4560.00	1.16	3.87	-0.82
50059.00	B18	M-020705-	transmemt	54859.00	TMEM103	3532.00	0.85	4.18	-0.89
50059.00	B19	M-009493-	spermine c	54498.00	SMOX	3038.00	0.92	4.11	-0.88
50059.00	B20	M-005994-	pyroglutan	54858.00	PGPEP1	3653.00	0.99	4.04	-0.86
50059.00	B21	M-013757-	transmemt	54499.00	TMCO1	3528.00	1.84	3.19	-0.68
50059.00	B23	M-020512-	RNA-bindir	54502.00	FLJ20273	3584.00	5.08	0.05	0.01
50059.00	C02	M-013754-	5'-3' exorit	54464.00	XRN1	3239.00	0.86	4.17	-0.89
50059.00	C04	M-016936-	family witl	54463.00	FAM134B	2224.00	1.21	3.82	-0.81
50059.00	C05	M-008405-	lipoyltrans	51601.00	LIPT1	3570.00	1.43	3.60	-0.77
50059.00	C06	M-013753-	KIAA1128	54462.00	KIAA1128	2927.00	2.56	2.47	-0.53
50059.00	C07	M-017973-	nucleolar p	51602.00	NOP5/NOF	3261.00	0.52	4.51	-0.96
50059.00	C08	M-013389-	F-box and \	54461.00	FBXW5	3968.00	3.10	1.93	-0.41

50059.00	C09	M-015132-	KIAA0859	51603.00	KIAA0859	4738.00	1.98	3.05	-0.65
50059.00	C10	M-013388-	mitochond	54460.00	MRPS21	1704.00	2.11	2.92	-0.62
50059.00	C11	M-003691-	phosphatic	51604.00	PIGT	3168.00	5.62	0.59	0.13
50059.00	C12	M-021337-	proline rich	54458.00	PRR13	1857.00	1.99	3.04	-0.65
50059.00	C13	M-017324-	CGI-09 pro	51605.00	CGI-09	4144.00	2.92	2.11	-0.45
50059.00	C14	M-013387-	Mov10l1, M	54456.00	MOV10L1	3923.00	5.53	0.50	0.11
50059.00	C15	M-020967-	chromosor	51608.00	C7orf20	4379.00	1.78	3.25	-0.69
50059.00	C16	M-022191-	F-box prote	54455.00	FBXO42	4912.00	3.54	1.49	-0.32
50059.00	C17	M-020926-	DPH5 hom	51611.00	DPH5	3293.00	0.91	4.12	-0.88
50059.00	C18	M-022640-	ATPase fan	54454.00	ATAD2B	3123.00	0.54	4.49	-0.96
50059.00	C19	M-020898-	ERGIC and	51614.00	ERGIC3	2592.00	2.35	2.68	-0.57
50059.00	C20	M-008173-	Ras and Ra	54453.00	RIN2	3040.00	3.03	2.00	-0.43
50059.00	C21	M-008848-	HMP19 prc	51617.00	HMP19	3603.00	4.19	0.84	-0.18
50059.00	C23	M-021482-	chromosor	51622.00	C7orf28A	3753.00	3.70	1.33	-0.28
50059.00	D02	M-010666-	glycerophc	54857.00	GDPD2	3104.00	0.81	4.22	-0.90
50059.00	D04	M-019400-	gon-4-like	54856.00	GON4L	4442.00	1.19	3.84	-0.82
50059.00	D05	M-020510-	zinc finger,	54503.00	ZDHHC13	3323.00	0.27	4.76	-1.02
50059.00	D06	M-020700-	family with	54855.00	FAM46C	3552.00	1.52	3.51	-0.75
50059.00	D07	M-005828-	carboxype	54504.00	CPVL	4266.00	1.24	3.79	-0.81
50059.00	D08	M-020696-	family with	54854.00	FAM83E	4084.00	1.49	3.54	-0.75
50059.00	D09	M-013759-	DEAH (Asp	54505.00	DHX29	2975.00	2.72	2.31	-0.49
50059.00	D10	M-015363-	WD repeat	54853.00	WDR55	4519.00	1.66	3.37	-0.72
50059.00	D11	M-031080-	ADAMTS-li	54507.00	ADAMTSL4	4470.00	2.35	2.68	-0.57
50059.00	D12	M-020694-	ankyrin rep	54851.00	ANKRD49	4289.00	2.38	2.65	-0.57
50059.00	D13	M-025114-	3-hydroxyr	54511.00	HMGCLL1	3374.00	1.87	3.16	-0.67
50059.00	D14	M-020685-	hypothetic	54849.00	FLJ20186	3744.00	1.63	3.40	-0.73
50059.00	D15	M-013760-	exosome c	54512.00	EXOSC4	4180.00	2.54	2.49	-0.53
50059.00	D16	M-020674-	SID1 transr	54847.00	SIDT1	4687.00	3.76	1.27	-0.27
50059.00	D17	M-020495-	tudor dom	54513.00	TDRD4	3519.00	1.65	3.38	-0.72
50059.00	D18	M-020672-	RNA bindir	54845.00	RBM35A	3819.00	2.49	2.54	-0.54
50059.00	D19	M-012904-	DEAD (Asp	54514.00	DDX4	4046.00	4.45	0.58	-0.12
50059.00	D20	M-013555-	synaptotag	54843.00	SYTL2	3253.00	3.32	1.71	-0.36
50059.00	D21	M-015662-	amyloid be	54518.00	APBB1IP	4635.00	5.67	0.64	0.14
50059.00	D23	M-016945-	coiled-coil	54520.00	CCDC93	4082.00	2.01	3.02	-0.64
50059.00	E02	M-021199-	potassium	54442.00	KCTD5	3021.00	0.20	4.83	-1.03
50059.00	E04	M-021208-	chromosor	54440.00	CXorf9	4165.00	1.25	3.78	-0.81
50059.00	E05	M-020872-	dynein, cyt	51626.00	DYNC2LI1	4345.00	0.97	4.06	-0.87
50059.00	E06	M-024337-	RNA bindir	54439.00	RBM27	2759.00	2.32	2.71	-0.58
50059.00	E07	M-007319-	solute carr	51629.00	SLC25A39	4719.00	3.56	1.47	-0.31
50059.00	E08	M-021214-	glucose-fru	54438.00	GFOD1	4153.00	0.75	4.28	-0.91
50059.00	E09	M-020770-	LUC7-like 2	51631.00	LUC7L2	3666.00	2.32	2.71	-0.58
50059.00	E10	M-023584-	sema dom	54437.00	SEMA5B	3502.00	0.74	4.29	-0.91
50059.00	E11	M-008553-	OTU doma	51633.00	OTUD6B	3701.00	1.57	3.46	-0.74
50059.00	E12	M-016937-	SH3 domai	54436.00	SH3TC1	3209.00	1.31	3.72	-0.79
50059.00	E13	M-020763-	RNA bindir	51634.00	RBMX2	1818.00	1.38	3.65	-0.78
50059.00	E14	M-013386-	nucleolar p	54433.00	NOLA1	3511.00	1.88	3.15	-0.67
50059.00	E15	M-009573-	dehydroge	51635.00	DHRS7	2517.00	0.99	4.04	-0.86

50059.00	E16	M-016906-	Yip1 doma	54432.00	YIPF1	2997.00	1.64	3.40	-0.72
50059.00	E17	M-020723-	chromosor	51637.00	C14orf166	3331.00	0.48	4.55	-0.97
50059.00	E18	M-013752-	DnaJ (Hsp4	54431.00	DNAJC10	2455.00	1.67	3.36	-0.72
50059.00	E19	M-020260-	splicing fac	51639.00	SF3B14	1524.00	8.01	2.98	0.64
50059.00	E20	M-013751-	sialic acid	54414.00	SIAE	3460.00	9.36	4.33	0.93
50059.00	E21	M-017512-	mitochond	51642.00	MRPL48	4141.00	6.81	1.78	0.38
50059.00	E23	M-020255-	transmem	51643.00	TMBIM4	1913.00	11.19	6.16	1.32
50059.00	F02	M-020665-	FLJ20160 p	54842.00	FLJ20160	3310.00	9.00	3.97	0.85
50059.00	F04	M-016581-	basic, imm	54841.00	BIVM	3048.00	3.54	1.49	-0.32
50059.00	F05	M-018913-	WD repeat	54521.00	WDR44	3860.00	6.06	1.03	0.22
50059.00	F06	M-020660-	leucine ric	54839.00	LRRC49	4257.00	10.15	5.12	1.09
50059.00	F07	M-026394-	ankyrin rep	54522.00	ANKRD16	3846.00	10.06	5.03	1.08
50059.00	F08	M-019421-	chromosor	54838.00	C10orf26	3094.00	4.17	0.86	-0.18
50059.00	F09	M-020489-	asparagine	54529.00	ASNSD1	4440.00	12.57	7.54	1.61
50059.00	F10	M-020655-	B-box and	54836.00	BSPRY	4311.00	9.56	4.53	0.97
50059.00	F11	M-020485-	hypothetic	54530.00	FLJ20054	3188.00	4.71	0.32	-0.07
50059.00	F12	M-020650-	ganglioside	54834.00	GDAP2	3516.00	10.89	5.86	1.25
50059.00	F13	M-023917-	mesoderm	54531.00	MIER2	4496.00	19.80	**14.77**	3.15
50059.00	F14	M-020641-	vacuolar p	54832.00	VPS13C	3702.00	12.51	7.48	1.60
50059.00	F15	M-027186-	ubiquitin s	54532.00	USP53	2124.00	1.74	3.29	-0.70
50059.00	F16	M-020637-	bestrophin	54831.00	BEST2	3757.00	11.18	6.15	1.31
50059.00	F17	M-013373-	mitochond	54534.00	MRPL50	3540.00	6.16	1.13	0.24
50059.00	F18	M-020634-	nucleopori	54830.00	NUP62CL	3723.00	5.35	0.32	0.07
50059.00	F19	M-020481-	coiled-coil	54535.00	CCHCR1	4580.00	9.45	4.42	0.95
50059.00	F20	M-021479-	asporin	54829.00	ASPN	3749.00	8.96	3.93	0.84
50059.00	F21	M-021404-	exocyst co	54536.00	EXOC6	3938.00	11.28	6.25	1.33
50059.00	F23	M-015216-	roundabou	54538.00	ROBO4	3216.00	17.66	**12.63**	2.70
50059.00	G02	M-009084-	neuroligin	54413.00	NLGN3	4269.00	1.24	3.79	-0.81
50059.00	G04	M-007559-	solute carr	54407.00	SLC38A2	3650.00	0.55	4.48	-0.96
50059.00	G05	M-020317-	yippee-like	51646.00	YPEL5	5046.00	1.70	3.33	-0.71
50059.00	G06	M-009593-	hydroxyaci	54363.00	HAO1	5097.00	1.69	3.34	-0.71
50059.00	G07	M-020340-	family with	51647.00	FAM96B	4333.00	1.78	3.25	-0.69
50059.00	G08	M-018039-	unc-93 hor	54346.00	UNC93A	3489.00	1.95	3.08	-0.66
50059.00	G09	M-012973-	mitochond	51649.00	MRPS23	3371.00	0.80	4.23	-0.90
50059.00	G10	M-017492-	dolichyl-ph	54344.00	DPM3	4701.00	1.30	3.73	-0.80
50059.00	G11	M-012940-	mitochond	51650.00	MRPS33	3373.00	2.28	2.75	-0.59
50059.00	G12	M-032251-	guanine nu	54331.00	GNG2	3969.00	3.91	1.12	-0.24
50059.00	G13	M-007271-	peptidyl-tR	51651.00	PTRH2	3801.00	2.68	2.35	-0.50
50059.00	G14	M-021227-	syntrophin	54221.00	SNTG2	3697.00	1.14	3.89	-0.83
50059.00	G15	M-004696-	vacuolar p	51652.00	VPS24	3639.00	4.95	0.08	-0.02
50059.00	G16	M-021231-	syntrophin	54212.00	SNTG1	3112.00	3.63	1.40	-0.30
50059.00	G17	M-020418-	GINS comp	51659.00	GINS2	3579.00	2.29	2.74	-0.58
50059.00	G18	M-006255-	potassium	54207.00	KCNK10	4681.00	4.14	0.89	-0.19
50059.00	G19	M-020459-	brain prote	51660.00	BRP44L	3655.00	4.60	0.43	-0.09
50059.00	G20	M-017016-	ERBB rece	54206.00	ERRFI1	4030.00	8.86	3.83	0.82
50059.00	G21	M-009436-	FK506 bin	51661.00	FKBP7	3411.00	11.87	6.84	1.46
50059.00	G23	M-019266-	zinc finger	51663.00	ZFR	2838.00	16.14	**11.11**	2.37

50059.00	H02	M-010577-	breast carc	54828.00	BCAS3	1913.00	6.27	1.24	0.27
50059.00	H04	M-021311-	family with	54827.00	FAM55D	2507.00	9.45	4.42	0.95
50059.00	H05	M-016098-	NADH dehy	54539.00	NDUFB11	2413.00	5.35	0.32	0.07
50059.00	H06	M-020631-	zinc finger,	54826.00	ZH2C2	1779.00	2.36	2.67	-0.57
50059.00	H07	M-015342-	hypothetic	54540.00	FLJ10404	1646.00	3.04	1.99	-0.42
50059.00	H08	M-018994-	chromosor	54823.00	C1orf26	1663.00	5.41	0.38	0.08
50059.00	H09	M-010855-	DNA-dama	54541.00	DDIT4	2689.00	6.95	1.92	0.41
50059.00	H10	M-031581-	FLJ20105 p	54821.00	FLJ20105	2348.00	10.01	4.98	1.06
50059.00	H11	M-020453-	ring finger	54542.00	RC3H2	2740.00	13.43	8.40	1.79
50059.00	H12	M-020618-	zinc finger,	54819.00	ZCCHC10	2830.00	7.56	2.53	0.54
50059.00	H13	M-013762-	translocase	54543.00	TOMM7	2296.00	2.70	2.33	-0.50
50059.00	H14	M-030406-	suppressor	54816.00	SUHW4	2747.00	2.26	2.77	-0.59
50059.00	H15	M-020449-	cysteine-ri	54544.00	CRCT1	1534.00	3.72	1.31	-0.28
50059.00	H16	M-015311-	GATA zinc	54815.00	GATAD2A	3526.00	6.58	1.55	0.33
50059.00	H17	M-006999-	ring finger	54546.00	RNF186	2149.00	1.72	3.31	-0.71
50059.00	H18	M-005875-	glutaminyl-	54814.00	QPCTL	2366.00	6.80	1.77	0.38
50059.00	H19	M-017396-	sidekick ho	54549.00	SDK2	3322.00	4.12	0.91	-0.19
50059.00	H20	M-020611-	kelch-like 2	54813.00	KLHL28	3023.00	5.59	0.56	0.12
50059.00	H21	M-018938-	EF-hand ca	54550.00	EFCBP2	2712.00	13.09	8.06	1.72
50059.00	H23	M-013374-	MAGE-like	54551.00	MAGEL2	2480.00	3.75	1.28	-0.27
50059.00	I02	M-013399-	N-acetylne	54187.00	NANS	2465.00	3.69	1.34	-0.28
50059.00	I04	M-020812-	chromosor	54149.00	C21orf91	3034.00	5.70	0.67	0.14
50059.00	I05	M-017197-	ankyrin rep	51665.00	ASB1	3382.00	10.41	5.38	1.15
50059.00	I06	M-008542-	mitochond	54148.00	MRPL39	3093.00	5.82	0.79	0.17
50059.00	I07	M-013339-	ankyrin rep	51666.00	ASB4	3961.00	7.42	2.39	0.51
50059.00	I08	M-010901-	H2B histon	54145.00	H2BFS	2022.00	5.64	0.61	0.13
50059.00	I09	M-019158-	negative re	51667.00	NUB1	3318.00	10.16	5.13	1.10
50059.00	I10	M-008460-	polymerase	54107.00	POLE3	2620.00	11.49	6.46	1.38
50059.00	I11	M-010908-	chromosor	51668.00	C1orf41	2506.00	11.77	6.74	1.44
50059.00	I12	M-025410-	hypothetic	54103.00	tcag7.1314	3144.00	10.62	5.59	1.20
50059.00	I13	M-015281-	transmeml	51669.00	TMEM66	1045.00	3.35	1.68	-0.36
50059.00	I14	M-012919-	chloride in	54102.00	CLIC6	1840.00	7.77	2.74	0.59
50059.00	I15	M-020505-	tubulin pol	51673.00	TPPP3	3373.00	8.45	3.42	0.73
50059.00	I16	M-015462-	family with	54097.00	FAM3B	2563.00	10.42	5.39	1.15
50059.00	I17	M-009678-	membrane	51678.00	MPP6	2769.00	6.57	1.54	0.33
50059.00	I18	M-006998-	SET domai	54093.00	SETD4	1952.00	9.78	4.75	1.02
50059.00	I19	M-021189-	LSM7 hom	51690.00	LSM7	2876.00	6.54	1.51	0.32
50059.00	I20	M-016908-	chromosor	54084.00	C21orf29	3111.00	10.13	5.10	1.09
50059.00	I21	M-017030-	LSM8 hom	51691.00	LSM8	2526.00	11.09	6.06	1.29
50059.00	I23	M-006365-	cleavage a	51692.00	CPSF3	2846.00	4.15	0.88	-0.19
50059.00	J02	M-020609-	zinc finger	54811.00	ZNF562	4351.00	3.03	2.00	-0.43
50059.00	J04	M-031141-	sterile alph	54809.00	SAMD9	3722.00	3.47	1.56	-0.33
50059.00	J05	M-015743-	guanine nu	54552.00	GNL3L	3280.00	9.27	4.24	0.91
50059.00	J06	M-017498-	dymeclin	54808.00	DYM	3439.00	4.97	0.06	-0.01
50059.00	J07	M-017975-	DEAD (Asp	54555.00	DDX49	3016.00	3.35	1.68	-0.36
50059.00	J08	M-020605-	zinc finger	54807.00	ZNF586	3166.00	5.09	0.06	0.01
50059.00	J09	M-013763-	small gluta	54557.00	SGTB	4492.00	14.36	9.33	1.99

50059.00	J10	M-018831-	tRNA isope	54802.00	TRIT1	3202.00	2.31	2.72	-0.58
50059.00	J11	M-020413-	spermatog	54558.00	SPATA6	3355.00	12.16	7.13	1.52
50059.00	J12	M-018372-	family with	54801.00	FAM29A	2543.00	7.67	2.64	0.56
50059.00	J13	M-013803-	erythrocyt	54566.00	EPB41L4B	3492.00	4.95	0.08	-0.02
50059.00	J14	M-020604-	kelch-like 2	54800.00	KLHL24	2952.00	5.32	0.29	0.06
50059.00	J15	M-013764-	UDP glucur	54575.00	UGT1A10	2293.00	6.11	1.08	0.23
50059.00	J16	M-020602-	dachsous 2	54798.00	DCHS2	4004.00	9.32	4.29	0.92
50059.00	J17	M-013765-	UDP glucur	54577.00	UGT1A7	2896.00	3.25	1.78	-0.38
50059.00	J18	M-020600-	mediator c	54797.00	MED18	4261.00	10.35	5.32	1.14
50059.00	J19	M-031996-	UDP glucur	54579.00	UGT1A5	3190.00	4.83	0.20	-0.04
50059.00	J20	M-032217-	basonuclin	54796.00	BNC2	2244.00	9.58	4.55	0.97
50059.00	J21	M-013048-	SCAN dom	54581.00	SCAND2	2582.00	3.10	1.93	-0.41
50059.00	J23	M-012960-	guanine nu	54584.00	GNB1L	2451.00	4.24	0.79	-0.17
50059.00	K02	M-031393-	chromosor	54083.00	C21orf30	2221.00	1.49	3.54	-0.76
50059.00	K04	M-015218-	chromosor	54072.00	C21orf42	3106.00	7.50	2.47	0.53
50059.00	K05	M-021254-	trafficking	51693.00	TRAPPC2L	2912.00	5.39	0.36	0.08
50059.00	K06	M-020789-	chromosor	54069.00	C21orf45	2930.00	4.37	0.66	-0.14
50059.00	K07	M-021156-	headcase h	51696.00	HECA	3989.00	13.79	8.76	1.87
50059.00	K08	M-016949-	chromosor	54065.00	C21orf51	2773.00	5.34	0.31	0.07
50059.00	K09	M-009764-	vacuolar pı	51699.00	VPS29	3102.00	13.31	8.28	1.77
50059.00	K10	M-031405-	chromosor	54059.00	C21orf57	2860.00	4.30	0.73	-0.15
50059.00	K11	M-021051-	peptidyl ar	51702.00	PADI3	2333.00	2.31	2.72	-0.58
50059.00	K12	M-015217-	chromosor	54058.00	C21orf58	2630.00	5.10	0.07	0.01
50059.00	K13	M-015860-	endomucir	51705.00	EMCN	2746.00	6.92	1.89	0.40
50059.00	K14	M-013199-	poly(rC) biı	54039.00	PCBP3	1486.00	3.03	2.00	-0.43
50059.00	K15	M-004996-	selenoprot	51714.00	SELT	2316.00	9.28	4.25	0.91
50059.00	K16	M-013507-	ferritin, he	53940.00	FTHL17	2600.00	3.81	1.22	-0.26
50059.00	K17	M-015407-	calcium bir	51719.00	CAB39	3638.00	14.35	9.32	1.99
50059.00	K18	M-009868-	peptidylprc	53938.00	PPIL3	3303.00	9.14	4.11	0.88
50059.00	K19	M-020905-	F-box prote	51725.00	FBXO40	2017.00	1.44	3.59	-0.77
50059.00	K20	M-007436-	solute carr	53919.00	SLCO1C1	3897.00	13.09	8.06	1.72
50059.00	K21	M-015861-	DnaJ (Hsp4	51726.00	DNAJB11	2914.00	9.75	4.72	1.01
50059.00	K23	M-013358-	polymeras	51728.00	POLR3K	3145.00	5.21	0.18	0.04
50059.00	L02	M-020591-	potassium	54793.00	KCTD9	2048.00	4.44	0.59	-0.12
50059.00	L04	M-013776-	KIAA1546	54790.00	KIAA1546	2761.00	3.01	2.02	-0.43
50059.00	L05	M-026125-	chromosor	54586.00	C9orf11	2695.00	2.71	2.32	-0.49
50059.00	L06	M-020585-	DnaJ (Hsp4	54788.00	DNAJB12	3722.00	5.86	0.83	0.18
50059.00	L07	M-017976-	LINE-1 type	54596.00	L1TD1	3751.00	3.71	1.32	-0.28
50059.00	L08	M-020574-	chromosor	54785.00	C17orf59	1848.00	4.33	0.70	-0.15
50059.00	L09	M-021767-	Nedd4 fam	54602.00	NDFIP2	4128.00	8.21	3.18	0.68
50059.00	L10	M-004282-	alkB, alkyla	54784.00	ALKBH4	2974.00	2.49	2.54	-0.54
50059.00	L11	M-020410-	DEAD (Asp	54606.00	DDX56	2110.00	2.18	2.85	-0.61
50059.00	L12	M-020566-	non-SMC e	54780.00	NSMCE4A	2443.00	9.78	4.75	1.02
50059.00	L13	M-004176-	INO80 com	54617.00	INOC1	2634.00	2.89	2.14	-0.46
50059.00	L14	M-007002-	ring finger	54778.00	RNF111	3383.00	10.20	5.17	1.10
50059.00	L15	M-031874-	F-box and l	54620.00	FBXL19	1550.00	2.06	2.97	-0.63
50059.00	L16	M-018404-	chromosor	54777.00	C10orf92	2862.00	6.43	1.40	0.30

50059.00	L17	M-020362- hypothetic	54621.00	FLJ20674	2703.00	4.48	0.55	-0.12
50059.00	L18	M-008720- DIRAS fami	54769.00	DIRAS2	4468.00	5.60	0.57	0.12
50059.00	L19	M-020355- ADP-ribosy	54622.00	ARL15	4398.00	3.93	1.10	-0.23
50059.00	L20	M-022583- hydroceph	54768.00	HYDIN	4011.00	8.78	3.75	0.80
50059.00	L21	M-020349- Paf1, RNA	54623.00	PAF1	2756.00	3.08	1.95	-0.41
50059.00	L23	M-027389- hairy and e	54626.00	HES2	3111.00	1.86	3.17	-0.67
50059.00	M02	M-019068- pelota hon	53918.00	PELO	2131.00	1.60	3.43	-0.73
50059.00	M04	M-008828- RAB24, me	53917.00	RAB24	3157.00	4.91	0.12	-0.02
50059.00	M05	M-013343- WW doma	51729.00	WBP11	1630.00	2.27	2.76	-0.59
50059.00	M06	M-008126- dual oxidas	53905.00	DUOX1	2551.00	2.39	2.64	-0.56
50059.00	M07	M-020886- ureidoprop	51733.00	UPB1	4679.00	8.36	3.33	0.71
50059.00	M08	M-028307- claudin 22	53842.00	CLDN22	2611.00	4.56	0.47	-0.10
50059.00	M09	M-020883- selenoprot	51734.00	SEPX1	3567.00	3.20	1.83	-0.39
50059.00	M10	M-012987- mucin-like	53841.00	MUPCDH	3982.00	4.39	0.64	-0.13
50059.00	M11	M-017028- HIG1 doma	51751.00	HIGD1B	4029.00	13.60	8.57	1.83
50059.00	M12	M-006997- tripartite m	53840.00	TRIM34	3437.00	10.88	5.85	1.25
50059.00	M13	M-017716- chromosor	51754.00	C9orf127	2657.00	7.94	2.91	0.62
50059.00	M14	M-014035- chromosor	53838.00	C11orf24	3281.00	7.50	2.47	0.53
50059.00	M15	M-020231- chromosor	51759.00	C9orf78	3360.00	8.63	3.60	0.77
50059.00	M16	M-017419- FXYD doma	53828.00	FXYD4	4429.00	10.41	5.38	1.15
50059.00	M17	M-020736- synaptotag	51760.00	SYT17	3472.00	8.67	3.64	0.78
50059.00	M18	M-003670- FXYD doma	53827.00	FXYD5	3504.00	13.33	8.30	1.77
50059.00	M19	M-008744- RAB8B, me	51762.00	RAB8B	4974.00	20.37	**15.34**	3.28
50059.00	M20	M-013055- FXYD doma	53826.00	FXYD6	4908.00	13.79	8.76	1.87
50059.00	M21	M-017494- skeletal mu	51763.00	SKIP	3447.00	14.27	9.24	1.97
50059.00	M23	M-020691- guanine nu	51764.00	GNG13	3254.00	6.48	1.45	0.31
50059.00	N02	M-017337- tripartite m	54765.00	TRIM44	4283.00	3.18	1.85	-0.40
50059.00	N04	M-009270- zinc finger,	54764.00	ZRANB1	2597.00	5.62	0.59	0.13
50059.00	N05	M-013769- KIAA1383	54627.00	KIAA1383	5479.00	8.82	3.79	0.81
50059.00	N06	M-017062- ropporin, r	54763.00	ROPN1	3128.00	8.15	3.12	0.67
50059.00	N07	M-022254- family with	54629.00	FAM63B	3880.00	14.82	**9.79**	2.09
50059.00	N08	M-020545- GRAM don	54762.00	GRAMD1C	2415.00	8.49	3.46	0.74
50059.00	N09	M-016946- TBC1 doma	54662.00	TBC1D13	3412.00	12.46	7.43	1.59
50059.00	N10	M-013774- proprotein	54760.00	PCSK4	4127.00	10.59	5.56	1.19
50059.00	N11	M-020315- WD repeat	54663.00	WDR74	4902.00	9.75	4.72	1.01
50059.00	N12	M-017013- kelch doma	54758.00	KLHDC4	4186.00	18.51	**13.48**	2.88
50059.00	N13	M-020307- transmemb	54664.00	TMEM106I	3960.00	11.89	6.86	1.47
50059.00	N14	M-013773- family with	54757.00	FAM20A	3935.00	5.39	0.36	0.08
50059.00	N15	M-020299- round sper	54665.00	RSBN1	4295.00	10.62	5.59	1.19
50059.00	N16	M-007946- interleukin	54756.00	IL17RD	2538.00	7.80	2.77	0.59
50059.00	N17	M-018214- leucine rich	54674.00	LRRN3	4385.00	16.53	**11.50**	2.46
50059.00	N18	M-026260- family with	54754.00	FAM22F	3409.00	10.27	5.24	1.12
50059.00	N19	M-017910- cardiolipin	54675.00	CRLS1	4403.00	12.45	7.42	1.58
50059.00	N20	M-020530- fibronectin	54752.00	FNDC8	4430.00	18.08	**13.05**	2.79
50059.00	N21	M-015310- GTP bindin	54676.00	GTPBP2	4123.00	18.29	**13.26**	2.83
50059.00	N23	M-016316- chromosor	54680.00	C1orf181	3018.00	12.43	7.40	1.58
50059.00	O02	M-013056- FXYD doma	53822.00	FXYD7	1469.00	4.70	0.33	-0.07

50059.00	O04	M-021244- Down synd	53820.00	DSCR6	3670.00	17.14	**12.11**	2.59
50059.00	O05	M-005745- transmemb	51768.00	TM7SF3	4534.00	15.33	**10.30**	2.20
50059.00	O06	M-005210- prostate tu	53635.00	PTOV1	4222.00	22.50	**17.47**	3.73
50059.00	O07	M-020374- remodeling	51773.00	RSF1	3706.00	7.83	2.80	0.60
50059.00	O08	M-013403- beta-carot	53630.00	BCMO1	4766.00	6.97	1.94	0.41
50059.00	O09	M-015384- myozenin	51778.00	MYOZ2	2505.00	11.02	5.99	1.28
50059.00	O10	M-020624- syntaxin 1	53407.00	STX18	3605.00	10.15	5.12	1.09
50059.00	O11	M-020378- jumonji do	51780.00	JMJD1B	3093.00	8.34	3.31	0.71
50059.00	O12	M-010710- two pore s	53373.00	TPCN1	3471.00	4.64	0.39	-0.08
50059.00	O13	M-010155- coenzyme	51805.00	COQ3	2878.00	13.00	7.97	1.70
50059.00	O14	M-017570- nucleopori	53371.00	NUP54	2996.00	6.71	1.68	0.36
50059.00	O15	M-013402- UDP-N-ace	51809.00	GALNT7	3446.00	11.75	6.72	1.44
50059.00	O16	M-013086- zinc finger,	53349.00	ZFYVE1	3114.00	5.62	0.59	0.13
50059.00	O17	M-009521- cat eye syn	51816.00	CECR1	1628.00	7.13	2.10	0.45
50059.00	O18	M-014229- transmemb	53346.00	TM6SF1	3429.00	3.56	1.47	-0.31
50059.00	O19	M-018637- CPX chrom	53336.00	CPXCR1	5113.00	10.66	5.63	1.20
50059.00	O20	M-008858- nudix (nucl	53343.00	NUDT9	3737.00	6.56	1.53	0.33
50059.00	O21	M-014617- BTB (POZ)	53339.00	BTBD1	4251.00	6.94	1.91	0.41
50059.00	O23	M-007940- interleukin	53342.00	IL17D	2297.00	14.80	**9.77**	2.09
50059.00	P02	M-013772- filamin bin	54751.00	FBLIM1	2203.00	10.71	5.68	1.21
50059.00	P04	M-013378- ependymir	54749.00	EPDR1	2478.00	4.44	0.59	-0.13
50059.00	P05	M-018215- MANSC do	54682.00	MANSC1	2832.00	11.55	6.52	1.39
50059.00	P06	M-020243- hypothetic	54744.00	DKFZp566I	2529.00	7.04	2.01	0.43
50059.00	P07	M-020288- ATP bindin	54707.00	ATPBD1B	2545.00	14.62	**9.59**	2.05
50059.00	P08	M-013771- lymphocyt	54742.00	LY6K	3296.00	10.98	5.95	1.27
50059.00	P09	M-007001- membrane	54708.00	MARCH5	1666.00	6.06	1.03	0.22
50059.00	P10	M-020214- FEV (ETS o	54738.00	FEV	1861.00	9.94	4.91	1.05
50059.00	P11	M-007640- solute carr	54716.00	SLC6A20	2304.00	7.64	2.61	0.56
50059.00	P12	M-021680- M-phase p	54737.00	HSMPP8	3245.00	6.53	1.50	0.32
50059.00	P13	M-021361- butyrophili	54718.00	BTN2A3	3465.00	23.43	**18.40**	3.93
50059.00	P14	M-026511- RAB39, me	54734.00	RAB39	2403.00	21.39	**16.36**	3.49
50059.00	P15	M-007085- zinc finger	84146.00	ZNF644	2701.00	9.74	4.71	1.01
50059.00	P16	M-018216- solute carr	54733.00	SLC35F2	2355.00	12.48	7.45	1.59
50059.00	P17	M-015498- chromosor	54073.00	C21orf41	2448.00	14.95	**9.92**	2.12
50059.00	P18	M-007924- transmemb	54732.00	TMED9	3845.00	25.83	**20.80**	4.44
50059.00	P19	M-016404- chromosor	54143.00	C21orf74	1398.00	15.38	**10.35**	2.21
50059.00	P20	M-009927- OTU doma	54726.00	OTUD4	2250.00	6.22	1.19	0.26
50059.00	P21	M-021204- DKFZp434A	54441.00	DKFZP434A	2608.00	9.89	4.86	1.04
50059.00	P23	M-015341- pseudouric	54517.00	PUS7	1377.00	2.61	2.42	-0.51
					3253.50	5.03	3.16	
				MAD3			9.49	
				MADc			4.68	
50059.00	C22				2896.00	32.80		
50059.00	D22				4451.00	31.54		
50059.00	E22				1805.00	36.45		2817.00
50059.00	F22				2438.00	39.46		2918.00
				mn	2897.50	35.07		2867.50

					sd	1128.13	3.59	71.42
50059.00	G22					720.00	1.67	567.00
50059.00	H22					556.00	1.26	890.00
50059.00	I22					588.00	0.34	753.00
50059.00	J22					904.00	1.77	933.00
					mn	682.67	1.12	858.67
					sd	192.35	0.72	94.00
					3psSD		10.78	
					3ngSD		2.17	
					SumSD		12.96	
					DiffMn		33.94	
					SmovrDiff		0.38	
					1minus		0.62	

50059.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	471.00	0.42	317.00
50059.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	111.00	7.21	129.00
50059.00	I03	D-001206-	siControl non-targetin			3076.00	8.71	2542.00
50059.00	J03	D-001206-	siControl non-targetin			3815.00	7.00	3899.00
50059.00	K03	D-001600-	siGLO RISC-free siRNA			4590.00	7.36	4557.00
50059.00	L03	D-001600-	siGLO RISC-free siRNA			4203.00	9.47	4007.00

Cell Coun	**% inf**	**Abs Dev**	**rZ**	**Cell Count**	**% inf**	**Abs Dev**	**rZ**
3579.00	2.07	0.36	-0.16	2805.00	3.99	4.82	-0.81
1500.00	0.87	1.56	-0.70	2637.00	4.02	4.79	-0.81
1048.00	4.58	2.15	0.96	1454.00	2.27	6.54	-1.10
1238.00	1.29	1.14	-0.51	1219.00	2.38	6.43	-1.08
2520.00	0.95	1.48	-0.66	2185.00	3.20	5.61	-0.94
2881.00	1.91	0.52	-0.23	1855.00	6.52	2.29	-0.38
2182.00	0.73	1.70	-0.76	2447.00	5.39	3.42	-0.57
2084.00	1.25	1.18	-0.53	4079.00	6.79	2.02	-0.34
2643.00	2.42	0.01	0.00	2354.00	6.75	2.06	-0.35
2088.00	1.92	0.51	-0.23	1941.00	3.40	5.41	-0.91
1360.00	1.84	0.59	-0.26	315.00	54.60	**45.79**	7.69
2125.00	2.07	0.36	-0.16	3127.00	8.25	0.56	-0.09
1932.00	2.69	0.26	0.12	1520.00	3.62	5.19	-0.87
1467.00	2.32	0.11	-0.05	3250.00	3.32	5.49	-0.92
1465.00	2.12	0.31	-0.14	3158.00	8.14	0.67	-0.11
1429.00	3.99	1.56	0.70	2905.00	6.82	1.99	-0.34
1475.00	2.71	0.28	0.13	2476.00	3.92	4.89	-0.82
2378.00	2.61	0.18	0.08	2588.00	2.90	5.91	-0.99
2421.00	3.72	1.29	0.57	1431.00	2.10	6.71	-1.13
1594.00	4.02	1.59	0.71	1733.00	3.12	5.69	-0.96
4013.00	0.75	1.68	-0.75	3255.00	0.80	8.01	-1.35
1567.00	1.98	0.45	-0.20	1806.00	0.94	7.87	-1.32
3608.00	1.05	1.38	-0.62	4536.00	0.44	8.37	-1.41
4233.00	1.20	1.23	-0.55	3391.00	1.24	7.57	-1.27
5045.00	0.12	2.31	-1.03	3457.00	1.65	7.16	-1.20
4606.00	0.24	2.19	-0.98	3706.00	0.84	7.97	-1.34
2827.00	0.14	2.29	-1.02	2086.00	0.67	8.14	-1.37
2434.00	0.37	2.06	-0.92	2812.00	1.24	7.57	-1.27
2671.00	0.56	1.87	-0.83	2459.00	1.71	7.10	-1.19
3515.00	0.40	2.03	-0.91	2615.00	0.34	8.47	-1.42
3694.00	0.32	2.11	-0.94	2613.00	0.88	7.93	-1.33
3536.00	0.11	2.32	-1.03	1822.00	0.88	7.93	-1.33
3613.00	0.25	2.18	-0.97	2491.00	0.84	7.97	-1.34
2738.00	0.84	1.59	-0.71	2026.00	1.33	7.48	-1.26
2811.00	0.36	2.07	-0.93	2804.00	1.43	7.38	-1.24
2721.00	1.32	1.11	-0.49	1632.00	0.18	8.63	-1.45
3416.00	0.23	2.20	-0.98	2179.00	0.92	7.89	-1.33
4933.00	0.77	1.66	-0.74	1947.00	0.77	8.04	-1.35
4619.00	0.95	1.48	-0.66	2830.00	0.92	7.89	-1.33
2450.00	1.18	1.25	-0.56	2631.00	1.75	7.06	-1.19
3507.00	0.94	1.49	-0.67	3231.00	7.27	1.54	-0.26
3107.00	0.19	2.24	-1.00	1455.00	5.15	3.66	-0.61
3063.00	0.59	1.84	-0.82	2998.00	3.87	4.94	-0.83
3959.00	1.11	1.32	-0.59	3237.00	9.02	0.21	0.04
3969.00	0.30	2.13	-0.95	2330.00	2.36	6.45	-1.08
3453.00	1.10	1.33	-0.59	2796.00	13.91	5.10	0.86

3623.00	0.97	1.46	-0.65	3365.00	9.51	0.70	0.12
1667.00	1.62	0.81	-0.36	1662.00	14.92	6.11	1.03
3409.00	2.61	0.18	0.08	2305.00	18.31	9.50	1.60
2181.00	0.23	2.20	-0.98	1867.00	7.07	1.74	-0.29
3549.00	0.39	2.04	-0.91	2724.00	6.98	1.84	-0.31
3443.00	0.61	1.82	-0.81	1987.00	14.04	5.23	0.88
3805.00	0.68	1.75	-0.78	2337.00	9.33	0.52	0.09
3776.00	1.67	0.76	-0.34	3358.00	13.01	4.20	0.71
2924.00	0.85	1.58	-0.70	2304.00	8.59	0.22	-0.04
3861.00	0.60	1.83	-0.82	2251.00	4.93	3.88	-0.65
2778.00	0.68	1.75	-0.78	2381.00	7.52	1.29	-0.22
4930.00	1.30	1.13	-0.51	3312.00	9.39	0.58	0.10
4405.00	2.38	0.05	-0.02	2811.00	16.12	7.31	1.23
4003.00	1.12	1.31	-0.58	3179.00	13.24	4.43	0.74
2565.00	0.35	2.08	-0.93	5233.00	7.32	1.49	-0.25
3293.00	0.09	2.34	-1.04	3811.00	1.99	6.82	-1.15
3522.00	0.54	1.89	-0.84	4249.00	3.15	5.66	-0.95
3676.00	0.44	1.99	-0.89	4182.00	3.54	5.27	-0.89
5111.00	0.49	1.94	-0.87	3499.00	5.14	3.67	-0.62
3503.00	0.26	2.17	-0.97	3733.00	7.47	1.34	-0.22
3243.00	0.52	1.91	-0.85	2989.00	7.96	0.85	-0.14
4036.00	0.52	1.91	-0.85	3139.00	4.68	4.13	-0.69
4108.00	0.54	1.89	-0.85	4147.00	8.51	0.30	-0.05
2975.00	0.50	1.93	-0.86	4214.00	7.17	1.64	-0.28
3810.00	0.60	1.83	-0.82	3175.00	4.44	4.37	-0.73
2477.00	0.36	2.07	-0.92	2939.00	7.18	1.63	-0.27
2980.00	0.77	1.66	-0.74	2377.00	5.93	2.88	-0.48
3853.00	0.36	2.07	-0.92	3963.00	12.67	3.86	0.65
5094.00	0.86	1.57	-0.70	4056.00	12.55	3.74	0.63
3650.00	0.63	1.80	-0.80	3703.00	8.16	0.65	-0.11
4431.00	1.69	0.74	-0.33	3045.00	6.08	2.73	-0.46
3543.00	1.04	1.39	-0.62	3339.00	12.07	3.26	0.55
3568.00	0.59	1.84	-0.82	3245.00	14.21	5.40	0.91
4082.00	0.10	2.33	-1.04	4512.00	12.01	3.20	0.54
4704.00	1.53	0.90	-0.40	3689.00	1.55	7.26	-1.22
4181.00	2.44	0.01	0.00	3676.00	4.46	4.35	-0.73
3833.00	1.75	0.68	-0.30	3726.00	3.30	5.51	-0.93
2776.00	3.67	1.24	0.56	3164.00	9.13	0.32	0.05
3384.00	2.01	0.42	-0.19	4122.00	11.67	2.86	0.48
3974.00	1.43	1.00	-0.44	3019.00	3.35	5.46	-0.92
2728.00	3.23	0.80	0.36	2113.00	8.47	0.34	-0.06
4158.00	2.50	0.07	0.03	3289.00	4.74	4.07	-0.68
4306.00	3.23	0.80	0.36	3954.00	5.24	3.57	-0.60
4042.00	3.24	0.81	0.36	3649.00	7.21	1.60	-0.27
1431.00	1.82	0.61	-0.27	1652.00	1.33	7.48	-1.26
1873.00	0.80	1.63	-0.73	3070.00	2.77	6.04	-1.02
1804.00	1.05	1.38	-0.62	2299.00	2.70	6.11	-1.03

2231.00	1.97	0.46	-0.20	3227.00	8.15	0.66	-0.11	
3188.00	1.35	1.08	-0.48	2396.00	3.38	5.43	-0.91	
1796.00	1.00	1.43	-0.64	2002.00	4.15	4.66	-0.78	
1060.00	6.23	3.80	1.69	841.00	13.67	4.86	0.82	
4222.00	6.80	4.37	1.95	4049.00	16.70	7.89	1.32	
3581.00	3.07	0.64	0.29	4122.00	10.55	1.74	0.29	
1835.00	3.49	1.06	0.47	3963.00	10.45	1.64	0.27	
3654.00	4.21	1.78	0.80	3533.00	24.74	**15.93**	2.68	
3464.00	3.20	0.77	0.35	3337.00	14.38	5.57	0.94	
2816.00	2.70	0.27	0.12	2384.00	7.93	0.88	-0.15	
2733.00	2.16	0.27	-0.12	1567.00	7.47	1.34	-0.23	
2996.00	2.84	0.41	0.18	2108.00	12.71	3.90	0.66	
2580.00	0.31	2.12	-0.95	1898.00	7.43	1.38	-0.23	
3271.00	2.38	0.05	-0.02	2681.00	9.96	1.15	0.19	
2826.00	1.27	1.16	-0.52	2791.00	14.76	5.95	1.00	
3782.00	1.96	0.47	-0.21	2286.00	5.86	2.95	-0.50	
1886.00	5.67	3.24	1.45	1790.00	8.60	0.21	-0.04	
2312.00	2.72	0.29	0.13	2512.00	10.35	1.54	0.26	
3051.00	4.59	2.16	0.96	2863.00	15.58	6.77	1.14	
1916.00	0.99	1.44	-0.64	1765.00	5.61	3.20	-0.54	
2815.00	3.30	0.87	0.39	2627.00	8.95	0.14	0.02	
2320.00	2.72	0.29	0.13	2491.00	3.13	5.68	-0.95	
3250.00	1.78	0.65	-0.29	3090.00	5.21	3.60	-0.61	
3269.00	4.31	1.88	0.84	3480.00	6.90	1.91	-0.32	
3644.00	3.24	0.81	0.36	4000.00	5.38	3.44	-0.58	
3536.00	6.33	3.90	1.74	3676.00	13.00	4.19	0.70	
3985.00	8.58	**6.15**	2.75	3817.00	5.87	2.94	-0.49	y
4714.00	4.01	1.58	0.70	5754.00	16.86	8.05	1.35	
4623.00	2.14	0.29	-0.13	4014.00	10.39	1.58	0.27	
4936.00	2.78	0.35	0.15	5193.00	11.92	3.11	0.52	
3794.00	2.85	0.42	0.19	5103.00	10.43	1.62	0.27	
4661.00	2.72	0.29	0.13	4594.00	11.45	2.64	0.44	
3634.00	3.71	1.28	0.57	3549.00	17.27	8.46	1.42	
3583.00	1.09	1.34	-0.60	3023.00	7.77	1.04	-0.17	
3896.00	1.08	1.35	-0.60	3643.00	4.06	4.75	-0.80	
3351.00	2.24	0.19	-0.09	3597.00	13.12	4.31	0.72	
2879.00	2.74	0.31	0.14	4143.00	17.36	8.55	1.44	
2472.00	1.86	0.57	-0.25	3191.00	11.00	2.19	0.37	
3663.00	2.62	0.19	0.08	3067.00	7.04	1.77	-0.30	
3473.00	5.13	2.70	1.20	4724.00	14.33	5.52	0.93	
4540.00	7.14	**4.71**	2.10	3959.00	22.38	**13.57**	2.28	y
2693.00	1.89	0.54	-0.24	2807.00	4.67	4.14	-0.70	
3420.00	3.68	1.25	0.56	4976.00	12.66	3.85	0.65	
3208.00	3.99	1.56	0.70	4839.00	16.68	7.87	1.32	
3724.00	4.03	1.60	0.71	3603.00	12.63	3.82	0.64	
2869.00	2.51	0.08	0.04	4907.00	17.91	9.10	1.53	
3477.00	4.69	2.26	1.01	4824.00	23.78	**14.97**	2.51	y

3174.00	3.81	1.38	0.62	4123.00	8.25	0.56	-0.09
3706.00	8.55	**6.12**	2.73	3957.00	14.05	5.24	0.88
3791.00	1.77	0.66	-0.30	4515.00	9.97	1.16	0.19
2376.00	0.67	1.76	-0.78	1992.00	5.07	3.74	-0.63
2451.00	2.28	0.15	-0.07	1886.00	4.08	4.73	-0.79
3224.00	3.60	1.17	0.52	1618.00	16.07	7.26	1.22
4719.00	4.37	1.94	0.86	2946.00	8.66	0.15	-0.03
2909.00	3.78	1.35	0.60	1363.00	9.76	0.95	0.16
3173.00	4.41	1.98	0.88	3194.00	15.31	6.50	1.09
3281.00	1.83	0.60	-0.27	2629.00	7.19	1.62	-0.27
2680.00	0.93	1.50	-0.67	2377.00	4.46	4.35	-0.73
3245.00	1.39	1.04	-0.47	2283.00	4.16	4.65	-0.78
3203.00	1.56	0.87	-0.39	2222.00	5.18	3.63	-0.61
3512.00	2.99	0.56	0.25	3426.00	9.81	1.00	0.17
3235.00	1.51	0.92	-0.41	2162.00	5.37	3.44	-0.58
3339.00	5.75	3.32	1.48	2854.00	11.56	2.75	0.46
4083.00	2.35	0.08	-0.04	4575.00	10.89	2.08	0.35
3883.00	2.99	0.56	0.25	4392.00	8.47	0.34	-0.06
3577.00	4.36	1.93	0.86	3584.00	15.12	6.31	1.06
3686.00	1.55	0.88	-0.39	3591.00	4.96	3.85	-0.65
2881.00	5.94	3.51	1.56	3180.00	7.52	1.29	-0.22
2332.00	2.40	0.03	-0.01	3798.00	7.08	1.73	-0.29
2490.00	6.99	**4.56**	2.03	2731.00	13.40	4.59	0.77
2301.00	3.35	0.92	0.41	2860.00	3.92	4.89	-0.82
3106.00	4.70	2.27	1.01	3221.00	5.90	2.91	-0.49
1881.00	5.26	2.83	1.26	3326.00	10.91	2.10	0.35
2712.00	7.93	**5.50**	2.45	3860.00	13.71	4.90	0.82
2699.00	5.63	3.20	1.43	4341.00	16.06	7.25	1.22
2563.00	6.59	4.16	1.86	3819.00	16.00	7.19	1.21
2491.00	6.50	4.07	1.82	3873.00	13.48	4.67	0.78
1085.00	1.66	0.77	-0.34	2458.00	5.13	3.68	-0.62
2604.00	5.88	3.45	1.54	3509.00	9.23	0.42	0.07
2817.00	3.34	0.91	0.40	3102.00	6.42	2.39	-0.40
3910.00	8.34	**5.91**	2.64	4252.00	17.03	8.22	1.38
2556.00	2.00	0.43	-0.19	2835.00	8.85	0.04	0.01
2553.00	7.87	**5.44**	2.43	2762.00	12.31	3.50	0.59
2522.00	2.62	0.19	0.08	2388.00	4.31	4.50	-0.76
3040.00	2.63	0.20	0.09	4103.00	6.75	2.06	-0.35
2585.00	5.42	2.99	1.33	3379.00	9.29	0.48	0.08
2681.00	4.36	1.93	0.86	3484.00	7.06	1.75	-0.29
4669.00	0.81	1.62	-0.72	4501.00	9.18	0.37	0.06
3355.00	1.52	0.91	-0.41	4030.00	9.06	0.25	0.04
2790.00	1.58	0.85	-0.38	2868.00	9.97	1.16	0.19
3245.00	1.69	0.74	-0.33	3498.00	5.55	3.26	-0.55
2000.00	0.50	1.93	-0.86	2650.00	2.26	6.55	-1.10
2289.00	0.79	1.64	-0.73	2933.00	8.11	0.70	-0.12
4502.00	2.47	0.04	0.02	4765.00	17.00	8.19	1.38

3038.00	0.53	1.90	-0.85	2654.00	5.58	3.23	-0.54	
3007.00	6.52	4.09	1.83	4034.00	19.73	10.92	1.84	
1751.00	1.71	0.72	-0.32	2600.00	7.31	1.50	-0.25	
3317.00	2.53	0.10	0.05	3377.00	10.25	1.44	0.24	
2815.00	2.52	0.09	0.04	2688.00	5.21	3.60	-0.61	
2529.00	4.55	2.12	0.95	2582.00	9.22	0.41	0.07	
3922.00	4.46	2.03	0.91	4090.00	9.12	0.31	0.05	
3128.00	2.49	0.06	0.03	2517.00	4.81	4.00	-0.67	
4832.00	8.57	**6.14**	2.74	4860.00	13.75	4.94	0.83	
3662.00	3.52	1.09	0.49	3370.00	3.09	5.72	-0.96	
3829.00	15.54	**13.11**	5.85	3992.00	12.15	3.34	0.56	
2336.00	10.02	**7.59**	3.39	3442.00	7.70	1.11	-0.19	
2613.00	5.20	2.77	1.24	4093.00	5.57	3.24	-0.54	
2890.00	6.96	4.53	2.02	2985.00	15.58	6.77	1.14	
2838.00	10.18	**7.75**	3.46	2425.00	15.55	6.74	1.13	
4020.00	6.22	3.79	1.69	3550.00	12.11	3.30	0.55	
3170.00	2.62	0.19	0.08	3341.00	8.77	0.04	-0.01	
4307.00	12.12	**9.69**	4.33	3690.00	17.59	8.78	1.47	
2644.00	4.05	1.62	0.72	3042.00	14.04	5.23	0.88	
4094.00	14.95	**12.52**	5.59	3368.00	22.06	**13.25**	2.23	y
2269.00	2.95	0.52	0.23	3416.00	11.48	2.67	0.45	
1887.00	1.59	0.84	-0.38	2482.00	7.53	1.28	-0.21	
2958.00	4.23	1.80	0.80	2883.00	11.93	3.12	0.52	
2458.00	4.72	2.29	1.02	3080.00	12.86	4.05	0.68	
2294.00	4.66	2.23	1.00	1980.00	3.13	5.68	-0.95	
2336.00	7.83	**5.40**	2.41	2582.00	12.82	4.01	0.67	
2978.00	1.98	0.45	-0.20	3244.00	4.13	4.68	-0.79	
3016.00	6.57	4.14	1.85	2352.00	16.54	7.73	1.30	
2570.00	5.41	2.98	1.33	2438.00	10.46	1.65	0.28	
1852.00	1.35	1.08	-0.48	2804.00	1.93	6.88	-1.16	
3971.00	7.45	**5.02**	2.24	4627.00	12.08	3.27	0.55	
3154.00	3.65	1.22	0.54	3541.00	10.73	1.92	0.32	
3190.00	1.38	1.05	-0.47	4858.00	6.83	1.98	-0.33	
3298.00	3.46	1.03	0.46	3294.00	14.39	5.58	0.94	
2729.00	2.71	0.28	0.13	2668.00	8.17	0.64	-0.11	
2741.00	2.33	0.10	-0.04	1942.00	8.14	0.67	-0.11	
2479.00	2.02	0.41	-0.18	2916.00	13.41	4.60	0.77	
2446.00	0.70	1.73	-0.77	2800.00	9.25	0.44	0.07	
1445.00	0.97	1.46	-0.65	1617.00	10.27	1.46	0.24	
3160.00	2.63	0.20	0.09	4297.00	23.16	**14.35**	2.41	
1985.00	1.56	0.87	-0.39	2183.00	14.43	5.62	0.94	
2216.00	0.99	1.44	-0.64	1630.00	10.49	1.68	0.28	
1987.00	1.51	0.92	-0.41	2390.00	21.80	**12.99**	2.18	
2044.00	0.78	1.65	-0.74	1973.00	7.96	0.85	-0.14	
3152.00	2.79	0.36	0.16	2763.00	26.13	**17.32**	2.91	
1619.00	2.41	0.02	-0.01	1803.00	4.66	4.15	-0.70	
2892.00	1.00	1.43	-0.64	2236.00	9.62	0.81	0.14	

2901.00	2.34	0.09	-0.04	3196.00	17.62	8.81	1.48	
4616.00	3.83	1.40	0.63	3190.00	9.56	0.75	0.13	
2719.00	1.62	0.81	-0.36	3512.00	10.36	1.55	0.26	
2122.00	3.72	1.29	0.58	2831.00	14.06	5.25	0.88	
2537.00	1.26	1.17	-0.52	2705.00	4.62	4.19	-0.70	
2199.00	2.14	0.29	-0.13	2360.00	9.28	0.47	0.08	
3250.00	0.62	1.81	-0.81	3108.00	9.20	0.39	0.07	
3839.00	1.22	1.21	-0.54	2896.00	10.53	1.72	0.29	
2359.00	0.89	1.54	-0.69	2084.00	7.29	1.52	-0.26	
2594.00	0.50	1.93	-0.86	2849.00	7.48	1.33	-0.22	
3355.00	1.94	0.49	-0.22	3489.00	20.81	12.00	2.02	
2875.00	1.01	1.42	-0.63	3194.00	16.69	7.88	1.32	
3211.00	0.78	1.65	-0.74	2737.00	9.21	0.40	0.07	
4663.00	0.90	1.53	-0.68	2159.00	4.91	3.90	-0.66	
4225.00	2.75	0.32	0.14	3471.00	13.54	4.73	0.79	
2753.00	1.45	0.98	-0.44	2426.00	15.09	6.28	1.05	
2327.00	0.99	1.44	-0.64	1278.00	7.36	1.45	-0.24	
3515.00	1.34	1.09	-0.49	2199.00	12.73	3.92	0.66	
4005.00	2.85	0.42	0.19	2741.00	12.84	4.03	0.68	
4642.00	2.46	0.03	0.01	2429.00	12.52	3.71	0.62	
3798.00	1.69	0.74	-0.33	2152.00	12.97	4.16	0.70	
4570.00	4.20	1.77	0.79	2116.00	13.42	4.61	0.77	
2960.00	5.84	3.41	1.52	2581.00	13.75	4.94	0.83	
4123.00	2.74	0.31	0.14	2533.00	4.46	4.35	-0.73	
3006.00	6.25	3.82	1.71	1849.00	12.87	4.06	0.68	
2311.00	2.90	0.47	0.21	1713.00	6.48	2.33	-0.39	
1973.00	0.86	1.57	-0.70	2645.00	6.96	1.85	-0.31	
1491.00	0.40	2.03	-0.91	2441.00	12.17	3.36	0.56	
3068.00	1.56	0.87	-0.39	3529.00	15.08	6.27	1.05	
2241.00	1.92	0.51	-0.23	2636.00	13.62	4.81	0.81	
2944.00	3.97	1.54	0.69	3216.00	26.59	17.78	2.99	y
1148.00	3.22	0.79	0.35	2681.00	25.07	16.26	2.73	
1919.00	1.46	0.97	-0.43	2747.00	17.07	8.26	1.39	
3417.00	1.43	1.00	-0.44	2456.00	9.85	1.04	0.18	
2536.00	1.26	1.17	-0.52	2346.00	7.29	1.52	-0.26	
2453.00	4.65	2.22	0.99	4239.00	30.36	21.55	3.62	y
2788.00	2.33	0.10	-0.04	2901.00	12.41	3.60	0.60	
2223.00	1.39	1.04	-0.46	1851.00	4.48	4.33	-0.73	
2876.00	1.32	1.11	-0.50	2650.00	10.23	1.42	0.24	
1043.00	1.73	0.70	-0.31	2809.00	6.16	2.65	-0.45	
2842.00	6.65	4.22	1.88	3384.00	18.47	9.66	1.62	
2335.00	2.70	0.27	0.12	2561.00	12.73	3.92	0.66	
3582.00	8.24	5.81	2.59	3694.00	13.13	4.32	0.73	
3217.00	7.52	5.09	2.27	4201.00	21.64	12.83	2.16	y
2874.00	3.86	1.43	0.64	3647.00	20.81	12.00	2.02	y
2970.00	8.69	6.26	2.79	2990.00	10.87	2.06	0.35	
1246.00	1.52	0.91	-0.40	1934.00	7.96	0.85	-0.14	

3926.00	11.49	9.06	4.04	3367.00	23.88	15.07	2.53	y	
4718.00	8.16	5.73	2.56	4893.00	19.48	10.67	1.79	y	
3165.00	10.08	7.65	3.42	4561.00	20.02	11.21	1.88	y	
3283.00	5.88	3.45	1.54	2615.00	13.00	4.19	0.70		
4309.00	6.03	3.60	1.61	3893.00	15.03	6.22	1.04		
2660.00	6.69	4.26	1.90	2410.00	14.36	5.55	0.93		
2577.00	6.13	3.70	1.65	2562.00	27.64	18.83	3.16		
3379.00	10.60	8.17	3.65	2083.00	15.89	7.08	1.19		
2828.00	2.30	0.13	-0.06	3097.00	10.91	2.10	0.35		
4009.00	20.53	18.10	8.08	2954.00	28.74	19.93	3.35	y	
3242.00	4.26	1.83	0.82	2196.00	13.43	4.62	0.78		
3403.00	13.05	10.62	4.74	2589.00	19.24	10.43	1.75		
2696.00	7.97	5.54	2.48	2784.00	12.79	3.98	0.67		
1466.00	8.73	6.30	2.81	1461.00	17.32	8.51	1.43		
2368.00	6.55	4.12	1.84	3091.00	5.99	2.82	-0.47		
3104.00	9.95	7.52	3.36	3545.00	14.53	5.72	0.96		
3207.00	6.61	4.18	1.87	3403.00	17.57	8.76	1.47		
4732.00	15.60	13.17	5.88	3673.00	19.33	10.52	1.77		
2534.00	14.88	12.45	5.56	2782.00	19.05	10.24	1.72	x	debris a,b
1646.00	8.75	6.32	2.82	1895.00	8.76	0.05	-0.01		
1194.00	5.19	2.76	1.23	1897.00	5.75	3.06	-0.52		
1390.00	9.06	6.63	2.96	2040.00	4.90	3.91	-0.66		
2501.00	7.96	5.53	2.47	3233.00	6.65	2.16	-0.36		
1512.00	8.47	6.04	2.69	1942.00	5.46	3.35	-0.56	x	toxic b,c
1205.00	4.90	2.47	1.10	2425.00	5.86	2.95	-0.50		
1064.00	3.38	0.95	0.43	1332.00	3.45	5.36	-0.90		
1312.00	14.63	12.20	5.45	1155.00	9.35	0.54	0.09		
1770.00	6.78	4.35	1.94	938.00	3.09	5.72	-0.96		
1429.00	4.97	2.54	1.13	2468.00	4.58	4.23	-0.71		
1800.00	12.94	10.51	4.69	3066.00	11.94	3.13	0.53	y	
1249.00	11.29	8.86	3.96	2951.00	9.39	0.58	0.10	y	
1996.00	6.96	4.53	2.02	1884.00	4.30	4.51	-0.76		
2270.00	7.05	4.62	2.06	1940.00	6.86	1.95	-0.33		
1992.00	7.73	5.30	2.37	997.00	5.32	3.49	-0.59	x	toxic b,c
3146.00	13.70	11.27	5.03	1817.00	10.90	2.09	0.35		
1823.00	16.79	14.36	6.41	2780.00	16.44	7.63	1.28	y	
1443.00	5.68	3.25	1.45	2789.00	5.95	2.86	-0.48		
1818.00	1.98	0.45	-0.20	1788.00	2.40	6.41	-1.08		
1644.00	8.70	6.27	2.80	1337.00	6.13	2.68	-0.45		
2965.00	2.43	1.51		2865.50	8.81	4.02	0.00		
		4.54				12.06			
		2.24				5.95			
		2718.00	35.69		3423.00	19.52			
		3820.00	39.76		4845.00	15.89			
26.66		4266.00	42.50						
32.28		3109.00	21.39						
29.47		3478.25	34.84						

3.98	695.62	9.39
1.06	1446.00	4.56
0.67	707.00	1.41
2.66	440.00	0.91
3.00	916.00	1.86
2.11	687.67	1.39
1.26	238.59	0.47
11.93		28.17
3.77		1.42
15.69		29.59
27.36		33.44
0.57		0.88
0.43		0.12

2.21	504.00	7.14
1.55	299.00	7.36
6.73	4352.00	11.58
2.31	4193.00	13.93
11.72	4926.00	21.95
5.59	3306.00	18.85

					cell_ct	percent inf	Abs Devtn
50060.00	A02	M-021105- hypothetic	55101.00	FLJ10241	2276.00	0.83	2.48
50060.00	A04	M-020782- ribonucleas	54913.00	RPP25	1360.00	0.96	2.35
50060.00	A05	M-018088- phosphatid	54872.00	PIGG	2230.00	1.57	1.74
50060.00	A06	M-021083- hypothetic	55073.00	FLJ10120	1359.00	2.94	0.37
50060.00	A07	M-015134- palmdelphi	54873.00	PALMD	1813.00	0.61	2.70
50060.00	A08	M-021031- chromosom	55049.00	C19orf60	2599.00	10.66	**7.35**
50060.00	A09	M-020718- formin bin	54874.00	FNBP1L	943.00	0.53	2.78
50060.00	A10	M-016321- WD repeat	55100.00	WDR70	1462.00	0.82	2.49
50060.00	A11	M-020720- chromosom	54875.00	C9orf39	722.00	1.25	2.06
50060.00	A12	M-021103- hypothetic	55099.00	FLJ10232	372.00	1.08	2.23
50060.00	A13	M-020725- chromosom	54876.00	C4orf30	933.00	2.14	1.17
50060.00	A14	M-018141- hypothetic	55096.00	FLJ10213	1724.00	2.38	0.93
50060.00	A15	M-027338- zinc finger,	54877.00	ZCCHC2	1491.00	2.82	0.49
50060.00	A16	M-023688- sterile alph	55095.00	SAMD4B	841.00	3.69	0.38
50060.00	A17	M-005855- dipeptidyl-	54878.00	DPP8	660.00	3.79	0.48
50060.00	A18	M-016826- G patch do	55094.00	GPATCH1	938.00	5.01	1.70
50060.00	A19	M-004584- BCL6 co-re	54880.00	BCOR	351.00	9.97	**6.66**
50060.00	A20	M-021102- chromosom	55093.00	C8orf32	1289.00	3.34	0.03
50060.00	A21	M-020741- testis expre	54881.00	TEX10	817.00	8.08	4.77
50060.00	A23	M-014405- ankyrin rep	54882.00	ANKHD1	1855.00	9.06	5.75
50060.00	B02	M-021239- chromosom	55317.00	C20orf29	892.00	0.45	2.86
50060.00	B04	M-021241- radical S-ac	55316.00	RSAD1	2608.00	0.35	2.96
50060.00	B05	M-016822- chromosom	55102.00	C14orf103	3848.00	0.39	2.92
50060.00	B06	M-007507- solute carri	55315.00	SLC29A3	2506.00	0.96	2.35
50060.00	B07	M-021106- FLJ10246	55104.00	FLJ10246	4288.00	0.21	3.10
50060.00	B08	M-021260- transmemb	55314.00	TMEM144	2698.00	0.67	2.64
50060.00	B09	M-021111- G patch do	55105.00	GPATCH2	2141.00	0.56	2.75
50060.00	B10	M-021262- hypothetic	55313.00	FLJ11151	1945.00	1.08	2.23
50060.00	B11	M-018142- schlafen fa	55106.00	SLFN12	3251.00	1.14	2.17
50060.00	B12	M-021317- zinc finger	55311.00	ZNF444	3032.00	0.40	2.91
50060.00	B13	M-027200- transmemb	55107.00	TMEM16A	3884.00	1.08	2.23
50060.00	B14	M-015868- DEAD (Asp-	55308.00	DDX19A	2169.00	0.69	2.62
50060.00	B15	M-018143- BSD domai	55108.00	BSDC1	3131.00	2.43	0.88
50060.00	B16	M-010286- serine palm	55304.00	SPTLC3	1978.00	0.35	2.96
50060.00	B17	M-016706- mago-nash	55110.00	FLJ10292	2222.00	0.50	2.81
50060.00	B18	M-019267- GTPase, IM	55303.00	GIMAP4	2203.00	0.45	2.86
50060.00	B19	M-021132- pleckstrin h	55111.00	PLEKHJ1	3408.00	1.58	1.73
50060.00	B20	M-015372- brix domai	55299.00	BXDC2	2375.00	0.46	2.85
50060.00	B21	M-016701- WD repeat	55112.00	WDR60	3472.00	3.46	0.15
50060.00	B23	M-015745- XK, Kell blo	55113.00	XKR8	2706.00	0.52	2.79
50060.00	C02	M-021099- transmemb	55092.00	TMEM51	3187.00	2.20	1.11
50060.00	C04	M-013356- mediator o	55090.00	MED9	2725.00	3.23	0.08
50060.00	C05	M-016097- coiled-coil	54883.00	CCDC49	2563.00	3.20	0.11
50060.00	C06	M-007561- solute carri	55089.00	SLC38A4	2876.00	2.89	0.42
50060.00	C07	M-018094- retinol satu	54884.00	RETSAT	2410.00	4.94	1.63
50060.00	C08	M-019131- chromosom	55088.00	C10orf118	3387.00	7.35	4.04

50060.00	C09	M-020747- TBC1 doma	54885.00	TBC1D8B	2463.00	5.44	2.13
50060.00	C10	M-014634- chromoson	55086.00	CXorf57	2685.00	6.26	2.95
50060.00	C11	M-020752- plasticity re	54886.00	RP11-35N6	2322.00	2.89	0.42
50060.00	C12	M-021094- sine oculis	55084.00	SOBP	2254.00	2.93	0.38
50060.00	C13	M-013360- chromoson	54887.00	C6orf107	2379.00	3.74	0.43
50060.00	C14	M-022129- kinesin fam	55083.00	KIF26B	1754.00	4.45	1.14
50060.00	C15	M-018217- NOL1/NOP	54888.00	NSUN2	1618.00	2.84	0.47
50060.00	C16	M-021093- hypothetic	55082.00	FLJ10154	1839.00	10.11	**6.80**
50060.00	C17	M-004281- alkB, alkyla	54890.00	ALKBH5	2005.00	8.73	5.42
50060.00	C18	M-004021- TAP bindin	55080.00	TAPBPL	1298.00	3.54	0.23
50060.00	C19	M-020757- hypothetic	54891.00	FLJ20309	2311.00	6.79	3.48
50060.00	C20	M-016985- FEZ family	55079.00	FEZF2	3688.00	12.12	**8.81**
50060.00	C21	M-018283- non-SMC c	54892.00	NCAPG2	2580.00	6.28	2.97
50060.00	C23	M-020758- myotubula	54893.00	MTMR10	1908.00	4.45	1.14
50060.00	D02	M-007011- ring finger	55298.00	RNF121	2725.00	3.93	0.62
50060.00	D04	M-018638- coiled-coil	55297.00	CCDC91	3579.00	3.13	0.18
50060.00	D05	M-008335- Rho GTPas	55114.00	ARHGAP17	2920.00	5.31	2.00
50060.00	D06	M-020732- TBC1 doma	55296.00	TBC1D19	2752.00	2.22	1.09
50060.00	D07	M-021133- transmemb	55116.00	TMEM39B	2110.00	4.64	1.33
50060.00	D08	M-020312- kelch-like 2	55295.00	KLHL26	1915.00	2.92	0.39
50060.00	D09	M-007373- solute carri	55117.00	SLC6A15	2209.00	4.84	1.53
50060.00	D10	M-014646- SAPS doma	55291.00	SAPS3	3109.00	3.38	0.07
50060.00	D11	M-009527- cartilage ac	55118.00	CRTAC1	3751.00	2.45	0.86
50060.00	D12	M-010365- ras homolo	55288.00	RHOT1	2726.00	3.01	0.30
50060.00	D13	M-021143- PRP38 pre-	55119.00	PRPF38B	2733.00	1.39	1.92
50060.00	D14	M-017988- transmemb	55287.00	TMEM40	2462.00	1.02	2.29
50060.00	D15	M-021486- Fanconi an	55120.00	FANCL	1866.00	1.07	2.24
50060.00	D16	M-021257- chromoson	55286.00	C4orf19	2926.00	3.35	0.04
50060.00	D17	M-031863- chromoson	55122.00	C6orf166	1912.00	1.15	2.16
50060.00	D18	M-020984- RNA bindin	55285.00	RBM41	2872.00	1.25	2.06
50060.00	D19	M-032250- centrosom	55125.00	CEP192	2998.00	2.37	0.94
50060.00	D20	M-017987- leucine rich	55282.00	LRRC36	2319.00	3.02	0.29
50060.00	D21	M-015939- HEAT repea	55127.00	HEATR1	1914.00	0.63	2.68
50060.00	D23	M-007007- tripartite m	55128.00	TRIM68	1923.00	0.36	2.95
50060.00	E02	M-013795- uveal auto	55075.00	UACA	2995.00	2.50	0.81
50060.00	E04	M-017698- oxidation r	55074.00	OXR1	3505.00	2.97	0.34
50060.00	E05	M-007004- ring finger	54894.00	RNF43	2115.00	4.44	1.13
50060.00	E06	M-021078- chromoson	55071.00	C9orf40	1668.00	1.92	1.39
50060.00	E07	M-020760- PQ loop re	54896.00	PQLC2	1667.00	1.20	2.11
50060.00	E08	M-019393- de-etiolate	55070.00	DET1	1299.00	2.85	0.46
50060.00	E09	M-020764- castor zinc	54897.00	CASZ1	2569.00	2.26	1.05
50060.00	E10	M-018206- chromoson	55069.00	C7orf42	2316.00	2.89	0.42
50060.00	E11	M-009531- elongation	54898.00	ELOVL2	2830.00	2.51	0.80
50060.00	E12	M-021077- ecto-NOX c	55068.00	ENOX1	2908.00	2.68	0.63
50060.00	E13	M-020771- lymphocyte	54900.00	LAX1	1504.00	1.80	1.51
50060.00	E14	M-021074- chromoson	55064.00	C9orf68	1729.00	0.98	2.33
50060.00	E15	M-020772- CDK5 regul	54901.00	CDKAL1	1574.00	1.40	1.91

50060.00	E16	M-016988- zinc finger,	55063.00	ZCWPW1	2497.00	2.72	0.59
50060.00	E17	M-020774- Meckel syn	54903.00	MKS1	881.00	2.16	1.15
50060.00	E18	M-018205- WD repeat	55062.00	WIPI1	1347.00	0.37	2.94
50060.00	E19	M-009395- cytochrom	54905.00	CYP2W1	3274.00	1.10	2.21
50060.00	E20	M-021072- sushi doma	55061.00	SUSD4	3267.00	1.62	1.69
50060.00	E21	M-016970- coiled-coil	54908.00	CCDC99	3285.00	2.13	1.18
50060.00	E23	M-015364- sema doma	54910.00	SEMA4C	2100.00	1.43	1.88
50060.00	F02	M-020874- transmemb	55281.00	TMEM140	2629.00	1.86	1.45
50060.00	F04	M-016322- CWF19-like	55280.00	CWF19L1	2081.00	2.55	0.76
50060.00	F05	M-017701- transmemb	55129.00	TMEM16K	1948.00	5.34	2.03
50060.00	F06	M-020800- zinc finger	55279.00	ZNF654	2615.00	2.79	0.52
50060.00	F07	M-013357- armadillo r	55130.00	ARMC4	1981.00	3.23	0.08
50060.00	F08	M-010132- glutaminyl-	55278.00	QRSL1	1186.00	3.29	0.02
50060.00	F09	M-021145- RNA bindin	55131.00	RBM28	3515.00	11.12	**7.81**
50060.00	F10	M-020785- phosphoglu	55276.00	PGM2	2693.00	5.76	2.45
50060.00	F11	M-013350- La ribonucl	55132.00	LARP2	2602.00	2.00	1.31
50060.00	F12	M-017048- vacuolar pr	55275.00	VPS53	2005.00	4.79	1.48
50060.00	F13	M-018144- S1 RNA bin	55133.00	SRBD1	1678.00	5.42	2.11
50060.00	F14	M-013349- PHD finger	55274.00	PHF10	1909.00	10.58	**7.27**
50060.00	F15	M-021146- WD repeat	55135.00	WDR79	1442.00	1.46	1.85
50060.00	F16	M-020645- transmemb	55273.00	TMEM100	2133.00	3.00	0.31
50060.00	F17	M-010934- fidgetin	55137.00	FIGN	2597.00	6.55	3.24
50060.00	F18	M-013348- IMP3, U3 s	55272.00	IMP3	3179.00	2.93	0.38
50060.00	F19	M-021150- family with	55138.00	FAM90A1	2026.00	2.76	0.55
50060.00	F20	M-020621- nudix (nucl	55270.00	NUDT15	1801.00	5.33	2.02
50060.00	F21	M-021152- ankyrin rep	55139.00	ANKZF1	830.00	0.84	2.47
50060.00	F23	M-015940- elongation	55140.00	ELP3	2237.00	0.36	2.95
50060.00	G02	M-019377- Zwilch, kine	55055.00	ZWILCH	2940.00	1.97	1.34
50060.00	G04	M-021033- ATG16 auto	55054.00	ATG16L1	3632.00	2.12	1.19
50060.00	G05	M-015365- KIAA1797	54914.00	KIAA1797	2427.00	2.88	0.43
50060.00	G06	M-017564- mitochond	55052.00	MRPL20	2221.00	0.77	2.54
50060.00	G07	M-018095- YTH domai	54915.00	YTHDF1	4060.00	7.17	3.86
50060.00	G08	M-013794- chromosom	55051.00	C14orf102	2924.00	2.60	0.71
50060.00	G09	M-020793- chromosom	54916.00	C14orf101	2775.00	2.31	1.00
50060.00	G10	M-018204- vacuolar pr	55048.00	VPS37C	1091.00	0.55	2.76
50060.00	G11	M-010711- CKLF-like M	54918.00	CMTM6	3528.00	1.53	1.78
50060.00	G12	M-021012- pleckstrin h	55041.00	PLEKHB2	3539.00	1.84	1.47
50060.00	G13	M-018096- HEAT repea	54919.00	HEATR2	2635.00	1.18	2.13
50060.00	G14	M-021006- epsin 3	55040.00	EPN3	2472.00	0.40	2.91
50060.00	G15	M-017059- dihydrouri	54920.00	DUS2L	2515.00	4.93	1.62
50060.00	G16	M-021001- tRNA meth	55039.00	TRMT12	2768.00	0.94	2.37
50060.00	G17	M-020794- Ras interac	54922.00	RASIP1	2441.00	0.66	2.65
50060.00	G18	M-016957- Pentatricop	55037.00	PTCD3	3238.00	0.86	2.45
50060.00	G19	M-020797- Lck interac	54923.00	LIME1	3550.00	2.62	0.69
50060.00	G20	M-030953- coiled-coil	55036.00	CCDC40	2514.00	1.67	1.64
50060.00	G21	M-018838- zinc finger	54925.00	ZNF434	3281.00	0.73	2.58
50060.00	G23	M-020803- coiled-coil-	54927.00	CHCHD3	1820.00	0.49	2.82

50060.00	H02	M-020596- paraspeckl	55269.00	PSPC1	2224.00	0.99	2.32
50060.00	H04	M-010013- enoyl Coen	55268.00	ECHDC2	2541.00	0.91	2.40
50060.00	H05	M-021161- centrosom	55142.00	CEP27	1698.00	2.06	1.25
50060.00	H06	M-016459- transmem	55266.00	TMEM19	2110.00	0.28	3.03
50060.00	H07	M-021163- cell divisior	55143.00	CDCA8	799.00	4.01	0.70
50060.00	H08	M-020225- chromoson	55264.00	C21orf77	3304.00	3.45	0.14
50060.00	H09	M-015747- leucine rich	55144.00	LRRC8D	3288.00	1.82	1.49
50060.00	H10	M-016464- chromoson	55262.00	C7orf43	2681.00	0.71	2.60
50060.00	H11	M-021313- THAP dom	55145.00	THAP1	2445.00	1.51	1.80
50060.00	H12	M-018806- transmem	55260.00	TMEM143	3358.00	2.00	1.31
50060.00	H13	M-016699- zinc finger,	55146.00	ZDHHC4	1687.00	1.13	2.18
50060.00	H14	M-027150- cancer sus	55259.00	CASC1	2302.00	0.52	2.79
50060.00	H15	M-016689- RNA bindin	55147.00	RBM23	4679.00	2.27	1.04
50060.00	H16	M-020368- hypothetic	55258.00	FLJ10916	1954.00	0.72	2.59
50060.00	H17	M-016489- chromoson	55148.00	C14orf130	2847.00	0.67	2.64
50060.00	H18	M-006381- chromoson	55257.00	C20orf20	1778.00	0.45	2.86
50060.00	H19	M-016486- PAP associ	55149.00	PAPD1	2594.00	0.93	2.38
50060.00	H20	M-020394- acireductor	55256.00	ADI1	1749.00	0.23	3.08
50060.00	H21	M-021165- hypothetic	55150.00	FLJ10490	2906.00	1.20	2.11
50060.00	H23	M-021168- transmem	55151.00	TMEM38B	2579.00	0.74	2.57
50060.00	I02	M-016976- nucleolar p	55035.00	NOL8	2052.00	2.19	1.12
50060.00	I04	M-007541- solute carri	55032.00	SLC35A5	1383.00	5.71	2.40
50060.00	I05	M-020806- transmem	54929.00	TMEM161	3106.00	7.47	4.16
50060.00	I06	M-006093- ubiquitin s	55031.00	USP47	3587.00	4.96	1.65
50060.00	I07	M-020807- chromoson	54930.00	C14orf94	1774.00	2.20	1.11
50060.00	I08	M-020989- F-box prote	55030.00	FBXO34	3015.00	4.54	1.23
50060.00	I09	M-020813- RNA (guani	54931.00	RG9MTD1	2554.00	3.60	0.29
50060.00	I10	M-016959- chromoson	55028.00	C17orf80	3176.00	8.75	5.44
50060.00	I11	M-018097- hypothetic	54932.00	FLJ20433	4470.00	5.46	2.15
50060.00	I12	M-020982- HEAT repe	55027.00	HEATR3	2558.00	1.84	1.47
50060.00	I13	M-006028- rhomboid,	54933.00	RHBDL2	1863.00	0.43	2.88
50060.00	I14	M-018099- family with	55026.00	FAM70A	2549.00	3.53	0.22
50060.00	I15	M-020816- chromoson	54934.00	C12orf41	1827.00	1.15	2.16
50060.00	I16	M-019168- B-cell scaff	55024.00	BANK1	2534.00	2.92	0.39
50060.00	I17	M-020823- spermatog	54937.00	SOHLH2	2148.00	2.70	0.61
50060.00	I18	M-018934- phosphoty	55022.00	PID1	3559.00	5.14	1.83
50060.00	I19	M-016311- seryl-tRNA	54938.00	SARS2	3044.00	3.06	0.25
50060.00	I20	M-020975- hypothetic	55020.00	FLJ20699	3794.00	7.04	3.73
50060.00	I21	M-016966- COMM dor	54939.00	COMMD4	2775.00	4.94	1.63
50060.00	I23	M-020825- OCIA doma	54940.00	OCIAD1	2901.00	2.72	0.59
50060.00	J02	M-020405- WD repeat	55255.00	WDR41	3710.00	13.72	**10.41**
50060.00	J04	M-020434- transmem	55254.00	TMEM39A	2196.00	18.58	**15.27**
50060.00	J05	M-015807- DALR antic	55152.00	DALRD3	2960.00	11.69	**8.38**
50060.00	J06	M-020515- tRNA-yW s	55253.00	TYW1	3614.00	9.30	5.99
50060.00	J07	M-021169- SDA1 dom	55153.00	SDAD1	1995.00	15.84	**12.53**
50060.00	J08	M-022638- additional	55252.00	ASXL2	2373.00	13.11	**9.80**

50060.00	J09	M-021170- misato hon	55154.00	MSTO1	3075.00	9.89	**6.58**
50060.00	J10	M-021138- protein-L-is	55251.00	PCMTD2	1892.00	13.58	**10.27**
50060.00	J11	M-020492- aspartyl-tR	55157.00	DARS2	3029.00	15.09	**11.78**
50060.00	J12	M-021036- chromoson	55248.00	C1orf75	1701.00	17.52	**14.21**
50060.00	J13	M-017095- ring finger	55159.00	RFWD3	904.00	17.48	**14.17**
50060.00	J14	M-020939- nei endonu	55247.00	NEIL3	2546.00	10.21	**6.90**
50060.00	J15	M-017096- Rho guanin	55160.00	ARHGEF10	2787.00	5.96	2.65
50060.00	J16	M-020869- coiled-coil	55246.00	CCDC25	2637.00	10.16	**6.85**
50060.00	J17	M-020386- transmemb	55161.00	TMEM33	1977.00	3.44	0.13
50060.00	J18	M-013347- solute carri	55244.00	SLC47A1	2933.00	5.35	2.04
50060.00	J19	M-009715- pyridoxami	55163.00	PNPO	4134.00	10.14	**6.83**
50060.00	J20	M-019453- kin of IRRE	55243.00	KIRREL	2828.00	6.51	3.20
50060.00	J21	M-020737- SHQ1 hom	55164.00	SHQ1	3398.00	9.71	**6.40**
50060.00	J23	M-006893- centrosom	55165.00	CEP55	2578.00	9.50	6.19
50060.00	K02	M-020969- chromoson	55018.00	C17orf73	1652.00	13.62	**10.31**
50060.00	K04	M-021301- chromoson	55017.00	C14orf119	3712.00	14.36	**11.05**
50060.00	K05	M-007005- ring finger	54941.00	RNF125	2835.00	12.91	**9.60**
50060.00	K06	M-007006- membrane	55016.00	MARCH1	3302.00	11.75	**8.44**
50060.00	K07	M-016099- chromoson	54942.00	C9orf6	2815.00	5.79	2.48
50060.00	K08	M-021324- PRP39 pre-	55015.00	PRPF39	3448.00	15.31	**12.00**
50060.00	K09	M-021397- chromoson	54943.00	C21orf55	2556.00	4.69	1.38
50060.00	K10	M-020965- syntaxin 17	55014.00	STX17	3530.00	7.39	4.08
50060.00	K11	M-007330- solute carri	54946.00	SLC41A3	3232.00	8.76	5.45
50060.00	K12	M-016108- coiled-coil	55013.00	CCDC109B	2344.00	9.90	**6.59**
50060.00	K13	M-010285- acyltransfe	54947.00	AYTL1	2495.00	2.65	0.66
50060.00	K14	M-018203- protein ph	55012.00	PPP2R3C	2790.00	3.80	0.49
50060.00	K15	M-013354- mitochond	54948.00	MRPL16	2212.00	3.03	0.28
50060.00	K16	M-020963- PIH1 doma	55011.00	PIH1D1	3301.00	2.61	0.70
50060.00	K17	M-020834- chromoson	54949.00	C11orf79	2189.00	1.32	1.99
50060.00	K18	M-020943- chromoson	55010.00	C12orf48	2672.00	1.83	1.48
50060.00	K19	M-018218- COMM do	54951.00	COMMD8	3370.00	1.96	1.35
50060.00	K20	M-020936- chromoson	55009.00	C19orf24	4040.00	5.22	1.91
50060.00	K21	M-018098- tRNA selen	54952.00	TRSPAP1	3934.00	7.65	4.34
50060.00	K23	M-010667- chromoson	54953.00	C1orf27	2357.00	1.87	1.44
50060.00	L02	M-021197- 2-oxogluta	55239.00	OGFOD1	3106.00	10.43	**7.12**
50060.00	L04	M-007328- amino acid	55238.00	FLJ10815	4110.00	6.57	3.26
50060.00	L05	M-020768- centromer	55166.00	CENPQ	3031.00	9.67	6.36
50060.00	L06	M-021159- chromoson	55237.00	C14orf115	1776.00	4.05	0.74
50060.00	L07	M-020828- male-speci	55167.00	MSL2L1	2413.00	7.67	4.36
50060.00	L08	M-006403- ubiquitin-a	55236.00	UBE1L2	1776.00	6.19	2.88
50060.00	L09	M-007008- mitochond	55168.00	MRPS18A	3420.00	9.06	5.75
50060.00	L10	M-021129- smu-1 supp	55234.00	SMU1	557.00	14.54	**11.23**
50060.00	L11	M-007773- protein arg	55170.00	PRMT6	2687.00	7.59	4.28
50060.00	L12	M-021097- MOB1, Mp	55233.00	MOBK1B	3127.00	6.59	3.28
50060.00	L13	M-020887- TBCC doma	55171.00	TBCCD1	2892.00	5.71	2.40
50060.00	L14	M-021023- coiled-coil	55231.00	CCDC87	2331.00	2.49	0.82
50060.00	L15	M-020906- chromoson	55172.00	C14orf104	1417.00	1.62	1.69

50060.00	L16	M-006088- ubiquitin sp	55230.00	USP40	1745.00	2.46	0.85
50060.00	L17	M-013345- mitochond	55173.00	MRPS10	2085.00	2.49	0.82
50060.00	L18	M-021021- hypothetic	55228.00	FLJ10781	4264.00	6.14	2.83
50060.00	L19	M-020921- integrator	55174.00	INTS10	2598.00	4.23	0.92
50060.00	L20	M-010668- leucine rich	55227.00	LRRC1	3389.00	4.43	1.12
50060.00	L21	M-020928- kelch-like 1	55175.00	KLHL11	2731.00	6.15	2.84
50060.00	L23	M-013628- Sec61 alph	55176.00	SEC61A2	1304.00	2.99	0.32
50060.00	M02	M-020931- family with	55007.00	FAM118A	2142.00	3.92	0.61
50060.00	M04	M-012966- hypothetic	55006.00	FLJ20628	2916.00	2.74	0.57
50060.00	M05	M-032024- family with	54954.00	FAM120C	2719.00	2.02	1.29
50060.00	M06	M-020923- required fo	55005.00	RMND1	1876.00	2.03	1.28
50060.00	M07	M-020836- chromosom	54955.00	C1orf109	2793.00	6.12	2.81
50060.00	M08	M-020916- chromosom	55004.00	C11orf59	1596.00	4.45	1.14
50060.00	M09	M-020837- poly (ADP-	54956.00	PARP16	2703.00	6.22	2.91
50060.00	M10	M-020912- PAK1 intera	55003.00	PAK1IP1	2554.00	5.01	1.70
50060.00	M11	M-020838- thioredoxi	54957.00	TXNL4B	3789.00	5.36	2.05
50060.00	M12	M-020908- transmemb	55002.00	TMCO3	2947.00	7.97	4.66
50060.00	M13	M-020840- transmemb	54958.00	TMEM160	1569.00	5.48	2.17
50060.00	M14	M-020902- tetratricop	55001.00	TTC22	2776.00	3.13	0.18
50060.00	M15	M-016965- odontogen	54959.00	ODAM	2686.00	5.06	1.75
50060.00	M16	M-018202- taurine upr	55000.00	TUG1	2672.00	2.69	0.62
50060.00	M17	M-020841- gem (nucle	54960.00	GEMIN8	3009.00	4.65	1.34
50060.00	M18	M-020896- tescalcin	54997.00	TESC	3429.00	5.37	2.06
50060.00	M19	M-020843- TIMELESS i	54962.00	TIPIN	3205.00	12.48	9.17
50060.00	M20	M-018689- MOCO sulp	54996.00	MOSC2	2868.00	6.94	3.63
50060.00	M21	M-016312- chromosom	54964.00	C1orf56	3408.00	7.98	4.67
50060.00	M23	M-013784- phosphatid	54965.00	PIGX	2744.00	7.94	4.63
50060.00	N02	M-014402- N-acetyltra	55226.00	NAT10	3823.00	11.82	8.51
50060.00	N04	M-027483- ribonucleo	55225.00	RAVER2	1835.00	11.06	7.75
50060.00	N05	M-020973- family with	55177.00	FAM82C	2968.00	6.00	2.69
50060.00	N06	M-007010- tripartite	55223.00	TRIM62	3616.00	5.42	2.11
50060.00	N07	M-015450- RNA methy	55178.00	RNMTL1	2873.00	7.10	3.79
50060.00	N08	M-020832- leucine rich	55222.00	LRRC20	2329.00	6.14	2.83
50060.00	N09	M-019129- lines homo	55180.00	LINS1	5334.00	16.65	13.34
50060.00	N10	M-020914- kelch doma	55220.00	KLHDC8A	3531.00	15.63	12.32
50060.00	N11	M-016480- chromosom	55181.00	C17orf71	4385.00	13.23	9.92
50060.00	N12	M-020899- exonucleas	55218.00	EXDL2	2231.00	13.54	10.23
50060.00	N13	M-021044- chromosom	55182.00	C1orf164	2432.00	7.61	4.30
50060.00	N14	M-031958- trimethylly	55217.00	TMLHE	1738.00	5.47	2.16
50060.00	N15	M-027983- RAP1 intera	55183.00	RIF1	3428.00	6.18	2.87
50060.00	N16	M-020871- chromosom	55216.00	C11orf57	3777.00	6.33	3.02
50060.00	N17	M-013129- chromosom	55184.00	C20orf12	3009.00	4.19	0.88
50060.00	N18	M-022320- Fanconi an	55215.00	FANCI	3562.00	14.88	11.57
50060.00	N19	M-007327- solute carri	55186.00	SLC25A36	4235.00	23.66	20.35
50060.00	N20	M-004272- leprecan-li	55214.00	LEPREL1	4944.00	5.30	1.99
50060.00	N21	M-021567- vacuolar pr	55187.00	VPS13D	3312.00	3.29	0.02
50060.00	N23	M-021081- resistance	55188.00	RIC8B	2181.00	2.98	0.33

50060.00	O02	M-031860- 3-oxoacyl-	54995.00	OXSM	2287.00	1.97	1.34
50060.00	O04	M-032154- chromoson	54994.00	C20orf11	3335.00	6.87	3.56
50060.00	O05	M-020846- chromoson	54967.00	CXorf48	2442.00	4.91	1.60
50060.00	O06	M-021470- zinc finger	54993.00	ZSCAN2	1844.00	4.72	1.41
50060.00	O07	M-015366- transmem	54968.00	TMEM70	4044.00	11.85	**8.54**
50060.00	O08	M-027330- chromoson	54991.00	C1orf159	3121.00	8.39	5.08
50060.00	O09	M-020849- chromoson	54969.00	C4orf27	2718.00	11.04	**7.73**
50060.00	O10	M-022215- zinc finger	54989.00	ZNF770	2183.00	3.89	0.58
50060.00	O11	M-018220- tetratricop	54970.00	TTC12	2502.00	6.04	2.73
50060.00	O12	M-031212- hypothetic	54988.00	FLJ20581	2120.00	10.09	**6.78**
50060.00	O13	M-019041- transmem	54972.00	TMEM132	2072.00	4.92	1.61
50060.00	O14	M-031916- chromoson	54987.00	C1orf123	2262.00	4.51	1.20
50060.00	O15	M-013789- cleavage a	54973.00	CPSF3L	3535.00	5.04	1.73
50060.00	O16	M-004707- host cell fa	54985.00	HCFC1R1	3326.00	5.20	1.89
50060.00	O17	M-020857- chromoson	54976.00	C20orf27	2635.00	7.89	4.58
50060.00	O18	M-006722- chromoson	54981.00	C9orf95	3382.00	11.21	**7.90**
50060.00	O19	M-007331- solute carri	54977.00	SLC25A38	2264.00	9.10	5.79
50060.00	O20	M-020863- chromoson	54980.00	C2orf42	1835.00	5.18	1.87
50060.00	O21	M-018201- chromoson	54978.00	C2orf18	2284.00	6.70	3.39
50060.00	O23	M-020862- HRAS-like s	54979.00	HRASLS2	1456.00	5.29	1.98
50060.00	P02	M-017098- regulator o	55213.00	RCBTB1	2568.00	3.12	0.19
50060.00	P04	M-020766- developme	55211.00	DPPA4	994.00	1.31	2.00
50060.00	P05	M-010039- nudix (nucl	55190.00	NUDT11	880.00	9.20	5.89
50060.00	P06	M-008191- ATPase fa	55210.00	ATAD3A	2235.00	1.25	2.06
50060.00	P07	M-007723- NAD synth	55191.00	NADSYN1	2939.00	5.61	2.30
50060.00	P08	M-028069- SET domai	55209.00	SETD5	1383.00	3.62	0.31
50060.00	P09	M-021141- DnaJ (Hsp4	55192.00	DNAJC17	893.00	3.81	0.50
50060.00	P10	M-020261- DCN1, defe	55208.00	DCUN1D2	627.00	0.64	2.67
50060.00	P11	M-008692- polybromo	55193.00	PBRM1	1064.00	1.13	2.18
50060.00	P12	M-020294- ADP-ribosy	55207.00	ARL8B	1468.00	3.27	0.04
50060.00	P13	M-021255- chromoson	55194.00	C1orf78	1400.00	2.64	0.67
50060.00	P14	M-027143- strawberry	55206.00	SBNO1	2203.00	5.72	2.41
50060.00	P15	M-020507- chromoson	55195.00	C14orf105	815.00	1.10	2.21
50060.00	P16	M-007009- zinc finger	55205.00	ZNF532	1489.00	1.07	2.24
50060.00	P17	M-020502- chromoson	55196.00	C12orf35	2150.00	5.53	2.22
50060.00	P18	M-006413- golgi phosp	55204.00	GOLPH3L	1596.00	1.19	2.12
50060.00	P19	M-016272- adaptor pr	55198.00	APPL2	2147.00	2.79	0.52
50060.00	P20	M-017097- leucine-ric	55203.00	LGI2	928.00	6.25	2.94
50060.00	P21	M-015922- family with	55199.00	FAM86C	1607.00	4.79	1.48
50060.00	P23	M-016881- microtubul	55201.00	MAP1S	2339.00	2.35	0.96
				MAD	2524.50	3.31	2.13
							6.38
				corrected MAD			3.15
50060.00	C22		2682.00	43.89			
50060.00	D22		1857.00	8.02			
50060.00	E22				1799.00	12.90	
50060.00	F22				1996.00	19.84	

					mn	1897.50	16.37
					sd	139.30	4.91
50060.00	G22					374.00	0.80
50060.00	H22					636.00	1.26
50060.00	I22					307.00	1.63
50060.00	J22			1053.00	4.75		
					mn	471.50	1.44
					sd	232.64	0.26
					3psSD		14.73
					3ngSD		0.79
					SumSD		15.52
					DiffMn		14.92
					SmovrDiff		1.04
					1minus		-0.04
50060.00	G03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	196.00	3.57
50060.00	H03	M-003290-	polo-like ki	5347.00	PLK1 SMAF	149.00	4.03
50060.00	I03	D-001206-	siControl non-targetin			2255.00	6.21
50060.00	J03	D-001206-	siControl non-targetin			2282.00	16.43
50060.00	K03	D-001600-	siGLO RISC-free siRNA			4560.00	14.39
50060.00	L03	D-001600-	siGLO RISC-free siRNA			4394.00	9.13

Robust Z	**cell_ct**	**percent inf**	**Abs Devtn**	**Robust Z**	**cell_ct**	**percent inf**	**Abs Devtn**	**Robust Z**
-0.79	3828.00	5.12	1.72	0.62	2457.00	7.12	**4.98**	2.99
-0.75	1720.00	5.93	2.53	0.91	1043.00	3.07	0.93	0.56
-0.55	1457.00	2.95	0.45	-0.16	1158.00	4.92	2.78	1.67
-0.12	2043.00	7.10	3.70	1.33	1635.00	11.99	**9.85**	5.91
-0.86	1935.00	2.64	0.76	-0.27	1626.00	3.87	1.73	1.04
2.34	2792.00	5.19	1.79	0.64	2366.00	5.20	3.06	1.84
-0.88	1166.00	4.89	1.49	0.53	678.00	3.54	1.40	0.84
-0.79	1219.00	7.88	4.48	1.60	984.00	5.39	3.25	1.95
-0.66	1703.00	8.40	5.00	1.79	1123.00	4.45	2.31	1.39
-0.71	449.00	4.68	1.28	0.46	233.00	1.72	0.42	-0.25
-0.37	732.00	5.46	2.06	0.74	799.00	1.63	0.51	-0.31
-0.30	1890.00	8.47	5.07	1.82	1478.00	6.36	**4.22**	2.53
-0.16	1982.00	10.24	**6.84**	2.45	1397.00	4.08	1.94	1.16
0.12	495.00	11.72	**8.32**	2.98	453.00	3.53	1.39	0.84
0.15	1436.00	5.85	2.45	0.88	960.00	1.67	0.47	-0.28
0.54	891.00	7.07	3.67	1.32	1459.00	3.91	1.77	1.06
2.12	348.00	8.05	4.65	1.67	467.00	7.28	**5.14**	3.09
0.01	1691.00	5.03	1.63	0.58	2737.00	5.59	**3.45**	2.07
1.52	1452.00	17.42	**14.02**	5.03	2354.00	7.01	**4.87**	2.92
1.83	1285.00	10.58	**7.18**	2.58	1214.00	5.11	2.97	1.78
-0.91	1597.00	3.94	0.54	0.20	861.00	1.51	0.63	-0.38
-0.94	2749.00	5.49	2.09	0.75	3699.00	3.57	1.43	0.86
-0.93	2526.00	3.13	0.27	-0.10	2923.00	0.89	1.25	-0.75
-0.75	1875.00	3.04	0.36	-0.13	2556.00	2.03	0.11	-0.06
-0.99	4558.00	2.59	0.81	-0.29	4579.00	0.98	1.16	-0.69
-0.84	2348.00	3.28	0.12	-0.04	2121.00	0.42	1.72	-1.03
-0.88	1372.00	3.21	0.19	-0.07	977.00	0.82	1.32	-0.79
-0.71	2272.00	4.89	1.49	0.53	1740.00	0.63	1.51	-0.90
-0.69	2549.00	4.04	0.64	0.23	2428.00	2.22	0.08	0.05
-0.93	2919.00	3.01	0.39	-0.14	1991.00	0.10	2.04	-1.22
-0.71	1427.00	1.05	2.35	-0.84	2419.00	0.41	1.73	-1.04
-0.83	1426.00	1.75	1.65	-0.59	2079.00	0.63	1.51	-0.91
-0.28	2842.00	4.47	1.07	0.38	2281.00	1.23	0.91	-0.55
-0.94	1922.00	2.76	0.64	-0.23	2497.00	0.48	1.66	-1.00
-0.90	2099.00	1.81	1.59	-0.57	2602.00	0.15	1.99	-1.19
-0.91	1398.00	1.65	1.75	-0.63	1554.00	0.39	1.75	-1.05
-0.55	2153.00	3.90	0.50	0.18	3283.00	0.40	1.74	-1.05
-0.91	2832.00	9.53	**6.13**	2.20	3915.00	1.10	1.04	-0.62
0.05	3150.00	15.14	**11.74**	4.21	4273.00	1.83	0.31	-0.19
-0.89	2827.00	2.97	0.43	-0.15	3902.00	0.62	1.52	-0.91
-0.36	4361.00	10.55	**7.15**	2.56	2540.00	1.93	0.21	-0.13
-0.03	2027.00	4.00	0.60	0.21	2054.00	0.49	1.65	-0.99
-0.04	2687.00	4.47	1.07	0.38	2970.00	3.77	1.63	0.98
-0.14	2651.00	8.37	4.97	1.78	2493.00	1.68	0.46	-0.27
0.52	3203.00	4.46	1.06	0.38	3453.00	2.95	0.81	0.49
1.28	2721.00	9.85	**6.45**	2.31	2083.00	2.59	0.45	0.27

0.68	2895.00	5.01	1.61	0.58	1674.00	2.15	0.01	0.01
0.94	3118.00	14.05	**10.65**	3.82	3056.00	4.55	2.41	1.45
-0.14	3288.00	10.10	**6.70**	2.40	3545.00	3.24	1.10	0.66
-0.12	2324.00	5.29	1.89	0.68	2157.00	3.62	1.48	0.89
0.14	2476.00	6.42	3.02	1.08	2811.00	1.71	0.43	-0.26
0.36	2108.00	6.21	2.81	1.01	1927.00	2.49	0.35	0.21
-0.15	2787.00	3.77	0.37	0.13	1487.00	2.69	0.55	0.33
2.16	2064.00	7.51	4.11	1.47	1585.00	5.05	2.91	1.75
1.72	2995.00	3.14	0.26	-0.09	2144.00	5.64	**3.50**	2.10
0.07	3915.00	1.56	1.84	-0.66	2702.00	1.96	0.18	-0.11
1.11	4635.00	8.41	5.01	1.80	2808.00	3.92	1.78	1.07
2.80	5215.00	7.67	4.27	1.53	4256.00	8.27	**6.13**	3.68
0.94	4053.00	5.67	2.27	0.82	2654.00	5.84	**3.70**	2.22
0.36	3138.00	2.29	1.11	-0.40	2107.00	5.17	3.03	1.82
0.19	2218.00	1.13	2.27	-0.81	2646.00	1.51	0.63	-0.38
-0.06	4542.00	6.05	2.65	0.95	3021.00	6.39	**4.25**	2.55
0.63	3733.00	2.46	0.94	-0.33	3988.00	10.03	**7.89**	4.74
-0.35	4395.00	2.39	1.01	-0.36	3498.00	8.38	**6.24**	3.74
0.42	3751.00	3.97	0.57	0.21	3295.00	9.29	**7.15**	4.29
-0.12	2770.00	1.12	2.28	-0.82	2102.00	8.14	**6.00**	3.60
0.49	3475.00	2.50	0.90	-0.32	2884.00	13.18	**11.04**	6.62
0.02	3725.00	0.59	2.81	-1.01	2703.00	3.26	1.12	0.67
-0.27	2954.00	0.81	2.59	-0.93	2282.00	2.06	0.08	-0.05
-0.10	2927.00	2.32	1.08	-0.38	1932.00	5.64	**3.50**	2.10
-0.61	2639.00	1.71	1.69	-0.61	2630.00	6.43	**4.29**	2.57
-0.73	3364.00	1.40	2.00	-0.72	1983.00	2.52	0.38	0.23
-0.71	1984.00	1.81	1.59	-0.57	1985.00	5.89	**3.75**	2.25
0.01	2949.00	2.17	1.23	-0.44	3079.00	8.57	**6.43**	3.86
-0.69	2185.00	1.10	2.30	-0.82	1995.00	2.81	0.67	0.40
-0.66	3162.00	0.51	2.89	-1.04	2835.00	4.41	2.27	1.36
-0.30	4015.00	2.12	1.28	-0.46	3057.00	5.56	**3.42**	2.05
-0.09	4654.00	3.89	0.49	0.18	2915.00	11.32	**9.18**	5.51
-0.85	2039.00	0.34	3.06	-1.09	1969.00	1.57	0.57	-0.34
-0.94	2955.00	0.95	2.45	-0.88	2669.00	1.35	0.79	-0.47
-0.26	3024.00	7.71	4.31	1.54	2957.00	4.23	2.09	1.25
-0.11	3123.00	8.45	5.05	1.81	2198.00	4.55	2.41	1.45
0.36	2114.00	7.43	4.03	1.44	2380.00	8.28	**6.14**	3.68
-0.44	2126.00	6.30	2.90	1.04	2347.00	2.51	0.37	0.22
-0.67	2205.00	2.68	0.72	-0.26	2787.00	1.72	0.42	-0.25
-0.15	1352.00	7.32	3.92	1.41	1012.00	3.46	1.32	0.79
-0.34	2193.00	4.79	1.39	0.50	2388.00	5.40	3.26	1.96
-0.13	1454.00	8.18	4.78	1.72	1464.00	8.06	**5.92**	3.55
-0.26	2417.00	4.59	1.19	0.43	2141.00	2.71	0.57	0.34
-0.20	2819.00	4.36	0.96	0.35	3257.00	5.43	3.29	1.98
-0.48	1366.00	5.34	1.94	0.70	1360.00	3.75	1.61	0.97
-0.74	1311.00	3.05	0.35	-0.12	1327.00	1.28	0.86	-0.52
-0.61	1873.00	5.39	1.99	0.72	1667.00	2.64	0.50	0.30

-0.19	2365.00	6.89	3.49	1.25	2750.00	5.85	**3.71**	2.23
-0.37	952.00	8.61	5.21	1.87	843.00	5.10	2.96	1.78
-0.94	2779.00	2.63	0.77	-0.28	2150.00	2.14	0.00	0.00
-0.70	3234.00	6.28	2.88	1.03	2670.00	3.07	0.93	0.56
-0.54	2863.00	5.03	1.63	0.59	2926.00	2.12	0.02	-0.01
-0.38	2370.00	6.75	3.35	1.20	2678.00	5.49	3.35	2.01
-0.60	2257.00	6.56	3.16	1.13	2076.00	2.65	0.51	0.31
-0.46	2643.00	1.51	1.89	-0.68	3412.00	0.94	1.20	-0.72
-0.24	2515.00	0.95	2.45	-0.88	3097.00	0.39	1.75	-1.05
0.64	2888.00	6.75	3.35	1.20	3424.00	1.61	0.53	-0.32
-0.17	3408.00	1.88	1.52	-0.54	3115.00	0.55	1.59	-0.96
-0.03	1276.00	0.78	2.62	-0.94	2203.00	0.14	2.00	-1.20
-0.01	1620.00	1.17	2.23	-0.80	1175.00	1.02	1.12	-0.67
2.48	3577.00	9.78	**6.38**	2.29	3522.00	2.47	0.33	0.20
0.78	2354.00	2.72	0.68	-0.24	1567.00	1.40	0.74	-0.44
-0.42	1805.00	0.72	2.68	-0.96	2814.00	0.60	1.54	-0.92
0.47	3239.00	1.23	2.17	-0.77	2341.00	0.56	1.58	-0.95
0.67	1335.00	1.57	1.83	-0.65	2590.00	2.36	0.22	0.13
2.31	3025.00	1.88	1.52	-0.54	2630.00	1.90	0.24	-0.14
-0.59	2369.00	0.97	2.43	-0.87	1641.00	1.46	0.68	-0.41
-0.10	2847.00	0.70	2.70	-0.97	2699.00	4.04	1.90	1.14
1.03	3353.00	1.16	2.24	-0.80	2957.00	1.18	0.96	-0.57
-0.12	4378.00	0.75	2.65	-0.95	3805.00	2.00	0.14	-0.09
-0.17	4119.00	0.87	2.53	-0.90	2542.00	0.83	1.31	-0.79
0.64	2432.00	1.73	1.67	-0.60	2290.00	1.40	0.74	-0.45
-0.79	1202.00	1.00	2.40	-0.86	1868.00	1.45	0.69	-0.42
-0.94	2889.00	0.31	3.09	-1.11	3172.00	0.38	1.76	-1.06
-0.43	3758.00	4.47	1.07	0.38	3719.00	0.40	1.74	-1.04
-0.38	2383.00	2.98	0.42	-0.15	3634.00	0.55	1.59	-0.95
-0.14	2412.00	3.73	0.33	0.12	2381.00	0.21	1.93	-1.16
-0.81	1822.00	2.31	1.09	-0.39	1705.00	0.47	1.67	-1.00
1.23	3530.00	7.31	3.91	1.40	3110.00	1.22	0.92	-0.55
-0.23	3465.00	3.61	0.21	0.08	2495.00	1.72	0.42	-0.25
-0.32	4138.00	8.72	5.32	1.91	2300.00	0.87	1.27	-0.76
-0.88	1728.00	2.08	1.32	-0.47	839.00	0.48	1.66	-1.00
-0.57	3562.00	4.80	1.40	0.50	3357.00	2.32	0.18	0.11
-0.47	2714.00	3.68	0.28	0.10	2505.00	0.40	1.74	-1.04
-0.68	1985.00	1.96	1.44	-0.51	1576.00	1.02	1.12	-0.67
-0.92	2607.00	1.76	1.64	-0.59	1786.00	0.62	1.52	-0.91
0.51	2605.00	7.45	4.05	1.45	2326.00	0.39	1.75	-1.05
-0.75	2138.00	5.47	2.07	0.74	2394.00	2.97	0.83	0.50
-0.85	2252.00	2.89	0.51	-0.18	2570.00	1.13	1.01	-0.61
-0.78	3480.00	3.65	0.25	0.09	1844.00	0.87	1.27	-0.76
-0.22	3518.00	4.12	0.72	0.26	2790.00	2.83	0.69	0.42
-0.52	2339.00	6.41	3.01	1.08	2918.00	3.67	1.53	0.92
-0.82	1741.00	2.64	0.76	-0.27	2023.00	5.44	3.30	1.98
-0.90	2053.00	3.21	0.19	-0.07	870.00	1.49	0.65	-0.39

-0.74	2131.00	3.00	0.40	-0.14	2166.00	1.52	0.62	-0.37
-0.77	1995.00	5.46	2.06	0.74	2457.00	2.52	0.38	0.23
-0.40	1035.00	9.57	**6.17**	2.21	701.00	1.71	0.43	-0.26
-0.96	1104.00	5.07	1.67	0.60	1487.00	0.47	1.67	-1.00
0.22	481.00	6.03	2.63	0.94	424.00	3.30	1.16	0.70
0.04	2629.00	9.24	**5.84**	2.10	1918.00	1.77	0.37	-0.22
-0.47	2826.00	7.86	4.46	1.60	1881.00	1.12	1.02	-0.61
-0.83	2527.00	8.59	5.19	1.86	1462.00	1.57	0.57	-0.34
-0.57	2697.00	8.49	5.09	1.83	2517.00	1.95	0.19	-0.12
-0.42	1996.00	5.26	1.86	0.67	1957.00	1.64	0.50	-0.30
-0.70	655.00	1.68	1.72	-0.62	375.00	0.53	1.61	-0.96
-0.89	1412.00	2.90	0.50	-0.18	2117.00	1.46	0.68	-0.41
-0.33	3356.00	9.54	**6.14**	2.20	3394.00	2.06	0.08	-0.05
-0.83	1981.00	4.14	0.74	0.27	2118.00	2.64	0.50	0.30
-0.84	1879.00	1.81	1.59	-0.57	2267.00	0.66	1.48	-0.89
-0.91	1615.00	0.93	2.47	-0.88	2059.00	1.51	0.63	-0.38
-0.76	2685.00	4.13	0.73	0.26	2927.00	1.47	0.67	-0.40
-0.98	1968.00	6.66	3.26	1.17	1719.00	5.88	**3.74**	2.24
-0.67	2546.00	2.32	1.08	-0.39	2649.00	2.79	0.65	0.39
-0.82	2534.00	0.95	2.45	-0.88	2727.00	1.28	0.86	-0.51
-0.36	2437.00	0.86	2.54	-0.91	2266.00	1.24	0.90	-0.54
0.76	1509.00	1.13	2.27	-0.81	664.00	2.11	0.03	-0.02
1.32	2677.00	3.55	0.15	0.05	2065.00	2.18	0.04	0.02
0.52	2360.00	1.82	1.58	-0.56	2112.00	3.79	1.65	0.99
-0.35	1166.00	1.29	2.11	-0.76	906.00	1.43	0.71	-0.42
0.39	1034.00	2.03	1.37	-0.49	1452.00	1.52	0.62	-0.37
0.09	2873.00	1.91	1.49	-0.53	3061.00	3.27	1.13	0.68
1.73	3287.00	3.86	0.46	0.17	3013.00	3.82	1.68	1.01
0.68	2531.00	1.78	1.62	-0.58	2500.00	1.80	0.34	-0.20
-0.47	1843.00	0.76	2.64	-0.95	1761.00	1.53	0.61	-0.36
-0.92	1117.00	0.45	2.95	-1.06	1288.00	1.40	0.74	-0.45
0.07	1569.00	4.21	0.81	0.29	1859.00	3.50	1.36	0.81
-0.69	1825.00	3.73	0.33	0.12	1651.00	1.39	0.75	-0.45
-0.13	2814.00	2.06	1.34	-0.48	3242.00	2.34	0.20	0.12
-0.20	2301.00	1.04	2.36	-0.84	2279.00	1.54	0.60	-0.36
0.58	3146.00	3.21	0.19	-0.07	3973.00	5.94	**3.80**	2.28
-0.08	1905.00	0.42	2.98	-1.07	2105.00	0.71	1.43	-0.86
1.18	3692.00	4.17	0.77	0.28	2861.00	2.73	0.59	0.35
0.52	2375.00	1.68	1.72	-0.61	2807.00	2.64	0.50	0.30
-0.19	2742.00	2.22	1.18	-0.42	3297.00	1.85	0.29	-0.17
3.31	2951.00	12.23	**8.83**	3.17	2432.00	4.03	1.89	1.13
4.85	1661.00	8.61	5.21	1.87	1760.00	2.16	0.02	0.01
2.66	2906.00	5.33	1.93	0.69	1489.00	0.87	1.27	-0.76
1.90	3512.00	6.01	2.61	0.94	1578.00	0.63	1.51	-0.90
3.98	1139.00	4.21	0.81	0.29	938.00	1.28	0.86	-0.52
3.11	2670.00	4.72	1.32	0.47	2186.00	1.24	0.90	-0.54

2.09	2705.00	7.54	4.14	1.49	1248.00	0.96	1.18	-0.71
3.27	2271.00	6.43	3.03	1.09	2000.00	0.85	1.29	-0.77
3.74	2185.00	9.38	5.98	2.14	3282.00	2.07	0.07	-0.04
4.52	1390.00	4.03	0.63	0.23	1593.00	2.07	0.07	-0.04
4.50	799.00	6.63	3.23	1.16	772.00	2.20	0.06	0.04
2.19	2127.00	6.02	2.62	0.94	1826.00	1.53	0.61	-0.36
0.84	2368.00	1.60	1.80	-0.64	2249.00	1.47	0.67	-0.40
2.18	1844.00	3.69	0.29	0.10	2664.00	4.09	1.95	1.17
0.04	1121.00	4.46	1.06	0.38	1255.00	0.72	1.42	-0.85
0.65	1726.00	4.29	0.89	0.32	1396.00	5.52	3.38	2.03
2.17	2693.00	3.19	0.21	-0.07	2663.00	3.57	1.43	0.86
1.02	2203.00	2.32	1.09	-0.39	1132.00	1.41	0.73	-0.44
2.03	1977.00	3.29	0.11	-0.04	2147.00	2.42	0.28	0.17
1.97	1224.00	0.90	2.50	-0.90	2038.00	5.20	3.06	1.84
3.28	2865.00	2.62	0.78	-0.28	2373.00	3.37	1.23	0.74
3.51	3688.00	3.09	0.31	-0.11	2284.00	1.36	0.78	-0.47
3.05	1937.00	2.58	0.82	-0.29	2736.00	1.50	0.64	-0.38
2.68	3151.00	3.90	0.50	0.18	2759.00	3.04	0.90	0.54
0.79	3130.00	1.28	2.12	-0.76	4488.00	2.01	0.13	-0.08
3.82	3582.00	5.95	2.55	0.91	3766.00	5.87	3.73	2.24
0.44	2844.00	1.02	2.38	-0.85	3374.00	1.07	1.07	-0.64
1.30	1987.00	1.76	1.64	-0.59	1753.00	2.68	0.54	0.33
1.73	2371.00	1.43	1.97	-0.70	2186.00	2.33	0.19	0.12
2.09	808.00	1.61	1.79	-0.64	482.00	3.32	1.18	0.71
-0.21	2021.00	0.84	2.56	-0.92	1178.00	1.02	1.12	-0.67
0.15	1728.00	1.33	2.07	-0.74	2203.00	2.13	0.01	0.00
-0.09	2754.00	1.45	1.95	-0.70	2440.00	1.68	0.46	-0.28
-0.23	2468.00	2.23	1.17	-0.42	2779.00	1.87	0.27	-0.16
-0.63	2520.00	1.63	1.77	-0.63	2031.00	2.02	0.12	-0.07
-0.47	2396.00	1.67	1.73	-0.62	2794.00	3.61	1.47	0.89
-0.43	3216.00	2.08	1.32	-0.47	3533.00	2.38	0.24	0.14
0.61	3079.00	1.92	1.48	-0.53	2929.00	4.51	2.37	1.42
1.38	3685.00	5.07	1.67	0.60	3373.00	10.08	7.94	4.77
-0.46	1980.00	0.71	2.69	-0.96	2933.00	2.56	0.42	0.25
2.26	4163.00	6.03	2.63	0.94	3351.00	6.89	4.75	2.85
1.04	2469.00	1.86	1.54	-0.55	1630.00	0.80	1.34	-0.81
2.02	3374.00	1.78	1.62	-0.58	2749.00	3.27	1.13	0.68
0.24	2099.00	1.52	1.88	-0.67	1528.00	1.37	0.77	-0.46
1.38	1661.00	0.30	3.10	-1.11	1543.00	1.43	0.71	-0.43
0.92	1835.00	1.09	2.31	-0.83	1246.00	1.85	0.29	-0.18
1.83	2390.00	1.42	1.98	-0.71	2354.00	1.49	0.65	-0.39
3.57	283.00	3.53	0.13	0.05	150.00	4.00	1.86	1.12
1.36	2421.00	0.66	2.74	-0.98	2203.00	1.77	0.37	-0.22
1.04	2863.00	1.15	2.25	-0.80	2628.00	2.59	0.45	0.27
0.76	2894.00	0.48	2.92	-1.04	2097.00	0.81	1.33	-0.80
-0.26	4174.00	0.86	2.54	-0.91	2804.00	1.64	0.50	-0.30
-0.54	2215.00	2.98	0.42	-0.15	1855.00	1.99	0.15	-0.09

-0.27	3188.00	1.10	2.30	-0.82	1808.00	1.22	0.92	-0.55
-0.26	1784.00	1.01	2.39	-0.86	2158.00	2.13	0.01	0.00
0.90	4009.00	2.89	0.51	-0.18	3078.00	1.72	0.42	-0.25
0.29	4050.00	2.10	1.30	-0.47	2492.00	1.97	0.17	-0.10
0.35	2670.00	1.54	1.86	-0.67	1419.00	1.83	0.31	-0.18
0.90	2246.00	3.34	0.06	-0.02	1233.00	2.03	0.11	-0.07
-0.10	2144.00	0.93	2.47	-0.88	1432.00	1.40	0.74	-0.45
0.19	1693.00	1.54	1.86	-0.67	1436.00	0.70	1.44	-0.87
-0.18	3358.00	3.42	0.02	0.01	2413.00	2.07	0.07	-0.04
-0.41	3182.00	1.16	2.24	-0.80	3250.00	2.40	0.26	0.16
-0.41	2229.00	3.10	0.30	-0.11	2416.00	3.81	1.67	1.00
0.89	2043.00	2.59	0.81	-0.29	2052.00	4.09	1.95	1.17
0.36	1239.00	0.56	2.84	-1.01	980.00	1.22	0.92	-0.55
0.92	1414.00	3.47	0.07	0.02	1862.00	5.64	**3.50**	2.10
0.54	1983.00	2.67	0.73	-0.26	2978.00	4.16	2.02	1.21
0.65	2567.00	2.22	1.18	-0.42	2764.00	3.22	1.08	0.65
1.48	2022.00	2.42	0.98	-0.35	1824.00	0.71	1.43	-0.86
0.69	1735.00	1.79	1.61	-0.58	2128.00	2.63	0.49	0.30
-0.06	2392.00	2.17	1.23	-0.44	3090.00	1.17	0.98	-0.58
0.56	2296.00	1.79	1.61	-0.58	2477.00	2.95	0.81	0.48
-0.20	2212.00	0.54	2.86	-1.02	2891.00	0.93	1.21	-0.72
0.43	2483.00	3.02	0.38	-0.13	2039.00	0.59	1.55	-0.93
0.65	2418.00	1.41	1.99	-0.71	1506.00	1.53	0.61	-0.37
2.91	2427.00	5.40	2.00	0.72	2112.00	2.89	0.75	0.45
1.15	2967.00	1.52	1.88	-0.67	2213.00	0.63	1.51	-0.90
1.48	3593.00	3.67	0.27	0.10	2271.00	0.92	1.22	-0.73
1.47	3466.00	1.73	1.67	-0.60	3525.00	2.70	0.56	0.33
2.71	2360.00	2.88	0.52	-0.18	1973.00	0.51	1.63	-0.98
2.46	3461.00	5.81	2.41	0.86	2536.00	1.97	0.17	-0.10
0.85	2065.00	2.32	1.08	-0.38	2737.00	0.99	1.15	-0.69
0.67	2119.00	0.38	3.02	-1.08	2006.00	0.55	1.59	-0.95
1.20	2582.00	3.37	0.03	-0.01	2150.00	2.14	0.00	0.00
0.90	1227.00	1.06	2.34	-0.84	1153.00	2.69	0.55	0.33
4.24	3531.00	10.85	**7.45**	2.67	2159.00	1.99	0.15	-0.09
3.92	3196.00	7.01	3.61	1.29	2811.00	2.99	0.85	0.51
3.15	5032.00	13.36	**9.96**	3.57	2900.00	4.55	2.41	1.45
3.25	3174.00	5.70	2.30	0.83	3277.00	3.78	1.64	0.99
1.37	3477.00	5.92	2.52	0.91	1522.00	1.18	0.96	-0.57
0.68	2875.00	4.45	1.05	0.38	1920.00	1.46	0.68	-0.41
0.91	3381.00	4.50	1.10	0.39	2258.00	0.35	1.79	-1.07
0.96	4429.00	10.54	**7.14**	2.56	2491.00	2.45	0.31	0.19
0.28	3617.00	3.21	0.19	-0.07	2475.00	1.05	1.09	-0.65
3.68	2169.00	13.37	**9.97**	3.57	2375.00	4.51	2.37	1.42
6.47	2141.00	17.98	**14.58**	5.23	1641.00	8.59	**6.45**	3.87
0.63	5071.00	9.17	**5.77**	2.07	3100.00	1.77	0.37	-0.22
-0.01	1585.00	1.89	1.51	-0.54	1354.00	0.89	1.25	-0.75
-0.11	2036.00	0.54	2.86	-1.02	1465.00	0.82	1.32	-0.79

-0.43	2412.00	2.40	1.00	-0.36	1951.00	1.64	0.50	-0.30
1.13	3071.00	5.93	2.53	0.91	1622.00	3.51	1.37	0.83
0.51	2451.00	6.98	3.58	1.28	2409.00	2.74	0.60	0.36
0.45	1947.00	4.78	1.38	0.49	1754.00	2.91	0.77	0.46
2.71	2967.00	8.09	4.69	1.68	2906.00	6.09	**3.95**	2.37
1.62	1850.00	5.08	1.68	0.60	1969.00	1.83	0.31	-0.19
2.46	1416.00	8.62	5.22	1.87	1447.00	4.35	2.21	1.33
0.18	1972.00	4.21	0.81	0.29	1291.00	1.63	0.51	-0.31
0.87	2492.00	9.59	**6.19**	2.22	1559.00	5.00	2.86	1.72
2.16	1888.00	9.16	**5.76**	2.07	2015.00	6.05	**3.91**	2.35
0.51	2382.00	3.11	0.29	-0.10	2395.00	4.09	1.95	1.17
0.38	1760.00	5.28	1.88	0.68	1336.00	4.72	2.58	1.55
0.55	1672.00	3.89	0.49	0.18	1562.00	5.38	3.24	1.94
0.60	2962.00	3.78	0.38	0.14	1530.00	1.31	0.83	-0.50
1.46	1483.00	7.28	3.88	1.39	1661.00	2.17	0.03	0.02
2.51	2744.00	9.40	**6.00**	2.15	1509.00	5.17	3.03	1.82
1.84	1962.00	6.98	3.58	1.29	1682.00	3.27	1.13	0.68
0.59	1521.00	4.67	1.27	0.46	1203.00	3.41	1.27	0.76
1.08	1913.00	2.67	0.73	-0.26	1563.00	2.43	0.29	0.18
0.63	1596.00	3.51	0.11	0.04	1187.00	1.60	0.54	-0.32
-0.06	2649.00	8.57	5.17	1.85	3233.00	2.63	0.49	0.29
-0.64	1407.00	4.90	1.50	0.54	2349.00	1.23	0.91	-0.54
1.87	503.00	18.09	**14.69**	5.27	1572.00	10.56	**8.42**	5.05
-0.66	790.00	10.13	**6.73**	2.41	1866.00	1.45	0.69	-0.42
0.73	1676.00	14.80	**11.40**	4.09	3194.00	11.30	**9.16**	5.50
0.10	408.00	6.37	2.97	1.07	1432.00	5.10	2.96	1.78
0.16	160.00	7.50	4.10	1.47	1023.00	4.89	2.75	1.65
-0.85	444.00	6.53	3.13	1.12	1237.00	3.23	1.09	0.66
-0.69	370.00	3.51	0.11	0.04	1034.00	2.22	0.08	0.05
-0.01	934.00	8.14	4.74	1.70	2020.00	9.36	**7.22**	4.33
-0.21	803.00	6.72	3.32	1.19	1302.00	3.00	0.86	0.51
0.77	1258.00	3.58	0.18	0.06	1829.00	3.44	1.30	0.78
-0.70	1139.00	3.34	0.06	-0.02	2047.00	4.49	2.35	1.41
-0.71	1056.00	0.85	2.55	-0.91	1466.00	0.75	1.39	-0.83
0.71	1442.00	2.50	0.90	-0.32	1800.00	3.06	0.92	0.55
-0.68	1078.00	1.39	2.01	-0.72	1629.00	3.81	1.67	1.00
-0.16	2377.00	2.65	0.75	-0.27	3614.00	4.21	2.07	1.24
0.93	786.00	1.40	2.00	-0.72	257.00	4.67	2.53	1.52
0.47	1407.00	0.71	2.69	-0.96	700.00	1.71	0.43	-0.26
-0.31	951.00	1.47	1.93	-0.69	742.00	6.74	**4.60**	2.76
	2366.50	3.40	1.89		2157.50	2.14	1.13	
			5.66				3.38	
			2.79				1.67	
	3096.00	31.04			1947.00	22.14		
					1982.00	26.74	2898.00	16.60
	1422.00	30.66			1920.00	22.81		
					2336.00	16.70	2808.00	14.39

2259.00	30.85	2046.25	22.10		
		194.83	4.13	1183.70	0.27
420.00	1.19	335.00	4.78		
520.00	2.12	717.00	2.65		
314.00	1.91	897.00	0.33		
648.00	3.86	742.00	1.75		
494.00	2.63	785.33	1.58		
168.51	1.07	97.51	1.17		
	0.80		12.40		
	3.21		3.50		
	4.01		15.90		
	28.22		20.52		
	0.14		0.78		
	0.86		0.22		
293.00	2.39	365.00	0.55		
69.00	8.70	53.00	7.55		
2852.00	3.30	2499.00	4.48		
1825.00	10.69	1823.00	1.76		
4516.00	5.58	4030.00	3.05		
4941.00	3.42	3590.00	3.29		

x	toxic a,b,c
x	toxic b

y

y

y

y

y

y

y

y

y
y

x	debris a,b
x	debris a,b
y	
x	toxic b,c
x	toxic b
	0.03

						cell ct	% inf	AD
50061	A02	M-016111-	NECAP end	55707	NECAP2	306	28.105	18.61945
50061	A04	M-015459-	transmemb	55706	TMEM48	298	18.792	9.30645
50061	A05	M-021233-	hypothetic	55319	FLJ11184	283	26.502	17.01645
50061	A06	M-016863-	importin 9	55705	IPO9	588	19.558	10.07245
50061	A07	M-017100-	chromosor	55320	C14orf106	1063	13.452	3.96645
50061	A08	M-016902-	polymerase	55703	POLR3B	837	18.16	8.67445
50061	A09	M-021223-	chromosor	55322	C5orf22	1004	15.637	6.15145
50061	A10	M-017954-	coiled-coil	55702	CCDC94	696	26.58	17.09445
50061	A11	M-021333-	La ribonucl	55323	LARP6	468	40.171	30.68545
50061	A12	M-030269-	hypothetic	55701	FLJ10357	402	24.876	15.39045
50061	A13	M-021213-	chromosor	55325	C4orf20	533	23.265	13.77945
50061	A14	M-015538-	MAP7 dom	55700	MAP7D1	659	18.058	8.57245
50061	A15	M-008554-	1-acylglyce	55326	AGPAT5	501	34.132	24.64645
50061	A16	M-020404-	isoleucyl-tF	55699	IARS2	1463	19.139	9.65345
50061	A17	M-008473-	lin-7 homo	55327	LIN7C	611	26.187	16.70145
50061	A18	M-017110-	FLJ10324 p	55698	FLJ10324	2082	10.855	1.36945
50061	A19	M-021211-	chromosor	55328	C10orf59	1769	13.397	3.91145
50061	A20	M-015729-	Vac14 hom	55697	VAC14	1741	23.435	13.94945
50061	A21	M-021209-	meiosis-spe	55329	MNS1	1203	18.869	9.38345
50061	A23	M-021194-	cappuccinc	55330	CNO	1112	21.763	12.27745
50061	B02	M-010894-	vacuolar pr	55737	VPS35	1691	12.596	3.11045
50061	B04	M-013826-	neuroblast	55672	NBPF1	1642	6.3946	3.09095
50061	B05	M-018888-	kelch repea	55709	KBTBD4	3974	9.5873	0.10175
50061	B06	M-015708-	kelch repea	84078	KBTBD7	2625	12.038	2.55245
50061	B07	M-018704-	male sterili	55711	MLSTD1	1817	6.5493	2.93625
50061	B08	M-013526-	protocadhe	56129	PCDHB7	1564	6.9693	2.51625
50061	B09	M-017955-	zinc finger	55713	ZNF334	4647	9.8558	0.37025
50061	B10	M-013280-	protocadhe	56128	PCDHB8	4019	6.5937	2.89185
50061	B11	M-020773-	polymerase	55718	POLR3E	2694	7.7951	1.69045
50061	B12	M-013279-	protocadhe	56127	PCDHB9	1010	9.3069	0.17865
50061	B13	M-016268-	chromosor	55719	C10orf6	1584	11.869	2.38345
50061	B14	M-013529-	protocadhe	56123	PCDHB13	1955	11.918	2.43245
50061	B15	M-017111-	TSR1, 20S r	55720	TSR1	3139	6.69	2.79555
50061	B16	M-013277-	protocadhe	56114	PCDHGA1	2299	11.309	1.82345
50061	B17	M-021202-	IQ motif co	55721	IQCC	3253	7.5623	1.92325
50061	B18	M-013276-	protocadhe	56113	PCDHGA2	4196	13.513	4.02745
50061	B19	M-020549-	centrosom	55722	CEP72	1222	8.2651	1.22045
50061	B20	M-013275-	protocadhe	56112	PCDHGA3	4152	10.164	0.67845
50061	B21	M-020553-	ASF1 anti-s	55723	ASF1B	2440	6.8033	2.68225
50061	B23	M-020643-	chromosor	55726	C12orf11	3676	9.5484	0.06285
50061	C02	M-021186-	RNA bindin	55696	RBM22	627	4.3062	5.17935
50061	C04	M-020709-	jumonji do	55693	JMJD2D	1020	8.3333	1.15225
50061	C05	M-009430-	phytocerar	55331	PHCA	716	4.7486	4.73695
50061	C06	M-015452-	LUC7-like (	55692	LUC7L	579	6.9085	2.57705
50061	C07	M-021191-	damage-re	55332	DRAM	1529	6.998	2.48755
50061	C08	M-017109-	FERM dom	55691	FRMD4A	2467	7.1747	2.31085

50061	C09	M-021176-	synaptojan	55333	SYNJ2BP	907	6.505	2.98055
50061	C10	M-006697-	phosphofu	55690	PACS1	1030	6.9903	2.49525
50061	C11	M-007574-	solute carri	55334	SLC39A9	1121	9.4558	0.02975
50061	C12	M-017141-	YEATS dom	55689	YEATS2	991	4.6418	4.84375
50061	C13	M-015435-	nipsnap ho	55335	NIPSNAP3E	791	9.9874	0.50185
50061	C14	M-017953-	tRNA 5-me	55687	TRMU	1408	9.9432	0.45765
50061	C15	M-017504-	F-box and l	55336	FBXL8	1518	10.804	1.31845
50061	C16	M-020853-	melanoreg	55686	MREG	3377	7.1069	2.37865
50061	C17	M-020478-	hypothetic	55337	FLJ11286	3130	7.508	1.97755
50061	C18	M-031749-	chromoson	55684	C9orf86	4166	6.6251	2.86045
50061	C19	M-020475-	hypothetic	55338	FLJ11292	2840	18.592	9.10645
50061	C20	M-016928-	hypothetic	55683	FLJ10081	3448	10.934	1.44845
50061	C21	M-017101-	WD repeat	55339	WDR33	3699	10.408	0.92245
50061	C23	M-013342-	GTPase, IM	55340	GIMAP5	2479	8.9956	0.48995
50061	D02	M-013274-	protocadhe	56111	PCDHGA4	1688	4.4431	5.04245
50061	D04	M-013273-	protocadhe	56110	PCDHGA5	1464	6.5574	2.92815
50061	D05	M-020855-	chromoson	55731	C17orf63	2629	6.3903	3.09525
50061	D06	M-013272-	protocadhe	56109	PCDHGA6	2863	8.5575	0.92805
50061	D07	M-020930-	chromoson	55732	C1orf112	2361	5.7603	3.72525
50061	D08	M-013271-	protocadhe	56108	PCDHGA7	2451	4.1616	5.32395
50061	D09	M-009316-	hedgehog a	55733	HHAT	3019	4.4717	5.01385
50061	D10	M-013270-	protocadhe	56107	PCDHGA9	2324	6.9277	2.55785
50061	D11	M-021205-	DnaJ (Hsp4	55735	DNAJC11	4193	6.1054	3.38015
50061	D12	M-013294-	protocadhe	56106	PCDHGA10	817	6.12	3.36555
50061	D13	M-007259-	hypothetic	55739	FLJ10769	2740	7.2263	2.25925
50061	D14	M-013293-	protocadhe	56105	PCDHGA11	3448	4.6984	4.78715
50061	D15	M-021932-	enabled ho	55740	ENAH	2030	11.626	2.14045
50061	D16	M-013292-	protocadhe	56104	PCDHGB1	4620	5.9524	3.53315
50061	D17	M-020238-	chromoson	55744	C7orf44	2630	5.4373	4.04825
50061	D18	M-013291-	protocadhe	56103	PCDHGB2	3879	7.0895	2.39605
50061	D19	M-015523-	chromoson	55745	C14orf108	4319	5.3948	4.09075
50061	D20	M-013290-	protocadhe	56102	PCDHGB3	3882	4.3534	5.13215
50061	D21	M-013322-	nucleopori	55746	NUP133	3208	8.0112	1.47435
50061	D23	M-026372-	family with	55747	FAM21B	3563	10.356	0.87045
50061	E02	M-007016-	RUN and F	55680	RUFY2	4661	12.787	3.30145
50061	E04	M-020851-	LIM and se	55679	LIMS2	1119	10.188	0.70245
50061	E05	M-031865-	large subur	55341	LSG1	989	3.64	5.84555
50061	E06	M-010671-	IWS1 homo	55677	IWS1	1420	10.352	0.86645
50061	E07	M-015439-	spermatid	55342	STRBP	1290	10.388	0.90245
50061	E08	M-007527-	solute carri	55676	SLC30A6	3319	11.66	2.17445
50061	E09	M-010693-	solute carri	55343	SLC35C1	2192	7.8467	1.63885
50061	E10	M-019093-	SMEK hom	55671	SMEK1	3033	11.078	1.59245
50061	E11	M-020472-	phosphatid	55344	PLCXD1	1141	8.8519	0.63365
50061	E12	M-019128-	peroxisome	55670	PEX26	759	15.283	5.79745
50061	E13	M-027203-	chromoson	55345	C4orf21	716	14.106	4.62045
50061	E14	M-010670-	mitofusin 1	55669	MFN1	2719	12.909	3.42345
50061	E15	M-018101-	t-complex	55346	TCP11L1	1269	14.184	4.69845

50061	E16	M-020798-	chromoson	55668	C14orf118	1554	11.583	2.09745
50061	E17	M-020469-	abhydrolas	55347	ABHD10	2171	8.4754	1.01015
50061	E18	M-015536-	DENN/MAI	55667	DENND4C	1730	8.2659	1.21965
50061	E19	M-008123-	choline deh	55349	CHDH	1963	6.7753	2.71025
50061	E20	M-020796-	nuclear pro	55666	NPLOC4	1905	6.8766	2.60895
50061	E21	M-013047-	vanin 3	55350	VNN3	2072	8.3012	1.18435
50061	E23	M-013800-	chromoson	55352	C17orf79	2672	6.25	3.23555
50061	F02	M-013289-	protocadhe	56101	PCDHGB5	3290	11.55	2.06445
50061	F04	M-013288-	protocadhe	56100	PCDHGB6	2202	13.806	4.32045
50061	F05	M-005813-	CNDP dipe	55748	CNDP2	2557	14.47	4.98445
50061	F06	M-013287-	protocadhe	56099	PCDHGB7	1388	13.112	3.62645
50061	F07	M-013828-	cell divisior	55749	CCAR1	2256	15.115	5.62945
50061	F08	M-013286-	protocadhe	56098	PCDHGC4	2901	19.166	9.68045
50061	F09	M-020246-	transmemb	55751	TMEM34	3056	19.143	9.65745
50061	F10	M-013285-	protocadhe	56097	PCDHGC5	1606	10.336	0.85045
50061	F11	M-009703-	oxoglutarat	55753	OGDHL	1735	10.663	1.17745
50061	F12	M-015585-	chromoson	56063	C1orf91	1790	12.57	3.08445
50061	F13	M-020272-	transmemb	55754	TMEM30A	2195	12.711	3.22545
50061	F14	M-012866-	kelch-like 4	56062	KLHL4	1977	16.439	6.95345
50061	F15	M-020275-	integrator	55756	RC74	2145	12.96	3.47445
50061	F16	M-013154-	platelet der	56034	PDGFC	1354	21.566	12.08045
50061	F17	M-013806-	UDP-glucos	55757	UGCGL2	2228	10.413	0.92745
50061	F18	M-020561-	chromoson	56006	C19orf61	1980	17.525	8.03945
50061	F19	M-017112-	REST corep	55758	RCOR3	2550	11.294	1.80845
50061	F20	M-013837-	chromoson	56005	C19orf10	1934	8.3764	1.10915
50061	F21	M-003768-	DEAH (Asp-	55760	DHX32	1236	7.4434	2.04215
50061	F23	M-015541-	tetratricop	55761	TTC17	2560	7.0312	2.45435
50061	G02	M-017108-	up-regulate	55665	URG4	660	4.697	4.78855
50061	G04	M-020365-	zinc finger	55663	ZNF446	801	10.112	0.62645
50061	G05	M-017710-	lysosomal a	55353	LAPTM4B	758	3.0343	6.45125
50061	G06	M-013635-	DEAD (Asp-	55661	DDX27	333	12.012	2.52645
50061	G07	M-007449-	solute carri	55356	SLC22A15	564	8.8652	0.62035
50061	G08	M-027984-	PRP40 pre-	55660	PRPF40A	221	13.122	3.63645
50061	G09	M-020463-	TBC1 doma	55357	TBC1D2	548	9.854	0.36845
50061	G10	M-013825-	zinc finger	55659	ZNF416	662	13.142	3.65645
50061	G11	M-025105-	transmemb	55362	TMEM63B	377	10.08	0.59445
50061	G12	M-007015-	ring finger	55658	RNF126	376	8.2447	1.24085
50061	G13	M-021355-	hemogen	55363	HEMGN	437	4.5767	4.90885
50061	G14	M-015534-	zinc finger	55657	ZNF692	492	5.4878	3.99775
50061	G15	M-020439-	Impact hon	55364	IMPACT	768	12.24	2.75445
50061	G16	M-020270-	integrator	55656	INTS8	1785	6.7787	2.70685
50061	G17	M-019157-	transmemb	55365	TMEM176	1607	4.6671	4.81845
50061	G18	M-020232-	transmemb	55654	TMEM127	1433	5.5827	3.90285
50061	G19	M-015644-	transmemb	55374	TMCO6	825	7.6364	1.84915
50061	G20	M-010578-	breast carc	55653	BCAS4	1615	4.8916	4.59395
50061	G21	M-010669-	leucine rich	55379	LRRC59	580	6.5517	2.93385
50061	G23	M-019193-	minichrom	55388	MCM10	1277	13.626	4.14045

50061	H02	M-010445- nuclear RN	56001	NXF2	2322	15.935	6.44945
50061	H04	M-008445- nuclear RN	56000	NXF3	1329	12.566	3.08045
50061	H05	M-020277- zinc finger	55762	ZNF701	1845	11.599	2.11345
50061	H06	M-013599- nuclear RN	55998	NXF5	1104	5.4348	4.05075
50061	H07	M-013312- exocyst cor	55763	EXOC1	1461	12.663	3.17745
50061	H08	M-015574- kelch-like 7	55975	KLHL7	1700	6.6471	2.83845
50061	H09	M-016457- N-glycanas	55768	NGLY1	2041	9.7991	0.31355
50061	H10	M-020567- recombina	55974	RAG1AP1	977	14.023	4.53745
50061	H11	M-017357- exocyst cor	55770	EXOC2	1510	10.927	1.44145
50061	H12	M-020579- chromoson	55969	C20orf24	949	8.0084	1.47715
50061	H13	M-007019- proline rich	55771	PRR11	855	9.0058	0.47975
50061	H14	M-017222- NSFL1 (p97	55968	NSFL1C	945	8.1481	1.33745
50061	H15	M-020533- TBC1 doma	55773	TBC1D23	1520	13.684	4.19845
50061	H16	M-009094- NADH dehy	55967	NDUFA12	1212	16.007	6.52145
50061	H17	M-020536- chromoson	55776	C6orf64	1072	8.7687	0.71685
50061	H18	M-009879- adherens ju	55966	AJAP1	1401	7.3519	2.13365
50061	H19	M-027190- methyl-CpG	55777	MBD5	1830	10.765	1.27945
50061	H20	M-013840- kelch-like 9	55958	KLHL9	675	5.6296	3.85595
50061	H21	M-020540- chromoson	55778	C14orf131	795	5.5346	3.95095
50061	H23	M-017113- WD repeat	55779	WDR52	2381	6.0059	3.47965
50061	I02	M-020346- hypothetica	55652	FLJ20489	2783	7.8333	1.65225
50061	I04	M-013319- nucleolar p	55651	NOLA2	2305	7.3319	2.15365
50061	I05	M-020379- hypothetica	55415	PRO2964	1191	6.801	2.68455
50061	I06	M-015531- phosphatid	55650	PIGV	628	9.8726	0.38705
50061	I07	M-020376- chromoson	55421	C17orf85	1751	4.8544	4.63115
50061	I08	M-021139- Ly1 antibo	55646	LYAR	2846	4.4273	5.05825
50061	I09	M-021386- zinc finger	55422	ZNF331	1676	9.6062	0.12065
50061	I10	M-005981- O-sialoglyc	55644	OSGEP	1768	8.8801	0.60545
50061	I11	M-017104- KIAA1704	55425	KIAA1704	1276	4.0752	5.41035
50061	I12	M-016110- BTB (POZ)	55643	BTBD2	1224	6.2908	3.19475
50061	I13	M-015504- chromoson	55435	C4orf16	1157	5.7044	3.78115
50061	I14	M-021135- feline leuk	55640	FLVCR2	1492	6.0992	3.38635
50061	I15	M-015669- chromoson	55453	C14orf116	2296	3.8763	5.60925
50061	I16	M-021127- hypothetica	55638	FLJ20366	2076	5.4432	4.04235
50061	I17	M-015941- chondroitir	55454	GALNACT-2	1700	4.2941	5.19145
50061	I18	M-025947- chromodor	55636	CHD7	1290	5.5814	3.90415
50061	I19	M-013338- chromoson	55471	C2orf56	1895	6.8074	2.67815
50061	I20	M-021113- zinc finger	55634	ZNF673	1061	4.9953	4.49025
50061	I21	M-021387- presenilin a	55486	PARL	2157	6.7687	2.71685
50061	I23	M-008238- carbohydra	55501	CHST12	2681	6.1544	3.33115
50061	J02	M-013311- lin-37 hom	55957	LIN37	2718	13.907	4.42145
50061	J04	M-020592- zinc finger,	55954	ZMAT5	1827	11.932	2.44645
50061	J05	M-028653- chromoson	55780	C6orf70	3351	10.862	1.37645
50061	J06	M-031960- myosin VC	55930	MYO5C	2449	12.74	3.25445
50061	J07	M-018783- hypothetica	55783	FLJ11171	2421	6.361	3.12455
50061	J08	M-006378- DNA methy	55929	DMAP1	1321	13.02	3.53445
50061	J09	M-020810- multiple C2	55784	MCTP2	2907	6.8455	2.64005

50061	J10	M-017958-	chromoson	55924	C1orf183	882	7.7098	1.77575
50061	J11	M-007020-	zinc finger	55786	ZNF415	1751	8.4523	1.03325
50061	J12	M-031862-	NF-kappaB	55922	NKRF	838	6.0859	3.39965
50061	J13	M-020815-	chromoson	55787	CXorf15	2263	7.9982	1.48735
50061	J14	M-013835-	regulator o	55920	RCC2	1782	9.0909	0.39465
50061	J15	M-017956-	LMBR1 dor	55788	LMBRD1	1742	6.372	3.11355
50061	J16	M-013834-	CTTNBP2 N	55917	CTTNBP2NI	1256	5.7325	3.75305
50061	J17	M-013830-	DEP domai	55789	DEPDC1B	1346	9.2868	0.19875
50061	J18	M-016931-	nuclear tra	55916	NXT2	2305	8.1128	1.37275
50061	J19	M-016174-	chondroitir	55790	ChGn	1493	5.2244	4.26115
50061	J20	M-017118-	LanC lantib	55915	LANCL2	792	2.1465	7.33905
50061	J21	M-018103-	chromoson	55791	C1orf103	2039	6.6699	2.81565
50061	J23	M-017114-	family with	55793	FAM63A	1203	6.7332	2.75235
50061	K02	M-021109-	TBC1 doma	55633	TBC1D22B	1940	19.278	9.79245
50061	K04	M-007014-	KIAA1333	55632	KIAA1333	865	36.185	26.69945
50061	K05	M-013332-	nucleolar p	55505	NOLA3	1028	14.883	5.39745
50061	K06	M-021101-	zinc finger	55628	ZNF407	840	10.595	1.10945
50061	K07	M-007549-	solute carri	55508	SLC35E3	786	24.427	14.94145
50061	K08	M-020681-	sphingomy	55627	SMPD4	323	36.223	26.73745
50061	K09	M-013327-	DEAD (Asp-	55510	DDX43	312	34.295	24.80945
50061	K10	M-029987-	hypothetic	55626	FLJ20294	694	32.565	23.07945
50061	K11	M-013328-	sarcoma ar	55511	SAGE1	365	35.342	25.85645
50061	K12	M-021091-	zinc finger,	55625	ZDHHC7	272	36.029	26.54345
50061	K13	M-008358-	elaC homol	55520	ELAC1	320	27.187	17.70145
50061	K14	M-021087-	protein O-l	55624	POMGNT1	474	40.928	31.44245
50061	K15	M-007012-	tripartite m	55521	TRIM36	625	36	26.51445
50061	K16	M-021071-	THUMP do	55623	THUMPD1	168	36.905	27.41945
50061	K17	M-009050-	dehydroge	55526	DHTKD1	963	16.615	7.12945
50061	K18	M-015527-	tetratricop	55622	TTC27	418	37.799	28.31345
50061	K19	M-013807-	fem-1 hom	55527	FEM1A	650	20.769	11.28345
50061	K20	M-009655-	TRM1 tRN	55621	TRMT1	1063	19.097	9.61145
50061	K21	M-013808-	transmemb	55529	TMEM55A	2848	15.133	5.64745
50061	K23	M-007326-	SV2 relatec	55530	SVOP	1976	17.966	8.48045
50061	L02	M-031861-	erbb2 inter	55914	ERBB2IP	3236	16.656	7.17045
50061	L04	M-016113-	bridging int	55909	BIN3	1914	17.241	7.75545
50061	L05	M-017202-	DEAD (Asp-	55794	DDX28	2001	19.69	10.20445
50061	L06	M-013833-	hepatocellu	55908	LOC55908	2885	11.508	2.02245
50061	L07	M-020730-	PCI domair	55795	PCID2	3105	23.929	14.44345
50061	L08	M-009780-	cytidine mo	55907	CMAS	1011	28.586	19.10045
50061	L09	M-015373-	muscleblin	55796	MBNL3	556	28.058	18.57245
50061	L10	M-007025-	KIAA1166	55906	KIAA1166	1071	14.846	5.36045
50061	L11	M-008721-	methyltran	55798	METTL2B	1064	29.323	19.83745
50061	L12	M-007024-	zinc finger	55905	ZNF313	1006	23.757	14.27145
50061	L13	M-021246-	calcium cha	55799	CACNA2D3	1492	21.381	11.89545
50061	L14	M-021153-	thrombosp	55901	THSD1	1049	22.498	13.01245
50061	L15	M-017115-	sodium cha	55800	SCN3B	1118	24.329	14.84345
50061	L16	M-020987-	zinc finger	55900	ZNF302	450	23.111	13.62545

50061	L17	M-020444-	centaurin,	55803	CENTA2	376	18.085	8.59945
50061	L18	M-017653-	unc-45 hon	55898	UNC45A	538	16.729	7.24345
50061	L19	M-017116-	LRP2 bindi	55805	LRP2BP	1313	23.991	14.50545
50061	L20	M-008762-	mesoderm	55897	MESP1	1535	22.866	13.38045
50061	L21	M-015512-	ST6 (alpha-	55808	ST6GALNA	1158	12.09	2.60445
50061	L23	M-013831-	spermatog	55812	SPATA7	2055	19.416	9.93045
50061	M02	M-021069-	signal-tran	55620	STAP2	1202	2.8286	6.65695
50061	M04	M-023079-	dedicator	55619	DOCK10	479	7.5157	1.96985
50061	M05	M-013812-	ELMO/CED	55531	ELMOD1	395	7.5949	1.89065
50061	M06	M-004745-	taspase, th	55617	TASP1	288	11.111	1.62545
50061	M07	M-007324-	solute carri	55532	SLC30A10	309	9.0615	0.42405
50061	M08	M-017106-	developme	55616	DDEFL1	398	9.5477	0.06215
50061	M09	M-013813-	mastermin	55534	MAML3	381	6.8241	2.66145
50061	M10	M-004511-	chromoso	55612	C20orf42	464	9.0517	0.43385
50061	M11	M-017989-	cell divisio	55536	CDCA7L	572	5.4196	4.06595
50061	M12	M-012918-	coiled-coil	55610	CCDC132	451	11.086	1.60045
50061	M13	M-020845-	KCNQ1 do	55539	KCNQ1DN	503	10.736	1.25045
50061	M14	M-007013-	suppressor	55609	SUHW3	582	4.2955	5.19005
50061	M15	M-017352-	RNA bindin	55544	RBM38	407	9.0909	0.39465
50061	M16	M-021058-	ankyrin rep	55608	ANKRD10	300	11.667	2.18145
50061	M17	M-024021-	ZFP-36 for	55552	HSZFP36	620	7.0968	2.38875
50061	M18	M-021055-	leucine rich	55604	LRRC16	511	11.546	2.06045
50061	M19	M-015101-	SRY (sex de	55553	SOX6	369	13.55	4.06445
50061	M20	M-021046-	family with	55603	FAM46A	1119	9.7408	0.25525
50061	M21	M-005912-	kallikrein-r	55554	KLK15	1379	7.1791	2.30645
50061	M23	M-020894-	enolase su	55556	ENOSF1	683	6.1493	3.33625
50061	N02	M-012998-	defensin, b	55894	DEFB103A	1637	6.0476	3.43795
50061	N04	M-007023-	myoneurin	55892	MYNN	1591	8.9881	0.49745
50061	N05	M-010579-	UTP6, smal	55813	UTP6	1213	4.6991	4.78645
50061	N06	M-021082-	lens epithe	55891	LENEP	1478	4.6685	4.81705
50061	N07	M-020792-	translin-ass	55815	TSNAXIP1	857	4.9008	4.58475
50061	N08	M-013307-	golgin-like	55889	GOLGA	1581	7.4004	2.08515
50061	N09	M-017301-	jumonji do	55818	JMJD1A	728	14.148	4.66245
50061	N10	M-020508-	zinc finger	55888	ZNF167	1065	11.174	1.68845
50061	N11	M-007021-	ring finger	55819	RNF130	404	7.4257	2.05985
50061	N12	M-017223-	WD repeat	55884	WSB2	661	9.0772	0.40835
50061	N13	M-007022-	vacuolar pr	55823	VPS11	299	11.037	1.55145
50061	N14	M-020262-	gasdermin-	55876	GSDML	504	9.9206	0.43505
50061	N15	M-020878-	IQ motif an	55827	IQWD1	1048	8.4924	0.99315
50061	N16	M-013832-	COBW dom	55871	CBWD1	557	9.5153	0.02975
50061	N17	M-019353-	selenoprot	55829	SELS	281	11.388	1.90245
50061	N18	M-007445-	solute carri	55867	SLC22A11	677	9.6012	0.11565
50061	N19	M-010715-	transmemb	55831	TMEM111	824	5.3398	4.14575
50061	N20	M-018904-	transmemb	55863	TMEM126	1268	6.2303	3.25525
50061	N21	M-015562-	cullin-asso	55832	CAND1	1902	5.0999	4.38565
50061	N23	M-015809-	chromoso	55836	C6orf35	2031	6.0561	3.42945
50061	O02	M-021030-	CDKN2A in	55602	CDKN2AIP	304	11.513	2.02745

50061	O04	M-017664-	hypothetic	55601	FLJ20035	247	6.0729	3.41265
50061	O05	M-020942-	hypothetic	55565	LOC55565	131	10.687	1.20145
50061	O06	M-009035-	intelectin 1	55600	ITLN1	197	10.66	1.17445
50061	O07	M-013818-	dynein, ax	55567	DNAH3	371	4.3127	5.17285
50061	O08	M-021646-	RNA-bindi	55599	RNPC3	786	4.1985	5.28705
50061	O09	M-008707-	UDP-N-ace	55568	GALNT10	512	7.6172	1.86835
50061	O10	M-021026-	zinc finger,	55596	ZCCHC8	267	12.734	3.24845
50061	O11	M-020951-	chromoso	55571	C2orf29	213	15.023	5.53745
50061	O12	M-013823-	OTU domai	55593	OTUD5	111	17.117	7.63145
50061	O13	M-008137-	FAD-depen	55572	FOXRED1	73	21.918	12.43245
50061	O14	M-013822-	golgi autoa	55592	GOLGA2L1	391	8.4399	1.04565
50061	O15	M-020956-	CDV3 hom	55573	CDV3	299	11.037	1.55145
50061	O16	M-017105-	vezatin, ad	55591	VEZT	395	13.671	4.18545
50061	O17	M-015260-	stabilin 2	55576	STAB2	247	11.336	1.85045
50061	O18	M-023854-	intersex-lik	55588	IXL	715	5.5944	3.89115
50061	O19	M-020961-	hypothetic	55580	LOC55580	684	6.2865	3.19905
50061	O20	M-008723-	kinesin fam	55582	KIF27	1049	7.3403	2.14525
50061	O21	M-020582-	chromoso	55267	C22orf26	1186	9.4435	0.04205
50061	O23	M-020726-	gap junctio	57369	GJA9	385	4.6753	4.81025
50061	P02	M-009522-	enoyl Coen	55862	ECHDC1	1093	6.1299	3.35565
50061	P04	M-015079-	dysbindin (	55861	DBNDD2	1138	9.6661	0.18055
50061	P05	M-017926-	E2F-associ	55837	EAPP	760	11.447	1.96145
50061	P06	M-015096-	brain expre	55859	BEX1	281	9.2527	0.23285
50061	P07	M-013869-	WWC famil	55841	WWC3	834	6.5947	2.89085
50061	P08	M-018846-	transmemb	55858	TMEM165	842	5.9382	3.54735
50061	P09	M-018019-	Rho GTPas	55843	ARHGAP15	1283	8.0281	1.45745
50061	P10	M-017957-	chromoso	55857	C20orf19	995	6.6332	2.85235
50061	P11	M-017711-	chromoso	55845	C3orf10	129	10.078	0.59245
50061	P12	M-009794-	thioesteras	55856	THEM2	227	5.2863	4.19925
50061	P13	M-015565-	integrin alp	55846	ITFG2	938	7.0362	2.44935
50061	P14	M-020500-	family with	55855	FAM45B	647	9.7372	0.25165
50061	P15	M-020954-	zinc finger,	55847	ZCD1	757	4.3593	5.12625
50061	P16	M-020777-	zinc finger	55854	ZC3H15	246	7.3171	2.16845
50061	P17	M-020447-	chromoso	55848	C9orf46	560	4.1071	5.37845
50061	P18	M-027283-	chromoso	55853	C10orf110	382	4.9738	4.51175
50061	P19	M-015719-	asparagine	55849	ALG13	256	4.6875	4.79805
50061	P20	M-017117-	testis expre	55852	TEX2	455	3.2967	6.18885
50061	P21	M-021121-	uncharacte	55850	MDS032	776	5.1546	4.33095
50061	P23	M-008057-	presenilin	55851	PSENEN	737	7.7341	1.75145
					mdmdMAD		9.48555	3.1969
					3MAD			9.5907
					MADc			4.731412

50061	C22	Human4 P	RNAi	empty
50061	D22	Human4 P	RNAi	empty
50061	E22	Human4 P	RNAi	empty

50061	F22	Human4 Pc	RNAi	empty				

50061	G22	Human4 Pc	RNAi	empty				
50061	H22	Human4 Pc	RNAi	empty				
50061	I22	Human4 Pc	RNAi	empty				
50061	J22	Human4 Pc	RNAi	empty				

50061	G03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347
50061	H03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347
50061	I03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-	siControl non-targeting	
50061	J03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-	siControl non-targeting	
50061	K03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-	siGLO RISC-free siRNA	
50061	L03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-	siGLO RISC-free siRNA	

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
3.935284	2717	10.416	1.0195	-0.22307	1936	10.589	1.13705	0.084747
1.96695	2156	10.482	0.9535	-0.20863	1388	10.951	10.951	0.111728
3.596485	1140	13.509	2.0735	0.453696	1487	16.88	16.88	0.553629
2.128847	744	20.968	9.5325	2.085777	1964	20.061	20.061	0.790716
0.838323	546	21.245	9.8095	2.146386	1569	11.409	11.409	0.145863
1.833374	1597	17.909	6.4735	1.416446	2655	27.119	4.327	1.316765
1.30013	717	18.968	7.5325	1.648163	1011	22.057	3.102	0.939483
3.61297	1237	11.156	0.2795	-0.06116	1237	21.261	8.805	0.880155
6.485474	420	24.048	12.6125	2.759702	1220	17.049	21.837	0.566225
3.252824	520	28.654	17.2185	3.767526	1056	14.962	16.42725	0.410676
2.912334	835	21.198	9.7625	2.136102	1143	18.898	13.21846	0.704035
1.811816	1078	15.121	3.6855	0.806413	1640	21.768	13.6647	0.917943
5.209111	2051	14.822	3.3865	0.74099	1242	27.295	23.4367	1.329882
2.040289	1735	13.545	2.1095	0.461573	1894	19.219	13.9641	0.72796
3.529908	1094	23.035	11.5995	2.538051	1086	20.074	12.2932	0.791685
0.289438	2632	13.184	1.7485	0.382584	1246	14.767	8.517675	0.396143
0.826698	2267	14.513	3.0775	0.673378	1637	17.349	15.3087	0.588585
2.948264	2476	15.63	4.1945	0.917785	1154	21.317	4.278383	0.884329
1.983224	1894	20.011	8.5755	1.876378	827	18.138	12.01709	0.647391
2.594881	1310	17.405	5.9695	1.306168	750	18.4	4.759529	0.666918
0.657404	4996	18.695	7.2595	1.588429	3156	13.625	11.51493	0.311027
-0.65328	2304	10.938	0.4975	-0.10886	1353	12.047	11.12577	0.193415
0.021505	4968	12.581	1.1455	0.250643	3374	13.011	12.93223	0.265264
0.539469	3446	11.695	0.2595	0.05678	1926	14.434	16.054	0.371323
-0.62059	2286	7.4366	3.9989	-0.87499	1697	7.5427	20.8783	-0.1423
-0.53182	2316	11.054	0.3815	-0.08347	1565	7.9233	3.2518	-0.11393
0.078254	4318	14.868	3.4325	0.751055	2786	11.989	0.632	0.189092
-0.6112	3399	10.474	0.9615	-0.21038	1971	11.01	11.176	0.116125
-0.35728	2431	12.999	1.5635	0.342105	1979	14.704	4.459	0.391447
-0.03776	2356	12.818	1.3825	0.302501	633	17.22	17.22	0.57897
0.50375	4857	22.071	10.6355	2.327121	2820	19.504	19.504	0.749202
0.514107	2673	13.393	1.9575	0.428314	2348	15.204	15.204	0.428713
-0.59085	3812	10.388	1.0475	-0.2292	3150	11.079	11.079	0.121268
0.385392	4009	18.483	7.0475	1.542042	1746	13.803	13.803	0.324293
-0.40649	4052	20.163	8.7275	1.909637	3069	8.8628	8.8628	-0.04391
0.851215	6543	25.462	14.0265	3.069095	3853	15.91	15.91	0.481333
-0.25795	546	26.923	15.4875	3.388772	1773	9.0243	9.0243	-0.03187
0.143393	4900	19.878	8.4425	1.847277	3734	10.364	10.364	0.067977
-0.5669	4626	15.543	4.1075	0.898749	3033	14.87	14.87	0.403819
0.013284	4171	16.087	4.6515	1.01778	2219	6.8049	6.8049	-0.19729
-1.09467	2384	10.864	0.5715	-0.12505	3125	3.168	3.168	-0.46836
-0.24353	2428	13.097	1.6615	0.363548	3007	12.537	12.537	0.229936
-1.00117	3214	9.4586	1.9769	-0.43256	4297	9.8208	9.8208	0.027491
-0.54467	1762	9.9886	1.4469	-0.31659	3601	2.8881	2.8881	-0.48922
-0.52575	3844	11.55	0.1145	0.025053	4265	11.77	11.77	0.172769
-0.48841	3542	6.1547	5.2808	-1.15548	5591	7.3511	7.3511	-0.15658

-0.62995	1413	9.1295	2.306	-0.50457	2051	4.7294	4.7294	-0.35198
-0.52738	3204	8.7391	2.6964	-0.58999	2612	6.2404	6.2404	-0.23936
-0.00629	1808	11.394	0.0415	-0.00908	2194	11.531	11.531	0.154956
-1.02374	2581	7.9427	3.4928	-0.76425	2021	8.5106	8.5106	-0.07016
0.106068	845	11.124	0.3115	-0.06816	1317	7.5171	7.5171	-0.14421
0.096726	2805	6.5241	4.9114	-1.07465	1762	6.8672	6.8672	-0.19265
0.278659	1250	9.12	2.3155	-0.50665	925	7.2432	7.2432	-0.16462
-0.50274	3950	7.5443	3.8912	-0.85142	3286	9.9209	9.9209	0.034952
-0.41796	4601	12.606	1.1705	0.256113	2948	8.6499	8.6499	-0.05978
-0.60457	3029	9.9703	1.4652	-0.3206	3358	9.8571	9.8571	0.030197
1.924679	3004	18.209	6.7735	1.482088	2573	19.238	19.238	0.729376
0.306135	3536	7.7489	3.6866	-0.80665	2126	11.759	11.759	0.17195
0.194963	4400	9.4545	1.981	-0.43346	2146	8.5741	8.5741	-0.06543
-0.10355	2669	7.2312	4.2043	-0.91993	1418	10.79	10.79	0.099728
-1.06574	2558	8.5223	2.9132	-0.63743	2528	7.5949	7.5949	-0.13841
-0.61887	3171	7.9786	3.4569	-0.75639	2325	5.8925	5.8925	-0.26529
-0.65419	2954	7.8538	3.5817	-0.7837	3016	6.7971	6.7971	-0.19787
-0.19615	3586	7.1389	4.2966	-0.94013	3283	13.677	13.677	0.314902
-0.78734	2453	9.8247	1.6108	-0.35245	1675	12.119	12.119	0.198781
-1.12523	2044	6.3601	5.0754	-1.11053	2189	5.5276	5.5276	-0.29249
-1.05969	1736	6.2788	5.1567	-1.12832	2161	5.4604	5.4604	-0.2975
-0.54061	1492	5.496	5.9395	-1.2996	1658	5.2473	5.2473	-0.31338
-0.71441	2530	5.8893	5.5462	-1.21355	2036	7.9568	7.9568	-0.11144
-0.71132	1089	11.387	0.0485	-0.01061	735	4.2177	4.2177	-0.39012
-0.4775	2257	10.058	1.3775	-0.30141	1748	5.3776	5.3776	-0.30367
-1.01178	3226	7.0366	4.3989	-0.96251	2442	7.7805	7.7805	-0.12458
0.452391	1205	14.274	2.8385	0.621083	1009	10.208	10.208	0.05635
-0.74674	4274	7.9785	3.457	-0.75642	3016	5.504	5.504	-0.29425
-0.85561	1114	9.605	1.8305	-0.40053	1094	4.8446	4.8446	-0.3434
-0.50641	3610	9.6122	1.8233	-0.39895	2336	8.3904	8.3904	-0.07912
-0.86459	3490	9.0544	2.3811	-0.521	2225	6.427	6.427	-0.22546
-1.0847	3354	9.7496	1.6859	-0.36889	1155	5.0216	5.0216	-0.3302
-0.31161	2878	12.682	1.2465	0.272743	1461	4.5175	4.5175	-0.36778
0.183973	2768	10.188	1.2475	-0.27296	1157	7.5194	7.5194	-0.14404
0.697773	4316	11.608	0.1725	0.037744	5567	13.975	13.975	0.337113
0.148465	637	12.716	1.2805	0.280182	1399	7.0765	7.0765	-0.17705
-1.23548	2838	8.7738	2.6617	-0.5824	3333	10.801	10.801	0.100548
0.183127	2440	10.779	0.6565	-0.14365	2519	6.4311	6.4311	-0.22515
0.190736	3049	9.8721	1.5634	-0.34208	3697	8.0065	8.0065	-0.10773
0.459577	2794	10.773	0.6625	-0.14496	4932	9.0024	9.0024	-0.03351
-0.34638	2183	15.712	4.2765	0.935728	2644	6.5431	6.5431	-0.2168
0.33657	2200	13.864	2.4285	0.531373	3807	8.2217	8.2217	-0.09169
-0.13392	1781	13.981	2.5455	0.556973	2388	5.5276	5.5276	-0.29249
1.225311	1371	5.0328	6.4027	-1.40095	1180	5.1695	5.1695	-0.31918
0.976548	1782	11.616	0.1805	0.039495	2717	9.4958	9.4958	0.003268
0.723558	4086	11.429	0.0065	-0.00142	4478	8.7539	8.7539	-0.05203
0.993033	1298	13.405	1.9695	0.43094	1337	11.144	11.144	0.126112

0.443303	2092	10.134	1.3015	-0.28478	1699	5.7681	5.7681	-0.27457
-0.2135	1592	10.113	1.3225	-0.28937	1605	9.4081	9.4081	-0.00327
-0.25778	3325	7.0376	4.3979	-0.96229	1904	8.3508	8.3508	-0.08207
-0.57282	3187	9.6015	1.834	-0.40129	2082	5.0913	5.0913	-0.32501
-0.55141	2750	8.5818	2.8537	-0.62441	2422	7.5557	7.5557	-0.14133
-0.25032	2777	7.4901	3.9454	-0.86328	2010	6.8657	6.8657	-0.19276
-0.68384	3577	12.58	1.1445	0.250424	2971	4.0727	4.0727	-0.40093
0.436329	3815	18.244	6.8085	1.489747	2941	14.553	14.553	0.380193
0.913142	2612	16.73	5.2945	1.158473	2890	16.782	16.782	0.546325
1.05348	2345	12.708	1.2725	0.278432	2877	14.425	14.425	0.370653
0.766463	2709	10.779	0.6565	-0.14365	2176	9.2371	9.2371	-0.01601
1.189803	1889	12.176	0.7405	0.162027	1981	9.894	9.894	0.032947
2.045996	1797	25.543	14.1075	3.086818	2968	12.466	12.466	0.224644
2.041135	2528	17.642	6.2065	1.358025	2717	9.2749	9.2749	-0.0132
0.179745	1636	10.147	1.2885	-0.28193	1995	6.7168	6.7168	-0.20386
0.248858	2220	15.315	3.8795	0.848861	1579	11.843	11.843	0.17821
0.651909	2056	10.798	0.6375	-0.13949	1831	7.4823	7.4823	-0.1468
0.68171	2346	12.617	1.1815	0.25852	2507	10.73	10.73	0.095256
1.469635	1661	12.402	0.9665	0.211477	2328	7.4313	7.4313	-0.1506
0.734337	2506	12.57	1.1345	0.248236	3411	10.613	10.613	0.086536
2.553244	2208	15.987	4.5515	0.9959	2101	6.3303	6.3303	-0.23266
0.19602	1241	12.248	0.8125	0.177781	2044	7.6321	7.6321	-0.13564
1.699165	2279	20.667	9.2315	2.019916	2721	16.097	16.097	0.49527
0.382222	2218	12.489	1.0535	0.230513	2154	7.1959	7.1959	-0.16815
-0.23442	2644	9.3419	2.0936	-0.45809	1439	6.3933	6.3933	-0.22797
-0.43162	1450	11.379	0.0565	-0.01236	1362	5.7269	5.7269	-0.27764
-0.51874	2681	10.034	1.4015	-0.30666	3245	5.0847	5.0847	-0.3255
-1.01208	3068	10.398	1.0375	-0.22701	3533	12.737	12.737	0.244842
0.132402	2504	11.102	0.3335	-0.07297	1992	8.5843	8.5843	-0.06467
-1.36349	2586	11.64	0.2045	0.044746	1547	10.795	10.795	0.100101
0.533974	2800	11.464	0.0285	0.006236	2250	9.9556	9.9556	0.037538
-0.13111	1612	10.856	0.5795	-0.1268	1752	12.614	12.614	0.235675
0.768576	945	8.4656	2.9699	-0.64983	1628	3.0713	3.0713	-0.47556
0.077873	2392	13.127	1.6915	0.370112	1867	9.6411	9.6411	0.014098
0.772803	2492	10.634	0.8015	-0.17537	2172	12.155	12.155	0.201464
0.125639	1272	11.557	0.1215	0.026585	1033	7.2604	7.2604	-0.16334
-0.26226	1600	14.313	2.8775	0.629617	751	5.4594	5.4594	-0.29757
-1.0375	2003	8.3874	3.0481	-0.66695	1220	5.4918	5.4918	-0.29516
-0.84494	3840	18.828	7.3925	1.61753	1976	8.2996	8.2996	-0.08589
0.582162	1701	12.992	1.5565	0.340573	1335	8.3895	8.3895	-0.07919
-0.5721	3290	12.036	0.6005	0.131394	2314	5.7476	5.7476	-0.27609
-1.0184	2442	9.1319	2.3036	-0.50404	2844	3.6568	3.6568	-0.43193
-0.82488	2311	12.549	1.1135	0.243641	1536	8.9193	8.9193	-0.0397
-0.39082	2217	14.975	3.5395	0.774467	1565	10.99	10.99	0.114634
-0.97095	5966	19.544	8.1085	1.774196	3852	13.266	13.266	0.28427
-0.62008	2475	8.9697	2.4658	-0.53953	1684	5.7007	5.7007	-0.27959
0.875098	2338	9.367	2.0685	-0.4526	1505	4.9834	4.9834	-0.33305

1.363113	2288	15.428	3.9925	0.873587	4202	8.6625	8.6625	-0.05884
0.651064	1580	15.823	4.3875	0.960015	2394	12.197	12.197	0.204595
0.446685	1935	13.592	2.1565	0.471857	2621	10.988	10.988	0.114485
-0.85614	1089	11.754	0.3185	0.06969	2086	7.814	7.814	-0.12208
0.671565	1499	14.076	2.6405	0.57776	2672	10.254	10.254	0.059779
-0.59992	1984	11.442	0.0065	0.001422	3005	5.1913	5.1913	-0.31756
0.06627	1262	10.618	0.8175	-0.17887	3564	10.999	10.999	0.115305
0.959005	1534	10.104	1.3315	-0.29134	2195	7.3349	7.3349	-0.15779
0.304655	2220	19.91	8.4745	1.854279	2969	10.071	10.071	0.046139
-0.3122	1610	14.534	3.0985	0.677973	2240	8.75	8.75	-0.05232
-0.1014	1128	13.209	1.7735	0.388054	1428	6.5826	6.5826	-0.21386
-0.28267	1087	12.236	0.8005	0.175155	2095	7.3508	7.3508	-0.1566
0.887357	1411	15.379	3.9435	0.862865	2569	12.573	12.573	0.232619
1.378331	2343	15.962	4.5265	0.990429	2551	7.8793	7.8793	-0.11721
-0.15151	1303	9.2095	2.226	-0.48706	2179	4.0385	4.0385	-0.40348
-0.45095	2169	10.927	0.5085	-0.11126	4343	7.4373	7.4373	-0.15016
0.270416	2862	14.046	2.6105	0.571195	4571	7.832	7.832	-0.12074
-0.81497	1090	6.6972	4.7383	-1.03677	1666	5.5822	5.5822	-0.28842
-0.83505	1174	3.5775	7.858	-1.71938	1333	6.1515	6.1515	-0.24599
-0.73544	3163	10.433	1.0025	-0.21935	5137	6.4045	6.4045	-0.22713
-0.34921	3547	21.398	9.9625	2.179864	3656	13.211	13.211	0.28017
-0.45518	2603	9.9501	1.4854	-0.32502	4331	7.9427	7.9427	-0.11249
-0.56739	2633	13.787	2.3515	0.514524	4694	8.5002	8.5002	-0.07094
0.081804	1971	10.096	1.3395	-0.29309	2866	9.1068	9.1068	-0.02572
-0.97881	2685	12.663	1.2275	0.268585	5434	14.667	14.667	0.388689
-1.06908	2200	10.682	0.7535	-0.16487	4207	6.9408	6.9408	-0.18716
0.0255	1507	17.651	6.2155	1.359994	2428	11.326	11.326	0.139677
-0.12796	1823	16.182	4.7465	1.038567	3232	11.881	11.881	0.181043
-1.1435	2145	19.627	8.1915	1.792357	3422	12.478	12.478	0.225538
-0.67522	1629	7.919	3.5165	-0.76943	2093	6.0201	6.0201	-0.25578
-0.79916	1616	10.149	1.2865	-0.2815	3076	7.6398	7.6398	-0.13506
-0.71572	2281	8.1982	3.2373	-0.70834	3174	12.193	12.193	0.204297
-1.18553	2592	8.6806	2.7549	-0.60279	3177	10.261	10.261	0.0603
-0.85436	2592	9.9923	1.4432	-0.31578	3599	8.8636	8.8636	-0.04385
-1.09723	3325	21.564	10.1285	2.216186	2424	15.635	15.635	0.460837
-0.82516	2106	11.159	0.2765	-0.0605	3426	6.2755	6.2755	-0.23675
-0.56604	2311	13.76	2.3245	0.508617	4261	12.509	12.509	0.227849
-0.94903	2072	8.1564	3.2791	-0.71749	2360	5.8051	5.8051	-0.27181
-0.57422	2087	13.129	1.6935	0.370549	2860	12.343	12.343	0.215476
-0.70405	4026	11.451	0.0155	0.003392	3813	10.333	10.333	0.065667
0.934488	4393	12.429	0.9935	0.217385	5126	8.1545	8.1545	-0.0967
0.517066	1816	9.4163	2.0192	-0.44181	2211	12.121	12.121	0.19893
0.290917	4483	22.485	11.0495	2.417707	4581	24.427	24.427	1.116124
0.687839	3447	25.471	14.0355	3.071064	3949	19.929	19.929	0.780878
-0.66038	2978	8.8314	2.6041	-0.5698	3749	19.152	19.152	0.722966
0.747018	1815	8.8154	2.6201	-0.5733	2049	12.982	12.982	0.263103
-0.55798	3183	12.033	0.5975	0.130737	3194	8.9543	8.9543	-0.03709

-0.37531	2017	6.7427	4.6928	-1.02682	869	7.71	7.71	-0.12983
-0.21838	1854	11.866	0.4305	0.094196	1989	12.117	12.117	0.198632
-0.71853	2051	13.164	1.7285	0.378208	1718	9.6042	9.6042	0.011348
-0.31436	3034	15.425	3.9895	0.87293	3353	13.868	13.868	0.329138
-0.08341	3341	11.494	0.0585	0.0128	3230	16.966	16.966	0.560039
-0.65806	2223	15.655	4.2195	0.923256	2968	8.0526	8.0526	-0.1043
-0.79322	1273	10.134	1.3015	-0.28478	1435	11.568	11.568	0.157714
-0.04201	1975	15.241	3.8055	0.83267	2464	17.248	17.248	0.581057
-0.29014	4288	14.179	2.7435	0.600297	3092	12.387	12.387	0.218756
-0.90061	3153	8.817	2.6185	-0.57295	2560	5.9766	5.9766	-0.25903
-1.55113	2728	8.7977	2.6378	-0.57717	1803	4.437	4.437	-0.37378
-0.5951	3064	6.1684	5.2671	-1.15248	2859	5.6663	5.6663	-0.28215
-0.58172	1336	7.7096	3.7259	-0.81525	1527	3.7328	3.7328	-0.42626
2.069668	4753	19.398	7.9625	1.74225	5585	17.44	17.44	0.595367
5.643019	2611	19.763	8.3275	1.822114	2251	14.438	14.438	0.371621
1.140769	3787	14.154	2.7185	0.594827	3787	9.9551	9.9551	0.037501
0.234486	3709	15.179	3.7435	0.819104	2491	20.112	20.112	0.794517
3.157926	2182	25.298	13.8625	3.033211	1550	26.968	26.968	1.30551
5.651051	1840	25.272	13.8365	3.027522	2015	20.695	20.695	0.83797
5.243562	1490	18.389	6.9535	1.521474	1254	19.617	19.617	0.757624
4.87792	2627	15.683	4.2475	0.929382	2990	16.355	16.355	0.5145
5.464849	2697	15.647	4.2115	0.921505	2541	11.924	11.924	0.184247
5.610048	2040	23.333	11.8975	2.603255	3197	18.799	18.799	0.696656
3.741262	1693	27.23	15.7945	3.455945	1660	20.904	20.904	0.853547
6.645469	2312	18.339	6.9035	1.510533	1765	16.034	16.034	0.490575
5.603919	1530	23.137	11.7015	2.560369	1475	28.881	28.881	1.44809
5.795194	812	27.833	16.3975	3.587886	520	25.577	25.577	1.201836
1.506833	1919	16.936	5.5005	1.203547	1206	22.637	22.637	0.982711
5.984144	2124	25.141	13.7055	2.998858	1382	27.424	27.424	1.339497
2.384795	3085	19.643	8.2075	1.795858	1909	26.768	26.768	1.290604
2.031413	3162	26.344	14.9085	3.262083	1543	15.036	15.036	0.416192
1.193608	3685	19.213	7.7775	1.701771	2823	17.57	17.57	0.605056
1.792372	2239	15.766	4.3305	0.947543	2362	16.3	16.3	0.5104
1.515499	4176	21.193	9.7575	2.135008	4295	18.184	18.184	0.650819
1.639141	2137	20.73	9.2945	2.033701	1706	11.958	11.958	0.186781
2.156745	2188	23.446	12.0105	2.62798	1556	19.602	19.602	0.756506
0.427452	3648	12.473	1.0375	0.227012	3366	15.894	15.894	0.48014
3.052672	2537	16.949	5.5135	1.206392	1853	20.399	20.399	0.815908
4.036945	1152	17.795	6.3595	1.391502	796	18.97	18.97	0.709402
3.92535	622	32.476	21.0405	4.603806	549	30.237	30.237	1.549156
1.132949	1707	21.675	10.2395	2.240473	670	18.507	18.507	0.674893
4.192712	828	27.174	15.7385	3.443692	816	28.309	28.309	1.405458
3.016319	2166	19.898	8.4625	1.851653	1747	15.799	15.799	0.47306
2.514144	1852	20.788	9.3525	2.046391	2355	18.854	18.854	0.700756
2.750226	1757	13.546	2.1105	0.461792	1919	14.851	14.851	0.402403
3.137214	2446	18.275	6.8395	1.49653	1595	22.382	22.382	0.963705
2.879785	1212	21.287	9.8515	2.155576	969	20.743	20.743	0.841547

1.817523	917	30.098	18.6625	4.083484	792	24.747	24.747	1.139974
1.530928	3759	11.865	0.4295	0.093978	2173	18.086	18.086	0.643515
3.065776	2382	14.777	3.3415	0.731143	1618	17.12	17.12	0.571517
2.828004	2919	14.834	3.3985	0.743615	2791	13.436	13.436	0.29694
0.550459	2127	13.587	2.1515	0.470763	2232	11.918	11.918	0.1838
2.098834	3696	14.475	3.0395	0.665064	2485	10.101	10.101	0.048375
-1.40697	4480	6.5179	4.9176	-1.076	3394	7.2775	7.2775	-0.16207
-0.41633	3285	24.384	12.9485	2.833221	2492	22.552	22.552	0.976376
-0.3996	2621	3.0141	8.4214	-1.84266	2481	3.0633	3.0633	-0.47616
0.343544	2773	7.2485	4.187	-0.91614	2664	8.9715	8.9715	-0.03581
-0.08962	2987	9.5079	1.9276	-0.42177	2720	7.5735	7.5735	-0.14001
0.013136	1394	6.3128	5.1227	-1.12088	1165	5.4936	5.4936	-0.29502
-0.56251	2158	5.329	6.1065	-1.33614	1385	7.2202	7.2202	-0.16634
-0.0917	2079	8.177	3.2585	-0.71298	1792	6.4732	6.4732	-0.22201
-0.85935	2342	11.401	0.0345	-0.00755	2167	12.875	12.875	0.255128
0.338261	2290	12.62	1.1845	0.259177	2467	9.3231	9.3231	-0.0096
0.264287	1417	7.41	4.0255	-0.88081	2285	7.6149	7.6149	-0.13692
-1.09693	2191	10.726	0.7095	-0.15524	2258	13.508	13.508	0.302306
-0.08341	1410	5.5319	5.9036	-1.29175	1518	6.3241	6.3241	-0.23313
0.461057	2008	4.4821	6.9534	-1.52145	1556	5.0129	5.0129	-0.33085
-0.50487	3176	9.5718	1.8637	-0.40779	2790	9.2473	9.2473	-0.01525
0.435483	1605	9.9065	1.529	-0.33456	990	9.1919	9.1919	-0.01938
0.859035	2437	9.3968	2.0387	-0.44608	1029	7.1914	7.1914	-0.16848
0.053948	2050	13.463	2.0275	0.443631	1333	7.7269	7.7269	-0.12857
-0.48748	1995	12.18	0.7445	0.162902	1629	9.9448	9.9448	0.036733
-0.70513	1816	8.7004	2.7351	-0.59846	1840	4.837	4.837	-0.34396
-0.72662	2431	5.2242	6.2113	-1.35908	1812	6.3466	6.3466	-0.23145
-0.10514	3935	24.676	13.2405	2.897113	3184	23.367	23.367	1.03712
-1.01163	2902	4.1351	7.3004	-1.59738	3890	3.4704	3.4704	-0.44582
-1.0181	3297	11.526	0.0905	0.019802	2237	9.2535	9.2535	-0.01479
-0.969	2733	10.209	1.2265	-0.26837	2448	6.5768	6.5768	-0.21429
-0.4407	2320	5.4741	5.9614	-1.3044	2467	4.7021	4.7021	-0.35402
0.985425	3014	21.964	10.5285	2.303708	2788	24.032	24.032	1.086684
0.35686	3570	10.252	1.1835	-0.25896	4230	12.199	12.199	0.204744
-0.43536	2384	12.878	1.4425	0.315629	2205	11.655	11.655	0.164198
-0.08631	2380	10.882	0.5535	-0.12111	2848	6.4256	6.4256	-0.22556
0.327904	906	2.5386	8.8969	-1.9467	1378	5.8781	5.8781	-0.26637
0.091949	1660	11.024	0.4115	-0.09004	2270	6.2115	6.2115	-0.24152
-0.20991	1697	7.8374	3.5981	-0.78729	2658	8.0512	8.0512	-0.1044
0.006288	1669	5.7519	5.6836	-1.24361	2493	5.9767	5.9767	-0.25902
0.402089	1234	9.1572	2.2783	-0.49851	1478	7.2395	7.2395	-0.1649
0.024443	2388	11.683	0.2475	0.054155	3694	6.3346	6.3346	-0.23234
-0.87622	2798	10.758	0.6775	-0.14824	4189	10.026	10.026	0.042785
-0.68801	3000	7.5667	3.8688	-0.84652	4936	6.1791	6.1791	-0.24393
-0.92692	3409	8.5362	2.8993	-0.63439	3576	4.5861	4.5861	-0.36266
-0.72483	3056	9.6531	1.7824	-0.39	4010	3.7406	3.7406	-0.42568
0.428508	2636	5.1214	6.3141	-1.38157	3508	6.0433	6.0433	-0.25405

-0.72128	1953	6.6564	4.7791	-1.0457	3167	13.167	13.167	0.276891
0.253931	3342	5.9545	5.481	-1.19928	3822	5.102	5.102	-0.32421
0.248224	2623	7.5105	3.925	-0.85882	4423	9.7219	9.7219	0.02012
-1.0933	1695	7.6696	3.7659	-0.824	2091	4.3998	4.3998	-0.37655
-1.11744	3242	7.0327	4.4028	-0.96336	3081	7.9844	7.9844	-0.10938
-0.39488	2785	5.8528	5.5827	-1.22153	3980	4.7487	4.7487	-0.35054
0.686571	2700	6.5926	4.8429	-1.05966	2940	15.51	15.51	0.45152
1.170359	2708	4.9483	6.4872	-1.41944	3200	8.1875	8.1875	-0.09424
1.612933	768	6.1198	5.3157	-1.16311	833	11.765	11.765	0.172397
2.627641	1142	7.7933	3.6422	-0.79694	717	6.2762	6.2762	-0.2367
-0.221	1199	4.3369	7.0986	-1.55322	2301	4.9978	4.9978	-0.33198
0.327904	3996	5.8308	5.6047	-1.22635	2661	6.0128	6.0128	-0.25633
0.884609	2404	4.5341	6.9014	-1.51007	2493	5.1344	5.1344	-0.3218
0.391099	2840	6.1268	5.3087	-1.16158	1976	3.7449	3.7449	-0.42536
-0.82241	4326	4.4614	6.9741	-1.52598	3936	7.1138	7.1138	-0.17427
-0.67613	3943	15.876	4.4405	0.971612	2728	12.647	12.647	0.238134
-0.45341	5026	10.744	0.6915	-0.1513	3102	6.383	6.383	-0.22874
-0.00889	4569	9.258	2.1775	-0.47645	4696	5.4514	5.4514	-0.29817
-1.01666	2564	3.3541	8.0814	-1.76827	2843	5.5575	5.5575	-0.29026
-0.70923	2153	6.2239	5.2116	-1.14033	2400	10.167	10.167	0.053294
0.03816	4346	14.082	2.6465	0.579072	4864	17.373	17.373	0.590374
0.414559	2593	11.994	0.5585	0.122204	2702	14.064	14.064	0.343746
-0.04921	2622	6.7887	4.6468	-1.01675	2655	9.6422	9.6422	0.01418
-0.61099	5398	13.097	1.6615	0.363548	4341	14.029	14.029	0.341138
-0.74974	2078	6.9297	4.5058	-0.9859	2106	7.6448	7.6448	-0.13469
-0.30804	4229	11.114	0.3215	-0.07035	4997	15.129	15.129	0.423123
-0.60285	3886	12.069	0.6335	0.138614	3256	11.886	11.886	0.181415
0.125216	2488	8.7621	2.6734	-0.58496	1740	6.8391	6.8391	-0.19474
-0.88753	2103	4.1845	7.251	-1.58657	1554	5.4054	5.4054	-0.3016
-0.51768	3527	9.2713	2.1642	-0.47354	5060	10.119	10.119	0.049717
0.053187	2509	7.6126	3.8229	-0.83648	2938	6.8414	6.8414	-0.19457
-1.08345	3307	12.156	0.7205	0.15765	4604	14.466	14.466	0.373708
-0.45831	969	6.6047	4.8308	-1.05701	1768	6.2783	6.2783	-0.23654
-1.13675	2242	5.7984	5.6371	-1.23344	3418	5.1492	5.1492	-0.32069
-0.95357	3289	4.2566	7.1789	-1.57079	2906	2.8906	2.8906	-0.48903
-1.01408	2874	8.1768	3.2587	-0.71303	3074	5.4001	5.4001	-0.30199
-1.30803	901	9.101	2.3345	-0.5108	2063	4.7504	4.7504	-0.35042
-0.91536	3773	6.4405	4.995	-1.09294	2986	4.2867	4.2867	-0.38498
-0.37017	2934	6.2031	5.2324	-1.14489	1746	1.3746	1.3746	-0.60202
		11.4355	3.088			9.45195	9.06555	
			9.264				27.19665	
			4.57024				13.41701	

3778	34.966	3572	37.962	2013	31.446
2134	24.93	3242	40.253	1256	25.159
2522	41.911	3762	45.295	1969	30.066

	1809	39.912	2741	33.966	3680	38.886
mn	2560.75	35.42975	3329.25	39.369	2229.5	31.38925
sd	862.2534	7.584128	447.158	4.728319	1027.357	5.679539
	245	6.5306	1217	9.9425	1123	8.1033
	410	4.1463	1000	11.3	1581	3.8583
	570	4.7368	960	8.75	1275	5.2549
	716	5.4469	1516	7.124	1478	7.7808
mn	485.25	5.21515	1173.25	9.279125	1364.25	6.249325
sd	203.1508	1.025569	254.8743	1.774687	205.0096	2.040304
3posSD		22.75238		14.18496		17.03862
3negSD		3.076707		5.32406		6.120912
Sum3SD		25.82909		19.50902		23.15953
MnDiff		30.2146		30.08988		25.13993
SumovrMn		0.854855		0.648358		0.921225
1minus		0.145145		0.351642		0.078775
PLK1 SMAR	220	19.545	195	27.692	82	30.488
PLK1 SMAR	104	37.5	108	42.593	95	28.421
	2160	22.037	2398	39.283	2740	4.6715
	2506	31.445	1906	28.751	2166	11.357
	2125	46.447	5825	49.923	6486	22.186
	5078	55.849	4589	53.192	4347	19.163

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

X toxic b

x	toxic a,c
x	toxic a,b
x	toxic a
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,c
x	toxic a,c
X	toxic a,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b
x	toxic a,b

						cell ct	% inf	AD
50062	A02	M-020388-	ectonucleo	57089	ENTPD7	2091	11.143	0.825
50062	A04	M-021172-	phospholip	57088	PLSCR4	2256	13.475	3.157
50062	A05	M-013484-	testis expre	56154	TEX15	801	14.107	3.789
50062	A06	M-007416-	solute carri	57084	SLC17A6	1636	17.848	7.53
50062	A07	M-013485-	testis expre	56156	TEX13B	1451	15.713	5.395
50062	A08	M-010397-	DEAD (Asp-	57062	DDX24	1198	15.943	5.625
50062	A09	M-010167-	testis expre	56157	TEX13A	876	23.744	13.426
50062	A10	M-013200-	T-box 20	57057	TBX20	1892	22.516	12.198
50062	A11	M-013487-	testis expre	56158	TEX12	2703	23.307	12.989
50062	A12	M-020970-	disrupter o	57050	SAS10	1196	18.98	8.662
50062	A13	M-013488-	testis expre	56159	TEX11	1301	14.527	4.209
50062	A14	M-031983-	phospholip	57047	PLSCR2	749	26.035	15.717
50062	A15	M-017227-	necdin-like	56160	NDNL2	1896	13.66	3.342
50062	A16	M-016732-	twisted gas	57045	TWSG1	1506	14.874	4.556
50062	A17	M-007026-	ring finger	56163	RNF17	3100	13.161	2.843
50062	A18	M-013767-	arginyl-tRN	57038	RARS2	1155	13.939	3.621
50062	A19	M-013489-	tudor doma	56165	TDRD1	1007	17.875	7.557
50062	A20	M-013766-	ankyrin rep	57037	ANKMY2	1393	14.645	4.327
50062	A21	M-014716-	melanoma-	56169	MLZE	2358	19.169	8.851
50062	A23	M-009928-	dynein, axo	56171	DNAH7	1899	18.167	7.849
50062	B02	M-024217-	KIAA1345 p	57545	KIAA1345	3452	10.689	0.371
50062	B04	M-021960-	KIAA1344	57544	KIAA1344	2156	11.085	0.767
50062	B05	M-020509-	chromoson	57091	C20orf32	1922	14.932	4.614
50062	B06	M-027054-	kelch doma	57542	KLHDC5	3362	15.616	5.298
50062	B07	M-020263-	PEST prote	57092	PCNP	2945	14.363	4.045
50062	B08	M-021564-	patched do	57540	PTCHD2	1196	16.054	5.736
50062	B09	M-007030-	tripartite m	57093	TRIM49	2766	15.51	5.192
50062	B10	M-014053-	WD repeat	57539	WDR35	5043	15.467	5.149
50062	B11	M-015482-	chromoson	57095	C1orf128	1543	16.202	5.884
50062	B12	M-023424-	KIAA1328	57536	KIAA1328	3332	15.276	4.958
50062	B13	M-016115-	poly (ADP-r	57097	PARP11	3601	12.608	2.29
50062	B14	M-010726-	KIAA1324	57535	KIAA1324	4346	12.954	2.636
50062	B15	M-007031-	transmemk	57101	TMEM16B	3095	21.357	11.039
50062	B16	M-014032-	TBC1 doma	57533	TBC1D14	2689	19.115	8.797
50062	B17	M-016596-	chromoson	57102	C12orf4	4285	23.617	13.299
50062	B18	M-007193-	HECT doma	57531	HACE1	2993	17.34	7.022
50062	B19	M-020597-	chromoson	57103	C12orf5	4349	16.142	5.824
50062	B20	M-014025-	cingulin	57530	CGN	5527	11.326	1.008
50062	B21	M-009003-	patatin-like	57104	PNPLA2	3695	17.564	7.246
50062	B23	M-009507-	N-acetyltra	57106	NAT14	2361	11.902	1.584
50062	C02	M-015879-	chromoson	57035	C1orf63	1729	9.2539	1.0641
50062	C04	M-007417-	solute carri	57030	SLC17A7	1661	7.5256	2.7924
50062	C05	M-020537-	motile sper	56180	MOSPD1	2023	10.331	0.013
50062	C06	M-018658-	esophagea	57020	MGC16824	3013	7.7332	2.5848
50062	C07	M-017152-	family with	56181	FAM54B	1947	6.5742	3.7438
50062	C08	M-020666-	cytokine in	57019	CIAPIN1	1496	7.6203	2.6977

50062	C09	M-023261- leiomodin	56203	LMOD3	2017	6.8914	3.4266
50062	C10	M-022565- coenzyme	57017	COQ9	2319	5.4765	4.8415
50062	C11	M-022243- KIAA1370	56204	KIAA1370	1517	7.2512	3.0668
50062	C12	M-016924- calcium bi	57010	CABP4	1760	7.5	2.818
50062	C13	M-010716- sushi doma	56241	SUSD2	833	8.5234	1.7946
50062	C14	M-010719- coiled-coil	57003	CCDC47	1928	4.8755	5.4425
50062	C15	M-014084- zinc finger	56242	ZNF253	1322	7.9425	2.3755
50062	C16	M-020924- chromoson	57002	C7orf36	2099	6.8604	3.4576
50062	C17	M-021358- butyrophili	56244	BTNL2	1298	3.3898	6.9282
50062	C18	M-007390- solute carri	56996	SLC12A9	3913	16.228	5.91
50062	C19	M-021062- chromoson	56245	C21orf62	1331	8.1142	2.2038
50062	C20	M-013785- tubby like	56995	TULP4	2430	8.1481	2.1699
50062	C21	M-018522- melanocor	56246	MRAP	3107	10.943	0.625
50062	C23	M-007027- ring finger	56254	RNF20	3202	10.587	0.269
50062	D02	M-014024- retrotransp	57529	RGAG1	3907	12.798	2.48
50062	D04	M-024347- potassium	57528	KCTD16	2980	8.6913	1.6267
50062	D05	M-008671- peptidogly	57115	PGLYRP4	2254	8.6957	1.6223
50062	D06	M-024773- protocadhe	57526	PCDH19	2053	5.7964	4.5216
50062	D07	M-013202- zinc finger	57116	ZNF695	1352	6.5828	3.7352
50062	D08	M-014020- CASK intera	57524	CASKIN1	1502	4.1278	6.1902
50062	D09	M-015624- integrator	57117	INTS12	2416	9.851	0.467
50062	D10	M-030275- KIAA1305	57523	KIAA1305	1459	5.5517	4.7663
50062	D11	M-013193- serine pept	57119	SPINLW1	3449	7.2775	3.0405
50062	D12	M-026974- SLIT-ROBO	57522	SRGAP1	891	5.8361	4.4819
50062	D13	M-020440- nucleopori	57122	NUP107	1482	5.8704	4.4476
50062	D14	M-007192- HECT, C2 a	57520	HECW2	1887	9.168	1.15
50062	D15	M-010720- CD248 mol	57124	CD248	2142	6.8627	3.4553
50062	D16	M-022228- START dom	57519	STARD9	2047	7.6209	2.6971
50062	D17	M-015628- plexin dom	57125	PLXDC1	1103	10.245	0.073
50062	D18	M-010725- serine inco	57515	SERINC1	2276	6.239	4.079
50062	D19	M-020431- CD177 mol	57126	CD177	3081	12.009	1.691
50062	D20	M-023577- Cdc42 GTPa	57514	CDGAP	2882	12.006	1.688
50062	D21	M-020429- Rh family,	57127	RHBG	2107	4.2715	6.0465
50062	D23	M-015656- LYR motif c	57128	LYRM4	2767	6.8305	3.4875
50062	E02	M-015878- translocase	56993	TOMM22	3828	7.8631	2.4549
50062	E04	M-020728- chromoson	56988	C8orf17	1346	7.9495	2.3685
50062	E05	M-010717- thioredoxi	56255	TXNDC13	2135	12.459	2.141
50062	E06	M-015289- bobby sox	56987	BBX	2270	18.722	8.404
50062	E07	M-015425- SERTA dom	56256	SERTAD4	2887	11.223	0.905
50062	E08	M-018957- DTW doma	56986	DTWD1	1545	8.5437	1.7743
50062	E09	M-016636- bin3, bicoi	56257	BCDIN3	1458	10.151	0.167
50062	E10	M-015485- chromoson	56985	C17orf48	2784	12.787	2.469
50062	E11	M-021056- chromoson	56260	C8orf44	2696	13.205	2.887
50062	E12	M-016678- tumor necr	56984	TNFSF5IP1	1932	9.265	1.053
50062	E13	M-013836- hypothetic	56261	RP5-1022P	1916	12.787	2.469
50062	E14	M-016137- KTEL (Lys-T	56983	KTELC1	1506	10.425	0.107
50062	E15	M-026211- leucine rich	56262	LRRC8A	698	11.748	1.43

50062	E16	M-007029- PR domain	56980	PRDM10	1607	10.019	0.299
50062	E17	M-005829- carboxypep	56265	CPXM1	2151	14.598	4.28
50062	E18	M-024110- storkhead	56977	STOX2	1917	10.016	0.302
50062	E19	M-015493- cysteine co	56267	CCBL2	991	10.696	0.378
50062	E20	M-013791- family with	56975	FAM20C	2096	8.2538	2.0642
50062	E21	M-021048- immunity-r	56269	IRGC	2298	9.5735	0.7445
50062	E23	M-017119- WDR45-like	56270	WDR45L	3377	10.305	0.013
50062	F02	M-014011- CASK intera	57513	CASKIN2	2265	16.071	5.753
50062	F04	M-026468- G protein-c	57512	GPR158	2112	11.6	1.282
50062	F05	M-013186- mitochond	57129	MRPL47	2378	13.541	3.223
50062	F06	M-014004- componen	57511	COG6	2680	9.2164	1.1016
50062	F07	M-004698- chromatin	57132	CHMP1B	1810	13.867	3.549
50062	F08	M-014000- exportin 5	57510	XPO5	1697	9.5463	0.7717
50062	F09	M-020422- mannosida	57134	MAN1C1	2092	12.141	1.823
50062	F10	M-006848- mitochond	57509	MTUS1	1754	15.165	4.847
50062	F11	M-013846- deleted in	57135	DAZ4	2265	8.2561	2.0619
50062	F12	M-013999- integrator	57508	INTS2	1600	7.25	3.068
50062	F13	M-013867- chromosom	57136	C20orf3	1418	14.386	4.068
50062	F14	M-024395- zinc finger	57507	ZNF608	2161	7.6816	2.6364
50062	F15	M-031226- ral guanine	57139	RGL3	2441	12.372	2.054
50062	F16	M-024237- virus-induc	57506	VISA	1646	11.543	1.225
50062	F17	M-006032- arginyl ami	57140	RNPEPL1	2991	10.598	0.28
50062	F18	M-022665- metastasis	57504	MTA3	4890	10.429	0.111
50062	F19	M-010721- reticulon 4	57142	RTN4	4644	16.947	6.629
50062	F20	M-010288- neuroligin	57502	NLGN4X	3741	8.2866	2.0314
50062	F21	M-018724- transmem	57146	TMEM159	4547	8.9729	1.3451
50062	F23	M-013847- KIAA1219	57148	KIAA1219	4592	21.341	11.023
50062	G02	M-013798- carcinoem	56971	CEACAM19	3234	8.9981	1.3199
50062	G04	M-023237- ataxin 7-lik	56970	ATXN7L3	2555	5.8317	4.4863
50062	G05	M-024780- brain expre	56271	BEXL1	3065	9.2333	1.0847
50062	G06	M-020638- ribosomal	56969	RPL23AP13	2074	7.3288	2.9892
50062	G07	M-019077- gastrokine	56287	GKN1	1690	5.0888	5.2292
50062	G08	M-020626- chromosom	56967	C14orf132	3208	17.425	7.107
50062	G09	M-007611- solute carri	56301	SLC7A10	1946	9.815	0.503
50062	G10	M-013797- poly (ADP-	56965	PARP6	1207	11.682	1.364
50062	G11	M-005170- methyltran	56339	METTL3	1257	7.2395	3.0785
50062	G12	M-022323- hypothetic	56964	LOC56964	2010	7.3632	2.9548
50062	G13	M-009763- protein arg	56341	PRMT8	2214	11.698	1.38
50062	G14	M-013796- RGM doma	56963	RGMA	2514	5.5688	4.7492
50062	G15	M-013236- calcium bi	56344	CABP5	2691	7.9153	2.4027
50062	G16	M-023905- Src homolo	56961	SHD	1760	3.2955	7.0225
50062	G17	M-013237- eukaryotic	56478	EIF4ENIF1	3575	8.1399	2.1781
50062	G18	M-026172- chromosom	56959	C9orf102	3300	10.909	0.591
50062	G19	M-013973- DnaJ (Hsp4	56521	DNAJC12	2438	8.3675	1.9505
50062	G20	M-008670- OTU domai	56957	OTUD7B	2192	9.0785	1.2395
50062	G21	M-008443- carbohydra	56548	CHST7	2845	6.6081	3.7099
50062	G23	M-009219- cytochrom	56603	CYP26B1	4122	8.5153	1.8027

50062	H02	M-028159-	KIAA1257	57501	KIAA1257	2396	14.19	3.872
50062	H04	M-022984-	kinase D-in	57498	KIDINS220	2068	7.3017	3.0163
50062	H05	M-015432-	LYR motif c	57149	LYRM1	2383	13.512	3.194
50062	H06	M-025093-	leucine ric	57497	LRFN2	2919	6.9202	3.3978
50062	H07	M-018820-	chromoson	57150	C6orf162	1703	8.0446	2.2734
50062	H08	M-023887-	KIAA1239	57495	KIAA1239	1350	11.852	1.534
50062	H09	M-020384-	lysozyme-li	57151	LYZL6	2077	15.166	4.848
50062	H10	M-027036-	family with	57494	FAM80B	2141	12.891	2.573
50062	H11	M-013188-	secreted L	57152	SLURP1	1382	12.084	1.766
50062	H12	M-023585-	HEG homol	57493	HEG1	1668	9.5324	0.7856
50062	H13	M-018034-	solute carri	57153	SLC44A2	1572	11.641	1.323
50062	H14	M-013970-	AT rich inte	57492	ARID1B	1816	13.767	3.449
50062	H15	M-021981-	transmem	57156	TMEM63C	1693	8.3875	1.9305
50062	H16	M-021619-	outer dens	57489	ODF2L	1906	11.385	1.067
50062	H17	M-013189-	junctophili	57158	JPH2	930	12.258	1.94
50062	H18	M-025231-	family with	57488	FAM62B	1959	7.9632	2.3548
50062	H19	M-007032-	tripartite m	57159	TRIM54	2134	3.8425	6.4755
50062	H20	M-025438-	ataxin 7-lik	57485	ATXN7L1	2292	12.391	2.073
50062	H21	M-013839-	pellino hon	57161	PELI2	1930	5.544	4.774
50062	H23	M-013814-	pellino hon	57162	PELI1	1786	3.5274	6.7906
50062	I02	M-031943-	LIM homec	56956	LHX9	2019	5.9435	4.3745
50062	I04	M-020547-	matrix, ext	56955	MEPE	3189	6.8046	3.5134
50062	I05	M-018108-	ERO1-like b	56605	ERO1LB	2393	5.14	5.178
50062	I06	M-013214-	5',3'-nucleo	56953	NT5M	2294	15.039	4.721
50062	I07	M-012869-	small EDRK	56617	SERF1B	1212	8.0033	2.3147
50062	I08	M-015695-	phosphorib	56952	PRTFDC1	2788	11.442	1.124
50062	I09	M-005229-	N-acylsphir	56624	ASAH2	2578	12.878	2.56
50062	I10	M-020220-	chromoson	56951	C5orf15	1592	8.794	1.524
50062	I11	M-019191-	eukaryotic	56648	EIF5A2	2189	9.9589	0.3591
50062	I12	M-004914-	XPA binding	56949	XAB2	815	10.92	0.602
50062	I13	M-005243-	transmemb	56649	TMPRSS4	2016	16.171	5.853
50062	I14	M-020322-	chromoson	56948	C14orf124	1757	5.1793	5.1387
50062	I15	M-020682-	claudin dor	56650	CLDND1	1658	11.46	1.142
50062	I16	M-018261-	chromoson	56947	C2orf33	1804	9.7561	0.5619
50062	I17	M-014717-	chromoson	56651	C18orf2	2113	9.2286	1.0894
50062	I18	M-004081-	chromoson	56946	C11orf30	1289	7.758	2.56
50062	I19	M-009954-	neural prol	56654	NPDC1	2237	12.427	2.109
50062	I20	M-013219-	mitochond	56945	MRPS22	3643	10.211	0.107
50062	I21	M-009850-	polymerase	56655	POLE4	2030	9.3596	0.9584
50062	I23	M-007028-	tripartite m	56658	TRIM39	2541	12.554	2.236
50062	J02	M-010713-	ring finger	57484	RNF150	2912	9.1346	1.1834
50062	J04	M-024133-	KIAA1211 p	57482	KIAA1211	3175	8.5039	1.8141
50062	J05	M-017864-	aspartate b	57168	ASPHD2	2410	14.274	3.956
50062	J06	M-025003-	KIAA1210 p	57481	RP13-347D	1289	12.49	2.172
50062	J07	M-014074-	zinc finger,	57169	ZNFX1	1868	9.2612	1.0568
50062	J08	M-024745-	pleckstrin h	57480	PLEKHG1	1968	8.8415	1.4765
50062	J09	M-010493-	coronin, ac	57175	CORO1B	1632	10.233	0.085

50062	J10	M-023777- proline rich	57479	PRR12	3118	8.7556	1.5624
50062	J11	M-008268- valyl-tRNA	57176	VARS2	1509	11.597	1.279
50062	J12	M-024692- shroom far	57477	SHROOM4	1493	11.253	0.935
50062	J13	M-007034- zinc finger,	57178	ZMIZ1	1897	10.596	0.278
50062	J14	M-026529- GRAM dom	57476	GRAMD1B	2575	11.223	0.905
50062	J15	M-015433- KIAA1191	57179	KIAA1191	2398	16.972	6.654
50062	J16	M-030302- pleckstrin h	57475	PLEKHH1	1745	7.2206	3.0974
50062	J17	M-007565- solute carri	57181	SLC39A10	2610	8.5824	1.7356
50062	J18	M-013937- zinc finger	57474	ZNF490	2748	12.154	1.836
50062	J19	M-028250- ankyrin rep	57182	ANKRD50	3067	6.5536	3.7644
50062	J20	M-013934- zinc finger	57473	ZNF512B	3154	12.143	1.825
50062	J21	M-013849- chromoson	57184	C15orf17	3394	12.817	2.499
50062	J23	M-020359- NIPA-like d	57185	NPAL3	3150	8.5714	1.7466
50062	K02	M-020325- olfactomec	56944	OLFML3	2918	22.378	12.06
50062	K04	M-018808- enhancer o	56943	ENY2	3365	23.655	13.337
50062	K05	M-006256- potassium	56660	KCNK12	2669	20.382	10.064
50062	K06	M-020333- chromoson	56941	C3orf37	2494	20.249	9.931
50062	K07	M-015135- pannexin 2	56666	PANX2	1627	15.12	4.802
50062	K08	M-010501- transmemb	56937	TMEPAI	1351	18.653	8.335
50062	K09	M-015057- mucin 13, c	56667	MUC13	1763	21.044	10.726
50062	K10	M-020411- chromoson	56936	C14orf162	1628	22.789	12.471
50062	K11	M-015631- chromoson	56672	C11orf17	1999	26.413	16.095
50062	K12	M-020414- chromoson	56935	C11orf75	2142	30.719	20.401
50062	K13	M-020701- chromoson	56673	C11orf16	1052	32.414	22.096
50062	K14	M-008550- carbonic ar	56934	CA10	1712	32.535	22.217
50062	K15	M-020706- TMEM9 do	56674	TMEM9B	1050	31.619	21.301
50062	K16	M-031942- dihydrouric	56931	DUS3L	2000	25.35	15.032
50062	K17	M-013871- nuclear rec	56675	NRIP3	3534	18.308	7.99
50062	K18	M-019130- fem-1 hom	56929	FEM1C	963	18.588	8.27
50062	K19	M-008980- achaete-scu	56676	ASCL3	1474	30.258	19.94
50062	K20	M-006041- signal pept	56928	SPPL2B	2285	23.807	13.489
50062	K21	M-016756- SAR1 gene	56681	SAR1A	2886	19.889	9.571
50062	K23	M-013838- chromoson	56683	C21orf59	2954	16.994	6.676
50062	L02	M-019101- CCR4-NOT	57472	CNOT6	4165	16.086	5.768
50062	L04	M-027986- KIAA1189	57471	KIAA1189	3585	13.947	3.629
50062	L05	M-024244- chromoson	57186	C20orf74	3949	24.183	13.865
50062	L06	M-010724- leucine rich	57470	LRRC47	4256	10.949	0.631
50062	L07	M-025006- THO compl	57187	THOC2	2765	15.841	5.523
50062	L08	M-031129- KIAA1183 p	57469	KIAA1183	1801	13.604	3.286
50062	L09	M-015893- ATPase, Cla	57194	ATP10A	4508	18.722	8.404
50062	L10	M-007386- solute carri	57468	SLC12A5	4258	18.483	8.165
50062	L11	M-018004- ATPase, Cla	57205	ATP10D	3412	15.709	5.391
50062	L12	M-015488- hedgehog a	57467	HHATL	4240	20.094	9.776
50062	L13	M-014069- zinc finger	57209	ZNF248	4450	18.697	8.379
50062	L14	M-032088- splicing fac	57466	SFRS15	4657	19.54	9.222
50062	L15	M-025844- solute carri	57210	SLC45A4	2866	18.842	8.524
50062	L16	M-022880- TBC1 doma	57465	TBC1D24	2143	23.565	13.247

50062	L17	M-027524-	KIAA0495	57212	KIAA0495	4112	16.732	6.414
50062	L18	M-025451-	family with	57464	FAM40B	3964	23.36	13.042
50062	L19	M-013852-	chromosom	57213	C13orf1	5885	10.501	0.183
50062	L20	M-021515-	adhesion m	57463	AMIGO1	5075	11.488	1.17
50062	L21	M-022291-	KIAA1199	57214	KIAA1199	4247	19.543	9.225
50062	L23	M-021450-	THAP doma	57215	THAP11	2949	10.885	0.567
50062	M02	M-005530-	G protein-c	56927	GPR108	2460	5.1626	5.1554
50062	M04	M-010718-	nicalin hom	56926	NCLN	2658	16.14	5.822
50062	M05	M-013173-	junctophili	56704	JPH1	2722	14.475	4.157
50062	M06	M-015587-	latexin	56925	LXN	2106	10.114	0.204
50062	M07	M-013208-	resistin	56729	RETN	3344	15.102	4.784
50062	M08	M-020454-	sema doma	56920	SEMA3G	2254	13.398	3.08
50062	M09	M-018927-	SLC2A4 reg	56731	SLC2A4RG	2203	6.128	4.19
50062	M10	M-017205-	DEAH (Asp-	56919	DHX33	2910	8.0069	2.3111
50062	M11	M-017899-	BarH-like 1	56751	BARHL1	2748	7.0961	3.2219
50062	M12	M-007323-	hypothetic	56918	DKFZp547H	2315	5.9179	4.4001
50062	M13	M-022134-	formin 2	56776	FMN2	2172	12.983	2.665
50062	M14	M-023769-	Meis home	56917	MEIS3	1599	3.8149	6.5031
50062	M15	M-017449-	zinc finger	56829	ZC3HAV1	2321	16.415	6.097
50062	M16	M-020482-	exosome c	56915	EXOSC5	2048	17.773	7.455
50062	M17	M-013217-	interferon,	56832	IFNK	2318	6.6005	3.7175
50062	M18	M-020490-	core 1 synt	56913	C1GALT1	3061	8.2326	2.0854
50062	M19	M-013218-	SLAM famil	56833	SLAMF8	3143	11.295	0.977
50062	M20	M-015611-	chromosom	56912	C11orf60	3229	9.9412	0.3768
50062	M21	M-016241-	transcriptio	56849	TCEAL7	2586	10.17	0.148
50062	M23	M-021215-	chromosom	56851	C15orf24	2234	5.9087	4.4093
50062	N02	M-026129-	KIAA1161	57462	KIAA1161	2565	10.799	0.481
50062	N04	M-013894-	ISY1 splicin	57461	ISY1	1574	4.1931	6.1249
50062	N05	M-010581-	vang-like 2	57216	VANGL2	3445	15.53	5.212
50062	N06	M-013877-	transmemb	57458	TMCC3	3258	7.9804	2.3376
50062	N07	M-027882-	tetratricop	57217	TTC7A	2487	12.224	1.906
50062	N08	M-013876-	KIAA1143	57456	KIAA1143	1886	10.127	0.191
50062	N09	M-013854-	KIAA1244	57221	KIAA1244	2905	14.699	4.381
50062	N10	M-021445-	REX1, RNA	57455	REXO1	2831	4.2388	6.0792
50062	N11	M-027284-	SMEK hom	57223	SMEK2	2658	4.3642	5.9538
50062	N12	M-007884-	Down synd	57453	DSCAML1	2085	11.511	1.193
50062	N13	M-015717-	LYR motif c	57226	LYRM2	1515	9.901	0.417
50062	N14	M-021972-	UDP-N-ace	57452	GALNTL1	2439	13.612	3.294
50062	N15	M-013190-	sorting nex	57231	SNX14	1551	6.7054	3.6126
50062	N16	M-024304-	odz, odd O	57451	ODZ2	2155	5.9397	4.3783
50062	N17	M-024656-	zinc finger	57232	ZNF630	836	8.2536	2.0644
50062	N18	M-013873-	pleckstrin	57449	PLEKHG5	2780	3.3094	7.0086
50062	N19	M-021726-	family with	57234	FAM91A2	1762	3.9728	6.3452
50062	N20	M-013533-	NDRG fami	57446	NDRG3	3624	10.017	0.301
50062	N21	M-027537-	KIAA0492	57238	KIAA0492	2110	7.6303	2.6877
50062	N23	M-019335-	hypothetic	57245	FLJ20209	1957	4.3945	5.9235
50062	O02	M-017901-	chromosom	56911	C21orf7	1355	5.0923	5.2257

50062	O04	M-017289-	START dom	56910	STARD7	2533	11.291	0.973
50062	O05	M-013824-	bruno-like 4	56853	BRUNOL4	2650	3.9623	6.3557
50062	O06	M-023397-	spire homc	56907	SPIRE1	2357	6.6186	3.6994
50062	O07	M-013805-	follistatin-li	56884	FSTL5	3297	10.252	0.066
50062	O08	M-021460-	THAP doma	56906	THAP10	2749	10.113	0.205
50062	O09	M-006632-	UDP-glucos	56886	UGCGL1	1971	6.4434	3.8746
50062	O10	M-031882-	chromoson	56905	C15orf39	2523	4.7166	5.6014
50062	O11	M-017900-	potassium	56888	KCMF1	2532	9.4787	0.8393
50062	O12	M-015810-	SH3-domai	56904	SH3GLB2	2019	5.9931	4.3249
50062	O13	M-010220-	transmemb	56889	TM9SF3	3204	7.5531	2.7649
50062	O14	M-009500-	poly(A) pol	56903	PAPOLB	1936	8.936	1.382
50062	O15	M-021184-	lectin, gala	56891	LGALS14	1716	12.238	1.92
50062	O16	M-018033-	partner of	56902	PNO1	3278	5.2471	5.0709
50062	O17	M-015557-	chromoson	56892	C8orf4	2858	17.74	7.422
50062	O18	M-008192-	ankyrin rep	56899	ANKS1B	2500	5.28	5.038
50062	O19	M-021178-	ubiquilin 4	56893	UBQLN4	852	7.7465	2.5715
50062	O20	M-008694-	3-hydroxyb	56898	BDH2	4463	7.7974	2.5206
50062	O21	M-008581-	dihydropyr	56896	DPYSL5	3813	6.5565	3.7615
50062	O23	M-010072-	Werner hel	56897	WRNIP1	2622	5.6445	4.6735
50062	P02	M-007466-	solute carri	57419	SLC24A3	3080	6.3312	3.9868
50062	P04	M-021451-	WD repeat	57418	WDR18	2309	5.8467	4.4713
50062	P05	M-007580-	solute carri	57282	SLC4A10	2681	9.3995	0.9185
50062	P06	M-017892-	chromoson	57415	C3orf14	1961	4.9465	5.3715
50062	P07	M-024130-	KIAA0114	57291	KIAA0114	3202	7.183	3.135
50062	P08	M-020778-	rhomboid d	57414	RHBDD2	2415	4.6791	5.6389
50062	P09	M-008481-	CSRP2 bind	57325	CSRP2BP	3736	3.1317	7.1863
50062	P10	M-009525-	arsenic (+3	57412	AS3MT	1559	7.9538	2.3642
50062	P11	M-017962-	reticulocalb	57333	RCN3	2628	4.2618	6.0562
50062	P12	M-020761-	leucine-rich	57408	LRTM1	3016	7.4271	2.8909
50062	P13	M-020716-	zinc finger	57335	ZNF286A	3096	7.2351	3.0829
50062	P14	M-020759-	NmrA-like f	57407	NMRAL1	1932	4.9689	5.3491
50062	P15	M-007035-	zinc finger	57336	ZNF287	2820	3.2624	7.0556
50062	P16	M-009929-	cytochrome	57404	CYP20A1	1898	3.7935	6.5245
50062	P17	M-006035-	SUMO1/se	57337	SENP7	2641	4.8466	5.4714
50062	P18	M-015683-	transmemb	57393	TMEM27	2292	2.0942	8.2238
50062	P19	M-020719-	zinc finger	57343	ZNF304	2971	4.7122	5.6058
50062	P20	M-020748-	MRS2-like,	57380	MRS2L	3393	5.0693	5.2487
50062	P21	M-020721-	tweety hor	57348	TTYH1	2215	4.1535	6.1645
50062	P23	M-005439-	G protein-c	56834	GPR137	4437	2.0284	8.2896
					MAD		10.318	3.318
					MAD3			9.954
					MADc			4.91064
50062	C22	Human4 Pc	RNAi	empty				
50062	D22	Human4 Pc	RNAi	empty				
50062	E22	Human4 Pc	RNAi	empty				
50062	F22	Human4 Pc	RNAi	empty				

50062	G22	Human4 Pc	RNAi	empty
50062	H22	Human4 Pc	RNAi	empty
50062	I22	Human4 Pc	RNAi	empty
50062	J22	Human4 Pc	RNAi	empty

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.168003	1689	10.243	0.05	0.00982	2130	7.8404	0.9067	-0.22821
0.64289	2313	15.045	4.852	0.952948	2037	16.74	7.9929	2.011774
0.77159	1142	14.448	4.255	0.835695	946	12.156	3.4089	0.858004
1.533405	1740	14.828	4.635	0.910328	1895	11.768	3.0209	0.760346
1.098635	989	7.6845	2.5085	-0.49268	216	18.056	9.3089	2.343005
1.145472	855	9.9415	0.2515	-0.0494	1366	11.127	2.3799	0.599009
2.734063	1071	18.861	8.668	1.702422	1692	20.745	11.9979	3.019813
2.483994	1298	22.342	12.149	2.386101	1862	14.071	5.3239	1.34
2.645073	1822	27.387	17.194	3.376954	2532	25.118	16.3709	4.120476
1.763925	1347	15.219	5.026	0.987122	1414	11.245	2.4979	0.628709
0.857118	1487	14.19	3.997	0.785023	1743	17.671	8.9239	2.246103
3.200601	1027	22.006	11.813	2.32011	648	10.648	1.9009	0.478447
0.680563	1786	22.004	11.811	2.319717	1353	15.891	7.1439	1.798085
0.927781	996	23.193	13	2.55324	1293	16.396	7.6489	1.925191
0.578947	2210	17.964	7.771	1.526248	2450	12.204	3.4569	0.870085
0.737378	1596	16.416	6.223	1.222216	1424	21.067	12.3199	3.100859
1.538903	863	16.454	6.261	1.22968	1043	17.162	8.4149	2.11799
0.881148	1140	14.912	4.719	0.926826	945	16.085	7.3379	1.846914
1.802413	2126	13.17	2.977	0.584692	1629	19.091	10.3439	2.60351
1.598366	1951	14.454	4.261	0.836873	1575	17.27	8.5229	2.145173
0.07555	1817	14.915	4.722	0.927415	2803	9.7396	0.9925	0.249807
0.156191	2256	14.805	4.612	0.905811	3733	10.822	2.0749	0.522242
0.939592	1477	17.197	7.004	1.375607	2006	12.463	3.7159	0.935274
1.078882	3245	12.573	2.38	0.467439	2834	9.0332	0.2861	0.07201
0.823722	2760	9.3116	0.8814	-0.17311	3624	9.7406	0.9935	0.250059
1.168076	1331	9.9174	0.2756	-0.05413	1536	10.417	1.6699	0.420306
1.057296	2782	13.983	3.79	0.744368	3251	7.167	1.5801	-0.3977
1.048539	5125	18.341	8.148	1.600292	5035	12.612	3.8649	0.972777
1.198214	1601	12.992	2.799	0.549732	1220	10.902	2.1549	0.542378
1.009644	2910	22.302	12.109	2.378245	2605	16.238	7.4909	1.885423
0.466334	2022	9.8912	0.3018	-0.05927	2146	10.158	1.4109	0.355117
0.536794	3463	11.031	0.838	0.164586	3541	5.5916	3.1555	-0.79422
2.247976	2130	16.385	6.192	1.216128	2985	14.137	5.3899	1.356612
1.791416	2669	15.062	4.869	0.956287	2514	10.7	1.9529	0.491535
2.708201	3184	19.881	9.688	1.902753	2848	10.288	1.5409	0.387837
1.429956	2709	6.866	3.327	-0.65343	3256	6.6646	2.0825	-0.52416
1.185996	2867	11.789	1.596	0.313459	2513	8.3963	0.3508	-0.08829
0.205269	4165	13.902	3.709	0.728459	4441	8.2639	0.4832	-0.12162
1.475571	4282	14.409	4.216	0.828035	3401	9.703	0.9559	0.240595
0.322565	2829	8.024	2.169	-0.426	1770	7.2881	1.459	-0.36722
-0.21669	1222	12.357	2.164	0.425016	1414	5.0919	3.6552	-0.92
-0.56864	1704	7.6878	2.5052	-0.49203	1638	5.7998	2.9473	-0.74182
0.002647	2443	8.3504	1.8426	-0.36189	2341	9.4831	0.736	0.185248
-0.52637	4984	8.9085	1.2845	-0.25228	2087	6.229	2.5181	-0.63379
-0.76239	2073	7.2359	2.9571	-0.58078	2177	5.9256	2.8215	-0.71016
-0.54936	1930	10.984	0.791	0.155355	1301	7.2252	1.5219	-0.38305

-0.69779	1740	7.4713	2.7217	-0.53455	2044	7.8278	0.9193	-0.23138
-0.98592	2602	7.6095	2.5835	-0.50741	1752	6.6781	2.069	-0.52076
-0.62452	1529	9.7449	0.4481	-0.08801	1263	7.2842	1.4629	-0.3682
-0.57386	1533	7.5669	2.6261	-0.51577	1476	7.9268	0.8203	-0.20647
-0.36545	893	8.8466	1.3464	-0.26444	758	9.6306	0.8835	0.222373
-1.10831	1455	5.7045	4.4885	-0.88156	1594	6.5245	2.2226	-0.55942
-0.48375	1879	5.801	4.392	-0.8626	909	7.3707	1.3764	-0.34643
-0.7041	1666	8.5834	1.6096	-0.31613	1742	9.1274	0.3803	0.09572
-1.41085	1675	5.3731	4.8199	-0.94664	1414	4.7383	4.0088	-1.009
1.203509	3581	16.308	6.115	1.201005	2294	9.9826	1.2355	0.310969
-0.44878	1499	9.2061	0.9869	-0.19383	875	10.857	2.1099	0.531052
-0.44188	3201	12.777	2.584	0.507506	1653	9.6794	0.9323	0.234655
0.127275	2846	9.7681	0.4249	-0.08345	3053	7.3698	1.3773	-0.34666
0.054779	2115	11.631	1.438	0.282428	1956	9.2025	0.4554	0.114622
0.505026	2274	11.478	1.285	0.252378	2167	11.767	3.0199	0.760094
-0.33126	2571	7.9347	2.2583	-0.44354	3571	7.1689	1.5782	-0.39723
-0.33036	1723	7.8932	2.2998	-0.45169	1573	8.1373	0.6098	-0.15348
-0.92078	2320	9.2241	0.9689	-0.19029	1466	5.116	3.6311	-0.91393
-0.76063	1425	4	6.193	-1.21632	1895	7.3351	1.412	-0.35539
-1.26057	1624	5.4187	4.7743	-0.93769	1558	4.4288	4.3183	-1.0869
-0.0951	1602	7.8652	2.3278	-0.45719	2001	4.8476	3.8995	-0.98149
-0.97061	793	12.736	2.543	0.499453	711	6.6104	2.1367	-0.5378
-0.61917	2388	8.2915	1.9015	-0.37346	2232	6.1828	2.5643	-0.64542
-0.91269	1822	7.5741	2.6189	-0.51436	2092	5.7839	2.9632	-0.74582
-0.90571	1176	5.7823	4.4107	-0.86628	1489	6.313	2.4341	-0.61265
-0.23419	1188	9.2593	0.9337	-0.18338	1904	6.3025	2.4446	-0.61529
-0.70364	1529	9.3525	0.8405	-0.16508	1101	7.9019	0.8452	-0.21273
-0.54924	1093	4.849	5.344	-1.04958	1664	3.9062	4.8409	-1.21843
-0.01487	1193	9.8072	0.3858	-0.07577	1563	7.1657	1.5814	-0.39803
-0.83065	1724	7.1346	3.0584	-0.60068	1709	5.3833	3.3638	-0.84665
0.344354	2199	11.187	0.994	0.195225	3368	8.9074	0.1603	0.040347
0.343743	3171	13.34	3.147	0.61808	3090	9.1909	0.4438	0.111702
-1.23131	1121	9.3666	0.8264	-0.16231	1508	8.3554	0.3917	-0.09859
-0.71019	1988	5.3823	4.8107	-0.94484	2524	5.0713	3.6758	-0.92518
-0.49991	1347	8.7602	1.4328	-0.28141	3790	9.1029	0.3558	0.089553
-0.48232	908	8.0396	2.1534	-0.42293	1487	6.187	2.5601	-0.64436
0.435992	963	15.369	5.176	1.016582	2133	10.314	1.5669	0.394381
1.711386	1618	20.828	10.635	2.088747	2558	18.296	9.5489	2.403412
0.184294	1874	12.593	2.4	0.471367	2957	10.754	2.0069	0.505127
-0.36132	1301	7.5327	2.6603	-0.52249	2193	10.078	1.3309	0.334981
-0.03401	700	13.143	2.95	0.579389	1526	12.713	3.9659	0.998198
0.502786	1705	10.616	0.423	0.083079	2934	13.463	4.7159	1.186969
0.587907	1464	16.94	6.747	1.325132	3489	14.044	5.2969	1.333204
-0.21443	987	11.854	1.661	0.326226	2664	6.2688	2.4783	-0.62378
0.502786	1312	6.4024	3.7906	-0.74449	2148	5.4004	3.3467	-0.84235
0.021789	1533	8.0235	2.1695	-0.4261	2416	6.2086	2.5385	-0.63893
0.291204	544	20.772	10.579	2.077748	1108	13.899	5.1519	1.296708

-0.06089	682	12.317	2.124	0.41716	1114	11.041	2.2939	0.577364
0.871577	1792	23.717	13.524	2.656155	2778	15.299	6.5519	1.649082
-0.0615	1591	15.211	5.018	0.985551	4342	10.871	2.1239	0.534575
0.076976	1267	22.81	12.617	2.478018	1958	13.534	4.7869	1.20484
-0.42035	1707	8.0844	2.1086	-0.41414	2803	4.7449	4.0022	-1.00733
-0.15161	3548	11.415	1.222	0.240005	3013	5.1444	3.6027	-0.90678
-0.00265	2385	8.7631	1.4299	-0.28084	2154	9.5172	0.7701	0.19383
1.171538	2007	9.5167	0.6763	-0.13283	3053	5.7976	2.9495	-0.74237
0.261066	1604	8.4165	1.7765	-0.34891	2655	3.0132	5.7339	-1.44319
0.65633	1754	10.718	0.525	0.103112	2736	6.6886	2.0585	-0.51811
-0.22433	2821	7.7278	2.4652	-0.48417	4236	5.4769	3.2702	-0.82309
0.722716	2163	15.996	5.803	1.139727	2738	8.7655	0.0184	0.004631
-0.15715	1874	6.5635	3.6295	-0.71284	3238	2.7486	5.9985	-1.50979
0.371235	1515	9.4389	0.7541	-0.14811	2079	4.0404	4.7067	-1.18465
0.98704	1159	11.821	1.628	0.319744	2056	4.8638	3.8833	-0.97741
-0.41988	2597	11.359	1.166	0.229006	2312	4.8875	3.8596	-0.97144
-0.62477	1537	8.8484	1.3446	-0.26408	1693	4.7253	4.0218	-1.01227
0.828405	1060	6.9811	3.2119	-0.63083	1042	5.7582	2.9889	-0.75229
-0.53688	1603	6.1135	4.0795	-0.80123	1979	2.8297	5.9174	-1.48938
0.418275	1391	14.019	3.826	0.751438	1995	7.2682	1.4789	-0.37223
0.249458	1203	14.63	4.437	0.87144	1653	5.6261	3.121	-0.78554
0.057019	1439	7.7832	2.4098	-0.47329	2530	4.2292	4.5179	-1.13713
0.022604	2642	10.371	0.178	0.03496	3483	6.8332	1.9139	-0.48172
1.349926	3510	21.339	11.146	2.189109	3709	10.164	1.4169	0.356627
-0.41367	2716	14.838	4.645	0.912292	2546	5.6952	3.0519	-0.76815
-0.27392	3591	11.445	1.252	0.245897	3062	3.8863	4.8608	-1.22344
2.244718	2761	23.434	13.241	2.600573	3109	13.477	4.7299	1.190493
-0.26878	2040	4.3627	5.8303	-1.14509	3005	5.5241	3.223	-0.81121
-0.91359	1431	6.4291	3.7639	-0.73924	2037	3.2892	5.4579	-1.37373
-0.22089	1405	12.598	2.405	0.472349	2609	6.2476	2.4995	-0.62911
-0.60872	1344	7.5149	2.6781	-0.52599	1521	7.8895	0.8576	-0.21585
-1.06487	1028	8.9494	1.2436	-0.24425	1388	6.268	2.4791	-0.62398
1.447266	2564	11.817	1.624	0.318959	3548	10.147	1.3999	0.352348
-0.10243	1283	11.613	1.42	0.278892	940	5.9574	2.7897	-0.70215
0.277764	876	10.959	0.766	0.150445	1189	6.3078	2.4393	-0.61396
-0.6269	1538	5.2666	4.9264	-0.96756	1428	7.7731	0.974	-0.24515
-0.60171	1639	7.0165	3.1765	-0.62387	2051	7.1672	1.5799	-0.39765
0.281022	1242	12.56	2.367	0.464886	993	4.6324	4.1147	-1.03565
-0.96712	2606	7.2141	2.9789	-0.58507	2111	6.5846	2.1625	-0.54429
-0.48928	2014	8.3913	1.8017	-0.35386	2631	6.5374	2.2097	-0.55617
-1.43006	1548	9.6899	0.5031	-0.09881	1252	9.0256	0.2785	0.070097
-0.44355	2599	8.8496	1.3434	-0.26385	2195	9.0661	0.319	0.080291
0.120351	2761	18.363	8.17	1.604613	3022	13.236	4.4889	1.129834
-0.3972	1717	8.7944	1.3986	-0.27469	1874	9.8719	1.1248	0.283107
-0.25241	1806	10.41	0.217	0.042619	2192	8.8504	0.1033	0.026
-0.75548	2276	7.3814	2.8116	-0.55221	3355	9.8361	1.089	0.274096
-0.3671	3415	9.4583	0.7347	-0.1443	2530	7.8261	0.921	-0.23181

0.788492	1682	14.388	4.195	0.823911	3022	8.6036	0.1435	-0.03612
-0.61424	1871	6.6275	3.5655	-0.70028	3006	8.1836	0.5635	-0.14183
0.650424	1890	14.339	4.146	0.814287	2762	8.6894	0.0577	-0.01452
-0.69193	1629	10.866	0.673	0.132179	2072	5.4537	3.2934	-0.82893
-0.46295	1596	14.474	4.281	0.840802	2031	6.0069	2.7402	-0.6897
0.312383	969	15.273	5.08	0.997728	2741	7.7344	1.0127	-0.25489
0.987244	1281	13.505	3.312	0.650487	3098	5.326	3.4211	-0.86107
0.523964	2644	16.188	5.995	1.177436	3183	10.902	2.1549	0.542378
0.359627	1546	10.867	0.674	0.132376	3250	5.8462	2.9009	-0.73014
-0.15998	1808	11.007	0.814	0.159872	2773	6.383	2.3641	-0.59503
0.269415	1423	14.336	4.143	0.813698	2519	6.4708	2.2763	-0.57293
0.702352	1937	12.494	2.301	0.451923	3111	8.7753	0.0282	0.007098
-0.39313	1589	11.076	0.883	0.173424	3704	4.1037	4.6434	-1.16872
0.217283	2027	13.074	2.881	0.565837	3917	9.7268	0.9797	0.246586
0.395061	661	8.1694	2.0236	-0.39744	2137	11.09	2.3429	0.589697
-0.47953	2143	14.559	4.366	0.857496	3729	8.5278	0.2193	-0.0552
-1.31867	1924	7.8482	2.3448	-0.46053	2784	5.5675	3.1796	-0.80029
0.422145	1857	14.486	4.293	0.843158	3458	8.7623	0.0152	0.003826
-0.97217	1544	8.1606	2.0324	-0.39917	3326	8.659	0.0881	-0.02217
-1.38283	1252	9.6645	0.5285	-0.1038	1935	5.6331	3.114	-0.78378
-0.89082	2022	6.3798	3.8132	-0.74892	1517	6.0646	2.6825	-0.67517
-0.71547	2207	8.2465	1.9465	-0.3823	2600	8.1154	0.6317	-0.159
-1.05445	2299	9.3954	0.7976	-0.15665	2319	7.0289	1.7182	-0.43246
0.961382	1607	13.69	3.497	0.686822	1460	12.192	3.4449	0.867065
-0.47136	897	7.4693	2.7237	-0.53494	1025	9.561	0.8139	0.204855
0.228891	1448	9.7376	0.4554	-0.08944	2119	11.42	2.6729	0.672756
0.521317	1519	11.916	1.723	0.338402	2225	7.0112	1.7359	-0.43692
-0.31035	1210	11.901	1.708	0.335456	1463	11.415	2.6679	0.671498
-0.07313	1344	8.7798	1.4132	-0.27756	2220	10.901	2.1539	0.542126
0.122591	531	10.546	0.353	0.06933	731	12.312	3.5649	0.897268
1.191902	1421	16.186	5.993	1.177044	1670	13.413	4.6659	1.174384
-1.04644	1282	8.1123	2.0807	-0.40866	1555	12.347	3.5999	0.906077
0.232556	1509	16.435	6.242	1.225948	2585	14.855	6.1079	1.537329
-0.11443	2209	6.3377	3.8553	-0.75719	3175	8.4094	0.3377	-0.085
-0.22184	882	5.3288	4.8642	-0.95534	3301	13.329	4.5819	1.153242
-0.52132	1340	7.7612	2.4318	-0.47761	1626	10.086	1.3389	0.336995
0.429476	1798	7.119	3.074	-0.60374	2521	7.4574	1.2897	-0.32461
-0.02179	1843	5.1546	5.0384	-0.98956	3601	6.8592	1.8879	-0.47518
-0.19517	1632	5.2083	4.9847	-0.97901	2585	9.7099	0.9628	0.242332
0.455338	2367	5.4499	4.7431	-0.93156	3581	12.734	3.9869	1.003483
-0.24099	2614	6.8095	3.3835	-0.66453	2170	10.876	2.1289	0.535834
-0.36942	2393	3.9281	6.2649	-1.23045	3783	9.9392	1.1921	0.300046
0.805598	3456	16.233	6.04	1.186275	2510	18.486	9.7389	2.451234
0.442305	1267	10.734	0.541	0.106254	1830	15.628	6.8809	1.731889
-0.21521	2682	11.894	1.701	0.334082	2705	11.682	2.9349	0.7387
-0.30067	1886	8.6957	1.4973	-0.29407	1967	9.2018	0.4547	0.114446
-0.01731	2057	5.0073	5.1857	-1.01849	1643	8.4601	0.287	-0.07224

-0.31817	2800	9.5357	0.6573	-0.1291	3311	6.6445	2.1026	-0.52921
0.260455	1512	11.31	1.117	0.219382	1816	9.8568	1.1097	0.279306
0.190403	2922	12.012	1.819	0.357257	2919	14.697	5.9499	1.497561
0.056612	3070	9.3485	0.8445	-0.16586	2730	9.8535	1.1064	0.278476
0.184294	3630	11.267	1.074	0.210937	3349	10.749	2.0019	0.503869
1.355017	3353	18.67	8.477	1.664909	3764	17.96	9.2129	2.318842
-0.63075	1909	5.1336	5.0594	-0.99368	1854	8.2524	0.4947	-0.12451
-0.35344	3160	7.6582	2.5348	-0.49784	3618	7.0205	1.7266	-0.43458
0.373882	3537	10.093	0.1	-0.01964	3574	12.843	4.0959	1.030918
-0.76658	3670	7.5749	2.6181	-0.5142	3583	7.6472	1.0999	-0.27684
0.371642	3150	9.3651	0.8279	-0.1626	4409	12.202	3.4549	0.869582
0.508895	4419	14.709	4.516	0.886956	4700	13	4.2529	1.070434
-0.35568	3504	9.0753	1.1177	-0.21952	3794	12.203	3.4559	0.869833
2.455892	2180	26.514	16.321	3.205495	1863	17.391	8.6439	2.175628
2.715939	2033	20.659	10.466	2.055555	3401	21.641	12.8939	3.245332
2.049427	2241	23.427	13.234	2.599198	3375	10.044	1.2969	0.326423
2.022343	2449	14.087	3.894	0.764794	3346	8.0992	0.6479	-0.16307
0.977877	1840	11.359	1.166	0.229006	2124	9.9341	1.187	0.298762
1.697335	1891	14.913	4.72	0.927023	1238	15.59	6.8429	1.722325
2.184237	2777	16.241	6.048	1.187846	2822	17.824	9.0769	2.284612
2.539588	2492	17.416	7.223	1.418619	3019	12.653	3.9059	0.983096
3.277577	2653	20.015	9.822	1.929071	3465	13.535	4.7879	1.205091
4.154448	2997	25.225	15.032	2.952331	2594	18.774	10.0269	2.523722
4.499617	901	27.858	17.665	3.46946	1203	26.933	18.1859	4.577303
4.524258	2676	21.562	11.369	2.232907	2564	22.192	13.4449	3.384016
4.337724	1798	19.466	9.273	1.821246	1842	19.87	11.1229	2.79958
3.061108	2268	24.03	13.837	2.717629	1847	19.112	10.3649	2.608795
1.627079	3956	11.881	1.688	0.331528	3539	18.96	10.2129	2.570538
1.684098	2896	15.504	5.311	1.043097	2946	11.575	2.8279	0.711769
4.060571	2526	19.557	9.364	1.839118	2646	19.728	10.9809	2.763839
2.746892	4269	12.813	2.62	0.514576	3663	21.212	12.4649	3.137355
1.949033	3844	15.531	5.338	1.0484	3386	19.374	10.6269	2.674739
1.359497	3774	10.413	0.22	0.043209	3009	21.801	13.0539	3.285604
1.174592	2911	26.417	16.224	3.186443	1668	22.782	14.0349	3.532516
0.739008	2503	21.894	11.701	2.298112	3088	13.536	4.7889	1.205343
2.823461	2806	26.515	16.322	3.205691	2263	22.581	13.8339	3.481926
0.128496	3461	11.673	1.48	0.290677	3674	10.615	1.8679	0.470141
1.124701	1947	18.593	8.4	1.649786	2533	16.107	7.3599	1.852451
0.669159	1225	18.531	8.338	1.637609	1074	9.8696	1.1225	0.282528
1.711386	2081	24.123	13.93	2.735895	2571	14.352	5.6049	1.410726
1.662716	2551	16.974	6.781	1.331809	2921	17.939	9.1919	2.313557
1.09782	2109	17.686	7.493	1.471648	3346	14.943	6.1959	1.559478
1.990779	3611	20.991	10.798	2.12076	1506	23.639	14.8919	3.748219
1.706295	2824	19.334	9.141	1.795321	2122	17.436	8.6889	2.186954
1.877963	3393	20.808	10.615	2.084819	2562	17.994	9.2469	2.3274
1.735823	2699	18.933	8.74	1.716563	2172	13.996	5.2489	1.321123
2.697612	1897	23.3	13.107	2.574255	1305	22.759	14.0119	3.526728

1.306143	3172	9.9622	0.2308	-0.04533	2617	5.6171	3.13	-0.78781
2.655866	4390	17.973	7.78	1.528016	2932	8.2196	0.5275	-0.13277
0.037266	4148	14.923	4.73	0.928987	3438	7.7661	0.981	-0.24691
0.238258	3989	14.415	4.222	0.829214	3629	10.747	1.9999	0.503365
1.878574	3386	21.116	10.923	2.145311	4565	11.391	2.6439	0.665457
0.115464	3001	9.0636	1.1294	-0.22182	1709	11.644	2.8969	0.729136
-1.04984	1760	4.9432	5.2498	-1.03108	1654	4.8972	3.8499	-0.969
1.185589	2033	18.396	8.203	1.611094	2628	10.616	1.8689	0.470393
0.846529	1623	7.9482	2.2448	-0.44089	3241	8.7319	0.0152	-0.00383
-0.04154	2156	11.085	0.892	0.175192	3151	11.457	2.7099	0.682069
0.974211	4314	9.388	0.805	-0.1581	3816	14.649	5.9019	1.48548
0.627209	2737	17.282	7.089	1.392301	2319	13.325	4.5779	1.152235
-0.85325	1595	7.3354	2.8576	-0.56124	3115	7.191	1.5561	-0.39166
-0.47063	2455	5.336	4.857	-0.95393	3040	7.9934	0.7537	-0.1897
-0.65611	3299	4.8196	5.3734	-1.05535	2979	4.8338	3.9133	-0.98496
-0.89603	2600	8.1154	2.0776	-0.40805	2324	8.0034	0.7437	-0.18719
0.542699	2250	7.4222	2.7708	-0.54419	1658	10.374	1.6269	0.409483
-1.32429	2102	4.5671	5.6259	-1.10494	3405	9.2805	0.5334	0.134254
1.24159	2935	14.446	4.253	0.835302	2750	10.291	1.5439	0.388592
1.518132	1914	11.546	1.353	0.265733	2312	11.202	2.4549	0.617886
-0.75703	1290	2.4031	7.7899	-1.52996	1565	4.1534	4.5937	-1.15621
-0.42467	3942	7.9909	2.2021	-0.4325	4427	6.4378	2.3093	-0.58124
0.198956	2884	10.992	0.799	0.156926	3831	8.2224	0.5247	-0.13206
-0.07673	2849	5.5107	4.6823	-0.91962	4309	10.49	1.7429	0.43868
-0.03014	3141	8.1503	2.0427	-0.40119	3797	12.141	3.3939	0.854228
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0.097951	2222	12.286	2.093	0.411072	1689	9.9467	1.1996	0.301934
-1.24727	1198	4.8414	5.3516	-1.05107	1373	5.4625	3.2846	-0.82672
1.061369	3159	9.6866	0.5064	-0.09946	2294	10.026	1.2789	0.321893
-0.47603	2609	6.2476	3.9454	-0.77489	2208	6.8388	1.9083	-0.48031
0.388137	2534	17.245	7.052	1.385034	1965	16.641	7.8939	1.986856
-0.0389	1889	7.1996	2.9934	-0.58791	1699	10.359	1.6119	0.405707
0.892144	2359	17.677	7.484	1.469881	2115	15.414	6.6669	1.678027
-1.23796	2936	6.6757	3.5173	-0.69081	3308	4.5647	4.1824	-1.05269
-1.21243	2352	4.4218	5.7712	-1.13348	2764	6.1867	2.5604	-0.64444
0.242942	2404	12.063	1.87	0.367274	2597	12.476	3.7289	0.938546
-0.08492	1472	11.617	1.424	0.279678	1241	12.006	3.2589	0.820249
0.670788	1824	15.241	5.048	0.991443	2270	14.758	6.0109	1.512914
-0.73567	981	8.6646	1.5284	-0.30018	1778	5.3431	3.404	-0.85677
-0.89159	1961	8.1081	2.0849	-0.40948	2145	7.9254	0.8217	-0.20682
-0.42039	778	4.3702	5.8228	-1.14362	857	9.8016	1.0545	0.265413
-1.42723	3166	6.3803	3.8127	-0.74883	3047	4.7916	3.9555	-0.99558
-1.29213	2557	3.5589	6.6341	-1.30296	1973	2.6863	6.0608	-1.52547
-0.0613	4138	8.7482	1.4448	-0.28376	3710	6.7925	1.9546	-0.49196
-0.54732	2212	7.3237	2.8693	-0.56354	1869	6.4741	2.273	-0.5721
-1.20626	2169	10.143	0.05	-0.00982	2136	4.2603	4.4868	-1.12931
-1.06416	1115	5.5605	4.6325	-0.90984	820	3.0488	5.6983	-1.43423

0.198141	1088	11.121	0.928	0.182262	1954	6.9089	1.8382	-0.46267
-1.29427	1525	5.4426	4.7504	-0.93299	2572	3.4992	5.2479	-1.32087
-0.75334	1659	5.0633	5.1297	-1.00749	2781	5.2499	3.4972	-0.88023
-0.01344	2989	6.1224	4.0706	-0.79948	3508	10.205	1.4579	0.366946
-0.04175	1455	11.753	1.56	0.306389	2393	5.7668	2.9803	-0.75013
-0.78902	957	6.1651	4.0279	-0.79109	1919	7.2955	1.4516	-0.36536
-1.14067	1726	11.24	1.047	0.205634	2579	4.8856	3.8615	-0.97192
-0.17091	1835	9.5368	0.6562	-0.12888	2976	8.5013	0.2458	-0.06187
-0.88072	1214	4.5305	5.6625	-1.11213	3123	4.8031	3.944	-0.99269
-0.56304	1173	3.3248	6.8682	-1.34894	2499	4.8019	3.9452	-0.99299
-0.28143	1171	3.2451	6.9479	-1.36459	1982	7.114	1.6331	-0.41104
0.390988	1305	16.705	6.512	1.278977	2322	14.729	5.9819	1.505615
-1.03264	1685	2.908	7.285	-1.4308	3281	3.0479	5.6992	-1.43446
1.511412	2287	20.026	9.833	1.931231	3209	15.083	6.3359	1.594715
-1.02594	1399	4.1458	6.0472	-1.18769	3028	4.6235	4.1236	-1.03789
-0.52366	651	10.292	0.099	0.019444	982	6.6191	2.128	-0.53561
-0.51329	2549	11.887	1.694	0.332707	5360	8.8246	0.0775	0.019506
-0.76599	2671	9.9588	0.2342	-0.046	4925	4.2234	4.5237	-1.13859
-0.95171	743	8.7483	1.4447	-0.28374	1518	6.0606	2.6865	-0.67618
-0.81187	2318	3.063	7.13	-1.40035	1717	7.5713	1.1758	-0.29594
-0.91053	848	5.4245	4.7685	-0.93655	2060	6.9417	1.8054	-0.45441
-0.18704	1383	4.1938	5.9992	-1.17826	1784	5.157	3.5901	-0.90361
-1.09385	1111	3.1503	7.0427	-1.38321	1205	4.4813	4.2658	-1.07368
-0.63841	1862	9.3448	0.8482	-0.16659	2952	7.0122	1.7349	-0.43667
-1.1483	1719	2.3269	7.8661	-1.54493	1986	4.5821	4.165	-1.04831
-1.46341	1607	5.1649	5.0281	-0.98753	2769	5.0199	3.7272	-0.93812
-0.48144	617	5.0243	5.1687	-1.01515	1422	7.4543	1.2928	-0.32539
-1.23328	1084	3.2288	6.9642	-1.36779	2265	7.6821	1.065	-0.26806
-0.5887	1030	4.6602	5.5328	-1.08666	2570	8.3268	0.4203	-0.10579
-0.6278	1282	10.452	0.259	0.050868	2709	7.9365	0.8106	-0.20402
-1.08929	783	3.1928	7.0002	-1.37486	1594	5.8971	2.85	-0.71733
-1.4368	917	6.2159	3.9771	-0.78111	2996	3.972	4.7751	-1.20187
-1.32865	661	9.2284	0.9646	-0.18945	2163	4.0684	4.6787	-1.17761
-1.11419	855	3.5088	6.6842	-1.3128	1994	7.9238	0.8233	-0.20722
-1.67469	1576	1.5863	8.6067	-1.69038	3553	4.7284	4.0187	-1.01149
-1.14156	2144	8.3489	1.8441	-0.36219	3030	5.2145	3.5326	-0.88914
-1.06884	2370	9.3671	0.8259	-0.16221	3021	9.4009	0.6538	0.164558
-1.25534	1700	5.5882	4.6048	-0.9044	1771	4.6866	4.0605	-1.02201
-1.68809	2158	4.0778	6.1152	-1.20104	3025	3.8347	4.9124	-1.23643
		10.193	3.44025			8.7471	2.6845	
			10.32075				8.0535	
			5.09157				3.97306	

2626	34.463	2409	44.458	1663	33.734
2993	40.194	2499	47.059	3511	37.881
2879	29.871	2188	52.148	2747	31.416
5223	40.743	3407	40.945	2970	26.229

mn	3430.25	36.31775	2625.75	46.1525	2722.75	32.315
sd	1204.967	5.151338	536.9739	4.717243	775.9142	4.859407
	1036	7.1429	687	7.1325	1183	7.3542
	1228	4.5603	820	5	1960	5.7653
	1121	5.7092	617	9.7245	1251	10.791
	1239	6.5375	1490	4.8322	1655	8.6405
mn	1156	5.987475	903.5	6.6723	1512.25	8.13775
sd	96.08677	1.118302	399.9621	2.288396	364.0122	2.124065
3posSD		15.45401		14.15173		14.57822
3negSD		3.354907		6.865187		6.372196
Sum3SD		18.80892		21.01692		20.95042
MnDiff		30.33028		39.4802		24.17725
SumovrMn		0.620137		0.532341		0.866534
1minus		0.379863		0.467659		0.133466

x	toxic a,b,c
x	toxic a,b,c
X	toxic b, art a,b
x	toxic a,b,c

X toxic b

x debris a

Y	
Y	
X	debris a,c
X	toxic a
X	debris b,c
x	toxic a,b,c
X	toxic a,debris c,a
x	debris a,b,tox c
X	
X	toxic a
X	debris c
X	debris c
X	debris c
X	toxic c
Y	
X	toxic b,c

					cell ct	% inf	AD
50063	A02	M-014465- DENN/MA	57706	DENND1A	296	23.649	14.21225
50063	A04	M-013790- KIAA1295	57517	KIAA1295	235	15.319	5.88225
50063	A05	M-023051- zinc finger	57547	ZNF624	541	5.3604	4.07635
50063	A06	M-013788- zinc finger	58492	ZNF77	579	8.981	0.45575
50063	A07	M-014056- immunogl	57549	IGSF9	412	8.4951	0.94165
50063	A08	M-017123- zinc finger	58491	ZNF71	276	9.058	0.37875
50063	A09	M-024432- microtubul	57553	MICAL3	236	4.661	4.77575
50063	A10	M-013787- chromoso	58490	C20orf77	296	5.7432	3.69355
50063	A11	M-008843- neuroligin	57555	NLGN2	211	8.5308	0.90595
50063	A12	M-005929- family with	58489	FAM108C1	166	11.446	2.00925
50063	A13	M-014062- sema dom	57556	SEMA6A	248	16.935	7.49825
50063	A14	M-013786- phosphatid	58488	PCTP	127	8.6614	0.77535
50063	A15	M-023638- intraflagell	57560	IFT80	552	7.2464	2.19035
50063	A16	M-013782- zinc finger,	58486	ZBED5	463	12.959	3.52225
50063	A17	M-014063- arrestin do	57561	ARRDC3	307	13.681	4.24425
50063	A18	M-013781- trafficking	58485	TRAPPC1	397	8.8161	0.62065
50063	A19	M-029798- KIAA1377	57562	KIAA1377	197	12.69	3.25325
50063	A20	M-013780- chromoso	58483	C9orf27	419	11.695	2.25825
50063	A21	M-019270- kelch-like 8	57563	KLHL8	606	11.716	2.27925
50063	A23	M-023417- kelch-like 1	57565	KLHL14	1126	8.1705	1.26625
50063	B02	M-006835- non-SMC c	64151	NCAPG	3984	16.014	6.57725
50063	B04	M-003851- peptide de	64146	PDF	2748	11.645	2.20825
50063	B05	M-013792- chromoso	58493	C9orf80	3486	20.367	10.93025
50063	B06	M-014036- zinc finger,	64145	ZFYVE20	3709	15.503	6.06625
50063	B07	M-017389- junctional	58494	JAM2	2689	10.264	0.82725
50063	B08	M-013041- interferon	64135	IFIH1	3278	24.649	15.21225
50063	B09	M-013793- ovo-like 2 (	58495	OVOL2	1425	12.281	2.84425
50063	B10	M-013040- xylosyltran	64132	XYLT2	3346	10.759	1.32225
50063	B11	M-010073- lymphocyt	58496	LY6G5B	2451	13.505	4.06825
50063	B12	M-013749- xylosyltran	64131	XYLT1	2918	11.001	1.56425
50063	B13	M-013799- prune hom	58497	PRUNE	2987	10.278	0.84125
50063	B14	M-009653- lin-7 homo	64130	LIN7B	2425	8.7835	0.65325
50063	B15	M-018036- zinc finger	58499	ZNF462	625	9.44	0.00325
50063	B16	M-017822- Ras-relate	64121	RRAGC	1623	9.4886	0.05185
50063	B17	M-025860- zinc finger	58500	ZNF250	958	10.438	1.00125
50063	B18	M-015688- dihydrouri	64118	DUS1L	2310	10.39	0.95325
50063	B19	M-031984- proline ric	58503	PROL1	1729	11.683	2.24625
50063	B20	M-007573- solute carri	64116	SLC39A8	2114	7.5213	1.91545
50063	B21	M-019080- Rho GTPas	58504	ARHGAP22	1605	5.7944	3.64235
50063	B23	M-027193- DC2 protei	58505	DC2	1503	9.2482	0.18855
50063	C02	M-013646- signal reco	58477	SRPRB	1597	5.9487	3.48805
50063	C04	M-031980- tumor prot	58476	TP53INP2	876	6.5068	2.92995
50063	C05	M-022568- zinc finger	57567	ZNF319	1803	18.192	8.75525
50063	C06	M-013778- pleckstrin	58473	PLEKHB1	845	3.6686	5.76815
50063	C07	M-021865- signal-indu	57568	SIPA1L2	750	7.4667	1.97005
50063	C08	M-008271- sulfide qui	58472	SQRDL	1114	3.0521	6.38465

50063	C09	M-026514- Rho GTPas	57569	ARHGAP20	802	6.6085	2.82825
50063	C10	M-007876- chemokine	58191	CXCL16	371	6.1995	3.23725
50063	C11	M-021968- TRM5 tRN	57570	TRMT5	518	5.2124	4.22435
50063	C12	M-010046- neurogenic	58158	NEUROD4	1069	6.5482	2.88855
50063	C13	M-026680- KIAA1394	57571	KIAA1394	559	6.7979	2.63885
50063	C14	M-015869- neuroglobi	58157	NGB	717	6.1367	3.30005
50063	C15	M-031950- dedicator	57572	DOCK6	914	10.394	0.95725
50063	C16	M-021323- polypyrimi	58155	PTBP2	1271	8.0252	1.41155
50063	C17	M-014067- zinc finger	57573	ZNF471	1678	5.1847	4.25205
50063	C18	M-025427- mucin 3B,	57876	MUC3B	1265	4.7431	4.69365
50063	C19	M-013164- protocadh	57575	PCDH10	2835	13.086	3.64925
50063	C20	M-018639- solute carri	57864	SLC46A2	2793	8.8793	0.55745
50063	C21	M-014068- KIAA1407	57577	KIAA1407	1260	9.2063	0.23045
50063	C23	M-021995- KIAA1409	57578	KIAA1409	1765	4.7025	4.73425
50063	D02	M-015095- transmem	64114	TMBIM1	4105	11.62	2.18325
50063	D04	M-004430- modulator	64112	MOAP1	1229	12.693	3.25625
50063	D05	M-031985- serine argi	58506	SR-A1	1956	12.065	2.62825
50063	D06	M-019049- melanoma	64110	MAGEF1	3793	19.431	9.99425
50063	D07	M-031204- chromoso	58509	C19orf29	2822	13.005	3.56825
50063	D08	M-015207- centromer	64105	CENPK	1978	11.476	2.03925
50063	D09	M-008278- deoxyribo	58511	DNASE2B	3752	7.9691	1.46765
50063	D10	M-013888- tenomodul	64102	TNMD	3050	10	0.56325
50063	D11	M-022309- discs, large	58512	DLGAP3	3702	7.9957	1.44105
50063	D12	M-013887- leucine ric	64101	LRRC4	2482	8.8638	0.57295
50063	D13	M-016842- selenoprot	58515	SELK	3796	8.8514	0.58535
50063	D14	M-013046- epididymal	64100	ELSPBP1	2442	7.1253	2.31145
50063	D15	M-027166- family with	58516	FAM60A	1131	9.2838	0.15295
50063	D16	M-017821- parvin, ga	64098	PARVG	2477	8.9625	0.47425
50063	D17	M-021976- RNA bindin	58517	RBM25	2561	2.6552	6.78155
50063	D18	M-021335- erythrocyt	64097	EPB41L4A	4030	7.196	2.24075
50063	D19	M-031240- widely inte	58525	WIZ	3416	5.9133	3.52345
50063	D20	M-013886- SPARC rela	64094	SMOC2	2952	8.8076	0.62915
50063	D21	M-015884- MID1 inter	58526	MID1IP1	2812	7.5036	1.93315
50063	D23	M-024734- chromoso	58527	C6orf115	4178	15.462	6.02525
50063	E02	M-015864- cell adhesi	57863	CADM3	1753	5.9897	3.44705
50063	E04	M-014002- zinc finger	57862	ZNF410	793	12.106	2.66925
50063	E05	M-028640- family with	57579	FAM135A	2477	5.4098	4.02695
50063	E06	M-007585- solute carri	57835	SLC4A5	885	20.791	11.35425
50063	E07	M-010063- phosphatid	57580	PREX1	2498	5.1641	4.27265
50063	E08	M-008902- cytochrom	57834	CYP4F11	1507	4.5786	4.85815
50063	E09	M-024897- transmem	57583	TMEM181	1488	18.011	8.57425
50063	E10	M-014009- keratin ass	57830	KRTAP5-8	864	10.185	0.74825
50063	E11	M-004775- Rho GTPas	57584	ARHGAP21	1191	4.618	4.81875
50063	E12	M-013108- zona pelluc	57829	ZP4	965	5.0777	4.35905
50063	E13	M-022876- Crm, cram	57585	CRAMP1L	1648	5.8252	3.61155
50063	E14	M-014008- chromoso	57828	C19orf15	1122	4.5455	4.89125
50063	E15	M-014082- synaptotag	57586	SYT13	2185	4.5767	4.86005

50063	E16	M-014006-	chromoson	57827	C6orf47	2154	5.2925	4.14425
50063	E17	M-024112-	KIAA1430	57587	KIAA1430	2290	6.1135	3.32325
50063	E18	M-010057-	RAP2C, me	57826	RAP2C	1489	2.955	6.48175
50063	E19	M-026110-	KIAA1432	57589	KIAA1432	3423	6.5148	2.92195
50063	E20	M-014005-	histocompa	57824	HMHB1	2825	7.0442	2.39255
50063	E21	M-006861-	WD repeat	57590	WDFY1	3107	11.201	1.76425
50063	E23	M-007036-	zinc finger	57592	ZNF687	2992	4.2112	5.22555
50063	F02	M-013885-	SPARC rela	64093	SMOC1	4169	8.3713	1.06545
50063	F04	M-013045-	popeye dor	64091	POPDC2	2678	17.364	7.92725
50063	F05	M-015642-	myozenin 1	58529	MYOZ1	1879	20.596	11.15925
50063	F06	M-013884-	galactose-3	64090	GAL3ST2	2300	11.304	1.86725
50063	F07	M-031989-	lymphocyte	58530	LY6G6D	2195	18.087	8.65025
50063	F08	M-013044-	sorting nex	64089	SNX16	2961	9.794	0.35725
50063	F09	M-031990-	protamine	58531	PRM3	2668	10.832	1.39525
50063	F10	M-006414-	golgi phosp	64083	GOLPH3	2082	7.4448	1.99195
50063	F11	M-017557-	sorting nex	58533	SNX6	2065	9.4431	0.00635
50063	F12	M-013882-	phenazine	64081	PBLD	2735	11.846	2.40925
50063	F13	M-015070-	membrane	58538	MPP4	1374	16.885	7.44825
50063	F14	M-007505-	solute carri	64078	SLC28A3	2971	14.709	5.27225
50063	F15	M-013841-	transmemb	58986	TMEM8	2614	7.4216	2.01515
50063	F16	M-023671-	chromoson	64073	C19orf33	2544	7.5079	1.92885
50063	F17	M-007970-	interleukin	59067	IL21	2046	6.305	3.13175
50063	F18	M-008498-	neuronal P.	64067	NPAS3	2843	10.728	1.29125
50063	F19	M-009915-	ICEBERG ca	59082	ICEBERG	4380	10.251	0.81425
50063	F20	M-013881-	3-oxoacid C	64064	OXCT2	3579	8.1308	1.30595
50063	F21	M-016765-	chromoson	59271	C21orf63	2086	5.0336	4.40315
50063	F23	M-013508-	calcium cha	59283	CACNG8	3400	5.3529	4.08385
50063	G02	M-017122-	SLAM famil	57823	SLAMF7	1947	8.1664	1.27035
50063	G04	M-014017-	grainyhead	57822	GRHL3	501	13.573	4.13625
50063	G05	M-024234-	KIAA1442 p	57593	RP5-860F1	813	12.177	2.74025
50063	G06	M-014016-	chromoson	57821	C1orf114	681	6.1674	3.26935
50063	G07	M-014090-	homeobox	57594	HOMEZ	611	11.129	1.69225
50063	G08	M-019251-	cyclin B1 in	57820	CCNB1IP1	701	11.27	1.83325
50063	G09	M-014911-	PDZ domai	57595	PDZD4	492	11.992	2.55525
50063	G10	M-017813-	LSM2 hom	57819	LSM2	374	11.23	1.79325
50063	G11	M-014095-	likely ortho	57596	KIAA1446	755	6.0927	3.34405
50063	G12	M-010427-	KIAA1967	57805	KIAA1967	548	14.964	5.52725
50063	G13	M-023331-	BAH domai	57597	BAHCC1	363	19.835	10.39825
50063	G14	M-014013-	polymerase	57804	POLD4	952	8.1933	1.24345
50063	G15	M-016462-	WD repeat	57599	WDR48	432	9.2593	0.17745
50063	G16	M-016602-	GATA zinc f	57798	GATAD1	1651	11.69	2.25325
50063	G17	M-031785-	KIAA1456 p	57604	KIAA1456	1021	6.4643	2.97245
50063	G18	M-014022-	family with	57795	FAM5B	1012	15.909	6.47225
50063	G19	M-014106-	phosphatid	57605	PITPNM2	1314	12.329	2.89225
50063	G20	M-017511-	splicing fac	57794	SF4	3555	7.5949	1.84185
50063	G21	M-024203-	SLAIN moti	57606	SLAIN2	2531	14.066	4.62925
50063	G23	M-026476-	KIAA1462	57608	KIAA1462	2587	7.4604	1.97635

50063	H02	M-006013- protease, s	64063	PRSS22	3002	26.349	16.91225
50063	H04	M-019088- RNA bindin	64062	RBM26	2747	19.185	9.74825
50063	H05	M-017347- calcium ch	59284	CACNG7	2004	15.22	5.78325
50063	H06	M-013880- TSPY-like 2	64061	TSPYL2	3259	18.595	9.15825
50063	H07	M-017454- calcium ch	59285	CACNG6	2137	19.373	9.93625
50063	H08	M-025326- myosin IG	64005	MYO1G	1739	10.581	1.14425
50063	H09	M-008082- single imm	59307	SIGIRR	2448	18.342	8.90525
50063	H10	M-014718- transmem	63982	TMEM16C	2209	23.631	14.19425
50063	H11	M-006030- serine carb	59342	SCPEP1	2193	22.572	13.13525
50063	H12	M-019091- fidgetin-lik	63979	FIGNL1	2648	18.58	9.14325
50063	H13	M-006033- SUMO1/se	59343	SENP2	2339	15.69	6.25325
50063	H14	M-008363- PR domain	63977	PRDM15	2841	11.369	1.93225
50063	H15	M-017814- zinc finger	59348	ZNF350	2995	12.988	3.55125
50063	H16	M-008708- neurogeni	63974	NEUROD6	3394	11.196	1.75925
50063	H17	M-015890- kelch-like 1	59349	KLHL12	2075	8.9157	0.52105
50063	H18	M-009009- neurogeni	63973	NEUROG2	3410	5.2493	4.18745
50063	H19	M-013811- prostate ar	59351	PBOV1	2980	18.557	9.12025
50063	H20	M-026122- DMRT-like	63951	DMRTA1	2585	12.108	2.67125
50063	H21	M-013746- transmem	59353	TMEM35	3664	7.369	2.06775
50063	H23	M-016463- GC-rich pr	60313	GPBP1L1	1456	8.6538	0.78295
50063	I02	M-016344- ankyrin re	57763	ANKRA2	1274	8.0063	1.43045
50063	I04	M-015227- glucosidas	57733	GBA3	591	8.291	1.14575
50063	I05	M-022575- RAN bindin	57610	RANBP10	476	3.9916	5.44515
50063	I06	M-024148- zinc finger,	57732	ZFYVE28	685	8.9051	0.53165
50063	I07	M-022273- immunogl	57611	ISLR2	1194	11.809	2.37225
50063	I08	M-014609- spectrin, b	57731	SPTBN4	523	7.8394	1.59735
50063	I09	M-028936- KIAA1466	57612	KIAA1466	212	13.208	3.77125
50063	I10	M-022839- KIAA1641	57730	KIAA1641	858	9.9068	0.47005
50063	I11	M-027045- KIAA1467	57613	KIAA1467	292	3.4247	6.01205
50063	I12	M-016094- WD repeat	57728	WDR19	394	12.183	2.74625
50063	I13	M-014115- KIAA1468	57614	KIAA1468	320	10.312	0.87525
50063	I14	M-023428- KIAA1632	57724	KIAA1632	143	6.993	2.44375
50063	I15	M-024008- zinc finger	57615	ZNF492	979	11.134	1.69725
50063	I16	M-014170- neighbor o	57722	NOPE	1186	7.4199	2.01685
50063	I17	M-014119- teashirt fa	57616	TSHZ3	1224	6.5359	2.90085
50063	I18	M-014169- KIAA1627	57721	KIAA1627	1199	4.3369	5.09985
50063	I19	M-013178- vacuolar pr	57617	VPS18	2135	5.808	3.62875
50063	I20	M-031248- transmem	57719	TMEM16H	1787	3.4135	6.02325
50063	I21	M-014123- shroom fa	57619	SHROOM3	3849	5.456	3.98075
50063	I23	M-013166- stromal int	57620	STIM2	2093	5.2078	4.22895
50063	J02	M-021793- DMRT-like	63950	DMRTA2	4064	12.475	3.03825
50063	J04	M-015071- DMRT-like	63948	DMRTB1	3793	13.024	3.58725
50063	J05	M-013747- chromoso	60314	C12orf10	2402	11.241	1.80425
50063	J06	M-015059- DMRT-like	63947	DMRTC1	2050	9.0244	0.41235
50063	J07	M-013974- family with	60343	FAM3A	2041	19.304	9.86725
50063	J08	M-015058- DMRT-like	63946	DMRTC2	2089	13.787	4.35025
50063	J09	M-013941- arginine va	60370	AVPI1	2128	18.703	9.26625

50063	J10	M-013479- amyloid be	63941	APBA2BP	3000	11.4	1.96325
50063	J11	M-013068- exocyst cor	60412	EXOC4	2897	11.598	2.16125
50063	J12	M-013906- G-protein s	63940	GPSM3	3386	11.459	2.02225
50063	J13	M-017339- cadherin-lil	60437	CDH26	2112	10.795	1.35825
50063	J14	M-013905- chromoson	63939	C20orf177	3379	10.891	1.45425
50063	J15	M-013975- blepharoph	60467	BPESC1	2622	10.641	1.20425
50063	J16	M-013904- chromoson	63935	C20orf67	2594	6.7463	2.69045
50063	J17	M-009260- ELOVL fami	60481	ELOVL5	2336	12.115	2.67825
50063	J18	M-013903- zinc finger	63934	ZNF667	3808	8.3246	1.11215
50063	J19	M-007595- solute carri	60482	SLC5A7	2504	9.5447	0.10795
50063	J20	M-010730- coiled-coil	63933	CCDC90A	4078	10.152	0.71525
50063	J21	M-013976- hyaluronar	60484	HAPLN2	3074	13.175	3.73825
50063	J23	M-013070- salvador hc	60485	SAV1	3549	6.5371	2.89965
50063	K02	M-013156- protocadhe	57717	PCDHB16	1089	25.803	16.36625
50063	K04	M-019159- sema doma	57715	SEMA4G	844	34.36	24.92325
50063	K05	M-014129- zinc finger	57621	ZBTB2	683	25.622	16.18525
50063	K06	M-023323- KIAA1618	57714	KIAA1618	851	19.624	10.18725
50063	K07	M-023686- leucine rich	57622	LRFN1	858	28.904	19.46725
50063	K08	M-026395- Scm-like wi	57713	SFMBT2	832	20.192	10.75525
50063	K09	M-025840- ZFAT zinc fi	57623	ZFAT1	859	24.447	15.01025
50063	K10	M-014190- zinc finger	57711	ZNF529	585	23.932	14.49525
50063	K11	M-023134- KIAA1486 p	57624	KIAA1486	224	48.661	39.22425
50063	K12	M-021882- KIAA1614	57710	KIAA1614	134	44.03	34.59325
50063	K13	M-010912- kelch-like 1	57626	KLHL1	373	28.15	18.71325
50063	K14	M-007340- solute carri	57709	SLC7A14	694	19.597	10.16025
50063	K15	M-008971- dipeptidyl-	57628	DPP10	1553	14.81	5.37325
50063	K16	M-009375- glucosidase	57704	GBA2	1517	12.657	3.22025
50063	K17	M-007037- SH3 domai	57630	SH3RF1	1434	22.594	13.15725
50063	K18	M-023101- KIAA1604 p	57703	KIAA1604	276	32.246	22.80925
50063	K19	M-014131- leucine-rich	57631	LRCH2	1145	13.886	4.44925
50063	K20	M-026953- KIAA1602	57701	KIAA1602	1199	12.761	3.32425
50063	K21	M-019481- leucine rich	57633	LRRN1	3327	9.8888	0.45205
50063	K23	M-021272- E1A binding	57634	EP400	976	12.09	2.65325
50063	L02	M-013901- chromoson	63932	CXorf56	2588	25.193	15.75625
50063	L04	M-013050- mitochond	63931	MRPS14	4124	28.371	18.93425
50063	L05	M-013978- tRNA meth	60487	TRMT11	3576	21.756	12.31925
50063	L06	M-013917- chromoson	63930	C20orf51	4203	29.527	20.09025
50063	L07	M-013071- mitochond	60488	MRPS35	2020	24.356	14.91925
50063	L08	M-013916- hepatocellu	63928	LOC63928	3492	19.53	10.09325
50063	L09	M-015916- phosphopa	60490	PPCDC	2463	20.3	10.86325
50063	L10	M-016173- zinc finger	63925	ZNF335	2763	18.132	8.69525
50063	L11	M-013979- NIF3 NGG1	60491	NIF3L1	2422	24.071	14.63425
50063	L12	M-016168- cell death-i	63924	CIDEC	3538	20.04	10.60325
50063	L13	M-016774- coiled-coil	60492	CCDC90B	2132	20.966	11.52925
50063	L14	M-021879- tenascin N	63923	TNN	3551	14.756	5.31925
50063	L15	M-017125- FAST kinase	60493	FASTKD5	3185	15.039	5.60225
50063	L16	M-013915- CTF18, chro	63922	CHTF18	2777	11.523	2.08625

50063	L17	M-013980-	coiled-coil	60494	CCDC81	2595	10.636	1.19925
50063	L18	M-013914-	dJ467N11.	63921	DJ467N11.	2397	12.808	3.37125
50063	L19	M-003675-	heparanase	60495	HPSE2	3683	11.404	1.96725
50063	L20	M-018241-	transposon	63920	LOC63920	3541	12.228	2.79125
50063	L21	M-009468-	ATP/GTP bi	60509	AGBL5	3310	10.151	0.71425
50063	L23	M-009926-	chromosom	60526	C2orf43	2920	7.7055	1.73125
50063	M02	M-026315-	KIAA1600	57700	KIAA1600	1652	3.9952	5.44155
50063	M04	M-016175-	KIAA1598	57698	KIAA1598	1618	5.9333	3.50345
50063	M05	M-023061-	Rho GTPas	57636	ARHGAP23	1002	4.5908	4.84595
50063	M06	M-021955-	Fanconi an	57697	FANCM	781	4.3534	5.08335
50063	M07	M-021991-	KIAA1509	57641	KIAA1509	832	4.4471	4.98965
50063	M08	M-027082-	DEAD (Asp-	57696	DDX55	844	9.2417	0.19505
50063	M09	M-024094-	collagen, ty	57642	COL20A1	665	1.3534	8.08335
50063	M10	M-017121-	zinc finger	57693	ZNF317	268	4.1045	5.33225
50063	M11	M-021787-	zinc finger,	57643	ZSWIM5	307	7.8176	1.61915
50063	M12	M-014189-	melanoma	57692	MAGEE1	541	8.1331	1.30365
50063	M13	M-031354-	myosin, he	57644	MYH7B	520	8.0769	1.35985
50063	M14	M-025116-	KIAA1586	57691	KIAA1586	753	2.656	6.78075
50063	M15	M-017451-	pogo transp	57645	POGK	1086	3.3149	6.12185
50063	M16	M-019399-	trinucleoti	57690	TNRC6C	309	5.178	4.25875
50063	M17	M-019073-	DEAH (Asp-	57647	DHX37	1388	4.2507	5.18605
50063	M18	M-026791-	leucine rich	57689	LRRC4C	1024	3.7109	5.72585
50063	M19	M-010728-	KIAA1522	57648	KIAA1522	1302	4.2243	5.21245
50063	M20	M-024465-	zinc finger,	57688	ZSWIM6	1806	4.6512	4.78555
50063	M21	M-009736-	PHD finger	57649	PHF12	2042	5.4848	3.95195
50063	M23	M-014135-	KIAA1524	57650	KIAA1524	1074	3.9106	5.52615
50063	N02	M-007042-	UDP-N-ace	63917	GALNT11	1221	13.677	4.24025
50063	N04	M-019222-	engulfmen	63916	ELMO2	4005	11.885	2.44825
50063	N05	M-021270-	GUF1 GTPa	60558	GUF1	4088	13.601	4.16425
50063	N06	M-031754-	muted hom	63915	MUTED	3202	13.554	4.11725
50063	N07	M-010124-	signal pept	60559	SPCS3	3319	8.3158	1.12095
50063	N08	M-017820-	chromosom	63910	C20orf59	2490	14.498	5.06125
50063	N09	M-021268-	MAK10 hom	60560	MAK10	2488	6.4711	2.96565
50063	N10	M-013927-	G patch do	63906	GPATCH3	4609	8.5268	0.90995
50063	N11	M-004976-	RAD50 inte	60561	RINT1	3795	9.4335	0.00325
50063	N12	M-015357-	mannosida	63905	MANBAL	2600	7.4615	1.97525
50063	N13	M-014916-	short coile	60592	SCOC	1567	7.1474	2.28935
50063	N14	M-013926-	family with	63901	FAM111A	1209	6.4516	2.98515
50063	N15	M-006258-	potassium	60598	KCNK15	2227	7.5438	1.89295
50063	N16	M-017819-	NOL1/NOP	63899	NSUN3	3213	4.793	4.64375
50063	N17	M-013065-	DEAH (Asp-	60625	DHX35	1836	5.0654	4.37135
50063	N18	M-007724-	SH2 domai	63898	SH2D4A	2377	5.4691	3.96765
50063	N19	M-016121-	resistance	60626	RIC8A	2679	3.994	5.44275
50063	N20	M-013925-	family with	63895	FAM38B	2583	2.5165	6.92025
50063	N21	M-021269-	invasion in	60672	RP5-1077B	2723	4.1131	5.32365
50063	N23	M-017816-	chromosom	60673	C12orf44	1952	3.125	6.31175
50063	O02	M-008897-	KIAA1576	57687	KIAA1576	460	20.652	11.21525

50063	O04	M-014178-	cache dom	57685	CACHD1	1292	22.755	13.31825
50063	O05	M-026179-	KIAA1529	57653	KIAA1529	1315	6.1597	3.27705
50063	O06	M-017893-	zinc finger	57684	ZBTB26	701	9.2725	0.16425
50063	O07	M-024139-	KIAA1530 p	57654	KIAA1530	847	8.5006	0.93615
50063	O08	M-028011-	zinc finger,	57683	ZDBF2	1821	6.3701	3.06665
50063	O09	M-014143-	GRAM dom	57655	GRAMD1A	1134	8.2892	1.14755
50063	O10	M-030271-	chromodor	57680	CHD8	195	16.923	7.48625
50063	O11	M-007038-	calcium bir	57658	CALCOCO1	747	8.9692	0.46755
50063	O12	M-009946-	glycerol-3-p	57678	GPAM	259	10.811	1.37425
50063	O13	M-014149-	zinc finger	57659	ZBTB4	297	15.825	6.38825
50063	O14	M-023324-	ring finger	57674	RNF213	556	15.647	6.21025
50063	O15	M-026727-	CTD-bindin	57661	KIAA1542	922	5.6399	3.79685
50063	O16	M-024750-	KIAA1553	57673	KIAA1553	642	5.6075	3.82925
50063	O17	M-024077-	KIAA1543	57662	KIAA1543	634	8.6751	0.76165
50063	O18	M-025462-	KIAA1549 p	57670	KIAA1549	979	2.145	7.29175
50063	O19	M-020795-	pleckstrin h	57664	PLEKHA4	919	2.5027	6.93405
50063	O20	M-010729-	erythrocyte	57669	EPB41L5	1609	3.0454	6.39135
50063	O21	M-009103-	retinol deh	57665	RDH14	1423	4.2867	5.15005
50063	O23	M-023934-	KIAA1546 p	57667	KIAA1546	934	4.4968	4.93995
50063	P02	M-016131-	chromosom	63894	C14orf133	2088	6.9923	2.44445
50063	P04	M-032022-	thyroid ade	63892	THADA	2671	8.8731	0.56365
50063	P05	M-021267-	prokineticin	60675	PROK2	2088	7.3755	2.06125
50063	P06	M-007041-	ring finger	63891	RNF123	2828	4.0665	5.37025
50063	P07	M-005998-	pappalysin	60676	PAPPA2	3201	14.777	5.34025
50063	P08	M-013924-	chromosom	63877	C10orf84	2739	13.801	4.36425
50063	P09	M-015854-	bruno-like	60677	BRUNOL6	2753	10.679	1.24225
50063	P10	M-013049-	mitochond	63875	MRPL17	4010	7.3566	2.08015
50063	P11	M-003907-	eukaryotic	60678	EEFSEC	4245	10.86	1.42325
50063	P12	M-016130-	brevican	63827	BCAN	3405	8.928	0.50875
50063	P13	M-016648-	bruno-like	60680	BRUNOL5	298	14.765	5.32825
50063	P14	M-008788-	serine race	63826	SRR	2418	9.6361	0.19935
50063	P15	M-008360-	FK506 bind	60681	FKBP10	1513	11.17	1.73325
50063	P16	M-008368-	elastase 2A	63036	ELA2A	4670	6.8308	2.60595
50063	P17	M-017275-	stromal me	60682	SMAP1	2788	4.878	4.55875
50063	P18	M-019215-	BCL6 co-rep	63035	BCORL1	3332	5.2521	4.18465
50063	P19	M-016784-	FLJ12716 p	60684	FLJ12716	2416	8.7748	0.66195
50063	P20	M-015812-	chromosom	63027	C6orf85	3465	3.9538	5.48295
50063	P21	M-008570-	zinc finger,	60685	ZFAND3	2010	3.2338	6.20295
50063	P23	M-013989-	chromosom	60686	C14orf93	1344	7.4405	1.99625
					MAD		9.43675	3.31165
					MAD3			9.93495
					MADc			4.901242
50063	C22	Human4 Pc	RNAi	empty				
50063	D22	Human4 Pc	RNAi	empty				
50063	E22	Human4 Pc	RNAi	empty				
50063	F22	Human4 Pc	RNAi	empty				

50063	G22	Human4 Pc	RNAi	empty
50063	H22	Human4 Pc	RNAi	empty
50063	I22	Human4 Pc	RNAi	empty
50063	J22	Human4 Pc	RNAi	empty

50063	K03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-(	siGLO RISC-free siRNA
50063	L03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-(	siGLO RISC-free siRNA

50063	G03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347
50063	H03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347
50063	I03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-:	siControl non-targeting	
50063	J03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-:	siControl non-targeting	

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
2.899724	2236	7.1556	2.80455	-0.65302	3251	14.918	5.1316	1.001762
1.200155	3417	10.418	0.45785	0.106607	2217	10.419	0.6326	0.123493
-0.8317	1826	7.5575	2.40265	-0.55944	1852	5.0756	4.7108	-0.91962
-0.09299	3017	10.275	0.31485	0.073311	3324	9.627	0.1594	-0.03112
-0.19212	3201	4.7485	5.21165	-1.2135	2458	6.3873	3.3991	-0.66355
-0.07728	2921	9.1749	0.78525	-0.18284	1323	7.483	2.3034	-0.44966
-0.9744	4039	7.4523	2.50785	-0.58394	2515	5.169	4.6174	-0.90138
-0.75359	2487	7.2376	2.72255	-0.63393	3280	10.61	0.8236	0.160778
-0.18484	2131	3.9887	5.97145	-1.39041	974	5.4415	4.3449	-0.84819
0.409947	1317	13.364	3.40385	0.792563	1082	12.2	2.4136	0.471169
1.529867	1782	8.0247	1.93545	-0.45066	2599	7.349	2.4374	-0.47582
-0.15819	3083	9.8605	0.09965	-0.0232	2057	8.3131	1.4733	-0.28761
-0.4469	2403	4.8689	5.09125	-1.18546	1637	6.964	2.8224	-0.55097
0.718644	3824	10.251	0.29085	0.067722	3510	10.912	1.1256	0.219733
0.865954	3522	7.6377	2.32245	-0.54077	3255	8.0184	1.768	-0.34514
-0.12663	2726	6.1629	3.79725	-0.88416	2948	7.5645	2.2219	-0.43375
0.66376	3822	10.44	0.47985	0.11173	3584	12.528	2.7416	0.535199
0.460751	1769	4.1832	5.77695	-1.34512	1947	4.7252	5.0612	-0.98802
0.465035	1829	7.4904	2.46975	-0.57506	3134	8.679	1.1074	-0.21618
-0.25835	1915	6.423	3.53715	-0.8236	1975	6.3797	3.4067	-0.66504
1.341956	4831	14.428	4.46785	1.040308	4379	18.36	8.5736	1.673689
0.450549	3502	9.7087	0.25145	-0.05855	2150	9.2558	0.5306	-0.10358
2.230098	5655	15.19	5.22985	1.217734	4730	16.934	7.1476	1.395314
1.237696	4054	11.791	1.83085	0.426301	4034	12.419	2.6326	0.513921
0.168784	4739	8.6938	1.26635	-0.29486	4459	8.9482	0.8382	-0.16363
3.103754	4588	26.439	16.47885	3.836986	4393	22.354	12.5676	2.453375
0.580312	3183	8.891	1.06915	-0.24894	1297	9.4063	0.3801	-0.0742
0.269779	5618	11.107	1.14685	0.267036	4629	8.6196	1.1668	-0.22778
0.830045	3712	17.214	7.25385	1.689009	2640	14.205	4.4186	0.862574
0.319154	3380	7.8994	2.06075	-0.47983	4677	6.842	2.9444	-0.57479
0.17164	3322	11.71	1.74985	0.40744	3508	10.975	1.1886	0.232032
-0.13328	4385	9.8518	0.10835	-0.02523	3902	6.0226	3.7638	-0.73475
0.000663	1797	5.4535	4.50665	-1.04934	1500	6.3333	3.4531	-0.67409
0.010579	4122	6.9141	3.04605	-0.70925	2742	5.1787	4.6077	-0.89949
0.204285	2161	7.6354	2.32475	-0.5413	1857	9.5854	0.201	-0.03924
0.194492	4645	13.628	3.66785	0.854033	3942	7.8133	1.9731	-0.38518
0.458302	3989	8.1975	1.76265	-0.41042	3703	8.3986	1.3878	-0.27092
-0.39081	5253	15.762	5.80185	1.350921	4569	11.687	1.9006	0.371024
-0.74315	3784	3.8319	6.12825	-1.42692	3890	3.4961	6.2903	-1.22796
-0.03847	4194	7.2961	2.66405	-0.62031	2866	4.3964	5.39	-1.0522
-0.71167	4063	6.7192	3.24095	-0.75463	2710	6.0886	3.6978	-0.72186
-0.5978	3360	7.1131	2.84705	-0.66292	2044	12.769	2.9826	0.582246
1.786333	3488	25.975	16.01485	3.728947	3362	27.811	18.0246	3.518659
-1.17688	2810	3.0605	6.89965	-1.60654	1987	4.8817	4.9047	-0.95747
-0.40195	3934	6.7616	3.19855	-0.74476	2393	8.4831	1.3033	-0.25442
-1.30266	5793	5.2995	4.66065	-1.0852	4017	5.0784	4.708	-0.91907

-0.57705	3352	13.992	4.03185	0.938788	1223	12.428	2.6416	0.515678
-0.6605	3700	8.2432	1.71695	-0.39978	1731	7.9145	1.8719	-0.36542
-0.86189	2978	9.503	0.45715	-0.10644	2307	10.88	1.0936	0.213486
-0.58935	4277	13.374	3.41385	0.794891	3058	8.7966	0.9898	-0.19322
-0.5384	2333	3.7291	6.23105	-1.45086	1645	6.1398	3.6466	-0.71187
-0.67331	2563	10.105	0.14485	0.033727	958	5.428	4.3584	-0.85082
0.195308	4177	18.339	8.37885	1.950957	1894	17.001	7.2146	1.408393
-0.288	4392	9.1758	0.78435	-0.18263	1597	7.201	2.5854	-0.50471
-0.86755	4468	5.0358	4.92435	-1.1466	2380	6.8067	2.9797	-0.58168
-0.95765	2517	9.5749	0.38525	-0.0897	1188	7.7441	2.0423	-0.39869
0.744556	4555	8.5401	1.42005	-0.33065	2918	10.247	0.4606	0.089916
-0.11374	4196	10.701	0.74085	0.172502	1836	9.2593	0.5271	-0.1029
-0.04702	1368	10.015	0.05485	0.012771	755	6.3576	3.4288	-0.66935
-0.96593	2147	6.9399	3.02025	-0.70324	2228	5.9246	3.8618	-0.75388
0.445448	3089	5.6653	4.29485	-1.00003	4142	9.1502	0.6362	-0.1242
0.664372	2044	11.301	1.34085	0.312208	1804	12.639	2.8526	0.556868
0.536242	1765	6.4589	3.50125	-0.81524	1544	9.5207	0.2657	-0.05187
2.039126	3086	19.345	9.38485	2.185197	2380	17.815	8.0286	1.567297
0.72803	3312	13.104	3.14385	0.732024	2185	11.762	1.9756	0.385665
0.416068	3096	11.628	1.66785	0.388347	2353	14.407	4.6206	0.902007
-0.29944	5112	7.6095	2.35065	-0.54733	3310	5.9517	3.8347	-0.74859
0.11492	3462	11.063	1.10285	0.256791	2180	10.046	0.2596	0.050678
-0.29402	3198	8.1301	1.83005	-0.42611	2019	8.7172	1.0692	-0.20872
-0.1169	3011	7.3398	2.62035	-0.61013	2422	6.3171	3.4693	-0.67726
-0.11943	3449	5.1319	4.82825	-1.12422	2355	6.5817	3.2047	-0.6256
-0.4716	2951	3.8631	6.09705	-1.41966	1571	6.3654	3.421	-0.66783
-0.03121	1426	5.6101	4.35005	-1.01288	1023	13.392	3.6056	0.703865
-0.09676	4168	10.437	0.47685	0.111031	2891	7.7136	2.0728	-0.40464
-1.38364	2454	2.8932	7.06695	-1.64549	1653	4.6582	5.1282	-1.0011
-0.45718	4994	7.7693	2.19085	-0.51012	3269	6.5158	3.2706	-0.63847
-0.71889	3735	5.8902	4.06995	-0.94766	3110	6.3666	3.4198	-0.66759
-0.12837	2570	8.1323	1.82785	-0.4256	2567	10.83	1.0436	0.203726
-0.39442	3656	7.3578	2.60235	-0.60594	2616	6.9572	2.8292	-0.5523
1.229331	3587	12.88	2.91985	0.679867	2996	11.115	1.3286	0.259362
-0.7033	3403	7.1995	2.76065	-0.6428	3920	13.903	4.1166	0.803619
0.544607	2305	8.1562	1.80395	-0.42004	2663	15.096	5.3096	1.03651
-0.82162	4003	4.4217	5.53845	-1.28959	3624	7.8918	1.8946	-0.36985
2.316607	1846	11.213	1.25285	0.291717	1323	18.216	8.4296	1.645578
-0.87175	4682	3.695	6.26515	-1.4588	3103	5.4786	4.3078	-0.84094
-0.99121	3797	2.7127	7.24745	-1.68752	2782	5.284	4.5024	-0.87893
1.749404	3177	17.218	7.25785	1.68994	2057	18.23	8.4436	1.648311
0.152665	3169	6.5951	3.36505	-0.78353	2378	12.363	2.5766	0.502989
-0.98317	4208	8.8165	1.14365	-0.26629	2504	8.147	1.6394	-0.32003
-0.88938	1636	4.401	5.55915	-1.29441	2119	2.7843	7.0021	-1.36691
-0.73686	2968	6.0647	3.89545	-0.90703	3130	6.901	2.8854	-0.56327
-0.99796	2215	3.6117	6.34845	-1.47819	1304	4.0644	5.722	-1.11702
-0.9916	4401	5.317	4.64315	-1.08113	2429	5.4343	4.3521	-0.84959

-0.84555	2747	3.0579	6.90225	-1.60714	3003	4.329	5.4574	-1.06536
-0.67804	2854	9.5305	0.42965	-0.10004	3127	7.4832	2.3032	-0.44962
-1.32247	2004	4.3413	5.61885	-1.30831	1773	5.2453	4.5411	-0.88649
-0.59617	2630	4.2586	5.70155	-1.32757	3840	3.9583	5.8281	-1.13773
-0.48815	1844	4.6095	5.35065	-1.24586	2082	1.9693	7.8171	-1.52601
0.35996	3728	13.224	3.26385	0.759965	3389	12.659	2.8726	0.560773
-1.06617	2500	5.12	4.84015	-1.127	3863	3.9348	5.8516	-1.14232
-0.21738	3997	11.058	1.09785	0.255627	3380	14.734	4.9476	0.965842
1.617396	2699	18.155	8.19485	1.908114	2404	16.681	6.8946	1.345924
2.276821	1524	12.992	3.03185	0.705945	1855	11.213	1.4266	0.278493
0.380975	2681	13.502	3.54185	0.824695	2504	10.104	0.3176	0.062
1.76491	2835	15.45	5.48985	1.278274	2522	20.381	10.5946	2.068217
0.07289	3518	9.2951	0.66505	-0.15485	1763	13.33	3.5436	0.691761
0.284673	3478	7.9068	2.05335	-0.47811	2527	11.476	1.6896	0.329834
-0.40642	1254	6.6188	3.34135	-0.77801	1433	9.9791	0.1927	0.037618
0.001296	2238	10.054	0.09385	0.021852	1674	11.47	1.6836	0.328663
0.491559	2579	8.608	1.35215	-0.31484	1647	9.7146	0.0718	-0.01402
1.519666	2102	20.362	10.40185	2.421999	1973	18.348	8.5616	1.671347
1.075697	2751	13.74	3.77985	0.880112	2973	19.341	9.5546	1.865194
-0.41115	3555	11.449	1.48885	0.346668	2278	9.6576	0.1288	-0.02514
-0.39354	2623	7.663	2.29715	-0.53488	2356	5.1358	4.6506	-0.90786
-0.63897	2024	6.0277	3.93245	-0.91564	2177	6.9362	2.8502	-0.5564
0.263454	3005	8.0532	1.90695	-0.44402	2880	7.6736	2.1128	-0.41245
0.166131	1663	6.9152	3.04495	-0.709	4380	10.205	0.4186	0.081717
-0.26645	2924	5.472	4.48815	-1.04503	3554	5.5431	4.2433	-0.82835
-0.89837	2624	7.0122	2.94795	-0.68641	4273	5.289	4.4974	-0.87796
-0.83323	2918	4.3866	5.57355	-1.29776	4471	5.4574	4.329	-0.84508
-0.25919	4079	4.7561	5.20405	-1.21173	5423	10.603	0.8166	0.159412
0.843919	2892	13.451	3.49085	0.81282	2292	12.914	3.1276	0.610552
0.559093	3204	13.639	3.67885	0.856595	3245	15.285	5.4986	1.073405
-0.66705	3979	16.587	6.62685	1.543016	3319	14.221	4.4346	0.865697
0.34527	3402	14.345	4.38485	1.020982	3564	17.621	7.8346	1.529426
0.374038	3574	5.4561	4.50405	-1.04874	2779	8.0964	1.69	-0.32991
0.521347	3576	15.492	5.53185	1.288053	3278	12.843	3.0566	0.596692
0.365877	2897	8.0428	1.91735	-0.44644	1946	9.8664	0.08	0.015617
-0.68229	3414	6.7077	3.25245	-0.75731	2282	9.1148	0.6716	-0.13111
1.127724	2913	10.882	0.92185	0.214646	2986	9.0087	0.7777	-0.15182
2.121554	2958	9.9053	0.05485	-0.01277	2820	10.355	0.5686	0.110999
-0.2537	2196	8.6976	1.26255	-0.29398	2607	9.9731	0.1867	0.036447
-0.03621	2892	15.214	5.25385	1.223323	2808	9.5442	0.2422	-0.04728
0.45973	4446	8.6595	1.30065	-0.30285	3565	7.7419	2.0445	-0.39912
-0.60647	2291	5.9363	4.02385	-0.93693	2105	10.736	0.9496	0.185375
1.320533	1418	14.175	4.21485	0.981399	1330	14.662	4.8756	0.951787
0.590106	2165	10.577	0.61685	0.143629	2809	17.088	7.3016	1.425377
-0.37579	2570	8.9494	1.01075	-0.23535	3697	8.7098	1.0766	-0.21017
0.944505	3616	11.338	1.37785	0.320823	4174	13.56	3.7736	0.736661
-0.40323	3656	4.7593	5.20085	-1.21098	3633	9.1935	0.5929	-0.11574

3.450605	4360	12.477	2.51685	0.586031	4361	21.234	11.4476	2.234735
1.988935	2781	9.6728	0.28735	-0.06691	2775	12.937	3.1506	0.615042
1.179956	2988	13.286	3.32585	0.774401	2923	11.221	1.4346	0.280054
1.868557	4166	13.058	3.09785	0.721313	3552	11.515	1.7286	0.337447
2.027292	3483	8.039	1.92115	-0.44733	3256	10.627	0.8406	0.164097
0.233461	2628	11.377	1.41685	0.329904	2329	15.672	5.8856	1.148953
1.816937	3232	9.6844	0.27575	-0.06421	2491	14.452	4.6656	0.910792
2.896052	2984	13.271	3.31085	0.770908	2556	19.914	10.1276	1.977052
2.679984	2546	16.614	6.65385	1.549303	1645	19.635	9.8486	1.922587
1.865497	2363	15.616	5.65585	1.316926	1757	19.636	9.8496	1.922783
1.27585	3777	11.226	1.26585	0.294744	1855	14.933	5.1466	1.00469
0.394237	3469	10.666	0.70585	0.164352	1881	10.579	0.7926	0.154727
0.724561	5180	16.004	6.04385	1.407269	2912	21.463	11.6766	2.279439
0.35894	3642	9.1433	0.81685	-0.1902	3082	10.902	1.1156	0.217781
-0.10631	1597	10.394	0.43385	0.101019	2675	9.6075	0.1789	-0.03492
-0.85437	3846	5.9022	4.05795	-0.94487	2794	6.4424	3.344	-0.6528
1.860804	4021	21.363	11.40285	2.655075	2368	24.367	14.5806	2.846341
0.545015	2428	8.8962	1.06395	-0.24773	2084	15.019	5.2326	1.021478
-0.42188	2830	12.226	2.26585	0.527587	3316	13.842	4.0556	0.791711
-0.15975	1687	7.9431	2.01705	-0.46966	1425	9.0526	0.7338	-0.14325
-0.29185	3387	11.81	1.84985	0.430725	3226	12.027	2.2406	0.437397
-0.23377	2100	12.619	2.65885	0.619095	1582	9.9874	0.201	0.039238
-1.11097	2501	18.513	8.55285	1.991472	3208	18.61	8.8236	1.722493
-0.10847	2302	10.469	0.50885	0.118482	4134	11.03	1.2436	0.242768
0.48401	2408	26.495	16.53485	3.850025	1835	24.196	14.4096	2.81296
-0.32591	2775	11.784	1.82385	0.424671	2933	8.4555	1.3309	-0.25981
0.769448	830	8.7952	1.16495	-0.27125	679	12.077	2.2906	0.447158
0.095904	3222	13.16	3.19985	0.745063	2427	9.4355	0.3509	-0.0685
-1.22664	2392	12.249	2.28885	0.532943	1845	10.515	0.7286	0.142233
0.560317	1904	9.5588	0.40135	-0.09345	1412	5.0283	4.7581	-0.92885
0.178577	1618	10.878	0.91785	0.213715	1387	15.141	5.3546	1.045294
-0.4986	1806	10.908	0.94785	0.2207	2321	5.7303	4.0561	-0.79181
0.34629	2577	20.14	10.17985	2.370308	2251	25.766	15.9796	3.119446
-0.4115	2354	6.9244	3.03575	-0.70685	2201	6.8151	2.9713	-0.58004
-0.59186	1888	10.169	0.20885	0.048629	2758	7.5417	2.2447	-0.4382
-1.04052	2075	8.241	1.71915	-0.40029	1782	5.3311	4.4553	-0.86974
-0.74037	2737	8.1476	1.81255	-0.42204	3555	6.4979	3.2885	-0.64196
-1.22892	1869	5.297	4.66315	-1.08578	2858	2.6592	7.1272	-1.39133
-0.81219	2357	9.249	0.71115	-0.16559	3194	6.2617	3.5247	-0.68807
-0.86283	2601	14.225	4.26485	0.993041	3968	8.4929	1.2935	-0.25251
0.619894	4587	12.23	2.26985	0.528519	4669	19.148	9.3616	1.827518
0.731906	2812	14.047	4.08685	0.951595	2610	13.716	3.9296	0.767114
0.368121	2604	7.7573	2.20285	-0.51292	2599	11.543	1.7566	0.342913
-0.08413	2675	9.1589	0.80125	-0.18657	2099	9.5283	0.2581	-0.05038
2.013214	2162	12.165	2.20485	0.513384	2457	17.257	7.4706	1.458368
0.887581	2470	9.3927	0.56745	-0.13213	1637	10.324	0.5376	0.104947
1.890592	2341	10.679	0.71885	0.167379	2662	11.946	2.1596	0.421585

0.400562	2627	12.828	2.86785	0.667759	2843	16.426	6.6396	1.296145
0.44096	3351	16.234	6.27385	1.460823	2830	16.784	6.9976	1.366031
0.4126	3758	12.241	2.28085	0.53108	2345	18.337	8.5506	1.669199
0.277124	2939	8.098	1.86215	-0.43359	1960	10.816	1.0296	0.200993
0.296711	2807	11.186	1.22585	0.285431	3040	8.9803	0.8061	-0.15736
0.245703	2282	11.174	1.21385	0.282637	1896	10.97	1.1836	0.231056
-0.54893	2710	8.4502	1.50995	-0.35158	2880	11.146	1.3596	0.265413
0.546443	1553	11.719	1.75885	0.409536	2227	7.6785	2.1079	-0.41149
-0.22691	3293	9.3835	0.57665	-0.13427	3336	7.2542	2.5322	-0.49432
0.022025	1700	6.8824	3.07775	-0.71663	2187	7.4989	2.2875	-0.44655
0.145932	2806	10.941	0.98085	0.228384	3847	13.725	3.9386	0.768871
0.762715	2814	15.174	5.21385	1.214009	3883	18.002	8.2156	1.603802
-0.59162	2805	10.196	0.23585	0.054916	3804	5.9148	3.8716	-0.75579
3.339205	5140	10.447	0.48685	0.11336	4523	19.036	9.2496	1.805654
5.085089	1654	20.738	10.77785	2.509548	2004	19.261	9.4746	1.849577
3.302275	1689	16.045	6.08485	1.416815	2000	24.9	15.1136	2.950391
2.078504	2508	18.74	8.77985	2.044327	2643	24.442	14.6556	2.860982
3.971901	2785	10.485	0.52485	0.122208	3929	15.373	5.5866	1.090584
2.194393	2564	8.2293	1.73085	-0.40302	3637	11.301	1.5146	0.295672
3.06254	3089	14.471	4.51085	1.05032	3208	18.111	8.3246	1.625081
2.957465	2953	13.444	3.48385	0.81119	2748	17.504	7.7176	1.506586
8.00292	436	20.413	10.45285	2.433874	1467	15.951	6.1646	1.203418
7.058058	1738	11.738	1.77785	0.41396	2586	12.336	2.5496	0.497718
3.818063	1720	15.116	5.15585	1.200504	2415	17.101	7.3146	1.427914
2.072995	3494	14.11	4.14985	0.966264	4367	20.701	10.9146	2.130686
1.096304	3279	16.865	6.90485	1.607747	4120	16.845	7.0586	1.37794
0.657027	3233	14.785	4.82485	1.123433	4319	16.115	6.3286	1.235433
2.684473	2990	15.819	5.85885	1.364193	4210	14.299	4.5126	0.880924
4.653769	347	31.124	21.16385	4.927856	786	17.43	7.6436	1.49214
0.90778	2531	14.5	4.53985	1.057073	4955	17.175	7.3886	1.44236
0.678246	1780	13.539	3.57885	0.83331	2677	13.821	4.0346	0.787612
0.092232	4513	12.63	2.66985	0.621656	6239	18.368	8.5816	1.675251
0.541342	1292	16.486	6.52585	1.519499	2891	9.8582	0.0718	0.014016
3.214746	4320	15.046	5.08585	1.184205	3453	16.594	6.8076	1.328941
3.863153	4100	20.488	10.52785	2.451337	4989	18.841	9.0546	1.767587
2.513496	4372	14.433	4.47285	1.041472	3991	21.373	11.5866	2.26187
4.099012	3352	21.689	11.72885	2.730981	4053	25.043	15.2566	2.978306
3.043973	3527	11.483	1.52285	0.354585	3072	17.578	7.7916	1.521032
2.059325	5036	17.752	7.79185	1.814278	3153	22.518	12.7316	2.48539
2.216428	3550	16.366	6.40585	1.491558	2461	21.658	11.8716	2.317506
1.774091	2944	16.882	6.92185	1.611705	3415	23.602	13.8156	2.697002
2.985825	4148	16.321	6.36085	1.48108	3091	22.161	12.3746	2.415699
2.16338	3699	13.896	3.93585	0.916435	3287	27.168	17.3816	3.393137
2.352312	5069	17.775	7.81485	1.819634	2547	20.141	10.3546	2.021366
1.085286	4452	18.104	8.14385	1.896239	2779	20.619	10.8326	2.114678
1.143027	3198	18.699	8.73885	2.034781	2713	16.292	6.5056	1.269986
0.425657	2753	13.513	3.55285	0.827257	3080	17.435	7.6486	1.493116

0.244683	2251	13.638	3.67785	0.856362	3893	12.15	2.3636	0.461408
0.687836	2860	8.4266	1.53355	-0.35708	3209	10.751	0.9646	0.188304
0.401378	4057	13.187	3.22685	0.75135	4019	11.52	1.7336	0.338423
0.569499	2817	16.152	6.19185	1.441729	2256	16.401	6.6146	1.291264
0.145728	2377	17.543	7.58285	1.765614	3308	14.964	5.1776	1.010741
-0.35323	2962	13.201	3.24085	0.754609	3676	19.505	9.7186	1.89721
-1.11024	3608	6.2639	3.69625	-0.86065	3730	5.1475	4.6389	-0.90558
-0.71481	2045	8.1663	1.79385	-0.41769	2829	6.6808	3.1056	-0.60626
-0.98872	5046	11.732	1.77185	0.412563	5197	12.661	2.8746	0.561163
-1.03716	2117	5.5267	4.43345	-1.0323	2852	5.54	4.2464	-0.82896
-1.01804	2509	3.5074	6.45275	-1.50248	2500	4.76	5.0264	-0.98123
-0.0398	3919	6.124	3.83615	-0.89322	2929	7.238	2.5484	-0.49748
-1.64925	1866	3.4834	6.47675	-1.50807	1948	4.6201	5.1663	-1.00854
-1.08794	1206	7.131	2.82915	-0.65875	1313	1.904	7.8824	-1.53876
-0.33036	3054	5.1408	4.81935	-1.12215	3485	4.1894	5.597	-1.09261
-0.26598	2277	10.365	0.40485	0.094267	2903	8.8185	0.9679	-0.18895
-0.27745	2840	5.9155	4.04465	-0.94177	3844	8.897	0.8894	-0.17362
-1.38348	3100	8.3548	1.60535	-0.37379	3071	5.8938	3.8926	-0.75989
-1.24904	3327	10.249	0.28885	0.067257	3107	6.1796	3.6068	-0.7041
-0.86891	1657	3.9228	6.03735	-1.40576	2872	3.8997	5.8867	-1.14917
-1.05811	2271	7.3096	2.65055	-0.61716	4091	3.0066	6.7798	-1.32351
-1.16824	3297	13.436	3.47585	0.809328	4350	5.7241	4.0623	-0.79302
-1.0635	2961	8.4769	1.48325	-0.34536	3578	5.6177	4.1687	-0.81379
-0.9764	4070	10.983	1.02285	0.238164	5075	6.5419	3.2445	-0.63337
-0.80632	3699	9.7864	0.17375	-0.04046	4081	5.7829	4.0035	-0.78154
-1.1275	2038	4.4161	5.54405	-1.29089	2713	5.4184	4.368	-0.8527
0.865138	1341	12.528	2.56785	0.597906	2120	12.736	2.9496	0.575804
0.499516	2316	11.572	1.61185	0.375308	3483	14.097	4.3106	0.841491
0.849632	4401	10.816	0.85585	0.199279	4434	10.487	0.7006	0.136767
0.840042	1758	12.173	2.21285	0.515247	3661	13.494	3.7076	0.723776
-0.22871	2320	5.9914	3.96875	-0.9241	2845	8.3656	1.4208	-0.27736
1.032646	1894	11.827	1.86685	0.434683	2927	12.607	2.8206	0.550621
-0.60508	2034	8.6529	1.30725	-0.30438	2503	4.8342	4.9522	-0.96674
-0.18566	2737	10.047	0.08685	0.020222	4310	6.5893	3.1971	-0.62412
-0.00066	2975	6.7563	3.20385	-0.74599	2836	8.3921	1.3943	-0.27219
-0.40301	2804	8.7375	1.22265	-0.28469	2936	8.9237	0.8627	-0.16841
-0.4671	2559	4.025	5.93515	-1.38196	2264	4.5936	5.1928	-1.01371
-0.60906	915	12.022	2.06185	0.480087	1693	9.0372	0.7492	-0.14625
-0.38622	2526	8.0364	1.92375	-0.44793	3842	7.9906	1.7958	-0.35057
-0.94746	3461	7.6856	2.27455	-0.52961	4798	4.9812	4.8052	-0.93804
-0.89189	2227	3.9964	5.96375	-1.38862	3363	3.3601	6.4263	-1.25451
-0.80952	2739	6.4257	3.53445	-0.82297	5146	5.752	4.0344	-0.78757
-1.11048	2751	5.2708	4.68935	-1.09188	5229	3.4615	6.3249	-1.23471
-1.41194	3784	9.3816	0.57855	-0.13471	4373	5.4196	4.3668	-0.85246
-1.08618	2763	5.3565	4.60365	-1.07193	4509	5.1674	4.619	-0.90169
-1.28779	2808	8.084	1.87615	-0.43685	2790	3.2258	6.5606	-1.28072
2.288247	2909	8.2159	1.74425	-0.40614	2135	10.351	0.5646	0.110218

2.717321	4752	17.34	7.37985	1.718347	4290	18.065	8.2786	1.616101
-0.66862	3031	9.1719	0.78825	-0.18354	3961	8.3565	1.4299	-0.27914
-0.03351	2884	8.3564	1.60375	-0.37342	3060	7.2549	2.5315	-0.49418
-0.191	3915	8.2503	1.70985	-0.39813	3635	12.985	3.1986	0.624412
-0.62569	5396	11.675	1.71485	0.399291	3935	9.2249	0.5615	-0.10961
-0.23413	3384	15.396	5.43585	1.2657	3203	13.362	3.5756	0.698008
1.527419	2690	7.1004	2.85975	-0.66587	1752	7.3059	2.4805	-0.48423
-0.09539	2567	13.167	3.20685	0.746693	4120	11.335	1.5486	0.302309
0.280388	3541	9.1217	0.83845	-0.19523	2757	7.9434	1.843	-0.35978
1.303394	2164	12.338	2.37785	0.553666	2772	13.672	3.8856	0.758525
1.267077	2891	10.239	0.27885	0.064928	3041	8.1552	1.6312	-0.31843
-0.77467	2616	12.844	2.88385	0.671485	3626	8.0805	1.7059	-0.33302
-0.78128	2755	5.5172	4.44295	-1.03451	2792	5.9814	3.805	-0.74279
-0.1554	1939	22.228	12.26785	2.856484	2773	11.143	1.3566	0.264828
-1.48774	2181	7.8863	2.07385	-0.48288	2783	5.2821	4.5043	-0.8793
-1.41475	3021	6.852	3.10815	-0.72371	5725	4.559	5.2274	-1.02046
-1.30403	3071	18.333	8.37285	1.94956	4566	12.9	3.1136	0.607819
-1.05076	2724	8.7372	1.22295	-0.28476	2626	3.9223	5.8641	-1.14476
-1.0079	2198	7.5978	2.36235	-0.55006	4054	3.9221	5.8643	-1.1448
-0.49874	4008	9.3313	0.62885	-0.14642	2968	10.647	0.8606	0.168001
-0.115	2014	14.3	4.33985	1.010504	2456	12.622	2.8356	0.55355
-0.42056	1894	8.3421	1.61805	-0.37675	1432	5.4469	4.3395	-0.84713
-1.09569	1897	11.123	1.16285	0.270762	2096	9.1603	0.6261	-0.12222
1.089571	2598	20.593	10.63285	2.475785	2608	12.577	2.7906	0.544765
0.890438	2449	12.332	2.37185	0.552269	1718	10.594	0.8076	0.157655
0.253456	2426	9.7692	0.19095	-0.04446	1861	9.1349	0.6515	-0.12718
-0.42441	2165	13.58	3.61985	0.842857	2172	16.667	6.8806	1.343191
0.290386	2404	13.062	3.10185	0.722244	2018	13.28	3.4936	0.682001
-0.1038	2211	12.935	2.97485	0.692673	3313	17.386	7.5996	1.48355
1.087122	486	9.6708	0.28935	-0.06737	307	9.4463	0.3401	-0.06639
0.040673	1696	10.672	0.71185	0.165749	1592	6.093	3.6934	-0.721
0.353635	605	14.215	4.25485	0.990712	643	13.841	4.0546	0.791516
-0.53169	2428	15.239	5.27885	1.229144	3007	7.416	2.3704	-0.46274
-0.93012	1561	8.5202	1.43995	-0.33528	2277	8.0369	1.7495	-0.34153
-0.85379	2391	6.399	3.56115	-0.82919	2559	7.6592	2.1272	-0.41526
-0.13506	1541	8.6308	1.32935	-0.30953	2732	7.1742	2.6122	-0.50994
-1.11869	2317	10.703	0.74285	0.172967	4065	8.0197	1.7667	-0.34489
-1.26559	998	7.7154	2.24475	-0.52267	2357	3.9881	5.7983	-1.13191
-0.40729	1572	10.433	0.47285	0.1101	2324	7.5301	2.2563	-0.44046
		9.96015	2.90185			9.7864	3.4612	
			8.70555				10.3836	
			4.294738				5.122576	
	2080	31.827	2622	30.816	1501	36.775		
	4188	42.479	3097	31.611	4042	39.634		
	1753	31.375	1806	38.594	3218	28.931		
	3580	38.939	3023	36.553	3927	39.7		

mn	2900.25	36.155	2637	34.3935	3172	36.26
sd	1170.378	5.456605	591.9972	3.779262	1172.075	5.072703
	812	7.6355	1247	6.8164	1516	9.3668
	1629	4.911	766	4.6997	1767	8.206
	350	5.1429	566	6.8905	1476	4.1328
	1940	4.5361	823	6.5614	1630	6.0123
mn	1182.75	5.556375	850.5	6.242	1597.25	6.929475
sd	731.0939	1.40845	286.3849	1.037817	130.6277	2.326132
3posSD		16.36982		11.33778		15.21811
3negSD		4.225349		3.113451		6.978396
Sum3SD		20.59516		14.45124		22.1965
MnDiff		30.59863		28.1515		29.33053
SumovrMn		0.673075		0.513338		0.756771
1minus		0.326925		0.486662		0.243229
	2190	29.635	5851	18.424	1385	31.625
	5358	26.652	6297	23.281	6846	25.212
PLK1 SMAR	145	26.897	340	16.765	190	22.105
PLK1 SMAR	115	42.609	161	35.404	170	38.824
	677	9.3058	1996	12.275	2404	15.017
	3037	13.566	3267	15.549	3693	12.591

Y

Y

Y

x art a

Y

Y

Y

x	toxic a,b
x	toxic a,b
Y	
x	toxic a,b,c
x	toxic a
x	toxic a,b,c
X	debris a,b
X	debris a,c
X	debris a,c
X	debris a,c
X	debris a,c
X	debris a,c
X	debris a,c

					cell ct	% inf	AD
50064	A02	M-014232- stromal an	64940	FLJ13195	2636	3.1108	7.4582
50064	A04	M-013550- mitochond	64928	MRPL14	2415	4.3478	6.2212
50064	A05	M-014044- interferon	64163	IFRG15	2025	4.7407	5.8283
50064	A06	M-016339- tetratricop	64927	TTC23	1729	10.642	0.073
50064	A07	M-005934- leukocyte-	64167	LRAP	2807	7.2675	3.3015
50064	A08	M-031241- hypothetic	64926	FLJ21438	3356	7.36	3.209
50064	A09	M-018118- EF-hand ca	64168	EFCBP1	3465	15.267	4.698
50064	A10	M-019360- coiled-coil	64925	CCDC71	2284	5.6042	4.9648
50064	A11	M-004400- caspase re	64170	CARD9	1100	9.1818	1.3872
50064	A12	M-007526- solute carri	64924	SLC30A5	2075	9.494	1.075
50064	A13	M-005982- O-sialoglyc	64172	OSGEPL1	1551	9.6712	0.8978
50064	A14	M-014231- leucine ric	64922	LRRC19	2805	10.873	0.304
50064	A15	M-014045- spermatog	64173	SPATA1	2758	11.313	0.744
50064	A16	M-016926- CAS1 doma	64921	CASD1	2881	11.211	0.642
50064	A17	M-004271- leucine pro	64175	LEPRE1	1500	5.2	5.369
50064	A18	M-005082- B-cell CLL/l	64919	BCL11B	1105	13.846	3.277
50064	A19	M-013033- family with	64184	FAM12B	1407	11.158	0.589
50064	A20	M-015496- RAN bindin	64901	RANBP17	1626	15.252	4.683
50064	A21	M-007044- chromoson	64207	C14orf4	1666	6.0024	4.5666
50064	A23	M-017314- popeye do	64208	POPDC3	1982	11.1	0.531
50064	B02	M-026308- F-box and l	79176	FBXL15	3116	17.683	7.114
50064	B04	M-012894- zinc finger	79027	ZNF655	1630	14.601	4.032
50064	B05	M-014234- 5'-nucleoti	64943	NT5DC2	2603	11.602	1.033
50064	B06	M-014325- chromoson	79144	C20orf149	2817	8.0582	2.5108
50064	B07	M-013546- mitochond	64949	MRPS26	3099	8.648	1.921
50064	B08	M-014268- chromoson	78998	C8orf51	3237	17.084	6.515
50064	B09	M-013534- mitochond	64951	MRPS24	4436	6.3345	4.2345
50064	B10	M-012886- Ly6/neurot	66004	LYNX1	2564	9.2044	1.3646
50064	B11	M-013609- mitochond	64960	MRPS15	2911	4.878	5.691
50064	B12	M-014313- chromoson	79098	C1orf116	2757	10.301	0.268
50064	B13	M-019184- mitochond	64965	MRPS9	1974	7.3961	3.1729
50064	B14	M-013739- chromoson	64758	C14orf136	3066	6.1644	4.4046
50064	B15	M-019243- mitochond	64968	MRPS6	2901	6.8252	3.7438
50064	B16	M-014339- centromer	79172	CENPO	1837	12.357	1.788
50064	B17	M-019247- mitochond	64969	MRPS5	2869	10.561	0.008
50064	B18	M-015657- RNA bindin	79171	RBM42	2320	7.1121	3.4569
50064	B19	M-013572- mitochond	64975	MRPL41	4139	9.8575	0.7115
50064	B20	M-014338- ATPase fan	79170	ATAD4	3889	10.44	0.129
50064	B21	M-017608- mitochond	64976	MRPL40	4558	4.8267	5.7423
50064	B23	M-013573- mitochond	64978	MRPL38	2044	4.4521	6.1169
50064	C02	M-014230- chromoson	64897	C12orf43	2864	8.0656	2.5034
50064	C04	M-009854- poly(A) pol	64895	PAPOLG	2911	9.9279	0.6411
50064	C05	M-017823- MMS19-lik	64210	MMS19L	3434	11.386	0.817
50064	C06	M-012854- protocadhe	64881	PCDH20	4416	12.115	1.546
50064	C07	M-004887- DnaJ (Hsp4	64215	DNAJC1	2072	4.8263	5.7427
50064	C08	M-010732- CUB domai	64866	CDCP1	2062	13.046	2.477

50064	C09	M-015686- sema doma	64218	SEMA4A	3202	4.1849	6.3841
50064	C10	M-014227- regulatory	64864	RFXDC2	4042	11.034	0.465
50064	C11	M-007045- praja 1	64219	PJA1	2675	6.5421	4.0269
50064	C12	M-014226- methyltran	64863	METTL4	3267	11.448	0.879
50064	C13	M-016467- stimulated	64220	STRA6	2273	7.1271	3.4419
50064	C14	M-014225- armadillo r	64860	ARMCX5	2104	16.968	6.399
50064	C15	M-026504- roundabou	64221	ROBO3	2721	7.24	3.329
50064	C16	M-014224- oligonuclec	64859	OBFC2A	4165	5.9064	4.6626
50064	C17	M-017824- torsin fami	64222	TOR3A	1760	3.9205	6.6485
50064	C18	M-016331- von Willeb	64856	VWA1	1656	6.7029	3.8661
50064	C19	M-016093- G protein b	64223	GBL	1873	9.9306	0.6384
50064	C20	M-014222- chromoson	64853	C1orf80	3303	12.625	2.056
50064	C21	M-018276- HERPUD fa	64224	HERPUD2	3545	7.8984	2.6706
50064	C23	M-014047- ADP-ribosy	64225	ARL6IP2	5349	7.5154	3.0536
50064	D02	M-014336- chromoson	79169	C1orf35	3810	8.3202	2.2488
50064	D04	M-004156- chromoson	79161	C7orf23	2368	13.64	3.071
50064	D05	M-013574- mitochond	64979	MRPL36	2031	7.7794	2.7896
50064	D06	M-014330- nucleolar p	79159	NOL12	2727	10.341	0.228
50064	D07	M-012885- mitochond	64981	MRPL34	2317	6.9486	3.6204
50064	D08	M-031144- N-acetylglu	79158	GNPTAB	3106	10.753	0.184
50064	D09	M-013123- mitochond	65003	MRPL11	3873	12.058	1.489
50064	D10	M-014329- major facili	79157	MFSD11	3666	7.5832	2.9858
50064	D11	M-013498- mitochond	65005	MRPL9	2747	11.467	0.898
50064	D12	M-018423- pleckstrin h	79156	PLEKHF1	3283	7.5236	3.0454
50064	D13	M-007494- solute carri	65010	SLC26A6	2625	8.0762	2.4928
50064	D14	M-014328- TNFAIP3 in	79155	TNIP2	3309	8.7035	1.8655
50064	D15	M-007489- solute carri	65012	SLC26A10	4139	8.6494	1.9196
50064	D16	M-003997- glycerophо	79153	GDPD3	3529	12.978	2.409
50064	D17	M-014235- receptor ac	65055	REEP1	3296	13.926	3.357
50064	D18	M-009624- fatty acid 2	79152	FA2H	4717	7.6956	2.8734
50064	D19	M-014236- GC-rich prc	65056	GPBP1	5450	8.3486	2.2204
50064	D20	M-014327- zinc finger	79149	ZSCAN5	3916	10.521	0.048
50064	D21	M-031856- neurobeacl	65065	NBEAL1	4167	5.4476	5.1214
50064	D23	M-012858- mitochond	65080	MRPL44	2531	5.1758	5.3932
50064	E02	M-014221- terminal ur	64852	TUT1	3214	14.499	3.93
50064	E04	M-007393- solute carri	64849	SLC13A3	3800	15.474	4.905
50064	E05	M-017543- membrane	64232	MS4A5	2290	19.913	9.344
50064	E06	M-014220- YTH domai	64848	YTHDC2	2415	14.534	3.965
50064	E07	M-010731- PDZ and LII	64236	PDLIM2	3616	10.537	0.032
50064	E08	M-018059- spermatog	64847	SPATA20	2228	11.939	1.37
50064	E09	M-015651- rhomboid 5	64285	RHBDF1	2608	10.084	0.485
50064	E10	M-007055- membrane	64844	MARCH7	3759	8.6725	1.8965
50064	E11	M-007046- zinc finger	64288	ZNF323	2833	8.4716	2.0974
50064	E12	M-005239- glucosamin	64841	GNPNAT1	1590	7.1698	3.3992
50064	E13	M-018198- nucleolar c	64318	NOC3L	1750	10.629	0.06
50064	E14	M-024385- F-box and l	64839	FBXL17	1467	9.5433	1.0257
50064	E15	M-014091- fibrosin	64319	FBRS	1485	6.936	3.633

50064	E16	M-014219- fibronectin	64838	FNDC4	3303	6.267	4.302
50064	E17	M-007047- ring finger	64320	RNF25	3523	8.1749	2.3941
50064	E18	M-009355- elongation	64834	ELOVL1	3826	6.5342	4.0348
50064	E19	M-013028- SRY (sex de	64321	SOX17	3299	12.367	1.798
50064	E20	M-009273- cytochrom	64816	CYP3A43	4009	16.064	5.495
50064	E21	M-007049- ring finger	64326	RFWD2	4595	9.2057	1.3633
50064	E23	M-027196- exportin 4	64328	XPO4	1770	6.1017	4.4673
50064	F02	M-014326- coiled-coil-	79145	CHCHD7	4141	9.901	0.668
50064	F04	M-014324- PHD finger	79142	PHF23	1824	8.0592	2.5098
50064	F05	M-013330- vacuolar pr	65082	VPS33A	2410	12.531	1.962
50064	F06	M-014323- coiled-coil	79140	CCDC28B	2247	13.218	2.649
50064	F07	M-017285- nucleolar p	65083	NOL6	2398	6.9224	3.6466
50064	F08	M-010733- Der1-like d	79139	DERL1	2991	12.471	1.902
50064	F09	M-018130- transmem	65084	TMEM135	3262	9.3807	1.1883
50064	F10	M-018422- family with	79137	FAM134A	2977	15.888	5.319
50064	F11	M-014238- jumonji do	65094	JMJD4	2485	16.821	6.252
50064	F12	M-014319- lymphocyt	79136	LY6G6E	2349	8.3865	2.1825
50064	F13	M-012870- hypothetic	65095	FLJ12949	4393	8.7412	1.8278
50064	F14	M-014318- apolipopro	79135	APOO	4272	8.427	2.142
50064	F15	M-012871- UPF3 regul	65109	UPF3B	2684	10.32	0.249
50064	F16	M-014317- chromoso	79133	C20orf7	3484	11.079	0.51
50064	F17	M-012872- UPF3 regul	65110	UPF3A	3507	5.6173	4.9517
50064	F18	M-007060- ring finger	79102	RNF26	4322	10.689	0.12
50064	F19	M-016134- arginine/se	65117	RSRC2	5235	14.785	4.216
50064	F20	M-014314- Josephin d	79101	JOSD3	4861	15.923	5.354
50064	F21	M-014239- PRAME fa	65121	PRAMEF1	4155	6.3779	4.1911
50064	F23	M-014240- PRAME fa	65122	PRAMEF2	4442	10.536	0.033
50064	G02	M-007941- interleukin	64806	IL25	3398	11.654	1.085
50064	G04	M-008951- nicotinami	64802	NMNAT1	2505	14.251	3.682
50064	G05	M-013497- nuclear fac	64332	NFKBIZ	3425	9.3139	1.2551
50064	G06	M-014217- ARV1 hom	64801	ARV1	3371	11.391	0.822
50064	G07	M-010047- Rho GTPas	64333	ARHGAP9	1891	6.8747	3.6943
50064	G08	M-014216- CAP-bindin	64800	FLJ23588	2993	6.5486	4.0204
50064	G09	M-013029- HCLS1 bind	64342	HS1BP3	2023	6.7227	3.8463
50064	G10	M-014215- DEP domai	64798	DEPDC6	4037	12.336	1.767
50064	G11	M-014092- 5-azacytidi	64343	AZI2	3338	15.368	4.799
50064	G12	M-015437- required fo	64795	RMND5A	2092	8.0306	2.5384
50064	G13	M-017341- nucleored	64359	NXN	2617	16.049	5.48
50064	G14	M-012931- DEAD (Asp-	64794	DDX31	3536	14.593	4.024
50064	G15	M-018813- SIL1 homol	64374	SIL1	3065	10.669	0.1
50064	G16	M-014214- coiled-coil	64793	CCDC21	3172	11.885	1.316
50064	G17	M-007050- IKAROS fa	64375	IKZF4	1827	6.3492	4.2198
50064	G18	M-014213- RAB, mem	64792	RABL5	3384	12.264	1.695
50064	G19	M-007051- IKAROS fa	64376	IKZF5	3880	9.768	0.801
50064	G20	M-014212- chromoso	64789	C1orf176	3385	7.5037	3.0653
50064	G21	M-010067- carbohydr	64377	CHST8	4330	7.1824	3.3866
50064	G23	M-018120- gremlin 2,	64388	GREM2	4997	4.0024	6.5666

50064	H02	M-015259- hypothetic	79100	MGC4473	3042	9.8291	0.7399
50064	H04	M-014313- chromoson	79098	C1orf116	2635	20.569	10
50064	H05	M-018360- integrator	65123	INTS3	3151	13.678	3.109
50064	H06	M-007059- tripartite	79097	TRIM48	3419	17.227	6.658
50064	H07	M-014241- ankyrin rep	65124	ANKRD57	1959	4.9515	5.6175
50064	H08	M-014312- chromoson	79096	C11orf49	2102	6.6127	3.9563
50064	H09	M-007056- zinc finger	65243	ZNF643	2086	9.2522	1.3168
50064	H10	M-014311- chromoson	79095	C9orf16	3031	8.677	1.892
50064	H11	M-014242- spermatog	65244	SPATS2	4741	19.595	9.026
50064	H12	M-014310- ChaC, catio	79094	CHAC1	1495	10.569	0
50064	H13	M-031236- zinc finger,	65249	ZSWIM4	3301	8.1793	2.3897
50064	H14	M-014309- chromoson	79091	C16orf68	2836	9.9788	0.5902
50064	H15	M-014243- hypothetic	65250	FLJ13231	3924	12.997	2.428
50064	H16	M-014308- trafficking	79090	TRAPPC6A	3994	8.7882	1.7808
50064	H17	M-007057- zinc finger	65251	ZNF649	3483	7.5797	2.9893
50064	H18	M-014307- transmemb	79089	TMUB2	4336	16.582	6.013
50064	H19	M-008547- metallopho	65258	MPPE1	2006	5.8824	4.6866
50064	H20	M-014306- zinc finger	79088	ZNF426	3548	11.781	1.212
50064	H21	M-014245- chromoson	65260	C1orf163	3066	12.329	1.76
50064	H23	M-014247- chromoson	65265	C8orf33	3006	5.9215	4.6475
50064	I02	M-014211- transmemb	64788	TMEM112	2527	11.12	0.551
50064	I04	M-017269- EPS8-like 2	64787	EPS8L2	2597	16.404	5.835
50064	I05	M-017849- germ cell-l	64395	GMCL1	3356	7.2408	3.3282
50064	I06	M-016209- TBC1 doma	64786	TBC1D15	3264	18.474	7.905
50064	I07	M-016469- germ cell-l	64396	GMCL1L	2970	10.875	0.306
50064	I08	M-016229- GINS comp	64785	GINS3	2317	6.5602	4.0088
50064	I09	M-014093- zinc finger	64397	ZFP106	2928	12.773	2.204
50064	I10	M-014210- CREB regul	64784	CRTC3	3584	12.388	1.819
50064	I11	M-009388- membrane	64398	MPP5	3117	14.662	4.093
50064	I12	M-016332- interferon	64782	ISG20L1	2842	11.365	0.796
50064	I13	M-013018- hedgehog i	64399	HHIP	2772	10.209	0.36
50064	I14	M-010192- microtubul	64780	MICAL1	3869	5.7121	4.8569
50064	I15	M-018985- cadherin-lil	64403	CDH24	5312	13.517	2.948
50064	I16	M-013745- methenylte	64779	MTHFSD	3396	7.5972	2.9718
50064	I17	M-013099- cadherin-lil	64405	CDH22	3570	6.2465	4.3225
50064	I18	M-017856- fibronectin	64778	FNDC3B	2936	7.5272	3.0418
50064	I19	M-008489- regulator o	64407	RGS18	2775	10.27	0.299
50064	I20	M-016327- required fo	64777	RMND5B	2116	22.684	12.115
50064	I21	M-013019- Williams-B	64409	WBSCR17	3857	4.9261	5.6429
50064	I23	M-016252- kelch-like 2	64410	KLHL25	4885	3.9509	6.6181
50064	J02	M-014305- chromoson	79086	C19orf42	3772	15.721	5.152
50064	J04	M-007360- solute carri	79085	SLC25A23	2610	10.728	0.159
50064	J05	M-004319- pleckstrin	65977	PLEKHA3	2434	13.928	3.359
50064	J06	M-006895- WD repeat	79084	WDR77	2076	14.933	4.364
50064	J07	M-014249- phosphata	65979	PHACTR4	1403	14.184	3.615
50064	J08	M-018896- melanophil	79083	MLPH	1905	9.0814	1.4876
50064	J09	M-014250- bromodom	65980	BRD9	3325	10.917	0.348

50064	J10	M-006484- chromoson	79081	C11orf48	3428	17.386	6.817
50064	J11	M-014793- caprin fami	65981	CAPRIN2	2693	17.193	6.624
50064	J12	M-014304- coiled-coil	79080	CCDC86	2052	11.842	1.273
50064	J13	M-016474- zinc finger	65982	ZSCAN18	2612	16.08	5.511
50064	J14	M-014303- chromoson	79078	C1orf50	2190	12.785	2.216
50064	J15	M-014251- GRAM dom	65983	GRAMD3	3485	11.277	0.708
50064	J16	M-014302- XTP3-trans	79077	XTP3TPA	3893	13.409	2.84
50064	J17	M-014252- potassium	65987	KCTD14	3818	13.358	2.789
50064	J18	M-014300- defective in	79075	DCC1	3795	9.6443	0.9247
50064	J19	M-014253- zinc finger	65988	ZNF747	4094	11.822	1.253
50064	J20	M-014299- chromoson	79074	C2orf49	1932	11.491	0.922
50064	J21	M-014254- EGF-like-dc	65989	EGFL9	3761	11.274	0.705
50064	J23	M-014255- chromoson	65990	C16orf24	3390	7.6106	2.9584
50064	K02	M-013744- chromoson	64776	C11orf1	4355	21.355	10.786
50064	K04	M-016323- family with	64773	FAM113A	2659	20.233	9.664
50064	K05	M-007052- centaurin,	64411	CENTD3	2426	16.241	5.672
50064	K06	M-016330- chromoson	64771	C6orf106	3216	20.367	9.798
50064	K07	M-007053- GDNF-indu	64412	GZF1	3433	13.516	2.947
50064	K08	M-018127- coiled-coil	64770	CCDC14	2465	12.657	2.088
50064	K09	M-017127- chromoson	64417	C5orf28	3268	13.831	3.262
50064	K10	M-016326- chromoson	64769	C1orf149	3559	14.021	3.452
50064	K11	M-016254- transmemb	64418	TMEM168	3220	15.311	4.742
50064	K12	M-013742- S100P bind	64766	S100PBP	3184	13.788	3.219
50064	K13	M-016118- myotubula	64419	MTMR14	2720	19.228	8.659
50064	K14	M-019357- cAMP resp	64764	CREB3L2	2772	14.177	3.608
50064	K15	M-014096- sushi doma	64420	SUSD1	3308	13.694	3.125
50064	K16	M-007054- zinc finger	64763	ZNF574	1292	10.681	0.112
50064	K17	M-015375- ATG3 autop	64422	ATG3	4825	12.891	2.322
50064	K18	M-013741- family with	64762	FAM59A	2881	11.801	1.232
50064	K19	M-014097- chromoson	64423	C14orf173	2124	8.5687	2.0003
50064	K20	M-013740- poly (ADP-r	64761	PARP12	5626	11.127	0.558
50064	K21	M-014098- polymerase	64425	POLR1E	6136	10.789	0.22
50064	K23	M-027133- suppressor	64426	SUDS3	4603	5.844	4.725
50064	L02	M-014298- transmemb	79073	TMEM109	2089	23.839	13.27
50064	L04	M-014297- FAST kinase	79072	FASTKD3	3372	24.051	13.482
50064	L05	M-014256- chromoson	65992	C20orf116	4071	26.971	16.402
50064	L06	M-008861- ELOVL fami	79071	ELOVL6	2654	20.61	10.041
50064	L07	M-012884- mitochond	65993	MRPS34	3013	23.332	12.763
50064	L08	M-014296- KDEL (Lys-A	79070	KDELC1	1931	23.252	12.683
50064	L09	M-014258- hypothetica	65996	MGC2752	2845	22.32	11.751
50064	L10	M-004159- fat mass ar	79068	FTO	2585	17.756	7.187
50064	L11	M-014261- leucine rich	65999	LRRC61	1078	29.128	18.559
50064	L12	M-016359- methyltran	79066	METT10D	2366	19.019	8.45
50064	L13	M-023601- transmemb	66000	TMEM108	1527	24.689	14.12
50064	L14	M-014294- ATG9 autop	79065	ATG9A	2022	26.113	15.544
50064	L15	M-009127- cytochrome	66002	CYP4F12	4212	18.946	8.377
50064	L16	M-010369- proline rich	79057	PRRG3	4127	15.071	4.502

50064	L17	M-007511- solute carri	66035	SLC2A11	2667	11.211	0.642
50064	L18	M-008218- proline rich	79056	PRRG4	3303	18.498	7.929
50064	L19	M-021362- bol, boule-	66037	BOLL	3615	26.639	16.07
50064	L20	M-014293- nucleolar c	79050	NOC4L	4257	12.591	2.022
50064	L21	M-016377- cysteine-ric	78987	CRELD1	6245	18.975	8.406
50064	L23	M-019257- mitochond	78988	MRP63	4163	9.2962	1.2728
50064	M02	M-018720- retinoic aci	64760	RAI16	4888	9.4108	1.1582
50064	M04	M-009997- tensin 3	64759	TNS3	3960	8.8636	1.7054
50064	M05	M-014099- tetratricop	64427	TTC31	3575	6.5455	4.0235
50064	M06	M-019358- MOCO sulp	64757	MOSC1	4022	7.9314	2.6376
50064	M07	M-014100- nuclear pre	64428	NARFL	2787	5.2745	5.2945
50064	M08	M-013738- ATP syntha	64756	ATPAF1	2891	4.3929	6.1761
50064	M09	M-014101- zinc finger,	64429	ZDHHC6	3099	11.939	1.37
50064	M10	M-004000- chromosom	64755	C16orf58	2760	4.5652	6.0038
50064	M11	M-016752- chromosom	64430	C14orf135	3102	4.7066	5.8624
50064	M12	M-018576- coiled-coil	64753	CCDC136	3253	3.7196	6.8494
50064	M13	M-010142- mitochond	64432	MRPS25	2765	4.8825	5.6865
50064	M14	M-013735- major facili	64747	MFSD1	3814	11.51	0.941
50064	M15	M-025229- nucleolar p	64434	NOM1	3387	2.5096	8.0594
50064	M16	M-013734- methyltran	64745	METT11D1	4989	13.69	3.121
50064	M17	M-014171- dynein, axo	64446	DNAI2	3184	8.7312	1.8378
50064	M18	M-014209- stromal me	64744	SMAP1L	2355	6.1996	4.3694
50064	M19	M-007288- CUB and Su	64478	CSMD1	3864	7.971	2.598
50064	M20	M-014266- unkempt h	64718	UNKL	3524	7.0091	3.5599
50064	M21	M-006056- tryptase be	64499	TPSB2	2837	6.5915	3.9775
50064	M23	M-017178- cytoplasmi	64506	CPEB1	3038	7.1429	3.4261
50064	N02	M-015634- SECIS bindi	79048	SECISBP2	4131	11.038	0.469
50064	N04	M-014292- potassium	79047	KCTD15	3555	11.674	1.105
50064	N05	M-014267- collectin su	78989	COLEC11	3185	8.9796	1.5894
50064	N06	M-014290- transmemb	79041	TMEM38A	2911	11.439	0.87
50064	N07	M-010983- OTU domai	78990	OTUB2	2262	5.084	5.485
50064	N08	M-017128- DEAD (Asp-	79039	DDX54	1530	6.2745	4.2945
50064	N09	M-008427- prenylcyste	78991	PCYOX1L	3193	9.6774	0.8916
50064	N10	M-015889- zinc finger,	79038	ZFYVE21	1815	11.46	0.891
50064	N11	M-016133- Yip1 domai	78992	YIPF2	2947	6.9562	3.6128
50064	N12	M-014289- chromosom	79036	C19orf50	2622	7.8185	2.7505
50064	N13	M-018060- proline rich	78994	PRR14	3124	8.6748	1.8942
50064	N14	M-014288- oligonucleo	79035	OBFC2B	3892	11.434	0.865
50064	N15	M-018061- chromosom	78995	C17orf53	1826	7.2289	3.3401
50064	N16	M-016351- chromosom	79034	C7orf26	2672	15.157	4.588
50064	N17	M-010208- chromosom	78996	C7orf49	2345	4.307	6.262
50064	N18	M-021782- prion prote	79033	PRNPIP	3534	18.506	7.937
50064	N19	M-017342- ganglioside	78997	GDAP1L1	4131	9.9734	0.5956
50064	N20	M-014287- phosducin-	79031	PDCL3	4140	13.188	2.619
50064	N21	M-016297- leucine rich	78999	LRFN4	3809	7.3773	3.1917
50064	N23	M-014269- chromosom	79000	C1orf135	4937	9.4389	1.1301
50064	O02	M-014207- COP9 const	64708	COPS7B	5811	22.44	11.871

50064	O04	M-017417-	SPANX fam	64694	SPANXB2	2337	10.056	0.513
50064	O05	M-013509-	tektin 3	64518	TEKT3	3687	8.6249	1.9441
50064	O06	M-013844-	cutaneous	64693	CTAGE1	3566	11.245	0.676
50064	O07	M-021476-	C-type lecti	64581	CLEC7A	3597	11.704	1.135
50064	O08	M-013510-	golgi reasse	64689	GORASP1	3201	10.559	0.01
50064	O09	M-014173-	testis speci	64591	TSPY2	3045	4.532	6.037
50064	O10	M-012996-	SPANX fam	64663	SPANXC	2266	11.959	1.39
50064	O11	M-016132-	motile sper	64598	MOSPD3	2577	10.361	0.208
50064	O12	M-017414-	SPANX fam	64650	SPANXA2	1355	5.8303	4.7387
50064	O13	M-014174-	PERQ amin	64599	PERQ1	2649	10.57	0.001
50064	O14	M-013561-	SPANX fam	64649	SPANXB1	2839	9.9331	0.6359
50064	O15	M-008591-	phospholip	64600	PLA2G2F	1956	8.4356	2.1334
50064	O16	M-015060-	hippocamp	64645	HIAT1	3057	7.8835	2.6855
50064	O17	M-021275-	chromoson	60683	C21orf97	2129	4.697	5.872
50064	O18	M-013842-	early B-cell	64641	EBF2	3014	11.911	1.342
50064	O19	M-018725-	chromoson	79173	C19orf57	3471	13.973	3.404
50064	O20	M-013003-	vacuolar pr	64601	VPS16	3096	5.168	5.401
50064	O21	M-010856-	cysteine-ric	79174	CRELD2	3892	6.8602	3.7088
50064	O23	M-017597-	zinc finger	79175	ZNF343	2363	5.84	4.729
50064	P02	M-008899-	spermatog	79029	SPATA5L1	3209	22.842	12.273
50064	P04	M-014285-	AHNAK nuc	79026	AHNAK	1202	17.887	7.318
50064	P05	M-003998-	vitamin K e	79001	VKORC1	1313	16.451	5.882
50064	P06	M-014284-	chromoson	79025	C20orf195	1322	14.297	3.728
50064	P07	M-014270-	chromoson	79002	C19orf43	2393	8.6084	1.9606
50064	P08	M-014282-	nucleopori	79023	NUP37	1645	8.5106	2.0584
50064	P09	M-014271-	MIS12, MIN	79003	MIS12	1660	10.783	0.214
50064	P10	M-014281-	transmemb	79022	TMEM106C	3019	10.003	0.566
50064	P11	M-014272-	CUE domai	79004	CUEDC2	1713	16.229	5.66
50064	P12	M-014280-	chromoson	79020	C7orf25	1999	17.209	6.64
50064	P13	M-014273-	sodium cha	79005	SCNM1	1186	11.214	0.645
50064	P14	M-014279-	centromere	79019	CENPM	2161	8.746	1.823
50064	P15	M-014274-	meteorin, g	79006	METRN	2491	19.872	9.303
50064	P16	M-017343-	chromoson	79018	C17orf39	2099	15.769	5.2
50064	P17	M-014275-	dysbindin (	79007	DBNDD1	1515	7.9208	2.6482
50064	P18	M-014278-	chromoson	79017	C7orf24	929	11.733	1.164
50064	P19	M-003988-	GIY-YIG dor	79008	GIYD2	1143	10.936	0.367
50064	P20	M-014277-	chromoson	79016	C19orf58	2532	13.27	2.701
50064	P21	M-004255-	DEAD (Asp-	79009	DDX50	1676	11.933	1.364
50064	P23	M-016475-	chromoson	79014	C16orf67	2558	11.923	1.354
					MAD		10.569	2.9858
					MAD3			8.9574
					MADc			4.418984

50064	C22	Human4 Pc	RNAi	empty

50064	D22	Human4 Pc	RNAi	empty				
50064	E22	Human4 Pc	RNAi	empty				
50064	F22	Human4 Pc	RNAi	empty				

50064	G22	Human4 Pc	RNAi	empty				
50064	H22	Human4 Pc	RNAi	empty				
50064	I22	Human4 Pc	RNAi	empty				
50064	J22	Human4 Pc	RNAi	empty				

50064	I03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-:	siControl non-targeting	
50064	J03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-:	siControl non-targeting	
50064	K03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-(	siGLO RISC-free siRNA	
50064	L03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-(	siGLO RISC-free siRNA	
50064	G03	M-003290-	polo-like kinase 1 (Drosophila)					5347
50064	H03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-1.68776	4629	9.8077	1.8373	-0.41873	2646	3.7037	8.5843	-1.79695
-1.40783	1927	7.4728	4.1722	-0.95087	2404	5.0749	7.2131	-1.50992
-1.31892	1728	7.4074	4.2376	-0.96578	2135	7.3536	4.9344	-1.03292
0.01652	1925	7.6364	4.0086	-0.91359	1773	13.875	1.587	0.332207
-0.74712	2029	7.1464	4.4986	-1.02526	2457	7.6516	4.6364	-0.97054
-0.72619	2023	9.1448	2.5002	-0.56981	3776	10.54	1.748	-0.36591
1.06314	2310	12.857	1.212	0.276223	2221	10.401	1.887	-0.39501
-1.12352	1984	8.2157	3.4293	-0.78156	3600	6.3056	5.9824	-1.2523
-0.31392	1630	10.552	1.093	-0.2491	2242	8.9652	3.3228	-0.69556
-0.24327	2209	13.219	1.574	0.358726	2092	14.149	1.861	0.389563
-0.20317	1237	10.914	0.731	-0.1666	2213	9.0375	3.2505	-0.68043
0.068794	1812	7.2848	4.3602	-0.99372	2667	11.136	1.152	-0.24115
0.168364	2104	13.783	2.138	0.487265	2992	12.433	0.145	0.030353
0.145282	1824	11.678	0.033	0.007521	4188	14.518	2.23	0.466806
-1.21499	1374	11.645	0	0	2219	7.7512	4.5368	-0.94969
0.741573	1031	12.9	1.255	0.286023	843	8.3037	3.9843	-0.83403
0.133289	2023	11.616	0.029	-0.00661	1728	13.947	1.659	0.347279
1.059746	834	8.2734	3.3716	-0.76841	1623	13.309	1.021	0.213726
-1.0334	1417	8.6803	2.9647	-0.67568	1521	9.6647	2.6233	-0.54914
0.120163	2541	9.6812	1.9638	-0.44756	1029	10.593	1.695	-0.35481
1.609872	4052	16.683	5.038	1.148195	2808	19.587	7.299	1.5279
0.912427	923	20.693	9.048	2.062102	1321	14.686	2.398	0.501974
0.233764	3530	9.0652	2.5798	-0.58795	3958	12.809	0.521	0.109061
-0.56818	1825	12.11	0.465	0.105977	2280	11.974	0.314	-0.06573
-0.43472	2784	8.9799	2.6651	-0.60739	2358	15.013	2.725	0.570425
1.474321	2935	22.692	11.047	2.517688	3826	22.556	10.268	2.149401
-0.95825	2735	8.0804	3.5646	-0.8124	3843	12.542	0.254	0.05317
-0.3088	530	7.9245	3.7205	-0.84793	3180	20.094	7.806	1.634031
-1.28785	1658	10.374	1.271	-0.28967	3640	14.78	2.492	0.521651
-0.06065	1836	14.76	3.115	0.70993	2996	19.693	7.405	1.550089
-0.71802	1365	7.7656	3.8794	-0.88414	2946	15.716	3.428	0.717584
-0.99674	1651	9.9334	1.7116	-0.39009	2366	14.243	1.955	0.40924
-0.84721	2221	9.7704	1.8746	-0.42723	4226	10.341	1.947	-0.40757
0.404618	1262	12.678	1.033	0.235428	2877	14.32	2.032	0.425359
-0.00181	2270	9.8678	1.7772	-0.40504	2788	11.334	0.954	-0.1997
-0.78228	1493	7.1668	4.4782	-1.02061	1571	12.794	0.506	0.105921
-0.16101	4579	16.729	5.084	1.158679	2882	11.381	0.907	-0.18986
-0.02919	4518	13.966	2.321	0.528972	3103	11.247	1.041	-0.21791
-1.29946	5044	9.655	1.99	-0.45353	2409	13.117	0.829	0.173535
-1.38423	4261	13.025	1.38	0.314512	1186	9.1906	3.0974	-0.64838
-0.56651	3772	7.8473	3.7977	-0.86552	3208	8.9776	3.3104	-0.69297
-0.14508	2622	9.0008	2.6442	-0.60263	4669	14.371	2.083	0.436035
0.184884	3379	6.8363	4.8087	-1.09594	4874	8.5146	3.7734	-0.78989
0.349854	4536	14.065	2.42	0.551535	6683	13.647	1.359	0.28448
-1.29955	1637	3.6042	8.0408	-1.83255	2726	6.7498	5.5382	-1.15931
0.560536	1384	8.0202	3.6248	-0.82612	2391	9.7449	2.5431	-0.53235

-1.4447	2835	3.8095	7.8355	-1.78576	4153	9.15	3.138	-0.65688
0.105228	3125	11.584	0.061	-0.0139	5451	15.318	3.03	0.63427
-0.91127	3583	6.0564	5.5886	-1.27368	5661	9.38	2.908	-0.60873
0.198915	3172	11.854	0.209	0.047633	3351	14.264	1.976	0.413636
-0.77889	2099	11.91	0.265	0.060395	3116	13.286	0.998	0.208911
1.44807	1425	12.842	1.197	0.272805	2570	16.109	3.821	0.79985
-0.75334	1770	7.9661	3.6789	-0.83845	2720	6.9853	5.3027	-1.11001
-1.05513	2356	2.9711	8.6739	-1.97684	4839	7.7289	4.5591	-0.95436
-1.50453	1577	7.546	4.099	-0.93419	2290	5.5895	6.6985	-1.4022
-0.87488	1003	8.0758	3.5692	-0.81345	1352	2.8846	9.4034	-1.96841
-0.14447	2085	7.9616	3.6834	-0.83947	2563	13.773	1.485	0.310855
0.465265	2400	8.9167	2.7283	-0.6218	2427	13.02	0.732	0.15323
-0.60435	2495	10.261	1.384	-0.31542	2218	13.706	1.418	0.29683
-0.69102	3879	8.7651	2.8799	-0.65635	2563	7.9984	4.2896	-0.89794
-0.5089	4146	9.069	2.576	-0.58709	2398	6.6305	5.6575	-1.18429
0.694956	3115	21.509	9.864	2.248074	3181	14.964	2.676	0.560167
-0.63128	2858	9.0973	2.5477	-0.58064	2946	11.168	1.12	-0.23445
-0.0516	1733	12.579	0.934	0.212865	2565	14.074	1.786	0.373864
-0.81928	1493	8.1715	3.4735	-0.79163	2392	7.3161	4.9719	-1.04077
0.041639	2253	14.026	2.381	0.542646	2932	13.029	0.741	0.155114
0.336955	1540	18.961	7.316	1.667367	2583	14.789	2.501	0.523535
-0.67568	1653	10.708	0.937	-0.21355	4743	14.548	2.26	0.473086
0.203214	2023	16.906	5.261	1.199018	3526	15.372	3.084	0.645574
-0.68916	2210	9.5475	2.0975	-0.47803	2987	17.375	5.087	1.064862
-0.56411	1383	12.581	0.936	0.213321	1599	11.382	0.906	-0.18965
-0.42216	2396	10.225	1.42	-0.32363	3779	13.893	1.605	0.335975
-0.4344	1701	10.406	1.239	-0.28238	2920	13.014	0.726	0.151974
0.545148	1722	9.0592	2.5858	-0.58932	3383	15.016	2.728	0.571052
0.759677	1910	18.586	6.941	1.581902	2853	18.191	5.903	1.235676
-0.65024	2493	10.148	1.497	-0.34118	3908	12.308	0.02	0.004187
-0.50247	5608	16.387	4.742	1.080735	3345	11.51	0.778	-0.16286
-0.01086	4505	12.275	0.63	0.143581	1954	7.1648	5.1232	-1.07244
-1.15895	4373	16.625	4.98	1.134977	2002	10.839	1.449	-0.30332
-1.22046	4764	14.861	3.216	0.732949	1375	10.836	1.452	-0.30395
0.889345	2947	14.93	3.285	0.748674	2815	4.7602	7.5278	-1.5758
1.109984	2564	14.236	2.591	0.590507	4503	7.5949	4.6931	-0.98241
2.114513	2202	17.893	6.248	1.423962	4070	9.4103	2.8777	-0.60239
0.897265	1848	9.6861	1.9589	-0.44645	4012	10.169	2.119	-0.44357
-0.00724	3135	10.367	1.278	-0.29127	5219	10.634	1.654	-0.34623
0.310026	1389	11.519	0.126	-0.02872	2326	5.761	6.527	-1.3663
-0.10975	2413	8.247	3.398	-0.77443	4045	6.4524	5.8356	-1.22157
-0.42917	1367	8.0468	3.5982	-0.82005	4263	6.2163	6.0717	-1.27099
-0.47463	2268	8.9506	2.6944	-0.61407	4139	9.0602	3.2278	-0.67568
-0.76923	1721	11.505	0.14	-0.03191	2457	4.9654	7.3226	-1.53284
0.013578	1269	7.2498	4.3952	-1.0017	2207	10.104	2.184	-0.45718
-0.23211	1138	6.5026	5.1424	-1.17199	1402	8.0599	4.2281	-0.88507
-0.82213	683	11.42	0.225	-0.05128	1798	5.0056	7.2824	-1.52443

-0.97353	2467	6.6478	4.9972	-1.1389	4937	7.3729	4.9151	-1.02888
-0.54178	1648	10.012	1.633	-0.37217	4228	10.762	1.526	-0.31944
-0.91306	2119	6.4181	5.2269	-1.19125	2977	7.1884	5.0996	-1.0675
0.406881	4544	16.329	4.684	1.067516	3610	12.798	0.51	0.106758
1.243499	3771	16.335	4.69	1.068884	2299	15.659	3.371	0.705652
-0.30851	2467	6.0803	5.5647	-1.26823	1855	7.8167	4.4713	-0.93598
-1.01093	2407	11.965	0.32	0.07293	1186	5.8179	6.4701	-1.35439
-0.15117	4681	10.81	0.835	-0.1903	3074	17.306	5.018	1.050418
-0.56796	2634	9.4913	2.1537	-0.49084	1829	12.849	0.561	0.117434
0.443993	1537	8.1327	3.5123	-0.80048	2570	15.486	3.198	0.669438
0.599459	2404	13.894	2.249	0.512563	2874	19.346	7.058	1.477452
-0.82521	1914	8.9864	2.6586	-0.60591	2117	8.2664	4.0216	-0.84184
0.430416	2489	10.446	1.199	-0.27326	3197	19.299	7.011	1.467613
-0.26891	1560	15.064	3.419	0.779214	2131	16.33	4.042	0.846112
1.20367	1226	7.3409	4.3041	-0.98093	2189	12.197	0.091	-0.01905
1.414805	2007	14.748	3.103	0.707195	595	51.765	39.477	8.263724
-0.49389	1417	9.2449	2.4001	-0.547	1496	13.235	0.947	0.198236
-0.41362	2538	7.9196	3.7254	-0.84904	3190	12.288	0	0
-0.48473	3439	8.6944	2.9506	-0.67246	2630	10.684	1.604	-0.33577
-0.05635	1884	11.89	0.245	0.055837	1730	22.312	10.024	2.098325
0.115411	1967	16.726	5.081	1.157995	2374	17.86	5.572	1.166387
-1.12055	2241	7.1397	4.5053	-1.02679	1659	10.91	1.378	-0.28846
0.027156	1338	7.1001	4.5449	-1.03581	1807	9.5739	2.7141	-0.56814
0.954065	5819	13.782	2.137	0.487037	2838	10.712	1.576	-0.3299
1.211591	6651	20.162	8.517	1.941083	2033	18.446	6.158	1.289055
-0.94843	6967	16.894	5.249	1.196283	1347	7.0527	5.2353	-1.09591
-0.00747	6790	14.197	2.552	0.581618	691	7.8148	4.4732	-0.93638
0.245532	4338	7.8147	3.8303	-0.87295	1980	8.7879	3.5001	-0.73268
0.833223	4221	17.2	5.555	1.266023	1721	16.386	4.098	0.857835
-0.28402	4176	14.919	3.274	0.746167	3839	8.8825	3.4055	-0.71287
0.186016	3856	9.6214	2.0236	-0.46119	3538	8.5924	3.6956	-0.7736
-0.83601	1877	12.04	0.395	0.090023	1795	5.9053	6.3827	-1.33609
-0.9098	3606	10.427	1.218	-0.27759	3891	7.6073	4.6807	-0.97981
-0.8704	1875	6.9333	4.7117	-1.07383	1961	4.2835	8.0045	-1.67558
0.399866	2788	13.271	1.626	0.370577	3793	10.704	1.584	-0.33158
1.085996	3282	24.985	13.34	3.040278	2687	24.749	12.461	2.608462
-0.57443	1902	7.7813	3.8637	-0.88056	2122	10.462	1.826	-0.38224
1.240104	2190	26.804	15.159	3.454841	2500	26.68	14.392	3.012679
0.910617	2610	15.939	4.294	0.978632	3129	18.984	6.696	1.401674
0.02263	2886	11.504	0.141	-0.03213	3259	12.673	0.385	0.080592
0.297806	2378	8.9992	2.6458	-0.603	3063	12.014	0.274	-0.05736
-0.95493	1812	9.3267	2.3183	-0.52836	2462	7.3517	4.9363	-1.03332
0.383572	2542	15.106	3.461	0.788786	2125	16.612	4.324	0.905143
-0.18126	1922	9.4173	2.2277	-0.50771	2390	13.18	0.892	0.186722
-0.69367	2657	9.1833	2.4617	-0.56104	2179	7.8476	4.4404	-0.92951
-0.76638	3525	8.9645	2.6805	-0.6109	3071	9.5409	2.7471	-0.57505
-1.486	3816	10.613	1.032	-0.2352	1531	5.356	6.932	-1.45108

-0.16744	3225	11.969	0.324	0.073842	2005	6.3342	5.9538	-1.24631
2.262964	2378	16.947	5.302	1.208363	2651	18.936	6.648	1.391626
0.703555	3218	15.6	3.955	0.901372	2752	13.445	1.157	0.242195
1.506681	3550	19.014	7.369	1.679446	4408	16.742	4.454	0.932356
-1.27122	937	13.767	2.122	0.483619	1506	14.276	1.988	0.416148
-0.8953	2245	7.9287	3.7163	-0.84697	2210	13.62	1.332	0.278828
-0.29799	1113	19.587	7.942	1.810037	1924	14.917	2.629	0.550329
-0.42815	1431	14.885	3.24	0.738418	1861	13.434	1.146	0.239892
2.042551	3030	23.894	12.249	2.791632	4112	22.933	10.645	2.228319
0	1062	14.595	2.95	0.672325	1427	14.506	2.218	0.464294
-0.54078	1566	19.157	7.512	1.712037	2776	15.202	2.914	0.609988
-0.13356	2214	13.144	1.499	0.341632	2144	15.718	3.43	0.718002
0.549448	3024	20.8	9.155	2.086488	2905	19.759	7.471	1.563905
-0.40299	3644	12.569	0.924	0.210586	4105	11.157	1.131	-0.23675
-0.67647	2497	11.734	0.089	0.020284	3190	9.0596	3.2284	-0.6758
1.36072	2932	20.191	8.546	1.947693	3661	19.749	7.461	1.561812
-1.06056	3717	15.792	4.147	0.94513	1966	7.7823	4.5057	-0.94318
0.274271	4820	18.672	7.027	1.601502	3331	15.581	3.293	0.689324
0.398282	6006	21.961	10.316	2.351088	2782	11.538	0.75	-0.157
-1.05171	4654	12.677	1.032	0.2352	1100	9.3636	2.9244	-0.61216
0.124689	1985	15.214	3.569	0.8134	2201	10.223	2.065	-0.43227
1.320439	2666	11.328	0.317	-0.07225	3236	10.352	1.936	-0.40526
-0.75316	3129	9.5238	2.1212	-0.48344	4120	6.6748	5.6132	-1.17501
1.788873	3328	18.72	7.075	1.612442	5569	18.711	6.423	1.344527
0.069247	2800	10.786	0.859	-0.19577	4631	11.639	0.649	-0.13586
-0.90718	2746	8.0845	3.5605	-0.81146	2998	9.4396	2.8484	-0.59626
0.498757	2351	14.547	2.902	0.661386	3843	11.762	0.526	-0.11011
0.411633	2750	10.945	0.7	-0.15953	4291	10.021	2.267	-0.47455
0.926231	1877	11.774	0.129	0.0294	4456	14.048	1.76	0.368421
0.180132	2723	10.65	0.995	-0.22677	3251	13.073	0.785	0.164324
-0.08147	2220	12.748	1.103	0.251381	2481	11.245	1.043	-0.21833
-1.0991	4430	10.7	0.945	-0.21537	4923	10.075	2.213	-0.46325
0.667122	2601	9.2272	2.4178	-0.55103	4084	9.4515	2.8365	-0.59376
-0.67251	2590	5.9073	5.7377	-1.30766	3346	8.9958	3.2922	-0.68916
-0.97817	2423	7.4288	4.2162	-0.9609	3526	9.5009	2.7871	-0.58342
-0.68835	1716	8.7995	2.8455	-0.64851	2503	10.348	1.94	-0.4061
-0.06766	3133	9.767	1.878	-0.42801	3222	10.708	1.58	-0.33074
2.74158	1755	29.63	17.985	4.098906	2065	23.148	10.86	2.273325
-1.27697	3700	9.8108	1.8342	-0.41803	3217	10.32	1.968	-0.41196
-1.49765	3803	4.9698	6.6752	-1.52132	2861	7.5149	4.7731	-0.99915
1.165879	2678	20.836	9.191	2.094693	1756	8.2574	4.0306	-0.84373
0.035981	2497	15.058	3.413	0.777846	3073	10.348	1.94	-0.4061
0.760129	2350	19.787	8.142	1.855618	3396	8.9223	3.3657	-0.70454
0.987557	2133	14.909	3.264	0.743888	2255	9.3126	2.9754	-0.62284
0.818061	2021	20.485	8.84	2.014697	2093	13.33	1.042	0.218122
-0.33664	1867	11.302	0.343	-0.07817	1289	11.559	0.729	-0.1526
0.078751	2829	12.478	0.833	0.189846	2852	10.835	1.453	-0.30416

1.542662	3421	20.228	8.583	1.956125	2407	17.948	5.66	1.184808
1.498987	3850	23.247	11.602	2.644176	3188	15.339	3.051	0.638666
0.288075	1945	13.985	2.34	0.533302	1378	14.949	2.661	0.557027
1.247119	2847	17.668	6.023	1.372683	1848	14.881	2.593	0.542793
0.501473	2890	11.176	0.469	-0.10689	2352	17.602	5.314	1.11238
0.160218	4361	13.414	1.769	0.403167	2710	9.4096	2.8784	-0.60254
0.642682	3826	12.258	0.613	0.139707	2315	7.6026	4.6854	-0.9808
0.631141	3380	10.828	0.817	-0.1862	3406	11.421	0.867	-0.18149
-0.20926	4471	13.04	1.395	0.31793	3985	9.1092	3.1788	-0.66542
0.283549	6079	15.628	3.983	0.907753	3932	10.783	1.505	-0.31504
0.208645	6421	22.286	10.641	2.425158	1936	12.655	0.367	0.076824
0.159539	7163	22.714	11.069	2.522702	3368	10.6	1.688	-0.35335
-0.66948	5001	15.157	3.512	0.800409	1129	9.8317	2.4563	-0.51418
2.440833	4177	19.416	7.771	1.771065	4205	13.317	1.029	0.215401
2.186928	1777	15.926	4.281	0.97567	2335	24.069	11.781	2.466118
1.283553	2278	15.057	3.412	0.777618	2944	13.043	0.755	0.158044
2.217252	3633	17.203	5.558	1.266707	3028	18.692	6.404	1.34055
0.666895	4595	13.166	1.521	0.346646	4718	15.833	3.545	0.742075
0.472507	3642	12.685	1.04	0.237023	2962	26.232	13.944	2.918899
0.738179	3770	13.793	2.148	0.489544	4684	14.923	2.635	0.551585
0.781175	2580	21.163	9.518	2.169218	3613	15.527	3.239	0.67802
1.073097	3407	20.869	9.224	2.102214	3565	20.281	7.993	1.673175
0.728448	3587	19.32	7.675	1.749186	2935	17.479	5.191	1.086633
1.9595	2259	19.345	7.7	1.754883	3304	22.215	9.927	2.07802
0.816477	3590	16.017	4.372	0.996409	1922	19.407	7.119	1.490221
0.707176	2634	11.238	0.407	-0.09276	2562	14.169	1.881	0.39375
0.025345	1228	18.73	7.085	1.614721	1245	21.124	8.836	1.849641
0.52546	3302	15.899	4.254	0.969516	3750	17.173	4.885	1.022578
0.278797	2558	15.598	3.953	0.900916	2725	21.028	8.74	1.829545
-0.45266	2408	11.171	0.474	-0.10803	1589	25.425	13.137	2.749969
0.126273	3082	15.412	3.767	0.858525	4504	21.514	9.226	1.931279
0.049785	3779	13.39	1.745	0.397698	4285	19.837	7.549	1.580233
-1.06925	3521	10.736	0.909	-0.20717	2516	16.494	4.206	0.880442
3.002953	2963	20.351	8.706	1.984158	2553	16.53	4.242	0.887978
3.050928	3173	26.347	14.702	3.350688	4646	21.158	8.87	1.856758
3.711713	5622	21.932	10.287	2.344479	4989	21.006	8.718	1.82494
2.272242	4225	23.314	11.669	2.659446	3738	25.094	12.806	2.680681
2.88822	4056	17.061	5.416	1.234344	4313	24.855	12.567	2.630651
2.870117	2200	17.955	6.31	1.438093	2454	16.585	4.297	0.899491
2.659209	2858	22.393	10.748	2.449544	3702	24.338	12.05	2.522428
1.626392	3334	17.966	6.321	1.4406	3220	23.82	11.532	2.413995
4.199834	1319	22.82	11.175	2.54686	1236	30.016	17.728	3.711004
1.912204	2471	20.882	9.237	2.105176	2419	25.382	13.094	2.740968
3.195305	2174	17.157	5.512	1.256223	2159	26.401	14.113	2.954276
3.517551	5052	30.483	18.838	4.293311	2561	28.856	16.568	3.468181
1.895685	4510	18.78	7.135	1.626116	2618	19.939	7.651	1.601585
1.018786	3960	9.6717	1.9733	-0.44973	2187	25.926	13.638	2.854844

0.145282	1985	12.393	0.748	0.170474	1567	21.315	9.027	1.889623
1.794304	4141	16.325	4.68	1.066604	4092	20.552	8.264	1.729904
3.636583	7785	23.532	11.887	2.70913	4169	23.963	11.675	2.443929
0.457571	6537	12.682	1.037	0.236339	3553	9.4849	2.8031	-0.58677
1.902247	6675	23.101	11.456	2.610902	3901	21.712	9.424	1.972727
-0.28803	5368	9.7243	1.9207	-0.43774	1821	14.992	2.704	0.566029
-0.2621	4323	11.867	0.222	0.050595	3648	9.2928	2.9952	-0.62699
-0.38593	3368	9.709	1.936	-0.44123	4019	7.2406	5.0474	-1.05657
-0.9105	3220	9.2547	2.3903	-0.54477	3883	11.847	0.441	-0.09231
-0.59688	4604	14.075	2.43	0.553814	5427	15.607	3.319	0.694767
-1.19813	2592	11.188	0.457	-0.10415	3279	9.6371	2.6509	-0.55491
-1.39763	4314	7.5104	4.1346	-0.9423	3386	7.3243	4.9637	-1.03905
0.310026	3814	12.192	0.547	0.124665	4112	16.148	3.86	0.808014
-1.35864	2980	4.9329	6.7121	-1.52973	3964	6.6852	5.6028	-1.17283
-1.32664	3828	8.2288	3.4162	-0.77858	5298	7.7765	4.5115	-0.94439
-1.54999	2780	2.518	9.127	-2.08011	3599	5.8905	6.3975	-1.33919
-1.28683	2696	8.3828	3.2622	-0.74348	3215	6.1275	6.1605	-1.28958
0.212945	4288	14.576	2.931	0.667995	4678	14.793	2.505	0.524372
-1.82381	4100	3.7561	7.8889	-1.79793	4255	6.2985	5.9895	-1.25378
0.706271	3928	12.678	1.033	0.235428	6206	20.851	8.563	1.792494
-0.41589	3645	8.6694	2.9756	-0.67816	4499	10.247	2.041	-0.42724
-0.98878	1598	6.8836	4.7614	-1.08516	2897	8.7332	3.5548	-0.74413
-0.58792	3150	5.4603	6.1847	-1.40954	4078	9.1957	3.0923	-0.64731
-0.80559	4412	9.6102	2.0348	-0.46375	4913	10.727	1.561	-0.32676
-0.90009	3021	6.4217	5.2233	-1.19043	3584	7.2266	5.0614	-1.0595
-0.77531	3211	6.4466	5.1984	-1.18475	2780	7.8777	4.4103	-0.92321
0.106133	3901	13.509	1.864	0.424819	4336	8.8792	3.4088	-0.71356
0.250057	3158	13.585	1.94	0.442139	3624	15.342	3.054	0.639294
-0.35968	3210	10.062	1.583	-0.36078	3849	8.3398	3.9482	-0.82648
0.196878	2869	13.628	1.983	0.451939	4003	14.514	2.226	0.465969
-1.24124	1491	12.14	0.495	0.112814	2361	7.4121	4.8759	-1.02067
-0.97183	1964	11.405	0.24	-0.0547	2201	6.5879	5.7001	-1.1932
-0.20177	3228	10.285	1.36	-0.30995	4260	12.653	0.365	0.076405
0.20163	1771	9.3732	2.2718	-0.51776	2298	9.3124	2.9756	-0.62288
-0.81756	3851	8.4653	3.1797	-0.72468	4938	9.032	3.256	-0.68158
-0.62243	2003	11.133	0.512	-0.11669	2888	7.3753	4.9127	-1.02838
-0.42865	2110	10.047	1.598	-0.3642	4420	10.407	1.881	-0.39375
0.195746	3356	18.355	6.71	1.529256	3643	16.195	3.907	0.817853
-0.75585	1405	9.6797	1.9653	-0.44791	2085	8.9688	3.3192	-0.69481
1.038248	1495	9.4314	2.2136	-0.50449	4008	14.746	2.458	0.514533
-1.41707	1521	5.5884	6.0566	-1.38034	3211	8.8757	3.4123	-0.7143
1.796114	2090	8.8995	2.7455	-0.62572	4603	18.249	5.961	1.247817
-0.13478	5936	10.175	1.47	-0.33502	5442	8.9673	3.3207	-0.69512
0.59267	5634	16.01	4.365	0.994814	5049	14.181	1.893	0.396262
-0.72227	5393	10.681	0.964	-0.2197	2673	6.3599	5.9281	-1.24093
-0.25574	2721	7.5707	4.0743	-0.92856	3160	3.2278	9.0602	-1.89657
2.686364	3949	19.093	7.448	1.697451	3768	14.889	2.601	0.544468

-0.11609	2048	12.402	0.757	0.172526	2557	14.079	1.791	0.37491
-0.43994	3087	11.144	0.501	-0.11418	3464	11.605	0.683	-0.14297
0.152976	3184	8.5741	3.0709	-0.69988	3584	13.979	1.691	0.353977
0.256846	2995	9.3489	2.2961	-0.5233	2875	10.435	1.853	-0.38789
-0.00226	2565	9.4347	2.2103	-0.50374	2600	11.462	0.826	-0.17291
-1.36615	2259	6.6844	4.9606	-1.13056	2074	11.379	0.909	-0.19028
0.314552	2328	8.8058	2.8392	-0.64707	3141	9.774	2.514	-0.52626
-0.04707	5203	7.3611	4.2839	-0.97633	847	27.037	14.749	3.08741
-1.07235	2025	10.568	1.077	-0.24546	2008	10.807	1.481	-0.31002
0.000226	1997	10.966	0.679	-0.15475	2296	10.322	1.966	-0.41154
-0.1439	2036	8.7426	2.9024	-0.66148	2422	14.244	1.956	0.40945
-0.48278	1873	7.795	3.85	-0.87744	2119	15.715	3.427	0.717374
-0.60772	1260	5	6.645	-1.51444	3442	9.5293	2.7587	-0.57748
-1.32881	1320	5.3788	6.2662	-1.42811	2935	9.3697	2.9183	-0.61089
0.30369	2199	11.824	0.179	0.040795	3574	16.592	4.304	0.900957
0.770313	2675	14.206	2.561	0.58367	3086	23.785	11.497	2.406668
-1.22223	2484	8.7359	2.9091	-0.663	4222	12.577	0.289	0.060496
-0.83929	1975	6.1266	5.5184	-1.25768	2184	7.6007	4.6873	-0.98119
-1.07016	1124	4.0925	7.5525	-1.72127	1473	10.591	1.697	-0.35523
2.777335	2168	9.1328	2.5122	-0.57255	3371	16.642	4.354	0.911423
1.656037	609	18.062	6.417	1.462479	1523	17.4	5.112	1.070095
1.331075	780	18.59	6.945	1.582814	2524	12.163	0.125	-0.02617
0.843633	1647	18.64	6.995	1.594209	1924	13.877	1.589	0.332626
-0.44368	1203	14.464	2.819	0.64247	1327	11.153	1.135	-0.23759
-0.46581	1716	11.48	0.165	-0.0376	2397	11.431	0.857	-0.1794
0.048427	2056	9.7276	1.9174	-0.43699	1594	16.75	4.462	0.934031
-0.12808	2875	13.948	2.303	0.52487	2614	11.094	1.194	-0.24994
1.280837	2908	19.498	7.853	1.789753	1498	23.231	10.943	2.290699
1.502608	3820	22.88	11.235	2.560534	3080	21.006	8.718	1.82494
0.145961	1611	11.608	0.037	-0.00843	1827	16.475	4.187	0.876465
-0.41254	2980	11.376	0.269	-0.06131	2348	9.9659	2.3221	-0.48609
2.105235	2453	14.146	2.501	0.569995	2255	17.517	5.229	1.094587
1.176741	1296	13.966	2.321	0.528972	1762	13.507	1.219	0.255173
-0.59928	1430	12.308	0.663	0.151102	2105	9.5962	2.6918	-0.56347
0.263409	1069	15.716	4.071	0.927809	1326	16.063	3.775	0.790221
0.083051	5367	12.782	1.137	0.25913	2085	14.149	1.861	0.389563
0.611226	4849	15.385	3.74	0.852372	2523	13.238	0.95	0.198864
0.308668	4194	14.783	3.138	0.715172	1416	14.407	2.119	0.44357
0.306405	4390	11.936	0.291	0.066321	1424	15.801	3.513	0.735377
		11.645	2.9647			12.288	3.2278	
			8.8941				9.6834	
			4.387756				4.777144	
	2036	34.086	1752	37.842	1753	34.626		

	3332	30.132	4994	38.947	2763	41.911
	2969	31.021	2061	46.24	1750	44.629
	3815	36.304	6010	47.654	858	41.492
mn	3038	32.88575	3704.25	42.67075	1781	40.6645
sd	752.5357	2.839335	2120.652	4.991842	778.4596	4.259079
	942	5.6263	1378	6.9666	553	4.34
	1024	5.0781	2860	7.2378	490	11.224
	1416	1.2712	1363	5.2825	704	7.2443
	1842	5.1031	4586	17.074	1662	8.6643
mn	1306	4.269675	2546.75	9.140225	852.25	7.86815
sd	412.8825	2.014897	1530.131	5.359437	547.2503	2.871272
3posSD		8.518004		14.97553		12.77724
3negSD		6.044692		16.07831		8.613817
Sum3SD		14.5627		31.05384		21.39105
MnDiff		28.61608		33.53053		32.79635
SumovrMn		0.508899		0.926136		0.652239
1minus		0.491101		0.073864		0.347761
	2254	13.088	2340	18.077	2824	9.136
	1560	11.218	1992	18.524	2314	16.206
	6150	25.431	6454	23.35	5130	24.503
	4312	20.942	6849	29.055	6285	23.548
PLK1 SMAR	182	34.066	280	21.429	196	16.837
PLK1 SMAR	139	32.374	194	23.711	110	39.091

Y

Y

Y

Y

Y

X	debris a,b
X	debris a,b
X	debris a,b
X	debris a,b
	debris a,b
X	debris a,b
x	toxic a,b,c
	debris a,b
X	toxic a
X	debris a,b

Y

0.040625

						cell ct	% inf	AD
50065	A02	M-012929-	ankyrin rep	79754	ASB13	3221	13.443	2.965
50065	A04	M-009638-	zinc finger,	79752	ZFAND1	1838	5.6583	4.8197
50065	A05	M-014337-	zinc finger	79177	ZNF576	2664	8.0706	2.4074
50065	A06	M-007482-	solute carri	79751	SLC25A22	4025	9.0683	1.4097
50065	A07	M-030272-	thiamine tr	79178	THTPA	2728	6.9648	3.5132
50065	A08	M-014416-	zinc finger	79750	ZNF659	2004	12.126	1.648
50065	A09	M-016335-	EF-hand do	79180	EFHD2	1118	11.896	1.418
50065	A10	M-013977-	lectin, man	79748	LMAN1L	2075	5.7349	4.7431
50065	A11	M-014340-	chromoson	79183	C20orf121	1511	12.177	1.699
50065	A12	M-018412-	enoyl Coen	79746	ECHDC3	1941	10.046	0.432
50065	A13	M-005798-	BRCA1/BR	79184	BRCC3	1913	8.5729	1.9051
50065	A14	M-018986-	CAP-GLY do	79745	CLIP4	1443	10.326	0.152
50065	A15	M-014341-	fibronectin	79187	FSD1	2237	9.4323	1.0457
50065	A16	M-016550-	zinc finger	79744	ZNF419	1882	6.2168	4.2612
50065	A17	M-014342-	transmemb	79188	TMEM43	2440	7.0902	3.3878
50065	A18	M-014414-	chromoson	79742	CXorf36	2642	15.897	5.419
50065	A19	M-022561-	iroquois ho	79190	IRX6	1184	10.135	0.343
50065	A20	M-014413-	chromoson	79741	C10orf68	1275	7.9216	2.5564
50065	A21	M-022559-	iroquois ho	79191	IRX3	2013	14.307	3.829
50065	A23	M-024269-	iroquois ho	79192	IRX1	1765	8.5552	1.9228
50065	B02	M-014520-	ankyrin rep	79998	ANKRD53	5373	12.377	1.899
50065	B04	M-028493-	ELOVL fami	79993	ELOVL7	4163	9.8727	0.6053
50065	B05	M-014417-	zinc finger	79755	ZNF750	4274	4.7964	5.6816
50065	B06	M-014519-	chromoson	79992	C6orf59	5170	8.2592	2.2188
50065	B07	M-014418-	dehydroge	79758	DHRS12	7165	9.7976	0.6804
50065	B08	M-016208-	oligonucle	79991	OBFC1	5552	8.2493	2.2287
50065	B09	M-015785-	zinc finger	79759	ZNF668	6322	9.7754	0.7026
50065	B10	M-014518-	tetratricop	79989	TTC26	6323	12.921	2.443
50065	B11	M-014419-	gem (nucle	79760	GEMIN7	2578	11.365	0.887
50065	B12	M-014517-	zinc finger	79986	ZNF702	3539	9.579	0.899
50065	B13	M-018392-	chromoson	79762	C1orf115	4443	7.2699	3.2081
50065	B14	M-008936-	esterase 31	79984	FLJ21736	5423	8.3717	2.1063
50065	B15	M-014420-	isochorism	79763	ISOC2	3669	9.8392	0.6388
50065	B16	M-016605-	premature	79983	POF1B	3657	8.6136	1.8644
50065	B17	M-012935-	immune as	79765	hIAN2	3798	6.0295	4.4485
50065	B18	M-018817-	DnaJ (Hsp4	79982	DNAJB14	6567	11.801	1.323
50065	B19	M-012936-	engulfmen	79767	ELMO3	5698	16.725	6.247
50065	B20	M-015843-	FERM dom	79981	FRMD1	4745	6.7861	3.6919
50065	B21	M-014421-	chromoson	79768	C15orf29	4385	10.559	0.081
50065	B23	M-016546-	chromoson	79770	C5orf14	2323	6.1558	4.3222
50065	C02	M-014412-	hypothetic	79740	FLJ23049	1887	6.2003	4.2777
50065	C04	M-018159-	tubulin tyr	79739	TTLL7	3544	5.5869	4.8911
50065	C05	M-018424-	THO compl	79228	THOC6	2849	6.669	3.809
50065	C06	M-018158-	Bardet-Bie	79738	BBS10	3444	8.072	2.406
50065	C07	M-014343-	zinc finger	79230	ZNF557	4442	13.823	3.345
50065	C08	M-014410-	chromoson	79736	C17orf42	4183	12.814	2.336

50065	C09	M-005950-	membrane	79258	MMEL1	2412	6.0945	4.3835
50065	C10	M-014409-	TBC1 doma	79735	TBC1D17	2143	16.659	6.181
50065	C11	M-014344-	WD repeat	79269	WDR32	3627	9.3466	1.1314
50065	C12	M-014408-	potassium	79734	KCTD17	2274	4.4855	5.9925
50065	C13	M-029683-	olfactory re	79290	OR13A1	2709	8.5271	1.9509
50065	C14	M-014407-	E2F transcr	79733	E2F8	2458	11.473	0.995
50065	C15	M-014668-	chromoson	79363	C1orf89	1940	7.4742	3.0038
50065	C16	M-015892-	asparaginyl	79731	NARS2	3460	13.931	3.453
50065	C17	M-023561-	ZXD family	79364	ZXDC	3070	6.1564	4.3216
50065	C18	M-018156-	NOL1/NOP	79730	NSUN7	3860	13.782	3.304
50065	C19	M-010043-	basic helix-	79365	BHLHB3	4443	8.9354	1.5426
50065	C20	M-016447-	chromoson	79729	C1orf113	3247	6.4059	4.0721
50065	C21	M-014649-	nucleosom	79366	NSBP1	2211	11.171	0.693
50065	C23	M-013441-	UDP-GlcNA	79369	B3GNT4	1882	4.6759	5.8021
50065	D02	M-018397-	DSN1, MIN	79980	DSN1	3859	8.9401	1.5379
50065	D04	M-018705-	chromoson	79979	CXorf34	2215	18.014	7.536
50065	D05	M-016557-	multiple C2	79772	MCTP1	2904	13.085	2.607
50065	D06	M-014515-	grainyhead	79977	GRHL2	4048	13.908	3.43
50065	D07	M-014422-	growth hor	79774	GRTP1	3750	8.64	1.838
50065	D08	M-018816-	hypothetica	79974	FLJ21986	2916	7.0645	3.4135
50065	D09	M-018835-	zinc finger	79776	ZFHX4	3266	7.3791	3.0989
50065	D10	M-014513-	zinc finger	79973	ZNF442	2264	6.1396	4.3384
50065	D11	M-014425-	MICAL-like	79778	MICALL2	3055	10.704	0.226
50065	D12	M-018728-	G protein-c	79971	GPR177	3527	18.968	8.49
50065	D13	M-015438-	coiled-coil	79780	CCDC82	2880	10.66	0.182
50065	D14	M-014511-	zinc finger	79970	ZNF767	3545	5.7264	4.7516
50065	D15	M-016563-	IQ motif co	79781	IQCA	2856	13.27	2.792
50065	D16	M-014510-	chromoson	79969	C6orf134	3740	11.765	1.287
50065	D17	M-014426-	leucine rich	79782	LRRC31	3079	13.381	2.903
50065	D18	M-008416-	stearoyl-Co	79966	SCD5	2419	6.9037	3.5743
50065	D19	M-014427-	chromoson	79783	C7orf10	4119	16.436	5.958
50065	D20	M-022728-	hypothetica	79964	FLJ23529	3285	10.624	0.146
50065	D21	M-027149-	myosin, he	79784	MYH14	1560	7.6282	2.8498
50065	D23	M-009772-	hypothetica	79785	FLJ22655	2318	4.4435	6.0345
50065	E02	M-012928-	partner and	79728	PALB2	2793	6.8743	3.6037
50065	E04	M-018411-	lin-28 hom	79727	LIN28	3525	10.922	0.444
50065	E05	M-016384-	galactosida	79411	GLB1L	3789	7.4426	3.0354
50065	E06	M-022683-	WD repeat	79726	WDR59	2330	7.4678	3.0102
50065	E07	M-014347-	zinc finger,	79413	ZBED2	4787	15.751	5.273
50065	E08	M-021453-	THAP doma	79725	THAP9	3534	20.43	9.952
50065	E09	M-014348-	leucine rich	79414	LRFN3	2055	14.696	4.218
50065	E10	M-016138-	zinc finger	79724	ZNF768	3022	7.1476	3.3304
50065	E11	M-016389-	chromoson	79415	C17orf62	2769	8.7757	1.7023
50065	E12	M-014406-	ankyrin rep	79722	ANKRD55	3617	9.3448	1.1332
50065	E13	M-018131-	chromoson	79441	C4orf15	3429	16.273	5.795
50065	E14	M-014404-	vacuolar pr	79720	VPS37B	2211	8.2768	2.2012
50065	E15	M-014349-	leucine rich	79442	LRRC2	3431	9.5307	0.9473

50065	E16	M-015891-	hypothetica	79719	FLJ11506	3269	12.022	1.544
50065	E17	M-014350-	FYVE and c	79443	FYCO1	3947	6.5619	3.9161
50065	E18	M-012927-	transducin	79718	TBL1XR1	5409	10.723	0.245
50065	E19	M-014352-	WD repeat	79446	WDR25	2960	7.7703	2.7077
50065	E20	M-014403-	phosphopa	79717	PPCS	3715	7.8062	2.6718
50065	E21	M-003991-	chromosom	79447	C16orf53	4291	6.0126	4.4654
50065	E23	M-014353-	UL16 bindi	79465	ULBP3	2138	5.145	5.333
50065	F02	M-014508-	ATP-bindin	79963	ABCA11	1500	7.1333	3.3447
50065	F04	M-014507-	hypothetica	79962	FLJ13236	2492	9.3098	1.1682
50065	F05	M-018393-	chromosom	79786	C16orf44	3820	14.241	3.763
50065	F06	M-016580-	DENN/MAD	79961	DENND2D	2866	13.294	2.816
50065	F07	M-017131-	calmin (cal	79789	CLMN	5750	6.5739	3.9041
50065	F08	M-017133-	PHD finger	79960	PHF17	2959	10.341	0.137
50065	F09	M-014429-	chromosom	79794	C12orf49	3166	8.844	1.634
50065	F10	M-016487-	centrosom	79959	CEP76	3140	10.478	0
50065	F11	M-014430-	asparagine	79796	ALG9	2663	11.528	1.05
50065	F12	M-014506-	DENN/MAD	79958	DENND1C	2692	8.2838	2.1942
50065	F13	M-007064-	zinc finger	79797	ZNF408	2417	11.129	0.651
50065	F14	M-008054-	progestin a	79957	PAQR6	4294	10.852	0.374
50065	F15	M-003999-	armadillo r	79798	ARMC5	3162	8.697	1.781
50065	F16	M-005876-	KIAA1815	79956	KIAA1815	3186	10.013	0.465
50065	F17	M-014431-	UDP glucur	79799	UGT2A3	4066	7.0093	3.4687
50065	F18	M-015882-	PDZ domai	79955	PDZD7	5212	7.5403	2.9377
50065	F19	M-016781-	SHC SH2-do	79801	SHCBP1	3358	12.061	1.583
50065	F20	M-014505-	nucleolar p	79954	NOL10	3372	6.465	4.013
50065	F21	M-016570-	KIAA1822-l	79802	KIAA1822L	4681	6.5798	3.8982
50065	F23	M-018929-	vasohibin 2	79805	VASH2	2238	6.9705	3.5075
50065	G02	M-005978-	aminopept	79716	NPEPL1	1408	13.21	2.732
50065	G04	M-016444-	coiled-coil	79714	CCDC51	1942	10.35	0.128
50065	G05	M-014354-	family with	79567	FAM65A	1940	7.1649	3.3131
50065	G06	M-014401-	transmemb	79713	TMEM149	1397	9.4488	1.0292
50065	G07	M-014355-	chromosom	79568	C2orf47	2424	28.837	18.359
50065	G08	M-014400-	glycosyltra	79712	GTDC1	2373	10.24	0.238
50065	G09	M-014356-	family with	79570	FAM77C	1929	10.835	0.357
50065	G10	M-009516-	importin 4	79711	IPO4	1567	9.381	1.097
50065	G11	M-017478-	GRIP and c	79571	GCC1	3673	10.373	0.105
50065	G12	M-016180-	MORC fam	79710	MORC4	3655	13.297	2.819
50065	G13	M-018132-	tetratricop	79573	TTC13	1475	14.373	3.895
50065	G14	M-018152-	glycosyltra	79709	GLT25D1	4211	10.805	0.327
50065	G15	M-012913-	EPS8-like 3	79574	EPS8L3	2735	16.673	6.195
50065	G16	M-019418-	nucleolar p	79707	NOL9	3361	9.2532	1.2248
50065	G17	M-014357-	NF-kappaB	79576	NKAP	2462	8.7327	1.7453
50065	G18	M-014399-	PRKR intera	79706	PRKRIP1	3174	8.8217	1.6563
50065	G19	M-016914-	sperm asso	79582	SPAG16	4402	8.5416	1.9364
50065	G20	M-018410-	chromosom	79703	C11orf80	2841	6.371	4.107
50065	G21	M-014360-	hypothetica	79584	FLJ12684	1690	6.568	3.91
50065	G23	M-014361-	coronin 7	79585	CORO7	1678	8.4029	2.0751

50065	H02	M-014504-	chromoson	79953	C20orf39	2035	21.13	10.652
50065	H04	M-014502-	hypothetic	79951	FLJ11783	2973	16.347	5.869
50065	H05	M-014433-	glutathione	79807	GSTCD	2330	15.279	4.801
50065	H06	M-019417-	chromoson	79949	C10orf81	1909	10.896	0.418
50065	H07	M-021424-	tetratricop	79809	TTC21B	3494	15.283	4.805
50065	H08	M-010399-	dehydrodo	79947	DHDDS	3580	12.263	1.785
50065	H09	M-016139-	pentatrico	79810	PTCD2	1748	11.213	0.735
50065	H10	M-014500-	chromoson	79946	C10orf95	2108	18.359	7.881
50065	H11	M-014434-	SAFB-like, t	79811	SLTM	2325	12.989	2.511
50065	H12	M-008130-	L-2-hydrox	79944	L2HGDH	1784	15.695	5.217
50065	H13	M-014435-	multimerin	79812	MMRN2	2125	12.753	2.275
50065	H14	M-014499-	zinc finger	79943	ZNF696	2125	11.388	0.91
50065	H15	M-007065-	euchromat	79813	EHMT1	1872	10.31	0.168
50065	H16	M-021284-	chromoson	79940	C6orf155	2463	13.317	2.839
50065	H17	M-014436-	NIPA-like d	79815	NPAL2	3362	15.497	5.019
50065	H18	M-007547-	solute carri	79939	SLC35E1	2833	11.225	0.747
50065	H19	M-014437-	transducin-	79816	TLE6	1877	6.3932	4.0848
50065	H20	M-014495-	synaptopo	79933	SYNPO2L	2480	12.702	2.224
50065	H21	M-018160-	MOB1, Mp	79817	MOBKL2B	1449	11.732	1.254
50065	H23	M-014438-	zinc finger	79818	ZNF552	1364	10.704	0.226
50065	I02	M-004273-	hypothetic	79701	FLJ22222	3064	4.0144	6.4636
50065	I04	M-021798-	zyg-11 hon	79699	ZYG11B	2969	10.677	0.199
50065	I05	M-017704-	chondroitir	79586	CHPF	5247	21.86	11.382
50065	I06	M-014398-	zinc finger,	79698	ZMAT4	5919	16.945	6.467
50065	I07	M-014362-	cysteinyl-t	79587	CARS2	4067	11.384	0.906
50065	I08	M-014397-	chromoson	79697	C14orf169	3127	11.065	0.587
50065	I09	M-007061-	ring finger	79589	RNF128	3609	10.945	0.467
50065	I10	M-031970-	chromoson	79696	C14orf140	2782	13.767	3.289
50065	I11	M-017442-	mitochond	79590	MRPL24	2436	12.356	1.878
50065	I12	M-016429-	UDP-N-ace	79695	GALNT12	3791	20.232	9.754
50065	I13	M-014363-	chromoson	79591	C10orf76	3770	12.467	1.989
50065	I14	M-014396-	mannosida	79694	MANEA	2647	12.996	2.518
50065	I15	M-007062-	chromoson	79594	C1orf166	3212	10.679	0.201
50065	I16	M-018139-	yrdC doma	79693	YRDC	3429	15.281	4.803
50065	I17	M-017129-	Sin3A-asso	79595	SAP130	2706	14.893	4.415
50065	I18	M-014395-	zinc finger	79692	ZNF322A	2066	7.7928	2.6852
50065	I19	M-016380-	chromoson	79596	C13orf7	3942	13.115	2.637
50065	I20	M-018409-	queuine tR	79691	QTRTD1	3760	6.5957	3.8823
50065	I21	M-018133-	leucine-ricl	79598	LRRIQ2	3235	5.6569	4.8211
50065	I23	M-018660-	tectonic 1	79600	TECT1	3772	7.3701	3.1079
50065	J02	M-010672-	KIAA0319-l	79932	KIAA0319L	3809	14.781	4.303
50065	J04	M-016578-	TNFAIP3 in	79931	TNIP3	1941	11.901	1.423
50065	J05	M-019275-	WD repeat	79819	WDR78	3354	15.802	5.324
50065	J06	M-014494-	docking pr	79930	DOK3	3643	12.407	1.929
50065	J07	M-021281-	chromoson	79820	C14orf161	4197	7.3862	3.0918
50065	J08	M-014493-	MAP6 dom	79929	MAP6D1	3319	9.5812	0.8968
50065	J09	M-014439-	chromoson	79823	C2orf34	4242	6.5299	3.9481

50065	J10	M-014492-	glycine/arg	79927	GRRP1	3328	6.3702	4.1078
50065	J11	M-014440-	coiled-coil	79825	CCDC48	4654	22.583	12.105
50065	J12	M-014491-	hypothetic	79926	FLJ14124	4532	6.6417	3.8363
50065	J13	M-010734-	adipocyte-	79827	ASAM	4824	8.8516	1.6264
50065	J14	M-028510-	KPL2 prote	79925	FLJ23577	4051	10.738	0.26
50065	J15	M-014442-	methyltran	79828	METTL8	3798	13.77	3.292
50065	J16	M-018396-	mitochond	79922	MRM1	3280	6.0061	4.4719
50065	J17	M-014443-	N-acetyltra	79829	NAT11	2584	6.2693	4.2087
50065	J18	M-016799-	transcriptic	79921	TCEAL4	5106	12.848	2.37
50065	J19	M-007066-	zinc finger,	79830	ZMYM1	4343	9.6247	0.8533
50065	J20	M-014487-	chromosom	79919	C2orf54	2869	6.3437	4.1343
50065	J21	M-003983-	jumonji do	79831	JMJD5	1976	7.1862	3.2918
50065	J23	M-015243-	gem (nucle	79833	GEMIN6	2728	5.6452	4.8328
50065	K02	M-018699-	galactose-	79690	GAL3ST4	2006	15.354	4.876
50065	K04	M-014394-	STEAP fami	79689	STEAP4	2255	18.492	8.014
50065	K05	M-014364-	LAG1 hom	79603	LASS4	3639	12.888	2.41
50065	K06	M-016135-	chromosom	79686	C14orf139	2036	11.002	0.524
50065	K07	M-017594-	piggyBac tr	79605	PGBD5	5547	13.196	2.718
50065	K08	M-014392-	chromosom	79684	C11orf61	3346	13.987	3.509
50065	K09	M-014365-	family with	79607	FAM118B	4187	15.524	5.046
50065	K10	M-016703-	zinc finger,	79683	ZDHHC14	3448	16.85	6.372
50065	K11	M-016185-	resistance	79608	RIC3	3188	16.593	6.115
50065	K12	M-016338-	chromosom	79680	C22orf29	1720	12.965	2.487
50065	K13	M-014366-	chromosom	79609	C14orf138	2035	12.629	2.151
50065	K14	M-007814-	V-set doma	79679	VTCN1	3254	16.749	6.271
50065	K15	M-009760-	FLJ21963 p	79611	FLJ21963	4780	14.603	4.125
50065	K16	M-018408-	structural r	79677	SMC6	6197	11.376	0.898
50065	K17	M-013336-	NMDA rece	79612	NARG1L	4303	15.663	5.185
50065	K18	M-004279-	2-oxogluta	79676	OGFOD2	4175	7.2575	3.2205
50065	K19	M-018425-	chromosom	79614	C5orf23	5061	16.696	6.218
50065	K20	M-017130-	FAST kinas	79675	FASTKD1	4091	14.422	3.944
50065	K21	M-015658-	cyclin J-like	79616	CCNJL	4377	13.388	2.91
50065	K23	M-014367-	homeobox	79618	HMBOX1	3201	15.589	5.111
50065	L02	M-014486-	SET domair	79918	SETD6	4157	19.75	9.272
50065	L04	M-014485-	MAGI famil	79917	MAGIX	2860	23.881	13.403
50065	L05	M-005339-	NKF3 kinas	79834	SGK269	4515	22.99	12.512
50065	L06	M-004738-	ATPase fam	79915	ATAD5	4338	20.701	10.223
50065	L07	M-007067-	LON peptid	79836	LONRF3	2849	21.411	10.933
50065	L08	M-008132-	hypothetic	79912	FLJ22028	4175	23.88	13.402
50065	L09	M-019436-	transmemb	79838	TMC5	5479	19.474	8.996
50065	L10	M-014483-	butyrophili	79908	BTNL8	4552	20.562	10.084
50065	L11	M-014445-	coiled-coil	79839	CCDC102B	2645	15.879	5.401
50065	L12	M-014481-	MORN repe	79906	MORN1	3280	16.006	5.528
50065	L13	M-014446-	nonhomolo	79840	NHEJ1	3431	14.631	4.153
50065	L14	M-019479-	transmemb	79905	TMC7	2371	14.551	4.073
50065	L15	M-012937-	ATP/GTP bi	79841	AGBL2	3028	16.083	5.605
50065	L16	M-014479-	hypothetic	79903	FLJ14154	1656	21.316	10.838

50065	L17	M-016482- zinc finger	79842	ZBTB3	1916	15.501	5.023
50065	L18	M-014478- nucleopori	79902	NUP85	4397	11.963	1.485
50065	L19	M-018394- family with	79843	FAM124B	4102	17.504	7.026
50065	L20	M-017132- cytochrom	79901	CYBRD1	3878	17.818	7.34
50065	L21	M-014447- zinc finger,	79844	ZDHHC11	1805	21.884	11.406
50065	L23	M-007068- ring finger	79845	RNF122	2076	17.726	7.248
50065	M02	M-014390- ventricular	79674	VEPH1	2264	4.1519	6.3261
50065	M04	M-007063- zinc finger	79673	ZNF329	3058	6.4421	4.0359
50065	M05	M-014369- ribonuclea	79621	RNASEH2B	3772	13.176	2.698
50065	M06	M-012926- NLR family	79671	NLRX1	3620	7.9834	2.4946
50065	M07	M-014370- chromoson	79622	C16orf33	2533	9.6328	0.8452
50065	M08	M-026009- zinc finger,	79670	ZCCHC6	2777	4.9694	5.5086
50065	M09	M-014371- UDP-N-ace	79623	GALNT14	3265	17.703	7.225
50065	M10	M-014389- chromoson	79669	C3orf52	2660	7.8571	2.6209
50065	M11	M-014372- chromoson	79624	C6orf211	2815	12.398	1.92
50065	M12	M-015784- poly (ADP-	79668	PARP8	2901	8.1351	2.3429
50065	M13	M-016438- chromoson	79625	C4orf31	1554	5.3411	5.1369
50065	M14	M-014388- hypothetic	79667	FLJ13197	2303	5.3409	5.1371
50065	M15	M-014373- tumor necr	79626	TNFAIP8L2	3327	11.061	0.583
50065	M16	M-018407- pleckstrin	79666	PLEKHF2	2995	11.786	1.308
50065	M17	M-018134- opioid grov	79627	OGFRL1	3752	13.14	2.662
50065	M18	M-018727- DEAH (Asp-	79665	DHX40	1975	4.557	5.921
50065	M19	M-024332- SH3 domai	79628	SH3TC2	2459	8.4587	2.0193
50065	M20	M-004287- HSPB (heat	79663	HSPBAP1	3329	5.7375	4.7405
50065	M21	M-004343- occludin/EI	79629	OCEL1	2968	7.5809	2.8971
50065	M23	M-014374- chromoson	79630	C1orf54	3929	7.6355	2.8425
50065	N02	M-014477- hypothetic	79899	FLJ14213	2488	18.368	7.89
50065	N04	M-016574- zinc finger	79898	ZNF613	3052	14.318	3.84
50065	N05	M-019110- hypothetic	79846	FLJ21062	3520	21.222	10.744
50065	N06	M-014476- ribonuclea	79897	RPP21	3381	16.415	5.937
50065	N07	M-026283- transmemb	79847	TMEM180	4042	12.865	2.387
50065	N08	M-030400- ATPase, Cla	79895	ATP8B4	2901	10.789	0.311
50065	N09	M-016485- centrosom	79848	CSPP1	2273	12.89	2.412
50065	N10	M-007070- zinc finger	79894	ZNF672	1885	11.777	1.299
50065	N11	M-017027- PDZ domai	79849	PDZD3	2321	9.3494	1.1286
50065	N12	M-014475- zinc finger	79893	ZNF403	2391	5.9389	4.5391
50065	N13	M-014448- family with	79850	FAM57A	3387	16.268	5.79
50065	N14	M-014474- chromoson	79892	C10orf119	3319	11.992	1.514
50065	N15	M-014450- transmemb	79853	TM4SF20	2553	7.3639	3.1141
50065	N16	M-014473- zinc finger	79891	ZNF671	2348	5.6644	4.8136
50065	N17	M-014451- hypothetic	79854	FLJ22639	2891	6.4338	4.0442
50065	N18	M-014503- Ras and Ra	79890	RIN3	3031	16.1	5.622
50065	N19	M-014452- sorting nex	79856	SNX22	3635	5.7772	4.7008
50065	N20	M-014472- hypothetic	79887	FLJ22662	2568	7.243	3.235
50065	N21	M-031086- hypothetic	79860	FLJ21369	3339	7.8766	2.6014
50065	N23	M-009010- tubulin, alp	79861	TUBAL3	4702	5.806	4.672
50065	O02	M-026503- dynein, cyt	79659	DYNC2H1	2813	16.175	5.697

50065	O04	M-014385-	hypothetic	79657	FLJ21908	1332	11.486	1.008
50065	O05	M-018426-	elongation	79631	EFTUD1	1754	11.117	0.639
50065	O06	M-014384-	chromoson	79656	C1orf165	2075	11.181	0.703
50065	O07	M-015782-	chromoson	79632	C6orf60	4073	11.564	1.086
50065	O08	M-027468-	HECT doma	79654	HECTD3	3097	10.268	0.21
50065	O09	M-014375-	FAT tumor	79633	FAT4	3667	9.49	0.988
50065	O10	M-014383-	chromoson	79652	C16orf30	4120	13.301	2.823
50065	O11	M-014376-	secernin 3	79634	SCRN3	3634	14.557	4.079
50065	O12	M-014382-	chromoson	79650	C16orf57	1619	9.265	1.213
50065	O13	M-014377-	coiled-coil	79635	CCDC121	2799	8.9318	1.5462
50065	O14	M-024948-	MAP7 dom	79649	MAP7D3	2111	13.169	2.691
50065	O15	M-014378-	transmem	79639	TMEM53	1871	9.0326	1.4454
50065	O16	M-014381-	chromoson	79647	C1orf108	2334	8.2262	2.2518
50065	O17	M-015659-	hypothetic	79640	CTA-216E1	3975	3.5975	6.8805
50065	O18	M-016476-	EF-hand ca	79645	EFCAB1	2520	8.9683	1.5097
50065	O19	M-014379-	rogdi hom	79641	ROGDI	3393	15.031	4.553
50065	O20	M-014380-	steroid 5 al	79644	SRD5A2L	3666	13.066	2.588
50065	O21	M-009048-	arylsulfata	79642	ARSJ	2666	7.7644	2.7136
50065	O23	M-005060-	chromatin	79643	CHMP6	2704	4.5118	5.9662
50065	P02	M-014471-	chromoson	79886	C9orf82	2321	7.9707	2.5073
50065	P04	M-014470-	microtubul	79884	MAP9	2398	10.008	0.47
50065	P05	M-014454-	zinc finger	79862	ZNF669	2184	12.958	2.48
50065	P06	M-014469-	podocan-li	79883	PODNL1	1730	6.9942	3.4838
50065	P07	M-014455-	chromoson	79863	C18orf22	3137	7.2043	3.2737
50065	P08	M-014468-	zinc finger	79882	ZC3H14	2375	6.8632	3.6148
50065	P09	M-014456-	chromoson	79864	C11orf63	2172	7.1363	3.3417
50065	P10	M-006806-	dephospho	79877	DCAKD	1510	10.132	0.346
50065	P11	M-014457-	triggering r	79865	TREML2	2236	4.2934	6.1846
50065	P12	M-006405-	ubiquitin-a	79876	UBE1DC1	1559	3.5279	6.9501
50065	P13	M-014458-	chromoson	79866	C13orf34	2010	5.1244	5.3536
50065	P14	M-009001-	rabaptin, R	79874	RABEP2	3681	12.225	1.747
50065	P15	M-018161-	chromoson	79867	C12orf38	2629	7.6455	2.8325
50065	P16	M-014462-	nudix (nucl	79873	NUDT18	3392	6.8986	3.5794
50065	P17	M-014459-	chromoson	79868	CXorf45	3766	5.5231	4.9549
50065	P18	M-007069-	Cas-Br-M (	79872	CBLL1	2168	6.2731	4.2049
50065	P19	M-015842-	pre-mRNA	79869	FLJ12529	2707	6.6494	3.8286
50065	P20	M-014461-	chromoson	79871	C1orf82	1430	6.3636	4.1144
50065	P21	M-014460-	brain and a	79870	BAALC	1996	4.4088	6.0692
50065	P23	M-009382-	Rho GTPas	79658	ARHGAP10	3021	10.89	0.412
					MAD		10.478	3.0354
					MAD3			9.1062
					MADc			4.492392
50065	C22	Human4 Pc	RNAi	empty				
50065	D22	Human4 Pc	RNAi	empty				
50065	E22	Human4 Pc	RNAi	empty				
50065	F22	Human4 Pc	RNAi	empty				

50065	G22	Human4 Pc	RNAi	empty				
50065	H22	Human4 Pc	RNAi	empty				
50065	I22	Human4 Pc	RNAi	empty				
50065	J22	Human4 Pc	RNAi	empty				

50065	H03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347
50065	I03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-1	siControl non-targeting	
50065	J03	Human4 Pc	RNAi	library cont	Dharmacor	D-001206-1	siControl non-targeting	
50065	K03	Human4 Pc	RNAi	library cont	Dharmacor	D-001600-(	siGLO RISC-free siRNA	
50065	K22	Human4 Pc	RNAi	empty				
50065	G03	Human4 Pc	RNAi	library cont	Dharmacor	M-003290-	polo-like ki	5347

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.660005	4542	12.99	3.2727	0.823999	5385	19.536	9.745	2.352433
-1.07286	2238	5.8534	3.8639	-0.97285	3080	10.162	0.371	0.089559
-0.53588	3597	6.1718	3.5455	-0.89268	3325	7.1579	2.6331	-0.63563
-0.3138	4294	4.9837	4.7336	-1.19182	4550	6.7253	3.0657	-0.74006
-0.78203	1755	6.0969	3.6204	-0.91154	2017	8.5771	1.2139	-0.29303
0.366842	2354	7.6466	2.0707	-0.52136	2828	5.3041	4.4869	-1.08313
0.315645	1174	5.707	4.0103	-1.00971	1725	9.3333	0.4577	-0.11049
-1.05581	2431	8.1448	1.5725	-0.39592	1983	7.9677	1.8233	-0.44014
0.378195	1877	11.881	2.1637	0.544775	2222	9.0459	0.7451	-0.17987
-0.09616	2217	7.6229	2.0944	-0.52733	1802	9.3785	0.4125	-0.09958
-0.42407	1632	6.6789	3.0384	-0.76501	1929	7.1021	2.6889	-0.6491
-0.03383	2096	10.639	0.9217	0.232065	2526	8.3135	1.4775	-0.35667
-0.23277	2504	13.339	3.6217	0.91187	2962	4.7941	4.9969	-1.20625
-0.94854	3291	8.4169	1.3004	-0.32741	2773	5.3372	4.4538	-1.07514
-0.75412	2312	6.7474	2.9699	-0.74776	2432	4.6875	5.1035	-1.23198
1.206262	4592	8.6672	1.0501	-0.26439	2312	6.0554	3.7356	-0.90177
-0.07635	1479	8.1812	1.5361	-0.38676	1529	11.707	1.916	0.46252
-0.56905	1871	8.605	1.1123	-0.28005	2925	4.7521	5.0389	-1.21639
0.85233	2995	9.8164	0.0991	0.024951	2893	8.8835	0.9075	-0.21907
-0.42801	1092	8.4249	1.2924	-0.3254	1981	4.7451	5.0459	-1.21807
0.422715	4422	7.9376	1.7797	-0.44809	3952	12.424	2.633	0.635603
-0.13474	3229	11.799	2.0817	0.52413	2776	17.399	7.608	1.836563
-1.26472	3252	10.055	0.3377	0.085026	3316	10.253	0.462	0.111526
-0.4939	3372	8.274	1.4433	-0.36339	2954	11.645	1.854	0.447554
-0.15146	4515	8.7486	0.9687	-0.2439	4157	13.159	3.368	0.813032
-0.49611	4194	10.062	0.3447	0.086788	4409	9.6621	0.1289	-0.03112
-0.1564	3285	9.7717	0.0544	0.013697	3279	10.064	0.273	0.065902
0.543808	4803	12.492	2.7747	0.698613	4035	10.558	0.767	0.185153
0.197445	1687	13.456	3.7387	0.941328	3057	17.239	7.448	1.797939
-0.20012	1358	12.003	2.2857	0.575493	3493	9.791	0	0
-0.71412	2547	10.954	1.2367	0.311376	3137	8.5432	1.2478	-0.30122
-0.46886	2237	11.399	1.6817	0.423418	3652	7.7766	2.0144	-0.48627
-0.1422	1829	15.91	6.1927	1.559195	2726	11.445	1.654	0.399274
-0.41501	2113	10.175	0.4577	0.11524	2996	13.852	4.061	0.980321
-0.99023	2334	8.7404	0.9769	-0.24596	3566	8.4969	1.2941	-0.31239
0.294498	3579	15.731	6.0137	1.514127	4900	11.082	1.291	0.311646
1.390573	3409	12.232	2.5147	0.63315	4598	13.767	3.976	0.959802
-0.82181	2082	10.663	0.9457	0.238108	4117	5.6352	4.1558	-1.00321
0.01803	2391	10.456	0.7387	0.18599	3543	9.0601	0.7309	-0.17644
-0.96212	1015	15.369	5.6517	1.422983	2185	8.4668	1.3242	-0.31966
-0.95221	2071	5.1666	4.5507	-1.14577	2070	6.6667	3.1243	-0.7542
-1.08875	1868	4.818	4.8993	-1.23354	2939	5.3079	4.4831	-1.08222
-0.84788	2096	4.6756	5.0417	-1.2694	1919	6.9307	2.8603	-0.69047
-0.53557	3143	5.5043	4.213	-1.06075	3147	5.9739	3.8171	-0.92144
0.744592	4388	8.7511	0.9662	-0.24327	2921	14.105	4.314	1.041395
0.51999	2839	8.665	1.0523	-0.26495	3037	11.854	2.063	0.498006

-0.97576	2179	8.1689	1.5484	-0.38986	2378	9.4617	0.3293	-0.07949
1.375882	2207	11.871	2.1537	0.542258	2365	14.884	5.093	1.229445
-0.25185	3106	6.8577	2.8596	-0.71999	2863	6.7761	3.0149	-0.72779
-1.33392	2141	5.1845	4.5328	-1.14127	1930	4.4041	5.3869	-1.30039
-0.43427	1984	4.1331	5.5842	-1.40599	2247	1.0681	8.7229	-2.1057
0.221486	1530	9.8039	0.0866	0.021804	1722	10.918	1.127	0.272057
-0.66864	2463	7.7954	1.9219	-0.4839	2076	5.5395	4.2515	-1.02631
0.768633	3793	13.288	3.5707	0.899029	2978	8.3613	1.4297	-0.34513
-0.96198	4112	7.6362	2.0811	-0.52398	2984	5.6971	4.0939	-0.98826
0.735466	3409	11.352	1.6347	0.411584	3678	8.8635	0.9275	-0.2239
-0.34338	4094	5.7645	3.9528	-0.99523	4703	7.2507	2.5403	-0.61323
-0.90644	3369	5.8178	3.8995	-0.98181	5080	6.1614	3.6296	-0.87618
0.154261	2577	6.7132	3.0041	-0.75637	2245	3.7416	6.0494	-1.46032
-1.29154	1837	5.2803	4.437	-1.11715	2472	1.7395	8.0515	-1.94362
-0.34233	2424	10.644	0.9267	0.233324	2477	14.776	4.985	1.203374
1.677503	2965	13.794	4.0767	1.02643	1585	13.249	3.458	0.834758
0.580314	2434	14.503	4.7857	1.204942	1729	18.392	8.601	2.076272
0.763513	3684	10.722	1.0047	0.252963	2053	15.636	5.845	1.410977
-0.40914	2598	8.622	1.0953	-0.27577	1795	12.033	2.242	0.541216
-0.75984	2453	13.29	3.5727	0.899533	2002	9.5904	0.2006	-0.04842
-0.68981	2380	9.0336	0.6837	-0.17214	2333	10.716	0.925	0.223294
-0.96572	2234	10.295	0.5777	0.145453	1316	12.462	2.671	0.644777
0.050307	3564	15.965	6.2477	1.573043	3449	15.541	5.75	1.388044
1.889862	1726	16.744	7.0267	1.76918	2967	9.8079	0.0169	0.00408
0.040513	1631	11.649	1.9317	0.486363	2603	9.5275	0.2635	-0.06361
-1.0577	2239	9.2452	0.4721	-0.11887	2959	9.2937	0.4973	-0.12005
0.621495	1840	14.511	4.7937	1.206956	1837	13.337	3.546	0.856001
0.286484	2566	15.549	5.8317	1.468303	3414	9.8418	0.0508	0.012263
0.646204	1913	8.1025	1.6148	-0.40657	1775	8.7887	1.0023	-0.24195
-0.79563	1755	6.3818	3.3355	-0.83981	1425	8.6316	1.1594	-0.27988
1.326242	2758	13.017	3.2997	0.830797	2923	11.05	1.259	0.303921
0.032499	2185	5.9954	3.7219	-0.9371	2212	6.8716	2.9194	-0.70474
-0.63436	1858	8.9343	0.783	-0.19714	2219	6.1289	3.6621	-0.88403
-1.34327	1557	5.9088	3.8085	-0.9589	2887	5.3689	4.4221	-1.06749
-0.80218	2213	8.3597	1.3576	-0.34182	2073	4.438	5.353	-1.29221
0.098834	2421	9.7893	0.072	0.018128	2020	13.564	3.773	0.910798
-0.67568	2618	7.9068	1.8105	-0.45585	1569	10.771	0.98	0.236571
-0.67007	1198	3.3389	6.3784	-1.60595	737	8.5482	1.2428	-0.30001
1.173762	3282	6.9165	2.8008	-0.70518	1795	11.365	1.574	0.379962
2.215301	2938	11.777	2.0597	0.51859	2178	18.044	8.253	1.992266
0.938921	1486	11.978	2.2607	0.569198	1012	15.02	5.229	1.262275
-0.74134	2399	7.8366	1.8807	-0.47352	1758	12.912	3.121	0.753406
-0.37893	1931	5.8519	3.8654	-0.97323	1211	5.8629	3.9281	-0.94824
-0.25225	1555	8.1029	1.6144	-0.40647	1345	7.2119	2.5791	-0.62259
1.289959	2187	6.7215	2.9958	-0.75428	1963	11.819	2.028	0.489557
-0.48998	1458	7.4074	2.3099	-0.58159	853	7.7374	2.0536	-0.49574
-0.21087	2606	10.207	0.4897	0.123296	2478	9.6449	0.1461	-0.03527

0.343692	2838	8.1395	1.5778	-0.39726	1514	8.2563	1.5347	-0.37047
-0.87172	2729	3.0048	6.7125	-1.69007	1646	6.9866	2.8044	-0.67698
0.054537	3478	7.7918	1.9255	-0.4848	2774	10.238	0.447	0.107905
-0.60273	1540	4.7403	4.977	-1.25311	1314	12.1	2.309	0.55739
-0.59474	1684	3.9192	5.7981	-1.45984	1382	6.2952	3.4958	-0.84388
-0.99399	3259	4.1731	5.5442	-1.39592	2454	8.476	1.315	-0.31744
-1.18712	1433	3.3496	6.3677	-1.60326	1349	7.1905	2.6005	-0.62776
-0.74453	1997	9.364	0.3533	-0.08895	2477	8.8817	0.9093	-0.2195
-0.26004	1504	13.697	3.9797	1.002007	3164	9.4185	0.3725	-0.08992
0.837638	2146	10.531	0.8137	0.204873	3850	8.026	1.765	-0.42607
0.626838	1454	9.5598	0.1575	-0.03966	2478	12.066	2.275	0.549183
-0.86905	3516	6.57	3.1473	-0.79243	3529	4.9589	4.8321	-1.16646
-0.0305	2063	11.973	2.2557	0.567939	2021	7.7684	2.0226	-0.48825
-0.36373	2675	6.9533	2.764	-0.69592	3898	8.5428	1.2482	-0.30131
0	3222	11.173	1.4557	0.366516	2741	7.8803	1.9107	-0.46124
0.233728	2268	11.464	1.7467	0.439783	2264	6.0512	3.7398	-0.90278
-0.48843	2229	9.9596	0.2423	0.061006	2200	8.6818	1.1092	-0.26776
0.144912	1863	10.091	0.3737	0.09409	1719	8.4933	1.2977	-0.31326
0.083252	3462	8.4633	1.254	-0.31573	2437	6.8937	2.8973	-0.69941
-0.39645	2252	5.2842	4.4331	-1.11616	2500	10.08	0.289	0.069764
-0.10351	5330	10.206	0.4887	0.123045	2412	7.9602	1.8308	-0.44195
-0.77213	3608	7.3725	2.3448	-0.59037	3721	5.4286	4.3624	-1.05308
-0.65393	2891	5.4998	4.2175	-1.06188	2119	4.2945	5.4965	-1.32685
0.352374	2191	7.6221	2.0952	-0.52753	2046	6.9404	2.8506	-0.68813
-0.89329	1914	9.3521	0.3652	-0.09195	2549	5.7277	4.0633	-0.98088
-0.86773	3575	7.7203	1.997	-0.5028	2045	7.824	1.967	-0.47483
-0.78076	1368	6.0673	3.65	-0.919	2034	4.8181	4.9729	-1.20045
0.608139	1766	8.3239	1.3934	-0.35083	2315	11.447	1.656	0.399757
-0.02849	2732	6.4422	3.2751	-0.8246	2077	6.1627	3.6283	-0.87587
-0.73749	2740	4.4161	5.3012	-1.33473	1868	7.3876	2.4034	-0.58018
-0.2291	2595	6.0501	3.6672	-0.92333	1935	8.0103	1.7807	-0.42986
4.086687	2624	14.177	4.4597	1.122861	1640	12.927	3.136	0.757027
-0.05298	3989	7.6711	2.0462	-0.51519	2568	9.3458	0.4452	-0.10747
0.079468	2662	11.608	1.8907	0.47604	2054	11.149	1.358	0.32782
-0.24419	1456	8.3791	1.3382	-0.33693	1055	6.7299	3.0611	-0.73895
-0.02337	3298	9.9151	0.1978	0.049802	1973	11.353	1.562	0.377065
0.627505	2714	8.4009	1.3164	-0.33144	2407	8.5999	1.1911	-0.28753
0.867021	1514	19.947	10.2297	2.57563	1909	16.344	6.553	1.581887
0.07279	2807	11.329	1.6117	0.405793	3037	8.3635	1.4275	-0.3446
1.378998	2301	11.821	2.1037	0.529669	1543	11.925	2.134	0.515145
-0.27264	3026	8.8566	0.8607	-0.21671	2115	12.53	2.739	0.661192
-0.3885	2380	8.1933	1.524	-0.38371	1400	12.429	2.638	0.63681
-0.36869	2195	10.934	1.2167	0.30634	1871	7.643	2.148	-0.51852
-0.43104	4501	9.309	0.4083	-0.1028	3225	6.8217	2.9693	-0.71679
-0.91421	2176	7.9963	1.721	-0.43331	2626	6.3214	3.4696	-0.83756
-0.87036	2542	4.4847	5.2326	-1.31746	2286	5.5118	4.2792	-1.03299
-0.46191	1768	3.9593	5.758	-1.44975	1516	6.9261	2.8649	-0.69158

2.37112	1643	11.199	1.4817	0.373062	3063	15.736	5.945	1.435117
1.306431	2346	15.985	6.2677	1.578079	2593	16.236	6.445	1.555816
1.068696	1063	15.71	5.9927	1.508839	2327	7.5204	2.2706	-0.54812
0.093046	712	22.331	12.6137	3.175872	1466	10.709	0.918	0.221604
1.069586	2485	13.119	3.4017	0.856479	2473	10.352	0.561	0.135425
0.397338	2419	10.666	0.9487	0.238863	1594	13.551	3.76	0.90766
0.16361	1005	17.015	7.2977	1.837412	1214	12.932	3.141	0.758234
1.754299	2473	13.061	3.3437	0.841875	2468	10.818	1.027	0.247917
0.558945	1994	10.08	0.3627	0.09132	1988	12.022	2.231	0.538561
1.161297	1447	11.057	1.3397	0.337309	970	15.567	5.776	1.39432
0.506412	1912	16.004	6.2867	1.582863	2319	15.912	6.121	1.477603
0.202565	2035	10.221	0.5037	0.126821	2586	13.457	3.666	0.884969
-0.0374	1361	10.066	0.3487	0.087796	1658	16.526	6.735	1.625822
0.631957	1463	9.1593	0.558	-0.14049	1762	9.6481	0.1429	-0.0345
1.117222	1830	11.53	1.8127	0.456401	2032	10.384	0.593	0.14315
0.166281	2688	9.7098	0.0075	-0.00189	2200	13.682	3.891	0.939283
-0.90927	1573	7.5016	2.2157	-0.55787	1567	7.4027	2.3883	-0.57653
0.495059	1696	8.7264	0.9909	-0.24949	1990	12.362	2.571	0.620637
0.279139	1094	7.9525	1.7648	-0.44434	1399	4.1458	5.6452	-1.36275
0.050307	867	10.035	0.3177	0.07999	1724	8.6427	1.1483	-0.2772
-1.43879	2347	6.3911	3.3262	-0.83747	3438	4.1594	5.6316	-1.35946
0.044297	1803	12.978	3.2607	0.820978	2662	10.105	0.314	0.075799
2.533617	3140	18.089	8.3717	2.107823	3583	19.648	9.857	2.37947
1.439545	3756	14.963	5.2457	1.32076	4156	10.78	0.989	0.238744
0.201674	2366	8.5799	1.1374	-0.28637	2901	9.8931	0.1021	0.024647
0.130665	2955	10.761	1.0437	0.262782	3191	12.504	2.713	0.654915
0.103954	2134	9.8875	0.1702	0.042853	1902	11.725	1.934	0.466866
0.732127	2442	14.537	4.8197	1.213502	2346	15.388	5.597	1.35111
0.41804	2192	10.219	0.5017	0.126318	2288	9.7028	0.0882	-0.02129
2.171226	2604	14.055	4.3377	1.092144	2824	18.52	8.729	2.107171
0.442749	2662	6.0856	3.6317	-0.91439	2465	15.335	5.544	1.338316
0.560503	3707	10.952	1.2347	0.310872	3411	18.206	8.415	2.031372
0.044742	1941	8.1917	1.5256	-0.38411	3376	14.307	4.516	1.090158
1.069141	2535	8.7574	0.9599	-0.24168	2709	13.547	3.756	0.906694
0.982773	2653	7.9156	1.8017	-0.45363	2462	13.16	3.369	0.813273
-0.59772	2445	2.5767	7.1406	-1.79786	1310	8.4733	1.3177	-0.31809
0.586992	4194	10.515	0.7977	0.200845	3615	8.3264	1.4646	-0.35355
-0.86419	2551	5.3312	4.3861	-1.10433	2794	7.5161	2.2749	-0.54916
-1.07317	3197	5.1924	4.5249	-1.13928	3076	6.502	3.289	-0.79396
-0.69181	4711	6.177	3.5403	-0.89138	4379	13.542	3.751	0.905487
0.957842	3391	10.056	0.3387	0.085278	3054	15.619	5.828	1.406873
0.316758	1737	14.22	4.5027	1.133688	1954	17.861	8.07	1.94809
1.185115	1668	11.571	1.8537	0.466724	1461	17.796	8.005	1.932399
0.429393	2866	9.9093	0.192	0.048342	2207	19.755	9.964	2.405299
-0.68823	2088	6.7529	2.9644	-0.74638	1732	9.5266	0.2644	-0.06383
-0.19963	1493	8.7743	0.943	-0.23743	1354	11.448	1.657	0.399998
-0.87884	2736	9.0643	0.653	-0.16441	2158	14.133	4.342	1.048154

-0.91439	2852	7.3983	2.319	-0.58388	1385	14.44	4.649	1.122264
2.694556	3324	18.231	8.5137	2.143576	2652	17.421	7.63	1.841874
-0.85395	2252	6.1723	3.545	-0.89256	2232	12.59	2.799	0.675676
-0.36203	2821	8.1886	1.5287	-0.3849	2144	14.039	4.248	1.025463
0.057876	2279	16.849	7.1317	1.795616	2462	17.262	7.471	1.803492
0.732794	2177	15.158	5.4407	1.369857	2979	15.576	5.785	1.396493
-0.99544	1686	5.8126	3.9047	-0.98312	1098	8.561	1.23	-0.29692
-0.93685	1311	10.221	0.5037	0.126821	1134	7.9365	1.8545	-0.44767
0.527559	3197	12.23	2.5127	0.632647	3668	12.595	2.804	0.676883
-0.18994	2545	8.998	0.7193	-0.18111	3093	13.45	3.659	0.883279
-0.92029	2071	5.9392	3.7781	-0.95125	1575	5.7143	4.0767	-0.98411
-0.73275	2461	15.563	5.8457	1.471828	1712	11.624	1.833	0.442484
-1.07577	2331	9.2235	0.4938	-0.12433	2337	8.0017	1.7893	-0.43194
1.085391	1619	17.171	7.4537	1.876689	2521	17.771	7.98	1.926364
1.783905	1516	17.348	7.6307	1.921254	1693	20.083	10.292	2.484478
0.536463	2877	16.58	6.8627	1.727888	3059	17.13	7.339	1.771627
0.116642	1876	19.563	9.8457	2.478946	1463	18.865	9.074	2.190454
0.605023	3454	13.607	3.8897	0.979347	3294	20.735	10.944	2.64187
0.781098	1849	12.223	2.5057	0.630884	1934	14.995	5.204	1.25624
1.123232	3037	11.228	1.5107	0.380363	2036	21.709	11.918	2.876993
1.418398	3032	21.834	12.1167	3.050738	2226	15.499	5.708	1.377905
1.36119	2170	9.3548	0.3625	-0.09127	1237	18.674	8.883	2.144347
0.553603	1085	15.023	5.3057	1.335867	985	22.03	12.239	2.954482
0.47881	1750	8.6286	1.0887	-0.27411	1214	22.158	12.367	2.985381
1.395916	2082	15.658	5.9407	1.495747	2070	16.522	6.731	1.624856
0.918219	3002	12.192	2.4747	0.623079	2284	18.52	8.729	2.107171
0.199894	4083	9.6988	0.0185	-0.00466	3269	10.156	0.365	0.088111
1.154174	3413	14.093	4.3757	1.101712	3001	14.429	4.638	1.119608
-0.71688	3318	9.2224	0.4949	-0.12461	2710	15.203	5.412	1.306451
1.384118	3648	10.499	0.7817	0.196816	3254	9.6804	0.1106	-0.0267
0.877929	1859	10.92	1.2027	0.302815	2662	10.443	0.652	0.157392
0.647762	2207	12.415	2.6977	0.679226	3160	12.5	2.709	0.65395
1.137701	1822	18.222	8.5047	2.14131	2774	10.743	0.952	0.229812
2.063934	3478	16.791	7.0737	1.781013	3232	21.751	11.96	2.887132
2.983489	2357	13.661	3.9437	0.992943	2879	22.959	13.168	3.178741
2.785153	3744	15.037	5.3197	1.339392	3039	24.975	15.184	3.665402
2.275625	2216	21.48	11.7627	2.961608	2608	17.983	8.192	1.97754
2.43367	1595	26.395	16.6777	4.199104	2836	16.079	6.288	1.517917
2.983266	3428	17.182	7.4647	1.879459	3198	19.887	10.096	2.437164
2.002497	3944	21.045	11.3277	2.852084	5853	14.027	4.236	1.022566
2.244684	2710	23.358	13.6407	3.43445	4257	16.068	6.277	1.515261
1.202255	1665	15.195	5.4777	1.379173	2966	16.453	6.662	1.6082
1.230525	1829	15.145	5.4277	1.366584	2930	20.239	10.448	2.522136
0.924452	2727	12.541	2.8237	0.71095	2347	16.233	6.442	1.555092
0.906644	896	18.527	8.8097	2.218103	2435	13.306	3.515	0.848517
1.247665	2078	15.014	5.2967	1.333601	3417	12.994	3.203	0.773201
2.412523	1245	20.241	10.5237	2.649653	2081	11.437	1.646	0.397343

1.118113	1431	14.885	5.1677	1.301121	1793	15.393	5.602	1.352317
0.330559	2748	14.229	4.5117	1.135954	4592	8.9286	0.8624	-0.20818
1.563977	1612	15.074	5.3567	1.348708	4354	9.853	0.062	0.014967
1.633873	1653	15.366	5.6487	1.422227	3138	12.906	3.115	0.751958
2.538959	882	25.17	15.4527	3.890674	1095	11.05	1.259	0.303921
1.613394	987	17.021	7.3037	1.838923	2736	10.892	1.101	0.26578
-1.40818	2652	3.5822	6.1351	-1.54469	3410	6.2757	3.5153	-0.84859
-0.89839	2587	5.6823	4.035	-1.01593	3253	6.8245	2.9665	-0.71611
0.600571	1200	4.25	5.4673	-1.37655	3019	10.235	0.444	0.107181
-0.55529	2386	3.2691	6.4482	-1.62353	3113	6.2641	3.5269	-0.85139
-0.18814	2719	4.4134	5.3039	-1.33541	4059	8.8938	0.8972	-0.21658
-1.22621	2036	5.2554	4.4619	-1.12342	2274	8.4433	1.3477	-0.32533
1.608275	2960	9.5946	0.1227	-0.03089	3320	13.554	3.763	0.908384
-0.58341	3072	5.306	4.4113	-1.11068	3837	6.9846	2.8064	-0.67746
0.427389	2621	8.8897	0.8276	-0.20837	2901	7.1355	2.6555	-0.64103
-0.52153	2273	8.623	1.0943	-0.27552	3778	9.4494	0.3416	-0.08246
-1.14347	2037	4.9092	4.8081	-1.21058	1328	3.3133	6.4777	-1.56371
-1.14351	2338	5.6459	4.0714	-1.0251	2082	5.6676	4.1234	-0.99538
0.129775	2449	9.3099	0.4074	-0.10258	3205	8.5803	1.2107	-0.29226
0.291159	2560	12.656	2.9387	0.739905	3717	10.573	0.782	0.188774
0.592557	2904	10.572	0.8547	0.215196	3165	9.9842	0.1932	0.046638
-1.31801	1302	3.6866	6.0307	-1.51841	3065	4.4372	5.3538	-1.2924
-0.44949	1591	6.3482	3.3691	-0.84827	3675	5.6327	4.1583	-1.00381
-1.05523	2385	5.283	4.4343	-1.11647	5532	4.483	5.308	-1.28135
-0.64489	1732	7.2171	2.5002	-0.6295	2381	6.3839	3.4071	-0.82247
-0.63274	1414	6.6478	3.0695	-0.77284	2731	5.7488	4.0422	-0.97578
1.756303	2647	13.638	3.9207	0.987152	2745	23.024	13.233	3.194432
0.854778	2088	11.59	1.8727	0.471508	2520	12.222	2.431	0.586841
2.391599	3310	15.287	5.5697	1.402337	3579	18.664	8.873	2.141933
1.321568	1817	7.3198	2.3975	-0.60364	3225	13.891	4.1	0.989736
0.531343	3142	7.0337	2.6836	-0.67568	4105	9.1108	0.6802	-0.1642
0.069228	1947	6.0606	3.6567	-0.92068	2613	10.18	0.389	0.093904
0.536908	1918	7.2471	2.4702	-0.62195	1631	11.527	1.736	0.419069
0.289156	1180	11.61	1.8927	0.476543	2386	10.268	0.477	0.115147
-0.25122	1834	6.2159	3.5014	-0.88158	2320	9.2241	0.5669	-0.13685
-1.0104	1930	4.5596	5.1577	-1.2986	3280	7.7439	2.0471	-0.49417
1.288846	3212	13.2	3.4827	0.876873	2505	18.283	8.492	2.04996
0.337014	2707	9.9003	0.183	0.046076	3186	8.2863	1.5047	-0.36323
-0.69319	1567	7.7856	1.9317	-0.48636	2382	8.2284	1.5626	-0.37721
-1.0715	2089	7.3719	2.3454	-0.59052	2735	7.4223	2.3687	-0.5718
-0.90023	2440	3.3197	6.3976	-1.61079	2613	5.0517	4.7393	-1.14406
1.251449	2122	14.326	4.6087	1.160377	2804	9.5578	0.2332	-0.05629
-1.04639	2662	4.5079	5.2094	-1.31162	3225	4.6202	5.1708	-1.24823
-0.72011	986	11.055	1.3377	0.336806	2442	6.0197	3.7713	-0.91039
-0.57907	1561	10.57	0.8527	0.214692	3796	7.6923	2.0987	-0.50662
-1.03998	1156	5.3633	4.354	-1.09625	4089	7.8748	1.9162	-0.46257
1.268144	2390	11.464	1.7467	0.439783	3737	14.771	4.98	1.202167

0.224379	1327	3.8433	5.874	-1.47895	1600	8.8125	0.9785	-0.23621
0.14224	1778	4.2182	5.4991	-1.38456	2148	9.9162	0.1252	0.030223
0.156487	2525	7.2079	2.5094	-0.63182	3407	10.919	1.128	0.272298
0.241742	2418	7.8164	1.9009	-0.47861	4163	5.9813	3.8097	-0.91966
-0.04675	2129	12.259	2.5417	0.639948	1558	7.3171	2.4739	-0.5972
-0.21993	1755	4.9573	4.76	-1.19847	1983	5.7993	3.9917	-0.96359
0.628396	2697	15.276	5.5587	1.399567	2032	11.024	1.233	0.297645
0.90798	2286	12.248	2.5307	0.637179	3901	13.458	3.667	0.88521
-0.27001	691	11.867	2.1497	0.541251	1294	6.3369	3.4541	-0.83382
-0.34418	1515	11.287	1.5697	0.395218	1420	9.7887	0.0023	-0.00056
0.599013	1415	11.166	1.4487	0.364753	2036	13.261	3.47	0.837654
-0.32174	1121	5.5308	4.1865	-1.05408	1719	5.2356	4.5554	-1.09967
-0.50125	1495	6.8227	2.8946	-0.7288	2378	7.3171	2.4739	-0.5972
-1.53159	2753	3.923	5.7943	-1.45889	2610	4.023	5.768	-1.39239
-0.33606	1888	8.7924	0.9249	-0.23287	2267	6.352	3.439	-0.83017
1.013491	1601	9.6814	0.0359	-0.00904	3271	14.705	4.914	1.186234
0.576085	1944	7.6646	2.0527	-0.51683	2395	10.063	0.272	0.065661
-0.60404	1374	4.294	5.4233	-1.36548	2281	8.242	1.549	-0.37393
-1.32807	674	5.0445	4.6728	-1.17652	1401	6.5667	3.2243	-0.77834
-0.55812	2023	12.704	2.9867	0.75199	2204	8.0762	1.7148	-0.41395
-0.10462	3096	17.248	7.5307	1.896076	2687	12.877	3.086	0.744957
0.552044	1886	16.755	7.0377	1.771949	2569	11.639	1.848	0.446105
-0.77549	1306	22.052	12.3347	3.105626	1834	11.614	1.823	0.44007
-0.72872	2122	15.174	5.4567	1.373886	3488	9.031	0.76	-0.18346
-0.80465	1425	13.825	4.1077	1.034235	1348	9.9407	0.1497	0.036137
-0.74386	3077	9.7173	0	0	2946	8.0448	1.7462	-0.42153
-0.07702	1780	10.393	0.6757	0.170127	2210	7.8281	1.9629	-0.47384
-1.37668	1960	6.7857	2.9316	-0.73812	2658	6.4334	3.3576	-0.81052
-1.54708	1344	11.533	1.8157	0.457156	2500	8.2	1.591	-0.38407
-1.1917	1382	11.071	1.3537	0.340834	2517	10.528	0.737	0.177911
0.38888	2181	13.067	3.3497	0.843386	4386	13.406	3.615	0.872657
-0.63051	1587	14.556	4.8387	1.218286	2459	8.6621	1.1289	-0.27252
-0.79677	2600	10.769	1.0517	0.264797	2299	10.613	0.822	0.19843
-1.10295	1818	7.3157	2.4016	-0.60467	3563	8.7567	1.0343	-0.24968
-0.936	1557	10.405	0.6877	0.173149	2864	7.1229	2.6681	-0.64408
-0.85224	2662	9.7671	0.0498	0.012539	3714	7.1352	2.6558	-0.64111
-0.91586	1058	9.0737	0.6436	-0.16205	1165	7.1245	2.6665	-0.64369
-1.351	2396	5.6344	4.0829	-1.02799	1904	8.5609	1.2301	-0.29694
0.091711	1583	10.171	0.4537	0.114232	2821	17.653	7.862	1.897879
		9.7173	2.6836			9.791	2.799	
			8.0508				8.397	
			3.971728				4.14252	

1694	45.455	3407	40.71	2649	29.03
1992	36.245	2063	39.554	3176	40.271
3139	35.553	2447	30.854	1843	36.137
3479	37.223	3926	40.015	3720	33.199

mn	2576	38.619	2960.75	37.78325	2847	34.65925
sd	866.2867	4.608541	856.493	4.643872	799.4978	4.743285
	597	8.5427	756	5.291	1034	8.1238
	582	7.9038	689	7.9826	1367	9.4367
	710	6.6197	1199	8.2569	1025	10.341
	726	9.0909	578	11.765	1109	10.821
mn	653.75	8.039275	805.5	8.323875	1133.75	9.680625
sd	74.72784	1.063469	272.4096	2.655851	159.9945	1.185995
3posSD		13.82562		13.93162		14.22986
3negSD		3.190407		7.967552		3.557986
Sum3SD		17.01603		21.89917		17.78784
MnDiff		30.57973		29.45938		24.97863
SumovrMn		0.556448		0.743368		0.712123
1minus		0.443552		0.256632		0.287877
PLK1 SMAR	160	26.25	105	45.714	135	36.296
	2411	10.991	1617	7.9159	2092	9.369
	2208	10.915	2055	7.1533	2299	12.484
	5214	22.114	4478	21.974	5866	18.548
	5683	17.332	4318	16.79	6440	18.898
PLK1 SMAR	170	32.941	293	10.922	135	28.148

Y

Y

Y	
x	toxic b,c
X	debris a,c
x	debris a,c
x	debris a,c
X	debris a,c
x	toxic b
X	debris a,c
X	debris a,c
x	toxic ab

x toxic a,b,c

Y

0.03125

					cell ct	% inf	AD
50066	A02	M-027165- sushi, von	79987	SVEP1	3431	13.874	0.916
50066	A04	M-010678- l(3)mbt-lik	83746	L3MBTL2	3027	10.836	3.954
50066	A05	M-014521- hypothetic	79999	FLJ22659	3696	12.229	2.561
50066	A06	M-014578- hypothetic	80154	FLJ22795	1986	26.888	12.098
50066	A07	M-014522- KIAA1772	80000	KIAA1772	3809	24.941	10.151
50066	A08	M-014466- coiled-coil	79879	CCDC134	4127	23.867	9.077
50066	A09	M-019079- pecanex-lik	80003	PCNXL2	2575	23.767	8.977
50066	A10	M-014585- chromoson	80169	C17orf68	3059	15.136	0.346
50066	A11	M-014523- RNA bindin	80004	RBM35B	2346	15.772	0.982
50066	A12	M-014548- hypothetic	80076	FLJ13621	2837	15.615	0.825
50066	A13	M-018931- dedicator c	80005	DOCK5	1188	15.488	0.698
50066	A14	M-007813- CD276 mol	80381	CD276	2672	20.696	5.906
50066	A15	M-014524- hypothetic	80006	FLJ13611	1769	14.189	0.601
50066	A16	M-018563- programm	80380	PDCD1LG2	4155	24.116	9.326
50066	A17	M-014525- chromoson	80007	C10orf88	2261	11.101	3.689
50066	A18	M-007074- ring finger	80352	RNF39	3548	15.389	0.599
50066	A19	M-014526- transmemb	80008	TMEM156	2534	20.876	6.086
50066	A20	M-004741- tankyrase,	80351	TNKS2	2647	21.232	6.442
50066	A21	M-014527- RMI1, Rec	80010	RMI1	3027	22.167	7.377
50066	A23	M-014528- NEFA-inter	80011	NIP30	2315	19.352	4.562
50066	B02	M-014708- coiled-coil	83446	CCDC70	3893	8.6309	6.1591
50066	B04	M-014707- germ cell a	83445	GSG1	4898	25.194	10.404
50066	B05	M-008785- UBX domai	80700	UBXD1	3955	8.799	5.991
50066	B06	M-009848- zinc finger,	83444	ZNHIT4	4621	14.889	0.099
50066	B07	M-007424- solute carri	80704	SLC19A3	5818	20.368	5.578
50066	B08	M-014706- splicing fac	83443	SF3B5	2484	4.9517	9.8383
50066	B09	M-014618- testis speci	80705	TSGA10	5483	19.953	5.163
50066	B10	M-014705- SH3 domai	83442	SH3BGRL3	4695	13.695	1.095
50066	B11	M-016055- extraembry	80712	ESX1	5566	19.601	4.811
50066	B12	M-014704- hypothetic	83441	PP1057	4680	14.402	0.388
50066	B13	M-014619- transmemb	80723	TMEM22	4552	14.192	0.598
50066	B14	M-009945- elongation	83401	ELOVL3	4184	10.397	4.393
50066	B15	M-010674- SNAP25-int	80725	SNIP	5280	12.348	2.442
50066	B16	M-014698- zinc finger	81931	ZNF93	5076	13.002	1.788
50066	B17	M-025280- tweety hor	80727	TTYH3	4625	11.741	3.049
50066	B18	M-013475- SEH1-like (	81929	SEH1L	3581	11.421	3.369
50066	B19	M-023929- KIAA1680 p	80730	KIAA1680	4601	11.019	3.771
50066	B20	M-032282- Cdk5 and A	81928	CABLES2	5302	23.482	8.692
50066	B21	M-014620- solute carri	80736	SLC44A4	5101	11.194	3.596
50066	B23	M-014621- chromoson	80737	C6orf27	5987	15.734	0.944
50066	C02	M-014614- WD repeat	80349	WDR61	2934	7.2597	7.5303
50066	C04	M-016343- receptor ac	80346	REEP4	5003	19.588	4.798
50066	C05	M-015805- polyhomec	80012	PHC3	3173	16.136	1.346
50066	C06	M-014613- zinc finger	80345	ZSCAN16	5692	14.213	0.577
50066	C07	M-008465- chromoson	80013	C10orf97	5537	20.191	5.401
50066	C08	M-019051- WD repeat	80344	WDR23	5566	12.9	1.89

50066	C09	M-016585- WW and C	80014	WWC2	5628	25	10.21
50066	C10	M-024241- sel-1 suppr	80343	SEL1L2	4719	12.693	2.097
50066	C11	M-017134- chromoson	80017	C14orf159	4112	15.175	0.385
50066	C12	M-014612- TRAF3 inte	80342	TRAF3IP3	4332	9.2567	5.5333
50066	C13	M-014530- chromoson	80018	C12orf30	4055	34.747	19.957
50066	C14	M-009407- bactericida	80341	BPIL1	3925	9.707	5.083
50066	C15	M-018385- ubiquitin d	80019	UBTD1	5374	19.371	4.581
50066	C16	M-009564- patatin-like	80339	PNPLA3	5676	13.46	1.33
50066	C17	M-008133- FAD-depen	80020	FOXRED2	6217	11.903	2.887
50066	C18	M-016629- transmemb	80335	TMEM113	4850	10.495	4.295
50066	C19	M-015699- transmemb	80021	TMEM62	4547	11.634	3.156
50066	C20	M-021472- Kv channel	80333	KCNIP4	5809	20.675	5.885
50066	C21	M-014531- neurensin	80023	NRSN2	5307	13.115	1.675
50066	C23	M-007332- solute carri	80024	SLC24A6	4812	17.311	2.521
50066	D02	M-005947- family with	81926	FAM108A1	5968	15.382	0.592
50066	D04	M-007368- solute carri	81894	SLC25A28	3789	15.571	0.781
50066	D05	M-010982- chromoson	80739	C6orf25	5154	10.303	4.487
50066	D06	M-014696- chromoson	81892	C14orf156	4065	12.374	2.416
50066	D07	M-014622- lymphocyte	80740	LY6G6C	5454	11.973	2.817
50066	D08	M-007081- queuine tR	81890	QTRT1	3440	7.2093	7.5807
50066	D09	M-014623- lymphocyte	80741	LY6G5C	5738	28.703	13.913
50066	D10	M-014694- hydroxypyr	81888	HYI	5581	21.681	6.891
50066	D11	M-014624- proline rich	80742	PRR3	3807	23.273	8.483
50066	D12	M-018577- LAS1-like (	81887	LAS1L	2816	14.773	0.017
50066	D13	M-014625- THUMP do	80745	THUMPD2	3957	12.99	1.8
50066	D14	M-008958- RAB1B, me	81876	RAB1B	2185	7.2311	7.5589
50066	D15	M-016675- tRNA splici	80746	TSEN2	4491	14.273	0.517
50066	D16	M-014692- interferon	81875	ISG20L2	5573	18.859	4.069
50066	D17	M-014626- alanyl-tRN	80755	AARSD1	3655	9.5486	5.2414
50066	D18	M-014690- actin relate	81873	ARPC5L	6746	30.981	16.191
50066	D19	M-014627- transmemb	80757	TMEM121	4045	10.408	4.382
50066	D20	M-018575- SHANK-ass	81858	SHARPIN	3879	13.818	0.972
50066	D21	M-016618- proline rich	80758	PRR7	4604	20.308	5.518
50066	D23	M-016599- chromoson	80759	C6orf148	3028	15.125	0.335
50066	E02	M-024098- DnaJ (Hsp4	80331	DNAJC5	3878	6.4724	8.3176
50066	E04	M-014611- UL16 bindi	80329	ULBP1	3493	6.8995	7.8905
50066	E05	M-016587- F-box and l	80028	FBXL18	4846	11.494	3.296
50066	E06	M-015898- UL16 bindi	80328	ULBP2	5875	30.809	16.019
50066	E07	M-013165- sema doma	80031	SEMA6D	5426	17.269	2.479
50066	E08	M-016145- pseudouric	80324	PUS1	5569	10.163	4.627
50066	E09	M-014533- zinc finger	80032	ZNF556	5396	6.4307	8.3593
50066	E10	M-014610- coiled-coil	80323	CCDC68	5570	17.325	2.535
50066	E11	M-015646- family with	80034	FAM130A2	4541	15.701	0.911
50066	E12	M-014608- centrosom	80321	CEP70	3165	18.483	3.693
50066	E13	M-010927- family with	80039	FAM106A	4531	10.836	3.954
50066	E14	M-032231- Sp6 transcr	80320	SP6	3724	11.869	2.921
50066	E15	M-014538- hypothetic	80052	FLJ12331	4253	7.0538	7.7362

50066	E16	M-008812-	CXXC finger	80319	CXXC4	3832	5.5324	9.2576
50066	E17	M-014539-	hypothetica	80054	FLJ12355	5048	13.946	0.844
50066	E18	M-014607-	zinc finger	80317	ZKSCAN3	5872	10.065	4.725
50066	E19	M-008110-	GPI deacyla	80055	PGAP1	5730	16.405	1.615
50066	E20	M-014636-	cytoplasmi	80315	CPEB4	4862	7.2398	7.5502
50066	E21	M-018334-	leucine rich	80059	LRRTM4	6047	10.435	4.355
50066	E23	M-014541-	guanine nu	80060	FLJ12595	4192	5.6298	9.1602
50066	F02	M-014689-	mediator o	81857	MED25	4396	11.51	3.28
50066	F04	M-014688-	zinc finger	81856	ZNF611	5873	9.1606	5.6294
50066	F05	M-016148-	inter-alpha	80760	ITIH5	4812	12.219	2.571
50066	F06	M-018729-	sideroflexin	81855	SFXN3	4334	11.329	3.461
50066	F07	M-019188-	uroplakin 3	80761	UPK3B	3619	14.341	0.449
50066	F08	M-015288-	transmemb	81853	TMEM14B	2351	12.633	2.157
50066	F09	M-013419-	Nedd4 fam	80762	NDFIP1	3730	12.949	1.841
50066	F10	M-013622-	keratin ass	81851	KRTAP1-1	5148	11.694	3.096
50066	F11	M-014628-	chromosom	80763	C12orf39	4972	20.998	6.208
50066	F12	M-014685-	ST6 (alpha-	81849	ST6GALNAC	2541	9.2483	5.5417
50066	F13	M-003821-	THAP doma	80764	THAP7	2523	8.1649	6.6251
50066	F14	M-015457-	sprouty ho	81848	SPRY4	4316	18.536	3.746
50066	F15	M-014629-	START dom	80765	STARD5	3904	17.495	2.705
50066	F16	M-007080-	ring finger	81847	RNF146	3497	5.6334	9.1566
50066	F17	M-016724-	LIM domain	80774	LIMD2	3946	9.706	5.084
50066	F18	M-014684-	SET binding	81846	SBF2	5952	19.472	4.682
50066	F19	M-014631-	transmemb	80775	TMEM177	6468	13.358	1.432
50066	F20	M-007079-	tripartite m	81844	TRIM56	4885	12.958	1.832
50066	F21	M-014632-	hypothetica	80776	MGC4093	4701	9.3172	5.4728
50066	F23	M-014633-	cytochrome	80777	CYB5B	2949	1.3903	13.3997
50066	G02	M-026281-	leucine rich	80313	LRRC27	7048	24.83	10.04
50066	G04	M-014635-	CXXC finger	80312	CXXC6	4638	7.0073	7.7827
50066	G05	M-014543-	chromosom	80067	C2orf37	6351	13.069	1.721
50066	G06	M-024931-	kelch-like 1	80311	KLHL15	4417	14.308	0.482
50066	G07	M-028334-	hypothetica	80068	FLJ13105	4592	16.834	2.044
50066	G08	M-008876-	platelet de	80310	PDGFD	4414	10.172	4.618
50066	G09	M-014544-	chromosom	80069	C6orf208	5982	8.8098	5.9802
50066	G10	M-023135-	SPHK1 (sph	80309	SKIP	4193	10.398	4.392
50066	G11	M-014545-	coiled-coil	80071	CCDC15	4081	8.9929	5.7971
50066	G12	M-008629-	FAD1 flavin	80308	FLAD1	3727	10.33	4.46
50066	G13	M-014547-	hypothetica	80075	FLJ13544	3554	6.8092	7.9808
50066	G14	M-014606-	mediator o	80306	MED28	3268	3.3354	11.4546
50066	G15	M-008676-	tubulin, alp	80086	TUBA4B	3486	6.6839	8.1061
50066	G16	M-019390-	TraB doma	80305	TRABD	4747	7.352	7.438
50066	G17	M-014554-	hypothetica	80094	FLJ14107	5293	23.087	8.297
50066	G18	M-014605-	chromosom	80304	C2orf44	5123	14.542	0.248
50066	G19	M-017135-	zinc finger	80095	ZNF606	147	42.177	27.387
50066	G20	M-010673-	EF-hand do	80303	EFHD1	5029	10.678	4.112
50066	G21	M-014555-	family with	80097	FAM128B	4566	7.6873	7.1027
50066	G23	M-014556-	prefoldin su	80098	PFDN6L	3184	6.0616	8.7284

50066	H02	M-016662- vang-like 1	81839	VANGL1	4974	24.347	9.557
50066	H04	M-013464- sperm acro	81833	SPACA1	5504	30.124	15.334
50066	H05	M-018566- zinc finger	80778	ZNF34	5142	13.672	1.118
50066	H06	M-017249- neuropilin (	81832	NETO1	4936	26.357	11.567
50066	H07	M-026584- integrator (	80789	INTS5	4013	22.153	7.363
50066	H08	M-017616- neuropilin (	81831	NETO2	4611	14.335	0.455
50066	H09	M-014637- c-Maf-indu	80790	CMIP	3924	16.004	1.214
50066	H10	M-007437- solute carri	81796	SLCO5A1	4862	15.487	0.697
50066	H11	M-023422- additional s	80816	ASXL3	3900	22.897	8.107
50066	H12	M-007078- ring finger	81790	RNF170	2982	22.502	7.712
50066	H13	M-014639- KIAA1712	80817	KIAA1712	3002	8.8608	5.9292
50066	H14	M-013456- tigger trans	81789	TIGD6	3870	10.543	4.247
50066	H15	M-014640- zinc finger	80818	ZNF436	4197	22.445	7.655
50066	H16	M-030535- hypothetica	81787	DKFZP547L	3541	11.522	3.268
50066	H17	M-014641- KIAA1706 p	80820	KIAA1706	3874	10.325	4.465
50066	H18	M-007077- tripartite m	81786	TRIM7	4156	8.1328	6.6572
50066	H19	M-021963- DDHD dom	80821	DDHD1	5261	14.199	0.591
50066	H20	M-026106- dedicator c	81704	DOCK8	4845	13.375	1.415
50066	H21	M-024779- basic helix-	80823	BHLHB9	5530	14.593	0.197
50066	H23	M-013429- zinc finger	80829	ZFP91	3368	6.6508	8.1392
50066	I02	M-015750- pleckstrin h	80301	PLEKHQ1	3520	7.2443	7.5457
50066	I04	M-017693- signal pept	80274	SCUBE1	3955	10.442	4.348
50066	I05	M-014557- hypothetica	80099	FLJ21075	4284	13.749	1.041
50066	I06	M-014603- GrpE-like 1	80273	GRPEL1	4840	17.934	3.144
50066	I07	M-014560- zinc finger	80108	ZFP2	4680	23.782	8.992
50066	I08	M-009536- hydroxy-de	80270	HSD3B7	3768	14.809	0.019
50066	I09	M-014562- zinc finger	80110	ZNF614	4765	26.737	11.947
50066	I10	M-018942- zinc finger	80264	ZNF430	4300	19.884	5.094
50066	I11	M-014563- chromoson	80111	C3orf36	4024	23.882	9.092
50066	I12	M-007073- tripartite m	80263	TRIM45	4414	17.807	3.017
50066	I13	M-012945- Williams-Be	80112	WBSCR23	3483	6.6609	8.1291
50066	I14	M-016626- chromoson	80262	C16orf70	4514	16.017	1.227
50066	I15	M-012946- bicaudal C	80114	BICC1	4783	16.538	1.748
50066	I16	M-018562- EF-hand do	80258	EFHC2	4647	9.3609	5.4291
50066	I17	M-016595- BAI1-assoc	80115	BAIAP2L2	4231	19.452	4.662
50066	I18	M-019475- KIAA1539	80256	KIAA1539	4945	8.6957	6.0943
50066	I19	M-009028- ADP-ribosy	80117	ARL14	2302	9.9044	4.8856
50066	I20	M-010744- solute carri	80255	SLC35F5	6047	16.736	1.946
50066	I21	M-008525- hypothetica	80118	FLJ22684	6541	15.441	0.651
50066	I23	M-014564- PIF1 5'-to-3	80119	PIF1	5850	9.5897	5.2003
50066	J02	M-014680- chromoson	81698	C15orf5	5481	28.681	13.891
50066	J04	M-014679- exonucleas	81691	LOC81691	4491	8.8176	5.9724
50066	J05	M-013432- apolipopro	80830	APOL6	5044	17.645	2.855
50066	J06	M-014678- iron-sulfur	81689	ISCA1	5433	22.695	7.905
50066	J07	M-013433- apolipopro	80831	APOL5	4842	15.696	0.906
50066	J08	M-015706- chromoson	81688	C6orf62	4766	13.995	0.795
50066	J09	M-014642- SH3-bindin	80851	SH3BP5L	4936	11.73	3.06

50066	J10	M-015899- transmem	81671	TMEM49	4312	23.516	8.726
50066	J11	M-023449- glutamate	80852	GRIP2	3824	16.946	2.156
50066	J12	M-014677- cyclin L2	81669	CCNL2	3683	16.4	1.61
50066	J13	M-025357- jumonji C d	80853	JHDM1D	3390	17.404	2.614
50066	J14	M-012846- microtubul	81631	MAP1LC3B	4525	24.155	9.365
50066	J15	M-023148- KIAA1715	80856	KIAA1715	4661	20.275	5.485
50066	J16	M-006481- TSC22 dom	81628	TSC22D4	3697	12.659	2.131
50066	J17	M-028689- chromoso	80862	C6orf12	4180	17.727	2.937
50066	J18	M-019040- chromoso	81627	C1orf25	4974	22.859	8.069
50066	J19	M-016655- proline-ric	80863	PRRT1	4574	15.654	0.864
50066	J20	M-014676- chromoso	81626	C1orf14	4475	18.168	3.378
50066	J21	M-014645- EGF-like-d	80864	EGFL8	6227	13.345	1.445
50066	J23	M-008230- N-acetylne	80896	NPL	4552	13.576	1.214
50066	K02	M-016516- centrosom	80254	CEP63	5389	12.173	2.617
50066	K04	M-014602- DEP domai	80243	DEPDC2	3204	13.233	1.557
50066	K05	M-019137- valosin con	80124	VCPIP1	4691	23.385	8.595
50066	K06	M-014601- elongation	80237	ELL3	4884	15.93	1.14
50066	K07	M-010981- coiled-coil	80125	CCDC33	4658	12.173	2.617
50066	K08	M-012954- phosphatid	80235	PIGZ	3653	17.164	2.374
50066	K09	M-014567- chromoso	80127	C14orf45	3882	13.421	1.369
50066	K10	M-017139- chromoso	80233	C17orf70	4124	16.246	1.456
50066	K11	M-007071- tripartite	80128	TRIM46	3606	13.505	1.285
50066	K12	M-032006- WD repeat	80232	WDR26	3660	17.541	2.751
50066	K13	M-014568- chromoso	80129	C6orf97	3115	11.942	2.848
50066	K14	M-014600- chromoso	80231	CXorf21	4822	26.13	11.34
50066	K15	M-016488- leucine ric	80131	LRRC8E	5480	13.869	0.921
50066	K16	M-016355- RUN and F	80230	RUFY1	4138	14.741	0.049
50066	K17	M-014569- chromoso	80133	C1orf129	4034	13.014	1.776
50066	K18	M-015012- transmem	80228	TMEM142	4466	24.989	10.199
50066	K19	M-031267- brix domai	80135	BXDC5	5942	19.892	5.102
50066	K20	M-014599- WD repeat	80227	WDR71	4521	5.4192	9.3708
50066	K21	M-014572- zinc finger	80139	ZNF703	4073	15.443	0.653
50066	K23	M-021342- prostaglan	80142	PTGES2	3758	8.0628	6.7272
50066	L02	M-019333- galectin-3 i	81625	GALIG	4689	9.5116	5.2784
50066	L04	M-019046- defensin, b	81623	DEFB126	3658	9.9781	4.8119
50066	L05	M-006051- transmem	80975	TMPRSS5	4301	11.579	3.211
50066	L06	M-013454- unc-93 ho	81622	UNC93B1	4306	11.124	3.666
50066	L07	M-018567- gap junctio	81025	GJA10	4524	19.739	4.949
50066	L08	M-017143- Kazal-type	81621	KAZALD1	4302	14.575	0.215
50066	L09	M-014650- Z-DNA bin	81030	ZBP1	4125	13.721	1.069
50066	L10	M-003248- chromatin	81620	CDT1	4130	13.971	0.819
50066	L11	M-007510- solute carri	81031	SLC2A10	3731	12.034	2.756
50066	L12	M-014675- tetraspani	81619	TSPAN14	3320	21.777	6.987
50066	L13	M-007356- solute carri	81034	SLC25A32	3730	17.399	2.609
50066	L14	M-018574- integral me	81618	ITM2C	3885	15.521	0.731
50066	L15	M-013240- collectin su	81035	COLEC12	3828	15.569	0.779
50066	L16	M-014674- calcium bi	81617	CAB39L	4520	11.704	3.086

50066	L17	M-015661-	CLPTM1-lik	81037	CLPTM1L	4203	9.2553	5.5347
50066	L18	M-015674-	acyl-CoA sy	81616	ACSBG2	6203	18.507	3.717
50066	L19	M-008959-	phosphatid	81490	PTDSS2	5485	21.805	7.015
50066	L20	M-014673-	transmemk	81615	TMEM163	5566	11.319	3.471
50066	L21	M-014651-	radial spok	81492	RSHL1	6337	18.936	4.146
50066	L23	M-014652-	syncoilin, ir	81493	SYNC1	5530	17.649	2.859
50066	M02	M-014598-	hypothetic	80225	FLJ21477	7044	18.356	3.566
50066	M04	M-021287-	nucleotide	80224	NUBPL	5505	20.745	5.955
50066	M05	M-014574-	suppressor	80143	SIKE	6782	19.965	5.175
50066	M06	M-015897-	threonyl-tR	80222	TARS2	4923	26.325	11.535
50066	M07	M-019398-	Fraser sync	80144	FRAS1	5315	44.572	29.782
50066	M08	M-018561-	hypothetic	80221	FLJ20920	4682	23.003	8.213
50066	M09	M-014575-	THO compl	80145	THOC7	4919	26.977	12.187
50066	M10	M-018559-	coenzyme (	80219	COQ10B	3992	15.456	0.666
50066	M11	M-009861-	UDP-glucur	80146	UXS1	3908	21.213	6.423
50066	M12	M-014597-	N-acetyltra	80218	NAT13	4771	30.623	15.833
50066	M13	M-018387-	PQ loop rep	80148	PQLC1	4272	22.612	7.822
50066	M14	M-016621-	chromoson	80217	C10orf79	4048	14.452	0.338
50066	M15	M-014576-	zinc finger (	80149	ZC3H12A	3858	19.414	4.624
50066	M16	M-021283-	chromoson	80215	C21orf96	4336	29.036	14.246
50066	M17	M-004909-	asparagina	80150	ASRGL1	5223	18.955	4.165
50066	M18	M-012953-	TM2 doma	80213	TM2D3	4786	13.811	0.979
50066	M19	M-014577-	centromer	80152	CENPT	5423	17.315	2.525
50066	M20	M-014596-	coiled-coil (	80212	CCDC92	4312	8.5575	6.2325
50066	M21	M-017136-	enhancer o	80153	EDC3	5924	19.902	5.112
50066	M23	M-014580-	hypothetic	80157	FLJ21511	5836	22.344	7.554
50066	N02	M-014672-	non imprin	81614	NIPA2	4268	23.102	8.312
50066	N04	M-015844-	acidic (leuc	81611	ANP32E	5983	30.587	15.797
50066	N05	M-007907-	complemer	81494	CFHR5	5767	24.12	9.33
50066	N06	M-014671-	family with	81610	FAM83D	5631	23.264	8.474
50066	N07	M-008716-	transmemk	81501	TM7SF4	4605	22.041	7.251
50066	N08	M-017346-	sorting nex	81609	SNX27	3521	13.519	1.271
50066	N09	M-005896-	histocompa	81502	HM13	3152	55.171	40.381
50066	N10	M-014670-	FIP1 like 1 (	81608	FIP1L1	4974	26.96	12.17
50066	N11	M-019362-	HCCA2 pro	81532	HCCA2	3927	31.169	16.379
50066	N12	M-014248-	limb bud ar	81606	LBH	4644	31.611	16.821
50066	N13	M-016806-	integrin alp	81533	ITFG1	2965	29.848	15.058
50066	N14	M-014669-	ubiquitin re	81605	URM1	3150	13.048	1.742
50066	N15	M-007558-	solute carri	81539	SLC38A1	4162	35.656	20.866
50066	N16	M-010058-	phospholip	81579	PLA2G12A	4175	19.186	4.396
50066	N17	M-010675-	thioredoxir	81542	TXNDC1	3936	24.136	9.346
50066	N18	M-013445-	collagen, ty	81578	COL21A1	5514	28.346	13.556
50066	N19	M-014654-	leucine rich	81543	LRRC3	5659	23.644	8.854
50066	N20	M-016812-	glucose-fru	81577	GFOD2	6071	21.512	6.722
50066	N21	M-019423-	glyceropho	81544	GDPD5	4748	14.933	0.143
50066	N23	M-018163-	F-box prote	81545	FBXO38	4156	14.413	0.377
50066	O02	M-018047-	armadillo r	80210	ARMC9	4061	16.031	1.241

50066	O04	M-012952- chromoson	80209	C13orf23	2862	17.54	2.75
50066	O05	M-015296- chromoson	80161	CXYorf2	4991	12.803	1.987
50066	O06	M-017138- spastic par	80208	SPG11	3828	15.778	0.988
50066	O07	M-014584- chromoson	80167	C4orf29	3529	6.5174	8.2726
50066	O08	M-023411- formin hon	80206	FHOD3	4078	14.517	0.273
50066	O09	M-014586- intraflagell	80173	IFT74	4005	12.884	1.906
50066	O10	M-006723- hexokinase	80201	HKDC1	4731	27.542	12.752
50066	O11	M-015262- splA/ryano	80176	SPSB1	4241	15.633	0.843
50066	O12	M-016342- fuzzy homc	80199	FUZ	3560	10.309	4.481
50066	O13	M-027137- myc target	80177	MYCT1	3125	12.672	2.118
50066	O14	M-016143- MUS81 enc	80198	MUS81	4377	6.557	8.233
50066	O15	M-014588- chromoson	80178	C16orf59	2535	32.426	17.636
50066	O16	M-007072- ring finger	80196	RNF34	3527	13.071	1.719
50066	O17	M-017137- myosin hea	80179	MYOHD1	4920	11.585	3.205
50066	O18	M-018946- chromoson	80195	C10orf57	4139	13.989	0.801
50066	O19	M-014589- chromoson	80183	C13orf18	5375	16.093	1.303
50066	O20	M-014594- transmemk	80194	TMEM134	3659	8.7182	6.0718
50066	O21	M-014590- centrosom	80184	CEP290	4849	20.004	5.214
50066	O23	M-014591- chromoson	80185	C8orf41	4758	11.98	2.81
50066	P02	M-014665- coiled-coil	81576	CCDC130	4648	28.873	14.083
50066	P04	M-014664- apolipopro	81575	APOLD1	3836	15.537	0.747
50066	P05	M-014655- tudor dom	81550	TDRD3	2843	11.185	3.605
50066	P06	M-014663- ankyrin rep	81573	ANKRD13C	3869	18.713	3.923
50066	P07	M-016810- stathmin-li	81551	STMN4	3390	21.327	6.537
50066	P08	M-014662- p53 and DN	81572	PDRG1	3489	16.882	2.092
50066	P09	M-018568- EGFR-coam	81552	ECOP	3588	11.288	3.502
50066	P10	M-014661- chromoson	81571	C9orf45	3119	22.635	7.845
50066	P11	M-014656- family with	81553	FAM49A	2963	12.049	2.741
50066	P12	M-017179- ClpB casein	81570	CLPB	2428	17.463	2.673
50066	P13	M-013444- Williams-B	81554	WBSCR16	3880	17.758	2.968
50066	P14	M-014660- actin-like 8	81569	ACTL8	4237	19.755	4.965
50066	P15	M-018962- Yip1 domai	81555	YIPF5	3915	15.811	1.021
50066	P16	M-014659- family with	81566	FAM130A1	4491	11.289	3.501
50066	P17	M-014657- chromoson	81556	C15orf44	4001	12.897	1.893
50066	P18	M-010941- chromoson	81563	C1orf21	3766	12.825	1.965
50066	P19	M-017308- melanoma	81557	MAGED4	4178	11.584	3.206
50066	P20	M-014658- lectin, man	81562	LMAN2L	4588	16.739	1.949
50066	P21	M-018570- family with	81558	FAM117A	2956	14.31	0.48
50066	P23	M-007075- tripartite m	81559	TRIM11	3663	6.6066	8.1834
				medianthM	4314	14.791	4.1555
				2xMAD			8.311
				3mad			12.4665
				MADc			6.15014
50066	C22				2999	46.382	
50066	D22				4010	56.584	
50066	E22				5712	48.967	
50066	F22				4043	39.327	

					mn	4191	47.815
					sd	1123.828	7.12559
50066	G22					2747	5.2057
50066	H22					2257	11.21
50066	I22					3332	9.5138
50066	J22					1569	13.767
					mn	2386	11.49693
					sd	888.5511	2.141069
					3psSD		21.37677
					3ngSD		6.423206
					SumSD		27.79998
					DiffMn		36.31807
					SmovrDiff		0.765459
					1minus		0.234541

50066	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	952	11.345
50066	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	719	24.896
50066	I03	D-001206-	siControl non-targeting			4532	19.859
50066	J03	D-001206-	siControl non-targeting			5389	18.074
50066	K03	D-001600-	siGLO RISC-free siRNA			7070	19.632
50066	L03	D-001600-	siGLO RISC-free siRNA			6797	21.657

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-0.1491	3767	14.68	4.57	0.848121	2093	9.3645	3.7755	-0.5763
-0.64307	2871	11.146	1.036	0.192122	2577	9.8952	3.2448	-0.49527
-0.41658	2010	7.5622	2.5478	-0.47312	4106	3.9454	9.1946	-1.40371
1.966947	1004	36.056	25.946	4.816045	2044	20.646	7.506	1.146191
1.650369	3590	13.593	3.483	0.646347	3968	11.719	1.421	-0.21681
1.475739	3037	19.789	9.679	1.796481	3570	14.426	1.286	0.196503
1.459479	1923	16.745	6.635	1.231437	2156	11.642	1.498	-0.22857
0.056096	2083	12.818	2.708	0.502487	2508	10.845	2.295	-0.35025
0.159509	1747	12.65	2.54	0.471302	2561	6.8723	6.2677	-0.95682
0.133981	2706	15.706	5.596	1.038573	2286	6.168	6.972	-1.06435
0.113331	1705	14.545	4.435	0.823062	1713	6.2464	6.8936	-1.05238
0.960141	2388	16.374	6.264	1.162571	2483	8.1756	4.9644	-0.75783
-0.09788	3234	9.9876	0.1224	-0.02291	3794	5.9831	7.1569	-1.09258
1.516226	3005	18.037	7.927	1.471265	2643	9.1941	3.9459	-0.60232
-0.59999	1774	7.2717	2.8383	-0.52705	1848	4.3831	8.7569	-1.33688
0.097234	2939	11.432	1.322	0.245211	2722	7.6414	5.4986	-0.83939
0.989408	2722	12.858	2.748	0.509912	1575	6.6032	6.5368	-0.99791
1.047293	3796	14.568	4.458	0.827331	2499	10.524	2.616	-0.39927
1.199322	4360	19.243	9.133	1.695129	4837	18.813	5.673	0.866323
0.741609	3445	13.033	2.923	0.542397	1784	9.6973	3.4427	-0.52549
-1.00162	4122	4.4881	5.6219	-1.04375	3745	3.3378	9.8022	-1.49648
1.691506	3512	8.1435	1.9665	-0.36522	3491	14.294	1.154	0.176349
-0.97429	4030	3.2506	6.8594	-1.27346	2425	6.4742	6.6658	-1.0176
0.015935	3088	3.6269	6.4831	-1.20361	2929	8.8767	4.2633	-0.65078
0.906809	2466	7.5831	2.5269	-0.46924	3530	14.278	1.138	0.173906
-1.59985	1138	3.6028	6.5072	-1.20809	711	9.8453	3.2947	-0.50289
0.83933	2957	10.72	0.61	0.113046	3896	9.6766	3.4634	-0.52865
-0.17821	2464	4.3019	5.8081	-1.07832	1754	4.8461	8.2939	-1.26618
0.782096	3465	14.026	3.916	0.726723	5029	13.621	0.481	0.073593
-0.06325	3440	6.4244	3.6856	-0.68433	3907	9.8029	3.3371	-0.50937
-0.0974	4572	10.236	0.126	0.023203	3442	7.8152	5.3248	-0.81285
-0.71446	2077	5.4887	4.6213	-0.85802	2748	7.6419	5.4981	-0.83931
-0.39723	4172	6.6395	3.4705	-0.6444	4877	11.729	1.411	-0.21528
-0.29089	3099	8.1317	1.9783	-0.36741	3031	4.223	8.917	-1.36132
-0.49592	3131	3.7368	6.3732	-1.18321	2886	4.9203	8.2197	-1.25486
-0.54796	3157	6.8736	3.2364	-0.60094	3504	7.6769	5.4631	-0.83397
-0.61332	3807	7.854	2.256	-0.41896	3277	8.5749	4.5651	-0.69686
1.413139	5602	22.189	12.079	2.241981	4466	17.219	4.079	0.622947
-0.58486	4967	9.2209	0.8891	-0.16522	4828	7.7672	5.3728	-0.82018
0.15333	5645	8.2019	1.9081	-0.35438	4650	9.914	3.226	-0.4924
-1.22457	2583	5.0329	5.0771	-0.94262	1849	9.4105	3.7295	-0.56928
0.779982	3693	5.524	4.586	-0.85146	4910	10.998	2.142	-0.32689
0.218694	2718	9.1244	0.9856	-0.18314	2048	18.555	5.415	0.826931
-0.09398	3886	8.9552	1.1548	-0.21455	3460	8.4971	4.6429	-0.70874
0.878029	4940	23.806	13.696	2.542137	5645	26.732	13.592	2.07542
-0.30747	3826	8.8866	1.2234	-0.22728	5002	13.015	0.125	-0.01893

1.659962	4324	24.445	14.335	2.660751	4450	25.483	12.343	1.884719
-0.34113	2487	12.746	2.636	0.489122	2894	12.716	0.424	-0.06458
0.062438	2942	17.335	7.225	1.340956	3394	12.787	0.353	-0.05374
-0.89987	2091	7.3649	2.7451	-0.50975	3061	8.7226	4.4174	-0.67431
3.244804	2762	25.851	15.741	2.92174	3212	25.934	12.794	1.953579
-0.82665	3362	14.872	4.762	0.883762	3354	14.341	1.201	0.183525
0.744698	2134	9.7001	0.4099	-0.07627	3226	15.313	2.173	0.331933
-0.21642	2932	6.6166	3.4934	-0.64865	3773	11.847	1.293	-0.19727
-0.46958	3418	5.9099	4.2001	-0.77983	3004	6.9907	6.1493	-0.93874
-0.69852	2824	6.7635	3.3465	-0.62138	3302	6.5415	6.5985	-1.00733
-0.51332	4109	9.8077	0.3023	-0.0563	3095	14.346	1.206	0.184288
0.956726	4565	17.59	7.48	1.388291	3523	14.647	1.507	0.230246
-0.27251	4263	9.2423	0.8677	-0.16125	3905	10.858	2.282	-0.34827
0.409747	4199	12.098	1.988	0.368837	2865	12.077	1.063	-0.16215
0.096095	5081	6.0421	4.0679	-0.75529	5892	15.869	2.729	0.416825
0.126826	2131	6.2881	3.8219	-0.70963	2795	16.601	3.461	0.528589
-0.72974	4888	6.6694	3.4406	-0.63885	3970	7.5819	5.5581	-0.84847
-0.393	3399	6.2077	3.9023	-0.72455	4773	12.906	0.234	-0.03558
-0.4582	3703	7.2104	2.8996	-0.53842	5222	14.784	1.644	0.251164
-1.23277	3045	3.1527	6.9573	-1.29164	5429	6.2258	6.9142	-1.05553
2.262062	4817	19.763	9.653	1.791654	5887	32.835	19.695	3.007244
1.1203	2406	7.1072	3.0028	-0.55758	5198	23.624	10.484	1.600881
1.379156	2113	8.566	1.544	-0.28679	3670	19.046	5.906	0.901898
-0.00293	2198	6.9609	3.1491	-0.58474	1983	17.448	4.308	0.657911
-0.29284	2781	3.2362	6.8738	-1.27614	4196	12.178	0.962	-0.14673
-1.22922	1826	5.3669	4.7431	-0.88062	2054	10.419	2.721	-0.4153
-0.08423	2764	9.1534	0.9566	-0.17775	4766	14.226	1.086	0.165966
0.661448	4098	7.3694	2.7406	-0.50891	5505	15.186	2.046	0.312542
-0.8524	2114	3.1693	6.9407	-1.28855	3360	7.7083	5.4317	-0.82918
2.63246	4299	19.563	9.453	1.754529	6084	36.555	23.415	3.575225
-0.71267	3965	3.884	6.226	-1.15589	4660	8.6695	4.4705	-0.68242
-0.15821	3951	4.6064	5.5036	-1.02179	3108	14.125	0.985	0.150545
0.897053	3563	6.5114	3.5986	-0.66818	4275	11.205	1.935	-0.29529
0.054308	3373	2.4607	7.6493	-1.42009	4284	15.359	2.219	0.338956
-1.35259	2818	2.555	7.555	-1.40258	3415	6.9693	6.1707	-0.94201
-1.28314	1553	1.9961	8.1139	-1.50633	1655	2.9607	10.1793	-1.55405
-0.53609	3641	6.1796	3.9304	-0.72977	2820	5.3546	7.7854	-1.18855
2.604494	3364	10.048	0.062	-0.01169	3352	18.616	5.476	0.836245
0.402918	3209	5.4846	4.6254	-0.85878	4285	10.058	3.082	-0.47042
-0.7525	3204	4.1823	5.9277	-1.10052	3449	6.8136	6.3264	-0.96578
-1.35937	3958	3.2087	6.9013	-1.28124	5152	5.4348	7.7052	-1.1763
0.412023	3582	12.73	2.62	0.486152	4317	12.555	0.585	-0.08917
0.147964	3087	5.7337	4.3763	-0.81254	3877	8.8986	4.2414	-0.64744
0.600312	2393	9.3188	0.7912	-0.14705	1644	9.1849	3.9551	-0.60372
-0.64307	3301	5.1802	4.9298	-0.91528	3011	6.6091	6.5309	-0.997
-0.47511	2781	3.2003	6.9097	-1.2828	1799	5.7254	7.4146	-1.13193
-1.25805	2765	2.5316	7.5784	-1.40693	3292	5.9538	7.1862	-1.09706

-1.50543	2315	3.7581	6.3519	-1.17926	2437	3.0365	10.1035	-1.54248
-0.1374	2772	5.267	4.843	-0.89917	4615	10.531	2.609	-0.3982
-0.76844	3551	3.8862	6.2238	-1.15548	4888	9.2676	3.8724	-0.5911
0.262433	3696	6.8994	3.2106	-0.59615	3488	10.378	2.762	-0.42156
-1.22781	3799	4.7118	5.3982	-1.00223	4276	7.2965	5.8435	-0.89205
-0.70828	4998	7.7231	2.3869	-0.44325	3680	8.7228	4.4172	-0.67428
-1.48959	3148	2.1919	7.9181	-1.46998	2928	3.1762	9.9638	-1.52115
-0.53348	5038	6.8877	3.2223	-0.59833	3424	7.7395	5.4005	-0.82441
-0.91549	4957	5.8301	4.2799	-0.79464	5553	6.1768	6.9632	-1.06301
-0.4182	5053	11.973	1.863	0.345634	5362	21.391	8.251	1.25994
-0.56291	5696	10.341	0.231	0.042694	4117	12.072	1.068	-0.16291
-0.07317	5125	9.0927	1.0173	-0.18902	4195	13.349	0.209	0.032063
-0.35089	2062	6.5955	3.5145	-0.65257	2490	8.1526	4.9874	-0.76134
-0.29951	3184	5.3078	4.8022	-0.89159	3460	8.237	4.903	-0.74845
-0.50357	3236	5.0989	5.0111	-0.93037	4247	11.82	1.32	-0.20139
1.009245	4670	12.27	2.16	0.400765	4810	19.314	6.174	0.942817
-0.90123	2876	8.5188	1.5912	-0.29555	2699	10.634	2.506	-0.38247
-1.07739	2240	5	5.11	-0.94873	2459	11.387	1.753	-0.2675
0.608929	3844	14.334	4.224	0.783895	4694	19.28	6.14	0.937626
0.439665	4896	15.4	5.29	0.981772	4001	9.2727	3.8673	-0.59032
-1.48901	2504	3.7939	6.3161	-1.17261	3813	7.1859	5.9541	-0.90894
-0.82681	2857	15.296	5.186	0.962467	3759	11.998	1.142	-0.17421
0.761121	4160	11.755	1.645	0.305168	6165	22.936	9.796	1.495835
-0.233	5117	7.3285	2.7815	-0.5165	4905	9.1335	4.0065	-0.61157
-0.29804	4832	17.115	7.005	1.300119	3930	18.982	5.842	0.892127
-0.89003	3859	17.777	7.667	1.423003	3612	10.188	2.952	-0.45057
-2.17893	3197	4.3791	5.7309	-1.06399	3545	4.6544	8.4856	-1.29545
1.632321	4977	10.006	0.104	-0.01949	4634	17.026	3.886	0.593479
-1.26561	3373	4.2692	5.8408	-1.08439	2976	8.4341	4.7059	-0.71836
-0.27999	4037	4.0129	6.0971	-1.13196	2802	7.5303	5.6097	-0.85635
-0.07853	3131	13.478	3.368	0.625	1975	18.025	4.885	0.746009
0.332188	3190	9.5611	0.5489	-0.10208	3026	11.633	1.507	-0.22994
-0.75104	2162	4.8566	5.2534	-0.97535	2749	10.913	2.227	-0.33987
-0.97253	4254	8.7682	1.3418	-0.24926	3975	13.535	0.395	0.060462
-0.71429	3205	5.0546	5.0554	-0.9386	2307	9.7096	3.4304	-0.52361
-0.94276	2045	5.7213	4.3887	-0.81484	2957	13.257	0.117	0.018017
-0.72535	3443	8.7424	1.3676	-0.25405	2452	6.7292	6.4108	-0.97867
-1.29782	2739	3.8335	6.2765	-1.16526	2903	11.058	2.082	-0.31773
-1.86266	1987	4.8817	5.2283	-0.97069	1698	5.6537	7.4863	-1.14288
-1.3182	2285	7.4398	2.6702	-0.49584	2790	13.082	0.058	-0.0087
-1.20957	2918	4.9692	5.1408	-0.95445	3595	9.1794	3.9606	-0.60456
1.348912	3364	21.344	11.234	2.085128	3502	26.556	13.416	2.048548
-0.04049	3624	9.7958	0.3142	-0.05851	4670	19.4	6.26	0.955948
4.452907	4343	4.8814	5.2286	-0.97075	4809	9.2119	3.9281	-0.5996
-0.66877	6602	12.86	2.75	0.510284	3834	13.432	0.292	0.044736
-1.15505	3608	6.4302	3.6798	-0.68325	2950	8.6441	4.4959	-0.68629
-1.41938	2718	8.2046	1.9054	-0.35388	2285	10.372	2.768	-0.42247

1.553786	3691	6.99	3.12	-0.57934	4592	11.999	1.141	-0.17406
2.493114	5085	15.693	5.583	1.03616	4635	28.285	15.145	2.312537
-0.18195	4352	7.1461	2.9639	-0.55036	4158	8.3213	4.8187	-0.73558
1.880608	6419	22.963	12.853	2.385655	6103	20.023	6.883	1.05107
1.197046	4564	20.508	10.398	1.929945	3822	17.242	4.102	0.626458
-0.07414	4110	9.9027	0.2073	-0.03867	4070	11.4	1.74	-0.26552
0.197231	3271	11.342	1.232	0.228505	3236	10.97	2.17	-0.33117
0.113168	3115	10.883	0.773	0.143303	3899	14.234	1.094	0.167188
1.318019	3849	12.835	2.725	0.505643	2821	7.905	5.235	-0.79914
1.253793	3633	17.726	7.616	1.413536	4289	16.111	2.971	0.453774
-0.96424	2425	5.8969	4.2131	-0.78224	2902	9.0972	4.0428	-0.61711
-0.69072	3872	7.9029	2.2071	-0.40988	3334	5.5789	7.5611	-1.1543
1.244525	4550	25.099	14.989	2.78215	3813	25.256	12.116	1.85006
-0.53153	3394	12.994	2.884	0.535157	2842	8.4799	4.6601	-0.71137
-0.72616	3112	8.1298	1.9802	-0.36776	3164	9.4501	3.6899	-0.56323
-1.08261	3106	10.431	0.321	0.0594	3215	4.7589	8.3811	-1.2795
-0.09626	3787	13.309	3.199	0.593629	3149	6.256	6.884	-1.05092
-0.23024	4313	19.801	9.691	1.798708	3654	8.8123	4.3277	-0.66061
-0.03219	5492	15.896	5.786	1.073842	4740	13.671	0.531	0.081227
-1.32358	2281	6.0061	4.1039	-0.76197	3361	6.8432	6.2968	-0.96126
-1.22708	4142	3.4042	6.7058	-1.24495	3789	5.2784	7.8616	-1.20018
-0.70714	3645	8.8889	1.2211	-0.22685	2580	9.031	4.109	-0.62722
-0.16943	2455	15.031	4.921	0.913276	2533	18.358	5.218	0.796853
0.511045	4594	14.954	4.844	0.898983	4348	11.04	2.1	-0.32048
1.461918	4197	13.605	3.495	0.648574	4261	18.564	5.424	0.828305
0.002927	3538	9.8078	0.3022	-0.05628	3122	8.9366	4.2034	-0.64164
1.942395	3884	18.718	8.608	1.597676	3725	18.094	4.954	0.756544
0.828111	4317	20.662	10.552	1.958531	4273	17.365	4.225	0.645238
1.478178	4299	23.657	13.547	2.514479	3464	24.798	11.658	1.780131
0.490395	4662	29.665	19.555	3.629715	2887	16.176	3.036	0.463698
-1.32194	2604	7.9877	2.1223	-0.39414	2168	8.81	4.33	-0.66096
0.199345	4901	12.589	2.479	0.459979	2838	13.425	0.285	0.043667
0.284059	4294	17.327	7.217	1.339471	1796	13.196	0.056	0.008703
-0.88292	4084	4.4319	5.6781	-1.05418	2745	8.7067	4.4333	-0.67674
0.757869	3803	15.882	5.772	1.071243	3367	19.216	6.076	0.927855
-0.99108	4224	9.2566	0.8534	-0.1586	2599	6.6179	6.5221	-0.99566
-0.79455	2208	11.549	1.439	0.266929	1009	8.5233	4.6167	-0.70474
0.316253	5923	22.134	12.024	2.231772	4493	20.61	7.47	1.140695
0.105689	5837	14.939	4.829	0.896198	3873	6.8939	6.2461	-0.95352
-0.84572	4882	11.573	1.463	0.271384	4035	15.564	2.424	0.370256
2.258485	5719	20.738	10.628	1.972639	4345	31.807	18.667	2.850286
-0.97126	2806	5.4526	4.6574	-0.86472	3285	11.233	1.907	-0.29101
0.464054	3484	9.4145	0.6955	-0.12929	3867	20.326	7.186	1.097333
1.285174	5090	13.831	3.721	0.690526	4412	29.238	16.098	2.458043
0.147151	4026	9.2648	0.8452	-0.15708	3144	20.929	7.789	1.189401
-0.12943	4808	15.62	5.51	1.022609	2440	22.336	9.196	1.404225
-0.49771	4644	10.336	0.226	0.041766	3910	10.767	2.373	-0.36216

1.418667	3526	14.436	4.326	0.802829	3082	16.645	3.505	0.535307
0.350399	3102	8.5751	1.5349	-0.2851	2552	11.011	2.129	-0.32491
0.26162	2741	8.2816	1.8284	-0.33958	2708	18.131	4.991	0.762193
0.424868	2208	6.7482	3.3618	-0.62422	2760	15.181	2.041	0.311779
1.522567	3693	11.481	1.371	0.254307	2922	16.29	3.15	0.481104
0.891687	3796	8.2192	1.8908	-0.35117	3306	10.859	2.281	-0.34812
-0.34666	4259	11.388	1.278	0.237043	2888	11.565	1.575	-0.24032
0.477388	3764	10.308	0.198	0.036568	2520	6.1905	6.9495	-1.06092
1.31184	5196	17.379	7.269	1.349124	5036	20.929	7.789	1.189401
0.140322	4458	16.061	5.951	1.10447	4018	16.202	3.062	0.467668
0.549093	3516	13.766	3.656	0.67846	2609	11.614	1.526	-0.23284
-0.23512	5039	13.713	3.603	0.668622	4541	14.644	1.504	0.229788
-0.19756	3099	6.486	3.624	-0.67289	3300	8.697	4.443	-0.67822
-0.42568	5226	8.6682	1.4418	-0.26782	5080	12.264	0.876	-0.1336
-0.25333	4700	14.638	4.528	0.840325	3787	16.451	3.311	0.505686
1.397367	4837	22.328	12.218	2.267783	5111	27.509	14.369	2.194055
0.185199	5064	10.723	0.613	0.113603	4973	17.133	3.993	0.609816
-0.42568	4146	10.371	0.261	0.048263	4583	19.987	6.847	1.045573
0.385845	4230	15.934	5.824	1.080895	3319	24.194	11.054	1.68791
-0.22276	4651	14.384	4.274	0.793176	4384	17.336	4.196	0.640811
0.23658	4296	10.475	0.365	0.067568	3786	18.991	5.851	0.893501
-0.2091	4124	7.032	3.078	-0.57154	3917	18.764	5.624	0.858842
0.447144	2852	10.87	0.76	0.14089	3147	15.983	2.843	0.43423
-0.46324	2428	8.6903	1.4197	-0.26372	2112	18.466	5.326	0.813342
1.843698	4230	14.515	4.405	0.817493	3437	19.959	6.819	1.041298
-0.14992	3973	8.7591	1.3509	-0.25095	3899	10.464	2.676	-0.40843
-0.00813	4208	12.452	2.342	0.434549	3355	13.92	0.78	0.119245
-0.28894	4083	13.691	3.581	0.664538	2999	18.806	5.666	0.865255
1.658174	3679	14.841	4.731	0.878007	3432	26.719	13.579	2.073435
0.829412	5912	11.553	1.443	0.267672	5796	21.601	8.461	1.292003
-1.52384	5155	4.4617	5.6483	-1.04865	3936	5.9959	7.1441	-1.09063
0.106014	3460	12.63	2.52	0.46759	3619	17.767	4.627	0.706617
-1.09399	2326	4.2562	5.8538	-1.0868	2020	11.485	1.655	-0.25254
-0.85842	4684	7.3655	2.7445	-0.50963	6337	12.182	0.958	-0.14612
-0.78257	5002	11.695	1.585	0.29403	2971	16.19	3.05	0.465836
-0.52226	4597	13.726	3.616	0.671035	4334	23.858	10.718	1.636609
-0.59625	4993	5.0471	5.0629	-0.93999	3044	13.239	0.099	0.015268
0.804535	5074	14.367	4.257	0.790021	3920	27.602	14.462	2.208254
-0.03512	5195	10.221	0.111	0.020419	4320	18.38	5.24	0.800212
-0.17398	4573	8.2003	1.9097	-0.35467	2818	19.092	5.952	0.908922
-0.13333	5306	8.6317	1.4783	-0.2746	4422	14.45	1.31	0.200167
-0.44828	4375	7.9543	2.1557	-0.40034	3663	19.301	6.161	0.940833
1.135909	3015	19.867	9.757	1.810959	2990	32.575	19.435	2.967547
0.424055	4403	10.993	0.883	0.163721	2546	20.11	6.97	1.064353
0.118696	3927	12.35	2.24	0.415615	3757	21.666	8.526	1.301928
0.126501	5313	11.048	0.938	0.173931	2897	18.467	5.327	0.813495
-0.50194	3412	4.1032	6.0068	-1.1152	2016	14.831	1.691	0.25834

-0.90009	4333	6.0466	4.0634	-0.75446	2961	16.076	2.936	0.44843
0.604214	6910	10.188	0.078	0.014293	5755	22.832	9.692	1.479956
1.140462	5516	9.6265	0.4835	-0.08994	2948	19.267	6.127	0.935641
-0.56454	5292	11.357	1.247	0.231289	4441	19.95	6.81	1.039924
0.673968	6085	9.1701	0.9399	-0.17465	5723	18.085	4.945	0.75517
0.464705	3539	6.499	3.611	-0.67048	2912	13.255	0.115	0.017711
0.579662	5274	14.031	3.921	0.727651	4695	18.935	5.795	0.884951
0.968108	4943	25.005	14.895	2.764702	4131	22.053	8.913	1.361016
0.841282	4720	11.335	1.225	0.227205	4894	11.892	1.248	-0.1904
1.875404	5102	15.073	4.963	0.921072	4020	18.134	4.994	0.762652
4.842329	5323	26.996	16.886	3.134281	4247	37.203	24.063	3.674164
1.335254	5522	10.159	0.049	0.00891	4834	17.977	4.837	0.73868
1.981418	5414	14.463	4.353	0.807841	3464	12.644	0.496	-0.07558
0.108128	3920	8.699	1.411	-0.2621	2939	15.039	1.899	0.290098
1.044204	5544	9.127	0.983	-0.18266	3929	12.802	0.338	-0.05145
2.57425	3788	14.203	4.093	0.759578	3575	17.483	4.343	0.663255
1.271678	4829	13.771	3.661	0.679388	3188	14.711	1.571	0.240018
-0.05512	4010	9.9002	0.2098	-0.03913	1947	11.505	1.635	-0.24948
0.75169	3936	13.592	3.482	0.646161	3673	16.553	3.413	0.52126
2.316207	4647	18.937	8.827	1.638328	3728	22.988	9.848	1.503775
0.677058	5553	11.795	1.685	0.312593	4313	7.744	5.396	-0.82372
-0.15935	3419	5.2647	4.8453	-0.8996	3023	11.115	2.025	-0.30903
0.410397	5721	15.137	5.027	0.932952	3673	15.083	1.943	0.296816
-1.01355	4431	7.4024	2.7076	-0.50278	4569	10.199	2.941	-0.44889
0.831038	3674	7.8933	2.2167	-0.41166	3890	13.342	0.202	0.030995
1.228102	4445	10.191	0.081	0.01485	5730	26.457	13.317	2.033432
1.351351	3114	10.308	0.198	0.036568	2723	15.498	2.358	0.360179
2.568397	5170	25.841	15.731	2.919884	4823	23.243	10.103	1.542709
1.516876	5380	14.498	4.388	0.814338	3677	13.68	0.54	0.082601
1.377692	5834	19.901	9.791	1.817271	3833	15.132	1.992	0.304297
1.178835	6071	11.184	1.074	0.199176	4343	10.868	2.272	-0.34674
-0.20682	4553	11.136	1.026	0.190266	2843	10.095	3.045	-0.46477
6.565704	4595	45.419	35.309	6.554054	4311	53.932	40.792	6.228397
1.978654	4974	8.2027	1.9073	-0.35423	2893	17.283	4.143	0.632718
2.663029	5556	15.137	5.027	0.932952	4189	18.859	5.719	0.873347
2.734897	4214	17.964	7.854	1.457715	4464	22.267	9.127	1.39369
2.448237	3952	21.255	11.145	2.068607	3128	30.882	17.742	2.709054
-0.28341	4276	5.8466	4.2634	-0.79158	2741	13.061	0.079	-0.01191
3.392606	4631	14.489	4.379	0.812667	3980	25.352	12.212	1.864717
0.714618	4896	11.029	0.919	0.170404	3499	13.547	0.407	0.062295
1.519478	6594	14.998	4.888	0.90715	4331	17.825	4.685	0.715472
2.204015	6909	18.527	8.417	1.562222	5009	20.723	7.583	1.157948
1.439479	6383	8.554	1.556	-0.28902	5172	15.526	2.386	0.364454
1.092821	5549	6.9923	3.1177	-0.57891	4070	8.9681	4.1719	-0.63683
0.023089	4491	4.8987	5.2113	-0.96753	3490	7.765	5.375	-0.82052
-0.06146	2444	2.7414	7.3686	-1.36798	3486	5.7659	7.3741	-1.12575
0.201621	3603	6.0228	4.0872	-0.75887	2635	15.787	2.647	0.404305

0.446982	3824	13.363	3.253	0.603653	2221	24.403	11.263	1.719821
-0.32324	4575	8.5027	1.6073	-0.29854	3140	18.885	5.745	0.877316
0.160484	4708	10.918	0.808	0.1498	4129	20.586	7.446	1.13703
-1.34527	3311	11.024	0.914	0.169476	1594	28.921	15.781	2.409643
-0.04455	5319	13.612	3.502	0.649874	3638	23.2	10.06	1.536144
-0.31007	5217	10.063	0.047	-0.00891	2639	11.709	1.431	-0.21834
2.073286	6581	14.77	4.66	0.864828	4192	31.083	17.943	2.739744
0.136907	5062	9.7787	0.3313	-0.06168	2948	22.558	9.418	1.438121
-0.72876	4465	6.2262	3.8838	-0.72112	2933	15.274	2.134	0.325978
-0.34455	3385	10.192	0.082	0.015036	2139	16.924	3.784	0.577905
-1.33883	4763	3.4852	6.6248	-1.22992	2808	5.9829	7.1571	-1.09261
2.867414	2937	26.83	16.72	3.103467	1618	39.926	26.786	4.089919
-0.27967	4478	10.027	0.083	-0.01559	2474	19.038	5.898	0.900677
-0.52129	5873	8.7179	1.3921	-0.25859	4556	12.599	0.541	-0.08245
-0.1304	4859	7.7588	2.3512	-0.43663	3058	9.6795	3.4605	-0.52821
0.211702	6814	16.363	6.253	1.160529	5361	23.391	10.251	1.565306
-0.98742	4503	9.4382	0.6718	-0.12489	2897	13.738	0.598	0.091457
0.847623	4823	11.611	1.501	0.278438	4877	22.473	9.333	1.425143
-0.45706	3889	7.1227	2.9873	-0.5547	2742	15.937	2.797	0.427207
2.289704	5011	21.912	11.802	2.190563	3856	24.326	11.186	1.708065
0.121298	4141	8.6453	1.4647	-0.27207	3424	13.668	0.528	0.080769
-0.58633	3479	10.721	0.611	0.113231	2267	20.026	6.886	1.051528
0.637709	4914	20.228	10.118	1.87797	3235	20.495	7.355	1.123136
1.06274	4800	22	11.89	2.206898	2290	12.009	1.131	-0.17253
0.339992	3523	11.24	1.13	0.209571	1721	13.887	0.747	0.114207
-0.56958	4048	11.438	1.328	0.246325	3170	12.114	1.026	-0.1565
1.275418	4013	27.162	17.052	3.165095	3822	28.441	15.301	2.336355
-0.44584	3984	11.797	1.687	0.312964	2201	7.3149	5.8251	-0.88924
0.434462	2745	19.563	9.453	1.754529	1341	21.626	8.486	1.295821
0.482428	4499	14.914	4.804	0.891558	2846	15.355	2.215	0.338346
0.807136	4586	9.4854	0.6246	-0.11613	3595	11.127	2.013	-0.3072
0.16585	5350	20.579	10.469	1.943124	3180	17.767	4.627	0.706617
-0.56942	4421	5.3382	4.7718	-0.88595	4124	10.766	2.374	-0.36232
-0.30796	4972	15.447	5.337	0.990496	3146	12.715	0.425	-0.06474
-0.31967	2673	10.625	0.515	0.095411	2931	12.112	1.028	-0.15681
-0.52145	4098	10.2	0.09	0.016521	2822	9.4968	3.6432	-0.5561
0.316741	4094	14.24	4.13	0.766446	3764	14.506	1.366	0.208718
-0.07821	1995	18.095	7.985	1.482031	2115	17.967	4.827	0.737153
-1.33077	2566	7.4045	2.7055	-0.50239	3242	10.364	2.776	-0.4237
	3943.5	10.111	3.64		3462	13.139	4.42535	
			7.28				8.8507	
			10.92				13.27605	
			5.3872				6.549518	
3971	48.25		2960	50.574				
4660	37.897		4455	43.098				
4208	36.145		3454	30.602				
4433	46.785		5347	51.506				

4318	42.26925	4054	43.945
295.9155	6.131459	1062.934	9.658596
1341	5.742	1491	6.7069
1526	7.1429	1725	9.7971
1664	8.2332	1358	14.728
2285	11.291	2071	11.106
1825	8.889033	1718	11.87703
404.3031	2.150412	356.5515	2.554273
	0		28.97579
	6.451236		7.66282
	6.451236		36.63861
	33.38022		32.06797
	0.193265		1.14253
	0.806735		-0.14253

397	2.267	448	15.402
462	6.4935	271	26.199
3587	10.315	4492	13.446
4859	11.196	4016	22.46
7739	27.329	6945	29.057
7007	24.647	7212	34.068

y

y

y

y

y

y

y

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y

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y

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y

y

y

					cell ct	% inf	AD
50067	A02	M-004735- transketola	84076	TKTL2	4482	11.334	7.506
50067	A04	M-018597- chromoson	84075	C14orf155	3939	16.349	2.491
50067	A05	M-007322- solute carri	83447	SLC25A31	4472	10.711	8.129
50067	A06	M-014787- glutamine	84074	QRICH2	3341	14.098	4.742
50067	A07	M-014709- pseudouric	83448	PUS7L	4476	12.913	5.927
50067	A08	M-016346- MYCBP ass	84073	MYCBPAP	3712	15.194	3.646
50067	A09	M-014710- polyamine	83449	PMFBP1	4065	12.374	6.466
50067	A10	M-018596- HORMA do	84072	HORMAD1	3189	15.553	3.287
50067	A11	M-019419- leucine ric	83450	LRRC48	3585	27.364	8.524
50067	A12	M-018191- armadillo r	84071	ARMC2	3828	22.048	3.208
50067	A13	M-007082- hypothetic	83459	DKFZP761	3137	19.318	0.478
50067	A14	M-014786- chromoson	84070	C12orf25	3433	16.633	2.207
50067	A15	M-014711- transmemb	83460	TMEM93	3489	22.356	3.516
50067	A16	M-014785- pleckstrin	84069	PLEKHN1	4332	24.492	5.652
50067	A17	M-016149- cell divisior	83461	CDCA3	4839	14.3	4.54
50067	A18	M-014784- solute carri	84068	SLC10A7	3502	13.649	5.191
50067	A19	M-008827- MAX dimer	83463	MXD3	3058	13.734	5.106
50067	A20	M-014783- chromoson	84067	C11orf56	4219	23.536	4.696
50067	A21	M-008061- anterior ph	83464	APH1B	3922	18.511	0.329
50067	A23	M-016679- glycosyltra	83468	GLT8D2	4763	21.163	2.323
50067	B02	M-009755- coenzyme	84274	COQ5	5639	24.88	6.04
50067	B04	M-013518- keratin ass	83899	KRTAP9-2	5467	16.59	2.25
50067	B05	M-018600- chromoson	84077	C3orf20	5344	11.808	7.032
50067	B06	M-013500- keratin ass	83755	KRTAP4-12	5057	12.32	6.52
50067	B07	M-015708- kelch repea	84078	KBTBD7	3844	13.476	5.364
50067	B08	M-014881- zinc finger,	84327	ZBED3	3785	8.0845	10.7555
50067	B09	M-014788- ankyrin rep	84079	ANKRD27	2279	9.1707	9.6693
50067	B10	M-017010- hypothetic	84326	MGC13114	3784	9.8309	9.0091
50067	B11	M-014789- chromoson	84080	C16orf48	4061	14.627	4.213
50067	B12	M-008575- componen	84342	COG8	3930	16.718	2.122
50067	B13	M-014790- coiled-coil	84081	CCDC55	3978	14.706	4.134
50067	B14	M-017534- G elongatic	84340	GFM2	3394	12.11	6.73
50067	B15	M-010025- zinc finger,	84083	ZRANB3	3754	22.456	3.616
50067	B16	M-014888- elongation	84337	ELOF1	3739	23.562	4.722
50067	B17	M-021407- F-box prote	84085	FBXO30	3293	18.524	0.316
50067	B18	M-014887- transmemb	84336	TMEM101	3281	13.167	5.673
50067	B19	M-017298- ADP-ribosy	84100	ARL6	5270	11.575	7.265
50067	B20	M-014885- chromoson	84334	C14orf153	4681	25.272	6.432
50067	B21	M-007321- solute carri	84102	SLC41A2	5609	9.8057	9.0343
50067	B23	M-014791- chromoson	84103	C4orf17	5713	29.914	11.074
50067	C02	M-014782- chromoson	84066	C1orf49	3940	15.305	3.535
50067	C04	M-014781- chromoson	84065	C1orf160	5106	18.273	0.567
50067	C05	M-014712- deoxyhypu	83475	DOHH	4789	17.979	0.861
50067	C06	M-018923- kin of IRRE	84063	KIRREL2	4379	18.589	0.251
50067	C07	M-014713- Rho GTPas	83478	ARHGAP24	3784	18.155	0.685
50067	C08	M-018190- implantatic	84061	RP11-217H	3508	22.577	3.737

50067	C09	M-009916- DEAD (Asp-	83479	DDX59	3130	12.78	6.06
50067	C10	M-014780- hypothetic	84060	DKFZP564	3605	22.469	3.629
50067	C11	M-009748- pseudouric	83480	PUS3	3326	31.269	12.429
50067	C12	M-018961- WD repeat	84058	WDR54	3034	21.358	2.518
50067	C13	M-013490- scratch hor	83482	SCRT1	2818	33.286	14.446
50067	C14	M-014779- meiotic nu	84057	MND1	3181	13.329	5.511
50067	C15	M-014714- plasmalem	83483	PLVAP	3239	21.025	2.185
50067	C16	M-014778- katanin p6	84056	KATNAL1	4367	25.647	6.807
50067	C17	M-014719- tetratricop	83538	TTC25	4004	12.188	6.652
50067	C18	M-014777- elastin mic	84034	EMILIN2	4026	14.655	4.185
50067	C19	M-008532- carbohydra	83539	CHST9	4116	8.1633	10.6767
50067	C20	M-008985- UDP-GlcNA	84002	B3GNT5	5803	20.558	1.718
50067	C21	M-015441- family with	83541	FAM110A	4825	17.637	1.203
50067	C23	M-014721- chromoson	83543	C9orf58	4400	23.341	4.501
50067	D02	M-007089- polycomb	84333	PCGF5	5527	18.69	0.15
50067	D04	M-014884- DPY30 dom	84332	DYDC2	3294	10.413	8.427
50067	D05	M-009955- pterin-4 al	84105	PCBD2	4188	10.888	7.952
50067	D06	M-010968- chromoson	84331	C16orf14	5209	17.124	1.716
50067	D07	M-018654- PML-RARA	84106	PRAM1	4099	30.105	11.265
50067	D08	M-014882- zinc finger	84330	ZNF414	3476	19.045	0.205
50067	D09	M-017509- Zic family	84107	ZIC4	4360	26.606	7.766
50067	D10	M-006282- hydrogen v	84329	HVCN1	4177	19.033	0.193
50067	D11	M-007084- polycomb	84108	PCGF6	4345	21.611	2.771
50067	D12	M-016918- leucine zip	84328	LZIC	3630	15.041	3.799
50067	D13	M-010746- G protein-	84109	GPR103	4263	6.6854	12.1546
50067	D14	M-015061- cytokine in	84324	CIP29	3141	17.638	1.202
50067	D15	M-018995- zinc finger	84124	ZNF394	3391	14.686	4.154
50067	D16	M-014879- THO compl	84321	THOC3	4188	19.628	0.788
50067	D17	M-014794- RUN doma	84127	RUNDC2A	3394	7.5133	11.3267
50067	D18	M-014878- chromoson	84319	C3orf26	4715	21.866	3.026
50067	D19	M-014795- WD repeat	84128	WDR75	4717	10.854	7.986
50067	D20	M-014877- coiled-coil	84318	CCDC77	5108	8.9272	9.9128
50067	D21	M-008129- acyl-Coenz	84129	ACAD11	5439	22.835	3.995
50067	D23	M-026005- centrosom	84131	CEP78	5294	17.303	1.537
50067	E02	M-005973- transmemb	84000	TMPRSS13	6188	12.427	6.413
50067	E04	M-013538- regeneratir	83998	REG4	4058	14.49	4.35
50067	E05	M-014722- dynein, axo	83544	DNAL1	5017	26.37	7.53
50067	E06	M-015103- cortactin b	83992	CTTNBP2	5010	21.178	2.338
50067	E07	M-014723- retbindin	83546	RTBDN	4008	20.259	1.419
50067	E08	M-016828- chromoson	83989	C5orf21	4241	37.02	18.18
50067	E09	M-008787- Rab interac	83547	RILP	4359	24.18	5.34
50067	E10	M-014776- neurocalcir	83988	NCALD	3817	22.95	4.11
50067	E11	M-013499- componen	83548	COG3	4296	29.702	10.862
50067	E12	M-014775- coiled-coil	83987	CCDC8	1472	27.649	8.809
50067	E13	M-010745- membrane	83552	MFRP	2691	21.293	2.453
50067	E14	M-014774- integrin alp	83986	ITFG3	3942	22.019	3.179
50067	E15	M-018578- transmemb	83590	TMUB1	3035	18.682	0.158

50067	E16	M-003987- spinster ho	83985	SPNS1	4032	37.326	18.486
50067	E17	M-014725- THAP doma	83591	THAP2	4267	27.537	8.697
50067	E18	M-014773- family with	83982	FAM14A	3772	17.63	1.21
50067	E19	M-021354- nudix (nucl	83594	NUDT12	4808	29.264	10.424
50067	E20	M-007581- solute carri	83959	SLC4A11	5472	23.41	4.57
50067	E21	M-019017- SRY (sex de	83595	SOX7	5358	20.605	1.765
50067	E23	M-017207- BCL2-like 1	83596	BCL2L12	5523	16.386	2.454
50067	F02	M-017006- coiled-coil	84317	CCDC115	5667	13.182	5.658
50067	F04	M-014876- LSM domai	84316	LSMD1	5709	32.317	13.477
50067	F05	M-010747- zinc and rir	84133	ZNRF3	5730	14.066	4.774
50067	F06	M-014875- MON1 ho	84315	MON1A	5668	27.1	8.26
50067	F07	M-016907- translocas	84134	TOMM40L	4672	20.655	1.815
50067	F08	M-010979- transmem	84314	TMEM107	3443	25.908	7.068
50067	F09	M-014796- UTP15, U3	84135	UTP15	3263	6.7423	12.0977
50067	F10	M-004699- vacuolar pr	84313	VPS25	4082	20.725	1.885
50067	F11	M-014797- likely orth	84137	PHAX	5212	25.902	7.062
50067	F12	M-014874- breast can	84312	BRMS1L	3048	12.762	6.078
50067	F13	M-014798- solute carri	84138	SLC7A6OS	3933	12.764	6.076
50067	F14	M-019256- mitochond	84311	MRPL45	3690	16.098	2.742
50067	F15	M-022697- hypothetic	84140	FLJ13305	3789	14.225	4.615
50067	F16	M-014873- hypothetic	84310	MGC11257	3979	26.967	8.127
50067	F17	M-014799- transmem	84141	TMEM166	4550	14.703	4.137
50067	F18	M-014872- nudix (nucl	84309	NUDT16L1	4956	14.911	3.929
50067	F19	M-016775- coiled-coil	84142	CCDC98	6754	32.322	13.482
50067	F20	M-014871- limitrin	84308	MGC3047	6551	20.119	1.279
50067	F21	M-021617- synapse de	84144	SYDE2	5396	14.066	4.774
50067	F23	M-007085- zinc finger	84146	ZNF644	6086	20.358	1.518
50067	G02	M-014771- FKSG43 ge	83957	FKSG43	4955	5.7921	13.0479
50067	G04	M-006842- Rac GTPas	83956	RACGAP1P	4162	26.766	7.926
50067	G05	M-014727- receptor (c	83597	RTP3	5565	31.123	12.283
50067	G06	M-014770- nascent-po	83955	NACAP1	4850	18.082	0.758
50067	G07	M-021352- transmem	83604	TMEM47	4507	14	4.84
50067	G08	M-014768- Fc recepto	83953	FCAMR	3736	13.33	5.51
50067	G09	M-014728- cerebral ca	83605	CCM2	5373	15.615	3.225
50067	G10	M-005902- IMP2 inner	83943	IMMP2L	4845	36.388	17.548
50067	G11	M-031449- chromoso	83606	C22orf13	4333	20.194	1.354
50067	G12	M-013536- TM2 doma	83941	TM2D1	4088	19.643	0.803
50067	G13	M-014729- AMME chr	83607	AMMECR1	3389	12.6	6.24
50067	G14	M-014767- TatD DNas	83940	TATDN1	2623	25.658	6.818
50067	G15	M-016886- chromoso	83608	C18orf21	4870	20.821	1.981
50067	G16	M-014766- eukaryotic	83939	EIF2A	4745	16.354	2.486
50067	G17	M-014731- chromoso	83636	C19orf12	5022	27.758	8.918
50067	G18	M-014765- chromoso	83938	C10orf11	5428	47.126	28.286
50067	G19	M-025325- zinc finger,	83637	ZMIZ2	4870	18.686	0.154
50067	G20	M-017587- Ras associa	83937	RASSF4	4562	26.282	7.442
50067	G21	M-016160- testis expr	83639	TEX101	5009	17.728	1.112
50067	G23	M-021286- family with	83640	FAM103A1	5697	15.552	3.288

50067	H02	M-014870- zinc finger	84307	ZNF397	6179	20.489	1.649
50067	H04	M-014869- programm	84306	PDCD2L	5168	24.787	5.947
50067	H05	M-014800- MYST histo	84148	MYST1	4372	46.317	27.477
50067	H06	M-014868- within bgcr	84305	WIBG	4340	14.171	4.669
50067	H07	M-014801- ribonucleas	84153	RNASEH2C	5094	31.429	12.589
50067	H08	M-014867- nudix (nucl	84304	NUDT22	4076	8.0716	10.7684
50067	H09	M-024715- brix domai	84154	BXDC1	4419	20.502	1.662
50067	H10	M-014866- coiled-coil-	84303	CHCHD6	5222	18.211	0.629
50067	H11	M-028249- KIAA1109	84162	KIAA1109	5278	19.723	0.883
50067	H12	M-021290- chromoson	84300	C6orf125	3881	22.778	3.938
50067	H13	M-016458- activating s	84164	ASCC2	3492	19.158	0.318
50067	H14	M-014864- chromoson	84299	C17orf37	3933	19.502	0.662
50067	H15	M-018267- NLR family,	84166	NLRC5	4321	12.381	6.459
50067	H16	M-018613- chromoson	84298	C12orf31	4752	35.816	16.976
50067	H17	M-014802- chromoson	84167	C19orf44	4057	16.564	2.276
50067	H18	M-014863- GINS comp	84296	GINS4	4834	23.397	4.557
50067	H19	M-010679- anthrax to	84168	ANTXR1	5533	25.357	6.517
50067	H20	M-014861- chromoson	84294	C8orf53	5687	15.966	2.874
50067	H21	M-008022- lysyl oxidas	84171	LOXL4	6660	26.727	7.887
50067	H23	M-013391- polymerase	84172	POLR1B	5724	20.65	1.81
50067	I02	M-015442- chromoson	83932	C1orf124	4862	18.326	0.514
50067	I04	M-018591- STARD3 N-	83930	STARD3NL	6528	13.312	5.528
50067	I05	M-014732- family with	83641	FAM107B	4649	18.327	0.513
50067	I06	M-013521- keratin ass	83902	KRTAP17-1	5611	9.4101	9.4299
50067	I07	M-009396- selenoprot	83642	RP3-402G1	5219	10.979	7.861
50067	I08	M-013519- keratin ass	83900	KRTAP9-3	5838	6.0123	12.8277
50067	I09	M-018943- coiled-coil	83643	CCDC3	4943	17.297	1.543
50067	I10	M-013517- keratin ass	83897	KRTAP3-2	4887	6.9777	11.8623
50067	I11	M-015197- chromoson	83648	C8orf13	5066	15.101	3.739
50067	I12	M-013516- keratin ass	83896	KRTAP3-1	3419	11.582	7.258
50067	I13	M-012899- acyl-malon	83650	AMAC1L2	5118	22.118	3.278
50067	I14	M-013515- keratin ass	83895	KRTAP1-5	5109	12.214	6.626
50067	I15	M-025874- chromoson	83652	C8orf7	5401	20.348	1.508
50067	I16	M-014763- tetratricop	83894	TTC29	4459	15.699	3.141
50067	I17	M-015204- chromoson	83655	C8orf14	5752	23.644	4.804
50067	I18	M-014762- spermatog	83893	SPATA16	4569	10.79	8.05
50067	I19	M-015198- chromoson	83656	C8orf12	6572	24.422	5.582
50067	I20	M-018189- potassium	83892	KCTD10	5286	14.321	4.519
50067	I21	M-012921- tektin 1	83659	TEKT1	6780	18.569	0.271
50067	I23	M-012909- talin 2	83660	TLN2	5013	18.352	0.488
50067	J02	M-010680- chromoson	84293	C10orf58	5119	34.265	15.425
50067	J04	M-014860- mitogen-ac	84292	MORG1	4357	18.981	0.141
50067	J05	M-019225- Src-like-ada	84174	SLA2	6619	26.031	7.191
50067	J06	M-014859- hypothetic	84291	MGC2408	6346	29.751	10.911
50067	J07	M-028916- myosin, he	84176	MYH16	5135	19.241	0.401
50067	J08	M-014858- calpain, sm	84290	CAPNS2	4271	22.735	3.895
50067	J09	M-018602- major facili	84179	MFSD7	5259	26.659	7.819

50067	J10	M-007088- inhibitor of	84289	ING5	3933	31.808	12.968
50067	J11	M-017349- chromodor	84181	CHD6	4610	33.297	14.457
50067	J12	M-014857- EF-hand ca	84288	EFCAB2	3349	28.635	9.795
50067	J13	M-025310- hypothetica	84182	FLJ22374	3885	20.438	1.598
50067	J14	M-021403- zinc finger,	84287	ZDHHC16	4710	29.193	10.353
50067	J15	M-014804- zinc finger,	84186	ZCCHC7	4083	30.345	11.505
50067	J16	M-014856- transmemb	84286	TMEM175	4905	20.367	1.527
50067	J17	M-014805- transmemb	84187	TMEM164	5053	28.735	9.895
50067	J18	M-018192- hypothetica	84285	MGC11102	5607	35.135	16.295
50067	J19	M-014806- male sterili	84188	MLSTD2	6865	30.022	11.182
50067	J20	M-006805- chromoson	84284	C1orf57	4870	22.197	3.357
50067	J21	M-004305- SLIT and NT	84189	SLITRK6	4899	15.717	3.123
50067	J23	M-026900- chromoson	84190	C12orf26	5685	26.895	8.055
50067	K02	M-014761- sorting nex	83891	SNX25	4142	27.33	8.49
50067	K04	M-014760- spermatog	83890	SPATA9	4222	12.577	6.263
50067	K05	M-014734- poly (ADP-r	83666	PARP9	4711	32.987	14.147
50067	K06	M-031103- WD repeat	83889	WDR87	4795	21.105	2.265
50067	K07	M-019134- sestrin 2	83667	SESN2	5911	21.215	2.375
50067	K08	M-018587- fibroblast g	83888	FGFBP2	4079	17.235	1.605
50067	K09	M-016681- cysteine-ric	83690	CRISPLD1	4194	21.102	2.262
50067	K10	M-018585- tubulin tyro	83887	TTLL2	4440	22.297	3.457
50067	K11	M-014735- CD99 mole	83692	CD99L2	5306	22.654	3.814
50067	K12	M-005971- protease, s	83886	PRSS27	4448	13.422	5.418
50067	K13	M-004788- hydroxyste	83693	HSDL1	4461	23.223	4.383
50067	K14	M-007479- solute carri	83884	SLC25A2	4381	17.051	1.789
50067	K15	M-014736- chromoson	83695	C12orf32	4330	15.635	3.205
50067	K16	M-018583- tetraspanir	83882	TSPAN10	5141	32.231	13.391
50067	K17	M-019414- NIK and IKK	83696	NIBP	4641	20.147	1.307
50067	K18	M-014758- eukaryotic	83880	IFP38	5174	16.216	2.624
50067	K19	M-007588- solute carri	83697	SLC4A9	5405	25.18	6.34
50067	K20	M-018582- Usher synd	83878	USHBP1	6514	31.993	13.153
50067	K21	M-014737- calneuron 1	83698	CALN1	5331	21.534	2.694
50067	K23	M-014738- SH3 domai	83699	SH3BGRL2	4681	18.586	0.254
50067	L02	M-014855- transmemb	84283	TMEM79	3830	13.368	5.472
50067	L04	M-007087- ring finger	84282	RNF135	5204	16.66	2.18
50067	L05	M-015124- family with	84191	FAM96A	6325	19.636	0.796
50067	L06	M-014854- hypothetica	84281	MGC13057	6189	12.183	6.657
50067	L07	M-014808- SET domair	84193	SETD3	6252	16.843	1.997
50067	L08	M-017963- BTB (POZ) c	84280	BTBD10	6436	21.924	3.084
50067	L09	M-006079- ubiquitin sp	84196	USP48	6041	27.479	8.639
50067	L10	M-014853- chromoson	84279	C2orf7	6244	22.982	4.142
50067	L11	M-018662- thioredoxir	84203	TXNDC2	4423	12.706	6.134
50067	L12	M-014852- hippocamp	84278	HIATL2	3689	15.641	3.199
50067	L13	M-022292- ring finger a	84206	RKHD3	3946	27.978	9.138
50067	L14	M-017510- Williams Be	84277	WBSCR18	5194	34.405	15.565
50067	L15	M-014816- ankyrin rep	84210	ANKRD20A	5309	17.725	1.115
50067	L16	M-018610- nicolin 1	84276	NICN1	6160	30.179	11.339

50067	L17	M-014819- zinc finger	84215	ZNF541	5500	19.909	1.069
50067	L18	M-007366- solute carri	84275	SLC25A33	6978	31.155	12.315
50067	L19	M-014820- transmemb	84216	TMEM117	6143	35.357	16.517
50067	L20	M-014851- chromosom	84273	C4orf14	6340	26.388	7.548
50067	L21	M-015735- zinc finger,	84217	ZMYND12	5653	20.785	1.945
50067	L23	M-014821- TBC1 doma	84218	TBC1D3	6364	25.456	6.616
50067	M02	M-013037- TM2 doma	83877	TM2D2	4749	16.951	1.889
50067	M04	M-016832- maestro	83876	MRO	5053	25.965	7.125
50067	M05	M-017350- junctional a	83700	JAM3	4643	26.147	7.307
50067	M06	M-014757- beta-carote	83875	BCDO2	6488	22.842	4.002
50067	M07	M-010677- UNC-112 re	83706	URP2	4454	20.656	1.816
50067	M08	M-014756- TBC1 doma	83874	TBC1D10A	4299	18.586	0.254
50067	M09	M-014739- tRNA phosp	83707	TRPT1	5960	24.95	6.11
50067	M10	M-013514- hemicentin	83872	HMCN1	5373	22.204	3.364
50067	M11	M-014741- espin	83715	ESPN	3927	25.159	6.319
50067	M12	M-009735- RAB34, me	83871	RAB34	3157	12.037	6.803
50067	M13	M-014742- cysteine-ric	83716	CRISPLD2	4104	27.68	8.84
50067	M14	M-014755- testis-speci	83863	TTTY5	4400	31.295	12.455
50067	M15	M-017950- yippee-like	83719	YPEL3	4652	27.064	8.224
50067	M16	M-014754- transmemb	83862	TMPIT	4769	23.779	4.939
50067	M17	M-003996- family with	83723	FAM57B	4845	27.307	8.467
50067	M18	M-018730- radial spok	83861	RSHL2	4631	18.506	0.334
50067	M19	M-021435- inhibin, bet	83729	INHBE	5143	17.15	1.69
50067	M20	M-026403- TAF3 RNA p	83860	TAF3	4017	11.576	7.264
50067	M21	M-007477- solute carri	83733	SLC25A18	4170	13.094	5.746
50067	M23	M-019426- ATG10 auto	83734	ATG10	4106	21.676	2.836
50067	N02	M-014850- Yip1 domai	84272	YIPF4	5087	21.663	2.823
50067	N04	M-019036- polymerase	84271	POLDIP3	5976	28.464	9.624
50067	N05	M-014822- WD repeat	84219	WDR24	6995	31.48	12.64
50067	N06	M-016972- chromosom	84270	C9orf89	7089	17.929	0.911
50067	N07	M-015458- chromosom	84221	C21orf56	4541	15.019	3.821
50067	N08	M-014849- coiled-coil-	84269	CHCHD5	5479	9.0345	9.8055
50067	N09	M-014823- hypothetica	84222	DKFZp434N	6851	26.565	7.725
50067	N10	M-014848- RPA interac	84268	RPAIN	6017	27.987	9.147
50067	N11	M-014824- IQ motif co	84223	IQCG	5071	15.894	2.946
50067	N12	M-018609- chromosom	84267	C9orf64	4007	25.48	6.64
50067	N13	M-014826- zinc finger,	84225	ZMYND15	3003	9.6237	9.2163
50067	N14	M-014847- alkB, alkyla	84266	ALKBH7	5115	18.123	0.717
50067	N15	M-014827- chromosom	84226	C2orf16	4471	14.561	4.279
50067	N16	M-014846- polymerase	84265	POLR3GL	6918	27.956	9.116
50067	N17	M-014828- regulator o	84227	RGSL2	6139	16.306	2.534
50067	N18	M-010184- hydroxyste	84263	HSDL2	5029	13.78	5.06
50067	N19	M-018785- coiled-coil (	84229	CCDC135	6639	19.069	0.229
50067	N20	M-014845- chromosom	84262	C7orf48	6254	17.829	1.011
50067	N21	M-007086- TNF recept	84231	TRAF7	5251	16.911	1.929
50067	N23	M-018603- MAF1 hom	84232	MAF1	4185	17.18	1.66
50067	O02	M-019443- ATPase fam	83858	ATAD3B	4216	9.63	9.21

50067	O04	M-016838-	transmemb	83857	TMTC1	5095	18.979	0.139
50067	O05	M-024979-	H2A histon	83740	H2AFB3	5392	22.719	3.879
50067	O06	M-014752-	fibronectin	83856	FSD1L	5388	20.193	1.353
50067	O07	M-014743-	MARVEL d	83742	MARVELD1	4974	11.661	7.179
50067	O08	M-007809-	angiopoieti	83854	ANGPTL6	5113	20.595	1.755
50067	O09	M-027146-	glutamate-	83743	GRWD1	6353	21.423	2.583
50067	O10	M-014750-	synaptotag	83851	SYT16	4373	27.304	8.464
50067	O11	M-026258-	zinc finger	83744	ZNF484	4120	16.092	2.748
50067	O12	M-023602-	family with	83850	FAM62C	4812	18.703	0.137
50067	O13	M-007342-	solute carri	81893	SLC7A5P1	2387	15.165	3.675
50067	O14	M-013513-	synaptotag	83849	SYT15	4868	14.03	4.81
50067	O15	M-013466-	keratin ass	81850	KRTAP1-3	6107	17.521	1.319
50067	O16	M-006259-	potassium	83795	KCNK16	4253	17.635	1.205
50067	O17	M-005933-	lon peptida	83752	LONP2	4666	17.617	1.223
50067	O18	M-018188-	armadillo r	83787	ARMC10	5391	26.322	7.482
50067	O19	M-022184-	taste recep	83756	TAS1R3	4145	24.511	5.671
50067	O20	M-018955-	FKSG44 ge	83786	FKSG44	5354	15.521	3.319
50067	O21	M-008304-	retinol bin	83758	RBP5	4302	24.361	5.521
50067	O23	M-014744-	RNA bindin	83759	RBM4B	3736	12.313	6.527
50067	P02	M-014844-	F-box and	84261	FBXW9	3015	15.224	3.616
50067	P04	M-014843-	trichoplein	84260	TCHP	4885	17.687	1.153
50067	P05	M-014829-	transmemb	84233	TMEM126	5859	18.416	0.424
50067	P06	M-014842-	DCN1, defe	84259	DCUN1D5	5678	15.358	3.482
50067	P07	M-014830-	hypothetic	84234	DKFZp547	5755	16.56	2.28
50067	P08	M-014841-	synaptotag	84258	SYT3	5018	11.618	7.222
50067	P09	M-019378-	rhomboid	84236	RHBDD1	5915	23.297	4.457
50067	P10	M-014839-	FLYWCH-ty	84256	FLYWCH1	5267	8.3539	10.4861
50067	P11	M-023682-	ATPase typ	84239	ATP13A4	4150	2.9398	15.9002
50067	P12	M-007556-	solute carri	84255	SLC37A3	4746	11.61	7.23
50067	P13	M-014831-	zinc finger,	84240	ZCCHC9	4940	9.3522	9.4878
50067	P14	M-018606-	GTPase act	84253	GARNL3	6163	14.603	4.237
50067	P15	M-021844-	zinc finger,	84243	ZDHHC18	1685	31.691	12.851
50067	P16	M-014838-	SH3-domai	84251	SGIP1	6038	12.62	6.22
50067	P17	M-007755-	hypothetic	84245	MGC3207	6068	20.353	1.513
50067	P18	M-014837-	ankyrin rep	84250	ANKRD32	4363	8.4116	10.4284
50067	P19	M-014834-	mediator o	84246	MED10	2931	8.7342	10.1058
50067	P20	M-014836-	pleckstrin	84249	PSD2	5277	11.01	7.83
50067	P21	M-014835-	leucine zip	84247	LDOC1L	5216	7.1319	11.7081
50067	P23	M-018604-	forty-two-t	84248	FYTTD1	4490	13.363	5.477
					MAD	4713	18.841	4.709
					3MAD			14.127
					MADc			6.96932
50067	C22					4863	60.395	
50067	D22					4281	46.998	
50067	E22					3672	51.471	
50067	F22					5037	48.64	
					mn	4463.25	51.876	

					sd	618.6762	5.972268
50067	G22					1890	18.095
50067	H22					2915	11.046
50067	I22					1628	6.3882
50067	J22		3352	21.122			
					mn	2271.5	8.7171
					sd	910.0464	3.293562
					3psSD		17.9168
					3ngSD		9.880686
					SumSD		27.79749
					DiffMn		43.1589
					SmovrDiff		0.644073
					1minus		0.355927
50067	G03	M-003290-	polo-like ki	5347	PLK1 SMA	986	11.968
50067	H03	M-003290-	polo-like ki	5347	PLK1 SMA	960	3.6458
50067	I03	D-001206-	siControl non-targetin			5713	10.31
50067	J03	D-001206-	siControl non-targetin			5615	26.572
50067	K03	D-001600-	siGLO RISC-free siRNA			5270	25.465
50067	L03	D-001600-	siGLO RISC-free siRNA			6698	29.606

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-1.07715	3395	7.7467	7.9333	-1.21937	3013	9.5254	4.1746	-0.77951
-0.35757	3984	22.716	7.036	1.082757	2850	17.474	3.774	0.703285
-1.16654	5488	16.29	0.61	0.094504	3082	13.303	0.397	-0.07481
-0.68055	3205	11.482	4.198	-0.64492	2079	12.843	0.857	-0.16062
-0.85059	4308	11.56	4.12	-0.63292	2472	8.5761	5.1239	-0.9566
-0.52329	4301	23.134	7.454	1.147042	1691	21.762	8.062	1.503201
-0.92792	5178	14.639	1.041	-0.1594	2796	12.411	1.289	-0.24121
-0.47178	5688	19.427	3.747	0.576943	2762	14.989	1.289	0.239714
1.222931	4894	29.751	14.071	2.164669	2349	34.994	21.294	3.9716
0.46016	3557	17.29	1.61	0.248294	2185	12.403	1.297	-0.2427
0.068443	2568	8.7617	6.9183	-1.06327	1777	8.6663	5.0337	-0.93977
-0.31682	4032	14.881	0.799	-0.12219	3079	13.738	0.038	0.006343
0.504353	2881	20.201	4.521	0.695976	1903	16.553	2.853	0.531474
0.81084	4050	20.074	4.394	0.676445	2932	21.248	7.548	1.407316
-0.65157	4552	15.29	0.39	-0.05929	2733	13.758	0.058	0.010074
-0.74498	3911	14.498	1.182	-0.18109	2244	11.497	2.203	-0.41171
-0.73278	3692	13.272	2.408	-0.36963	2451	14.035	0.335	0.061747
0.673667	3655	24.679	8.999	1.384647	2173	13.438	0.262	-0.04962
-0.04735	3654	15.298	0.382	-0.05806	3195	13.74	0.04	0.006716
0.333175	3088	11.917	3.763	-0.57802	4047	13.516	0.184	-0.03507
0.866512	6051	17.468	1.788	0.275668	3905	24.558	10.858	2.024788
-0.32299	4717	11.851	3.829	-0.58817	3438	19.459	5.759	1.073582
-1.00914	5684	10.662	5.018	-0.77103	3454	9.8437	3.8563	-0.72013
-0.93567	6267	15.685	0.005	0.001461	3997	11.434	2.266	-0.42346
-0.7698	5635	17.125	1.445	0.222918	2570	16.148	2.448	0.455923
-1.54341	4922	7.7408	7.9392	-1.22028	1993	6.7235	6.9765	-1.3022
-1.38755	3341	7.5726	8.1074	-1.24614	2559	7.7765	5.9235	-1.10576
-1.29282	3469	12.28	3.4	-0.52219	1136	10.739	2.961	-0.55311
-0.60465	4912	13.721	1.959	-0.30058	2322	9.1301	4.5699	-0.85325
-0.30462	4442	12.765	2.915	-0.44761	1711	8.007	5.693	-1.06276
-0.59331	3813	16.103	0.423	0.065745	2270	12.775	0.925	-0.1733
-0.9658	6031	22.666	6.986	1.075068	1320	10.379	3.321	-0.62027
0.518702	5769	22.257	6.577	1.012168	2153	8.0353	5.6647	-1.05748
0.677398	4069	22.02	6.34	0.97572	1440	11.389	2.311	-0.43186
-0.04549	4615	21.408	5.728	0.8816	1771	9.825	3.875	-0.72362
-0.81414	4781	15.75	0.07	0.011457	1883	12.427	1.273	-0.23822
-1.04257	4826	15.126	0.554	-0.08451	3165	7.0458	6.6542	-1.24207
0.922759	4447	33.191	17.511	2.693706	2862	17.121	3.421	0.637433
-1.29644	4390	15.353	0.327	-0.0496	2704	4.3639	9.3361	-1.74237
1.588821	4909	36.993	21.313	3.278415	3860	17.772	4.072	0.758876
-0.50737	3930	10.891	4.789	-0.73581	4731	10.188	3.512	-0.6559
-0.0815	4150	12.386	3.294	-0.50589	4534	14.402	0.702	0.13021
-0.12368	4615	15.666	0.014	-0.00146	3985	10.489	3.211	-0.59975
-0.03616	4143	20.71	5.03	0.774255	3187	14.026	0.326	0.060068
-0.09843	5474	17.136	1.456	0.22461	3223	21.222	7.522	1.402465
0.536064	4374	18.839	3.159	0.486514	2494	17.562	3.862	0.719701

-0.86967	4238	10.217	5.463	-0.83946	1901	3.9453	9.7547	-1.82046
0.520567	4485	17.235	1.555	0.239835	2647	11.145	2.555	-0.47738
1.783244	3931	24.345	8.665	1.333281	1756	15.148	1.448	0.269375
0.361154	3255	19.601	3.921	0.603702	2013	13.91	0.21	0.038429
2.072656	2576	23.059	7.379	1.135507	1253	16.76	3.06	0.57009
-0.79089	4277	17.302	1.622	0.250139	1961	10.964	2.736	-0.51114
0.313373	3666	13.557	2.123	-0.3258	1281	11.163	2.537	-0.47402
0.976566	4997	24.855	9.175	1.411714	2600	17.154	3.454	0.643589
-0.95461	4184	9.608	6.072	-0.93312	2077	12.229	1.471	-0.27516
-0.60063	4898	9.8612	5.8188	-0.89418	1362	3.8179	9.8821	-1.84423
-1.5321	4292	12.232	3.448	-0.52958	1536	4.362	9.338	-1.74273
0.246365	4620	16.472	0.792	0.122494	2898	5.4175	8.2825	-1.54583
-0.17276	4294	12.017	3.663	-0.56264	2743	4.3019	9.3981	-1.75394
0.645687	3386	19.492	3.812	0.586939	3072	7.1615	6.5385	-1.22049
-0.02167	5366	25.177	9.497	1.461234	5234	12.801	0.899	-0.16845
-1.2093	2756	14.224	1.456	-0.22323	2414	5.5924	8.1076	-1.5132
-1.14114	4060	18.941	3.261	0.502201	3772	9.7561	3.9439	-0.73647
-0.24637	4897	15.152	0.528	-0.08051	3764	2.8959	10.8041	-2.01623
1.616227	5021	37.064	21.384	3.289334	3667	16.171	2.471	0.460213
0.029271	4432	23.127	7.447	1.145965	1766	5.7758	7.9242	-1.47899
1.114169	5388	26.151	10.471	1.611026	3491	15.726	2.026	0.377199
0.027549	5404	19.689	4.009	0.617236	3195	13.865	0.165	0.030034
0.397456	5497	25.523	9.843	1.514445	2809	16.625	2.925	0.544906
-0.54525	4102	18.625	2.945	0.453603	2662	11.796	1.904	-0.35593
-1.74416	2414	12.262	3.418	-0.52496	2004	4.8902	8.8098	-1.64419
-0.17261	3363	13.351	2.329	-0.35748	2011	8.7021	4.9979	-0.93309
-0.59618	3820	14.346	1.334	-0.20446	1234	10.13	3.57	-0.66672
0.112923	4677	20.291	4.611	0.709817	3503	18.87	5.17	0.963705
-1.62537	4141	12.944	2.736	-0.42008	2077	9.5811	4.1189	-0.76912
0.434045	5431	24.121	8.441	1.298832	2796	15.093	1.393	0.259115
-1.14602	4340	11.359	4.321	-0.66383	2204	8.2123	5.4877	-1.02446
-1.42249	4821	18.191	2.511	0.386858	2769	8.3424	5.3576	-1.00019
0.573083	4208	22.624	6.944	1.068609	1869	15.142	1.442	0.268256
-0.22068	4218	20.65	4.97	0.765028	2938	14.261	0.561	0.103907
-0.92032	5357	10.006	5.674	-0.87191	5860	10.444	3.256	-0.60815
-0.62431	3797	14.011	1.669	-0.25598	3867	12.775	0.925	-0.1733
1.080306	6823	25.722	10.042	1.54505	3912	16.283	2.583	0.481106
0.335327	5031	19.519	3.839	0.591091	3912	14.801	1.101	0.204643
0.203463	4713	16.359	0.679	0.105115	2810	8.4342	5.2658	-0.98307
2.608432	5815	30.576	14.896	2.291546	3062	19.366	5.666	1.056233
0.766072	4626	21.509	5.829	0.897133	3454	12.884	0.816	-0.15297
0.589584	6082	24.975	9.295	1.430169	3628	19.763	6.063	1.130292
1.558402	5953	28.406	12.726	1.957822	3321	21.168	7.468	1.392392
1.263825	1702	12.808	2.872	-0.44099	1621	18.692	4.992	0.9305
0.351828	5082	22.609	6.929	1.066302	3401	14.849	1.149	0.213597
0.455999	4787	13.662	2.018	-0.30966	2642	13.285	0.415	-0.07816
-0.02281	3212	7.1295	8.5505	-1.31429	2314	11.279	2.421	-0.45238

2.652339	6228	24.663	8.983	1.382186	1922	17.43	3.73	0.695077
1.247754	6749	28.019	12.339	1.898305	3670	18.747	5.047	0.94076
-0.17376	4117	5.708	9.972	-1.5329	1393	4.0201	9.6799	-1.80651
1.495555	5870	24.855	9.175	1.411714	3251	14.611	0.911	0.169199
0.655588	6016	13.979	1.701	-0.2609	2913	8.033	5.667	-1.05791
0.253109	4439	11.602	4.078	-0.62646	2621	10.416	3.284	-0.61337
-0.35226	4628	9.2913	6.3887	-0.98183	2963	12.082	1.618	-0.30258
-0.81199	5252	16.813	1.133	0.174936	4457	14.404	0.704	0.130583
1.933618	6226	31.577	15.897	2.445489	4987	28.153	14.453	2.695427
-0.68515	5162	11.798	3.882	-0.59632	4848	12.108	1.592	-0.29773
1.185051	4434	22.17	6.49	0.998788	3359	18.547	4.847	0.90345
0.260284	3983	22.295	6.615	1.018012	2697	19.244	5.544	1.033474
1.014016	3376	23.193	7.513	1.156115	2260	21.416	7.716	1.438656
-1.73599	3313	6.2179	9.4621	-1.45448	1788	7.774	5.926	-1.10623
0.270328	5042	26.735	11.055	1.700839	4225	22.343	8.643	1.611585
1.013155	4340	20.507	4.827	0.743036	3524	15.494	1.794	0.33392
-0.87225	2402	12.032	3.648	-0.56033	1839	8.211	5.489	-1.02471
-0.87196	2723	10.723	4.957	-0.76164	1820	4.2857	9.4143	-1.75696
-0.39358	3995	16.195	0.515	0.079894	3232	7.271	6.429	-1.20006
-0.66233	2514	11.018	4.662	-0.71628	2515	9.7018	3.9982	-0.7466
1.165967	4809	23.872	8.192	1.260538	2639	16.484	2.784	0.518603
-0.59375	3633	11.974	3.706	-0.56925	2536	10.607	3.093	-0.57774
-0.5639	5044	12.688	2.992	-0.45945	3544	6.0666	7.6334	-1.42474
1.934335	5772	27.841	12.161	1.87093	5314	24.84	11.14	2.077395
0.183375	5458	14.841	0.839	-0.12834	4985	11.314	2.386	-0.44585
-0.68515	5428	12.012	3.668	-0.56341	4228	11.755	1.945	-0.36358
0.217668	4292	17.847	2.167	0.333955	4253	6.1368	7.5632	-1.41164
-1.87233	6054	13.528	2.152	-0.33026	5726	12.889	0.811	-0.15204
1.137127	2723	26.956	11.276	1.734826	2435	22.834	9.134	1.70318
1.762295	4290	29.254	13.574	2.088235	3499	21.749	8.049	1.500776
-0.10891	2441	10.651	5.029	-0.77272	4156	10.01	3.69	-0.68911
-0.69462	4348	13.615	2.065	-0.31688	3061	14.211	0.511	0.09458
-0.79075	3788	9.7413	5.9387	-0.91262	3415	10.425	3.275	-0.61169
-0.46289	5015	10.13	5.55	-0.85284	4569	6.3471	7.3529	-1.37241
2.517749	4793	33.194	17.514	2.694167	3733	20.975	7.275	1.356388
0.194137	3534	21.307	5.627	0.866068	2650	11.962	1.738	-0.32497
0.115076	3038	18.499	2.819	0.434226	2679	11.497	2.203	-0.41171
-0.8955	3712	12.581	3.099	-0.4759	2670	7.8652	5.8348	-1.08921
0.978144	1618	20.89	5.21	0.801937	1178	10.102	3.598	-0.67194
0.284102	3976	17.631	1.951	0.300736	2941	12.173	1.527	-0.2856
-0.35685	5083	12.493	3.187	-0.48944	3540	5.9605	7.7395	-1.44453
1.279465	6100	20.77	5.09	0.783482	2719	9.8566	3.8434	-0.71772
4.058502	5398	37.921	22.241	3.421132	3696	20.373	6.673	1.244086
-0.02224	3349	11.287	4.393	-0.67491	2723	3.8193	9.8807	-1.84397
1.067679	3922	22.642	6.962	1.071377	2983	10.929	2.771	-0.51767
-0.1597	4410	20.68	5	0.769641	3526	8.962	4.738	-0.88461
-0.47193	5705	12.761	2.919	-0.44822	3600	6.1667	7.5333	-1.40607

0.236465	5531	14.446	1.234	-0.18908	4975	15.276	1.576	0.293253
0.853168	5946	29.331	13.651	2.100077	5598	24.116	10.416	1.942334
3.942422	4052	39.931	24.251	3.73025	3757	47.99	34.29	6.395974
-0.67008	4748	13.079	2.601	-0.39932	3322	14.389	0.689	0.127785
1.806202	5166	29.907	14.227	2.18866	4278	32.445	18.745	3.49609
-1.54526	4926	13.54	2.14	-0.32842	3082	11.486	2.214	-0.41376
0.23833	4876	22.416	6.736	1.03662	3643	19.407	5.707	1.063881
-0.0904	4394	13.564	2.116	-0.32473	3628	11.825	1.875	-0.35052
0.126555	4521	19.443	3.763	0.579403	2910	16.254	2.554	0.475697
0.564904	4020	19.055	3.375	0.519733	2412	12.604	1.096	-0.2052
0.045485	2991	13.173	2.507	-0.38486	3194	14.621	0.921	0.171064
0.094844	3828	20.324	4.644	0.714892	2300	15.087	1.387	0.257995
-0.92692	2658	8.8789	6.8011	-1.04525	2446	5.1513	8.5487	-1.59549
2.435675	4242	30.174	14.494	2.229722	2861	23.558	9.858	1.838241
-0.32672	2929	12.632	3.048	-0.46806	1843	8.3559	5.3441	-0.99768
0.653722	4254	26.046	10.366	1.594878	1881	11.43	2.27	-0.42421
0.934955	5106	23.619	7.939	1.22163	3884	16.813	3.113	0.579977
-0.41252	4490	10.869	4.811	-0.73919	3302	4.3307	9.3693	-1.74857
1.131531	5028	26.85	11.17	1.718525	4655	21.375	7.675	1.431007
0.259566	3807	18.492	2.812	0.433149	4455	8.5073	5.1927	-0.96943
-0.0739	3745	28.144	12.464	1.917529	4670	27.709	14.009	2.6126
-0.79333	4617	20.468	4.788	0.737038	4022	12.904	0.796	-0.14924
-0.07375	2958	22.887	7.207	1.109055	3233	20.384	6.684	1.246138
-1.3532	4247	18.696	3.016	0.464522	4430	12.348	1.352	-0.25296
-1.12809	3960	16.768	1.088	0.168015	3787	11.83	1.87	-0.34959
-1.84074	2948	11.737	3.943	-0.6057	3910	7.3913	6.3087	-1.17762
-0.22154	3583	18.811	3.131	0.482208	4413	12.441	1.259	-0.23561
-1.70222	2900	10.379	5.301	-0.81455	4022	8.2297	5.4703	-1.02122
-0.53664	3414	16.755	1.075	0.166016	4280	9.5561	4.1439	-0.77378
-1.04157	3470	15.764	0.084	0.01361	3312	14.13	0.43	0.079469
0.470204	2981	22.409	6.729	1.035544	3446	19.791	6.091	1.135516
-0.95088	3274	11.393	4.287	-0.65861	3473	8.3501	5.3499	-0.99876
0.216233	2829	16.26	0.58	0.08989	4309	16.988	3.288	0.612623
-0.45083	3173	15.254	0.426	-0.06482	3056	11.78	1.92	-0.35892
0.689163	3541	17.622	1.942	0.299352	3745	18.932	5.232	0.975271
-1.15521	2507	11.488	4.192	-0.64399	2842	12.597	1.103	-0.20651
0.800795	5382	20.996	5.316	0.818239	2952	23.34	9.64	1.797573
-0.64856	4927	17.191	1.511	0.233069	4600	12.913	0.787	-0.14756
-0.03903	4959	14.459	1.221	-0.18709	4699	11.641	2.059	-0.38485
-0.07016	3441	10.433	5.247	-0.80624	3927	13.038	0.662	-0.12424
2.213128	4522	21.207	5.527	0.850689	3958	21.728	8.028	1.496859
0.020088	3784	17.151	1.471	0.226917	3305	17.64	3.94	0.734252
1.031664	4837	10.75	4.93	-0.75749	5406	16.963	3.263	0.607959
1.565432	4462	20.574	4.894	0.75334	5408	21.616	7.916	1.475965
0.057394	3513	11.358	4.322	-0.66399	4639	14.809	1.109	0.206135
0.558735	3635	11.197	4.483	-0.68875	4232	10.232	3.468	-0.64769
1.121774	4120	17.767	2.087	0.321651	5455	18.772	5.072	0.945424

1.860583	2353	17.637	1.957	0.301659	4352	23.46	9.76	1.819959
2.074234	4196	16.969	1.289	0.198927	4371	20.339	6.639	1.237744
1.405302	2858	12.141	3.539	-0.54357	3623	13.442	0.258	-0.04888
0.229147	3211	9.4986	6.1814	-0.94994	4119	11.92	1.78	-0.3328
1.485367	2888	15.166	0.514	-0.07836	3969	20.005	6.305	1.175437
1.650663	4272	23.596	7.916	1.218092	4034	19.683	5.983	1.115369
0.21896	4077	10.081	5.599	-0.86038	5026	16.037	2.337	0.435216
1.419651	2495	17.475	1.795	0.276745	3312	13.979	0.279	0.051301
2.337961	4455	18.945	3.265	0.502816	4796	23.332	9.632	1.796081
1.604317	4300	12.488	3.192	-0.49021	4888	15.732	2.032	0.378319
0.481539	3939	15.232	0.448	-0.06821	4985	16.349	2.649	0.493419
-0.44825	4536	9.3915	6.2885	-0.96642	5951	13.594	0.106	-0.02052
1.155636	4026	10.432	5.248	-0.8064	5652	17.268	3.568	0.664856
1.218053	4237	19.802	4.122	0.634614	4879	23.058	9.358	1.744967
-0.8988	3738	11.932	3.748	-0.57571	4294	13.67	0.03	-0.00634
2.029753	4684	22.011	6.331	0.974336	5975	21.975	8.275	1.542936
0.324852	3725	11.946	3.734	-0.57356	5384	15.119	1.419	0.263965
0.340636	4159	17.721	2.041	0.314577	6551	15.585	1.885	0.350896
-0.23044	2591	7.4875	8.1925	-1.25923	3472	11.175	2.525	-0.47178
0.324422	4126	13.888	1.792	-0.2749	4628	22.926	9.226	1.720343
0.495888	4153	15.555	0.125	-0.01853	4587	13.298	0.402	-0.07574
0.547112	3875	21.006	5.326	0.819777	5238	22.184	8.484	1.581924
-0.77755	3360	6.0417	9.6383	-1.48158	3795	6.0343	7.6657	-1.43076
0.628756	3903	17.935	2.255	0.347488	3818	25.065	11.365	2.119368
-0.25684	1168	6.3356	9.3444	-1.43638	2972	4.677	9.023	-1.68397
-0.46002	3915	16.986	1.306	0.201542	5135	20.779	7.079	1.319825
1.921278	4083	28.68	13	1.99996	3269	26.981	13.281	2.476793
0.187393	2958	12.711	2.969	-0.45591	3093	9.57	4.13	-0.77119
-0.37665	3869	10.804	4.876	-0.74919	5173	6.1473	7.5527	-1.40968
0.909558	5545	25.951	10.271	1.580268	5999	16.236	2.536	0.472339
1.887128	7236	27.004	11.324	1.742208	6783	20.271	6.571	1.225059
0.386408	5720	12.15	3.53	-0.54219	6348	8.7272	4.9728	-0.92841
-0.03659	4318	10.259	5.421	-0.833	4985	5.998	7.702	-1.43754
-0.7853	3957	11.17	4.51	-0.6929	4223	9.6614	4.0386	-0.75414
-0.31294	4099	10.49	5.19	-0.79748	4534	11.976	1.724	-0.32235
0.114071	3712	9.2942	6.3858	-0.98138	4247	19.331	5.631	1.049704
-0.95533	3489	7.6813	7.9987	-1.22943	5248	6.955	6.745	-1.25901
-0.28669	3223	12.876	2.804	-0.43053	5021	11.153	2.547	-0.47588
0.442367	3192	9.1479	6.5321	-1.00388	3742	8.9524	4.7476	-0.8864
1.239432	3300	18.818	3.138	0.483285	6465	27.873	14.173	2.643194
0.594176	3713	12.389	3.291	-0.50543	5633	13.51	0.19	-0.03619
-0.88029	2467	9.6473	6.0327	-0.92708	3870	14.444	0.744	0.138045
-0.45916	2317	8.4161	7.2639	-1.11642	2920	9.1096	4.5904	-0.85707
1.311032	3337	13.126	2.554	-0.39209	3779	17.306	3.606	0.671945
2.233216	3327	21.821	6.141	0.945115	4492	20.058	6.358	1.185324
-0.16013	2007	15.047	0.633	-0.09666	4368	17.193	3.493	0.650865
1.626845	4534	28.606	12.926	1.98858	4955	14.733	1.033	0.191958

0.153243	2683	15.654	0.026	-0.00331	2963	9.2811	4.4189	-0.82508
1.766887	3869	19.437	3.757	0.57848	6939	22.035	8.335	1.554129
2.369815	4632	28.282	12.602	1.938752	5809	21.725	8.025	1.496299
1.082889	3483	21.131	5.451	0.839	4998	14.086	0.386	0.071261
0.278937	2538	10.599	5.081	-0.78071	5404	10.77	2.93	-0.54733
0.94916	4761	22.117	6.437	0.990637	5492	9.614	4.086	-0.76298
-0.27119	4242	8.5101	7.1699	-1.10197	4044	10.93	2.77	-0.51748
1.022194	4181	17.46	1.78	0.274438	4680	16.004	2.304	0.42906
1.048309	3920	20.944	5.264	0.810242	5500	28.018	14.318	2.670243
0.574088	4790	14.614	1.066	-0.16325	5769	19.015	5.315	0.990755
0.260427	4438	20.46	4.78	0.735808	5900	21.847	8.147	1.519058
-0.03659	3839	12.868	2.812	-0.43176	5732	20.586	6.886	1.283821
0.876556	3232	17.358	1.678	0.258751	5782	30.249	16.549	3.086431
0.482543	3064	14.752	0.928	-0.14202	5132	19.934	6.234	1.162192
0.906545	3861	16.887	1.207	0.186316	5247	24.814	11.114	2.072545
-0.97628	2575	11.767	3.913	-0.60109	3477	11.418	2.282	-0.42645
1.268273	3491	21.054	5.374	0.827159	3851	27.032	13.332	2.486307
1.786975	3276	20.452	4.772	0.734577	3976	27.716	14.016	2.613906
1.179886	3565	30.21	14.53	2.235258	5321	29.337	15.637	2.9163
0.708534	4478	18.736	3.056	0.470674	4249	17.369	3.669	0.683697
1.214753	4323	18.876	3.196	0.492204	4976	20.86	7.16	1.334935
-0.04807	3534	19.44	3.76	0.578942	4280	11.893	1.807	-0.33784
-0.24263	3361	10.8	4.88	-0.7498	4114	12.883	0.817	-0.15316
-1.04243	3549	11.496	4.184	-0.64276	3840	11.276	2.424	-0.45294
-0.82461	2959	10.443	5.237	-0.80471	4372	17.338	3.638	0.677914
0.406783	4710	21.423	5.743	0.883907	4020	21.219	7.519	1.401906
0.404918	5060	17.767	2.087	0.321651	4661	22.806	9.106	1.697957
1.380766	3963	13.02	2.66	-0.40839	4030	15.881	2.181	0.406114
1.81352	5268	14.749	0.931	-0.14249	5902	20.112	6.412	1.195397
-0.13086	4337	7.9548	7.7252	-1.18737	7051	18.04	4.34	0.808871
-0.5484	2763	7.1299	8.5501	-1.31423	4017	8.7628	4.9372	-0.92177
-1.4071	2949	6.1716	9.5084	-1.4616	3857	10.526	3.174	-0.59285
1.108286	3616	15.487	0.193	-0.02899	4367	12.663	1.037	-0.1942
1.312323	3242	16.687	1.007	0.155558	4792	30.822	17.122	3.193323
-0.42285	3610	7.6731	8.0069	-1.23069	5012	14.385	0.685	0.127039
0.952604	3150	16.381	0.701	0.108499	3224	22.084	8.384	1.56327
-1.32255	2025	3.358	12.322	-1.89431	2465	6.2069	7.4931	-1.39857
-0.10302	2747	15.326	0.354	-0.05375	3655	21.505	7.805	1.455258
-0.61412	2990	7.7258	7.9542	-1.22258	2735	11.408	2.292	-0.42831
1.307875	4478	12.93	2.75	-0.42223	4519	15.003	1.303	0.242325
-0.36374	4201	11.616	4.064	-0.62431	4716	12.15	1.55	-0.2899
-0.72618	3247	5.0508	10.6292	-1.63397	3352	8.0549	5.6451	-1.05383
0.032715	6104	17.398	1.718	0.264903	5596	16.119	2.419	0.450513
-0.14521	5236	14.572	1.108	-0.16971	4245	13.946	0.246	0.045145
-0.27693	4074	9.1311	6.5489	-1.00646	3448	7.1056	6.5944	-1.23092
-0.23833	5135	12.522	3.158	-0.48498	3815	11.769	1.931	-0.36097
-1.32165	4805	16.483	0.803	0.124185	3019	10.732	2.968	-0.55442

0.019801	3143	18.549	2.869	0.441915	3705	15.304	1.604	0.298476
0.556439	2554	19.303	3.623	0.557873	2985	17.521	3.821	0.712052
0.193993	3395	18.085	2.405	0.370557	3580	11.788	1.912	-0.35743
-1.03023	2378	11.648	4.032	-0.61939	4515	10.698	3.002	-0.56076
0.251674	3049	13.873	1.807	-0.27721	6232	14.409	0.709	0.131516
0.370481	2872	20.299	4.619	0.711047	4161	9.0363	4.6637	-0.87075
1.214322	2604	22.273	6.593	1.014628	3922	16.548	2.848	0.530542
-0.39444	2225	12.764	2.916	-0.44776	3131	13.286	0.414	-0.07798
-0.0198	2574	20.085	4.405	0.678136	3298	18.648	4.948	0.922292
-0.52745	1034	14.603	1.077	-0.16494	1835	15.695	1.995	0.371416
-0.69031	2160	12.778	2.902	-0.44561	4250	11.035	2.665	-0.4979
-0.1894	3558	20.573	4.893	0.753186	5644	16.088	2.388	0.44473
-0.17304	2350	21.957	6.277	0.966031	4168	16.339	2.639	0.491553
-0.17563	1892	21.036	5.356	0.82439	3245	18.274	4.574	0.852523
1.073419	3021	21.251	5.571	0.857455	4808	19.738	6.038	1.125629
0.813566	1640	28.78	13.1	2.015339	2643	21.945	8.245	1.537339
-0.47637	2730	16.996	1.316	0.203079	4615	14.995	1.295	0.240833
0.792043	3238	23.317	7.637	1.175185	4022	19.766	6.066	1.130852
-0.93668	2395	10.647	5.033	-0.77333	1993	11.44	2.26	-0.42234
-0.51899	3119	16.961	1.281	0.197697	2736	15.863	2.163	0.402756
-0.16558	4267	8.0384	7.6416	-1.17451	3214	12.788	0.912	-0.17088
-0.06098	4406	15.388	0.292	-0.04421	4207	18.588	4.888	0.911099
-0.49976	3524	12.174	3.506	-0.5385	5132	12.276	1.424	-0.26639
-0.32729	3369	9.0531	6.6269	-1.01846	4135	14.51	0.81	0.150357
-1.0364	3378	6.6903	8.9897	-1.38183	4305	10.105	3.595	-0.67139
0.639374	3018	16.468	0.788	0.121878	4279	19.397	5.697	1.062016
-1.50475	3404	10.311	5.369	-0.82501	4665	14.469	0.769	0.142709
-2.2816	2038	4.8577	10.8223	-1.66367	3101	7.9652	5.7348	-1.07056
-1.03755	2487	15.239	0.441	-0.06713	3495	13.619	0.081	-0.01586
-1.36151	2601	9.6117	6.0683	-0.93255	3574	9.9888	3.7112	-0.69306
-0.60809	3649	10.003	5.677	-0.87237	4516	14.128	0.428	0.079096
1.843795	2758	16.28	0.6	0.092966	4119	24.035	10.335	1.927224
-0.89263	4723	10.481	5.199	-0.79886	4137	16.606	2.906	0.541361
0.216951	4055	11.171	4.509	-0.69275	3492	12.543	1.157	-0.21658
-1.49647	3345	9.2078	6.4722	-0.99467	4120	11.068	2.632	-0.49174
-1.45018	2431	6.088	9.592	-1.47446	2331	14.286	0.586	0.108571
-1.12364	4330	8.776	6.904	-1.06107	4588	10.615	3.085	-0.57625
-1.68009	5107	7.1275	8.5525	-1.3146	4087	10.717	2.983	-0.55722
-0.78602	5158	12.233	3.447	-0.52942	4158	16.354	2.654	0.494351
	4051	15.6755	4.3935		3628	13.704	3.622	
			13.1805				10.866	
			6.50238				5.36056	
5192	61.267		4438	40.514				
4320	57.361		3287	52.997				
4181	46.616		3300	52.091				
4071	52.321		4617	45.094				
4441	54.39125		3910.5	47.674				

510.9279	6.346542	716.2078	5.937626
1895	19.103	1972	3.9554
2025	18.765	1251	9.9121
1821	13.729	2072	14.189
1754	9.8632	3084	11.349
1866.667	14.11907	2135.667	11.8167
141.1536	4.463701	918.157	2.176471
	0		17.81288
	13.3911		6.529413
	13.3911		24.34229
	40.27218		35.8573
	0.332515		0.678866
	0.667485		0.321134

816	25.735	880	21.591
757	13.474	425	30.118
3596	18.215	3438	14.02
3833	12.81	3805	10.145
5378	27.241	7740	30.491
6269	27.389	5206	16.116

y

y

y

y

y

y

y

x debris a,b

x debris b

					cell ct	% inf	AD
50068	A02	M-007095- tripartite m	84851	TRIM52	3884	11.432	6.408
50068	A04	M-014989- hypothetic	84848	MGC16121	4315	17.312	0.528
50068	A05	M-018614- zinc finger	84364	ZNF289	4116	20.627	2.787
50068	A06	M-014988- hypothetic	84847	MGC16075	3759	12.264	5.576
50068	A07	M-014889- small nucle	84366	PRAC	3980	12.06	5.78
50068	A08	M-014987- PHD finger	84844	PHF5A	1907	24.489	6.649
50068	A09	M-013558- hook hom	84376	HOOK3	3879	25.625	7.785
50068	A10	M-014986- hypothetic	84843	MGC15705	3323	18.026	0.186
50068	A11	M-003653- chromosom	84417	C2orf40	2935	11.789	6.051
50068	A12	M-014985- 4-hydroxyp	84842	HPDL	2627	12.219	5.621
50068	A13	M-018616- chromosom	84418	C5orf32	2537	8.8687	8.9713
50068	A14	M-014984- hypothetic	84841	MGC15634	2487	19.582	1.742
50068	A15	M-021496- chromosom	84419	C15orf48	2826	31.953	14.113
50068	A16	M-016157- retina and	84839	RAXL1	2626	18.203	0.363
50068	A17	M-004219- caspase re	84433	CARD11	3394	18.739	0.899
50068	A18	M-014983- zinc finger	84838	ZNF496	2483	11.639	6.201
50068	A19	M-014891- zinc finger	84436	ZNF528	3102	13.314	4.526
50068	A20	M-009831- abhydrolas	84836	ABHD14B	4510	26.497	8.657
50068	A21	M-026510- KIAA1826	84437	KIAA1826	3317	9.5267	8.3133
50068	A23	M-022058- KIAA1822	84439	KIAA1822	3418	15.828	2.012
50068	B02	M-019119- KIAA1737	85457	KIAA1737	2687	5.7313	12.1087
50068	B04	M-015106- tankyrase 1	85456	TNKS1BP1	3000	15.1	2.74
50068	B05	M-018181- hypothetic	84856	MGC16291	2750	9.0182	8.8218
50068	B06	M-013729- dispatched	85455	DISP2	4409	14.947	2.893
50068	B07	M-015846- zinc finger	84858	ZNF503	3334	11.428	6.412
50068	B08	M-025222- KIAA1751	85452	KIAA1751	3413	8.9364	8.9036
50068	B09	M-014993- leucine-rich	84859	LRCH3	3003	10.856	6.984
50068	B10	M-022950- unkempt h	85451	UNK	2479	18.959	1.119
50068	B11	M-015847- kelch-like 2	84861	KLHL22	2762	8.4359	9.4041
50068	B12	M-015104- KIAA1754	85450	KIAA1754	2187	9.1449	8.6951
50068	B13	M-016031- MYC induc	84864	MINA	3240	13.395	4.445
50068	B14	M-024163- KIAA1755 p	85449	RP5-1054A	3112	7.6478	10.1922
50068	B15	M-018182- hypothetic	84865	FLJ14397	2179	7.6641	10.1759
50068	B16	M-021916- zinc finger	85446	ZFHX2	2806	16.964	0.876
50068	B17	M-008420- carbonyl re	84869	CBR4	2541	25.58	7.74
50068	B18	M-013728- contactin a	85445	CNTNAP4	3169	13.443	4.397
50068	B19	M-012849- R-spondin	84870	RSPO3	2524	14.937	2.903
50068	B20	M-025887- leucine rich	85444	LRRCC1	2493	15.564	2.276
50068	B21	M-014994- ATP/GTP bi	84871	AGBL4	4152	15.125	2.715
50068	B23	M-014995- zinc finger	84872	ZC3H10	3732	17.658	0.182
50068	C02	M-014982- upregulate	84833	USMG5	6399	25.426	7.586
50068	C04	M-014980- chromosom	84830	C6orf105	4992	21.374	3.534
50068	C05	M-018023- RAB11 fam	84440	RAB11FIP4	3109	16.79	1.05
50068	C06	M-018317- SFT2 doma	84826	SFT2D3	4861	29.521	11.681
50068	C07	M-024802- FERM and	84443	FRMPD3	3003	18.914	1.074
50068	C08	M-014977- hypothetic	84821	MGC13168	4457	21.158	3.318

50068	C09	M-014900-	DOT1-like,	84444	DOT1L	2742	25.237	7.397
50068	C10	M-007945-	interleukin	84818	IL17RC	3943	28.405	10.565
50068	C11	M-026306-	leucine zip	84445	LZTS2	2857	17.396	0.444
50068	C12	M-015928-	thioredoxi	84817	TXNL5	2368	23.775	5.935
50068	C13	M-007090-	synovial ap	84447	SYVN1	1901	14.571	3.269
50068	C14	M-010131-	reticulon 4	84816	RTN4IP1	1858	24.058	6.218
50068	C15	M-014893-	zinc finger	84449	ZNF333	3475	19.885	2.045
50068	C16	M-014976-	phosphatid	84814	PPAPDC3	4178	27.382	9.542
50068	C17	M-007091-	zinc finger	84450	ZNF512	2982	24.95	7.11
50068	C18	M-005065-	phospholip	84812	PLCD4	3308	26.421	8.581
50068	C19	M-021807-	KIAA1799	84455	KIAA1799	2737	12.751	5.089
50068	C20	M-014974-	BUD13 hor	84811	BUD13	4101	28.773	10.933
50068	C21	M-024729-	l(3)mbt-lik	84456	L3MBTL3	4970	19.678	1.838
50068	C23	M-014894-	phytanoyl-	84457	PHYHIPL	7158	19.307	1.467
50068	D02	M-026275-	kinase non	85442	KNDC1	4777	11.304	6.536
50068	D04	M-031725-	dedicator c	85440	DOCK7	5243	19.168	1.328
50068	D05	M-014996-	zinc finger	84874	ZNF514	4935	18.257	0.417
50068	D06	M-016182-	stonin 2	85439	STON2	3783	17.843	0.003
50068	D07	M-014997-	poly (ADP-	84875	PARP10	4196	25.882	8.042
50068	D08	M-018644-	chromosom	85438	C4orf35	5109	13.369	4.471
50068	D09	M-014998-	transmemb	84876	TMEM142	3838	18.343	0.503
50068	D10	M-016700-	zinc finger	85437	ZCRB1	4187	21.4	3.56
50068	D11	M-016698-	zinc finger	84878	ZBTB45	3879	14.23	3.61
50068	D12	M-013668-	Zic family n	85416	ZIC5	3338	16.687	1.153
50068	D13	M-014999-	major facili	84879	MFSD2	4197	17.846	0.006
50068	D14	M-016798-	rhophilin,	85415	RHPN2	3956	8.822	9.018
50068	D15	M-015000-	RNA pseud	84881	RPUSD4	2242	18.064	0.224
50068	D16	M-004231-	solute carri	85414	SLC45A3	2963	8.9436	8.8964
50068	D17	M-016296-	zinc finger,	84885	ZDHHC12	3318	15.793	2.047
50068	D18	M-007450-	solute carri	85413	SLC22A16	4800	16.812	1.028
50068	D19	M-015001-	chromosom	84886	C1orf198	4142	17.335	0.505
50068	D20	M-021297-	chromosom	85411	C6orf114	3797	17.303	0.537
50068	D21	M-006040-	signal pept	84888	SPPL2A	5919	21.524	3.684
50068	D23	M-007614-	solute carri	84889	SLC7A3	4295	13.062	4.778
50068	E02	M-031715-	chromosom	84808	C1orf170	6064	14.726	3.114
50068	E04	M-004227-	T-cell activ	84807	TA-NFKBH	3917	10.85	6.99
50068	E05	M-026303-	ligand depe	84458	LCOR	4265	19.742	1.902
50068	E06	M-007357-	major facili	84804	MFSD9	4906	14.798	3.042
50068	E07	M-024776-	zinc finger,	84460	ZMAT1	4662	13.213	4.627
50068	E08	M-010291-	lung cance	84803	MAG1	3393	11.612	6.228
50068	E09	M-027096-	KIAA1786	84462	KIAA1786	3825	17.307	0.533
50068	E10	M-014971-	chromosom	84798	C19orf48	4068	20.723	2.883
50068	E11	M-014895-	BTB (POZ)	84464	BTBD12	3197	15.734	2.106
50068	E12	M-014970-	hypothetic	84797	MGC13090	2763	15.889	1.951
50068	E13	M-014896-	multiple E	84465	MEGF11	3773	18.659	0.819
50068	E14	M-014969-	hypothetic	84796	MGC13053	2841	11.052	6.788
50068	E15	M-014897-	multiple E	84466	MEGF10	3987	17.532	0.308

50068	E16	M-010185- chromoson	84795	C10orf33	3495	20	2.16
50068	E17	M-018619- fibrillin 3	84467	FBN3	3886	7.4112	10.4288
50068	E18	M-014968- hypothetic	84792	MGC12966	5459	22.074	4.234
50068	E19	M-014898- family with	84498	FAM120B	3410	15.572	2.268
50068	E20	M-014967- chromoson	84791	C1orf97	3938	16.023	1.817
50068	E21	M-022605- spire homo	84501	SPIRE2	3611	12.407	5.433
50068	E23	M-014899- junctophili	84502	JPH4	6112	14.791	3.049
50068	F02	M-018641- naked cutic	85409	NKD2	6386	17.632	0.208
50068	F04	M-018984- naked cutic	85407	NKD1	5084	14.26	3.58
50068	F05	M-015855- chromoson	84890	C10orf22	5378	13.109	4.731
50068	F06	M-019284- ELL associa	85403	EAF1	3978	14.756	3.084
50068	F07	M-015002- zinc finger	84891	ZSCAN10	3525	11.433	6.407
50068	F08	M-008229- regulator o	85397	RGS8	2931	7.7107	10.1293
50068	F09	M-018718- chromoson	84892	C3orf39	3532	10.306	7.534
50068	F10	M-015221- chromoson	85395	C21orf70	3983	18.529	0.689
50068	F11	M-017404- F-box prote	84893	FBXO18	4397	18.558	0.718
50068	F12	M-024559- KIAA1671	85379	CTA-221G9	2995	13.189	4.651
50068	F13	M-018624- leucine rich	84894	LINGO1	3599	14.198	3.642
50068	F14	M-010118- tubulin, ga	85378	TUBGCP6	2996	10.414	7.426
50068	F15	M-017149- family with	84895	FAM73B	3396	13.84	4
50068	F16	M-015102- MICAL-like	85377	MICALL1	2864	17.772	0.068
50068	F17	M-018184- ATPase fam	84896	ATAD1	3847	20.328	2.488
50068	F18	M-024445- KIAA1666	85376	KIAA1666	3939	17.669	0.171
50068	F19	M-015003- transformi	84897	TBRG1	3602	12.021	5.819
50068	F20	M-021516- family with	85369	FAM40A	3735	15.77	2.07
50068	F21	M-015203- plexin dom	84898	PLXDC2	4109	13.921	3.919
50068	F23	M-015004- transmemb	84899	TMTC4	2820	10.177	7.663
50068	G02	M-014966- tubulin, alp	84790	TUBA1C	1643	8.947	8.893
50068	G04	M-017148- zinc finger	84775	ZNF607	4778	11.239	6.601
50068	G05	M-023663- zinc finger	84503	ZNF527	4478	11.791	6.049
50068	G06	M-014961- hypothetic	84773	MGC13010	3990	16.266	1.574
50068	G07	M-010588- GH3 domai	84514	GHDC	3726	20.934	3.094
50068	G08	M-014959- hypothetic	84769	FKSG24	5457	13.304	4.536
50068	G09	M-017291- minichrom	84515	MCM8	4645	23.574	5.734
50068	G10	M-010079- SPRY doma	84767	SPRYD5	4281	12.894	4.946
50068	G11	M-014901- dynactin 5	84516	DCTN5	3394	12.994	4.846
50068	G12	M-014958- EF-hand ca	84766	EFCAB4B	3732	28.778	10.938
50068	G13	M-015387- actin relate	84517	ARPM1	4110	36.131	18.291
50068	G14	M-014957- zinc finger	84765	ZNF577	2557	42.511	24.671
50068	G15	M-014902- cornifelin	84518	CNFN	3098	40.93	23.09
50068	G16	M-015099- hypothetic	84752	MGC4655	4881	18.336	0.496
50068	G17	M-019003- jagunal ho	84522	JAGN1	5054	20.578	2.738
50068	G18	M-008931- fucosyltran	84750	FUT10	2407	15.123	2.717
50068	G19	M-014903- zinc finger	84524	ZC3H8	5940	26.953	9.113
50068	G20	M-014950- hypothetic	84740	MGC10981	5225	29.301	11.461
50068	G21	M-013413- homeodom	84525	HOP	6473	25.29	7.45
50068	G23	M-014904- zinc finger	84527	ZNF559	5858	31.922	14.082

50068	H02	M-017978- zinc finger,	85364	ZCCHC3	4316	30.885	13.045
50068	H04	M-007100- tripartite m	85363	TRIM5	4998	22.909	5.069
50068	H05	M-007097- transmemb	84900	TMEM118	3919	10.487	7.353
50068	H06	M-016827- chromoson	85362	C20orf158	5603	22.702	4.862
50068	H07	M-018625- nuclear fac	84901	NFATC2IP	3648	22.999	5.159
50068	H08	M-013705- DiGeorge s	85359	DGCR6L	4798	40.496	22.656
50068	H09	M-021334- coiled-coil	84902	CCDC123	3738	28.117	10.277
50068	H10	M-031491- KIAA1644 p	85352	KIAA1644	3852	16.822	1.018
50068	H11	M-015005- hypothetic	84903	FLJ14641	3445	17.997	0.157
50068	H12	M-018890- B melanom	85319	BAGE2	3168	11.458	6.382
50068	H13	M-015264- zinc finger	84905	ZNF341	2892	20.678	2.838
50068	H14	M-018894- B melanom	85318	BAGE3	3437	19.319	1.479
50068	H15	M-015007- hypothetic	84908	FLJ14668	3466	13.993	3.847
50068	H16	M-007820- progestin a	85315	PAQR8	4386	22.481	4.641
50068	H17	M-015008- transmemb	84910	TMEM87B	4367	39.707	21.867
50068	H18	M-010401- peptidylpro	85313	PPIL4	3595	20.473	2.633
50068	H19	M-018627- zinc finger	84911	ZNF382	3963	19.404	1.564
50068	H20	M-030807- Fas (TNFRS	85302	FBF1	3771	19.226	1.386
50068	H21	M-007545- solute carri	84912	SLC35B4	6542	34.668	16.828
50068	H23	M-015010- chromoson	84915	C12orf34	4116	11.832	6.008
50068	I02	M-005824- carnosine d	84735	CNDP1	4320	14.398	3.442
50068	I04	M-008357- chromobox	84733	CBX2	5010	24.511	6.671
50068	I05	M-014905- PEPP subfa	84528	PEPP-2	5233	20.485	2.645
50068	I06	M-014948- hypothetic	84730	MGC2452	3442	22.777	4.937
50068	I07	M-014906- chromoson	84529	C15orf41	3586	33.993	16.153
50068	I08	M-014947- splA/ryano	84727	SPSB2	4634	21.515	3.675
50068	I09	M-030175- KIAA1853	84530	KIAA1853	3776	15.89	1.95
50068	I10	M-004320- pleckstrin h	84725	PLEKHA8	4268	18.51	0.67
50068	I11	M-015219- chromoson	84536	C21orf67	4192	27.6	9.76
50068	I12	M-008728- phosphatid	84720	PIGO	4832	27.276	9.436
50068	I13	M-015220- chromoson	84537	C21orf69	4329	26.912	9.072
50068	I14	M-014945- hypothetic	84719	MGC5457	3387	16.74	1.1
50068	I15	M-028015- KIAA1843 p	84540	KIAA1843	4630	33.218	15.378
50068	I16	M-014944- hepatoma-	84717	HDGF2	4864	33.326	15.486
50068	I17	M-014907- kelch repea	84541	KBTBD8	5564	15.421	2.419
50068	I18	M-010682- ovary-spec	84709	OSAP	4438	20.82	2.98
50068	I19	M-022692- KIAA1841	84542	KIAA1841	7098	37.532	19.692
50068	I20	M-014939- brain expre	84707	BEX2	4927	36.432	18.592
50068	I21	M-019126- mitochond	84545	MRPL43	6817	19.818	1.978
50068	I23	M-013578- piggyBac tr	84547	PGBD1	5425	24.848	7.008
50068	J02	M-018800- collagen, ty	85301	COL27A1	6452	17.855	0.015
50068	J04	M-027139- ataxia, cere	85300	ATCAY	5876	24.115	6.275
50068	J05	M-015014- FLT3-intera	84922	FIZ1	5786	12.703	5.137
50068	J06	M-013663- keratin ass	85293	KRTAP3-3	5195	21.713	3.873
50068	J07	M-015015- family with	84923	FAM104A	5742	17.99	0.15
50068	J08	M-030880- keratin ass	85286	KRTAP4-9	4661	21.583	3.743
50068	J09	M-015016- zinc finger	84924	ZNF566	5159	30.781	12.941

50068	J10	M-013656-	keratin ass	85285	KRTAP4-10	4403	18.26	0.42
50068	J11	M-015017-	SPRY doma	84926	SPRYD3	4095	17.631	0.209
50068	J12	M-013323-	histone clu	85236	HIST1H2BK	3628	26.571	8.731
50068	J13	M-015018-	hypothetica	84928	FLJ14803	4391	20.314	2.474
50068	J14	M-013324-	histone clu	85235	HIST1H2AH	4654	21.659	3.819
50068	J15	M-007908-	fibrinogen	84929	FIBCD1	3545	16.812	1.028
50068	J16	M-027562-	chromosom	85028	C1orf79	5913	21.191	3.351
50068	J17	M-015019-	hypothetica	84931	FLJ14816	4366	18.346	0.506
50068	J18	M-007099-	chromosom	85026	C9orf37	5220	23.065	5.225
50068	J19	M-010370-	RAB2B, me	84932	RAB2B	5249	27.262	9.422
50068	J20	M-015052-	transmemb	85025	TMEM60	4809	18.715	0.875
50068	J21	M-015020-	chromosom	84933	C8orf76	4182	16.571	1.269
50068	J23	M-015021-	chromosom	84934	C12orf52	4011	18.724	0.884
50068	K02	M-004173-	glutamic py	84706	GPT2	5480	11.679	6.161
50068	K04	M-014938-	GTP bindin	84705	GTPBP3	6217	12.611	5.229
50068	K05	M-014908-	transmemb	84548	TMEM185A	5654	14.096	3.744
50068	K06	M-013590-	cytochrom	84701	COX4I2	6422	21.52	3.68
50068	K07	M-018620-	RNA bindin	84549	RBM13	5223	17.787	0.053
50068	K08	M-015302-	myosin XVI	84700	MYO18B	6734	20.775	2.935
50068	K09	M-014909-	par-6 partit	84552	PARD6G	4393	17.778	0.062
50068	K10	M-014937-	cAMP resp	84699	CREB3L3	5723	20.129	2.289
50068	K11	M-014910-	chromosom	84553	C6orf168	5009	17.449	0.391
50068	K12	M-014936-	calcyphosin	84698	CAPS2	4120	18.859	1.019
50068	K13	M-013579-	microtubul	84557	MAP1LC3A	4726	22.852	5.012
50068	K14	M-014935-	connexin 6	84694	CX62	5232	20.814	2.974
50068	K15	M-014890-	metallothio	84560	MT4	5064	16.785	1.055
50068	K16	M-016691-	methylmal	84693	MCEE	6878	31.419	13.579
50068	K17	M-007389-	solute carri	84561	SLC12A8	4263	22.191	4.351
50068	K18	M-018621-	coiled-coil	84692	CCDC54	5072	17.764	0.076
50068	K19	M-015672-	lysozyme-li	84569	LYZL1	4668	18.445	0.605
50068	K20	M-014934-	testes deve	84691	NYD-SP18	4674	18.271	0.431
50068	K21	M-014912-	collagen, ty	84570	COL25A1	4744	16.02	1.82
50068	K23	M-014913-	N-acetylglu	84572	GNPTG	5256	16.762	1.078
50068	L02	M-014753-	RALBP1 ass	85021	REPS1	6384	23.606	5.766
50068	L04	M-015051-	chromosom	85019	C18orf45	6009	17.441	0.399
50068	L05	M-016348-	chromosom	84935	C13orf33	5703	19.499	1.659
50068	L06	M-015050-	chromosom	85016	C11orf70	5952	23.068	5.228
50068	L07	M-017961-	zinc finger,	84936	ZFYVE19	5608	16.78	1.06
50068	L08	M-010054-	ubiquitin sp	85015	USP45	5751	13.737	4.103
50068	L09	M-007098-	zinc and rin	84937	ZNRF1	6586	21.546	3.706
50068	L10	M-015049-	transmemb	85014	TMEM141	6808	22.929	5.089
50068	L11	M-005788-	ATG4 autop	84938	ATG4C	5356	19.529	1.689
50068	L12	M-015048-	transmemb	85013	TMEM128	4198	19.295	1.455
50068	L13	M-019083-	melanoma	84939	MUM1	4275	10.713	7.127
50068	L14	M-018635-	transcriptio	85012	TCEAL3	5015	12.203	5.637
50068	L15	M-015022-	coronin 6	84940	CORO6	5935	10.059	7.781
50068	L16	M-008968-	alanine-gly	85007	AGXT2L2	6678	21.114	3.274

50068	L17	M-015023- hematopoi	84941	HSH2D	6846	19.793	1.953
50068	L18	M-021293- chromosor	85006	C21orf124	7225	36.028	18.188
50068	L19	M-015024- WD repeat	84942	WDR73	6738	30.84	13
50068	L20	M-008204- RAS-like, es	85004	RERG	5839	18.702	0.862
50068	L21	M-015025- maelstrom	84944	MAEL	5871	28.496	10.656
50068	L23	M-005874- abhydrolas	84945	ABHD13	4880	16.209	1.631
50068	M02	M-016751- spermatog	84690	SPATA22	6534	22.391	4.551
50068	M04	M-017476- chromosor	84688	C9orf24	6993	24.124	6.284
50068	M05	M-010681- par-6 partit	84612	PARD6B	5728	26.816	8.976
50068	M06	M-014931- histidine tr	84681	HINT2	6759	18.923	1.083
50068	M07	M-014914- zinc finger	84614	ZBTB37	7461	27.409	9.569
50068	M08	M-009753- 1-aminocy	84680	PHACS	5365	29.152	11.312
50068	M09	M-009895- 5'-nucleoti	84618	NT5C1A	7148	22.552	4.712
50068	M10	M-007627- solute carri	84679	SLC9A7	5712	22.689	4.849
50068	M11	M-019064- zinc finger,	84619	ZGPAT	5628	25.675	7.835
50068	M12	M-014930- F-box and l	84678	FBXL10	5006	16.6	1.24
50068	M13	M-008402- ST6 beta-ga	84620	ST6GAL2	4371	33.608	15.768
50068	M14	M-014929- Down synd	84677	DSCR8	5387	15.797	2.043
50068	M15	M-023003- zinc finger	84622	ZNF594	6064	15.765	2.075
50068	M16	M-007093- tripartite m	84676	TRIM63	6570	27.656	9.816
50068	M17	M-021455- kin of IRRE	84623	KIRREL3	6445	29.682	11.842
50068	M18	M-007092- tripartite m	84675	TRIM55	5931	22.189	4.349
50068	M19	M-024901- fibronectin	84624	FNDC1	6700	16.104	1.736
50068	M20	M-006080- ubiquitin sp	84669	USP32	7550	24.49	6.65
50068	M21	M-025366- KRAB-A dor	84626	KRBA1	5935	17.27	0.57
50068	M23	M-022608- zinc finger	84627	ZNF469	4347	29.377	11.537
50068	N02	M-015044- ubiquitin-li	84993	UBL7	3635	8.5282	9.3118
50068	N04	M-015043- phosphatid	84992	PIGY	5080	17.598	0.242
50068	N05	M-016354- LTV1 homo	84946	LTV1	5216	10.429	7.411
50068	N06	M-005158- RNA bindin	84991	RBM17	6231	23.11	5.27
50068	N07	M-015026- serine activ	84947	SERAC1	5564	14.252	3.588
50068	N08	M-015041- chromosor	84987	C12orf62	4566	15.506	2.334
50068	N09	M-013595- tigger trans	84948	TIGD5	5705	10.552	7.288
50068	N10	M-018322- Rho GTPase	84986	ARHGAP19	4210	15.891	1.949
50068	N11	M-014833- PRP38 pre-	84950	PRPF38A	3295	13.536	4.304
50068	N12	M-015040- family with	84985	FAM83A	2807	13.894	3.946
50068	N13	M-010589- tensin 4	84951	TNS4	3607	21.431	3.591
50068	N14	M-015039- chromosor	84984	C3orf34	4021	20.095	2.255
50068	N15	M-019002- cingulin-like	84952	CGNL1	4348	13.408	4.432
50068	N16	M-015036- FERM dom	84978	FRMD5	4808	15.807	2.033
50068	N17	M-015027- MICAL C-te	84953	MICALCL	4808	14.621	3.219
50068	N18	M-013596- dispatched	84976	DISP1	4597	18.73	0.89
50068	N19	M-018630- MPN doma	84954	MPND	3763	12.463	5.377
50068	N20	M-018634- major facili	84975	MFSD5	4286	16.356	1.484
50068	N21	M-018185- NudC doma	84955	NUDCD1	4740	10.401	7.439
50068	N23	M-010429- synaptotag	84958	SYTL1	4074	16.2	1.64
50068	O02	M-017147- family with	84668	FAM126A	6487	19.3	1.46

50068	O04	M-014927- resistin like	84666	RETNLB	4448	19.852	2.012
50068	O05	M-021292- netrin G2	84628	NTNG2	5446	32.372	14.532
50068	O06	M-010902- myopalladi	84665	MYPN	4230	13.877	3.963
50068	O07	M-014915- SLIT and N	84631	SLITRK2	5579	16.257	1.583
50068	O08	M-014926- chondroiti	84664	CSPG4LYP2	5318	17.356	0.484
50068	O09	M-014917- actin filame	84632	AFAP1L2	4501	19.951	2.111
50068	O10	M-014925- chromoso	84663	CYorf15B	4747	29.492	11.652
50068	O11	M-007954- interleukin	84639	IL1F10	4070	12.26	5.58
50068	O12	M-014923- dpy-30-like	84661	HDPY-30	2691	11.334	6.506
50068	O13	M-014918- hippocamp	84641	HIATL1	4280	17.967	0.127
50068	O14	M-018085- coiled-coil	84660	CCDC62	4506	26.254	8.414
50068	O15	M-016823- chromoso	84645	C22orf23	2679	15.416	2.424
50068	O16	M-018193- ribonuclea	84659	RNASE7	4789	20.422	2.582
50068	O17	M-010290- phospholip	84647	PLA2G12B	4562	16.616	1.224
50068	O18	M-008332- cytokine-li	84656	N-PAC	4559	23.448	5.608
50068	O19	M-009333- diacylglyce	84649	DGAT2	4798	22.072	4.232
50068	O20	M-015845- spermatog	84654	SPZ1	5248	22.999	5.159
50068	O21	M-014920- emopamil	84650	EBPL	5787	29.031	11.191
50068	O23	M-014921- serine pept	84651	SPINK7	4112	10.263	7.577
50068	P02	M-015034- transmem	84972	TMEM137	3997	15.387	2.453
50068	P04	M-005790- ATG4 auto	84971	ATG4D	3096	15.536	2.304
50068	P05	M-008533- Cbl-interac	84959	STS-1	5199	25.851	8.011
50068	P06	M-015033- chromoso	84970	C1orf94	4233	6.7801	11.0599
50068	P07	M-014951- hypothetic	84744	MGC10701	4802	21.095	3.255
50068	P08	M-015032- TOX high	84969	TOX2	4918	20.13	2.29
50068	P09	M-014949- chromoso	84734	C1orf90	4669	9.9807	7.8593
50068	P10	M-018632- paraneopla	84968	PNMA6A	4735	15.692	2.148
50068	P11	M-014972- chromoso	84800	C14orf151	4206	16.548	1.292
50068	P12	M-015031- LSM10, U7	84967	LSM10	2565	14.035	3.805
50068	P13	M-014933- MS4A13 pr	84689	NYD-SP21	3002	14.091	3.749
50068	P14	M-018631- immunogl	84966	IGSF21	4884	15.766	2.074
50068	P15	M-013582- keratin ass	84616	KRTAP4-4	5657	17.147	0.693
50068	P16	M-015030- alkB, alkyla	84964	ALKBH6	3331	13.029	4.811
50068	P17	M-008567- ARD1 hom	84779	ARD1B	4601	13.932	3.908
50068	P18	M-021473- jub, ajuba	84962	JUB	4998	18.988	1.148
50068	P19	M-014919- late cornifi	84648	LCE3D	3799	10.74	7.1
50068	P20	M-018319- KIAA1984	84960	KIAA1984	5018	10.701	7.139
50068	P21	M-021300- hematolog	90861	HN1L	3348	7.4074	10.4326
50068	P23	M-017713- splA/ryano	90864	SPSB3	3401	7.1744	10.6656
				MAD	4315.5	17.8445	3.9135
				3MAD			11.7405
				MADc			5.79198
50068	C22				3795	57.444	
50068	D22				5112	49.237	
50068	E22				3110	45.691	
50068	F22				4071	52.395	
				mn	4022	51.19175	

					sd	831.4193	4.987242
50068	G22					2552	17.712
50068	H22					2814	13.504
50068	I22					2795	15.349
50068	J22					3063	15.051
					mn	2890.667	14.63467
					sd	149.5471	0.990458
					3psSD		14.96173
					3ngSD		2.971373
					SumSD		17.9331
					DiffMn		36.55708
					SmovrDiff		0.490551
					1minus		0.509449

50068	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	1865	11.153
50068	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	1116	16.577
50068	I03	D-001206-	siControl non-targetin			5216	29.812
50068	J03	D-001206-	siControl non-targetin			4799	21.275
50068	K03	D-001600-	siGLO RISC-free siRNA			7825	31.642
50068	L03	D-001600-	siGLO RISC-free siRNA			7160	27.486

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-1.10713	2791	9.4231	11.7269	-1.53251	2379	10.593	5.057	-0.72597
-0.09194	3588	15.608	5.542	-0.72404	3333	15.332	0.318	-0.04498
0.480406	4267	29.201	8.051	1.052794	2773	22.07	6.42	0.92327
-0.96349	2291	16.019	5.131	-0.67032	2044	12.867	2.783	-0.3992
-0.99871	3721	13.41	7.74	-1.01136	2622	11.67	3.98	-0.57121
1.14719	1659	28.149	6.999	0.91528	1206	18.905	3.255	0.468461
1.343323	3373	27.127	5.977	0.781687	2216	20.758	5.108	0.734736
0.031336	3763	31.331	10.181	1.331221	2095	15.179	0.471	-0.06696
-1.0455	3540	17.768	3.382	-0.44169	2514	11.814	3.836	-0.55051
-0.97126	2564	17.551	3.599	-0.47006	1307	5.7383	9.9117	-1.42359
-1.54969	2675	10.579	10.571	-1.38142	2108	7.0209	8.6291	-1.23928
0.299984	2845	22.988	1.838	0.24065	1367	17.922	2.272	0.327204
2.435868	1727	37.695	16.545	2.163103	1740	32.644	16.994	2.44275
0.061896	1666	22.689	1.539	0.201565	1047	15.855	0.205	0.030177
0.154438	1770	16.949	4.201	-0.54875	2396	15.359	0.291	-0.0411
-1.0714	3170	19.842	1.308	-0.17059	1854	18.608	2.958	0.425782
-0.7822	2363	8.7177	12.4323	-1.62472	2364	18.486	2.836	0.408251
1.493876	4622	31.415	10.265	1.342201	3145	30.525	14.875	2.138251
-1.43609	2279	16.323	4.827	-0.63058	1746	7.1019	8.5481	-1.22764
-0.34815	1765	21.643	0.493	0.064836	1217	14.462	1.188	-0.17
-2.09137	3527	7.4001	13.7499	-1.79695	1645	4.2553	11.3947	-1.6367
-0.47384	3363	11.329	9.821	-1.28338	2592	7.4074	8.2426	-1.18374
-1.52388	4825	18.487	2.663	-0.34771	2953	5.4182	10.2318	-1.46959
-0.50026	5042	26.874	5.724	0.748616	2979	13.159	2.491	-0.35724
-1.10782	4792	11.415	9.735	-1.27214	3492	5.7847	9.8653	-1.41692
-1.53801	4808	14.372	6.778	-0.88561	3003	4.0626	11.5874	-1.66439
-1.20658	4040	10.842	10.308	-1.34704	2426	4.5342	11.1158	-1.59662
0.192421	5143	19.561	1.589	-0.20732	2509	15.823	0.173	0.025579
-1.62442	5559	11.333	9.817	-1.28286	2440	8.5246	7.1254	-1.0232
-1.50201	4038	17.112	4.038	-0.52744	1604	4.6135	11.0365	-1.58522
-0.76822	3294	18.124	3.026	-0.39516	2705	9.0943	6.5557	-0.94133
-1.76049	5272	8.5357	12.6143	-1.64851	2645	9.3006	6.3494	-0.91169
-1.75767	4768	12.605	8.545	-1.11658	1998	4.8549	10.7951	-1.55053
-0.15202	5602	19.797	1.353	-0.17647	2434	8.8332	6.8168	-0.97885
1.335554	3855	31.518	10.368	1.355665	2254	15.484	0.166	-0.02314
-0.75993	4965	11.098	10.052	-1.31357	3458	12.637	3.013	-0.43225
-0.50199	3751	18.022	3.128	-0.40849	3150	13.397	2.253	-0.32304
-0.39373	4224	15.625	5.525	-0.72182	2749	18.116	2.466	0.355082
-0.46953	3999	14.229	6.921	-0.9043	3222	7.2315	8.4185	-1.20902
-0.0322	3458	11.828	9.322	-1.21815	2898	12.146	3.504	-0.50281
1.308965	6339	27.386	6.236	0.815543	6651	18.478	2.828	0.407101
0.609377	5834	26.226	5.076	0.663911	4315	12.19	3.46	-0.49648
-0.18206	4411	7.436	13.714	-1.79226	4185	7.0729	8.5771	-1.23181
2.015977	6530	28.959	7.809	1.02116	5006	17.799	2.149	0.309529
0.184652	5413	15.592	5.558	-0.72613	3826	7.9456	7.7044	-1.1064
0.572084	5644	16.867	4.283	-0.55947	2860	8.8112	6.8388	-0.98201

1.276334	4855	28.404	7.254	0.948613	3236	12.824	2.826	-0.40538
1.823297	6276	32.33	11.18	1.461807	2846	19.079	3.429	0.493465
-0.07743	4491	18.637	2.513	-0.3281	2391	7.5282	8.1218	-1.16638
1.023916	4378	16.766	4.384	-0.57267	1965	7.5318	8.1182	-1.16586
-0.56518	2636	11.039	10.111	-1.32129	2057	3.403	12.247	-1.75917
1.072776	2961	25.16	4.01	0.524567	2453	15.369	0.281	-0.03966
0.352297	6284	25.095	3.945	0.51607	3195	11.017	4.633	-0.66504
1.646674	6242	26.29	5.14	0.672277	3368	18.527	2.877	0.414142
1.226783	5384	28.975	7.825	1.023252	2545	10.963	4.687	-0.6728
1.480754	4873	29.633	8.483	1.109264	2151	8.8796	6.7704	-0.97219
-0.87941	3928	18.203	2.947	-0.38483	1846	9.9133	5.7367	-0.82364
1.886833	4892	35.998	14.848	1.941277	3321	21.53	5.88	0.845672
0.316558	6167	30.89	9.74	1.273575	4416	13.859	1.791	-0.25665
0.252504	6391	21.468	0.318	0.04196	4815	7.3936	8.2564	-1.18572
-1.12923	4241	11.884	9.266	-1.21083	3995	13.016	2.634	-0.37779
0.228506	5340	17.397	3.753	-0.49019	4233	14.836	0.814	-0.11625
0.071219	6150	19.22	1.93	-0.25189	4915	18.311	2.661	0.383103
-0.00026	3972	24.119	2.969	0.388491	2532	16.351	0.701	0.101452
1.387695	5603	25.736	4.586	0.59986	3517	17.6	1.95	0.280933
-0.77271	5184	14.969	6.181	-0.80757	3786	9.6144	6.0356	-0.8666
0.086067	5343	22.31	1.16	0.152024	3446	14.364	1.286	-0.18408
0.613866	5464	25.055	3.905	0.510842	3800	18.237	2.587	0.372469
-0.62405	4423	11.282	9.868	-1.28952	2886	9.6327	6.0173	-0.86397
-0.19985	3782	10.656	10.494	-1.37135	2298	13.446	2.204	-0.316
0.000259	5351	19.697	1.453	-0.18954	3271	10.364	5.286	-0.75888
-1.55776	4231	10.778	10.372	-1.3554	2113	4.07	11.58	-1.66332
0.037897	5263	28.102	6.952	0.909136	2903	28.384	12.734	1.83059
-1.53676	5025	8.4179	12.7321	-1.66391	2775	16.072	0.422	0.06136
-0.3542	4612	18.387	2.763	-0.36078	1871	12.026	3.624	-0.52005
-0.17826	6118	17.751	3.399	-0.44391	4325	10.312	5.338	-0.76635
-0.08797	5734	16.097	5.053	-0.66012	3581	10.276	5.374	-0.77152
-0.09349	4988	17.281	3.869	-0.50535	3242	11.258	4.392	-0.63041
0.635275	6158	16.125	5.025	-0.65646	4235	9.1617	6.4883	-0.93165
-0.82571	3562	19.68	1.47	-0.19176	3739	11.688	3.962	-0.56862
-0.53842	5532	15.13	6.02	-0.78652	5768	15.777	0.127	0.018968
-1.20762	5883	18.664	2.486	-0.32457	3900	13.282	2.368	-0.33956
0.327608	4507	26.026	4.876	0.637768	2111	9.0005	6.6495	-0.95481
-0.52599	5294	21.156	0.006	0.001176	4610	10.607	5.043	-0.72396
-0.79964	5524	17.361	3.789	-0.49489	2952	5.7249	9.9251	-1.42551
-1.07606	4947	26.319	5.169	0.676068	2588	13.524	2.126	-0.30479
-0.0928	4348	19.457	1.693	-0.22091	2202	5.8583	9.7917	-1.40635
0.49698	5817	26.319	5.169	0.676068	3733	15.859	0.209	0.030752
-0.36438	4090	17.726	3.424	-0.44718	1165	6.0944	9.5556	-1.37242
-0.33762	4411	18.998	2.152	-0.28091	2739	13.582	2.068	-0.29645
0.140625	4085	17.674	3.476	-0.45398	2536	14.826	0.824	-0.11769
-1.17274	4900	25.918	4.768	0.62365	2484	9.3398	6.3102	-0.90605
-0.05395	5872	30.381	9.231	1.20704	2977	12.832	2.818	-0.40423

0.372153	5653	26.181	5.031	0.658029	3545	14.104	1.546	-0.22144
-1.80134	6017	12.116	9.034	-1.1805	3624	6.181	9.469	-1.35997
0.730234	7247	42.873	21.723	2.839955	3884	21.421	5.771	0.830009
-0.39235	5022	30.307	9.157	1.197367	2485	11.469	4.181	-0.60009
-0.31449	5008	15.495	5.655	-0.73881	3168	7.3232	8.3268	-1.19584
-0.9388	4653	11.799	9.351	-1.22194	3166	9.3809	6.2691	-0.90015
-0.52719	5225	18.316	2.834	-0.37006	4993	11.937	3.713	-0.53284
-0.03669	6112	14.545	6.605	-0.86299	5269	14.557	1.093	-0.15635
-0.61887	3649	8.4681	12.6819	-1.65735	3555	10.352	5.298	-0.7606
-0.8176	5593	16.109	5.041	-0.65855	3895	12.632	3.018	-0.43297
-0.53324	3879	15.88	5.27	-0.68849	3762	19.298	3.648	0.524935
-1.10696	4795	11.366	9.784	-1.27854	3434	10.513	5.137	-0.73747
-1.74963	4267	7.9681	13.1819	-1.72271	2749	33.212	17.562	2.524371
-1.30154	5666	14.137	7.013	-0.91633	2659	12.335	3.315	-0.47565
0.118181	5120	21.133	0.017	-0.00183	3450	24.232	8.582	1.233949
0.123188	4462	15.374	5.776	-0.75463	3210	21.433	5.783	0.831733
-0.80378	3768	20.435	0.715	-0.09307	2619	16.571	0.921	0.133066
-0.62958	4712	26.273	5.123	0.670055	3005	19.834	4.184	0.601958
-1.28289	4472	14.781	6.369	-0.83214	2762	12.925	2.725	-0.39086
-0.69139	5180	16.004	5.146	-0.67228	2856	15.966	0.316	0.046128
-0.01252	5509	32.656	11.506	1.504421	2415	28.033	12.383	1.780151
0.428783	5325	31.174	10.024	1.310698	2203	27.463	11.813	1.698242
-0.0303	5756	37.144	15.994	2.091078	3659	23.23	7.58	1.089962
-1.00544	6548	34.407	13.257	1.733306	3933	26.112	10.462	1.504104
-0.35817	5030	24.453	3.303	0.43215	4220	22.18	6.53	0.939077
-0.6774	4780	18.912	2.238	-0.29215	3488	13.819	1.831	-0.2624
-1.32381	4334	18.182	2.968	-0.38758	2769	14.879	0.771	-0.11007
-1.53618	1799	15.231	5.919	-0.77332	1737	13.644	2.006	-0.28754
-1.14046	4994	24.549	3.399	0.444699	4406	18.112	2.462	0.354507
-1.04515	4222	16.888	4.262	-0.55672	2931	10.577	5.073	-0.72827
-0.27253	3996	22.973	1.823	0.238689	3901	17.355	1.705	0.245726
0.53341	5003	26.484	5.334	0.697636	4246	24.235	8.585	1.23438
-0.78393	5537	15.008	6.142	-0.80247	4281	9.5538	6.0962	-0.8753
0.989213	5254	28.512	7.362	0.96273	4425	28.362	12.712	1.827428
-0.85472	4324	20.999	0.151	-0.01935	3796	10.933	4.717	-0.67711
-0.83745	4415	17.939	3.211	-0.41934	3124	17.19	1.54	0.222016
1.887696	3594	32.053	10.903	1.425599	2365	19.746	4.096	0.589312
3.15721	3851	30.771	9.621	1.258019	4002	42.829	27.179	3.906331
4.258734	3855	42.516	21.366	2.79329	3516	39.59	23.94	3.440888
3.98577	3580	36.089	14.939	1.953172	2757	29.924	14.274	2.051887
0.084859	4637	13.155	7.995	-1.04469	2701	12.255	3.395	-0.48714
0.471946	4863	12.832	8.318	-1.08691	3175	9.1339	6.5161	-0.93564
-0.46987	2794	12.527	8.623	-1.12678	1763	12.762	2.888	-0.41429
1.572606	5911	24.784	3.634	0.475417	4577	25.497	9.847	1.415729
1.977994	5433	27.259	6.109	0.798942	4652	25.494	9.844	1.415298
1.285484	5787	21.773	0.623	0.081829	4765	13.473	2.177	-0.31212
2.430516	5355	23.66	2.51	0.328492	5021	18.642	2.992	0.430668

2.251475	4353	26.487	5.337	0.698028	4108	23.856	8.206	1.179918
0.874399	5282	19.084	2.066	-0.26967	4139	11.863	3.787	-0.54347
-1.27029	4450	11.82	9.33	-1.2192	3412	6.5651	9.0849	-1.30478
0.83866	5690	21.933	0.783	0.102743	3386	12.552	3.098	-0.44446
0.889937	4608	26.085	4.935	0.64548	3376	19.668	4.018	0.578104
3.910839	4915	37.396	16.246	2.124019	2936	21.969	6.319	0.908756
1.773573	4658	32.675	11.525	1.506904	3399	18.123	2.473	0.356088
-0.17654	4802	22.074	0.924	0.121175	2922	12.628	3.022	-0.43354
0.02633	3700	28.892	7.742	1.012402	2866	13.608	2.042	-0.29272
-1.10265	2425	9.6907	11.4593	-1.49753	1966	13.123	2.527	-0.36241
0.489211	3509	21.317	0.167	0.022222	2575	14.019	1.631	-0.23366
0.254576	3273	16.926	4.224	-0.55176	2552	17.751	2.101	0.302631
-0.66497	4903	18.621	2.529	-0.33019	2750	6.7636	8.8864	-1.27625
0.800503	4537	20.013	1.137	-0.14823	4381	23.944	8.294	1.192563
3.774616	4028	36.346	15.196	1.986766	3344	34.898	19.248	2.766649
0.453817	4202	22.323	1.173	0.153723	3445	16.633	0.983	0.141975
0.269252	4266	24.191	3.041	0.397902	3209	16.204	0.554	0.080328
0.238519	3352	19.391	1.759	-0.22954	3286	16.677	1.027	0.148298
2.90462	6422	35.939	14.789	1.933564	5075	27.764	12.114	1.741496
-1.03807	4278	21.996	0.846	0.110979	3550	10.366	5.284	-0.75859
-0.59505	4135	8.2709	12.8791	-1.68312	5032	11.208	4.442	-0.6376
1.150988	4168	11.132	10.018	-1.30913	4215	12.052	3.598	-0.51631
0.455889	5090	23.438	2.288	0.299472	4341	21.308	5.658	0.813771
0.851609	2949	18.481	2.669	-0.34849	2820	16.064	0.414	0.06021
2.788079	3636	33.196	12.046	1.575008	2990	24.615	8.965	1.288986
0.633721	4110	15.669	5.481	-0.71607	4112	15.856	0.206	0.030321
-0.33745	2277	11.638	9.512	-1.24299	2560	12.031	3.619	-0.51933
0.1149	3371	11.718	9.432	-1.23253	3459	11.593	4.057	-0.58227
1.684312	3810	20.709	0.441	-0.05725	3257	16.181	0.531	0.077023
1.628372	4317	20.778	0.372	-0.04823	3080	10.325	5.325	-0.76448
1.565527	4024	25.298	4.148	0.542606	3046	14.741	0.909	-0.1299
-0.19069	3572	17.777	3.373	-0.44052	2521	11.027	4.623	-0.6636
2.654274	4346	23.608	2.458	0.321694	4337	18.285	2.635	0.379367
2.67292	4615	37.27	16.12	2.107549	4042	25.383	9.733	1.399347
-0.41842	3868	10.367	10.783	-1.40913	4619	13.877	1.773	-0.25406
0.513728	3646	20.269	0.881	-0.11477	3324	11.221	4.429	-0.63573
3.399097	5339	35.4	14.25	1.863108	5363	24.688	9.038	1.299476
3.209179	3837	41.621	20.471	2.676298	3320	33.404	17.754	2.551962
0.34073	5886	20.557	0.593	-0.07712	5575	16.52	0.87	0.125737
1.209172	5662	31.349	10.199	1.333574	4611	13.121	2.529	-0.3627
0.001813	5596	16.994	4.156	-0.54287	5994	12.045	3.605	-0.51732
1.082618	5297	20.313	0.837	-0.10902	5152	20.613	4.963	0.7139
-0.88769	4889	10.697	10.453	-1.36599	5850	7.7607	7.8893	-1.13297
0.667906	5043	21.138	0.012	-0.00118	5633	12.604	3.046	-0.43699
0.025121	3817	15.562	5.588	-0.73005	4029	15.115	0.535	-0.07616
0.645461	2914	18.257	2.893	-0.37777	4154	14.54	1.11	-0.15879
2.233519	5002	31.847	10.697	1.398671	5236	25.497	9.847	1.415729

0.071737	5111	22.031	0.881	0.115554	4085	12.95	2.7	-0.38727
-0.03686	3865	28.176	7.026	0.918809	4230	15.626	0.024	-0.00273
1.506652	4261	27.224	6.074	0.794367	3009	17.381	1.731	0.249463
0.426365	2687	14.738	6.412	-0.83776	3010	15.814	0.164	0.024285
0.658583	3949	20.815	0.335	-0.0434	3089	16.057	0.407	0.059204
-0.17826	3637	21.941	0.791	0.103789	2768	8.9234	6.7266	-0.96589
0.577782	4970	26.439	5.289	0.691754	4438	13.384	2.266	-0.3249
0.086585	2677	17.706	3.444	-0.4498	2216	9.6119	6.0381	-0.86695
0.901333	5440	25.018	3.868	0.506005	4283	15.293	0.357	-0.05058
1.625955	5512	34.888	13.738	1.796181	4306	17.812	2.162	0.311397
0.150294	4756	21.573	0.423	0.055685	4638	13.583	2.067	-0.29631
-0.21987	5033	19.571	1.579	-0.20601	4688	17.129	1.479	0.21325
0.151848	4570	21.532	0.382	0.050326	4677	14.304	1.346	-0.1927
-1.06449	5971	13.7	7.45	-0.97345	5365	15.676	0.026	0.004455
-0.90358	5541	23.678	2.528	0.330844	4807	15.061	0.589	-0.08392
-0.64719	4583	11.804	9.346	-1.22129	4485	13.579	2.071	-0.29688
0.634584	5620	23.185	2.035	0.266401	5402	21.177	5.527	0.794946
-0.00993	4334	23.719	2.569	0.336204	4991	26.107	10.457	1.503386
0.505958	4374	22.908	1.758	0.230192	4197	29.14	13.49	1.939227
-0.01148	3081	20.513	0.637	-0.08287	4133	23.179	7.529	1.082633
0.394425	4034	17.179	3.971	-0.51868	3422	14.319	1.331	-0.19055
-0.06828	3676	14.771	6.379	-0.83345	2892	12.31	3.34	-0.47924
0.175156	3347	13.027	8.123	-1.06142	3291	18.961	3.311	0.476508
0.864558	4308	21.936	0.786	0.103136	4160	20.793	5.143	0.739766
0.512692	4145	23.498	2.348	0.307315	3826	25.536	9.886	1.421333
-0.18293	5044	14.433	6.717	-0.87763	4380	13.516	2.134	-0.30594
2.343672	4713	24.592	3.442	0.45032	4900	24.306	8.656	1.244583
0.750434	4400	23.409	2.259	0.295682	4066	29.267	13.617	1.957476
-0.0139	5983	18.185	2.965	-0.38718	4662	20.957	5.307	0.763332
0.103678	5694	25.501	4.351	0.569141	4227	22.167	6.517	0.937209
0.073636	5700	25.386	4.236	0.554109	6010	30.083	14.433	2.074735
-0.315	6683	31.767	10.617	1.388214	5476	27.52	11.87	1.706433
-0.1869	6627	25.502	4.352	0.569272	5693	33.462	17.812	2.560296
0.994738	5287	16.89	4.26	-0.55646	3741	15.664	0.014	0.00273
-0.06967	5006	31.662	10.512	1.374488	4331	15.008	0.642	-0.09154
0.285654	5387	26.62	5.47	0.715414	5328	23.236	7.586	1.090824
0.90185	7586	39.388	18.238	2.384407	5672	23.431	7.781	1.118845
-0.18379	5736	29.027	7.877	1.030049	5507	17.941	2.291	0.329934
-0.70917	4075	21.89	0.74	0.097123	4104	19.274	3.624	0.521486
0.639073	5768	26.907	5.757	0.752929	6100	26.18	10.53	1.513876
0.877852	4429	30.413	9.263	1.211223	4176	20.761	5.111	0.735167
0.290833	3694	28.018	6.868	0.898156	3037	26.605	10.955	1.574948
0.250432	3193	32.289	11.139	1.456448	2346	22.762	7.112	1.02271
-1.23127	3507	17.308	3.842	-0.50182	3127	13.751	1.899	-0.27217
-0.97402	4842	25.671	4.521	0.591363	3334	18.836	3.186	0.458546
-1.34419	3519	18.272	2.878	-0.37581	3403	9.4916	6.1584	-0.88424
0.564487	4186	26.015	4.865	0.63633	2899	19.041	3.391	0.488004

0.336413	4885	23.378	2.228	0.291629	4265	13.669	1.981	-0.28395
3.139427	5311	38.223	17.073	2.232122	5480	25.42	9.77	1.404664
2.243706	5907	46.927	25.777	3.369882	4609	28.358	12.708	1.826853
0.14805	4794	20.588	0.562	-0.07307	4799	20.525	4.875	0.701254
1.839008	4761	39.719	18.569	2.427674	3973	31.311	15.661	2.251198
-0.28237	5820	28.557	7.407	0.968612	4099	22.835	7.185	1.0332
0.784965	6747	16.318	4.832	-0.63123	5480	20.693	5.043	0.725396
1.084172	5872	13.692	7.458	-0.97449	5662	18.792	3.142	0.452223
1.548952	4669	26.023	4.873	0.637376	5517	26.518	10.868	1.562446
0.186206	5382	14.363	6.787	-0.88678	6505	22.183	6.533	0.939508
1.651335	5322	28.504	7.354	0.961684	6759	28.037	12.387	1.780726
1.952268	3651	28.129	6.979	0.912665	4032	21.131	5.481	0.788336
0.812762	4372	23.102	1.952	0.255552	7181	23.2	7.55	1.085651
0.836415	4267	26.107	4.957	0.648356	5070	17.692	2.042	0.294153
1.351956	3387	25.391	4.241	0.554763	3940	26.218	10.568	1.519336
-0.21487	3622	17.145	4.005	-0.52313	4424	11.641	4.009	-0.57537
2.721608	4984	35.152	14.002	1.83069	3936	34.223	18.573	2.669652
-0.35351	3659	12.189	8.961	-1.17096	5332	21.099	5.449	0.783738
-0.35903	4804	24.063	2.913	0.38117	5815	22.442	6.792	0.976726
1.69398	5334	36.314	15.164	1.982583	5581	34.653	19.003	2.731443
2.043774	4213	37.171	16.021	2.094608	3842	25.95	10.3	1.480825
0.750089	4601	27.255	6.105	0.798419	5853	29.421	13.771	1.979606
-0.3005	5599	24.683	3.533	0.462215	5900	20.898	5.248	0.754854
1.147362	6557	22.236	1.086	0.142351	5351	18.875	3.225	0.46415
-0.09919	4505	22.486	1.336	0.17503	4732	27.663	12.013	1.726982
1.991115	5500	47.891	26.741	3.495893	3341	36.636	20.986	3.016399
-1.60848	2689	13.871	7.279	-0.9511	2747	11.722	3.928	-0.56373
-0.04256	4102	23.745	2.595	0.339603	4036	20.738	5.088	0.731862
-1.2803	3906	15.643	5.507	-0.71947	3679	15.901	0.251	0.036787
0.909102	3838	24.831	3.681	0.481561	4271	25.661	10.011	1.439296
-0.62025	4091	18.04	3.11	-0.40614	5185	16.066	0.416	0.060498
-0.40375	2918	15.113	6.037	-0.78875	4208	18.227	2.577	0.371032
-1.25907	2843	15.406	5.744	-0.75045	3142	7.9885	7.6615	-1.10024
-0.33728	2857	16.556	4.594	-0.60012	3466	21.091	5.441	0.782588
-0.74387	2741	25.392	4.242	0.554893	3291	22.03	6.38	0.917522
-0.68206	3324	24.699	3.549	0.464306	2832	16.102	0.452	0.065671
0.619218	2974	18.931	2.219	-0.28967	2599	20.777	5.127	0.737467
0.388555	2922	24.333	3.183	0.416464	3845	26.606	10.956	1.575092
-0.76597	2886	12.301	8.849	-1.15632	3753	14.762	0.888	-0.12689
-0.35178	3576	19.855	1.295	-0.16889	4808	12.646	3.004	-0.43096
-0.55655	3177	17.343	3.807	-0.49725	4255	15.182	0.468	-0.06653
0.152884	4547	25.005	3.855	0.504306	5862	20.914	5.264	0.757153
-0.92913	3501	23.308	2.158	0.282479	4330	17.136	1.486	0.214256
-0.25699	4434	29.883	8.733	1.141943	5474	23.073	7.423	1.067401
-1.28514	5858	20.314	0.836	-0.10889	5484	11.834	3.816	-0.54764
-0.28393	4956	20.682	0.468	-0.06078	3543	8.3545	7.2955	-1.04764
0.251296	6019	26.499	5.349	0.699597	5130	16.043	0.393	0.057192

0.3466	3888	23.148	1.998	0.261565	3876	18.395	2.745	0.395174
2.50821	5286	41.6	20.45	2.673553	5620	36.335	20.685	2.973145
-0.685	4319	19.31	1.84	-0.24013	5223	14.742	0.908	-0.12976
-0.27409	4004	24.351	3.201	0.418817	5683	19.338	3.688	0.530683
-0.08434	6002	25.392	4.242	0.554893	6755	23.849	8.199	1.178912
0.363693	3957	27.496	6.346	0.829922	5403	22.932	7.282	1.047139
2.01097	4039	36.692	15.542	2.031994	5107	31.095	15.445	2.220159
-0.96418	4608	13.607	7.543	-0.98561	3873	15.931	0.281	0.041098
-1.12405	4543	21.352	0.202	0.026797	3267	10.162	5.488	-0.78791
0.02115	3512	23.121	1.971	0.258035	4438	23.051	7.401	1.064239
1.451921	4764	28.401	7.251	0.94822	5838	26.122	10.472	1.505541
-0.41929	2462	15.881	5.269	-0.68836	3848	17.646	1.996	0.287543
0.445012	2635	11.917	9.233	-1.20652	4448	12.028	3.622	-0.51976
-0.2121	2951	7.5568	13.5932	-1.77647	3893	10.917	4.733	-0.67941
0.967458	5095	28.479	7.329	0.958416	5661	22.24	6.59	0.947699
0.729889	6265	34.222	13.072	1.709124	6139	28.914	13.264	1.90675
0.889937	5220	16.82	4.33	-0.56561	5571	16.765	1.115	0.160944
1.931378	5836	24.829	3.679	0.4813	6523	28.821	13.171	1.893386
-1.30897	2778	9.1073	12.0427	-1.57379	2496	8.8942	6.7558	-0.97009
-0.42429	4089	21.668	0.518	0.068104	3399	11.68	3.97	-0.56977
-0.39857	2677	15.951	5.199	-0.67921	1982	9.7376	5.9124	-0.84889
1.382342	3141	21.426	0.276	0.03647	3465	14.949	0.701	-0.10001
-1.9103	2487	25.613	4.463	0.583782	2569	8.4469	7.2031	-1.03436
0.561207	3531	32.767	11.617	1.51893	4676	17.151	1.501	0.216412
0.394597	1781	30.657	9.507	1.243118	2454	17.441	1.791	0.258085
-1.3577	2920	18.288	2.862	-0.37372	4198	14.293	1.357	-0.19428
-0.37163	2929	22.636	1.486	0.194637	4090	13.056	2.594	-0.37204
-0.22384	3258	23.91	2.76	0.361171	3762	8.6922	6.9578	-0.99911
-0.65772	2202	17.666	3.484	-0.45503	2386	14.669	0.981	-0.14025
-0.64805	1633	15.309	5.841	-0.76313	2377	7.825	7.825	-1.12373
-0.35886	2689	22.797	1.647	0.215683	4270	15.691	0.041	0.00661
-0.12043	2506	31.524	10.374	1.356449	4103	18.157	2.507	0.360973
-0.83141	2234	15.712	5.438	-0.71045	4299	17.283	1.633	0.23538
-0.6755	2743	13.38	7.77	-1.01528	3406	9.7181	5.9319	-0.85169
0.197428	2175	10.529	10.621	-1.38795	4172	12.224	3.426	-0.4916
-1.22661	1717	11.415	9.735	-1.27214	2578	7.8743	7.7757	-1.11665
-1.23334	2861	15.904	5.246	-0.68535	4293	9.4107	6.2393	-0.89587
-1.80199	2421	13.383	7.767	-1.01489	2333	11.316	4.334	-0.62208
-1.84222	2727	14.925	6.225	-0.81332	1810	5.3591	10.2909	-1.47808
	4426	21.147	5.169		3552.5	15.645	4.702	
			15.507				14.106	
			7.65012				6.95896	
4857	67.49		5197	52.492				
6058	60.961		6295	54.678				
5043	55.027		4878	47.294				
6133	62.791		4002	52.774				
5522.75	61.56725		5093	51.8095				

666.4035	5.154899	947.299	3.163021
2872	11.281	2779	14.969
3044	19.941	2589	16.222
2230	19.91	2379	9.3317
3021	22.509	3113	8.9303
2765	20.78667	2693.667	11.49467
463.4663	1.491665	378.0282	4.098907
	0		9.489062
	4.474995		12.29672
	4.474995		21.78578
	40.78058		40.31483
	0.109733		0.540391
	0.890267		0.459609

1211	18.91	971	19.67
582	18.213	365	20.822
4062	20.162	5180	21.448
4621	18.026	5677	17.685
6972	31.297	5879	32.829
6728	31.436	5642	29.599

y

y
y
y

y

y

y

y

y

y

y

y

y

y

y

y

						cell ct	% inf	AD
50069	A02	M-013676-	keratin ass	85280	KRTAP9-4	3994	14.747	3.463
50069	A04	M-013657-	keratin ass	85287	KRTAP4-7	4567	21.524	3.314
50069	A05	M-007758-	DIX domai	85458	DIXDC1	2555	14.325	3.885
50069	A06	M-013660-	keratin ass	85289	KRTAP4-5	2843	19.522	1.312
50069	A07	M-029941-	KIAA1731	85459	KIAA1731	3182	14.142	4.068
50069	A08	M-013661-	keratin ass	85291	KRTAP4-2	4038	15.602	2.608
50069	A09	M-024214-	KIAA1729	85460	KIAA1729	2735	22.413	4.203
50069	A10	M-013655-	keratin ass	85282	KRTAP4-14	3910	11.816	6.394
50069	A11	M-023088-	tetratricop	85461	TANC1	4533	21.112	2.902
50069	A12	M-013686-	keratin ass	85294	KRTAP2-4	3207	14.157	4.053
50069	A13	M-024060-	KIAA1727	85462	KIAA1727	3171	13.718	4.492
50069	A14	M-021300-	hematolog	90861	HN1L	3413	9.4931	8.7169
50069	A15	M-026513-	zinc finger	85463	ZC3H12C	4528	15.57	2.64
50069	A16	M-015053-	MSTP150	85027	MST150	4132	22.798	4.588
50069	A17	M-027817-	selenoprot	85465	SELI	6783	29.191	10.981
50069	A18	M-015046-	family with	85002	FAM86B1	2519	16.038	2.172
50069	A19	M-013685-	G elongati	85476	GFM1	3988	9.4534	8.7566
50069	A20	M-015115-	similar to Z	90816	MGC12518	4925	23.005	4.795
50069	A21	M-015062-	scinderin	85477	SCIN	4064	15.723	2.487
50069	A23	M-015072-	coiled-coil	85478	CCDC65	5299	17.324	0.886
50069	B02	M-005789-	ATG4 auto	115201	ATG4A	5371	18.47	0.26
50069	B04	M-016682-	zinc finger	115196	ZNF554	5375	14.195	4.015
50069	B05	M-007111-	synaptotag	94121	SYTL4	5857	11.525	6.685
50069	B06	M-007116-	membrane	115123	MARCH3	5223	13.67	4.54
50069	B07	M-016567-	synaptotag	94122	SYTL5	4239	9.5777	8.6323
50069	B08	M-007495-	solute carri	115111	SLC26A7	5972	24.246	6.036
50069	B09	M-008729-	Rho GTPas	94134	ARHGAP12	5467	13.261	4.949
50069	B10	M-027531-	hypothetic	115110	LOC11511	5666	12.248	5.962
50069	B11	M-018543-	retinitis pig	94137	RP1L1	6882	21.011	2.801
50069	B12	M-015608-	coiled-coil	115098	CCDC124	3840	11.094	7.116
50069	B13	M-008705-	forkhead b	94234	FOXQ1	4716	14.97	3.24
50069	B14	M-015167-	5'-nucleoti	115024	NT5C3L	4667	14.42	3.79
50069	B15	M-031976-	guanine nu	94235	GNG8	5303	8.7309	9.4791
50069	B16	M-007497-	solute carri	115019	SLC26A9	6169	25.677	7.467
50069	B17	M-012473-	H2A histon	94239	H2AFV	6004	31.446	13.236
50069	B18	M-015607-	chromosom	115004	C6orf150	5440	19.485	1.275
50069	B19	M-015094-	epithelial s	94240	EPSTI1	5239	21.378	3.168
50069	B20	M-026194-	zinc finger	114991	ZNF618	5953	27.768	9.558
50069	B21	M-009689-	testis speci	95681	TSGA14	4159	23.299	5.089
50069	B23	M-023053-	hypothetic	96597	LOC96597	6543	18.6	0.39
50069	C02	M-018599-	B melanom	85317	BAGE4	5079	16.992	1.218
50069	C04	M-015975-	SPOC doma	90853	SPOCD1	4316	14.62	3.59
50069	C05	M-018419-	DnaJ (Hsp4	85479	DNAJC5B	4778	22.771	4.561
50069	C06	M-007104-	zinc finger	90850	ZNF598	4441	12.385	5.825
50069	C07	M-013671-	thymic stro	85480	TSLP	5920	12.111	6.099
50069	C08	M-016510-	transcripti	90843	TCEAL8	5708	16.538	1.672

50069	C09	M-032199- scratch hor	85508	SCRT2	6074	15.147	3.063
50069	C10	M-030737- hypothetica	90835	LOC90835	5109	18.497	0.287
50069	C11	M-015063- galanin-like	85569	GALP	4419	9.1423	9.0677
50069	C12	M-025188- zinc finger	90827	ZNF479	2734	6.9861	11.2239
50069	C13	M-015064- GTP-bindin	85865	GTPBP10	4148	14.007	4.203
50069	C14	M-024046- hypothetica	90826	LOC90826	5573	9.4384	8.7716
50069	C15	M-019454- polyribonu	87178	PNPT1	5065	10.563	7.647
50069	C16	M-016425- transmemb	90809	TMEM55B	6095	15.422	2.788
50069	C17	M-030187- hypothetica	87769	RP11-151A	4518	15.516	2.694
50069	C18	M-019132- angel homo	90806	ANGEL2	6216	18.356	0.146
50069	C19	M-027120- ankyrin rep	88455	ANKRD13A	4981	14.475	3.735
50069	C20	M-015529- coiled-coil	90799	CCDC45	7684	23.217	5.007
50069	C21	M-015066- CG016	88523	RP11-298P	4609	19.787	1.577
50069	C23	M-015067- chromoson	88745	C6orf153	4185	7.3596	10.8504
50069	D02	M-031729- vasorin	114990	VASN	5072	11.08	7.13
50069	D04	M-008459- WD repeat	114987	WDR31	5926	23.912	5.702
50069	D05	M-013363- hypothetica	96610	LOC96610	4212	13.841	4.369
50069	D06	M-015605- hypothetica	114984	LOC114984	4499	8.9353	9.2747
50069	D07	M-015126- LIM and se	96626	LIMS3	6122	30.154	11.944
50069	D08	M-018176- testis speci	114960	TSGA13	4650	14.538	3.672
50069	D09	M-018116- myosin reg	103910	MRLC2	5112	20.872	2.662
50069	D10	M-016004- Morf4 fami	114932	MRFAP1L1	4882	16.673	1.537
50069	D11	M-004277- egl nine ho	112398	EGLN2	4352	11.673	6.537
50069	D12	M-015604- G protein-c	114928	GPRASP2	4818	25.612	7.402
50069	D13	M-004274- egl nine ho	112399	EGLN3	4465	19.754	1.544
50069	D14	M-015490- chromoson	114926	C8orf40	4319	17.11	1.1
50069	D15	M-015859- proline-rich	112476	PRRT2	5892	21.385	3.175
50069	D16	M-015182- chromoson	114915	C5orf26	6369	34.652	16.442
50069	D17	M-015252- exonucleas	112479	EXOD1	6543	28.962	10.752
50069	D18	M-016683- C1q and tu	114905	C1QTNF7	5683	26.746	8.536
50069	D19	M-008352- spermidine	112483	SAT2	5909	27.467	9.257
50069	D20	M-019178- C1q and tu	114904	C1QTNF6	3789	19.161	0.951
50069	D21	M-021299- chromoson	112487	C14orf126	4222	10.043	8.167
50069	D23	M-015508- chromoson	112495	C6orf51	3706	9.7949	8.4151
50069	E02	M-017154- pygopus ho	90780	PYGO2	6125	11.641	6.569
50069	E04	M-018525- hypothetica	90768	MGC45800	6249	17.459	0.751
50069	E05	M-007101- tripartite m	89122	TRIM4	6681	13.606	4.604
50069	E06	M-017468- P antigen fa	90737	PAGE5	4627	20.705	2.495
50069	E07	M-025312- dpy-19-like	89231	DPY19L1P1	6854	26.218	8.008
50069	E08	M-015525- family with	90736	FAM104B	5516	20.123	1.913
50069	E09	M-015282- testis speci	89765	TSGA2	5257	17.577	0.633
50069	E10	M-005932- SEC11 hom	90701	SEC11C	5396	15.289	2.921
50069	E11	M-008758- serpin pept	89777	SERPINB12	4799	13.315	4.895
50069	E12	M-016556- coiled-coil	90693	CCDC126	3933	17.544	0.666
50069	E13	M-015231- serpin pept	89778	SERPINB11	4062	13.22	4.99
50069	E14	M-007103- leucine rich	90678	LRSAM1	3184	10.867	7.343
50069	E15	M-018172- sialic acid b	89790	SIGLEC10	4417	15.033	3.177

50069	E16	M-015521- chromoson	90668	C14orf121	6553	16.069	2.141
50069	E17	M-015069- galactose-3	89792	GAL3ST3	5484	9.6098	8.6002
50069	E18	M-013720- transducin	90665	TBL1Y	6233	18.193	0.017
50069	E19	M-018348- neuron nav	89795	NAV3	5925	12.338	5.872
50069	E20	M-031256- zinc finger	90649	ZNF486	5555	17.642	0.568
50069	E21	M-017554- neuron nav	89796	NAV1	4479	11.855	6.355
50069	E23	M-006370- neuron nav	89797	NAV2	5296	8.4592	9.7508
50069	F02	M-013893- C1q and tu	114902	C1QTNF5	315	21.587	3.377
50069	F04	M-014749- C1q and tu	114900	C1QTNF4	5505	12.407	5.803
50069	F05	M-013438- sorting nex	112574	SNAG1	3774	11.288	6.922
50069	F06	M-014681- C1q and tu	114899	C1QTNF3	4989	18.541	0.331
50069	F07	M-015566- chromoson	112609	C6orf117	5972	22.019	3.809
50069	F08	M-017146- C1q and tu	114898	C1QTNF2	4923	21.227	3.017
50069	F09	M-015117- RWD doma	112611	RWDD2	4678	16.781	1.429
50069	F10	M-014686- C1q and tu	114897	C1QTNF1	4745	14.9	3.31
50069	F11	M-022934- tubulin, alp	112714	TUBA3E	3556	18.813	0.603
50069	F12	M-008415- oxysterol b	114885	OSBPL11	4675	16.941	1.269
50069	F13	M-008628- retinol deh	112724	RDH13	4432	17.577	0.633
50069	F14	M-009912- oxysterol b	114883	OSBPL9	5323	16.363	1.847
50069	F15	M-007942- interleukin	112744	IL17F	5081	14.682	3.528
50069	F16	M-009508- oxysterol b	114882	OSBPL8	5471	15.281	2.929
50069	F17	M-015150- chromoson	112752	C14orf179	4804	12.261	5.949
50069	F18	M-009234- oxysterol b	114881	OSBPL7	6072	12.368	5.842
50069	F19	M-015151- syntaxin 1E	112755	STX1B2	6989	11.518	6.692
50069	F20	M-009437- oxysterol b	114880	OSBPL6	7304	18.113	0.097
50069	F21	M-016364- chromoson	112770	C1orf85	5896	17.368	0.842
50069	F23	M-015118- keratin 71	112802	KRT71	4372	11.436	6.774
50069	G02	M-019000- zinc finger,	90637	ZFAND2A	217	6.4516	11.7584
50069	G04	M-010256- START dom	90627	STARD13	5216	26.361	8.151
50069	G05	M-024661- protein pho	89801	PPP1R3F	4120	12.354	5.856
50069	G06	M-018887- Lyrm7 hom	90624	LYRM7	4920	6.8293	11.3807
50069	G07	M-006260- potassium	89822	KCNK17	5208	14.689	3.521
50069	G08	M-015506- zinc finger	90594	ZNF439	4013	12.011	6.199
50069	G09	M-010371- FYVE, RhoG	89846	FGD3	4952	14.762	3.448
50069	G10	M-031228- zinc finger	90592	ZNF700	3544	19.47	1.26
50069	G11	M-015107- FCH and dc	89848	FCHSD1	3803	25.585	7.375
50069	G12	M-015824- zinc finger	90589	ZNF625	3227	25.875	7.665
50069	G13	M-026687- ATG16 auto	89849	ATG16L2	4195	22.122	3.912
50069	G14	M-015520- chromoson	90580	C19orf52	4251	12.35	5.86
50069	G15	M-026207- family with	89853	FAM125B	4307	13.838	4.372
50069	G16	M-031235- zinc finger	90576	ZNF799	6619	25.835	7.625
50069	G17	M-015291- kelch-like 6	89857	KLHL6	4122	10.553	7.657
50069	G18	M-015519- coiled-coil	90550	CCDC109A	5314	14.791	3.419
50069	G19	M-015073- leucine zipp	89866	LZTR2	4763	15.893	2.317
50069	G20	M-018310- chromoson	90529	C1orf201	4264	8.0441	10.1659
50069	G21	M-008303- phospholip	89869	PLCZ1	5670	16.049	2.161
50069	G23	M-007102- tripartite m	89870	TRIM15	6103	13.944	4.266

50069	H02	M-009274-	oxysterol b	114879	OSBPL5	6557	18.225	0.015
50069	H04	M-022161-	forkhead-a	114827	FHAD1	4925	26.985	8.775
50069	H05	M-015253-	similar to R	112812	MGC19604	4662	17.503	0.707
50069	H06	M-022995-	SET and MY	114826	SMYD4	5334	22.235	4.025
50069	H07	M-018686-	chromoson	112817	C10orf65	3380	14.675	3.535
50069	H08	M-024302-	MSTP101	114825	MST101	5070	22.11	3.9
50069	H09	M-015254-	WD repeat	112840	WDR89	4158	20.924	2.714
50069	H10	M-015165-	paraneopla	114824	PNMA5	5165	28.771	10.561
50069	H11	M-010373-	chromoson	112849	C14orf149	4606	19.062	0.852
50069	H12	M-015163-	rhophilin, R	114822	RHPN1	3822	19.754	1.544
50069	H13	M-003986-	coiled-coil	112869	CCDC101	4744	21.058	2.848
50069	H14	M-025127-	zinc finger	114821	ZNF452	4234	28.909	10.699
50069	H15	M-007113-	PHD finger	112885	PHF21B	4302	14.179	4.031
50069	H16	M-022194-	KIAA1922 p	114819	KIAA1922	5239	28.288	10.078
50069	H17	M-015152-	vacuolar pr	112936	VPS26B	4858	22.417	4.207
50069	H18	M-030564-	KIAA1920 p	114817	KIAA1920	4110	9.1727	9.0373
50069	H19	M-015575-	galactosida	112937	GLB1L3	4432	16.855	1.355
50069	H20	M-023084-	UDP-N-ace	114805	GALNT13	3936	14.914	3.296
50069	H21	M-015255-	coiled-coil	112942	CCDC104	4953	37.876	19.666
50069	H23	M-015576-	KTI12 hom	112970	KTI12	4507	14.045	4.165
50069	I02	M-016396-	dual oxidas	90527	DUOXA1	4517	13.682	4.528
50069	I04	M-022237-	Src homolo	90525	SHF	3641	15.737	2.473
50069	I05	M-017487-	aquaporin	89872	AQP10	4749	21.331	3.121
50069	I06	M-015915-	chromoson	90523	C6orf142	4749	24.847	6.637
50069	I07	M-007481-	solute carri	89874	SLC25A21	4748	30.455	12.245
50069	I08	M-015128-	Yip1 intera	90522	YIF1B	3840	23.984	5.774
50069	I09	M-015068-	fetal and a	89885	FATE1	2223	10.616	7.594
50069	I10	M-028873-	hypothetica	90520	LOC90520	3763	21.1	2.89
50069	I11	M-015109-	SLAM famil	89886	SLAMF9	3581	11.589	6.621
50069	I12	M-015516-	secernin 2	90507	SCRN2	2515	26.203	7.993
50069	I13	M-023876-	zinc finger	89887	ZNF628	2662	12.81	5.4
50069	I14	M-015114-	leucine rich	90506	LRRC46	3213	9.4927	8.7173
50069	I15	M-015802-	kelch repea	89890	KBTBD6	4440	14.662	3.548
50069	I16	M-027894-	hypothetica	90499	LOC90499	4832	14.694	3.516
50069	I17	M-015136-	WD repeat	89891	WDR34	3828	17.45	0.76
50069	I18	M-015480-	chromoson	90488	C12orf23	5490	16.393	1.817
50069	I19	M-015507-	transmemb	89894	TMEM116	3471	17.862	0.348
50069	I20	M-019412-	zinc finger	90462	ZNF605	6295	24.527	6.317
50069	I21	M-015078-	chromoson	89927	C16orf45	4801	26.453	8.243
50069	I23	M-030307-	papilin, prc	89932	PAPLN	5044	17.843	0.367
50069	J02	M-022965-	ring finger	114804	RNF157	3977	15.615	2.595
50069	J04	M-005905-	myb-like, S	114803	MYSM1	4895	16.65	1.56
50069	J05	M-015222-	RNA pseud	113000	RPUSD1	4238	23.313	5.103
50069	J06	M-015162-	KIAA1913	114801	KIAA1913	4896	17.096	1.114
50069	J07	M-008649-	phospholip	113026	PLCD3	3035	16.639	1.571
50069	J08	M-022684-	coiled-coil	114800	CCDC85A	3812	18.73	0.52
50069	J09	M-015495-	family with	113115	FAM54A	2817	13.028	5.182

50069	J10	M-023413- establishm	114799	ESCO1	4184	29.039	10.829
50069	J11	M-015256- cell divisio	113130	CDCA5	3754	20.325	2.115
50069	J12	M-021768- SLIT and N	114798	SLITRK1	3347	22.289	4.079
50069	J13	M-022014- AHNAK nuc	113146	AHNAK2	3213	17.647	0.563
50069	J14	M-027097- transmem	114795	TMEM132	2736	13.596	4.614
50069	J15	M-015583- serum amy	113174	SAAL1	4194	17	1.21
50069	J16	M-024572- leucine ric	114794	LRRC62	4001	16.371	1.839
50069	J17	M-023899- chromoso	113177	C19orf36	3716	13.025	5.185
50069	J18	M-031993- formin-like	114793	FMNL2	3964	11.251	6.959
50069	J19	M-015226- secretory c	113178	SCAMP4	5577	29.155	10.945
50069	J20	M-015161- kelch-like 3	114792	KLHL32	4891	18.81	0.6
50069	J21	M-015584- hypothetic	113179	LOC11317	6191	21.58	3.37
50069	J23	M-008821- carbohydra	113189	CHST14	3516	12.059	6.151
50069	K02	M-015113- zinc finger	90441	ZNF622	5665	29.214	11.004
50069	K04	M-004393- Bcl2 modif	90427	BMF	3731	26.534	8.324
50069	K05	M-008340- ras homol	89941	RHOT2	6120	32.565	14.355
50069	K06	M-019427- ATPase, H+	90423	ATP6V1E2	5409	27.066	8.856
50069	K07	M-018681- hypothetic	89944	LOC89944	3893	32.802	14.592
50069	K08	M-022219- chromoso	90417	C15orf23	4449	31.31	13.1
50069	K09	M-015510- kinesin ligh	89953	KLC4	1341	57.494	39.284
50069	K10	M-019187- coiled-coil	90416	CCDC32	2801	26.562	8.352
50069	K11	M-017787- chromoso	89958	C9orf140	3980	25.276	7.066
50069	K12	M-003707- multiple co	90411	MCFD2	3439	28.758	10.548
50069	K13	M-031880- ATP bindin	89978	ATPBD4	2145	26.713	8.503
50069	K14	M-017747- intraflagell	90410	IFT20	3354	32.528	14.318
50069	K15	M-023894- midnolin	90007	MIDN	4246	14.908	3.302
50069	K16	M-015245- transmem	90407	TMEM41A	4151	20.381	2.171
50069	K17	M-031877- killer cell in	90011	KIR3DX1	3225	16.372	1.838
50069	K18	M-015244- thyroid hor	90390	THRAP6	4573	19.375	1.165
50069	K19	M-019166- synaptotag	90019	SYT8	5248	24.314	6.104
50069	K20	M-018755- chromoso	90381	C15orf42	5018	28.956	10.746
50069	K21	M-024870- chromoso	90025	C6orf157	5805	24.72	6.51
50069	K23	M-018683- chromoso	90050	C14orf152	5740	19.895	1.685
50069	L02	M-015160- tubulin, ga	114791	TUBGCP5	4244	24.175	5.965
50069	L04	M-007355- solute carri	114789	SLC25A25	3680	24.484	6.274
50069	L05	M-019048- cancer susc	113201	CASC4	3628	24.063	5.853
50069	L06	M-007869- CUB and S	114788	CSMD3	3769	22.818	4.608
50069	L07	M-031238- hypothetic	113230	LOC11323	3278	25.351	7.141
50069	L08	M-015158- G protein r	114787	GPRIN1	3078	30.507	12.297
50069	L09	M-018653- solute carri	113235	SLC46A1	2504	31.03	12.82
50069	L10	M-025942- XK, Kell blo	114786	XKR4	3792	30.301	12.091
50069	L11	M-015586- chromoso	113246	C12orf57	4111	33.155	14.945
50069	L12	M-015157- methyl-Cp	114785	MBD6	3193	29.533	11.323
50069	L13	M-016523- La ribonucl	113251	LARP4	2846	24.596	6.386
50069	L14	M-007868- CUB and S	114784	CSMD2	4057	39.537	21.327
50069	L15	M-025295- glucocortic	113263	GLCCI1	3330	26.547	8.337
50069	L16	M-023922- KIAA1881	114782	KIAA1881	2119	26.239	8.029

50069	L17	M-016385- transmem	113277	TMEM106	4797	33.646	15.436
50069	L18	M-016128- BTB (POZ)	114781	BTBD9	5008	30.671	12.461
50069	L19	M-015119- chromoso	113278	C20orf54	6307	42.302	24.092
50069	L20	M-013421- polycystic	114780	PKD1L2	6574	32.705	14.495
50069	L21	M-016568- similar to e	113386	LOC11338	6264	30.556	12.346
50069	L23	M-016199- SFT2 doma	113402	SFT2D1	5977	29.245	11.035
50069	M02	M-031237- hypothetic	90379	LOC90379	5973	25.264	7.054
50069	M04	M-028185- sterile alph	90378	SAMD1	5855	24.475	6.265
50069	M05	M-015130- coiled-coil	90060	CCDC120	5153	16.845	1.365
50069	M06	M-016393- family with	90362	FAM110B	5371	20.387	2.177
50069	M07	M-013719- lacritin	90070	LACRT	5313	27.649	9.439
50069	M08	M-015082- chromoso	90355	C5orf30	3795	32.358	14.148
50069	M09	M-019334- zinc finger	90075	ZNF30	3932	29.196	10.986
50069	M10	M-015790- ATP bindin	90353	ATPBD3	4348	25.483	7.273
50069	M11	M-016702- pleckstrin	90102	PHLDB2	4286	20.135	1.925
50069	M12	M-022844- fer-1-like 5	90342	FER1L5	3226	23.218	5.008
50069	M13	M-023782- hypothetic	90113	LOC90113	3552	17.23	0.98
50069	M14	M-023812- zinc finger	90333	ZNF468	2988	19.277	1.067
50069	M15	M-029408- hypothetic	90120	LOC90120	3812	34.706	16.496
50069	M16	M-017806- exocyst co	90332	EXOC3L2	4494	29.239	11.029
50069	M17	M-015211- TSR2, 20S	90121	TSR2	5060	32.688	14.478
50069	M18	M-031883- THAP dom	90326	THAP3	4249	19.04	0.83
50069	M19	M-023760- keratin 8 p	90133	KRT8P12	5929	24.287	6.077
50069	M20	M-015139- coiled-coil	90324	CCDC97	6708	38.283	20.073
50069	M21	M-015097- BTB (POZ)	90135	BTBD6	4336	15.383	2.827
50069	M23	M-015297- tetraspani	90139	TSPAN18	5792	27.762	9.552
50069	N02	M-008608- peptidogly	114771	PGLYRP3	5815	16.836	1.374
50069	N04	M-008638- peptidogly	114770	PGLYRP2	3945	21.47	3.26
50069	N05	M-016193- testis expre	113419	TEX261	4938	16.646	1.564
50069	N06	M-004411- caspase-1	114769	COP1	4807	14.416	3.794
50069	N07	M-018278- chromoso	113444	C1orf212	4478	33.318	15.108
50069	N08	M-016960- cytoglobin	114757	CYGB	3778	13.446	4.764
50069	N09	M-008374- arginine de	113451	ADC	4616	26.083	7.873
50069	N10	M-015156- leucine ric	114659	LRRC37B	3678	16.694	1.516
50069	N11	M-015127- transmem	113452	TMEM54	3848	18.997	0.787
50069	N12	M-017103- erythrobla	114625	ERMAP	3929	17.943	0.267
50069	N13	M-022902- tubulin, alp	113457	TUBA3D	3318	29.928	11.718
50069	N14	M-007460- solute carri	114571	SLC22A9	3505	15.578	2.632
50069	N15	M-015379- DNA helica	113510	HEL308	3992	26.478	8.268
50069	N16	M-015155- mal, T-cell	114569	MAL2	3846	18.435	0.225
50069	N17	M-010750- CKLF-like	113540	CMTM1	4301	18.159	0.051
50069	N18	M-020285- EF-hand do	114327	EFHC1	4349	30.306	12.096
50069	N19	M-019422- cytochrom	113612	CYP2U1	4595	28.118	9.908
50069	N20	M-015186- paralemmi	114299	PALM2	4997	17.05	1.16
50069	N21	M-015597- major facili	113655	MFSD3	5610	11.979	6.231
50069	N23	M-008640- alpha tubul	113691	MGC16703	5283	20.803	2.593
50069	O02	M-023807- zinc finger	90321	ZNF766	3606	12.451	5.759

50069	O04	M-023805- zinc finger	90317	ZNF616	4841	13.344	4.866
50069	O05	M-015819- chromoson	90141	C14orf143	3620	9.1436	9.0664
50069	O06	M-015518- tumor prot	90313	TP53I13	4960	8.5484	9.6616
50069	O07	M-015558- heparan su	90161	HS6ST2	3778	15.061	3.149
50069	O08	M-015125- kelch-like 1	90293	KLHL13	4375	19.68	1.47
50069	O09	M-019331- FERM dom	90167	FRMD7	4166	33.581	15.371
50069	O10	M-023593- chromoson	90288	C3orf25	3899	14.773	3.437
50069	O11	M-024190- elastin mic	90187	EMILIN3	3312	17.935	0.275
50069	O12	M-015081- carcinoeml	90273	CEACAM21	2975	12.269	5.941
50069	O13	M-018309- chromoson	90198	C19orf49	2830	13.074	5.136
50069	O14	M-026305- chromoson	90271	C10orf75	2784	20.941	2.731
50069	O15	M-017629- WAP four-c	90199	WFDC8	2795	11.628	6.582
50069	O16	M-018991- family with	90268	FAM105B	3890	12.185	6.025
50069	O17	M-013643- sorting nex	90203	SNX21	3910	25.601	7.391
50069	O18	M-024315- unc-5 hom	90249	UNC5A	4169	26.913	8.703
50069	O19	M-018444- zinc finger,	90204	ZSWIM1	4441	26.12	7.91
50069	O20	M-015515- zinc finger	90233	ZNF551	3648	18.914	0.704
50069	O21	M-018173- urocortin 2	90226	UCN2	3739	16.315	1.895
50069	O23	M-015511- KIAA2013	90231	KIAA2013	3946	21.262	3.052
50069	P02	M-005922- lactamase,	114294	LACTB	3207	17.431	0.779
50069	P04	M-007513- solute carri	114134	SLC2A13	3449	21.398	3.188
50069	P05	M-015600- kelch doma	113730	KLHDC7B	3697	11.388	6.822
50069	P06	M-015190- urocortin 3	114131	UCN3	2388	14.992	3.218
50069	P07	M-015199- outer dens	113746	ODF3	2607	16.532	1.678
50069	P08	M-012974- tripartite m	114088	TRIM9	2153	9.9861	8.2239
50069	P09	M-015601- chromoson	113763	C7orf29	2059	24.575	6.365
50069	P10	M-009383- Williams Be	114049	WBSCR22	1782	14.759	3.451
50069	P11	M-021298- phosphoin	113791	PIK3IP1	1788	17.841	0.369
50069	P12	M-016405- chromoson	114043	C21orf90	1554	20.399	2.189
50069	P13	M-016309- chromoson	113802	C1orf59	2092	28.967	10.757
50069	P14	M-016163- chromoson	114041	C21orf88	2552	18.339	0.129
50069	P15	M-015492- family with	113828	FAM83F	2617	21.207	2.997
50069	P16	M-016161- chromoson	114038	C21orf84	2655	14.237	3.973
50069	P17	M-007540- solute carri	113829	SLC35A4	3179	12.677	5.533
50069	P18	M-016652- chromoson	114036	C21orf82	3303	21.375	3.165
50069	P19	M-015111- zinc finger	113835	ZNF257	3647	28.27	10.06
50069	P20	M-016651- chromoson	114035	C21orf81	3202	18.676	0.466
50069	P21	M-007115- zinc finger,	114026	ZIM3	3689	19.789	1.579
50069	P23	M-018386- target of E	114034	TOE1	4067	26.063	7.853
				mdmdMAD	4396	18.209	4.611
				2MAD			9.222
				3MAD			13.833
				MADc			6.82428
50069	C22				5606	54.299	
50069	D22				5287	53.622	
50069	E22				4391	51.56	
50069	F22				5927	48.541	

					mn	5302.75	52.0055
					sd	661.6103	2.58679
50069	G22					2868	9.4142
50069	H22					2646	23.583
50069	I22					2054	14.849
50069	J22					3468	19.377
					mn	2722.667	19.26967
					sd	710.1108	4.367989
					3psSD		7.76037
					3ngSD		13.10397
					SumSD		20.86434
					DiffMn		32.73583
					SmovrDiff		0.637355
					1minus		0.362645

50069	G03	M-003290-	polo-like ki	5347	PLK1 SMA	674	15.282
50069	H03	M-003290-	polo-like ki	5347	PLK1 SMA	1244	18.971
50069	I03	D-001206-	siControl non-targetin			3465	22.54
50069	J03	D-001206-	siControl non-targetin			4061	20.734
50069	K03	D-001600-	siGLO RISC-free siRNA			6293	40.775
50069	L03	D-001600-	siGLO RISC-free siRNA			4459	28.773

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-0.50731	3531	12.659	1.531	-0.21269	3769	12.337	1.783	-0.26976
0.485766	3532	19.394	5.204	0.720805	3834	17.058	2.938	0.4449
-0.56914	2587	14.65	0.46	0.063272	3575	14.434	0.314	0.047684
0.192401	2015	21.836	7.646	1.059273	2664	14.827	0.707	0.107176
-0.59596	2149	11.354	2.836	-0.39356	4050	16.025	1.905	0.288526
-0.38202	4443	13.842	0.348	-0.04872	5680	14.806	0.686	0.103997
0.616036	2042	22.674	8.484	1.175423	3326	24.654	10.534	1.594767
-0.9368	2809	19.9	5.71	0.790938	3651	15.941	1.821	0.275811
0.425393	2529	13.365	0.825	-0.11483	3982	15.218	1.098	0.166364
-0.59376	1306	10.873	3.317	-0.46023	2572	13.142	0.978	-0.1479
-0.65809	2135	16.066	1.876	0.259534	1916	10.177	3.943	-0.59673
-1.27719	2524	12.48	1.71	-0.2375	3301	11.815	2.305	-0.34877
-0.38671	2614	14.04	0.15	-0.02128	3088	13.925	0.195	-0.02937
0.672452	3094	24.661	10.471	1.450827	4739	20.743	6.623	1.002728
1.609254	4146	33.237	19.047	2.639486	4044	35.163	21.043	3.185599
-0.31813	642	19.315	5.125	0.709855	1517	15.359	1.239	0.187709
-1.28301	1291	16.499	2.309	0.319549	2668	9.2204	4.8996	-0.74154
0.702785	3802	26.854	12.664	1.754783	3381	18.87	4.75	0.719197
-0.36429	3493	13.37	0.82	-0.11414	2398	14.345	0.225	0.034211
-0.12968	3393	16.475	2.285	0.316223	3708	19.714	5.594	0.84696
0.038246	4520	7.7655	6.4245	-0.89094	4314	8.5999	5.5201	-0.83547
-0.58819	3976	6.4889	7.7011	-1.06788	4548	10.884	3.236	-0.48971
-0.97944	4665	7.8242	6.3658	-0.8828	4935	9.1388	4.9812	-0.75389
-0.66513	2811	5.1939	8.9961	-1.24737	4584	14.791	0.671	0.101726
-1.26479	2563	3.3945	10.7955	-1.49677	4524	9.107	5.013	-0.75871
0.884635	3147	10.709	3.481	-0.48296	5170	18.066	3.946	0.597489
-0.72506	2633	8.0137	6.1763	-0.85654	4667	16.456	2.336	0.35377
-0.8735	2831	8.6542	5.5358	-0.76776	4239	6.8648	7.2552	-1.09813
0.410593	3018	10.57	3.62	-0.50223	5216	9.2408	4.8792	-0.73845
-1.0426	2078	4.3792	9.8108	-1.36029	3303	8.4771	5.6429	-0.85406
-0.47463	2152	9.2937	4.8963	-0.67913	4362	12.173	1.947	-0.29458
-0.55522	2257	6.1143	8.0757	-1.1198	4688	8.2978	5.8222	-0.8812
-1.38888	2826	5.5202	8.6698	-1.20215	4919	8.6196	5.5004	-0.83249
1.094328	2683	15.095	0.905	0.124951	6022	21.886	7.766	1.175753
1.939692	3251	18.025	3.835	0.531057	6236	27.037	12.917	1.955501
0.186979	3943	8.8765	5.3135	-0.73695	5767	21.172	7.052	1.067669
0.464371	2757	7.8709	6.3191	-0.87633	4617	13.039	1.081	-0.16349
1.400734	3206	16.687	2.497	0.345607	5438	26.683	12.563	1.901913
0.745866	2305	9.5011	4.6889	-0.65038	4775	22.45	8.33	1.26113
0.057295	3088	4.4689	9.7211	-1.34786	4087	15.317	1.197	0.181351
-0.17833	4350	6.9195	7.2705	-1.0082	5387	12.66	1.46	-0.22086
-0.52592	4187	10.843	3.347	-0.46439	5899	12.731	1.389	-0.21011
0.668495	3847	17.052	2.862	0.396197	5338	18.809	4.689	0.709963
-0.85342	3649	8.4133	5.7767	-0.80115	4438	11.469	2.651	-0.40115
-0.89357	3925	9.4777	4.7123	-0.65362	6137	13.15	0.97	-0.14669
-0.24486	3306	7.4713	6.7187	-0.93172	6370	17.755	3.635	0.55041

-0.44869	3740	10.642	3.548	-0.49225	4958	6.5752	7.5448	-1.14197
0.042202	2918	14.496	0.306	0.041927	4277	12.626	1.494	-0.22601
-1.32859	2218	9.2426	4.9474	-0.68621	4901	8.4269	5.6931	-0.86166
-1.64455	1700	5.6471	8.5429	-1.18456	2237	3.755	10.365	-1.56888
-0.61574	3291	10.665	3.525	-0.48906	3561	5.9253	8.1947	-1.24035
-1.28521	3458	7.9237	6.2663	-0.86901	5499	4.0735	10.0465	-1.52067
-1.12041	3917	14.526	0.336	0.046085	5046	10.186	3.934	-0.59537
-0.40839	3483	9.9627	4.2273	-0.5864	4727	7.8062	6.3138	-0.95562
-0.39462	2816	17.152	2.962	0.410057	3360	9.4643	4.6557	-0.70462
0.021541	2740	22.372	8.182	1.133564	5107	19.561	5.441	0.823799
-0.54716	3171	12.804	1.386	-0.19259	4913	4.193	9.927	-1.50258
0.73385	5014	17.511	3.321	0.459815	5645	11.408	2.712	-0.41039
0.231233	3260	15.583	1.393	0.192589	4346	12.172	1.948	-0.29473
-1.58982	3341	9.4882	4.7018	-0.65217	4092	9.3842	4.7358	-0.71674
-1.04465	3285	2.344	11.846	-1.64238	3410	6.0704	8.0496	-1.21838
0.835693	4131	6.4875	7.7025	-1.06807	3971	13.498	0.622	-0.09401
-0.64007	2766	1.9884	12.2016	-1.69166	3467	8.0185	6.1015	-0.92348
-1.35893	2389	1.9674	12.2226	-1.69457	2689	5.3923	8.7277	-1.32103
1.750368	2695	8.3488	5.8412	-0.81009	4892	16.128	2.008	0.304118
-0.53793	2413	4.2271	9.9629	-1.38137	3940	9.4924	4.6276	-0.70037
0.390224	2596	7.4345	6.7555	-0.93682	3517	12.283	1.837	-0.27793
-0.22508	2748	8.5153	5.6747	-0.78702	3493	13.112	1.008	-0.15244
-0.95776	2197	7.3737	6.8163	-0.94524	2571	5.2898	8.8302	-1.33655
1.084803	2527	13.732	0.458	-0.06397	2802	10.992	3.128	-0.47336
0.226398	2632	12.31	1.88	-0.26106	2513	8.5953	5.5247	-0.83617
-0.16104	2365	8.6258	5.5642	-0.7717	2796	9.9428	4.1772	-0.63218
0.465397	2927	12.231	1.959	-0.27201	3390	9.2625	4.8575	-0.73517
2.409485	3371	21.27	7.08	0.980824	4633	21.304	7.184	1.087651
1.575697	2443	17.806	3.616	0.500703	5597	14.401	0.281	0.042689
1.250974	3625	17.462	3.272	0.453024	4968	19.122	5.002	0.757344
1.356627	3776	21.504	7.314	1.013257	4613	17.126	3.006	0.455194
0.139502	2871	16.998	2.808	0.388712	2241	13.342	0.778	-0.11762
-1.19661	2621	8.1267	6.0633	-0.84088	2396	5.0918	9.0282	-1.36652
-1.23297	2276	7.2496	6.9404	-0.96245	2931	9.9625	4.1575	-0.6292
-0.96245	6596	8.6416	5.5484	-0.76951	6669	14.515	0.395	0.059946
-0.1099	4336	12.2	1.99	-0.27631	5338	18.247	4.127	0.624888
-0.6745	3785	7.9789	6.2111	-0.86136	4960	12.319	1.801	-0.27248
0.365753	2924	9.3365	4.8535	-0.67319	3519	16.397	2.277	0.344839
1.173604	3922	7.3177	6.8723	-0.95301	5226	11.806	2.314	-0.35014
0.280469	2654	8.3271	5.8629	-0.8131	3718	15.573	1.453	0.220104
-0.09261	2808	5.4131	8.7769	-1.21699	5501	11.543	2.577	-0.38995
-0.42788	2879	3.7166	10.4734	-1.45213	5010	9.5409	4.5791	-0.69302
-0.71715	3698	8.3288	5.8612	-0.81286	4365	12.623	1.497	-0.22646
-0.09745	2678	8.8125	5.3775	-0.74582	3858	14.438	0.318	0.04829
-0.73107	2907	6.5015	7.6885	-1.06613	3254	5.8082	8.3118	-1.25807
-1.07586	2379	7.356	6.834	-0.9477	2190	7.9452	6.1748	-0.93458
-0.4654	1838	12.514	1.676	-0.23278	2114	10.88	3.24	-0.49031

-0.31359	2886	8.3853	5.8047	-0.80503	2978	5.7085	8.4115	-1.27316
-1.26009	2678	5.6385	8.5515	-1.18575	3527	6.1242	7.9958	-1.21024
-0.00234	2287	10.057	4.133	-0.57333	3849	9.1712	4.9488	-0.74899
-0.86031	4313	5.0777	9.1123	-1.26348	5606	6.279	7.841	-1.1868
-0.08309	3386	6.4973	7.6927	-1.06672	3625	6.9241	7.1959	-1.08915
-0.93109	3219	7.8906	6.2994	-0.8736	3633	4.4041	9.7159	-1.47062
-1.42869	4857	7.8649	6.3251	-0.87716	3919	5.4606	8.6594	-1.31069
0.494997	4515	5.9801	8.2099	-1.1384	5250	13.905	0.215	-0.03239
-0.8502	4427	6.8218	7.3682	-1.02174	5364	12.136	1.984	-0.30018
-1.01417	2986	3.148	11.042	-1.53094	3969	9.0451	5.0749	-0.76808
0.04865	3711	10.698	3.492	-0.48449	4764	17.38	3.26	0.493644
0.558301	4042	10.762	3.428	-0.47562	5774	20.038	5.918	0.896006
0.442244	2361	15.036	0.846	0.116773	4002	13.643	0.477	-0.07206
-0.20925	3481	10.629	3.561	-0.49405	5308	15.637	1.517	0.229792
-0.48489	2781	12.585	1.605	-0.22294	4877	15.542	1.422	0.215411
0.088508	1840	8.75	5.44	-0.75449	3883	17.615	3.495	0.529217
-0.18581	2819	26.712	12.522	1.735101	3799	21.927	7.807	1.181959
-0.09261	3349	13.138	1.052	-0.1463	4668	18.723	4.603	0.696944
-0.2705	3597	23.964	9.774	1.35422	4508	23.669	9.549	1.44566
-0.51683	3811	20.467	6.277	0.869526	3961	16.259	2.139	0.323949
-0.42906	2376	11.406	2.784	-0.38636	4926	12.87	1.25	-0.18907
-0.87159	2876	9.0403	5.1497	-0.71425	3707	6.2315	7.8885	-1.19399
-0.85591	4082	7.9618	6.2282	-0.86373	6199	12.115	2.005	-0.30336
-0.98047	4773	14.854	0.664	0.091547	6842	13.607	0.513	-0.07751
-0.01407	4874	18.281	4.091	0.56654	6565	18.187	4.067	0.615806
-0.12324	3650	15.205	1.015	0.140197	5168	10.971	3.149	-0.47654
-0.99249	3305	15.976	1.786	0.24706	4900	11.122	2.998	-0.45368
-1.72288	5159	8.8777	5.3123	-0.73679	6159	19.597	5.477	0.829249
1.194558	5045	14.351	0.161	0.02183	5844	24.538	10.418	1.577207
-0.85797	5735	8.5963	5.5937	-0.77579	4829	13.17	0.95	-0.14366
-1.66753	3775	4.4768	9.7132	-1.34676	4217	7.4223	6.6977	-1.01373
-0.51581	3382	7.9834	6.2066	-0.86074	5509	17.553	3.433	0.519832
-0.90823	2678	5.6759	8.5141	-1.18056	3306	8.0157	6.1043	-0.92391
-0.50511	3605	10.485	3.705	-0.51401	5457	16.584	2.464	0.373147
0.184781	3192	11.028	3.162	-0.43875	4510	21.153	7.033	1.064793
1.080847	2937	16.99	2.8	0.387603	4399	24.596	10.476	1.585987
1.123342	3609	17.678	3.488	0.482962	3231	12.69	1.43	-0.21632
0.573394	3641	17.111	2.921	0.404374	4205	26.754	12.634	1.912661
-0.85855	1826	10.843	3.347	-0.46439	2667	10.874	3.246	-0.49122
-0.64051	4045	12.237	1.953	-0.27118	5484	20.04	5.92	0.896309
1.117481	3299	20.37	6.18	0.856081	4587	23.654	9.534	1.443389
-1.12188	3174	17.486	3.296	0.45635	4052	12.858	1.262	-0.19089
-0.50086	2891	13.49	0.7	-0.09751	5110	21.507	7.387	1.118381
-0.33938	3934	20.412	6.222	0.861903	5166	21.796	7.676	1.162129
-1.48952	3048	8.4318	5.7582	-0.79859	4372	6.8847	7.2353	-1.09511
-0.31652	3612	10.05	4.14	-0.5743	5487	16.986	2.866	0.434001
-0.62497	3745	12.31	1.88	-0.26106	4829	13.419	0.701	-0.10596

0.002345	4706	9.7535	4.4365	-0.6154	5512	10.559	3.561	-0.53891
1.285996	4187	22.235	8.045	1.114576	4058	21.168	7.048	1.067063
-0.10345	3969	12.346	1.844	-0.25607	3795	11.542	2.578	-0.3901
0.589952	5290	21.682	7.492	1.037928	5001	16.637	2.517	0.38117
-0.51786	2790	14.91	0.72	0.099309	3087	11.014	3.106	-0.47003
0.571635	4097	18.379	4.189	0.580123	4356	19.467	5.347	0.80957
0.397844	3384	19.09	4.9	0.67867	2707	18.36	4.24	0.641994
1.547709	3825	27.634	13.444	1.862893	3818	29.387	15.267	2.311239
0.124995	3374	13.485	0.705	-0.0982	3550	16.479	2.359	0.357252
0.226398	3497	16.242	2.052	0.283928	2925	13.231	0.889	-0.13442
0.41748	4141	18.305	4.115	0.569866	3058	13.767	0.353	-0.05329
1.567931	3508	21.009	6.819	0.944649	3902	20.964	6.844	1.036182
-0.59054	3543	9.7093	4.4807	-0.62152	2514	8.1941	5.9259	-0.8969
1.476932	3548	22.632	8.442	1.169601	3213	20.728	6.608	1.000457
0.616622	4292	18.756	4.566	0.632376	5185	20.212	6.092	0.922346
-1.32414	4614	6.8054	7.3846	-1.02401	4267	8.2494	5.8706	-0.88853
-0.19841	5081	19.445	5.255	0.727874	4460	13.52	0.6	-0.09068
-0.48283	4674	14.163	0.027	-0.00423	4142	13.496	0.624	-0.09431
2.881916	4108	18.33	4.14	0.573331	3891	20.175	6.055	0.916745
-0.61017	4752	11.174	3.016	-0.41851	4468	7.0949	7.0251	-1.06329
-0.66337	3966	8.825	5.365	-0.74409	3727	11.296	2.824	-0.42734
-0.36224	4127	8.0204	6.1696	-0.85561	2496	9.8157	4.3043	-0.65142
0.457484	5117	13.094	1.096	-0.15239	3946	14.749	0.629	0.095368
0.972703	3160	11.614	2.576	-0.35753	3273	14.36	0.24	0.036482
1.794475	6030	26.75	12.56	1.740368	5767	26.756	12.636	1.912964
0.846243	3529	15.557	1.367	0.188985	2508	19.896	5.776	0.874511
-1.11264	2252	10.036	4.154	-0.57624	1781	7.9169	6.2031	-0.93886
0.423634	3804	17.087	2.897	0.401048	3874	11.9	2.22	-0.33591
-0.97007	3122	15.983	1.793	0.24803	4013	9.7433	4.3767	-0.66238
1.171406	4315	35.782	21.592	2.99223	3512	25.513	11.393	1.724801
-0.79115	3780	14.894	0.704	0.097091	2838	9.0557	5.0643	-0.76647
-1.27725	2794	9.6278	4.5622	-0.63282	2183	7.4668	6.6532	-1.007
-0.51976	3989	22.336	8.146	1.128575	4263	17.429	3.309	0.501061
-0.51507	4125	19.152	4.962	0.687263	3610	9.0582	5.0618	-0.76609
-0.11122	3850	25.143	10.953	1.517633	3727	20.982	6.862	1.038907
-0.26611	4221	16.134	1.944	0.268959	4531	11.653	2.467	-0.3733
-0.05085	3839	23.365	9.175	1.271197	4516	17.139	3.019	0.457162
0.925812	3942	17.047	2.857	0.395504	5591	23.788	9.668	1.463674
1.20804	5159	31.014	16.824	2.331371	5506	31.202	17.082	2.58599
-0.05363	5054	19.509	5.319	0.736744	5589	13.401	0.719	-0.10869
-0.38011	4070	11.966	2.224	-0.30874	5232	12.424	1.696	-0.25659
-0.22845	4125	14.691	0.501	0.068955	5860	14.42	0.3	0.045565
0.747918	4394	19.549	5.359	0.742288	4473	21.999	7.879	1.192859
-0.16309	4995	19.88	5.69	0.788166	5199	12.579	1.541	-0.23312
-0.23006	4398	16.007	1.817	0.251357	3596	11.958	2.162	-0.32713
0.076345	4325	23.052	8.862	1.227815	4159	26.425	12.305	1.862858
-0.7592	2385	13.208	0.982	-0.13659	2256	8.422	5.698	-0.8624

1.586981	3932	28.077	13.887	1.924294	4317	24.183	10.063	1.523468
0.310069	3898	18.368	4.178	0.578598	3972	14.98	0.86	0.130336
0.597865	3697	24.506	10.316	1.429343	4090	16.601	2.481	0.37572
-0.08235	3521	18.83	4.64	0.642633	3283	9.8995	4.2205	-0.63874
-0.67597	3271	12.106	2.084	-0.28933	3295	9.651	4.469	-0.67636
-0.17716	3398	16.745	2.555	0.353646	4977	12.317	1.803	-0.27278
-0.26933	4873	17.279	3.089	0.42766	3927	8.9127	5.2073	-0.78812
-0.75964	4467	20.215	6.025	0.834598	3651	11.531	2.589	-0.39177
-1.01959	4694	11.951	2.239	-0.31082	4622	12.008	2.112	-0.31956
1.603979	5167	25.431	11.241	1.557551	5418	25.083	10.963	1.659708
0.088068	4807	15.394	1.204	0.166393	5433	8.9085	5.2115	-0.78876
0.493972	6546	20.914	6.724	0.931481	6408	26.561	12.441	1.883445
-0.90119	3997	14.086	0.104	-0.0149	4275	7.9298	6.1902	-0.93691
1.612624	6062	16.711	2.521	0.348933	6957	24.594	10.474	1.585684
1.219909	4107	16.265	2.075	0.287116	3858	17.911	3.791	0.574025
2.103665	5468	22.257	8.067	1.117625	6609	25.995	11.875	1.797765
1.297866	7000	19.329	5.139	0.711796	6655	30.098	15.978	2.418869
2.138394	4353	22.49	8.3	1.14992	3924	32.441	18.321	2.773548
1.919763	5401	18.182	3.992	0.552818	4745	23.477	9.357	1.416595
5.756651	4237	14.444	0.254	0.03472	4518	19.699	5.579	0.844689
1.224012	2993	17.374	3.184	0.440827	2611	21.639	7.519	1.138363
1.035567	3823	24.614	10.424	1.444312	4737	26.451	12.331	1.866793
1.545804	3929	11.962	2.228	-0.30929	3505	16.491	2.371	0.359069
1.246139	3302	21.744	7.554	1.046522	2992	22.326	8.206	1.242359
2.098243	4314	29.346	15.156	2.100182	3591	28.209	14.089	2.132916
-0.48371	5357	11.387	2.803	-0.38899	4584	11.933	2.187	-0.33091
0.318275	4837	17.304	3.114	0.431125	5289	14.672	0.552	0.083712
-0.26919	4525	16.331	2.141	0.296264	4108	21.495	7.375	1.116564
0.170861	4499	15.203	1.013	0.13992	4587	16.852	2.732	0.413716
0.8946	5393	21.75	7.56	1.047353	6393	25.387	11.267	1.705727
1.574818	6290	27.727	13.537	1.875783	4443	21.54	7.42	1.123376
0.954093	6211	29.303	15.113	2.094222	5261	28.265	14.145	2.141393
0.247059	3374	10.759	3.431	-0.47603	4730	16.702	2.582	0.391009
0.874231	6128	13.659	0.531	-0.07408	4429	20.095	5.975	0.904635
0.919511	4746	15.908	1.718	0.237635	5482	18.387	4.267	0.646081
0.857819	4411	16.822	2.632	0.364318	4118	16.44	2.32	0.351348
0.675383	5236	15.202	1.012	0.139781	5009	14.554	0.434	0.065849
1.046557	3885	14.646	0.456	0.062718	3894	16.076	1.956	0.296247
1.802095	3481	17.725	3.535	0.489476	3333	18.842	4.722	0.714958
1.878733	4417	20.67	6.48	0.897662	3360	23.601	9.481	1.435366
1.771909	4139	21.261	7.071	0.979577	2869	18.578	4.458	0.674994
2.190121	5334	19.948	5.758	0.797591	3647	13.957	0.163	-0.02452
1.659369	4114	21.609	7.419	1.02781	3217	16.257	2.137	0.323646
0.935923	3545	17.066	2.876	0.398137	3575	24.336	10.216	1.546629
3.125311	4249	29.701	15.511	2.149386	3427	25.328	11.208	1.696796
1.221814	5165	23.621	9.431	1.30668	2994	23.848	9.728	1.472757
1.176681	4541	14.16	0.03	-0.00464	2468	12.196	1.924	-0.2911

2.26207	5343	19.427	5.237	0.725379	4057	16.342	2.222	0.336513
1.826127	5903	25.563	11.373	1.575847	5016	25.299	11.179	1.692406
3.530482	6755	29.474	15.284	2.117923	6586	22.745	8.625	1.305787
2.12418	6403	27.503	13.313	1.844736	4208	8.3413	5.7787	-0.87462
1.809275	4596	17.211	3.021	0.418234	5550	20.018	5.898	0.892979
1.617167	4794	20.129	5.939	0.822678	5200	14.635	0.515	0.078111
1.033809	4587	16.961	2.771	0.383584	6094	20.217	6.097	0.923103
0.918192	4380	26.689	12.499	1.731914	4853	14.733	0.613	0.092946
-0.19987	5306	13.664	0.526	-0.07339	4066	8.0177	6.1023	-0.9236
0.319155	5492	17.298	3.108	0.430293	4612	7.6323	6.4877	-0.98194
1.383296	4794	20.505	6.315	0.874793	4287	7.9776	6.1424	-0.92967
2.073332	3757	17.567	3.377	0.467577	3138	13.512	0.608	-0.09189
1.609987	4736	19.51	5.32	0.736883	3723	10.449	3.671	-0.55556
1.0659	5954	14.075	0.115	-0.01642	3166	14.498	0.378	0.057372
0.282228	4664	22.041	7.851	1.087687	2911	15.802	1.682	0.254769
0.733997	3127	13.24	0.95	-0.13216	2351	9.9532	4.1668	-0.63061
-0.14346	4181	24.731	10.541	1.460529	3876	19.298	5.178	0.783987
0.1565	4139	20.947	6.757	0.936055	2529	11.032	3.088	-0.4673
2.417398	6290	36.105	21.915	3.036999	3865	24.373	10.253	1.55223
1.616288	5469	22.966	8.776	1.215895	4123	19.961	5.841	0.88435
2.121689	7110	38.847	24.657	3.417049	3658	23.018	8.898	1.347113
0.121771	5259	9.5075	4.6825	-0.64949	3113	4.69	9.43	-1.42734
0.890643	6507	28.508	14.318	1.984032	4054	11.569	2.551	-0.38601
2.941556	6229	32.156	17.966	2.489656	5716	26.067	11.947	1.808664
-0.41411	4314	11.59	2.6	-0.36085	2477	9.891	4.229	-0.64003
1.399855	5285	18.127	3.937	0.545195	4363	12.148	1.972	-0.29837
-0.20119	5840	7.7568	6.4332	-0.89215	3674	10.996	3.124	-0.47275
0.477853	3391	9.6432	4.5468	-0.63069	3181	12.575	1.545	-0.23373
-0.22904	3145	10.079	4.111	-0.57028	3100	11.839	2.281	-0.34514
-0.55581	4949	12.346	1.844	-0.25607	3842	17.126	3.006	0.455194
2.214006	6649	36.336	22.146	3.069017	3449	44.042	29.922	4.529684
-0.69795	6983	18.302	4.112	0.56945	3380	21.834	7.714	1.167881
1.153821	5139	12.96	1.23	-0.17097	2744	23.652	9.532	1.443086
-0.222	5186	15.156	0.966	0.133405	3311	17.94	3.82	0.578415
0.11547	3477	11.475	2.715	-0.37679	3297	25.296	11.176	1.691952
-0.03898	4047	9.6615	4.5285	-0.62815	2886	13.652	0.468	-0.07069
1.717251	3799	25.48	11.29	1.564343	2873	28.542	14.422	2.183325
-0.38554	4477	12.598	1.592	-0.22114	2799	21.365	7.245	1.096885
1.211703	5188	25.944	11.754	1.628654	2811	18.179	4.059	0.614595
0.033117	5853	16.385	2.195	0.303748	2684	10.469	3.651	-0.55253
-0.00733	5730	21.675	7.485	1.036958	3853	12.614	1.506	-0.22782
1.772641	5605	28.689	14.499	2.00912	4075	22.994	8.874	1.34348
1.452021	5152	20.031	5.841	0.809095	3771	17.714	3.594	0.544204
-0.16983	6204	19.036	4.846	0.671185	3545	10.437	3.683	-0.55737
-0.91292	5347	8.8274	5.3626	-0.74376	4388	8.9562	5.1638	-0.78153
0.380113	6699	18.809	4.619	0.639722	4424	13.156	0.964	-0.14578
-0.84375	4609	6.5524	7.6376	-1.05908	3766	7.6474	6.4726	-0.97966

-0.7129	4403	18.873	4.683	0.648593	3934	14.743	0.623	0.09446
-1.3284	4081	7.6207	6.5693	-0.91101	3074	7.0592	7.0608	-1.0687
-1.41562	4608	7.5521	6.6379	-0.92052	3002	9.1939	4.9261	-0.74555
-0.46129	3923	10.502	3.688	-0.51165	2760	14.855	0.735	0.111414
0.215554	4844	21.305	7.115	0.985675	3138	18.642	4.522	0.684683
2.252545	5953	35.679	21.489	2.977954	3522	29.302	15.182	2.298372
-0.5035	4795	11.512	2.678	-0.37166	2594	9.4449	4.6751	-0.70756
-0.04015	4435	13.596	0.594	-0.08282	2912	14.08	0.04	-0.0059
-0.87042	3249	9.7876	4.4024	-0.61067	2605	6.9482	7.1718	-1.0855
-0.75246	2410	6.3071	7.8829	-1.09308	1749	9.4911	4.6289	-0.70056
0.400335	3861	21.601	7.411	1.026702	2545	16.267	2.147	0.32516
-0.96435	5196	10.354	3.836	-0.53217	3497	10.695	3.425	-0.51832
-0.88273	5555	11.611	2.579	-0.35794	2559	10.16	3.96	-0.59931
1.083191	4661	16.649	2.459	0.34034	3125	20.448	6.328	0.958071
1.275446	6300	25.222	11.032	1.528583	5390	22.412	8.292	1.255378
1.159243	4289	17.463	3.273	0.453162	4062	9.2073	4.9127	-0.74352
0.103308	4821	14.644	0.454	0.062441	3063	8.0966	6.0234	-0.91166
-0.27754	4065	11.734	2.456	-0.34089	4499	6.7571	7.3629	-1.11443
0.447373	4559	11.735	2.455	-0.34076	3976	12.123	1.997	-0.30215
-0.114	3421	9.734	4.456	-0.6181	5143	13.125	0.995	-0.15047
0.467302	4914	24.522	10.332	1.431561	4421	19.52	5.4	0.817593
-0.99952	4730	5.1797	9.0103	-1.24934	4290	10.816	3.304	-0.5
-0.47141	3749	10.456	3.734	-0.51803	2313	12.668	1.452	-0.21965
-0.24574	3839	12.425	1.765	-0.24512	2180	17.661	3.541	0.536181
-1.20495	3951	14.224	0.034	0.004227	1968	14.787	0.667	0.10112
0.932846	3235	17.434	3.244	0.449143	2313	19.498	5.378	0.814262
-0.50555	2115	7.565	6.625	-0.91873	1796	5.6236	8.4964	-1.28602
-0.05393	3044	7.1616	7.0284	-0.97464	1589	10.006	4.114	-0.62262
0.320913	2699	12.486	1.704	-0.23666	2555	16.751	2.631	0.398427
1.57643	2881	20.514	6.324	0.87604	2032	31.693	17.573	2.660317
0.01905	4240	21.203	7.013	0.971538	2508	19.099	4.979	0.753862
0.439314	3921	10.814	3.376	-0.46841	3353	22.577	8.457	1.280355
-0.58204	3596	11.652	2.538	-0.35226	2781	7.5872	6.5328	-0.98877
-0.81063	4647	8.9735	5.2165	-0.72351	2739	13.91	0.21	-0.03164
0.463932	2723	9.1443	5.0457	-0.69983	2350	17.021	2.901	0.439299
1.474295	4169	30.631	16.441	2.278287	2222	15.887	1.767	0.267636
0.068432	2731	8.312	5.878	-0.81519	2260	10.708	3.412	-0.51635
0.231526	2217	7.7582	6.4318	-0.89195	2390	12.887	1.233	-0.1865
1.150891	2643	15.702	1.512	0.209083	2677	14.158	0.038	0.005904
	3848.5	14.1935	4.8749		3971.5	14.119	4.4635	
			9.7498				8.927	
			14.6247				13.3905	
			7.214852				6.60598	
4755	58.17		5459	55.523				
3679	50.122		3898	37.712				
2800	37.143		4117	41.827				
4459	50.819		4736	44.954				

3923.25	49.0635	4552.5	45.004
875.6302	8.74126	700.8198	7.613988
2372	16.484	3621	11.102
2128	9.1635	2865	11.902
2417	15.143	2800	13.5
2766	12.581	3087	10.528
2437	12.29583	2917.333	11.97667
319.4699	2.999933	150.487	1.487406
	0		22.84196
	8.999798		4.462219
	8.999798		27.30418
	36.76767		33.02733
	0.244775		0.826715
	0.755225		0.173285

828	3.1401	793	12.358
704	16.051	510	18.627
5870	20.102	4558	23.322
3834	21.127	5236	13.999
7130	20.491	7047	33.603
5486	19.96	6458	32.332

y

y

y

y

y

y

y

y

y

y

y

y

					cell ct	% inf	AD
50070	A02	M-008202- Cdk5 and A	91768	CABLES1	3088	10.848	5.732
50070	A04	M-019346- zinc finger	91752	ZNF804A	3887	16.285	0.295
50070	A05	M-015610- potassium	115207	KCTD12	3000	15.933	0.647
50070	A06	M-030308- lin-52 hom	91750	LIN52	3315	11.192	5.388
50070	A07	M-008662- OMA1 hom	115209	OMA1	2102	18.316	1.736
50070	A08	M-010748- KIAA1919	91749	KIAA1919	3631	30.102	13.522
50070	A09	M-015715- DNA-dama	115265	DDIT4L	2915	14.237	2.343
50070	A10	M-031938- chromosom	91748	C14orf43	2616	15.558	1.022
50070	A11	M-009144- RAB42, me	115273	RAB42	2773	14.497	2.083
50070	A12	M-015332- YTH domai	91746	YTHDC1	1880	20.691	4.111
50070	A13	M-007343- solute carri	115286	SLC25A26	2350	8.8511	7.7289
50070	A14	M-008463- isopenteny	91734	IDI2	3431	8.8021	7.7779
50070	A15	M-013128- F-box prote	115290	FBXO17	2372	18.002	1.422
50070	A16	M-016847- similar to C	91695	dJ222E13.2	2938	9.5303	7.0497
50070	A17	M-015168- protein-L-is	115294	PCMTD1	3258	16.697	0.117
50070	A18	M-007108- LON peptid	91694	LONRF1	3003	16.284	0.296
50070	A19	M-018700- leucine rich	115353	LRRC42	2865	13.333	3.247
50070	A20	M-016704- chromosom	91689	C22orf32	3535	12.277	4.303
50070	A21	M-018177- guanylate b	115361	GBP4	3993	21.563	4.983
50070	A23	M-018178- guanylate b	115362	GBP5	4507	18.749	2.169
50070	B02	M-006319- chromosom	133686	C5orf33	3938	11.757	4.823
50070	B04	M-018199- proline-rich	133619	PRRC1	3855	28.742	12.162
50070	B05	M-016564- family with	91775	FAM55C	4193	10.971	5.609
50070	B06	M-015146- secretoglob	92304	SCGB3A1	4184	20.22	3.64
50070	B07	M-015514- CHMP fami	91782	CHMP7	2639	15.764	0.816
50070	B08	M-015112- integrator c	92105	INTS4	2601	11.572	5.008
50070	B09	M-016544- alkB, alkyla	91801	ALKBH8	4092	18.426	1.846
50070	B10	M-022081- dual specifi	92235	DUSP27	4008	21.507	4.927
50070	B11	M-022006- chromosom	91828	C14orf73	2877	12.826	3.754
50070	B12	M-004544- synaptotag	94120	SYTL3	3098	20.239	3.659
50070	B13	M-021318- WD repeat	91833	WDR20	3514	12.123	4.457
50070	B14	M-015191- hypothetica	94107	MGC14327	2561	8.7075	7.8725
50070	B15	M-015779- chordin-like	91851	CHRDL1	2997	17.851	1.271
50070	B16	M-015090- Thy-1 co-tr	94105	LOC94105	3549	22.147	5.567
50070	B17	M-031986- calmodulin	91860	CALML4	5227	21.599	5.019
50070	B18	M-012984- chromosom	94104	C21orf66	6333	34.423	17.843
50070	B19	M-015143- MARVEL do	91862	MARVELD3	5387	27.269	10.689
50070	B20	M-017002- ORM1-like	94103	ORMDL3	5503	13.847	2.733
50070	B21	M-018174- RFT1 homo	91869	RFT1	5012	40.882	24.302
50070	B23	M-015535- tetratricope	91875	TTC5	5443	38.288	21.708
50070	C02	M-027536- centromere	91687	CENPL	3229	6.4416	10.1384
50070	C04	M-018482- synaptotag	91683	SYT12	2631	9.008	7.572
50070	C05	M-026730- leucine rich	115399	LRRC56	4223	18.968	2.388
50070	C06	M-023874- hypothetica	91664	LOC91664	3971	9.8968	6.6832
50070	C07	M-015612- chromosom	115416	C7orf30	3750	16.24	0.34
50070	C08	M-018277- myeloid-as	91663	MYADM	3514	19.294	2.714

50070	C09	M-015613- zinc finger	115509	ZNF689	4111	18.876	2.296
50070	C10	M-008413- Boc homol	91653	BOC	4056	16.297	0.283
50070	C11	M-024508- FCH domai	115548	FCHO2	4869	29.883	13.303
50070	C12	M-017426- ATP syntha	91647	ATPAF2	3669	17.443	0.863
50070	C13	M-004121- RAC/CDC4	115557	GEFT	3194	13.431	3.149
50070	C14	M-023635- ES cell asso	91646	ECAT8	2962	24.173	7.593
50070	C15	M-007118- zinc finger	115560	ZNF501	3405	11.747	4.833
50070	C16	M-016402- nexilin (F a	91624	NEXN	3859	17.854	1.274
50070	C17	M-015169- family with	115572	FAM46B	3365	32.214	15.634
50070	C18	M-016878- DEP domai	91614	DEPDC7	4851	34.343	17.763
50070	C19	M-007341- solute carri	115584	SLC5A11	3739	13.319	3.261
50070	C20	M-015463- churchill d	91612	CHURC1	5465	19.195	2.615
50070	C21	M-013424- tumor necr	115650	TNFRSF13C	4407	13.342	3.238
50070	C23	M-021944- tetratricop	115669	TTC6	5309	23.357	6.777
50070	D02	M-016367- sideroflexi	94097	SFXN5	4305	12.102	4.478
50070	D04	M-009005- heat shock	94086	HSPB9	6365	19.152	2.572
50070	D05	M-015249- chromoso	91894	C11orf52	5626	24.369	7.789
50070	D06	M-010686- sideroflexi	94081	SFXN1	4860	32.778	16.198
50070	D07	M-015537- T-cell imm	91937	TIMD4	4785	26.228	9.648
50070	D08	M-027335- leukocyte	94059	LENG9	3632	18.943	2.363
50070	D09	M-017758- NDUFA12-	91942	NDUFA12L	4007	25.206	8.626
50070	D10	M-017180- synapse as	94056	SYAP1	4199	22.72	6.14
50070	D11	M-019366- arrestin do	91947	ARRDC4	2484	7.4879	9.0921
50070	D12	M-016903- zinc finger	94039	ZNF101	4413	26.558	9.978
50070	D13	M-030501- hypothetic	91948	LOC91948	3929	23.517	6.937
50070	D14	M-018442- ferritin mit	94033	FTMT	2980	12.315	4.265
50070	D15	M-015904- componen	91949	COG7	3356	15.673	0.907
50070	D16	M-013687- calcium/ca	94032	CAMK2N2	4767	12.482	4.098
50070	D17	M-018483- chromoso	91966	CXorf40A	4283	8.8022	7.7778
50070	D18	M-005897- HtrA serine	94031	HTRA3	4347	5.7971	10.7829
50070	D19	M-015144- zinc finger	91975	ZNF300	3614	9.2418	7.3382
50070	D20	M-023786- leucine ric	94030	LRRC4B	5131	11.674	4.906
50070	D21	M-018208- myozenin	91977	MYOZ3	3779	10.347	6.233
50070	D23	M-023892- chromoso	91978	C19orf20	4282	6.5624	10.0176
50070	E02	M-008344- RAS-like, fa	91608	RASL10B	3990	10.476	6.104
50070	E04	M-016764- schlafen fa	91607	SLFN11	4017	18.82	2.24
50070	E05	M-015170- nitric oxide	115677	NOSTRIN	4020	28.234	11.654
50070	E06	M-015142- coiled-coil	91603	CCDC16	4276	21.749	5.169
50070	E07	M-009225- sorting nex	115703	SNX26	3307	9.3741	7.2059
50070	E08	M-018881- plexin A4,	91584	PLXNA4B	3851	16.022	0.558
50070	E09	M-015870- chromoso	115708	C14orf172	3546	21.404	4.824
50070	E10	M-019332- ribosomal	91582	RPS19BP1	3679	15.955	0.625
50070	E11	M-026975- chromoso	115749	C12orf56	3952	17.738	1.158
50070	E12	M-016859- chromoso	91574	C12orf65	3879	20.263	3.683
50070	E13	M-015333- DIS3 mitoti	115752	DIS3L	2720	15.735	0.845
50070	E14	M-016403- UBX domai	91544	UBXD5	2445	11.411	5.169
50070	E15	M-018083- ADP-ribosy	115761	ARL11	3588	14.381	2.199

50070	E16	M-018357- hypothetic	91531	DKFZp434F	2746	11.799	4.781
50070	E17	M-018367- chromoson	115795	C3orf24	3019	13.647	2.933
50070	E18	M-015710- ankyrin rep	91526	ANKRD44	3918	14.395	2.185
50070	E19	M-015615- IQ motif co	115811	IQCD	4933	17.819	1.239
50070	E20	M-015532- family with	91523	FAM113B	3790	7.3087	9.2713
50070	E21	M-008577- dehydroge	115817	DHRS1	2416	3.0215	13.5585
50070	E23	M-006860- WD repeat	115825	WDFY2	5600	17.571	0.991
50070	F02	M-010685- tweety hor	94015	TTYH2	4674	7.9589	8.6211
50070	F04	M-016780- serine hydr	94009	SERHL	4902	29.886	13.306
50070	F05	M-017087- family with	92002	FAM58A	5069	14.263	2.317
50070	F06	M-013702- phosphatid	94005	PIGS	4703	13.289	3.291
50070	F07	M-007358- mitochond	92014	MCART1	5045	19.722	3.142
50070	F08	M-017220- ATPase inh	93974	ATPIF1	3036	17.194	0.614
50070	F09	M-030590- similar to R	92017	LOC92017	4617	26.099	9.519
50070	F10	M-018078- Ca2+-depe	93664	CADPS2	3361	10.622	5.958
50070	F11	M-015145- hypothetic	92070	MGC21675	4398	16.712	0.132
50070	F12	M-015110- Rho GTPas	93663	ARHGAP18	3209	12.808	3.772
50070	F13	M-005887- gamma-glu	92086	GGTLA4	4021	18.677	2.097
50070	F14	M-013732- capping pr	93661	CAPZA3	3461	28.633	12.053
50070	F15	M-015250- zinc finger	92092	ZC3HAV1L	3889	28.079	11.499
50070	F16	M-015236- tight juncti	93643	TJAP1	2753	14.384	2.196
50070	F17	M-016833- tetratricop	92104	TTC30A	3529	13.347	3.233
50070	F18	M-024154- transcriptic	93624	MGC21874	3887	10.188	6.392
50070	F19	M-010186- oxidoreduc	92106	OXNAD1	4931	24.092	7.512
50070	F20	M-015093- Mof4 famil	93621	MRFAP1	5291	28.067	11.487
50070	F21	M-008886- dermatan s	92126	DSEL	4603	13.122	3.458
50070	F23	M-024787- hypothetic	92129	RP11-321G	3209	14.927	1.653
50070	G02	M-010684- collagen, ty	91522	COL23A1	6606	14.033	2.547
50070	G04	M-031465- intestine-sp	91464	ISX	4215	14.069	2.511
50070	G05	M-008520- RAB3C, me	115827	RAB3C	4577	14.027	2.553
50070	G06	M-005341- hypothetic	91461	LOC91461	4098	25.842	9.262
50070	G07	M-015489- thioredoxir	115861	TXNL6	2779	8.1684	8.4116
50070	G08	M-007107- ring finger	91445	RNF185	4873	14.262	2.318
50070	G09	M-015487- collagen tri	115908	CTHRC1	3781	13.859	2.721
50070	G10	M-016958- chromoson	91442	C19orf40	4289	32.618	16.038
50070	G11	M-030773- chromoson	115939	C16orf42	4626	25.984	9.404
50070	G12	M-016382- premature	91431	LOC91431	4111	22.403	5.823
50070	G13	M-016210- hypothetic	115948	MGC20983	3143	15.017	1.563
50070	G14	M-015098- XRCC6 binc	91419	XRCC6BP1	3034	11.668	4.912
50070	G15	M-016539- zinc finger	115950	ZNF653	2692	25.111	8.531
50070	G16	M-022933- coiled-coil	91409	CCDC74B	3635	10.316	6.264
50070	G17	M-007119- ring finger	115992	RNF166	3182	11.565	5.015
50070	G18	M-027988- basic trans	91408	BTF3L4	3847	15.025	1.555
50070	G19	M-015684- chromoson	116028	C16orf75	4756	21.068	4.488
50070	G20	M-018379- SEC14 and	91404	SESTD1	4570	21.685	5.105
50070	G21	M-015183- odd-skippe	116039	OSR2	3769	15.15	1.43
50070	G23	M-023580- leucine rich	116064	LRRC58	3280	10.945	5.635

50070	H02	M-019201- F-box prote	93611	FBXO44	3945	7.3764	9.2036
50070	H04	M-015606- WD repeat	93594	WDR67	3093	20.757	4.177
50070	H05	M-018531- metadherir	92140	MTDH	3245	33.867	17.287
50070	H06	M-021481- calcium cha	93589	CACNA2D4	3973	13.466	3.114
50070	H07	M-022582- actin-bund	92154	ABBA-1	3964	25.732	9.152
50070	H08	M-015453- RNA (guani	93587	RG9MTD2	3385	10.812	5.768
50070	H09	M-031924- transmemk	92162	TMEM88	2899	13.211	3.369
50070	H10	M-028197- chromosor	93556	C3orf50	3224	18.734	2.154
50070	H11	M-015522- mitochond	92170	MTG1	2976	10.988	5.592
50070	H12	M-017760- AN1, ubiqu	93550	ANUBL1	2633	17.812	1.232
50070	H13	M-013677- protocadhe	92211	PCDH21	2839	21.839	5.259
50070	H14	M-009097- NAD(P) dep	93517	HSPC105	3170	18.36	1.78
50070	H15	M-023470- hypothetic	92216	DKFZp434E	4021	18.105	1.525
50070	H16	M-016369- chromosor	93487	C14orf32	4192	16.412	0.168
50070	H17	M-018175- RCSD doma	92241	RCSD1	3833	23.663	7.083
50070	H18	M-015089- zinc finger	93474	ZNF670	3573	21.411	4.831
50070	H19	M-024491- LMBR1 dor	92255	LMBRD2	4392	24.636	8.056
50070	H20	M-027963- hypothetic	93463	LOC93463	4772	33.759	17.179
50070	H21	M-019052- mitochond	92259	MRPS36	3724	20.784	4.204
50070	H23	M-024517- hypothetic	92270	LOC92270	3858	8.2167	8.3633
50070	I02	M-016515- zinc finger	91392	ZNF502	3249	14.281	2.299
50070	I04	M-026040- UDP-N-acte	91373	UAP1L1	3855	16.576	0.004
50070	I05	M-024521- LysM, puta	116068	LYSMD3	2805	26.845	10.265
50070	I06	M-015141- ankyrin rep	91369	ANKRD40	4361	24.123	7.543
50070	I07	M-016830- basic leucir	116071	BATF2	3070	10.358	6.222
50070	I08	M-015248- similar to R	91368	MGC13017	2223	20.738	4.158
50070	I09	M-015172- disrupted ir	116093	DIRC1	2716	15.059	1.521
50070	I10	M-019004- low density	91355	LRP5L	2970	11.616	4.964
50070	I11	M-008255- forkhead b	116113	FOXP4	2112	10.275	6.305
50070	I12	M-024102- hypothetic	91351	FLJ31033	2619	32.073	15.493
50070	I13	M-023716- zinc finger	116115	ZNF526	2666	22.693	6.113
50070	I14	M-032237- Der1-like d	91319	DERL3	3972	19.587	3.007
50070	I15	M-008380- flavin-conta	116123	RP11-45J16	3067	13.89	2.69
50070	I16	M-015077- chromosor	91304	C19orf6	3478	17.108	0.528
50070	I17	M-015173- leucine rich	116135	LRRC3B	2982	21.932	5.352
50070	I18	M-016549- chromosor	91300	C19orf22	2707	14.777	1.803
50070	I19	M-012978- kelch doma	116138	KLHDC3	4096	33.13	16.55
50070	I20	M-015085- transmemk	91289	TMEM112E	3555	22.982	6.402
50070	I21	M-008669- monad	116143	LOC116143	4165	29.892	13.312
50070	I23	M-015622- nuclear unc	116150	NUS1	2923	19.535	2.955
50070	J02	M-028862- maltase-glu	93432	LOC93432	4083	27.945	11.365
50070	J04	M-031128- hypothetic	93429	DKFZp434J	3491	16.213	0.367
50070	J05	M-016843- zinc finger	92285	ZNF585B	4014	25.561	8.981
50070	J06	M-015298- synaptoner	93426	SYCE1	3815	15.99	0.59
50070	J07	M-005803- calpain 13	92291	CAPN13	4735	23.21	6.63
50070	J08	M-015564- myosin ligh	93408	MYLC2PL	4511	13.146	3.434
50070	J09	M-010292- glycine-N-a	92292	GLYATL1	3664	31.386	14.806

50070	J10	M-015075- transmemb	93377	TMEM10	3947	12.567	4.013
50070	J11	M-027086- transmemb	92293	TMEM132	4775	26.283	9.703
50070	J12	M-016195- hypothetic	93349	LOC93349	2912	12.946	3.634
50070	J13	M-015539- transmemb	92305	TMEM129	4248	20.88	4.3
50070	J14	M-015563- family with	93343	FAM125A	3680	8.4239	8.1561
50070	J15	M-022355- MEX3A pro	92312	MEX3A	6011	33.239	16.659
50070	J16	M-031247- sarcoma ar	93323	NY-SAR-48	3695	15.101	1.479
50070	J17	M-015087- chromoson	92342	C1orf156	4749	11.96	4.62
50070	J18	M-021840- LEM domai	93273	LEMD1	5296	24.094	7.514
50070	J19	M-016142- SCY1-like 1	92344	SCYL1BP1	5273	24.844	8.264
50070	J20	M-016370- coiled-coil	93233	CCDC114	4940	17.146	0.566
50070	J21	M-015540- hypothetic	92345	LOC92345	4253	8.6527	7.9273
50070	J23	M-018714- chromoson	92346	C1orf105	3335	16.312	0.268
50070	K02	M-015247- chromoson	91283	C9orf30	4898	14.598	1.982
50070	K04	M-015526- family with	91272	FAM44B	4216	14.16	2.42
50070	K05	M-015272- chromoson	116151	C20orf108	5350	14.935	1.645
50070	K06	M-007568- solute carri	91252	SLC39A13	5887	16.12	0.46
50070	K07	M-019242- phosphatas	116154	PHACTR3	5088	21.403	4.823
50070	K08	M-018475- gamma-glu	91227	GGTL4	4749	11.687	4.893
50070	K09	M-015174- cysteine/ty	116159	CYYR1	4315	16.593	0.013
50070	K10	M-013362- hypothetic	91219	LOC91219	4022	22.974	6.394
50070	K11	M-010751- CKLF-like	116173	CMTM5	3153	21.059	4.479
50070	K12	M-022339- nucleopori	91181	NUP210L	4153	25.957	9.377
50070	K13	M-008606- transglutar	116179	TGM7	2979	9.6677	6.9123
50070	K14	M-018250- eEF1A2 bin	91156	DKFZp434	4621	16.966	0.386
50070	K15	M-015623- transmemb	116211	TM4SF19	3753	25.793	9.213
50070	K16	M-017443- tigger trans	91151	TIGD7	4807	23.32	6.74
50070	K17	M-015499- family with	116224	FAM122A	3648	10.389	6.191
50070	K18	M-016511- transmemb	91147	TMEM67	3616	16.565	0.015
50070	K19	M-021402- zinc finger,	116225	ZMYND19	4637	17.102	0.522
50070	K20	M-007353- solute carri	91137	SLC25A46	5328	25.113	8.533
50070	K21	M-021429- family with	116228	FAM36A	3330	15.015	1.565
50070	K23	M-023290- hypothetic	116236	LOC11623	3775	10.808	5.772
50070	L02	M-017912- per1-like d	93210	PERLD1	6159	33.236	16.656
50070	L04	M-016852- chromoson	93190	C1orf158	4756	13.373	3.207
50070	L05	M-017271- crumbs hor	92359	CRB3	5413	11.454	5.126
50070	L06	M-015148- immunoglo	93185	IGSF8	5125	15.278	1.302
50070	L07	M-015283- splA/ryano	92369	SPSB4	5213	11.855	4.725
50070	L08	M-017388- phosphatid	93183	PIGM	4369	17.601	1.021
50070	L09	M-008557- acid phosp	92370	ACPL2	6788	30.701	14.121
50070	L10	M-015212- olfactomec	93145	OLFM2	4698	15.858	0.722
50070	L11	M-015691- zinc finger	92379	ZFP62	6120	25.114	8.534
50070	L12	M-015888- zinc finger	93134	ZNF561	5232	34.518	17.938
50070	L13	M-016545- mitochond	92399	MRRF	4602	22.599	6.019
50070	L14	M-015896- transmemb	93129	TMEM142	4706	24.139	7.559
50070	L15	M-015074- RNA bindin	92400	RBM18	5681	28.182	11.602
50070	L16	M-015550- transmemb	93109	TMEM44	6597	22.237	5.657

50070	L17	M-015932- chromatin	92421	CHMP4C	5501	19.687	3.107
50070	L18	M-006231- potassium	93107	KCNG4	6073	27.499	10.919
50070	L19	M-015189- proline rich	92454	PRR8	5797	17.561	0.981
50070	L20	M-016912- nicotinate	93100	NAPRT1	4187	20.97	4.39
50070	L21	M-029657- hypothetic	92482	LOC92482	5022	17.583	1.003
50070	L23	M-008908- lactate deh	92483	LDHAL6B	5846	24.803	8.223
50070	M02	M-008540- l(3)mbt-like	91133	L3MBTL4	6561	26.658	10.078
50070	M04	M-023998- zinc finger	91115	ZNF506	5386	26.457	9.877
50070	M05	M-015483- TLC domair	116238	TLCD1	5478	17.233	0.653
50070	M06	M-007106- tripartite m	91107	TRIM47	5829	13.965	2.615
50070	M07	M-016569- chromoson	116254	C6orf72	5859	28.52	11.94
50070	M08	M-008466- ankyrin rep	91074	ANKRD30A	4579	26.294	9.714
50070	M09	M-010062- monoacylg	116255	MOGAT1	5190	10.154	6.426
50070	M10	M-015246- coiled-coil	91057	CCDC34	4984	20.104	3.524
50070	M11	M-004896- acyl-CoA sy	116285	ACSM1	3715	26.729	10.149
50070	M12	M-015530- DKFZp761E	91056	DKFZp761E	3242	12.523	4.057
50070	M13	M-015175- chromoson	116328	C8orf34	4476	16.309	0.271
50070	M14	M-018356- hypothetic	91050	DKFZp761E	4266	21.753	5.173
50070	M15	M-015176- pannexin 3	116337	PANX3	5166	9.4077	7.1723
50070	M16	M-005856- dipeptidyl-	91039	DPP9	5957	18.751	2.171
50070	M17	M-028370- hypothetic	116349	LOC11634	4121	19.801	3.221
50070	M18	M-016077- LAG1 homo	91012	LASS5	4867	14.732	1.848
50070	M19	M-008654- retinol binc	116362	RBP7	5350	11.869	4.711
50070	M20	M-019007- formin-like	91010	FMNL3	4700	14.851	1.729
50070	M21	M-007496- solute carri	116369	SLC26A8	3600	12.194	4.386
50070	M23	M-016303- LY6/PLAUR	116372	LYPD1	5992	19.009	2.429
50070	N02	M-019416- dermokine	93099	DMKN	4697	13.498	3.082
50070	N04	M-016562- chromoson	93081	C13orf27	3170	17.35	0.77
50070	N05	M-015803- sperm anti	92521	SPECC1	5448	21.366	4.786
50070	N06	M-018734- coenzyme	93058	COQ10A	5202	16.763	0.183
50070	N07	M-027129- coiled-coil	92558	CCDC64	4758	12.085	4.495
50070	N08	M-018509- polycystic	93035	PKHD1L1	4174	9.7748	6.8052
50070	N09	M-015776- fibronectin	92565	FANK1	3549	5.41	11.17
50070	N10	M-009865- 5'-nucleoti	93034	NT5C1B	5194	11.417	5.163
50070	N11	M-013061- ankyrin rep	92591	ASB16	3728	11.803	4.777
50070	N12	M-015841- UDP-GlcNA	93010	B3GNT7	4761	18.925	2.345
50070	N13	M-007109- zinc finger	92595	ZNF764	3267	16.253	0.327
50070	N14	M-016531- zinc finger	92999	ZBTB47	3858	7.5428	9.0372
50070	N15	M-018359- MOB1, Mp	92597	MOBKL1A	4477	29.663	13.083
50070	N16	M-015561- membrane	92979	MARCH9	3761	20.5	3.92
50070	N17	M-015147- TRAF-inter	92610	TIFA	3730	21.448	4.868
50070	N18	M-015251- peroxisom	92960	PEX11G	2865	21.745	5.165
50070	N19	M-030821- hypothetic	92659	LOC92659	4397	14.146	2.434
50070	N20	M-015560- methionyl-	92935	MARS2	3359	10.182	6.398
50070	N21	M-017150- chromoson	92667	C20orf72	4542	18.098	1.518
50070	N23	M-019009- D-tyrosyl-t	92675	DTD1	4206	15.359	1.221
50070	O02	M-008579- cAMP resp	90993	CREB3L1	3682	6.5182	10.0618

50070	O04	M-025858- zinc finger	90987	ZNF251	4837	18.131	1.551
50070	O05	M-023837- hypothetic	116412	LOC116412	2989	15.657	0.923
50070	O06	M-015603- DEAH (Asp-	90957	DHX57	4059	25.696	9.116
50070	O07	M-016540- transmem	116441	TM4SF18	4075	17.055	0.475
50070	O08	M-016663- endothelial	90952	ESAM	4609	24.083	7.503
50070	O09	M-008558- RAB39B, m	116442	RAB39B	4990	19.639	3.059
50070	O10	M-007105- tripartite m	90933	TRIM41	3547	18.664	2.084
50070	O11	M-007918- glutamate	116444	GRIN3B	3411	24.186	7.606
50070	O12	M-027619- zinc finger	90874	ZNF697	2765	7.4503	9.1297
50070	O13	M-031788- oligodendr	116448	OLIG1	2861	10.94	5.64
50070	O14	M-029533- chromosom	90871	C9orf123	2199	7.7763	8.8037
50070	O15	M-015193- hypothetic	114130	MGC16384	4406	20.132	3.552
50070	O16	M-029232- similar to T	90868	COE2	5842	24.101	7.521
50070	O17	M-015149- hypothetic	112597	MGC4677	3172	14.912	1.668
50070	O18	M-015122- interleukin	90865	IL33	2944	20.686	4.106
50070	O19	M-017735- tuberoinfu	113091	TIP39	3155	8.5261	8.0539
50070	O20	M-017713- splA/ryano	90864	SPSB3	3393	13.911	2.669
50070	O21	M-008421- UDP glycos	133688	UGT3A1	4196	9.5567	7.0233
50070	O23	M-016007- calcyphosi	133690	CAPSL	2564	11.193	5.387
50070	P02	M-015088- coiled-coil	92922	CCDC102A	2831	9.6079	6.9721
50070	P04	M-008326- ubiquitin-c	92912	UBE2Q2	3579	12.35	4.23
50070	P05	M-015552- family with	92689	FAM114A1	3848	10.785	5.795
50070	P06	M-016347- heterogene	92906	HNRPLL	4248	18.079	1.499
50070	P07	M-018989- transmem	92691	TMEM169	3753	15.055	1.525
50070	P08	M-015116- IMP4, U3 s	92856	IMP4	3824	9.3619	7.2181
50070	P09	M-018685- transmem	92703	TMEM183	3035	15.453	1.127
50070	P10	M-015555- receptor ac	92840	REEP6	3576	18.96	2.38
50070	P11	M-015918- arrestin do	92714	ARRDC1	2350	21.362	4.782
50070	P12	M-015702- zinc finger	92822	ZNF276	3548	13.698	2.882
50070	P13	M-016561- WD repeat	92715	WDR85	3956	14.737	1.843
50070	P14	M-019163- histone clu	92815	HIST3H2A	4432	19.63	3.05
50070	P15	M-018429- otopetrin 2	92736	OTOP2	3851	11.192	5.388
50070	P16	M-016551- hypothetic	92806	MGC16385	3863	15.506	1.074
50070	P17	M-018708- delta/notc	92737	DNER	3968	10.837	5.743
50070	P18	M-015553- SH3KBP1 b	92799	SHKBP1	4044	19.585	3.005
50070	P19	M-007562- solute carri	92745	SLC38A5	3738	7.6779	8.9021
50070	P20	M-013541- helicase (D	92797	HELB	5279	21.86	5.28
50070	P21	M-010095- chromosom	92747	C20orf114	3739	9.4678	7.1122
50070	P23	M-016558- chromosom	92749	C2orf39	3499	15.519	1.061
				MAD	3946	16.5845	4.7815
				MAD3			14.3445
				MADc			7.07662
50070	C22				4701	53.967	
50070	D22				4654	51.955	
50070	E22				2667	34.346	
50070	F22				3328	54.387	
				mn	3837.5	48.66375	

					sd	1006.97	9.603998
50070	G22					1196	12.207
50070	H22					1664	10.938
50070	I22					1121	12.578
50070	J22					2218	11.587
					mn	1667.667	11.701
					sd	548.5092	0.825922
					3psSD		28.81199
					3ngSD		2.477766
					SumSD		31.28976
					DiffMn		36.96275
					SmovrDiff		0.846521
					1minus		0.153479

50070	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	688	10.029
50070	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	415	9.1566
50070	I03	D-001206-	siControl non-targeting			3717	20.285
50070	J03	D-001206-	siControl non-targeting			3787	19.039
50070	K03	D-001600-	siGLO RISC-free siRNA			6110	26.727
50070	L03	D-001600-	siGLO RISC-free siRNA			6344	28.121

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-0.81063	1696	8.3726	2.6974	-0.55951	3167	7.0098	5.1802	-0.97459
-0.04232	2766	14.317	3.247	0.67443	4343	10.937	1.253	-0.23638
-0.09206	2113	12.873	1.803	0.374683	2708	11.004	1.186	-0.22378
-0.76202	2445	5.0307	6.0393	-1.25323	3305	3.0257	9.1643	-1.7235
0.244679	2332	11.792	0.722	0.150289	2659	14.442	2.252	0.422474
1.910163	3063	26.216	15.146	3.144435	3964	29.818	17.628	3.312775
-0.33173	1794	9.1416	1.9284	-0.39988	2196	6.7395	5.4505	-1.0254
-0.14506	2501	9.876	1.194	-0.24744	1871	6.1464	6.0436	-1.13689
-0.29499	2324	15.62	4.55	0.944908	2100	11.952	0.238	-0.04558
0.580291	1226	10.522	0.548	-0.11334	1667	9.838	2.352	-0.44296
-1.09281	1036	3.4749	7.5951	-1.57618	1295	10.502	1.688	-0.31815
-1.09973	3340	9.5808	1.4892	-0.30871	3351	8.7138	3.4762	-0.65428
0.200307	1918	6.7779	4.2921	-0.89054	2642	17.298	5.108	0.95933
-0.99683	2148	13.92	2.85	0.592021	2351	5.5296	6.6604	-1.25283
0.015897	1858	12.594	1.524	0.316768	2549	13.731	1.541	0.288823
-0.04246	2211	21.122	10.052	2.087018	2985	17.655	5.465	1.026437
-0.45947	1489	9.9396	1.1304	-0.23423	2696	16.988	4.798	0.901058
-0.60869	2341	16.916	5.846	1.213933	3305	16.036	3.846	0.722105
0.703514	2221	18.595	7.525	1.562461	2905	14.94	2.75	0.516085
0.305866	2728	15.982	4.912	1.020052	4151	19.104	6.914	1.298812
-0.68218	4514	12.605	1.535	0.319052	4479	11.721	0.469	-0.08901
1.717981	5107	28.118	17.048	3.539254	5562	19.885	7.695	1.445621
-0.79325	4633	12.67	1.6	0.332545	3723	3.6261	8.5639	-1.61064
0.513734	3158	8.3914	2.6786	-0.55561	2562	10.226	1.964	-0.37003
-0.11595	3645	12.373	1.303	0.270893	3320	7.4699	4.7201	-0.88811
-0.70832	2136	2.8558	8.2142	-1.7047	2432	5.5099	6.6801	-1.25654
0.260223	4923	12.696	1.626	0.337942	3284	5.877	6.313	-1.18753
0.6956	4151	14.888	3.818	0.792959	4039	19.683	7.493	1.40765
-0.53112	3625	11.09	0.02	0.004567	2479	3.9935	8.1965	-1.54158
0.516419	2345	8.5288	2.5412	-0.52709	2180	8.8991	3.2909	-0.61945
-0.63046	4060	13.596	2.526	0.524764	1695	4.8968	7.2932	-1.37178
-1.1131	1757	7.9681	3.1019	-0.64348	2101	4.0457	8.1443	-1.53177
0.17897	2103	10.128	0.942	-0.19513	2372	9.4857	2.7043	-0.50919
0.786039	3546	15.116	4.046	0.840287	3116	12.516	0.326	0.060434
0.708601	3814	8.731	2.339	-0.48512	3296	7.6153	4.5747	-0.86077
2.520766	5425	18.765	7.695	1.59775	4086	12.139	0.051	-0.01043
1.509831	5558	21.141	10.071	2.090962	4987	7.9807	4.2093	-0.79209
-0.38684	4206	15.24	4.17	0.866027	5175	10.957	1.233	-0.23262
3.433489	2923	29.969	18.899	3.923486	3615	22.296	10.106	1.898828
3.06693	3972	29.079	18.009	3.738739	5242	18.504	6.314	1.186027
-1.4333	4651	8.5788	2.4912	-0.51671	3112	9.608	2.582	-0.4862
-1.07064	2813	5.2968	5.7732	-1.19799	3612	6.3123	5.8777	-1.10571
0.336813	3867	7.3183	3.7517	-0.77837	4860	12.263	0.073	0.012876
-0.94504	3158	9.658	1.412	-0.29269	3405	5.2863	6.9037	-1.29857
-0.04868	4464	8.3109	2.7591	-0.57232	3258	10.712	1.478	-0.27867
0.382881	3270	6.1468	4.9232	-1.02155	2357	12.728	0.538	0.100285

0.323813	4561	12.804	1.734	0.36036	2776	16.354	4.164	0.781881
-0.04063	3737	7.9476	3.1224	-0.64774	2522	8.2078	3.9822	-0.7494
1.879216	4085	21.028	9.958	2.067505	2856	25.805	13.615	2.558432
0.121315	2400	6.7917	4.2783	-0.88768	2070	8.599	3.591	-0.67586
-0.44562	2364	10.829	0.241	-0.04961	2773	5.9142	6.2758	-1.18054
1.072334	1988	13.028	1.958	0.406858	1910	15.131	2.941	0.551988
-0.68359	2376	8.4175	2.6525	-0.55019	1837	12.194	0.004	-9.4E-05
0.179394	2881	9.7883	1.2817	-0.26564	3319	14.402	2.212	0.414955
2.208611	2607	9.8581	1.2119	-0.25115	2867	10.708	1.482	-0.27942
2.509461	4329	19.727	8.657	1.797443	3547	19.594	7.404	1.39092
-0.46145	1675	7.1045	3.9655	-0.82275	2003	5.8412	6.3488	-1.19426
0.368891	2590	9.4208	1.6492	-0.34193	4018	11.498	0.692	-0.13092
-0.4582	980	10.306	0.764	-0.15818	2230	6.5919	5.5981	-1.05315
0.957025	3400	21	9.93	2.061693	3801	9.2607	2.9293	-0.55148
-0.63342	2101	6.8539	4.2161	-0.87477	2970	12.121	0.069	-0.01382
0.362814	3588	16.276	5.206	1.081081	3612	11.794	0.396	-0.07528
1.100031	3033	15.134	4.064	0.844024	2765	18.987	6.797	1.276819
2.28831	2538	4.2947	6.7753	-1.40601	2657	14.49	2.3	0.431496
1.362727	3715	18.466	7.396	1.535683	2717	12.44	0.25	0.046148
0.333281	2237	10.907	0.163	-0.03342	2153	11.983	0.207	-0.03976
1.218308	3276	19.475	8.405	1.745132	2144	14.972	2.782	0.5221
0.86701	2562	10.265	0.805	-0.16669	2451	15.871	3.681	0.69109
-1.28544	2385	10.901	0.169	-0.03467	1604	7.1696	5.0204	-0.94455
1.409359	1929	18.248	7.178	1.490431	2927	30.851	18.661	3.506953
0.979634	2135	15.972	4.902	1.017977	2038	17.566	5.376	1.009707
-0.60332	1831	10.268	0.802	-0.16606	1905	16.85	4.66	0.875117
-0.1288	3431	21.277	10.207	2.119193	1752	15.811	3.621	0.679811
-0.57973	3465	8.9466	2.1234	-0.44036	3014	12.376	0.186	0.034117
-1.09972	4005	10.662	0.408	-0.08428	3809	13.888	1.698	0.318335
-1.52437	2747	6.225	4.845	-1.00531	2255	2.5277	9.6623	-1.81712
-1.0376	1766	10.079	0.991	-0.2053	961	10.822	1.368	-0.258
-0.6939	2360	2.7966	8.2734	-1.71698	1571	12.222	0.032	0.005169
-0.88142	2564	10.998	0.072	-0.01453	1728	8.4491	3.7409	-0.70404
-1.41623	2840	6.2324	4.8376	-1.00378	2964	1.9231	10.2669	-1.93077
-0.86319	3677	9.4098	1.6602	-0.34421	4361	9.7455	2.4445	-0.46035
0.315899	3767	11.627	0.557	0.116038	2450	13.551	1.361	0.254988
1.646196	2656	15.324	4.254	0.883464	3605	19.029	6.839	1.284714
0.729798	3460	16.156	5.086	1.056171	4225	13.846	1.656	0.310441
-1.0189	2330	6.4378	4.6322	-0.96114	2136	5.9457	6.2443	-1.17462
-0.07949	4229	12.06	0.99	0.20592	3528	16.412	4.222	0.792784
0.681045	3382	15.169	4.099	0.851289	3480	13.879	1.689	0.316644
-0.08895	4518	11.554	0.484	0.100884	2654	11.492	0.698	-0.13205
0.163002	4142	16.248	5.178	1.075269	2405	12.848	0.658	0.122842
0.51981	2865	10.611	0.459	-0.09486	2380	12.689	0.499	0.092954
-0.12004	3374	13.189	2.119	0.440279	2338	13.259	1.069	0.200099
-0.73107	2187	16.232	5.162	1.071948	1831	22.774	10.584	1.98868
-0.31138	4436	20.018	8.948	1.857849	2672	17.066	4.876	0.91572

-0.67624	4357	12.073	1.003	0.208619	1858	13.778	1.588	0.297658
-0.4151	3505	26.79	15.72	3.263586	2340	18.889	6.699	1.258398
-0.3094	4734	19.983	8.913	1.850583	3453	22.415	10.225	1.921197
0.174448	3391	16.455	5.385	1.118238	3316	20.326	8.136	1.528518
-1.31077	3424	13.989	2.919	0.606344	2748	14.956	2.766	0.519093
-1.91659	1424	5.8989	5.1711	-1.07301	1850	8.1622	4.0278	-0.75797
0.139403	4458	27.658	16.588	3.443766	4884	19.82	7.63	1.433402
-1.21889	3381	5.8267	5.2433	-1.08799	3142	5.697	6.493	-1.22137
1.87964	5722	22.003	10.933	2.269897	4757	22.598	10.408	1.955597
-0.32805	4265	11.841	0.771	0.16046	3226	8.4625	3.7275	-0.70152
-0.46569	5521	13.349	2.279	0.473492	4432	11.191	0.999	-0.18863
0.443361	5360	18.153	7.083	1.47071	3276	16.026	3.836	0.720226
0.086129	4166	13.346	2.276	0.472869	1803	8.7077	3.4823	-0.65543
1.344498	5673	22.563	11.493	2.386142	2768	15.788	3.598	0.675488
-0.84256	3917	6.5101	4.5599	-0.94613	1845	9.5935	2.5965	-0.48892
0.018017	3045	9.0312	2.0388	-0.4228	2910	12.062	0.128	-0.02491
-0.53366	3470	9.683	1.387	-0.2875	1943	7.5142	4.6758	-0.87978
0.295692	3730	12.359	1.289	0.267987	2842	9.5004	2.6896	-0.50642
1.702578	3188	18.256	7.186	1.492091	2148	16.527	4.337	0.814401
1.624292	4578	22.368	11.298	2.345664	2527	16.502	4.312	0.809702
-0.31095	3404	10.165	0.905	-0.18745	2667	10.461	1.729	-0.32585
-0.45749	3078	9.974	1.096	-0.22709	1961	7.2922	4.8978	-0.92151
-0.90389	4615	6.5655	4.5045	-0.93463	2790	12.222	0.032	0.005169
1.060888	4473	16.968	5.898	1.224727	3463	16.806	4.616	0.866846
1.622597	5167	16.741	5.671	1.177606	3788	9.1341	3.0559	-0.57528
-0.48929	4639	15.413	4.343	0.901939	3471	10.545	1.645	-0.31006
-0.23422	3030	11.716	0.646	0.134512	1775	5.6338	6.5562	-1.23325
-0.36055	5285	13.321	2.251	0.46768	5245	10.105	2.085	-0.39277
-0.35547	4863	10.343	0.727	-0.1505	2629	10.65	1.54	-0.29033
-0.3614	4059	14.043	2.973	0.617553	3476	12.86	0.67	0.125097
1.308181	4568	18.695	7.625	1.583219	2536	20.071	7.881	1.480584
-1.18928	2941	9.5546	1.5154	-0.31415	2288	10.795	1.395	-0.26307
-0.32819	5280	12.008	0.938	0.195126	3699	13.923	1.733	0.324915
-0.38514	3751	7.9712	3.0988	-0.64284	2204	11.025	1.165	-0.21984
2.2657	4142	20.521	9.451	1.962262	2766	31.634	19.444	3.654138
1.328247	5450	17.67	6.6	1.370449	2482	24.819	12.629	2.373089
0.822215	3290	14.286	3.216	0.667995	2046	18.671	6.481	1.217419
-0.2215	2969	11.317	0.247	0.051688	2296	15.418	3.228	0.605937
-0.69475	3020	8.9073	2.1627	-0.44852	2234	12.668	0.478	0.089006
1.204883	3794	23.01	11.94	2.478931	2381	21.756	9.566	1.797322
-0.8858	3076	6.567	4.503	-0.93432	1650	5.697	6.493	-1.22137
-0.70931	2703	7.0292	4.0408	-0.83838	1969	5.6374	6.5526	-1.23257
-0.22037	4510	13.193	2.123	0.441109	3948	14.564	2.374	0.445406
0.633565	4775	13.55	2.48	0.515216	3486	6.5978	5.5922	-1.05204
0.720754	5491	17.92	6.85	1.422344	3762	12.892	0.702	0.131112
-0.20271	4525	9.6354	1.4346	-0.29738	5001	6.7786	5.4114	-1.01805
-0.79692	2791	8.4558	2.6142	-0.54224	3406	3.7874	8.4026	-1.58032

-1.3012	3453	4.8074	6.2626	-1.29958	3138	7.9987	4.1913	-0.7887
0.589618	4356	14.899	3.829	0.795242	3140	12.675	0.485	0.090322
2.442197	4290	20.513	9.443	1.960601	3795	29.908	17.718	3.329693
-0.44068	3928	4.6843	6.3857	-1.32513	3533	6.9063	5.2837	-0.99405
1.292637	4701	17.124	6.054	1.25711	3162	17.932	5.742	1.078506
-0.81571	4119	12.115	1.045	0.217337	3246	9.1189	3.0711	-0.57814
-0.47671	3309	12.451	1.381	0.287084	2358	9.542	2.648	-0.4986
0.303747	5580	17.24	6.17	1.281189	3339	13.267	1.077	0.201603
-0.79084	3729	6.6506	4.4194	-0.91697	2506	10.255	1.935	-0.36458
0.173459	3343	10.081	0.989	-0.20488	2315	11.793	0.397	-0.07547
0.742515	3542	8.9497	2.1203	-0.43972	3150	16.857	4.667	0.876433
0.250897	4394	12.016	0.946	0.196787	2343	16.133	3.943	0.740339
0.214862	2709	11	0.07	-0.01412	2452	12.072	0.118	-0.02303
-0.02438	4273	13.457	2.387	0.495911	2638	13.04	0.85	0.158933
1.000266	3783	14.592	3.522	0.731515	1758	13.424	1.234	0.231115
0.682035	3396	12.603	1.533	0.318637	2758	5.7288	6.4612	-1.21539
1.137761	3869	11.347	0.277	0.057915	2242	14.451	2.261	0.424165
2.426935	3403	19.424	8.354	1.734546	3103	20.432	8.242	1.548443
0.593433	4654	11.667	0.597	0.124341	1872	5.8226	6.3674	-1.19776
-1.18246	3523	4.5416	6.5284	-1.35476	2971	8.9869	3.2031	-0.60295
-0.32551	3111	9.5468	1.5232	-0.31577	2988	11.178	1.012	-0.19108
-0.0012	4875	10.482	0.588	-0.12164	4330	9.6767	2.5133	-0.47328
1.449915	2865	14.38	3.31	0.687508	2442	17.731	5.541	1.040723
1.065268	4485	19.331	8.261	1.715241	4310	14.037	1.847	0.346344
-0.87987	4067	7.942	3.128	-0.6489	3687	8.652	3.538	-0.6659
0.586933	2375	13.853	2.783	0.578113	2297	10.535	1.655	-0.31194
-0.21557	2328	4.854	6.216	-1.28991	2853	8.4823	3.7077	-0.6978
-0.7021	3955	9.7345	1.3355	-0.27681	3389	12.216	0.026	0.004041
-0.8916	2293	7.1958	3.8742	-0.80379	1747	6.411	5.779	-1.08715
2.188686	2382	18.22	7.15	1.484618	2863	24.625	12.435	2.336622
0.863195	3562	10.303	0.767	-0.1588	3613	17.271	5.081	0.954254
0.424284	4502	16.948	5.878	1.220575	4035	18.959	6.769	1.271556
-0.38076	3367	11.642	0.572	0.119151	3093	13.256	1.066	0.199535
0.073976	3513	14.831	3.761	0.781127	3947	14.644	2.454	0.460444
0.755657	3089	10.91	0.16	-0.0328	3546	13.818	1.628	0.305177
-0.25542	3785	18.653	7.583	1.574501	3362	7.3766	4.8134	-0.90564
2.338051	3407	18.609	7.539	1.565367	3523	16.435	4.245	0.797107
0.904033	5499	22.677	11.607	2.409806	4358	18.311	6.121	1.149748
1.880488	4253	16.412	5.342	1.109312	6050	17.14	4.95	0.92963
0.416936	3611	9.028	2.042	-0.42346	3327	9.5582	2.6318	-0.49556
1.605357	5646	13.673	2.603	0.540748	3824	23.3	11.11	2.087555
-0.0525	3957	7.7837	3.2863	-0.68176	3750	10.827	1.363	-0.25706
1.268473	4221	11.158	0.088	0.018682	5405	15.19	3	0.563079
-0.08401	4271	8.6631	2.4069	-0.49921	4115	10.96	1.23	-0.23205
0.936252	4308	11.328	0.258	0.053971	5630	16.075	3.885	0.729436
-0.4859	3717	8.5015	2.5685	-0.53276	4268	10.989	1.201	-0.2266
2.091606	2832	11.441	0.371	0.077428	3878	18.592	6.402	1.202569

-0.56771	4021	8.0826	2.9874	-0.61971	4663	8.8784	3.3116	-0.62334
1.370499	3354	16.13	5.06	1.050774	3850	16.312	4.122	0.773987
-0.51416	2673	6.9211	4.1489	-0.86082	2296	10.801	1.389	-0.26194
0.606999	3400	8.7353	2.3347	-0.48422	3366	10.22	1.97	-0.37116
-1.15318	3892	8.6331	2.4369	-0.50544	3058	5.8535	6.3365	-1.19195
2.353454	3110	16.752	5.682	1.17989	4187	20.444	8.254	1.550699
-0.20963	3666	7.9651	3.1049	-0.6441	4632	6.5846	5.6054	-1.05452
-0.65349	3634	10.402	0.668	-0.13825	4636	6.8809	5.3091	-0.99882
1.06117	6215	17.233	6.163	1.279736	5445	14.766	2.576	0.483377
1.167153	4505	20.91	9.84	2.043011	4844	13.398	1.208	0.226228
0.079346	4567	15.349	4.279	0.888654	4001	8.4729	3.7171	-0.69957
-1.12085	4297	6.586	4.484	-0.93038	4598	3.719	8.471	-1.59318
-0.03851	2310	10.563	0.507	-0.10483	3140	8.535	3.655	-0.68789
-0.28071	4158	9.3795	1.6905	-0.3505	6287	14.729	2.539	0.476422
-0.34261	2569	8.4079	2.6621	-0.55219	4478	9.3345	2.8555	-0.53761
-0.23309	2552	4.1928	6.8772	-1.42716	5118	10.531	1.659	-0.3127
-0.06564	3900	14.333	3.263	0.677751	4909	18.517	6.327	1.188471
0.680904	4244	18.332	7.262	1.507867	5879	16.244	4.054	0.761204
-0.69207	2946	8.3503	2.7197	-0.56414	4371	8.0988	4.0912	-0.76989
0.001201	2484	5.6361	5.4339	-1.12756	5348	10.527	1.663	-0.31345
0.902903	2210	19.095	8.025	1.666252	3338	22.259	10.069	1.891873
0.632293	2745	7.4681	3.6019	-0.74727	3178	17.464	5.274	0.990534
1.324432	3371	12.519	1.449	0.3012	3803	22.403	10.213	1.918941
-0.97742	3332	7.6531	3.4169	-0.70887	3301	10.936	1.254	-0.23657
0.05391	3427	7.5576	3.5124	-0.72869	3985	10.013	2.177	-0.41007
1.301257	3405	13.363	2.293	0.476398	4254	25.505	13.315	2.50204
0.951796	3982	13.184	2.114	0.439241	3800	19.842	7.652	1.437538
-0.87549	3425	4.4964	6.5736	-1.36414	4690	7.8465	4.3435	-0.81731
-0.00276	4422	8.0959	2.9741	-0.61695	4848	19.884	7.694	1.445433
0.073128	2540	6.4173	4.6527	-0.9654	4188	14.422	2.232	0.418714
1.205166	4140	11.932	0.862	0.17935	5540	21.444	9.254	1.738674
-0.22179	3561	10.643	0.427	-0.08822	5041	12.557	0.367	0.068141
-0.81628	3791	7.5442	3.5258	-0.73147	2555	8.9237	3.2663	-0.61483
2.35303	4221	16.986	5.916	1.228463	4046	16.881	4.691	0.880944
-0.45382	3021	9.8312	1.2388	-0.25674	4493	18.184	5.994	1.125875
-0.72499	2606	5.9862	5.0838	-1.05488	5014	10.311	1.879	-0.35405
-0.18462	3090	5.5663	5.5037	-1.14205	5518	16.636	4.446	0.83489
-0.66833	2663	7.8858	3.1842	-0.66056	4358	7.0445	5.1455	-0.96807
0.143642	2395	4.3006	6.7694	-1.40478	4834	15.391	3.201	0.600862
1.994808	2733	4.4274	6.6426	-1.37846	4702	19.46	7.27	1.365731
-0.10266	2524	4.0016	7.0684	-1.46685	4438	15.412	3.222	0.604809
1.205307	2906	11.046	0.024	-0.00457	4432	21.39	9.2	1.728523
2.53419	2678	12.92	1.85	0.38444	4493	25.351	13.161	2.473091
0.849911	2482	6.5673	4.5027	-0.93426	3722	18.861	6.671	1.253134
1.067529	2413	7.1695	3.9005	-0.80925	2609	14.488	2.298	0.43112
1.638847	2597	11.205	0.135	0.028439	4681	20.722	8.532	1.602956
0.798757	2388	6.4489	4.6211	-0.95884	3280	10.701	1.489	-0.28074

0.438416	2148	7.635	3.435	-0.71263	2954	13.304	1.114	0.208558
1.542332	3793	14.316	3.246	0.674223	4239	16.749	4.559	0.856132
0.13799	3524	7.8604	3.2096	-0.66584	3011	10.594	1.596	-0.30085
0.619717	3937	9.9568	1.1132	-0.23066	3395	14.786	2.596	0.487137
0.141098	4049	13.46	2.39	0.496533	2659	11.358	0.832	-0.15724
1.16136	3176	14.767	3.697	0.767842	1981	14.841	2.651	0.497475
1.42349	6344	19.404	8.334	1.730394	4274	14.904	2.714	0.509318
1.395087	5056	14.043	2.973	0.617553	4810	17.672	5.482	1.029632
0.09164	5023	12.522	1.452	0.301823	4453	8.8929	3.2971	-0.62062
-0.37016	4418	11.634	0.564	0.117491	5228	9.5065	2.6835	-0.50528
1.68661	3262	20.233	9.163	1.902479	3761	14.597	2.407	0.45161
1.372053	2644	28.328	17.258	3.582846	2398	14.762	2.572	0.482625
-0.9087	3433	10.108	0.962	-0.19928	4394	10.173	2.017	-0.37999
0.497342	3224	14.051	2.981	0.619214	4174	12.195	0.005	9.4E-05
1.433523	1940	23.402	12.332	2.560302	4283	32.08	19.89	3.737974
-0.57393	2419	9.7561	1.3139	-0.27233	2796	7.01	5.18	-0.97456
-0.03893	2472	13.552	2.482	0.515631	3470	11.383	0.807	-0.15254
0.730363	3120	16.154	5.084	1.055756	4150	11.518	0.672	-0.12717
-1.01416	2462	5.6052	5.4648	-1.13397	4134	7.015	5.175	-0.97362
0.306149	3348	14.456	3.386	0.703284	5814	10.01	2.18	-0.41063
0.454525	2884	16.436	5.366	1.114294	4344	11.948	0.242	-0.04634
-0.26178	3016	12.5	1.43	0.297256	5056	8.1883	4.0017	-0.75306
-0.66635	4022	12.108	1.038	0.215884	4858	6.6694	5.5206	-1.03858
-0.24496	3566	25.014	13.944	2.894923	4841	9.9566	2.2334	-0.42067
-0.62042	2936	15.327	4.257	0.884087	4597	9.8978	2.2922	-0.43172
0.342607	5253	19.17	8.1	1.68182	3789	5.8327	6.3573	-1.19586
-0.43615	4720	10.72	0.35	-0.07224	5432	8.7629	3.4271	-0.64505
0.108173	3540	13.305	2.235	0.464358	3698	16.549	4.359	0.818537
0.675676	5274	18.733	7.663	1.591107	5653	15.019	2.829	0.530935
0.025224	4503	10.326	0.744	-0.15402	4827	9.7576	2.4324	-0.45808
-0.63583	4229	13.975	2.905	0.603438	5192	10.921	1.269	-0.23939
-0.96228	3055	4.9427	6.1273	-1.27149	4074	3.8537	8.3363	-1.56786
-1.57907	4083	8.3762	2.6938	-0.55877	2916	4.0809	8.1091	-1.52515
-0.73022	3462	7.0191	4.0509	-0.84047	3958	10.46	1.73	-0.32604
-0.67568	2957	12.445	1.375	0.285839	2587	13.22	1.03	0.192768
0.330737	3451	10.519	0.551	-0.11396	3745	17.33	5.14	0.965345
-0.04684	3541	14.092	3.022	0.627724	2853	22.047	9.857	1.852022
-1.27769	2951	9.7933	1.2767	-0.2646	3010	9.0365	3.1535	-0.59362
1.848128	4064	21.998	10.928	2.268859	4190	23.532	11.342	2.131165
0.553301	3236	17.862	6.792	1.410304	3509	21.317	9.127	1.714801
0.687263	3617	19.519	8.449	1.754266	2431	17.195	5.005	0.939968
0.729232	2134	15.323	4.253	0.883257	2030	14.335	2.145	0.40236
-0.34459	4389	15.562	4.492	0.932868	4802	14.952	2.762	0.518341
-0.90474	3897	13.754	2.684	0.557562	3250	15.2	3.01	0.564958
0.213873	3811	12.91	1.84	0.382364	2943	12.504	0.314	0.058178
-0.17318	4785	8.255	2.815	-0.58392	3350	9.9104	2.2796	-0.42935
-1.42247	3131	5.5893	5.4807	-1.13727	2692	6.8351	5.3549	-1.00743

0.218537	4196	8.7703	2.2997	-0.47696	3498	15.466	3.276	0.61496
-0.13107	3095	8.8853	2.1847	-0.45309	2230	14.439	2.249	0.42191
1.28755	2981	13.385	2.315	0.480965	3597	17.737	5.547	1.041851
0.066487	2749	6.1477	4.9223	-1.02136	4089	12.301	0.111	0.020019
1.059616	2054	9.445	1.625	-0.3369	3882	22.798	10.608	1.993192
0.431633	4010	10.599	0.471	-0.09736	3533	10.558	1.632	-0.30762
0.293855	2404	9.4842	1.5858	-0.32877	3127	21.554	9.364	1.759351
1.074171	2367	7.6468	3.4232	-0.71018	2676	20.516	8.326	1.564233
-1.29076	3106	6.4392	4.6308	-0.96085	2966	10.823	1.367	-0.25781
-0.79763	1492	10.523	0.547	-0.11313	2706	15.484	3.294	0.618343
-1.24469	1156	6.3149	4.7551	-0.98665	2192	7.3905	4.7995	-0.90303
0.501299	2981	14.626	3.556	0.738573	5559	25.256	13.066	2.455234
1.06216	4088	14.946	3.876	0.804999	4355	39.013	26.823	5.041204
-0.23634	2612	8.3461	2.7239	-0.56501	3880	14.33	2.14	0.40142
0.579585	2971	8.8522	2.2178	-0.45996	2981	23.314	11.124	2.090187
-1.13874	3273	4.8274	6.2426	-1.29543	4146	15.002	2.812	0.527739
-0.37779	2979	3.4575	7.6125	-1.57979	4056	8.925	3.265	-0.61458
-0.9931	5056	6.3093	4.7607	-0.98782	3965	8.3733	3.8167	-0.71829
-0.76188	3349	2.986	8.084	-1.67767	3281	11.612	0.578	-0.1095
-0.98587	3182	14.205	3.135	0.651181	4472	10.219	1.971	-0.37134
-0.59838	1686	11.981	0.911	0.189521	3813	9.861	2.329	-0.43864
-0.81953	3725	10.47	0.6	-0.12413	4495	6.8743	5.3157	-1.00006
0.211188	1929	6.7392	4.3308	-0.89858	3595	9.3185	2.8715	-0.54062
-0.21613	2063	9.5977	1.4723	-0.30521	4090	8.6308	3.5592	-0.66989
-1.02063	2249	5.3802	5.6898	-1.18068	3613	2.8508	9.3392	-1.75638
-0.15989	1492	9.6515	1.4185	-0.29404	2384	9.4379	2.7521	-0.51817
0.335683	1483	4.1807	6.8893	-1.42967	5493	12.689	0.499	0.092954
0.67511	1315	16.046	4.976	1.033337	2785	14.111	1.921	0.360254
-0.40789	1763	8.7351	2.3349	-0.48427	3286	12.112	0.078	-0.01551
-0.26107	1610	8.1988	2.8712	-0.59559	3499	12.632	0.442	0.082239
0.430361	1863	12.024	0.954	0.198447	4838	20.463	8.273	1.55427
-0.76202	1009	6.5411	4.5289	-0.9397	4359	7.5705	4.6195	-0.8692
-0.1524	1262	5.7845	5.2855	-1.09675	4027	8.9397	3.2503	-0.61182
-0.81218	1970	9.9492	1.1208	-0.23224	4340	8.4562	3.7338	-0.70271
0.424002	2114	5.3926	5.6774	-1.1781	3564	8.3895	3.8005	-0.71524
-1.2586	1590	3.7107	7.3593	-1.52723	3084	3.1128	9.0772	-1.70713
0.745483	2196	3.2787	7.7913	-1.61691	4858	18.979	6.789	1.275316
-1.00566	2004	5.1397	5.9303	-1.2306	3322	3.1306	9.0594	-1.70379
-0.15057	2382	5.4996	5.5704	-1.15589	2324	8.3907	3.7993	-0.71502
	3369	11.068	3.255		3324.5	12.1945	3.5945	
			9.765				10.7835	
			4.8174				5.31986	
2258	47.653		3380	39.231				
2295	45.795		2469	37.303				
2894	51.9		1404	40.1				
5618	58.366		3156	43.504				
3266.25	50.9285		2602.25	40.0345				

1594.699	5.577991	887.8988	2.591552
2702	12.361	899	6.4516
2022	5.8853	781	6.9142
1104	11.051	1190	7.395
1924	12.11	1141	4.645
1683.333	9.6821	1037.333	6.318067
504.1045	3.330486	223.3391	1.468726
	0		7.774656
	9.991458		4.406178
	9.991458		12.18083
	41.2464		33.71643
	0.242238		0.361273
	0.757762		0.638727

399	14.536	308	16.234
408	3.9216	308	16.558
4219	13.961	3303	13.685
4240	7.5708	3981	10.55
5026	24.831	7454	22.887
4439	9.0336	6963	31.725

y

y
y

y

y

y

y

y

y

y

						cell ct	% inf	AD
50071	A02	M-010297-	phospholip	123745	PLA2G4E	4437	21.14	3.57
50071	A04	M-022414-	fibronectin	123722	FSD2	4040	14.356	3.214
50071	A05	M-031876-	mast cell i	116449	MIST	4583	28.322	10.752
50071	A06	M-022415-	WAS prote	123720	WHDC1	3676	7.9978	9.5722
50071	A07	M-015177-	chromosom	116461	C1orf19	2889	11.7	5.87
50071	A08	M-017061-	ATP/GTP bi	123624	AGBL1	3759	20.724	3.154
50071	A09	M-013928-	family with	116496	FAM129A	2869	10.526	7.044
50071	A10	M-016270-	non imprin	123606	NIPA1	2451	9.0983	8.4717
50071	A11	M-005663-	MAS-relate	116512	MRGPRD	3462	17.62	0.05
50071	A12	M-015473-	chromosom	123591	C15orf27	2253	16.822	0.748
50071	A13	M-012970-	apolipopro	116519	APOA5	3062	12.998	4.572
50071	A14	M-019368-	leucine ric	123355	LRRC28	2548	9.3014	8.2686
50071	A15	M-005664-	MAS-relate	116534	MRGPRE	3664	11.245	6.325
50071	A16	M-030423-	HIG1 doma	123346	HIGD2BP	4154	7.8479	9.7221
50071	A17	M-012941-	mitochond	116540	MRPL53	3627	11.856	5.714
50071	A18	M-015734-	threonyl-t	123283	TARSL2	1818	12.651	4.919
50071	A19	M-017497-	mitochond	116541	MRPL54	2584	9.017	8.553
50071	A20	M-018553-	organic so	123264	OSTbeta	2916	9.1907	8.3793
50071	A21	M-017539-	heat shock	116835	HSPA12B	3331	11.048	6.522
50071	A23	M-015194-	centrobin,	116840	CNTROB	2155	14.617	2.953
50071	B02	M-015950-	DC-STAMP	127579	DCST2	4753	10.057	7.513
50071	B04	M-007126-	zinc finger	127557	ZBTB8	5212	16.309	1.261
50071	B05	M-015689-	chromosom	123775	C16orf46	5696	14.203	3.367
50071	B06	M-010203-	IBR domai	127544	IBRDC3	5471	15.08	2.49
50071	B07	M-018383-	N-terminal	123803	NTAN1	4574	19.808	2.238
50071	B08	M-016743-	high-mobili	127540	HMGB4	2857	7.2104	10.3596
50071	B09	M-016243-	chromosom	123811	C16orf63	3073	20.404	2.834
50071	B10	M-016072-	leucine ric	127495	LRRC39	2736	23.026	5.456
50071	B11	M-018358-	leucine ric	123872	LRRC50	3002	15.09	2.48
50071	B12	M-027457-	S100 calciu	127482	S100A7L2	2798	15.082	2.488
50071	B13	M-022500-	hypothetic	123876	LOC12387	3142	30.172	12.602
50071	B14	M-027142-	podocan	127435	PODN	2431	19.457	1.887
50071	B15	M-018390-	DCN1, defe	123879	DCUN1D3	3408	17.371	0.199
50071	B16	M-015486-	chromosom	127428	C1orf83	2316	9.3264	8.2436
50071	B17	M-015694-	zymogen g	123887	ZG16	2966	9.0695	8.5005
50071	B18	M-016658-	zinc finger	127396	ZNF684	3043	8.9057	8.6643
50071	B19	M-027207-	neuritin 1-l	123904	NRN1L	3823	16.008	1.562
50071	B20	M-017479-	diencephal	127343	DMBX1	5103	17.558	0.012
50071	B21	M-010752-	CKLF-like	123920	CMTM3	3996	9.7598	7.8102
50071	B23	M-016247-	chromosom	123970	C16orf78	3779	5.9804	11.5896
50071	C02	M-009633-	mitochond	123263	MTFMT	6291	16.309	1.261
50071	C04	M-004071-	SUMO/sen	123228	SENP8	5242	26.555	8.985
50071	C05	M-015195-	chromosom	116841	C1orf142	6512	19.103	1.533
50071	C06	M-016276-	chromosom	123207	C15orf40	4854	15.595	1.975
50071	C07	M-015178-	liver expre	116842	LEAP2	3824	17.939	0.369
50071	C08	M-016579-	Leo1, Paf1/	123169	LEO1	3122	14.061	3.509

50071	C09	M-013459- chromoson	116843	C6orf192	3537	24.936	7.366
50071	C10	M-010296- degenerati	123099	DEGS2	3659	32.905	15.335
50071	C11	M-015179- leucine-rich	116844	LRG1	2960	14.865	2.705
50071	C12	M-007318- solute carri	123096	SLC25A29	2917	22.969	5.399
50071	C13	M-017917- mediator o	116931	MED12L	2579	25.94	8.37
50071	C14	M-007467- solute carri	123041	SLC24A4	2932	14.393	3.177
50071	C15	M-017538- WD repeat	116966	WDR17	2656	23.532	5.962
50071	C16	M-018293- membrane	123036	MTAC2D1	2759	14.172	3.398
50071	C17	M-008772- ADP-ribosy	116969	ART5	3650	39.452	21.882
50071	C18	M-021417- tetratricop	123016	TTC8	5006	36.656	19.086
50071	C19	M-014644- centaurin,	116983	CENTB5	4285	20.747	3.177
50071	C20	M-008999- acyl-CoA th	122970	ACOT4	4858	14.903	2.667
50071	C21	M-009302- centaurin,	116984	CENTD1	6288	29.628	12.058
50071	C23	M-009136- centaurin,	116985	CENTD2	2915	9.2624	8.3076
50071	D02	M-017014- myomesin	127294	MYOM3	5860	9.6587	7.9113
50071	D04	M-015867- chromoson	127281	C1orf93	5359	13.006	4.564
50071	D05	M-018294- spermatog	124044	SPATA2L	4808	16.057	1.513
50071	D06	M-019381- family with	127262	FAM79A	5262	13.417	4.153
50071	D07	M-016431- chromoson	124045	C16orf55	4451	15.794	1.776
50071	D08	M-016012- leucine rich	127255	LRRC44	4491	9.6192	7.9508
50071	D09	M-016237- NADPH oxi	124056	NOXO1	3633	13.185	4.385
50071	D10	M-021809- chromoson	127254	C1orf173	3291	26.77	9.2
50071	D11	M-018400- coiled-coil	124093	CCDC78	3362	22.606	5.036
50071	D12	M-021604- tRNA-yW s	127253	TYW3	2928	24.966	7.396
50071	D13	M-016410- IQ motif co	124152	IQCK	2966	22.994	5.424
50071	D14	M-015284- ankyrin rep	127247	ASB17	4157	20.399	2.829
50071	D15	M-016197- hypothetic	124216	LOC124216	3558	19.562	1.992
50071	D16	M-017569- ATPase, H+	127124	ATP6V1G3	2731	30.135	12.565
50071	D17	M-008923- hypothetic	124221	MGC52282	4146	15.292	2.278
50071	D18	M-008388- lysophosph	127018	LYPLAL1	4807	25.4	7.83
50071	D19	M-007910- progestin a	124222	PAQR4	4572	28.346	10.776
50071	D20	M-018376- ataxin 7-lik	127002	ATXN7L2	6795	35.305	17.735
50071	D21	M-018285- conserved	124245	NHN1	4842	12.144	5.426
50071	D23	M-008755- chromodor	124359	CDYL2	6417	21.879	4.309
50071	E02	M-019329- iron-sulfur	122961	ISCA2	6775	17.476	0.094
50071	E04	M-008321- jun dimeriz	122953	JDP2	4015	14.545	3.025
50071	E05	M-021010- centaurin,	116986	CENTG1	5110	18.16	0.59
50071	E06	M-016576- chromoson	122945	C14orf148	6841	27.525	9.955
50071	E07	M-020452- centaurin,	116987	CENTG2	5795	24.884	7.314
50071	E08	M-009027- glycoprotei	122876	GPHB5	4467	21.379	3.809
50071	E09	M-019127- centaurin,	116988	CENTG3	4309	22.627	5.057
50071	E10	M-009961- N-acetyltra	122830	NAT12	3745	20.134	2.564
50071	E11	M-026274- paired rela	117065	PRRXL1	2643	22.247	4.677
50071	E12	M-016437- FERM dom	122786	FRMD6	3088	14.67	2.9
50071	E13	M-015196- transcripti	117143	TADA1L	3127	31.148	13.578
50071	E14	M-016665- kelch doma	122773	KLHDC1	2817	21.157	3.587
50071	E15	M-008604- thioesteras	117145	THEM4	3858	26.672	9.102

50071	E16	M-016820- peptidylprc	122769	PPIL5	4404	28.906	11.336
50071	E17	M-021296- melanoma	117153	MIA2	3956	17.341	0.229
50071	E18	M-019012- mitochond	122704	MRPL52	3697	26.751	9.181
50071	E19	M-015201- SH2 domai	117157	SH2D1B	4635	28.328	10.758
50071	E20	M-017155- ribonuclea	122665	RNASE8	3610	27.784	10.214
50071	E21	M-015202- dermcidin	117159	DCD	3247	23.221	5.651
50071	E23	M-012920- WAP, follis	117166	WFIKKN1	5261	26.136	8.566
50071	F02	M-015949- solute carri	126969	SLC44A3	6760	19.822	2.252
50071	F04	M-019097- histone clu	126961	HIST2H3C	5266	22.826	5.256
50071	F05	M-022621- ankyrin rep	124401	ANKS3	5193	12.382	5.188
50071	F06	M-022072- hypothetic	126917	LOC126917	5527	19.794	2.224
50071	F07	M-015987- family with	124402	FAM100A	2463	12.992	4.578
50071	F08	M-016839- chromoson	126868	C1orf161	3774	17.276	0.294
50071	F09	M-016227- septin 12	124404	SEPT12	4342	13.058	4.512
50071	F10	M-019223- chromoson	126859	C1orf125	4758	15.027	2.543
50071	F11	M-022814- zinc finger	124411	ZNF720	3812	14.166	3.404
50071	F12	M-016017- kelch/anky	126823	KARCA1	3176	16.782	0.788
50071	F13	M-003993- hypothetic	124446	LOC124446	2671	28.866	11.296
50071	F14	M-016848- WD repeat	126820	WDR63	3475	21.842	4.272
50071	F15	M-016514- selectin lig	124460	SLIC1	4198	20.01	2.44
50071	F16	M-021340- UDP-Gal:be	126792	B3GALT6	2803	18.195	0.625
50071	F17	M-015996- transmem	124491	TMEM170	3945	16.705	0.865
50071	F18	M-016667- pseudouric	126789	PUSL1	5227	26.344	8.774
50071	F19	M-023220- heat shock	124535	HSF5	5512	26.379	8.809
50071	F20	M-022158- leucine rich	126755	LRRC38	5477	27.186	9.616
50071	F21	M-017248- musashi hc	124540	MSI2	6325	26.719	9.149
50071	F23	M-007359- hypothetic	124565	MGC15523	5220	28.831	11.261
50071	G02	M-017754- tubulin pol	122664	TPPP2	6438	14.647	2.923
50071	G04	M-015958- ribonuclea	122651	RNASE11	6335	22.194	4.624
50071	G05	M-018265- RAB3A inte	117177	RAB3IP	6436	11.498	6.072
50071	G06	M-010295- phospholip	122618	PLD4	4793	21.823	4.253
50071	G07	M-020361- synovial sa	117178	SSX2IP	6039	29.326	11.756
50071	G08	M-017761- chromoson	122616	C14orf79	4562	22.753	5.183
50071	G09	M-010293- HRAS-like s	117245	HRASLS5	3475	13.957	3.613
50071	G10	M-018297- trafficking	122553	TRAPPC6B	4235	28.689	11.119
50071	G11	M-013367- FtsJ homol	117246	FTSJ3	3889	27.256	9.686
50071	G12	M-021950- chromoson	122525	C14orf28	3163	15.302	2.268
50071	G13	M-007403- solute carri	117247	SLC16A10	2629	18.79	1.22
50071	G14	M-015934- family with	122509	FAM14B	3666	16.858	0.712
50071	G15	M-018649- UDP-N-ace	117248	GALNTL2	4145	34.596	17.026
50071	G16	M-015551- ankyrin rep	122416	ANKRD9	4114	19.908	2.338
50071	G17	M-015208- defensin, b	117285	DEFB118	4403	17.965	0.395
50071	G18	M-022008- tudor dom	122402	TDRD9	5293	19.686	2.116
50071	G19	M-008711- T-cell activ	117289	TAGAP	4656	28.651	11.081
50071	G20	M-015914- chromoson	122258	C13orf28	6259	17.591	0.021
50071	G21	M-013265- transmem	117532	TMC2	3826	6.7695	10.8005
50071	G23	M-010863- relaxin 3	117579	RLN3	4337	15.725	1.845

50071	H02	M-016008- chromoson	126731	C1orf96	4035	13.953	3.617
50071	H04	M-015599- chromoson	126695	C1orf172	5275	21.043	3.473
50071	H05	M-019272- Usher synd	124590	USH1G	4410	25.306	7.736
50071	H06	M-027713- Src homolo	126669	SHE	4272	12.687	4.883
50071	H07	M-004966- kinesin fam	124602	KIF19	3715	12.948	4.622
50071	H08	M-018657- tudor doma	126668	TDRD10	4970	17.586	0.016
50071	H09	M-010687- zona pelluc	124626	ZPBP2	3666	22.586	5.016
50071	H10	M-021788- hypothetica	126661	LOC126661	3611	30.684	13.114
50071	H11	M-016224- cytochrom	124637	CYB5D1	3707	13.515	4.055
50071	H12	M-027449- repetin	126638	RPTN	3046	22.029	4.459
50071	H13	M-023019- ubiquitin sp	124739	USP43	3221	32.971	15.401
50071	H14	M-016074- hypothetica	126626	MGC29891	3495	26.609	9.039
50071	H15	M-023016- KRAB-A do	124751	KRBA2	3207	22.95	5.38
50071	H16	M-023891- KIAA1957	126567	KIAA1957	4180	21.005	3.435
50071	H17	M-018784- chromoson	124773	C17orf64	4236	21.506	3.936
50071	H18	M-016461- ankyrin rep	126549	ANKRD41	4929	23.92	6.35
50071	H19	M-015837- chromoson	124783	C17orf46	6246	33.381	15.811
50071	H20	M-031244- hypothetica	126536	LOC12653	4918	26.698	9.128
50071	H21	M-016213- hexamthyl	124790	HEXIM2	5644	29.536	11.966
50071	H23	M-015641- LSM12 hon	124801	LSM12	4937	18.29	0.72
50071	I02	M-027206- FLJ40296 p	122183	FLJ40296	7026	15.3	2.27
50071	I04	M-018736- SLAIN moti	122060	SLAIN1	6161	18.731	1.161
50071	I05	M-015224- zinc finger	117608	ZNF354B	5094	23.263	5.693
50071	I06	M-016750- chromoson	122046	C13orf26	5748	13.97	3.6
50071	I07	M-007121- tripartite m	117854	TRIM6	5630	15.471	2.099
50071	I08	M-021595- hypothetica	121952	LOC12195	4414	11.192	6.378
50071	I09	M-015505- chromoson	118421	C21orf100	6551	14.12	3.45
50071	I10	M-021583- hypothetica	121951	FLJ40176	5828	21.071	3.501
50071	I11	M-018197- loss of hete	118426	LOH12CR1	4239	7.7377	9.8323
50071	I12	M-016184- chromoson	121793	C13orf16	3726	10.064	7.506
50071	I13	M-021637- olfactomec	118427	OLFM3	3059	12.292	5.278
50071	I14	M-006042- signal pept	121665	UNQ1887	3287	27.746	10.176
50071	I15	M-015215- anthrax tox	118429	ANTXR2	4756	18.398	0.828
50071	I16	M-027118- forkhead b	121643	FOXN4	5258	18.334	0.764
50071	I17	M-003683- small breas	118430	SBEM	5267	19.499	1.929
50071	I18	M-018551- transmemb	121601	TMEM16D	5606	16.179	1.391
50071	I19	M-026273- chromoson	118461	C10orf71	5235	14.288	3.282
50071	I20	M-015774- BTB (POZ)	121551	BTBD11	5042	10.432	7.138
50071	I21	M-027286- proline-rich	118471	PRAP1	5271	14.437	3.133
50071	I23	M-018086- zinc finger	118472	ZNF511	6716	13.386	4.184
50071	J02	M-018555- chromoson	126526	C19orf47	3705	16.977	0.593
50071	J04	M-023896- hypothetica	126520	LOC12652	3067	11.933	5.637
50071	J05	M-016216- coiled-coil	124808	CCDC43	5702	26.64	9.07
50071	J06	M-018558- F-box prote	126433	FBXO27	5432	16.09	1.48
50071	J07	M-018405- cyclin N-ter	124817	CNTD1	2781	18.339	0.769
50071	J08	M-027209- FLJ45909 p	126432	FLJ45909	3615	16.155	1.415
50071	J09	M-023299- transmemb	124842	TMEM132	4839	19.591	2.021

50071	J10	M-008905-	cytochrom	126410	CYP4F22	4301	27.482	9.912
50071	J11	M-019227-	WAP, follis	124857	WFIKKN2	3823	22.495	4.925
50071	J12	M-018427-	coiled-coil	126402	CCDC105	4217	24.069	6.499
50071	J13	M-016054-	beta-1,4-N	124872	B4GALNT2	3775	11.841	5.729
50071	J14	M-009224-	heat shock	126393	HSPB6	3673	24.694	7.124
50071	J15	M-017764-	sperm acro	124912	SPACA3	4873	22.963	5.393
50071	J16	M-017942-	zinc finger	126375	ZNF792	5262	16.724	0.846
50071	J17	M-008080-	seizure rela	124925	SEZ6	4979	19.482	1.912
50071	J18	M-015998-	leucine rich	126364	LRRC25	4485	15.719	1.851
50071	J19	M-018787-	ankyrin rep	124930	ANKRD13B	6599	15.199	2.371
50071	J20	M-018420-	chromoson	126353	C19orf21	5596	19.425	1.855
50071	J21	M-016443-	solute carri	124935	SLC43A2	5407	14.888	2.682
50071	J23	M-004706-	cytochrom	124936	CYB5D2	5971	12.376	5.194
50071	K02	M-026940-	achaete-sc	121549	ASCL4	5531	14.482	3.088
50071	K04	M-007123-	FYVE, RhoG	121512	FGD4	5754	11.436	6.134
50071	K05	M-027351-	coiled-coil-	118487	CHCHD1	5875	15.132	2.438
50071	K06	M-015698-	endoplasm	121506	ERP27	6364	13.891	3.679
50071	K07	M-018243-	zinc finger,	118490	ZMYND17	5792	16.575	0.995
50071	K08	M-019233-	histone clu	121504	HIST4H4	4464	13.284	4.286
50071	K09	M-016390-	tetratricop	118491	TTC18	6095	16.768	0.802
50071	K10	M-008306-	neural prec	121441	NEDD1	2743	18.666	1.096
50071	K11	M-026375-	chromoson	118611	C10orf90	3918	11.409	6.161
50071	K12	M-017998-	keratin 74	121391	KRT74	3792	24.736	7.166
50071	K13	M-016301-	BTB (POZ)	118663	BTBD16	2512	14.57	3
50071	K14	M-016283-	family with	121355	FAM112B	4420	11.29	6.28
50071	K15	M-016512-	phosphose	118672	PSTK	3780	14.921	2.649
50071	K16	M-008305-	tryptophan	121278	TPH2	5318	20.666	3.096
50071	K17	M-016290-	zinc finger	118738	ZNF488	5169	17.392	0.178
50071	K18	M-007122-	zinc finger	121274	ZNF641	3947	10.084	7.486
50071	K19	M-018541-	chromoson	118812	C10orf83	5506	17.508	0.062
50071	K20	M-015959-	chromoson	121273	C12orf54	5689	22.06	4.49
50071	K21	M-016349-	zinc finger,	118813	ZFYVE27	5682	6.9342	10.6358
50071	K23	M-018735-	catechol-O	118881	COMTD1	6431	6.4998	11.0702
50071	L02	M-018508-	NADH dehy	126328	NDUFA11	6592	19.463	1.893
50071	L04	M-015416-	GIPC PDZ d	126326	GIPC3	6750	21.822	4.252
50071	L05	M-023008-	chromoson	124944	C17orf49	6641	30.854	13.284
50071	L06	M-018417-	chromoson	126321	C19orf28	7422	31.393	13.823
50071	L07	M-016831-	zinc finger	124961	ZFP3	5891	18.723	1.153
50071	L08	M-015299-	MOB1, Mp	126308	MOBKL2A	2661	25.554	7.984
50071	L09	M-016666-	gamma-glu	124975	GGT6	5902	34.141	16.571
50071	L10	M-021303-	junctional	126306	JSRP1	5573	48.143	30.573
50071	L11	M-007344-	spinster ho	124976	SPNS2	4407	16.928	0.642
50071	L12	M-018656-	zinc finger	126299	ZNF428	4147	9.4044	8.1656
50071	L13	M-018295-	chromoson	124989	C17orf57	3371	22.872	5.302
50071	L14	M-007125-	zinc finger	126295	ZNF57	4803	17.635	0.065
50071	L15	M-017394-	mitochond	124995	MRPL10	5130	28.304	10.734
50071	L16	M-016446-	tumor necr	126282	TNFAIP8L1	5640	17.128	0.442

50071	L17	M-016825- WD repeat	124997	WDR81	5600	21.214	3.644
50071	L18	M-016537- EP300 inte	126272	EID2B	5774	15.778	1.792
50071	L19	M-019420- TBC1 doma	125058	TBC1D16	6324	19.133	1.563
50071	L20	M-016089- transmem	126259	TMIGD2	5524	20.293	2.723
50071	L21	M-016720- gap junctio	125111	GJC1	7242	12.842	4.728
50071	L23	M-016589- keratin 222	125113	KRT222P	5713	6.9666	10.6034
50071	M02	M-008778- Ras homol	121268	RHEBL1	6139	11.81	5.76
50071	M04	M-007401- solute carri	121260	SLC15A4	5762	27.317	9.747
50071	M05	M-016293- ankyrin rep	118932	ANKRD22	7339	26.202	8.632
50071	M06	M-027087- transmem	121256	TMEM132	7000	30.414	12.844
50071	M07	M-018547- sideroflexi	118980	SFXN2	6730	20.312	2.742
50071	M08	M-016513- leucine-ric	121227	LRIG3	6839	29.727	12.157
50071	M09	M-018369- PDZ domai	118987	PDZD8	5716	26.382	8.812
50071	M10	M-008855- orphan sho	121214	SDR-O	6093	24.175	6.605
50071	M11	M-015345- centaurin,	119016	CTGLF1	5929	28.15	10.58
50071	M12	M-016009- chromoson	121053	C12orf45	5285	29.063	11.493
50071	M13	M-016288- chromoson	119032	C10orf32	4127	20.257	2.687
50071	M14	M-026954- hypothetic	121006	LOC12100	4140	26.208	8.638
50071	M15	M-019380- lysozyme-li	119180	LYZL2	5918	17.945	0.375
50071	M16	M-016013- chromoson	120939	C12orf59	6332	17.925	0.355
50071	M17	M-026289- KIAA1975	119385	KIAA1975	6583	23.333	5.763
50071	M18	M-018642- coiled-coil	120935	CCDC38	6310	17.195	0.375
50071	M19	M-026311- glutathione	119391	GSTO2	5978	20.91	3.34
50071	M20	M-006323- leucine-ric	120892	LRRK2	6018	22.35	4.78
50071	M21	M-015697- chromoson	119392	C10orf78	6458	20.316	2.746
50071	M23	M-018828- family with	119395	FAM26A	5899	19.715	2.145
50071	N02	M-018414- WD repeat	126248	WDR88	5024	12.5	5.07
50071	N04	M-016620- zinc finger	126231	ZNF573	5134	11.94	5.63
50071	N05	M-018643- keratin 40	125115	KRT40	6133	15.033	2.537
50071	N06	M-023823- zinc finger	126208	ZNF787	6508	16.334	1.236
50071	N07	M-016543- chromoson	125144	C17orf45	6501	18.274	0.704
50071	N08	M-019146- NLR family,	126206	NLRP5	6416	19.031	1.461
50071	N09	M-017272- Smith-Mag	125170	SMCR7	6420	16.573	0.997
50071	N10	M-023659- hypothetic	126167	LOC12616	5563	11.541	6.029
50071	N11	M-007333- solute carri	125206	SLC5A10	5307	19.823	2.253
50071	N12	M-016814- hypothetic	126147	LOC12614	4150	14.289	3.281
50071	N13	M-015626- chromoson	125228	C18orf19	5470	22.431	4.861
50071	N14	M-008646- aldehyde d	126133	ALDH16A1	6077	22.429	4.859
50071	N15	M-007124- lipoxygena	125336	LOXHD1	5734	6.9759	10.5941
50071	N16	M-008824- carnitine p	126129	CPT1C	4954	8.3569	9.2131
50071	N17	M-019327- chromoson	125476	C18orf37	5221	8.9063	8.6637
50071	N18	M-016815- chromoson	126123	C19orf41	5166	14.131	3.439
50071	N19	M-016915- chromoson	125488	C18orf17	6240	19.423	1.853
50071	N20	M-015500- Josephin d	126119	JOSD2	5931	16.911	0.659
50071	N21	M-015524- claudin do	125875	CLDND2	4429	10.07	7.5
50071	N23	M-023813- zinc finger	125893	ZNF816A	4876	11.792	5.778
50071	O02	M-016039- DEP domai	120863	DEPDC4	6003	18.407	0.837

50071	O04	M-015992- chromoson	120534	C11orf46	5634	21.246	3.676
50071	O05	M-016086- clarin 3	119467	CLRN3	5560	19.209	1.639
50071	O06	M-008875- DPH4, JJJ3	120526	DPH4	5197	14.835	2.735
50071	O07	M-018378- chromoson	119504	C10orf104	5305	15.834	1.736
50071	O08	M-016407- adhesion m	120425	AMICA1	4925	12.995	4.575
50071	O09	M-010294- pancreatic	119548	PNLIPRP3	5236	13.541	4.029
50071	O10	M-018588- family with	120406	FAM55B	4978	27.802	10.232
50071	O11	M-018237- sideroflexir	119559	SFXN4	4030	18.362	0.792
50071	O12	M-015986- family with	120400	FAM55A	3440	8.8081	8.7619
50071	O13	M-005927- carboxypep	119587	CPXM2	3664	12.364	5.206
50071	O14	M-016573- PIH1 doma	120379	PIH1D2	4352	20.404	2.834
50071	O15	M-016572- chromoson	119710	C11orf74	4287	10.054	7.516
50071	O16	M-026516- hypothetic	120376	LOC120376	4457	15.033	2.537
50071	O17	M-019367- glycosyltra	120071	GYLTL1B	5486	12.742	4.828
50071	O18	M-014351- cytochrom	120227	CYP2R1	4451	10.47	7.1
50071	O19	M-007553- solute carri	120103	SLC36A4	5656	12.801	4.769
50071	O20	M-018706- transmemb	120224	TMEM45B	5425	10.286	7.284
50071	O21	M-026743- FAT tumor	120114	FAT3	5188	13.763	3.807
50071	O23	M-015982- chromoson	120196	C11orf69	4851	5.5452	12.0248
50071	P02	M-017913- chromoson	126074	C19orf39	3528	11.933	5.637
50071	P04	M-016889- zinc finger	126070	ZNF440	3689	14.367	3.203
50071	P05	M-023828- zinc finger	125919	ZNF543	2770	19.783	2.213
50071	P06	M-018758- zinc finger	126069	ZNF491	5449	24.225	6.655
50071	P07	M-027208- carcinoemb	125931	CEACAM20	2351	12.42	5.15
50071	P08	M-016909- zinc finger	126068	ZNF441	4779	15.589	1.981
50071	P09	M-015346- ribonucleo	125950	RAVER1	3964	17.255	0.315
50071	P10	M-024078- Purkinje ce	126006	PCP2	4342	8.5675	9.0025
50071	P11	M-019413- cytochrom	125965	COX6B2	4930	16.471	1.099
50071	P12	M-024079- trafficking	126003	TRAPPC5	4577	11.427	6.143
50071	P13	M-013004- exosome c	118460	EXOSC6	3103	17.241	0.329
50071	P14	M-017360- methyl-Cp	125997	MBD3L2	3944	15.847	1.723
50071	P15	M-015213- gene differ	118425	GDEP	5113	17.759	0.189
50071	P16	M-031920- hypothetic	125988	P117	4704	15.115	2.455
50071	P17	M-016408- IKK interac	121457	IKIP	4935	22.796	5.226
50071	P18	M-010298- N-acylsphir	125981	ASAH3	5353	11.732	5.838
50071	P19	M-012971- ribosomal	116832	RPL39L	3494	12.936	4.634
50071	P20	M-016230- calreticulin	125972	CALR3	4882	25.317	7.747
50071	P21	M-016922- junction-m	133746	JMY	4668	19.537	1.967
50071	P23	M-032031- zinc finger	133923	ZNF474	3514	14.798	2.772
				mdn	4662	17.572	4.568
				3MAD			13.704
				MADc			6.76064
50071	C22				2681	16.039	
50071	D22				2817	10.082	
50071	E22				1680	15.595	

50071	F22					3227	9.3275
					mn	2601.25	12.76088
					sd	656.5498	3.546961
50071	G22					4125	47.345
50071	I22					5019	49.173
50071	H22					6714	56.315
50071	J22					6516	50.89
					mn	5593.5	50.93075
					sd	1237.345	3.870362
					3psSD		11.61108
					3ngSD		10.64088
					SumSD		22.25197
					DiffMn		38.16988
					SmovrDiff		0.582972
					1minus		0.417028
50071	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	1482	40.013
50071	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	1120	41.518
50071	J03	D-001206-	siControl non-targeting			3438	39.122
50071	I03	D-001206-	siControl non-targeting			6104	45.724
50071	K03	D-001600-	siGLO RISC-free siRNA			7540	46.22
50071	L03	D-001600-	siGLO RISC-free siRNA			6864	49.985

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.527761	2435	4.4764	6.4736	-1.2999	3561	14.575	5.035	1.185287
-0.47569	2826	11.359	0.409	0.081274	2908	8.4594	1.0806	-0.25474
1.590086	3635	19.037	8.087	1.622063	3560	18.511	8.971	2.11209
-1.41617	2147	9.9674	0.9826	-0.19799	2261	6.7669	2.7731	-0.65327
-0.86856	2867	6.0342	4.9158	-0.98729	2219	10.41	0.87	0.204563
0.466228	3534	13.016	2.066	0.413794	4068	15.069	5.529	1.301609
-1.04221	2369	3.588	7.362	-1.47818	1949	7.3884	2.1516	-0.50693
-1.25339	1971	3.9574	6.9926	-1.40405	2556	8.6463	0.8937	-0.21073
0.0071	2745	9.5811	1.3689	-0.27551	2207	15.134	5.594	1.316914
-0.11094	2875	9.6	1.35	-0.27172	2104	9.981	0.441	0.103547
-0.67656	2284	9.1506	1.7994	-0.3619	2474	10.348	0.808	0.189964
-1.22335	2948	9.498	1.452	-0.29218	3732	15.648	6.108	1.437945
-0.93586	3507	8.982	1.968	-0.39573	3229	8.7953	0.7447	-0.17565
-1.43834	2900	5.3793	5.5707	-1.11871	3920	5.2551	4.2849	-1.00925
-0.84548	2913	8.5136	2.4364	-0.48973	4553	12.937	3.397	0.799591
-0.72789	2796	16.953	6.003	1.203855	2337	9.5421	0.0021	0.0002
-1.26541	2727	17.565	6.615	1.326668	4191	13.648	4.108	0.967009
-1.23972	2665	11.107	0.157	0.030703	4181	7.1992	2.3408	-0.55148
-0.965	3355	21.252	10.302	2.06656	3863	11.157	1.617	0.380458
-0.43709	2928	12.568	1.618	0.323891	4502	9.0849	0.4551	-0.10746
-1.11158	5200	2.9808	7.9692	-1.60003	4003	9.5678	0.0278	0.006252
-0.18682	4317	4.2622	6.6878	-1.34288	3757	7.0535	2.4865	-0.58579
-0.49833	5134	5.0838	5.8662	-1.17801	3606	8.7909	0.7491	-0.17668
-0.3686	5939	6.4826	4.4674	-0.8973	4536	10.538	0.998	0.234703
0.330738	5418	5.3525	5.5975	-1.12409	4303	8.7613	0.7787	-0.18365
-1.53264	3976	2.6157	8.3343	-1.6733	2257	2.7913	6.7487	-1.5894
0.418895	4616	6.4341	4.5159	-0.90703	2904	7.6791	1.8609	-0.43848
0.806728	6634	9.0292	1.9208	-0.38626	2875	7.7565	1.7835	-0.42025
-0.36713	5371	4.7105	6.2395	-1.25292	2423	6.8923	2.6477	-0.62374
-0.36831	4332	3.8089	7.1411	-1.43385	2299	8.047	1.493	-0.35185
1.863729	4674	13.543	2.593	0.51955	3295	13.414	3.874	0.911909
0.27882	5204	9.435	1.515	-0.30483	2438	8.3675	1.1725	-0.27638
-0.02973	3875	4.6452	6.3048	-1.26602	3310	11.511	1.971	0.463813
-1.21965	3249	4.7707	6.1793	-1.24084	1199	12.177	2.637	0.620635
-1.25765	4532	3.9276	7.0224	-1.41003	2593	6.7875	2.7525	-0.64842
-1.28188	4399	4.9329	6.0171	-1.20829	2960	6.2838	3.2562	-0.76703
-0.23134	4519	6.0854	4.8646	-0.97701	3386	9.1553	0.3847	-0.09088
-0.00207	6068	12.459	1.509	0.302017	5504	13.826	4.286	1.008922
-1.15554	6888	12.035	1.085	0.216931	5087	11.598	2.058	0.484299
-1.71457	6345	11.6	0.65	0.129637	5532	11.153	1.613	0.379516
-0.18682	4908	11.084	0.134	0.026088	5171	9.5146	0.0254	-0.00628
1.32872	4091	17.575	6.625	1.328675	4659	17.879	8.339	1.963274
0.226458	5198	10.389	0.561	-0.11338	4889	16.568	7.028	1.654575
-0.29243	4318	7.1561	3.7939	-0.76215	3048	8.727	0.813	-0.19173
0.054285	4134	7.2085	3.7415	-0.75163	2655	6.4407	3.0993	-0.73008
-0.51933	4549	10.156	0.794	-0.16014	2775	5.5495	3.9905	-0.93993

1.089246	3672	9.7222	1.2278	-0.24719	3359	15.927	6.387	1.50364
2.267981	3937	17.704	6.754	1.354562	3089	19.845	10.305	2.426204
-0.40041	4928	11.871	0.921	0.18402	2652	8.2579	1.2821	-0.30219
0.798297	3419	8.1603	2.7897	-0.56063	1904	10.819	1.279	0.300869
1.237753	2534	11.8	0.85	0.169772	2561	11.714	2.174	0.511613
-0.47022	3022	7.2138	3.7362	-0.75057	2424	8.5396	1.0004	-0.23586
0.881573	4216	14.303	3.353	0.672064	2802	11.813	2.273	0.534925
-0.50291	3604	11.099	0.149	0.029098	2551	8.9769	0.5631	-0.13289
3.23638	3322	21.884	10.934	2.193387	2867	22.672	13.132	3.091873
2.82281	5821	18.124	7.174	1.438846	4176	12.955	3.415	0.803829
0.46963	4376	14.374	3.424	0.686311	3897	15.704	6.164	1.451131
-0.39479	4441	10.065	0.885	-0.1784	4034	9.3456	0.1944	-0.04607
1.783263	5451	16.896	5.946	1.192416	5821	13.64	4.1	0.965125
-1.22911	2950	4.8136	6.1364	-1.23223	1823	5.4306	4.1094	-0.96793
-1.1705	4449	5.3945	5.5555	-1.11566	3509	7.8085	1.7315	-0.40801
-0.67538	4559	6.4268	4.5232	-0.9085	3427	9.075	0.465	-0.10979
-0.22409	4223	5.1859	5.7641	-1.15752	3332	5.4922	4.0478	-0.95342
-0.61459	4416	5.865	5.085	-1.02124	3460	8.7572	0.7828	-0.18462
-0.26299	3907	8.8815	2.0685	-0.4159	2711	7.2667	2.2733	-0.53558
-1.17634	5197	9.3708	1.5792	-0.31771	3547	5.7231	3.8169	-0.89905
-0.6489	4307	9.4033	1.5467	-0.31119	2769	3.6114	5.9286	-1.39629
1.360522	4038	14.785	3.835	0.768789	2284	10.902	1.362	0.320413
0.744604	3400	16.235	5.285	1.059769	2230	8.6099	0.9301	-0.2193
1.093683	3502	15.277	4.327	0.867522	2490	14.699	5.159	1.214486
0.801995	3117	13.699	2.749	0.550855	2457	11.437	1.897	0.446389
0.418156	4689	15.803	4.853	0.973077	2308	13.518	3.978	0.936398
0.294351	4295	18.929	7.979	1.60039	3078	11.339	1.799	0.423313
1.858256	3902	15.505	4.555	0.913276	3315	10.528	0.988	0.232348
-0.33725	4120	8.8107	2.1393	-0.43011	3103	7.1866	2.3534	-0.55444
1.157879	4912	18.689	7.739	1.552228	4217	16.41	6.87	1.617371
1.593636	5441	15.99	5.04	1.010604	4213	10.99	1.45	0.341134
2.622977	6421	23.299	12.349	2.477344	5715	12.686	3.146	0.740488
-0.80288	3961	10.906	0.044	-0.00963	4485	9.0078	0.5322	-0.12561
0.63707	3801	11.181	0.231	0.045553	5120	9.4922	0.0478	-0.01155
-0.0142	3406	10.217	0.733	-0.1479	4703	10.1	0.56	0.131568
-0.44774	2183	8.5204	2.4296	-0.48836	2345	7.6333	1.9067	-0.44926
0.086974	3502	13.649	2.699	0.540821	3031	12.372	2.832	0.666551
1.472198	4697	20.439	9.489	1.903411	4837	19.661	10.121	2.382878
1.081554	4843	20.69	9.74	1.95378	4614	19.788	10.248	2.412783
0.563112	4669	15.721	4.771	0.956622	3867	13.059	3.519	0.828318
0.74771	5068	19.89	8.94	1.79324	4228	13.198	3.658	0.861048
0.378958	4480	11.317	0.367	0.072845	4526	9.5007	0.0393	-0.00955
0.691503	4192	14.456	3.506	0.702767	3248	8.9901	0.5499	-0.12978
-0.42925	3185	9.2936	1.6564	-0.3332	2593	4.7821	4.7579	-1.12063
2.008094	3431	6.6744	4.2756	-0.85881	2062	9.2144	0.3256	-0.07696
0.530275	3634	8.1728	2.7772	-0.55812	3192	8.396	1.144	-0.26967
1.346026	4328	11.114	0.164	0.032108	2921	9.6542	0.1142	0.026596

1.676469	4762	13.251	2.301	0.460952	3926	10.647	1.107	0.260369
-0.03417	4102	5.9971	4.9529	-0.99473	4015	5.1308	4.4092	-1.03852
1.357712	4148	10.824	0.126	-0.02609	3484	9.4145	0.1255	-0.02985
1.590974	5477	16.925	5.975	1.198236	4641	15.385	5.845	1.376017
1.510508	4511	14.077	3.127	0.626711	5425	9.3456	0.1944	-0.04607
0.835572	4227	13.769	2.819	0.564903	3035	9.4234	0.1166	-0.02775
1.266744	5110	12.642	1.692	0.338741	4497	9.3173	0.2227	-0.05273
0.332809	5868	19.888	8.938	1.792838	5650	10.867	1.327	0.312172
0.777145	4265	10.012	0.938	-0.18904	4840	13.967	4.427	1.042123
-0.76768	3584	7.2545	3.6955	-0.7424	3927	2.9539	6.5861	-1.55111
0.328667	4975	15.839	4.889	0.980302	4926	13.276	3.736	0.879414
-0.67745	1716	6.5268	4.4232	-0.88843	1178	3.3956	6.1444	-1.4471
-0.04378	4455	9.4276	1.5224	-0.30631	4574	7.7394	1.8006	-0.42428
-0.66769	4978	7.8947	3.0553	-0.61393	5861	6.6371	2.9029	-0.68383
-0.37644	3323	8.5766	2.3734	-0.47709	5150	11.243	1.703	0.400708
-0.5038	3613	7.39	3.56	-0.71521	3089	2.1366	7.4034	-1.74356
-0.11685	2851	13.855	2.905	0.582161	2864	7.4721	2.0679	-0.48722
1.670552	2893	11.407	0.457	0.090906	3270	9.6942	0.1542	0.036015
0.631597	3199	8.3464	2.6036	-0.52328	4007	3.419	6.121	-1.44159
0.360617	3642	5.2718	5.6782	-1.14028	2695	3.7848	5.7552	-1.35546
0.092151	3866	10.916	0.034	-0.00763	2929	4.6774	4.8626	-1.14528
-0.12824	3861	7.2779	3.6721	-0.7377	4254	4.913	4.627	-1.08981
1.29751	6558	12.489	1.539	0.308037	4510	10.51	0.97	0.22811
1.302687	5159	10.215	0.735	-0.1483	3700	7.9459	1.5941	-0.37565
1.422055	5390	9.1651	1.7849	-0.35899	6013	9.4628	0.0772	-0.01847
1.352978	5657	15.821	4.871	0.976689	6748	10.388	0.848	0.199383
1.665375	5123	10.346	0.604	-0.12201	6372	12.006	2.466	0.58037
-0.43265	5086	11.738	0.788	0.15733	5611	11.905	2.365	0.556588
0.683663	3698	12.574	1.624	0.325095	4248	15.443	5.903	1.389674
-0.89844	4099	13.076	2.126	0.425834	3934	4.8551	4.6849	-1.10344
0.628787	5049	21.727	10.777	2.161881	4643	14.538	4.998	1.176575
1.738593	4472	26.319	15.369	3.083385	5378	27.705	18.165	4.276983
0.766348	4339	17.124	6.174	1.23817	4141	17.532	7.992	1.881567
-0.53471	3542	8.6392	2.3108	-0.46452	3103	6.671	2.869	-0.67585
1.644371	3813	16.391	5.441	1.091075	5518	15.295	5.755	1.354825
1.432409	3505	20.2	9.25	1.855449	2829	9.1198	0.4202	-0.09924
-0.33577	3311	3.7451	7.2049	-1.44665	3195	3.975	5.565	-1.31067
0.18016	2033	6.3453	4.6047	-0.92485	1556	3.7275	5.8125	-1.36895
-0.10561	3764	9.0861	1.8639	-0.37484	3043	6.2438	3.2962	-0.77644
2.518105	5031	26.198	15.248	3.059103	4613	19.684	10.144	2.388294
0.345529	3846	10.348	0.602	-0.12161	3694	9.3395	0.2005	-0.04751
0.058131	4692	13.662	2.712	0.54343	3394	5.0972	4.4428	-1.04643
0.312692	3907	9.7517	1.1983	-0.24127	4169	12.329	2.789	0.656426
1.63875	6078	13.047	2.097	0.420015	4393	8.2859	1.2541	-0.29559
0.00281	4108	6.962	3.988	-0.8011	4996	4.5036	5.0364	-1.18621
-1.59785	3015	3.0514	7.8986	-1.58586	4529	6.4032	3.1368	-0.73891
-0.2732	3697	10.982	0.032	0.005619	4533	5.3827	4.1573	-0.97921

-0.5353	3742	11.678	0.728	0.145289	4276	19.645	10.105	2.379111
0.513413	3484	15.786	4.836	0.969666	4608	24.457	14.917	3.512183
1.143975	3060	12.81	1.86	0.372454	3756	16.986	7.446	1.753001
-0.72256	3843	8.3789	2.5711	-0.51676	4524	19.12	9.58	2.25549
-0.68396	4118	12.725	1.775	0.355397	4505	10.855	1.315	0.309346
0.002071	4676	8.8751	2.0749	-0.41719	4341	14.974	5.434	1.279239
0.741646	3086	9.5593	1.3907	-0.27988	3808	15.94	6.4	1.506701
1.939461	5097	12.164	1.214	0.242818	4597	15.38	5.84	1.374839
-0.60009	3766	11.976	1.026	0.205091	2794	14.996	5.456	1.28442
0.659257	3984	5.7731	5.1769	-1.03968	3529	9.1527	0.3873	-0.09149
2.277743	2202	10.854	0.096	-0.02007	2121	21.216	11.676	2.749031
1.336708	3676	9.7661	1.1839	-0.23838	3114	23.764	14.224	3.349004
0.795487	3404	8.8132	2.1368	-0.42961	3256	14.22	4.68	1.101696
0.507792	3946	10.821	0.129	-0.02669	2832	11.017	1.477	0.347492
0.581898	4739	8.3351	2.6149	-0.52555	2712	11.431	1.891	0.444976
0.938964	5449	10.699	0.251	-0.05117	3610	14.848	5.308	1.24957
2.338388	5119	13.03	2.08	0.416603	4682	17.343	7.803	1.837063
1.349872	5154	9.9922	0.9578	-0.19301	4305	16.376	6.836	1.609366
1.769655	3576	10.766	0.184	-0.03773	3626	16.823	7.283	1.71462
0.106203	3953	5.2365	5.7135	-1.14736	2349	5.8748	3.6652	-0.86333
-0.33606	3838	10.526	0.424	-0.08589	5988	16.667	7.127	1.677887
0.171433	2622	23.684	12.734	2.554604	3200	23.031	13.491	3.176406
0.841784	3668	14.995	4.045	0.810931	3305	22.118	12.578	2.961423
-0.53279	2342	8.6678	2.2822	-0.45879	3315	7.9336	1.6064	-0.37855
-0.31077	2998	15.177	4.227	0.847454	3545	16.107	6.567	1.546025
-0.9437	2995	14.758	3.808	0.763371	2014	10.377	0.837	0.196792
-0.5106	4691	19.527	8.577	1.720394	4431	13.36	3.82	0.899194
0.517555	4852	21.063	10.113	2.028632	2898	16.322	6.782	1.59665
-1.45464	3934	7.4733	3.4767	-0.69849	2611	9.4983	0.0417	-0.01011
-1.11055	3147	10.359	0.591	-0.1194	2940	10.034	0.494	0.116027
-0.78099	2067	8.7567	2.1933	-0.44095	1726	8.1692	1.3708	-0.32307
1.504887	2623	12.581	1.631	0.3265	2087	13.321	3.781	0.890011
0.122178	3132	13.793	2.843	0.569719	2532	12.559	3.019	0.710584
0.112711	3867	7.2666	3.6834	-0.73997	2614	10.138	0.598	0.140516
0.285032	4496	9.2082	1.7418	-0.35034	3147	9.6282	0.0882	0.020474
-0.20605	3722	11.311	0.361	0.071641	3039	9.6413	0.1013	0.023559
-0.48575	2581	3.8357	7.1143	-1.42847	3601	6.0816	3.4584	-0.81464
-1.05611	4475	8.9832	1.9668	-0.39549	3650	4.0274	5.5126	-1.29834
-0.46371	3727	7.2713	3.6787	-0.73903	3578	7.5182	2.0218	-0.47636
-0.61917	3672	5.3649	5.5851	-1.1216	3742	6.5473	2.9927	-0.70498
-0.08801	3935	16.417	5.467	1.096292	4816	2.4709	7.0691	-1.66484
-0.83409	2119	14.11	3.16	0.633333	3582	3.1826	6.3574	-1.49726
1.341293	3961	19.212	8.262	1.657181	5647	9.2438	0.2962	-0.07004
-0.21921	3977	17.425	6.475	1.298574	4724	4.8264	4.7136	-1.1102
0.113451	2906	19.374	8.424	1.689691	4369	6.9352	2.6048	-0.61364
-0.2096	2743	13.416	2.466	0.494064	4840	5.7025	3.8375	-0.9039
0.29864	4160	20.913	9.963	1.998531	4988	7.2374	2.3026	-0.54248

1.465838	3615	22.075	11.125	2.231716	4804	13.301	3.761	0.885301
0.728185	3361	17.941	6.991	1.402122	4234	10.723	1.183	0.278264
0.961004	2800	16.679	5.729	1.148869	4082	6.9084	2.6316	-0.61995
-0.8477	2702	12.028	1.078	0.215526	3235	3.493	6.047	-1.42417
1.053451	3116	11.842	0.892	0.1782	3291	5.4695	4.0705	-0.95877
0.79741	2002	17.283	6.333	1.270078	3716	7.1313	2.4087	-0.56747
-0.12543	3118	13.855	2.905	0.582161	4934	6.6072	2.9328	-0.69088
0.282518	3165	20.158	9.208	1.847021	3965	8.2472	1.2928	-0.30471
-0.27409	2848	13.097	2.147	0.430048	4171	6.9288	2.6112	-0.61515
-0.351	5544	17.929	6.979	1.399714	6656	12.41	2.87	0.675499
0.274086	3811	23.38	12.43	2.493598	3996	5.6056	3.9344	-0.92672
-0.397	4490	16.481	5.531	1.109136	4717	8.0984	1.4416	-0.33975
-0.76857	4161	14.372	3.422	0.68591	4428	8.3559	1.1841	-0.27911
-0.45706	3839	14.118	3.168	0.634938	4436	9.6032	0.0632	0.014587
-0.90761	3177	15.392	4.442	0.8906	4186	7.8356	1.7044	-0.40163
-0.36091	3686	19.886	8.936	1.792437	4371	10.043	0.503	0.118146
-0.54448	3293	14.425	3.475	0.696546	4135	11.391	1.851	0.435557
-0.14747	4135	19.758	8.808	1.76675	4658	11.013	1.473	0.34655
-0.63426	2608	18.597	7.647	1.533766	3841	8.2531	1.2869	-0.30332
-0.11892	3155	8.5895	2.3605	-0.4745	3438	9.5404	0.0004	-0.0002
0.161819	1078	24.861	13.911	2.790799	1807	11.566	2.026	0.476764
-0.9116	3884	12.024	1.074	0.214723	4593	10.102	0.562	0.132039
1.059663	2948	20.149	9.199	1.845215	3627	17.811	8.271	1.947262
-0.44404	2286	10.455	0.495	-0.10014	3364	8.1748	1.3652	-0.32176
-0.9292	2677	14.158	3.208	0.642966	4102	8.3374	1.2026	-0.28347
-0.39212	2175	10.805	0.145	-0.0299	3761	13.932	4.392	1.033882
0.457649	2687	10.495	0.455	-0.09211	4742	15.183	5.643	1.328452
-0.02662	2782	12.797	1.847	0.369846	4847	16.959	7.419	1.746643
-1.10759	2347	7.0729	3.8771	-0.77884	3672	4.0577	5.4823	-1.2912
-0.00947	3331	12.579	1.629	0.326098	4794	7.6345	1.9055	-0.44898
0.663842	3110	15.016	4.066	0.815145	5508	15.142	5.602	1.318798
-1.57349	2691	9.4017	1.5483	-0.31151	4889	8.243	1.297	-0.3057
-1.63774	3238	3.5516	7.3984	-1.48548	4298	6.4216	3.1184	-0.73458
0.279707	4204	14.772	3.822	0.76618	5825	8.9614	0.5786	-0.13654
0.628639	2965	9.2074	1.7426	-0.3505	3939	4.5443	4.9957	-1.17662
1.964607	2687	11.202	0.252	0.049768	4653	9.0264	0.5136	-0.12123
2.044333	2497	15.419	4.469	0.896018	5460	10.421	0.881	0.207153
0.17025	2159	10.283	0.667	-0.13465	5670	8.0071	1.5329	-0.36124
1.180657	1471	22.366	11.416	2.290113	3020	13.179	3.639	0.856574
2.450803	1506	15.206	4.256	0.853274	5155	17.051	7.511	1.768306
4.521909	2816	35.227	24.277	4.871006	4612	33.348	23.808	5.60573
-0.09526	1930	7.8756	3.0744	-0.61776	3810	8.2677	1.2723	-0.29988
-1.20811	1835	6.267	4.683	-0.94057	3815	4.7182	4.8218	-1.13567
0.783949	2121	8.3451	2.6049	-0.52354	3520	7.2727	2.2673	-0.53417
0.009319	3210	10.654	0.296	-0.0602	4406	8.6927	0.8473	-0.19981
1.587424	2337	12.366	1.416	0.283354	4307	10.959	1.419	0.333835
-0.06567	2661	11.875	0.925	0.184822	3145	9.0938	0.4462	-0.10536

0.538706	2887	20.506	9.556	1.916856	4335	19.054	9.514	2.239949
-0.26536	2432	8.347	2.603	-0.52316	4058	8.9946	0.5454	-0.12872
0.230895	3659	11.151	0.201	0.039533	5417	16.264	6.724	1.582993
0.402477	3148	11.817	0.867	0.173183	4538	7.9771	1.5629	-0.36831
-0.69964	4298	9.3299	1.6201	-0.32592	6166	9.8605	0.3205	0.075173
-1.5687	4395	7.3493	3.6007	-0.72338	4226	3.3365	6.2035	-1.46102
-0.85229	4445	11.856	0.906	0.18101	5150	13.65	4.11	0.96748
1.441432	3299	21.128	10.178	2.041676	4571	29.381	19.841	4.671628
1.276506	3256	13.698	2.748	0.550655	5966	21.187	11.647	2.742202
1.899524	5053	25.727	14.777	2.964585	5637	30.247	20.707	4.875543
0.405287	3174	3.7177	7.2323	-1.45215	5015	13.918	4.378	1.030585
1.797907	3234	9.9876	0.9624	-0.19393	4768	17.722	8.182	1.926306
1.303131	2579	25.359	14.409	2.890736	5167	22.257	12.717	2.994153
0.976683	3282	12.249	1.299	0.259875	6902	17.676	8.136	1.915474
1.564645	2571	9.9961	0.9539	-0.19223	4522	20.168	10.628	2.50226
1.699691	3122	12.332	1.382	0.276531	3768	13.907	4.367	1.027995
0.397152	1621	7.7113	3.2387	-0.65073	3509	10.972	1.432	0.336896
1.277394	1996	10.02	0.93	-0.18743	3165	13.207	3.667	0.863167
0.055172	2443	6.9996	3.9504	-0.79355	4294	11.504	1.964	0.462165
0.052214	2417	9.4332	1.5168	-0.30519	5346	13.468	3.928	0.924624
0.852138	2416	8.6507	2.2993	-0.46222	4447	9.9843	0.4443	0.104324
-0.05576	3633	8.5604	2.3896	-0.48034	4990	9.8998	0.3598	0.084427
0.49374	3433	5.2432	5.7068	-1.14602	4600	9.8043	0.2643	0.06194
0.706738	3289	8.1788	2.7712	-0.55692	5539	13.992	4.452	1.04801
0.405879	3178	7.5205	3.4295	-0.68902	4257	11.534	1.994	0.469229
0.316982	3191	7.1451	3.8049	-0.76435	2907	5.9856	3.5544	-0.83724
-0.75022	4768	20.826	9.876	1.981072	5377	5.1888	4.3512	-1.02486
-0.83306	5448	22.394	11.444	2.295732	4634	5.8049	3.7351	-0.87979
-0.37556	4791	15.55	4.6	0.922306	5484	8.4792	1.0608	-0.25008
-0.18312	4613	10.926	0.024	-0.00562	4583	6.3496	3.1904	-0.75153
0.103836	4123	13.752	2.802	0.561491	6245	8.695	0.845	-0.19926
0.215808	3259	17.674	6.724	1.348542	3690	5.4743	4.0657	-0.95764
-0.14777	2530	11.858	0.908	0.181411	6465	12.049	2.509	0.590495
-0.89208	3261	8.893	2.057	-0.41359	5624	11.807	2.267	0.533512
0.332957	2573	11.97	1.02	0.203887	4175	8.6467	0.8933	-0.21064
-0.4856	2704	5.6583	5.2917	-1.06272	4404	10.876	1.336	0.314291
0.718719	3268	15.116	4.166	0.835213	3623	9.6881	0.1481	0.034578
0.718423	3195	12.05	1.1	0.219941	4043	10.908	1.368	0.321826
-1.56732	3074	3.4157	7.5343	-1.51275	4511	6.0297	3.5103	-0.82686
-1.36305	2141	3.6899	7.2601	-1.45773	3696	6.71	2.83	-0.66667
-1.28179	3216	13.277	2.327	0.46617	5275	10.427	0.887	0.208566
-0.50898	3070	17.036	6.086	1.220511	4653	14.206	4.666	1.0984
0.273791	3390	10.472	0.478	-0.09673	5480	10.201	0.661	0.15535
-0.09777	3927	14.948	3.998	0.801499	3791	9.9446	0.4046	0.094976
-1.10966	4463	14.788	3.838	0.769391	4038	13.323	3.783	0.890481
-0.85495	3728	9.5225	1.4275	-0.28727	3793	10.308	0.768	0.180545
0.123509	5638	14.331	3.381	0.677682	4677	3.9769	5.5631	-1.31023

0.54344	3952	10.071	0.879	-0.1772	5029	6.6614	2.8786	-0.67811
0.242137	5305	15.231	4.281	0.858291	4776	4.7948	4.7452	-1.11764
-0.40484	2766	6.3991	4.5509	-0.91406	5758	8.6315	0.9085	-0.21422
-0.25708	4170	5.012	5.938	-1.19242	5519	4.7472	4.7928	-1.12885
-0.67701	3752	6.7964	4.1536	-0.83433	6253	6.4929	3.0471	-0.71779
-0.59625	4362	11.967	1.017	0.203285	6624	12.077	2.537	0.597088
1.51317	3117	16.683	5.733	1.149672	6273	14.204	4.664	1.097929
0.116853	3686	10.635	0.315	-0.06402	5088	11.95	2.41	0.567184
-1.29631	2304	6.033	4.917	-0.98753	4757	6.769	2.771	-0.65278
-0.77034	3017	7.4909	3.4591	-0.69496	4143	7.217	2.323	-0.54729
0.418895	2504	10.383	0.567	-0.11459	4325	11.052	1.512	0.355733
-1.11202	3078	6.5302	4.4198	-0.88775	6377	13.141	3.601	0.847626
-0.37556	2570	5.4475	5.5025	-1.10502	4570	14.551	5.011	1.179636
-0.71443	4893	8.0114	2.9386	-0.59051	4973	11.1	1.56	0.367036
-1.05049	5407	6.3436	4.6064	-0.9252	5597	10.398	0.858	0.201737
-0.7057	6132	9.0346	1.9154	-0.38518	6255	14.181	4.641	1.092513
-1.07771	5392	5.8791	5.0709	-1.01841	4199	9.669	0.129	0.030081
-0.56341	5208	8.0453	2.9047	-0.58371	4140	14.227	4.687	1.103345
-1.77894	3934	2.9995	7.9505	-1.59628	2767	11.312	1.772	0.416955
-0.83409	3864	13.251	2.301	0.460952	3994	3.3801	6.1599	-1.45075
-0.47407	4083	15.111	4.161	0.83421	2937	5.1413	4.3987	-1.03605
0.32704	4694	20.111	9.161	1.837589	3146	7.2155	2.3245	-0.54764
0.984078	4443	13.077	2.127	0.426035	5456	7.368	2.172	-0.51173
-0.76206	1532	9.0078	1.9422	-0.39056	2505	1.8363	7.7037	-1.81427
-0.29332	3706	14.49	3.54	0.70959	3651	4.6836	4.8564	-1.14382
-0.04689	3124	14.853	3.903	0.782435	3486	4.0161	5.5239	-1.301
-1.3319	2430	8.1481	2.8019	-0.56308	2176	2.9871	6.5529	-1.54329
-0.16285	3274	16.768	5.818	1.16673	3504	5.6507	3.8893	-0.9161
-0.90894	2808	9.188	1.762	-0.35439	3052	2.9161	6.6239	-1.56001
-0.04896	2517	11.561	0.611	0.12181	3587	4.1539	5.3861	-1.26855
-0.25515	1810	5.0276	5.9224	-1.18929	3993	4.007	5.533	-1.30314
0.02766	3483	17.858	6.908	1.385466	4115	6.4885	3.0515	-0.71883
-0.36343	2844	7.1027	3.8473	-0.77286	2943	4.2474	5.2926	-1.24653
0.772708	3845	13.914	2.964	0.594001	3529	5.0723	4.4677	-1.0523
-0.86382	1849	2.8123	8.1377	-1.63384	3290	2.7356	6.8044	-1.60251
-0.68573	3338	10.725	0.225	-0.04595	3667	8.8901	0.6499	-0.15333
1.145602	4800	19.917	8.967	1.798658	3373	6.2556	3.2844	-0.77367
0.290653	3517	9.6389	1.3111	-0.26391	3093	6.9835	2.5565	-0.60227
-0.41032	4115	9.6719	1.2781	-0.25729	3678	4.6493	4.8907	-1.1519
	3672	10.954	3.367		3993.5	9.54125	2.8695	
			10.101				8.6085	
			4.98316				4.24686	

2083	12.578		2144	8.9086
1908	10.063		2166	10.434
1501	4.4637		1007	6.0576

1986	2.2155	1695	2.0649
1869.5	7.33005	1753	6.866275
255.8834	4.809178	542.6263	3.679081
3992	55.411	4086	27.288
3084	44.812	2676	31.39
5291	38.216	3690	38.618
4583	59.503	6419	35.784
4237.5	49.4855	4217.75	33.27
	9.734904		4.974603
	29.20471		14.92381
	14.42753		11.03724
	43.63225		25.96105
	42.15545		26.40373
	1.035032		0.983234
	-0.03503		0.016766

906	27.373	1180	19.915
620	19.032	818	17.359

3694	48.674	5750	8.2435
3613	33.49	3998	19.535

5693	41.015	5766	19.337
4074	37.923	6441	18.864

y

y

y

y

y

y

y

y

y

y

y

					cell ct	% inf	AD
50072	A02	M-015991- coiled-coil	133957	CCDC127	4749	5.3274	6.2826
50072	A04	M-019235- EGF-like, fil	133584	EGFLAM	4794	13.767	2.157
50072	A05	M-032029- VNFT9373	127614	UNQ9373	3651	14.024	2.414
50072	A06	M-018452- hypothetica	133558	FLJ40243	3905	10.986	0.624
50072	A07	M-016623- transmemb	127670	TEDDM1	2771	11.729	0.119
50072	A08	M-028413- hypothetica	133491	LOC133491	4692	26.79	15.18
50072	A09	M-027210- chromoson	127687	C1orf122	4164	9.1979	2.4121
50072	A10	M-007375- solute carri	133482	SLCO6A1	3025	15.835	4.225
50072	A11	M-016554- chromoson	127700	C1orf102	1826	13.089	1.479
50072	A12	M-027213- embigin ho	133418	EMB	2440	10.615	0.995
50072	A13	M-016893- hypothetica	127703	FLJ38984	2174	14.397	2.787
50072	A14	M-016729- chromoson	133383	C5orf35	3687	20.966	9.356
50072	A15	M-016598- kelch doma	127707	KLHDC7A	2947	14.489	2.879
50072	A16	M-007345- Na+/H+ exc	133308	NHEDC2	1307	10.635	0.975
50072	A17	M-015953- hypothetica	127731	FLJ32784	3017	8.1869	3.4231
50072	A18	M-008704- ectonucleo	133121	ENPP6	2769	13.218	1.608
50072	A19	M-008657- UBX domai	127733	UBXD3	1777	11.818	0.208
50072	A20	M-017748- otopetrin 1	133060	OTOP1	2574	28.322	16.712
50072	A21	M-016507- chromoson	127795	C1orf87	3572	14.726	3.116
50072	A23	M-016577- ADP-ribosy	127829	ARL8A	3576	17.31	5.7
50072	B02	M-003819- CCCTC-bin	140690	CTCFL	4665	5.6806	5.9294
50072	B04	M-013335- cerebellin	140689	CBLN4	3757	8.8635	2.7465
50072	B05	M-007272- chromoson	387357	C6orf190	3785	5.6803	5.9297
50072	B06	M-015240- chromoson	140688	C20orf112	3142	5.9835	5.6265
50072	B07	M-032019- Notch hom	388677	NOTCH2NL	1678	3.8737	7.7363
50072	B08	M-013334- WAP four-	140686	WFDC3	2913	4.8404	6.7696
50072	B09	M-028389- hypothetica	134121	LOC134121	3520	6.9886	4.6214
50072	B10	M-024291- chromoson	140683	C20orf70	2692	5.3492	6.2608
50072	B11	M-024274- hypothetica	134145	LOC13414	2768	2.8902	8.7198
50072	B12	M-015769- chromoson	140680	C20orf96	2297	6.5303	5.0797
50072	B13	M-016730- hypothetica	134187	FLJ25680	2752	2.4346	9.1754
50072	B14	M-007639- solute carri	140679	SLC32A1	2571	5.2898	6.3202
50072	B15	M-019326- DnaJ homo	134218	DNAJA5	3997	10.458	1.152
50072	B16	M-019043- actin-relate	140625	ACTRT2	3162	3.0361	8.5739
50072	B17	M-024339- actin filame	134265	AFAP1L1	2991	6.8873	4.7227
50072	B18	M-014089- zinc finger	140612	ZFP28	3355	2.623	8.987
50072	B19	M-016191- GrpE-like 2	134266	GRPEL2	5466	13.026	1.416
50072	B20	M-015230- selenoprot	140606	SELM	5337	10.418	1.192
50072	B21	M-018796- transmemb	134285	TMEM171	2838	6.413	5.197
50072	B23	M-016731- transmemb	134288	TMEM174	3044	4.1064	7.5036
50072	C02	M-016877- translocati	133022	TRAM1L1	3127	6.5878	5.0222
50072	C04	M-016333- chromoson	133015	C4orf28	5588	10.039	1.571
50072	C05	M-018809- synaptotag	127833	SYT2	4417	10.799	0.811
50072	C06	M-016011- chromoson	132989	C4orf36	3980	10.704	0.906
50072	C07	M-027211- golgi trans	127845	GOLT1A	3501	10.111	1.499
50072	C08	M-016532- phosducin-	132954	PDCL2	3075	10.829	0.781

50072	C09	M-016275- Fc receptor	127943	FCRLB	3960	12.247	0.637
50072	C10	M-018650- 2-aminoad	132949	AASDH	2865	20.489	8.879
50072	C11	M-015961- WD repeat	128025	WDR64	2489	10.566	1.044
50072	C12	M-019170- cytoplasm	132864	CPEB2	2489	7.3925	4.2175
50072	C13	M-016069- chromoso	128061	C1orf131	2510	9.9203	1.6897
50072	C14	M-018741- spermato	132851	SPATA4	1955	13.708	2.098
50072	C15	M-016668- Lix1 homol	128077	LIX1L	2789	13.302	1.692
50072	C16	M-008672- glucosami	132789	GNPDA2	2638	5.7998	5.8102
50072	C17	M-027618- 3-beta-hyd	128102	LOC12810	3169	12.307	0.697
50072	C18	M-009116- transmem	132724	TMPRSS11	3291	23.519	11.909
50072	C19	M-016538- spermato	128153	SPATA17	3917	14.399	2.789
50072	C20	M-015464- chromoso	132720	C4orf32	3258	11.51	0.1
50072	C21	M-018431- Kruppel-lik	128209	KLF17	3978	20.387	8.777
50072	C23	M-016058- transmem	128218	TMEM125	3255	5.2535	6.3565
50072	D02	M-015344- transcripti	140597	TCEAL2	3233	2.7529	8.8571
50072	D04	M-015229- defensin, b	140596	DEFB104A	5367	7.9188	3.6912
50072	D05	M-018455- LSM11, U7	134353	LSM11	3754	8.6574	2.9526
50072	D06	M-017198- chondrolec	140578	CHODL	2919	1.5074	10.1026
50072	D07	M-016919- chromoso	134359	C5orf37	4287	2.7525	8.8575
50072	D08	M-015228- S100 calciu	140576	S100A16	4245	4.2167	7.3933
50072	D09	M-005705- G protein-	134391	GPR151	3237	10.998	0.612
50072	D10	M-021149- zinc finger	140467	ZNF358	3735	6.3989	5.2111
50072	D11	M-003315- START do	134429	STARD4	2655	8.3616	3.2484
50072	D12	M-013090- myosin, lig	140465	MYL6B	2413	7.1695	4.4405
50072	D13	M-017004- WD repeat	134430	WDR36	2144	6.2034	5.4066
50072	D14	M-014295- ankyrin re	140462	ASB9	2557	8.3692	3.2408
50072	D15	M-028442- hypothetic	134466	LOC13446	2180	2.7064	8.9036
50072	D16	M-014301- ankyrin re	140461	ASB8	3341	5.1482	6.4618
50072	D17	M-016043- NudC dom	134492	NUDCD2	3444	13.415	1.805
50072	D18	M-012930- ankyrin re	140460	ASB7	3894	14.099	2.489
50072	D19	M-016328- ubiquitin-li	134510	UBLCP1	4406	10.35	1.26
50072	D20	M-013355- ankyrin re	140459	ASB6	4121	8.3475	3.2625
50072	D21	M-017945- ankyrin re	134548	ANKRD43	5671	9.2929	2.3171
50072	D23	M-015348- shroom fa	134549	SHROOM1	3923	8.4629	3.1471
50072	E02	M-016038- spermato	132671	SPATA18	4939	12.432	0.822
50072	E04	M-019325- lin-54 hom	132660	LIN54	2650	14.151	2.541
50072	E05	M-016052- chromoso	128229	C1orf182	3280	10.213	1.397
50072	E06	M-017752- zinc finger	132625	ZFP42	5364	13.386	1.776
50072	E07	M-009077- IQ motif co	128239	IQGAP3	3501	16.595	4.985
50072	E08	M-008699- adenosine	132612	ADAD1	4093	8.8688	2.7412
50072	E09	M-016460- apolipopro	128240	APOA1BP	2158	17.98	6.37
50072	E10	M-015609- transmem	132332	TMEM155	3092	15.718	4.108
50072	E11	M-008370- Rho guani	128272	ARHGEF19	3246	15.804	4.194
50072	E12	M-018450- chromoso	132321	C4orf33	1848	11.039	0.571
50072	E13	M-019054- mitochond	128308	MRPL55	2476	13.045	1.435
50072	E14	M-016016- sodium ch	132320	SCLT1	3477	20.851	9.241
50072	E15	M-017836- transmem	128338	TMEM77	2589	9.1927	2.4173

50072	E16	M-015633- OCIA doma	132299	OCIAD2	3377	13.118	1.508
50072	E17	M-018821- chromosom	128344	C1orf88	3616	14.546	2.936
50072	E18	M-017501- H1 histone	132243	H1FOO	2816	21.982	10.372
50072	E19	M-017770- chromosom	128346	C1orf162	3352	4.3854	7.2246
50072	E20	M-028163- ribosomal	132241	RPL32P3	3280	9.2378	2.3722
50072	E21	M-027376- TatD DNas	128387	TATDN3	4008	17.29	5.68
50072	E23	M-015430- chromosom	128414	C20orf58	4260	12.183	0.573
50072	F02	M-017458- ankyrin rep	140458	ASB5	3187	8.5033	3.1067
50072	F04	M-013267- ankyrin rep	140456	ASB11	3387	6.7316	4.8784
50072	F05	M-015517- chromosom	134553	C5orf24	5149	9.1862	2.4238
50072	F06	M-025429- mucin 17,	140453	MUC17	5043	16.042	4.432
50072	F07	M-018920- deaminase	134637	DEADC1	3461	16.816	5.206
50072	F08	M-007135- ring finger	140432	RNF113B	3284	3.5932	8.0168
50072	F09	M-028645- chromosom	134701	C6orf159	3390	5.3982	6.2118
50072	F10	M-015903- t-complex	140290	TCP10L	3408	12.5	0.89
50072	F11	M-024865- interleukin	134728	IRAK1BP1	3161	7.2762	4.3338
50072	F12	M-018675- keratin ass	140258	KRTAP13-1	3117	11.036	0.574
50072	F13	M-024722- chromosom	134829	C6orf213	3514	10.131	1.479
50072	F14	M-016659- ribosomal	140032	RPS4Y2	3947	18.216	6.606
50072	F15	M-017286- syntaxin bi	134957	STXBP5	4156	9.4562	2.1538
50072	F16	M-024825- hypothetic	139886	RP11-93B1	3444	16.696	5.086
50072	F17	M-015800- histidine tr	135114	HINT3	4086	8.2477	3.3623
50072	F18	M-015696- dedicator	139818	DOCK11	3304	33.596	21.986
50072	F19	M-016948- PARK2 co-r	135138	PACRG	3551	6.6742	4.9358
50072	F20	M-017003- chromosom	139804	CXorf55	4783	8.5511	3.0589
50072	F21	M-015266- beta-1,3-gl	135152	B3GAT2	6133	15.066	3.456
50072	F23	M-015985- chromosom	135154	C6orf57	5165	12.004	0.394
50072	G02	M-016728- chromosom	132228	C3orf45	5280	11.78	0.17
50072	G04	M-018739- synaptopo	132204	SYNPR	4075	12.54	0.93
50072	G05	M-015237- chromosom	128434	C20orf102	4133	19.526	7.916
50072	G06	M-016590- chromosom	132200	C3orf49	4372	7.731	3.879
50072	G07	M-024166- chromosom	128486	C20orf142	3415	8.3163	3.2937
50072	G08	M-016028- protein ph	132160	PPM1M	3830	3.577	8.033
50072	G09	M-010915- WAP four-	128488	WFDC12	3022	6.2872	5.3228
50072	G10	M-006728- glycerate k	132158	GLYCTK	3339	12.489	0.879
50072	G11	M-015238- chromosom	128497	C20orf165	1939	4.1774	7.4326
50072	G12	M-016325- IQ motif co	132141	IQCF1	2778	5.5076	6.1024
50072	G13	M-018447- teashirt far	128553	TSHZ2	2868	5.5439	6.0661
50072	G14	M-016727- receptor (	132112	RTP1	2963	4.8262	6.7838
50072	G15	M-017835- chromosom	128602	C20orf85	3630	3.0028	8.6072
50072	G16	M-007947- interleukin	132014	IL17RE	3807	12.398	0.788
50072	G17	M-024186- chromosom	128611	C20orf174	3706	16.217	4.607
50072	G18	M-016534- chromosom	132001	C3orf31	4768	14.66	3.05
50072	G19	M-015981- TBC1 doma	128637	TBC1D20	5938	5.9784	5.6316
50072	G20	M-016329- methyltran	131965	METTL6	5290	13.554	1.944
50072	G21	M-015265- chromosom	128653	C20orf141	4556	16.045	4.435
50072	G23	M-017306- cystatin-lik	128817	CSTL1	5994	15.682	4.072

50072	H02	M-027176-	pregnancy	139728	PNCK	3416	16.511	4.901
50072	H04	M-027215-	forkhead b	139628	FOXR2	3445	18.491	6.881
50072	H05	M-015378-	CD109 mol	135228	CD109	4349	10.117	1.493
50072	H06	M-015813-	melanoma	139599	MAGEE2	3695	17.997	6.387
50072	H07	M-016880-	retinoic aci	135250	RAET1E	3758	19.053	7.443
50072	H08	M-016141-	uracil phos	139596	UPRT	3824	19.456	7.846
50072	H09	M-016381-	serine-argi	135295	SRrp35	3630	15.234	3.624
50072	H10	M-032033-	OTU domai	139562	OTUD6A	3917	23.411	11.801
50072	H11	M-016793-	chromosom	135398	C6orf141	3904	23.028	11.418
50072	H12	M-018932-	melanoma	139422	MAGEB10	2807	23.299	11.689
50072	H13	M-028635-	FK506 bind	135521	FKBP1C	3523	6.7556	4.8544
50072	H14	M-032032-	SMEK hom	139420	SMEK3P	3726	15.003	3.393
50072	H15	M-007129-	tripartite m	135644	TRIM40	3671	17.107	5.497
50072	H16	M-007911-	patched do	139411	PTCHD1	4049	14.226	2.616
50072	H17	M-015285-	diffuse pan	135656	DPCR1	3599	17.088	5.478
50072	H18	M-018480-	FUN14 dom	139341	FUNDC1	3532	5.1529	6.4571
50072	H19	M-018926-	Williams-B	135886	WBSCR28	3722	10.613	0.997
50072	H20	M-015913-	chromosom	139324	CXorf43	3159	15.163	3.553
50072	H21	M-007130-	tripartite m	135892	TRIM50	3504	12.414	0.804
50072	H23	M-018513-	chromosom	135927	C7orf34	3263	6.7729	4.8371
50072	I02	M-032030-	SRSR846	131920	UNQ846	4445	9.3813	2.2287
50072	I04	M-023732-	hypothetica	131873	LOC131873	3073	11.878	0.268
50072	I05	M-013333-	cystatin 9-l	128821	CST9L	4847	20.961	9.351
50072	I06	M-016334-	nudix (nucl	131870	NUDT16	4435	14.408	2.798
50072	I07	M-017728-	chromosom	128826	C20orf166	4269	10.611	0.999
50072	I08	M-018760-	chromosom	131831	C3orf44	4549	21.895	10.285
50072	I09	M-017908-	TSPY-like 3	128854	TSPYL3	3649	10.989	0.621
50072	I10	M-016023-	urocanase	131669	UROC1	3021	18.239	6.629
50072	I11	M-008771-	bactericida	128859	BPIL3	2437	9.7251	1.8849
50072	I12	M-016037-	transmemb	131616	TMEM42	3019	10.831	0.779
50072	I13	M-010140-	chromosom	128861	C20orf71	3715	14.697	3.087
50072	I14	M-018377-	family with	131583	FAM43A	3158	10.925	0.685
50072	I15	M-015274-	chromosom	128864	C20orf144	3994	7.7116	3.8984
50072	I16	M-015301-	leucine rich	131578	LRRC15	3881	5.1018	6.5082
50072	I17	M-018075-	chromatin	128866	CHMP4B	3517	12.226	0.616
50072	I18	M-016714-	discoidin, C	131566	DCBLD2	3946	11.379	0.231
50072	I19	M-017679-	high-mobili	128872	HMG4L	3471	12.1	0.49
50072	I20	M-028137-	hypothetica	131544	DKFZp667C	6402	20.072	8.462
50072	I21	M-017694-	family with	128876	FAM83C	5204	24.731	13.121
50072	I23	M-031414-	GRB2-asso	128954	GAB4	4208	16.16	4.55
50072	J02	M-027214-	apolipopro	139322	APOOL	5128	14.392	2.782
50072	J04	M-016075-	family with	139285	FAM123B	4421	18.842	7.232
50072	J05	M-016794-	transmemb	135932	TMEM139	3688	11.253	0.357
50072	J06	M-024785-	chromosom	139231	CXorf39	4364	11.366	0.244
50072	J07	M-007131-	zinc finger	136051	ZNF786	4008	9.6557	1.9543
50072	J08	M-016018-	melanoma	139221	MUM1L1	2828	6.7539	4.8561
50072	J09	M-015349-	EMI domai	136227	EMID2	3504	21.005	9.395

50072	J10	M-018476- chromoson	139212	CXorf41	4717	15.603	3.993
50072	J11	M-016003- chromoson	136263	C7orf45	4328	19.524	7.914
50072	J12	M-017873- WD repeat	139170	WDR40B	2508	7.0973	4.5127
50072	J13	M-025330- hypothetic	136288	LOC13628	2706	9.5713	2.0387
50072	J14	M-018473- PAS domai	139135	PASD1	3740	8.9572	2.6528
50072	J15	M-007346- SVOP-like	136306	SVOPL	3427	9.8629	1.7471
50072	J16	M-016795- chromoson	139105	CXorf20	4004	7.6673	3.9427
50072	J17	M-016817- myotrophi	136319	MTPN	3609	5.9573	5.6527
50072	J18	M-017734- SLIT and N	139065	SLITRK4	5114	5.4556	6.1544
50072	J19	M-015997- leucine-ric	136332	LRGUK	5446	11.733	0.123
50072	J20	M-031963- olfactory r	138883	OR1N1	4167	9.5752	2.0348
50072	J21	M-007725- ankyrin rep	136371	ASB10	3805	13.246	1.636
50072	J23	M-016379- chromoson	136647	C7orf11	2622	10.336	1.274
50072	K02	M-015990- zinc finger,	131540	ZDHHC19	3279	4.5441	7.0659
50072	K04	M-016042- coiled-coil-	131474	CHCHD4	3788	10.929	0.681
50072	K05	M-016397- chromoson	128989	C22orf25	1765	12.295	0.685
50072	K06	M-018738- family with	131408	FAM131A	3990	11.579	0.031
50072	K07	M-010919- suppressor	129025	SUHW1	4116	14.772	3.162
50072	K08	M-016211- kelch repea	131377	KBTBD5	4492	8.6598	2.9502
50072	K09	M-010918- hypothetic	129026	LOC12902	4406	8.2615	3.3485
50072	K10	M-015984- lysozyme-li	131375	LYZL4	2413	3.6884	7.9216
50072	K11	M-024557- RUN and T	129049	RUTBC2	3176	4.534	7.076
50072	K12	M-018006- zona pelluc	131368	ZPLD1	3776	12.474	0.864
50072	K13	M-015347- EMI domai	129080	EMID1	2483	3.0608	8.5492
50072	K14	M-016533- family with	131177	FAM3D	3952	14.853	3.243
50072	K15	M-016583- ankyrin rep	129138	ANKRD54	2822	11.942	0.332
50072	K16	M-016024- DnaJ (Hsp4	131118	DNAJC19	3845	5.9558	5.6542
50072	K17	M-017065- coiled-coil	129285	CCDC128	4876	11.998	0.388
50072	K18	M-008546- copine IV	131034	CPNE4	3295	4.0061	7.6039
50072	K19	M-022729- hypothetic	129293	LOC12929	4146	4.9204	6.6896
50072	K20	M-016733- hypothetic	130951	LOC130951	4676	7.7203	3.8897
50072	K21	M-016669- transmemb	129303	TMEM150	3575	15.021	3.411
50072	K23	M-018998- nucleopori	129401	NUP35	3983	10.846	0.764
50072	L02	M-031891- chromoson	138724	C9orf131	5031	13.238	1.628
50072	L04	M-017493- chromoson	138716	C9orf23	3860	11.995	0.385
50072	L05	M-015935- chromoson	136895	C7orf31	3384	9.3085	2.3015
50072	L06	M-029567- AT rich inte	138715	ARID3C	4365	11.638	0.028
50072	L07	M-015293- ankyrin rep	136991	ASZ1	5547	15.54	3.93
50072	L08	M-026263- ankyrin rep	138649	ANKRD19	5617	13.797	2.187
50072	L09	M-019324- claudin 23	137075	CLDN23	3620	13.011	1.401
50072	L10	M-026208- peptidyl-tR	138428	PTRH1	2734	9.4001	2.2099
50072	L11	M-016324- coiled-coil	137196	CCDC26	4255	19.412	7.802
50072	L12	M-016278- family with	138311	FAM69B	2523	8.5216	3.0884
50072	L13	M-029365- otoconin 9	137202	OC90	3012	8.7649	2.8451
50072	L14	M-019397- chromoson	138241	C9orf85	2659	11.282	0.328
50072	L15	M-007133- zinc finger	137209	ZNF572	4285	13.722	2.112
50072	L16	M-026002- chromoson	138240	C9orf57	4657	15.589	3.979

50072	L17	M-016864-	glutamic-ox	137362	GOT1L1	4695	22.322	10.712
50072	L18	M-016365-	chromoson	138199	C9orf41	4213	13.672	2.062
50072	L19	M-016046-	family with	137392	FAM92A1	4703	10.057	1.553
50072	L20	M-015933-	chromoson	138162	C9orf116	4634	16.854	5.244
50072	L21	M-026897-	E2F transcr	144455	E2F7	3320	12.47	0.86
50072	L23	M-018941-	keratin 80	144501	KRT80	4147	13.238	1.628
50072	M02	M-018279-	hypothetica	130940	LOC130940	5538	7.8187	3.7913
50072	M04	M-018834-	MTERF dor	130916	MTERFD2	2160	12.315	0.705
50072	M05	M-016468-	hypothetica	129450	FLJ37953	3011	11.192	0.418
50072	M06	M-018460-	F-box prote	130888	FBXO36	4805	19.334	7.724
50072	M07	M-017774-	hypothetica	129530	LOC129530	4644	11.154	0.456
50072	M08	M-016045-	transmemb	130827	TMEM182	5821	10.6	1.01
50072	M09	M-016584-	MIT, micro	129531	MITD1	6208	22.552	10.942
50072	M10	M-016552-	PQ loop rep	130814	PQLC3	4269	13.118	1.508
50072	M11	M-018715-	DIS3 mitoti	129563	DIS3L2	5535	11.906	0.296
50072	M12	M-018692-	chromoson	130813	C2orf50	2980	11.946	0.336
50072	M13	M-006746-	hypothetica	129607	LOC129607	2846	15.706	4.096
50072	M14	M-023122-	malate deh	130752	MDH1B	3906	9.447	2.163
50072	M15	M-010299-	membrane	129642	MBOAT2	5428	17.502	5.892
50072	M16	M-016560-	transmemb	130733	TMEM178	5232	12.347	0.737
50072	M17	M-010914-	contactin a	129684	CNTNAP5	3824	9.1527	2.4573
50072	M18	M-016566-	hypothetica	130619	MGC35338	5112	9.7222	1.8878
50072	M19	M-015912-	taube nuss	129685	TBN	4368	5.8608	5.7492
50072	M20	M-016586-	zinc finger,	130617	ZFAND2B	5603	21.578	9.968
50072	M21	M-016932-	transmemb	129787	TMEM18	4482	16.756	5.146
50072	M23	M-014942-	chromoson	129790	C7orf13	3187	7.813	3.797
50072	N02	M-015957-	BTB (POZ) d	138151	BTBD14A	5716	15.238	3.628
50072	N04	M-007134-	ring finger	138065	RNF183	2834	12.915	1.305
50072	N05	M-016506-	amidohydr	144193	AMDHD1	3770	14.43	2.82
50072	N06	M-025981-	heparan-al	138050	HGSNAT	4390	12.688	1.078
50072	N07	M-007514-	solute carri	144195	SLC2A14	3414	6.1511	5.4589
50072	N08	M-017769-	hypothetica	138046	LOC138046	6462	11.962	0.352
50072	N09	M-018768-	BCDIN3 dor	144233	BCDIN3D	4943	22.719	11.109
50072	N10	M-016929-	WD repeat	138009	WDR21C	3634	16.07	4.46
50072	N11	M-016617-	GLI pathog	144321	GLIPR1L2	5269	16.815	5.205
50072	N12	M-015974-	leucine zip	137994	LETM2	2638	33.397	21.787
50072	N13	M-018737-	family with	144347	FAM101A	3490	18.739	7.129
50072	N14	M-015286-	unc-5 hom	137970	UNC5D	2945	21.392	9.782
50072	N15	M-016535-	zinc finger	144348	ZNF664	4114	17.307	5.697
50072	N16	M-010300-	1-acylglyce	137964	AGPAT6	3538	17.411	5.801
50072	N17	M-015852-	hypothetica	144360	FLJ32894	5483	11.964	0.354
50072	N18	M-008450-	peroxidasin	137902	PXDNL	3549	15.356	3.746
50072	N19	M-030130-	LYR motif c	144363	LYRM5	5676	14.693	3.083
50072	N20	M-025945-	hypothetica	137886	LOC137886	3961	14.592	2.982
50072	N21	M-017584-	copine VIII	144402	CPNE8	5682	13.745	2.135
50072	N23	M-015772-	WD repeat	144406	WDR66	5478	22.015	10.405
50072	O02	M-008396-	galactose m	130589	GALM	4963	19.222	7.612

50072	O04	M-017984- hypothetic	130576	LOC13057	3457	11.224	0.386
50072	O05	M-016726- hypothetic	129804	FLJ37440	4496	10.609	1.001
50072	O06	M-019328- LY6/PLAUR	130574	LYPD6	3765	14.555	2.945
50072	O07	M-013263- sialidase 4	129807	NEU4	4303	4.3923	7.2177
50072	O08	M-007128- zinc finger	130557	ZNF513	3676	9.7661	1.8439
50072	O09	M-022681- hypothetic	129852	FLJ40298	4954	17.44	5.83
50072	O10	M-016962- potassium	130535	KCTD18	5054	25.03	13.42
50072	O11	M-007127- tripartite	129868	TRIM43	4421	12.373	0.763
50072	O12	M-016653- zinc finger	130507	ZNF650	4640	22.802	11.192
50072	O13	M-016478- Bardet-Bie	129880	BBS5	3326	16.386	4.776
50072	O14	M-016029- odd-skippe	130497	OSR1	3640	15.275	3.665
50072	O15	M-027990- hypothetic	129881	LOC129881	4895	22.308	10.698
50072	O16	M-015727- sphingosin	130367	SGPP2	4502	7.53	4.08
50072	O17	M-031904- amyotroph	130029	ALS2CR16	3580	12.291	0.681
50072	O18	M-018537- adaptor-rel	130340	AP1S3	3736	10.278	1.332
50072	O19	M-027212- regenerati	130120	REG3G	5534	13.625	2.015
50072	O20	M-022669- pleckstrin	130271	PLEKHH2	5730	14.031	2.421
50072	O21	M-016049- raftlin fami	130132	RFTN2	5681	21.141	9.531
50072	O23	M-016356- hypothetic	130162	FLJ31438	4107	8.5707	3.0393
50072	P02	M-010970- sarcoglyca	137868	SGCZ	2974	5.8171	5.7929
50072	P04	M-015995- transmem	137835	TMEM71	2710	10.923	0.687
50072	P05	M-015840- glycosyltra	144423	GLT1D1	2320	6.3793	5.2307
50072	P06	M-031903- LY6/PLAUR	137797	LYPD2	2603	4.3796	7.2304
50072	P07	M-016337- bestrophin	144453	BEST3	4438	13.249	1.639
50072	P08	M-015426- transmem	137695	TMEM68	1625	7.5077	4.1023
50072	P09	M-015775- alpha-2-ma	144568	A2ML1	3416	9.8068	1.8032
50072	P10	M-016179- chromoso	137682	C8orf38	4478	16.972	5.362
50072	P11	M-016222- hypothetic	144577	FLJ32549	2142	7.423	4.187
50072	P12	M-016816- vacuolar pr	137492	VPS37A	3425	11.883	0.273
50072	P13	M-017966- chromoso	144608	C12orf60	3062	16.264	4.654
50072	P14	M-018491- ovostatin 2	144203	OVOS2	2991	11.568	0.042
50072	P15	M-022992- family with	144638	FAM10A3	2743	7.109	4.501
50072	P16	M-030232- hypothetic	144766	LOC14476	2761	9.8515	1.7585
50072	P17	M-030145- hypothetic	144678	LOC14467	4004	10.714	0.896
50072	P18	M-019322- hypothetic	144747	LOC14474	1833	9.9291	1.6809
50072	P19	M-015718- F-box and	144699	FBXL14	3298	11.552	0.058
50072	P20	M-030176- hypothetic	144742	LOC14474	2594	20.162	8.552
50072	P21	M-016177- RAD9 hom	144715	RAD9B	2126	13.735	2.125
50072	P23	M-015976- family with	144717	FAM109A	1980	8.0303	3.5797
				MAD	3650	11.6085	3.37765
				MAD3			10.13295
				MADc			4.998922
50072	C22				1062	8.4746	
50072	D22				1588	3.5894	
50072	E22				1489	12.424	
50072	F22				3014	11.513	
				mn	1788.25	9.00025	

					sd	848.4403	3.982863
50072	G22					4217	41.807
50072	H22					3689	53.212
50072	I22					4823	57.91
50072	J22					4101	46.135
					mn	4207.5	49.766
					sd	468.727	7.181678
					3psSD		21.54503
					3ngSD		11.94859
					SumSD		33.49362
					DiffMn		40.76575
					SmovrDiff		0.821612
					1minus		0.178388
50072	G03	M-003290-	polo-like ki	5347	PLK1 SMAF	558	6.9892
50072	H03	M-003290-	polo-like ki	5347	PLK1 SMAF	601	26.789
50072	I03	D-001206-:	siControl non-targeting			4035	11.673
50072	J03	D-001206-:	siControl non-targeting			4047	16.728
50072	K03	D-001600-(	siGLO RISC-free siRNA			4145	19.469
50072	L03	D-001600-(	siGLO RISC-free siRNA			5731	19.682

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-1.25649	3721	6.9874	2.8226	-0.59674	3014	7.5315	5.7985	-0.96532
0.431793	3101	13.995	4.185	0.883276	3639	18.274	4.944	0.824456
0.483204	3530	9.5751	0.2349	-0.05021	3123	19.18	5.85	0.975402
-0.12453	2984	11.83	2.02	0.426025	2976	16.331	3.001	0.500738
0.024105	4104	5.4825	4.3275	-0.91458	2930	10.648	2.682	-0.44609
3.036955	3418	23.61	13.8	2.913978	3575	21.846	8.516	1.419577
-0.48222	2868	3.8354	5.9746	-1.26245	3500	14.229	0.899	0.15053
0.845482	2820	7.1277	2.6823	-0.56711	3675	17.469	4.139	0.690337
0.296164	2841	12.144	2.334	0.492342	3188	21.55	8.22	1.370261
-0.19874	2091	8.1301	1.6799	-0.3554	2198	7.9618	5.3682	-0.89363
0.55782	1900	6.2632	3.5468	-0.74969	3007	11.872	1.458	-0.24216
1.871904	3165	13.997	4.187	0.883699	3958	21.147	7.817	1.303119
0.576224	2669	9.2544	0.5556	-0.11795	3288	10.036	3.294	-0.54805
-0.19474	1994	9.5286	0.2814	-0.06003	2020	7.6733	5.6567	-0.9417
-0.68447	2786	6.7121	3.0979	-0.65488	3269	8.6877	4.6423	-0.77269
0.321969	3745	9.3191	0.4909	-0.10428	3165	14.06	0.73	0.122373
0.041909	2015	7.9404	1.8696	-0.39546	2652	13.462	0.132	0.022742
3.343421	2012	27.535	17.725	3.742944	4363	30.85	17.52	2.919709
0.623634	3659	11.233	1.423	0.299938	4659	9.8948	3.4352	-0.57158
1.140546	2543	16.595	6.785	1.4324	4030	13.846	0.516	0.086719
-1.18584	3977	6.1856	3.6244	-0.76608	4624	7.7638	5.5662	-0.92662
-0.54912	3833	7.0702	2.7398	-0.57925	4218	15.742	2.412	0.402606
-1.1859	4118	6.508	3.302	-0.69799	3803	9.6766	3.6534	-0.60793
-1.12524	2445	7.1166	2.6934	-0.56945	4518	8.9641	4.3659	-0.72664
-1.54729	2808	6.5171	3.2929	-0.69607	2472	4.8544	8.4756	-1.41135
-1.35391	4325	9.9653	0.1553	0.032198	3804	12.224	1.106	-0.18352
-0.92418	4239	8.7992	1.0108	-0.21408	4155	10.782	2.548	-0.42377
-1.25213	4105	3.4105	6.3995	-1.35219	4117	10.444	2.886	-0.48008
-1.74404	4323	8.7671	1.0429	-0.22086	3376	11.789	1.541	-0.25599
-1.01586	3547	6.5689	3.2411	-0.68513	3365	10.045	3.285	-0.54656
-1.83518	3653	4.5168	5.2932	-1.11853	2773	9.304	4.026	-0.67001
-1.26401	3087	10.301	0.491	0.103098	3230	15.789	2.459	0.410437
-0.23015	5160	10.116	0.306	0.064026	4003	23.832	10.502	1.750459
-1.71485	4566	8.3224	1.4876	-0.31479	3730	15.684	2.354	0.392943
-0.94444	4188	10.196	0.386	0.080922	2733	13.721	0.391	0.065893
-1.79749	5328	7.958	1.852	-0.39175	3517	10.037	3.293	-0.54789
0.283561	6904	20.032	10.222	2.158299	6461	19.656	6.326	1.054707
-0.23815	6431	20.51	10.7	2.259254	6139	23.88	10.55	1.758456
-1.03932	3855	5.0584	4.7516	-1.00415	3511	12.589	0.741	-0.12271
-1.50074	4476	8.6908	1.1192	-0.23698	4124	8.8991	4.4309	-0.73747
-1.00436	4040	7.698	2.112	-0.44666	5263	17.386	4.056	0.676509
-0.31397	4316	7.1131	2.6969	-0.57019	6244	15.999	2.669	0.445424
-0.16193	4141	10.843	1.033	0.217569	4645	16.835	3.505	0.584708
-0.18094	5126	11.959	2.149	0.45327	5122	19.309	5.979	0.996894
-0.29956	5082	9.819	0.009	0.001299	4795	18.811	5.481	0.913924
-0.15593	3647	9.8437	0.0337	0.006516	3289	17.604	4.274	0.712829

0.127728	4763	10.603	0.793	0.166881	3969	22.701	9.371	1.562026
1.776483	4100	6.8049	3.0051	-0.63528	3323	18.688	5.358	0.893431
-0.20854	4187	9.6967	0.1133	-0.02453	3581	21.726	8.396	1.399584
-0.84338	3717	7.2908	2.5192	-0.53266	3123	11.687	1.643	-0.27299
-0.33771	3354	10.078	0.268	0.056	3125	24.384	11.054	1.842426
0.419991	4104	15.01	5.2	1.097646	3621	29.274	15.944	2.657136
0.338773	4013	5.7563	4.0537	-0.85675	2962	16.914	3.584	0.59787
-1.16199	4421	9.4323	0.3777	-0.08037	2960	17.905	4.575	0.762978
0.13973	5167	9.1542	0.6558	-0.13911	2958	24.104	10.774	1.795776
2.382614	6237	19.929	10.119	2.136546	3851	31.161	17.831	2.971523
0.55822	4434	18.245	8.435	1.780882	5052	30.998	17.668	2.944367
-0.0197	5056	11.669	1.859	0.392022	4614	27.958	14.628	2.43788
1.756079	4536	14.815	5.005	1.056461	5044	26.983	13.653	2.275438
-1.27127	3855	7.4968	2.3132	-0.48915	4440	11.036	2.294	-0.38145
-1.7715	4835	6.5357	3.2743	-0.69214	5176	12.519	0.811	-0.13437
-0.7381	4668	19.152	9.342	1.972442	4736	21.305	7.975	1.329442
-0.59035	3913	10.018	0.208	0.043328	2814	12.189	1.141	-0.18935
-2.02066	3311	4.4397	5.3703	-1.13482	2641	8.3302	4.9998	-0.83225
-1.77158	4490	6.9933	2.8167	-0.59549	1845	7.5339	5.7961	-0.96492
-1.47868	5138	11.97	2.16	0.455593	3633	20.451	7.121	1.18716
-0.12213	5565	18.005	8.195	1.730194	2888	15.132	1.802	0.300976
-1.04214	4396	14.126	4.316	0.910944	1927	17.385	4.055	0.676342
-0.64952	4135	10.931	1.121	0.236155	2218	23.084	9.754	1.625837
-0.88799	4329	15.292	5.482	1.157204	2632	19.453	6.123	1.020886
-1.08125	3136	11.639	1.829	0.385686	1920	21.354	8.024	1.337606
-0.648	3798	12.138	2.328	0.491075	3493	15.918	2.588	0.431929
-1.7808	3625	4.9931	4.8169	-1.01794	1540	9.7403	3.5897	-0.59732
-1.29234	4541	8.214	1.596	-0.33768	4333	16.963	3.633	0.606034
0.361378	5350	21.421	11.611	2.451658	2325	24.387	11.057	1.842926
0.498207	6020	21.595	11.785	2.488407	3582	23.311	9.981	1.663657
-0.25175	4611	10.128	0.318	0.06656	2632	13.336	0.006	0.001749
-0.65234	4025	15.106	5.296	1.117921	3378	11.308	2.022	-0.33613
-0.46322	5150	6.9709	2.8391	-0.60022	5357	11.424	1.906	-0.3168
-0.62926	2645	14.896	5.086	1.073569	2458	14.361	1.031	0.172522
0.164736	4963	2.4783	7.3317	-1.54907	4169	3.55	9.78	-1.62867
0.50861	3259	5.8607	3.9493	-0.8347	2384	9.5218	3.8082	-0.63372
-0.27916	5411	7.1706	2.6394	-0.55805	3990	6.7419	6.5881	-1.09688
0.355577	5290	7.7316	2.0784	-0.43956	4893	6.7648	6.5652	-1.09306
0.997515	3637	7.7261	2.0839	-0.44072	3369	4.8085	8.5215	-1.41899
-0.54806	4954	4.6629	5.1471	-1.08768	4187	7.7621	5.5679	-0.9269
1.274575	3461	3.2072	6.6028	-1.39512	3498	4.3168	9.0132	-1.50091
0.822077	4331	6.6036	3.2064	-0.6778	3483	9.532	3.798	-0.63202
0.839281	3495	4.8069	5.0031	-1.05726	3346	6.7244	6.6056	-1.09979
-0.11392	3293	15.062	5.252	1.108628	3346	6.7543	6.5757	-1.09481
0.287362	1868	3.8009	6.0091	-1.26973	2799	7.4312	5.8988	-0.98203
1.848899	3849	7.8722	1.9378	-0.40987	4358	11.634	1.696	-0.28182
-0.48326	3121	9.1317	0.6783	-0.14386	3750	8.0533	5.2767	-0.87839

0.301965	3718	10.059	0.249	0.051987	3814	12.48	0.85	-0.14087
0.587627	3113	8.0951	1.7149	-0.36279	3842	14.003	0.673	0.112876
2.075147	3923	10.324	0.514	0.107956	3837	13.683	0.353	0.059562
-1.44493	3576	5.8725	3.9375	-0.83221	5303	6.4115	6.9185	-1.15192
-0.47424	3249	4.8323	4.9777	-1.0519	4782	9.724	3.606	-0.60004
1.136545	2639	8.526	1.284	-0.27178	4383	13.895	0.565	0.094883
0.114925	3015	8.1592	1.6508	-0.34925	5467	15.054	1.724	0.287981
-0.62117	5506	5.9208	3.8892	-0.82201	5161	6.2197	7.1103	-1.18388
-0.97559	5697	6.8808	2.9292	-0.61925	4314	9.2258	4.1042	-0.68304
-0.48456	5867	4.9599	4.8501	-1.02495	5314	7.4332	5.8968	-0.9817
0.886891	5799	11.812	2.002	0.422223	5386	11.53	1.8	-0.29914
1.041725	5057	11.588	1.778	0.374914	3344	12.978	0.352	-0.0579
-1.60341	5462	5.639	4.171	-0.88152	3912	8.7423	4.5877	-0.76359
-1.24233	5043	3.9857	5.8243	-1.2307	4009	12.023	1.307	-0.21701
0.178338	5368	6.3338	3.4762	-0.73478	3367	13.959	0.629	0.105546
-0.86665	3350	9.7612	0.0488	-0.01091	2856	7.2129	6.1171	-1.0184
-0.11452	4891	5.3159	4.4941	-0.94976	3831	7.8309	5.4991	-0.91544
-0.29556	4416	6.9746	2.8354	-0.59944	3473	11.229	2.101	-0.34929
1.321785	3339	12.099	2.289	0.482838	3265	14.487	1.157	0.193514
-0.43055	3267	4.8056	5.0044	-1.05754	3206	11.135	2.195	-0.36495
1.017719	4425	12.859	3.049	0.643351	2880	19.479	6.149	1.025218
-0.6723	4382	6.7549	3.0551	-0.64584	4605	11.379	1.951	-0.3243
4.398448	3977	29.872	20.062	4.236522	3882	27.28	13.95	2.324921
-0.98707	4060	5.0246	4.7854	-1.01129	4071	8.1552	5.1748	-0.86141
-0.61161	4213	3.2281	6.5819	-1.39071	5210	12.265	1.065	-0.17669
0.691649	5233	6.9941	2.8159	-0.59532	5518	13.701	0.371	0.062561
0.079117	3470	4.0922	5.7178	-1.20821	5900	9.9661	3.3639	-0.5597
0.034307	4893	19.027	9.217	1.946042	3918	8.6524	4.6776	-0.77857
0.18634	2909	18.529	8.719	1.840864	4685	19.637	6.307	1.051542
1.583841	2861	30.129	20.319	4.2908	3499	15.547	2.217	0.370118
-0.77567	3592	10.245	0.435	0.091271	4845	14.448	1.118	0.187017
-0.65858	2287	8.6139	1.1961	-0.25322	2899	7.4508	5.8792	-0.97877
-1.60665	3488	4.7592	5.0508	-1.06734	3237	13.315	0.015	-0.00175
-1.06449	2619	8.9729	0.8371	-0.1774	3398	12.36	0.97	-0.16086
0.176138	2791	14.368	4.558	0.962054	3976	25.327	11.997	1.999537
-1.48654	2452	6.8515	2.9585	-0.62544	2974	10.188	3.142	-0.52273
-1.22044	2091	8.8953	0.9147	-0.19379	2836	14.774	1.444	0.241331
-1.21318	2243	14.712	4.902	1.034708	2819	13.019	0.311	-0.05107
-1.35675	2799	11.29	1.48	0.311976	3159	16.398	3.068	0.511901
-1.72151	3210	6.8536	2.9564	-0.625	4157	11.21	2.12	-0.35246
0.157934	3641	19.72	9.91	2.092404	3518	16.856	3.526	0.588207
0.921899	1859	15.976	6.166	1.301666	3325	28.541	15.211	2.535013
0.610432	2953	17.982	8.172	1.725336	3578	16.294	2.964	0.494574
-1.12626	3370	8.9021	0.9079	-0.19235	3924	12.538	0.792	-0.1312
0.389184	2297	13.017	3.207	0.676721	3848	21.57	8.24	1.373593
0.887491	2245	15.947	6.137	1.295541	3684	19.435	6.105	1.017887
0.814876	3328	15.835	6.025	1.271887	4751	21.069	7.739	1.290123

0.980711	4130	4.3099	5.5001	-1.16223	4058	16.634	3.304	0.55122
1.376797	5375	15.647	5.837	1.232181	3888	25.643	12.313	2.052185
-0.29836	5015	7.3579	2.4521	-0.51849	3664	8.3788	4.9512	-0.82416
1.277976	4514	7.9087	1.9013	-0.40216	4044	20.302	6.972	1.162335
1.489221	4330	11.986	2.176	0.458972	4711	15.39	2.06	0.343961
1.569838	4540	13.128	3.318	0.700164	2821	19.355	6.025	1.004558
0.725256	3156	7.9214	1.8886	-0.39948	3166	15.003	1.673	0.279484
2.361009	4725	11.704	1.894	0.399414	3300	22.97	9.64	1.606844
2.284393	3734	14.247	4.437	0.936499	3102	25.371	12.041	2.006868
2.338604	2768	14.668	4.858	1.025415	2931	22.279	8.949	1.491718
-0.97079	3488	4.3578	5.4522	-1.15211	3647	7.2114	6.1186	-1.01865
0.679046	3108	14.06	4.25	0.897004	3871	20.847	7.517	1.253136
1.099937	2546	11.115	1.305	0.275016	3417	23.881	10.551	1.758623
0.523613	4487	12.525	2.715	0.57281	3743	22.816	9.486	1.581186
1.096136	3057	10.37	0.56	0.117671	3746	19.621	6.291	1.048876
-1.2914	2911	9.1721	0.6379	-0.13533	3082	12.589	0.741	-0.12271
-0.19914	3158	12.571	2.761	0.582525	3336	25	11.67	1.945056
0.711053	2183	9.7114	0.0986	-0.02143	2383	15.946	2.616	0.436594
0.161135	2854	11.037	1.227	0.258542	3883	21.478	8.148	1.358266
-0.96733	2946	6.3815	3.4285	-0.72471	4257	10.218	3.112	-0.51773
-0.44554	3983	21.341	11.531	2.434762	5499	12.584	0.746	-0.12354
0.053912	2570	11.556	1.746	0.368156	5484	18.928	5.598	0.933417
1.870903	2602	11.261	1.451	0.305851	4164	18.396	5.066	0.844782
0.560021	3533	20.521	10.711	2.261577	4827	14.999	1.669	0.278817
-0.19954	3336	8.0336	1.7764	-0.37578	5201	10.575	2.755	-0.45825
2.057744	2527	14.721	4.911	1.036608	5368	27.18	13.85	2.30826
-0.12393	1873	5.9263	3.8837	-0.82084	4115	6.4642	6.8658	-1.14314
1.326386	2067	8.7567	1.0533	-0.22306	3274	14.722	1.392	0.232667
-0.37676	1960	8.0102	1.7998	-0.38072	3503	12.075	1.255	-0.20834
-0.15553	2654	16.202	6.392	1.349398	3485	15.868	2.538	0.423599
0.617833	2831	10.632	0.822	0.173006	3051	15.536	2.206	0.368285
-0.13673	3728	13.68	3.87	0.816748	4291	15.754	2.424	0.404606
-0.77955	3574	3.8612	5.9488	-1.257	3170	8.4858	4.8442	-0.80633
-1.30162	3316	5.4885	4.3215	-0.91331	4588	8.5004	4.8296	-0.8039
0.123527	3034	10.613	0.803	0.168993	3969	16.251	2.921	0.487409
-0.04591	3734	12.721	2.911	0.614205	5227	13.143	0.187	-0.03041
0.098321	2592	13.002	3.192	0.673553	4697	20.502	7.172	1.195657
1.693065	3938	11.605	1.795	0.378505	5444	13.666	0.336	0.05673
2.625066	3034	20.567	10.757	2.271292	5401	28.865	15.535	2.588993
0.910496	2788	16.033	6.223	1.313705	4881	18.111	4.781	0.797299
0.55682	3973	9.7408	0.0692	-0.01522	5643	9.4808	3.8492	-0.64055
1.447012	3518	9.8067	0.0033	-0.0013	4942	12.626	0.704	-0.11654
-0.07112	3253	4.6726	5.1374	-1.08563	5028	4.6937	8.6363	-1.43812
-0.04851	3608	6.8182	2.9918	-0.63247	7111	14.513	1.183	0.197846
-0.39064	3263	7.2326	2.5774	-0.54495	4821	7.4051	5.9249	-0.98638
-0.97113	3777	7.6516	2.1584	-0.45646	5026	8.9534	4.3766	-0.72842
1.879705	3080	11.688	1.878	0.396034	4827	11.394	1.936	-0.3218

0.799072	3519	12.049	2.239	0.472278	4804	10.033	3.297	-0.54855
1.583441	4883	8.417	1.393	-0.29481	6442	18.24	4.91	0.818791
-0.90243	3883	6.1293	3.6807	-0.77797	4829	13.46	0.13	0.022409
-0.40753	3314	4.4961	5.3139	-1.12291	3646	10.066	3.264	-0.54306
-0.53037	2944	7.2011	2.6089	-0.55161	4997	15.429	2.099	0.350458
-0.3492	2679	11.273	1.463	0.308386	4989	17.398	4.068	0.678508
-0.78841	4067	9.2943	0.5157	-0.10952	4579	12.841	0.489	-0.08072
-1.13048	2226	9.1195	0.6905	-0.14644	3995	9.7121	3.6179	-0.60202
-1.23085	3215	10.42	0.61	0.128231	5831	11.405	1.925	-0.31997
0.024905	4483	9.2572	0.5528	-0.11735	7243	18.956	5.626	0.938082
-0.40675	3638	12.012	2.202	0.464464	5224	17.075	3.745	0.624694
0.327571	3436	10.332	0.522	0.109645	5534	22.804	9.474	1.579187
-0.25455	2334	4.9272	4.8828	-1.03186	4024	12.972	0.358	-0.0589
-1.41318	4080	2.3284	7.4816	-1.58073	3851	2.3111	11.0189	-1.83508
-0.13593	3604	1.6926	8.1174	-1.71501	4816	11.441	1.889	-0.31397
0.13733	2689	8.7021	1.1079	-0.23459	3941	13.118	0.212	-0.03457
-0.0059	5316	9.8006	0.0094	-0.00259	5356	11.837	1.493	-0.24799
0.632836	3102	18.246	8.436	1.781093	5179	19.637	6.307	1.051542
-0.58987	3580	13.715	3.905	0.82414	5736	21.513	8.183	1.364097
-0.66954	3799	9.1077	0.7023	-0.14893	4766	11.687	1.643	-0.27299
-1.58436	2103	7.6082	2.2018	-0.46563	3872	10.124	3.206	-0.53339
-1.41521	3885	8.2883	1.5217	-0.32199	3852	8.5151	4.8149	-0.80145
0.173137	4334	17.028	7.218	1.52385	5021	16.65	3.32	0.553886
-1.70991	3156	6.0203	3.7897	-0.80099	3917	8.0419	5.2881	-0.88029
0.64904	3746	28.644	18.834	3.977166	5299	30.553	17.223	2.870226
0.066714	3476	18.383	8.573	1.810028	4716	17.875	4.545	0.75798
-1.13078	3819	14.768	4.958	1.046535	6000	15.05	1.72	0.287314
0.077917	2755	12.232	2.422	0.510928	5525	13.538	0.208	0.035404
-1.52081	3507	7.3282	2.4818	-0.52476	6621	12.007	1.323	-0.21967
-1.33791	2529	27.956	18.146	3.83186	6666	14.101	0.771	0.129204
-0.77781	3232	6.3428	3.4672	-0.73288	5277	7.1821	6.1479	-1.02353
0.682647	3180	13.774	3.964	0.836601	5411	15.746	2.416	0.403273
-0.15253	3397	13.541	3.731	0.787391	6276	17.065	3.735	0.623028
0.32597	4232	2.2448	7.5652	-1.59838	5014	7.7184	5.6116	-0.93418
0.077317	3948	2.9889	6.8211	-1.44123	4543	7.2199	6.1101	-1.01724
-0.4601	2794	2.2906	7.5194	-1.58871	5077	9.0014	4.3286	-0.72043
0.005901	3830	1.7232	8.0868	-1.70855	4695	7.5825	5.7475	-0.95683
0.78647	4475	4.3352	5.4748	-1.15689	5350	13.514	0.184	0.031405
0.437794	4382	2.7157	7.0943	-1.49893	6451	12.2	1.13	-0.18752
0.28056	2436	3.4483	6.3617	-1.3442	3787	4.0401	9.2899	-1.54701
-0.44178	3146	2.2568	7.5532	-1.59585	5056	7.5752	5.7548	-0.95804
1.561037	3910	6.0102	3.7998	-0.80313	4759	12.671	0.659	-0.10904
-0.61751	3063	0.78355	9.02645	-1.907	4018	5.7491	7.5809	-1.26228
-0.56884	4027	3.1785	6.6315	-1.40118	4944	11.044	2.286	-0.38011
-0.06531	3296	4.7633	5.0467	-1.06647	4879	12.257	1.073	-0.17802
0.422791	2812	5.0498	4.7602	-1.00596	5513	18.828	5.498	0.916756
0.796272	4418	4.6401	5.1699	-1.09249	6396	8.9744	4.3556	-0.72492

2.143162	3619	6.7146	3.0954	-0.65435	5560	11.906	1.424	-0.2365
0.412789	4088	2.9599	6.8501	-1.44735	6361	14.605	1.275	0.213174
-0.31037	4747	4.9505	4.8595	-1.02694	6880	11.032	2.298	-0.38211
1.049326	3353	1.9684	7.8416	-1.65676	6776	11.924	1.406	-0.2335
0.172337	3090	5.0162	4.7938	-1.01306	5789	14.994	1.664	0.277984
0.32597	3801	4.262	5.548	-1.17235	5843	11.022	2.308	-0.38378
-0.75812	6366	6.8018	3.0082	-0.63594	7636	7.6349	5.6951	-0.9481
0.14133	3010	14.551	4.741	1.000704	5748	17.31	3.98	0.663847
-0.08332	3425	7.7372	2.0728	-0.43838	5473	13.009	0.321	-0.05273
1.545433	4545	17.162	7.352	1.552151	6992	26.402	13.072	2.17864
-0.09092	4183	11.977	2.167	0.457072	6198	13.02	0.31	-0.0509
-0.20174	4201	8.3313	1.4787	-0.31291	6540	9.3884	3.9416	-0.65595
2.189172	3174	18.557	8.747	1.846777	6498	15.99	2.66	0.443925
0.301965	3447	18.306	8.496	1.793766	4660	13.884	0.554	0.09305
0.059513	3471	15.356	5.546	1.170721	3700	8.7027	4.6273	-0.77019
0.067515	4176	10.081	0.271	0.056634	4056	6.1391	7.1909	-1.19731
0.819677	2274	13.632	3.822	0.80661	3716	13.186	0.144	-0.02324
-0.43239	3336	12.8	2.99	0.63089	4760	19.475	6.145	1.024551
1.178954	3581	15.945	6.135	1.295119	6425	20.28	6.95	1.15867
0.147732	3238	7.7517	2.0583	-0.43532	5137	9.5386	3.7914	-0.63092
-0.49127	3118	9.2688	0.5412	-0.1149	5664	6.7797	6.5503	-1.09058
-0.37734	3538	8.1402	1.6698	-0.35327	5907	9.6157	3.7143	-0.61808
-1.14979	2569	8.0965	1.7135	-0.3625	5488	9.2566	4.0734	-0.67791
1.99433	5273	15.229	5.419	1.143899	7586	20.327	6.997	1.166501
1.029722	5037	16.855	7.045	1.487312	6886	25.632	12.302	2.050352
-0.75926	3801	5.5775	4.2325	-0.89451	4469	6.2878	7.0422	-1.17253
0.726057	5353	9.434	0.376	-0.08001	6080	18.783	5.453	0.909259
0.261356	2598	10.393	0.583	0.122529	4840	17.397	4.067	0.678341
0.564422	3659	13.501	3.691	0.778943	4530	16.093	2.763	0.461086
0.215947	4096	12.036	2.226	0.469533	5231	15.618	2.288	0.381947
-1.09172	2696	6.8249	2.9851	-0.63106	4035	6.6667	6.6633	-1.1094
0.070715	3666	6.874	2.936	-0.62069	6866	15.234	1.904	0.31797
2.222579	2846	15.601	5.791	1.222466	5108	22.475	9.145	1.524373
0.892492	2860	15.14	5.33	1.125102	3679	17.206	3.876	0.646519
1.041525	3527	10.462	0.652	0.137101	6715	20.447	7.117	1.186493
4.35864	2530	14.585	4.775	1.007885	4375	24.617	11.287	1.881246
1.426408	3652	11.473	1.663	0.350626	5272	21.491	8.161	1.360431
1.957122	2278	12.423	2.613	0.551267	6318	23.773	10.443	1.740629
1.139946	2202	5.2225	4.5875	-0.96949	4487	16.849	3.519	0.587041
1.16075	2125	7.9059	1.9041	-0.40275	4581	13.425	0.095	0.016577
0.071115	2311	8.7408	1.0692	-0.22642	5955	11.335	1.995	-0.33163
0.749662	3038	12.673	2.863	0.604068	6887	19.573	6.243	1.040879
0.617033	3456	16.175	6.365	1.343695	6565	18.096	4.766	0.7948
0.596829	2662	10.856	1.046	0.220315	6841	10.306	3.024	-0.50307
0.427392	2353	6.5873	3.2227	-0.68124	4834	9.4125	3.9175	-0.65193
2.081749	3670	16.267	6.457	1.363126	5477	14.807	1.477	0.246829
1.523028	4863	20.543	10.733	2.266223	4932	12.53	0.8	-0.13254

-0.07692	3406	8.1033	1.7067	-0.36106	5079	14.294	0.964	0.161359
-0.19994	2770	4.4765	5.3335	-1.12704	3721	6.853	6.477	-1.07837
0.589427	4421	19.498	9.688	2.045518	6110	17.021	3.691	0.615697
-1.44355	3610	12.216	2.406	0.507549	4986	9.627	3.703	-0.6162
-0.36856	3171	13.75	3.94	0.831532	5812	10.857	2.473	-0.41127
1.166552	2848	14.888	5.078	1.071879	5862	9.1607	4.1693	-0.69389
2.684879	3837	21.658	11.848	2.501713	5818	17.515	4.185	0.698001
0.152933	2716	8.3211	1.4889	-0.31506	5058	7.0384	6.2916	-1.04748
2.239183	3124	12.612	2.802	0.591185	4843	20.979	7.649	1.275129
0.955706	3006	14.305	4.495	0.948749	4655	14.307	0.977	0.163525
0.733458	3000	15.2	5.39	1.137774	6162	24.197	10.867	1.811271
2.140361	3237	19.802	9.992	2.109723	6670	31.409	18.079	3.012842
-0.81588	2431	7.8157	1.9943	-0.4218	6155	7.7335	5.5965	-0.93167
0.136529	2902	11.061	1.251	0.263611	5101	11.253	2.077	-0.34529
-0.26616	2574	10.14	0.33	0.069095	5639	14.843	1.513	0.252826
0.403387	4171	15.008	5.198	1.097223	5714	15.453	2.123	0.354457
0.484604	3540	16.441	6.631	1.399875	6743	18.182	4.852	0.809128
1.906911	3303	16.561	6.751	1.425219	5346	15.32	1.99	0.332298
-0.60769	3208	10.661	0.851	0.179131	5573	9.7075	3.6225	-0.60279
-1.15853	3468	15.946	6.136	1.29533	4888	5.8715	7.4585	-1.24189
-0.13713	3087	9.3618	0.4482	-0.09526	3520	4.0341	9.2959	-1.54801
-1.04607	3532	16.195	6.385	1.347919	3839	4.4803	8.8497	-1.47367
-1.44609	1909	10.739	0.929	0.195604	4751	6.0408	7.2892	-1.21368
0.328171	2303	15.979	6.169	1.3023	5089	10.886	2.444	-0.40644
-0.82034	1980	12.929	3.119	0.658135	2793	6.8385	6.4915	-1.08078
-0.36042	3453	8.1958	1.6142	-0.34152	4443	6.257	7.073	-1.17766
1.072931	2528	16.416	6.606	1.394595	5741	19.091	5.761	0.960574
-0.83728	2774	14.78	4.97	1.049069	3940	6.802	6.528	-1.08686
0.054912	2684	10.395	0.585	0.122951	3677	6.0919	7.2381	-1.20517
0.931301	2535	22.288	12.478	2.63477	4727	23.588	10.258	1.709807
-0.0081	2657	21.867	12.057	2.545854	5565	11.95	1.38	-0.22917
-0.90009	3367	11.494	1.684	0.355061	4619	16.172	2.842	0.474248
-0.35148	3585	10.265	0.455	0.095495	5721	10.767	2.563	-0.42626
-0.17894	2951	12.911	3.101	0.654334	5459	6.3382	6.9918	-1.16413
-0.33595	2450	15.224	5.414	1.142843	5408	10.688	2.642	-0.43943
-0.0113	3089	19.1	9.29	1.96146	6177	12.239	1.091	-0.18102
1.711069	2896	20.511	10.701	2.259465	5318	13.125	0.205	-0.0334
0.425392	2240	9.9554	0.1454	0.030107	4126	5.6714	7.6586	-1.27523
-0.71579	3298	8.5506	1.2594	-0.26659	4281	7.4982	5.8318	-0.97087
	3491.5	9.81285	3.1992		4379	13.3255	4.0555	
			9.5976				12.1665	
			4.734816				6.00214	
806	12.655		3453	21.952				
1606	10.834		1741	7.8116				
1293	2.5522		2828	7.9208				
1129	4.3401		1896	5.9072				
1208.5	7.595325		2479.5	10.8979				

333.4032	4.903024	807.2606	7.427171
2239	49.71	4348	50.851
3180	41.855	6411	61.816
3265	48.055	4353	47.232
2654	42.615	5596	59.936
2834.5	45.55875	5177	54.95875
	3.909287		7.032571
	11.72786		21.09771
	14.70907		22.28151
	26.43693		43.37922
	37.96343		44.06085
	0.696379		0.98453
	0.303621		0.01547

515	14.175	733	7.5034
584	7.363	527	20.873
2308	12.348	5571	18.094
3090	8.0583	4734	7.7102
5893	13.117	5679	21.078
6704	6.071	5460	17.399

y

y

y

y

x debris a

y

y

y

y

y

					cell ct	% inf	AD
50073	A02	M-018749- WD repeat	146845	WDR16	3294	10.929	1.519
50073	A04	M-010964- solute carri	146802	SLC47A2	3993	32.206	22.796
50073	A05	M-007137- tripartite m	140691	TRIM69	3866	7.2944	2.1156
50073	A06	M-030801- hypothetica	146795	LOC146795	4448	6.9469	2.4631
50073	A07	M-016526- chromosom	140699	C20orf132	4048	7.831	1.579
50073	A08	M-018511- EF-hand ca	146779	EFCAB3	5080	5.1181	4.2919
50073	A09	M-015241- sterile alph	140700	SAMD10	3921	5.8914	3.5186
50073	A10	M-030838- dynein, axc	146754	DNAH2	4771	6.3718	3.0382
50073	A11	M-015242- chromosom	140701	C20orf135	4401	13.156	3.746
50073	A12	M-016417- chromosom	146723	C17orf77	4262	10.465	1.055
50073	A13	M-018652- chromosom	140706	C20orf160	4200	10.81	1.4
50073	A14	M-030816- hypothetica	146713	HRNBP3	3799	11.714	2.304
50073	A15	M-021322- regulating	140730	RIMS4	3918	3.9816	5.4284
50073	A16	M-019318- UDP-GlcNA	146712	B3GNTL1	4938	12.13	2.72
50073	A17	M-015257- chromosom	140731	C20orf86	4232	7.0888	2.3212
50073	A18	M-015821- chromosom	146705	C17orf56	5437	15.431	6.021
50073	A19	M-016807- sperm asso	140732	SPAG4L	2217	12.539	3.129
50073	A20	M-018810- target of m	146691	TOM1L2	4942	13.638	4.228
50073	A21	M-015258- chromosom	140733	C20orf133	5032	6.6574	2.7526
50073	A23	M-019410- transmemb	140738	TMEM37	3534	4.2445	5.1655
50073	B02	M-032206- HERV-FRD	405754	HERV-FRD	5575	8.7892	0.6208
50073	B04	M-016525- hypothetica	149650	RP11-93B1	4543	4.7766	4.6334
50073	B05	M-015818- coiled-coil	146849	CCDC42	5335	4.5361	4.8739
50073	B06	M-016392- hypothetica	146268	FLJ31821	5664	12.112	2.702
50073	B07	M-030841- chromosom	146850	C17orf38	5250	6.0571	3.3529
50073	B08	M-016735- hypothetica	148697	FLJ30634	5004	4.6763	4.7337
50073	B09	M-016398- outer dens	146852	ODF4	5731	9.9459	0.5359
50073	B10	M-017378- CDC42 effe	148170	CDC42EP5	5388	8.1477	1.2623
50073	B11	M-016053- chromosom	146853	C17orf50	5752	10.57	1.16
50073	B12	M-024368- hypothetica	150084	LOC150084	5556	11.015	1.605
50073	B13	M-015815- schlafen fa	146857	SLFN13	4685	9.5624	0.1524
50073	B14	M-016527- chromosom	150082	C21orf13	5694	16.298	6.888
50073	B15	M-016419- acyl-malon	146861	AMAC1	3848	7.9262	1.4838
50073	B16	M-016165- chromosom	149992	C21orf99	5979	13.949	4.539
50073	B17	M-017877- unc-45 hom	146862	UNC45B	5773	17.565	8.155
50073	B18	M-015675- LSM14B, SC	149986	LSM14B	6257	13.872	4.462
50073	B19	M-030925- hypothetica	146880	MGC40489	6088	17.428	8.018
50073	B20	M-009125- chromosom	149954	C20orf186	5161	16.063	6.653
50073	B21	M-016059- CD300 mol	146894	CD300LG	5743	26.223	16.813
50073	B23	M-010460- hypothetica	146909	LOC146909	6295	17.299	7.889
50073	C02	M-015789- mannosyl (	146664	MGAT5B	5581	14.334	4.924
50073	C04	M-016884- chromosom	146562	C16orf71	4342	11.515	2.105
50073	C05	M-009081- ubiquitin-c	140739	UBE2F	4125	4.9697	4.4403
50073	C06	M-018764- hypothetica	146556	MGC45438	6236	15.763	6.353
50073	C07	M-018655- neurensin 1	140767	NRSN1	4382	6.1844	3.2256
50073	C08	M-005879- protease, s	146547	PRSS36	5774	9.0578	0.3522

50073	C09	M-016465- Smith-Mag	140771	SMCR5	4969	9.8611	0.4511
50073	C10	M-007139- zinc finger	146542	ZNF688	4859	6.9356	2.4744
50073	C11	M-017373- Smith-Mag	140775	SMCR8	3984	8.3584	1.0516
50073	C12	M-018331- zinc finger	146540	ZNF785	3627	13.758	4.348
50073	C13	M-013264- ribosomal	140801	RPL10L	3786	20.919	11.509
50073	C14	M-022800- similar to h	146489	LOC14648	6269	18.089	8.679
50073	C15	M-015267- keratin 72	140807	KRT72	3504	14.526	5.116
50073	C16	M-030697- hypothetic	146481	LOC146481	3691	22.108	12.698
50073	C17	M-015263- sulfiredoxi	140809	SRXN1	3236	5.8096	3.6004
50073	C18	M-008029- transmem	146456	TMED6	4938	14.905	5.495
50073	C19	M-015268- chromoso	140823	C20orf52	4265	13.411	4.001
50073	C20	M-030676- hypothetic	146443	LOC14644	4627	10.979	1.569
50073	C21	M-015269- neuralized	140825	NEURL2	3949	15.447	6.037
50073	C23	M-018137- brix domai	140826	BXDC1P	4622	22.22	12.81
50073	D02	M-015188- COMM do	149951	COMMD7	3551	9.434	0.024
50073	D04	M-018767- chromoso	149840	C20orf196	4216	10.223	0.813
50073	D05	M-017736- RUN doma	146923	RUNDC1	3483	6.7758	2.6342
50073	D06	M-018042- hypothetic	149836	MGC35023	3357	3.2767	6.1333
50073	D07	M-016420- essential	146956	EME1	5297	3.4925	5.9175
50073	D08	M-018306- prion prote	149830	PRNT	4169	8.5392	0.8708
50073	D09	M-030945- hypothetic	147004	LOC14700	4346	5.0391	4.3709
50073	D10	M-017408- WAP four-	149708	WFDC5	5303	9.3155	0.0945
50073	D11	M-016421- chromoso	147007	C17orf32	3124	7.8425	1.5675
50073	D12	M-018028- family with	149699	FAM112A	3202	5.4341	3.9759
50073	D13	M-016422- proline-ric	147011	PROCA1	3497	11.925	2.515
50073	D14	M-031303- hypothetic	149692	LOC14969	4018	10.229	0.819
50073	D15	M-008777- dehydroge	147015	DHRS13	5210	8.5797	0.8303
50073	D16	M-017780- adipogenin	149685	ADIG	2841	7.5326	1.8774
50073	D17	M-023046- potassium	147040	KCTD11	3322	4.2745	5.1355
50073	D18	M-015906- family with	149647	FAM71A	5989	12.389	2.979
50073	D19	M-030899- hypothetic	147080	LOC14708	5147	7.2081	2.2019
50073	D20	M-016524- pyrin and	149628	PYHIN1	3087	13.022	3.612
50073	D21	M-016423- chromoso	147081	C17orf69	6396	20.169	10.759
50073	D23	M-030882- hypothetic	147093	LOC14709	2861	13.072	3.662
50073	E02	M-016761- zinc finger	146434	ZNF597	6227	22.981	13.571
50073	E04	M-016777- chromoso	146433	C16orf77	5649	16.268	6.858
50073	E05	M-015271- zinc finger,	140831	ZSWIM3	4796	10.53	1.12
50073	E06	M-003985- GSG1-like	146395	GSG1L	5807	19.649	10.239
50073	E07	M-013266- WAP four-	140832	WFDC10A	5457	7.495	1.915
50073	E08	M-003995- hypothetic	146378	FLJ25404	4312	12.43	3.02
50073	E09	M-018231- chromoso	140836	C20orf179	4390	11.002	1.592
50073	E10	M-018990- hypothetic	146336	FLJ32252	4875	13.415	4.005
50073	E11	M-017258- defensin, b	140850	DEFB127	4147	8.7051	0.7049
50073	E12	M-016797- F-box and	146330	FBXL16	3908	10.415	1.005
50073	E13	M-010375- chromoso	140856	C20orf79	3529	13.262	3.852
50073	E14	M-016050- similar to h	146325	LOC14632	4085	8.2252	1.1848
50073	E15	M-024255- chromoso	140862	C20orf82	4830	12.712	3.302

50073	E16	M-030777- ring finger	146310	RNF151	3684	12.025	2.615
50073	E17	M-013695- WAP four-	140870	WFDC6	2980	5.2013	4.2087
50073	E18	M-015833- tektin 5	146279	TEKT5	5383	22.608	13.198
50073	E19	M-015275- chromoso	140873	C20orf173	4810	8.316	1.094
50073	E20	M-022571- brain expre	146227	BEAN	4185	23.441	14.031
50073	E21	M-015276- chromoso	140876	C20orf175	3907	4.5047	4.9053
50073	E23	M-017530- cystatin 11	140880	CST11	5543	10.554	1.144
50073	F02	M-021939- ring finger	149603	RNF187	4474	5.7443	3.6657
50073	F04	M-018368- chromoso	149563	C1orf64	5145	7.1914	2.2186
50073	F05	M-018341- notum pe	147111	NOTUM	4451	5.2797	4.1303
50073	F06	M-015707- chromoso	149499	C1orf92	2980	1.2752	8.1348
50073	F07	M-023295- hypothetic	147172	DKFZp667	4116	2.551	6.859
50073	F08	M-016956- coiled-coil	149483	CCDC17	4774	9.0071	0.4029
50073	F09	M-017591- WAS/WAS	147179	WIPF2	3410	3.4604	5.9496
50073	F10	M-027467- hypothetic	149478	LOC14947	4599	6.3275	3.0825
50073	F11	M-018766- keratin 25	147183	KRT25	4986	11.051	1.641
50073	F12	M-016955- coiled-coil	149473	CCDC24	3465	9.6104	0.2004
50073	F13	M-015962- transmem	147184	TMEM99	3650	3.7808	5.6292
50073	F14	M-018666- chromoso	149469	C1orf84	4005	5.6429	3.7671
50073	F15	M-015629- secretoglo	147199	SCGB1C1	4067	4.3521	5.0579
50073	F16	M-018640- chromoso	149466	C1orf210	3376	7.8495	1.5605
50073	F17	M-016885- START do	147323	STARD6	3179	4.2152	5.1948
50073	F18	M-016954- WD repeat	149465	WDR65	5029	12.965	3.555
50073	F19	M-015948- chromoso	147339	C18orf25	5070	9.5069	0.0969
50073	F20	M-016233- claudin 19	149461	CLDN19	4992	7.3117	2.0983
50073	F21	M-015579- chromoso	147341	C18orf23	5609	12.319	2.909
50073	F23	M-023544- collagen a	147372	CCBE1	2233	5.1948	4.2152
50073	G02	M-010754- CKLF-like	146225	CMTM2	6017	6.5481	2.8619
50073	G04	M-010753- CKLF-like	146223	CMTM4	6462	10.09	0.68
50073	G05	M-013461- defensin, b	140881	DEFB129	5187	7.3646	2.0454
50073	G06	M-030635- potassium	146212	KCTD19	5653	4.9354	4.4746
50073	G07	M-007138- suppressor	140883	SUHW2	5178	6.9911	2.4189
50073	G08	M-022592- RGD, leuci	146206	RLTPR	5870	9.029	0.381
50073	G09	M-015277- poly(A) bin	140886	PABPC5	4101	14.24	4.83
50073	G10	M-022578- zinc finger	146198	ZFP90	5222	5.8407	3.5693
50073	G11	M-016865- splicing fac	140890	SFRS12	3904	9.4006	0.0094
50073	G12	M-030605- hypothetic	146177	LOC14617	4180	10.622	1.212
50073	G13	M-015278- chromoso	140893	C20orf151	3528	6.4909	2.9191
50073	G14	M-018502- chromoso	146174	C16orf52	4477	12.799	3.389
50073	G15	M-015279- chromoso	140894	C20orf152	4536	7.7822	1.6278
50073	G16	M-018763- zinc finger	146050	ZSCAN29	4378	6.7839	2.6261
50073	G17	M-018256- R3H domai	140902	R3HDML	3340	3.6527	5.7573
50073	G18	M-016754- transmem	145978	TMEM83	4502	5.3754	4.0346
50073	G19	M-017598- chromoso	140947	C5orf20	4257	4.7921	4.6179
50073	G20	M-015692- neuregulin	145957	NRG4	5292	5.0454	4.3646
50073	G21	M-015287- mindbomb	142678	MIB2	5171	8.7024	0.7076
50073	G23	M-007536- solute carri	142680	SLC34A3	5227	5.6629	3.7471

50073	H02	M-015353- BCL2/aden	149428	BNIPL	5231	2.2175	7.1925
50073	H04	M-016953- chromosom	149421	C1orf215	5618	6.3546	3.0554
50073	H05	M-018996- cerebellin 2	147381	CBLN2	4990	14.729	5.319
50073	H06	M-018001- exocyst cor	149371	EXOC8	4246	3.7683	5.6417
50073	H07	M-031039- mitochond	147407	MCART2	3054	7.9895	1.4205
50073	H08	M-027614- hypothetica	149351	LOC149351	4420	4.4118	4.9982
50073	H09	M-017803- desmoglein	147409	DSG4	4200	6.1905	3.2195
50073	H10	M-022094- transmemb	149345	TMEM58	4816	13.642	4.232
50073	H11	M-015580- chromosom	147429	C18orf16	3193	4.5412	4.8688
50073	H12	M-016951- mannosida	149175	MANEAL	3679	3.0987	6.3113
50073	H13	M-018512- ankyrin rep	147463	ANKRD29	2623	2.9356	6.4744
50073	H14	M-027627- hypothetica	149134	LOC149134	2831	7.8064	1.6036
50073	H15	M-016399- adenomato	147495	APCDD1	2994	4.1082	5.3018
50073	H16	M-016950- cornichon h	149111	CNIH3	4396	7.2111	2.1989
50073	H17	M-023794- hypothetica	147645	LOC147645	3962	15.598	6.188
50073	H18	M-016740- DC-STAMP	149095	DCST1	5373	10.702	1.292
50073	H19	M-023796- hypothetica	147646	LOC147646	3532	15.657	6.247
50073	H20	M-021899- hypothetica	149086	LOC149086	4833	6.1039	3.3061
50073	H21	M-023802- hypothetica	147650	LOC147650	4577	5.9646	3.4454
50073	H23	M-015806- zinc finger	147657	ZNF480	4565	11.961	2.551
50073	I02	M-018499- spermatog	145946	SPATA8	4591	6.9266	2.4834
50073	I04	M-016378- transmemb	145942	TMCO5	3741	8.0727	1.3373
50073	I05	M-008590- intelectin 2	142683	ITLN2	5035	10.884	1.474
50073	I06	M-022324- mesoderm	145873	MESP2	6326	15.729	6.319
50073	I07	M-031158- ankyrin rep	142685	ASB15	3835	9.5176	0.1076
50073	I08	M-019125- hyaluronan	145864	HAPLN3	4166	5.8809	3.5291
50073	I09	M-013205- ankyrin rep	142686	ASB14	4921	11.38	1.97
50073	I10	M-015930- chromosom	145858	C15orf32	4121	7.5952	1.8148
50073	I11	M-013180- ankyrin rep	142689	ASB12	4566	13.382	3.972
50073	I12	M-030388- hypothetica	145845	LOC145845	4906	15.226	5.816
50073	I13	M-029647- chromosom	142827	C10orf129	3461	8.4658	0.9442
50073	I14	M-030417- hypothetica	145837	LOC145837	4179	13.544	4.134
50073	I15	M-015900- sterile alph	142891	SAMD8	3515	4.5804	4.8296
50073	I16	M-030497- hypothetica	145820	LOC145820	4580	9.5633	0.1533
50073	I17	M-015476- cofilin pseu	142913	CFLP1	3383	10.73	1.32
50073	I18	M-030513- hypothetica	145814	LOC145814	4584	8.7696	0.6404
50073	I19	M-016391- TruB pseud	142940	TRUB1	4057	14.814	5.404
50073	I20	M-022244- unc-13 hon	145790	UNC13C	4054	9.7928	0.3828
50073	I21	M-008487- membrane	143098	MPP7	4675	9.0481	0.3619
50073	I23	M-015451- hypothetica	143153	FLJ31958	4287	8.5374	0.8726
50073	J02	M-016739- FLJ25476 p	149076	FLJ25476	6520	12.239	2.829
50073	J04	M-021878- ring finger	149041	RC3H1	6888	8.2172	1.1928
50073	J05	M-015581- zinc finger	147660	ZNF578	6278	12.01	2.6
50073	J06	M-027496- KIAA1245	149013	KIAA1245	5512	9.0167	0.3933
50073	J07	M-015582- FLJ32214 p	147664	FLJ32214	4815	15.223	5.813
50073	J08	M-016995- GLIS family	148979	GLIS1	4345	9.4822	0.0722
50073	J09	M-023826- hypothetica	147670	LOC147670	3632	9.4163	0.0063

50073	J10	M-016073-	MOB1, Mp	148932	MOBKL2C	4105	11.352	1.942
50073	J11	M-016200-	chromosom	147685	C19orf18	3413	9.8447	0.4347
50073	J12	M-018573-	kinocilin	148930	L5	4049	12.176	2.766
50073	J13	M-023835-	zinc finger	147686	ZNF418	3370	10.059	0.649
50073	J14	M-031726-	chromosom	148898	C1orf213	4107	5.6245	3.7855
50073	J15	M-016201-	zinc finger	147687	ZNF417	3926	8.4819	0.9281
50073	J16	M-016738-	coiled-coil	148870	CCDC27	4428	9.9593	0.5493
50073	J17	M-016400-	zinc finger	147694	ZNF548	3251	6.4596	2.9504
50073	J18	M-007528-	solute carri	148867	SLC30A7	5036	17.752	8.342
50073	J19	M-009006-	hypothetica	147699	FLJ40125	4085	8.8862	0.5238
50073	J20	M-005106-	chromosom	148823	C1orf150	4226	8.6133	0.7967
50073	J21	M-018514-	LY6/PLAUR	147719	LYPD4	4696	6.8569	2.5531
50073	J23	M-027352-	hypothetica	147727	LOC147727	4586	8.3515	1.0585
50073	K02	M-022251-	hypothetica	145783	LOC145783	5569	4.4532	4.9568
50073	K04	M-016361-	GRINL1A co	145781	Gcom1	5035	6.1569	3.2531
50073	K05	M-008854-	FERM and	143162	FRMPD2	5963	9.8105	0.4005
50073	K06	M-016386-	family with	145773	FAM81A	5283	6.2465	3.1635
50073	K07	M-016716-	vesicle tran	143187	VTI1A	4465	2.6204	6.7896
50073	K08	M-030516-	hypothetica	145757	LOC145757	3466	5.049	4.361
50073	K09	M-029659-	hypothetica	143188	LOC143188	4808	9.505	0.095
50073	K10	M-016597-	LysM, puta	145748	LYSMD4	3458	5.8415	3.5685
50073	K11	M-016591-	DPY30 dom	143241	DYDC1	3906	9.319	0.091
50073	K12	M-032034-	nuclear loc	145741	NLF1	2933	7.3304	2.0796
50073	K13	M-007198-	HECT doma	143279	HECTD2	3376	5.8649	3.5451
50073	K14	M-016753-	chromosom	145645	C15orf43	2934	6.2713	3.1387
50073	K15	M-018330-	fibroblast g	143282	FGFBP3	3649	3.3434	6.0666
50073	K16	M-018762-	leucine rich	145581	LRFN5	4404	10.672	1.262
50073	K17	M-015704-	chromosom	143379	C10orf82	2927	4.8172	4.5928
50073	K18	M-021990-	tetratricop	145567	TTC7B	3295	5.0379	4.3721
50073	K19	M-016305-	chromosom	143384	C10orf46	4563	14.07	4.66
50073	K20	M-019407-	magnesium	145553	MDP-1	4943	8.1934	1.2166
50073	K21	M-018003-	synaptotag	143425	SYT9	4121	6.843	2.567
50073	K23	M-017778-	low density	143458	LDLRAD3	3340	4.2216	5.1884
50073	L02	M-016737-	hypothetica	148811	FLJ32569	6240	7.9167	1.4933
50073	L04	M-018560-	major facili	148808	MFSD4	5328	6.3626	3.0474
50073	L05	M-016202-	zinc finger	147741	ZNF560	5385	11.978	2.568
50073	L06	M-027544-	hypothetica	148756	LOC148756	3490	5.8453	3.5647
50073	L07	M-016866-	MDAC1	147744	MDAC1	5464	8.071	1.339
50073	L08	M-018554-	chromosom	148753	C1orf76	4288	6.0634	3.3466
50073	L09	M-015801-	transmemb	147798	TMC4	4649	10.368	0.958
50073	L10	M-015977-	ankyrin rep	148741	ANKRD35	5751	9.6853	0.2753
50073	L11	M-007140-	zinc finger	147807	ZNF524	3294	7.6199	1.7901
50073	L12	M-018751-	hemochrom	148738	HFE2	3930	17.761	8.351
50073	L13	M-031933-	zinc finger	147808	ZNF784	3398	10.653	1.243
50073	L14	M-018535-	chromosom	148646	C1orf188	3561	4.9424	4.4676
50073	L15	M-015954-	zinc finger	147837	ZNF563	2535	3.0375	6.3725
50073	L16	M-015655-	chromosom	148645	C1orf211	4192	16.913	7.503

50073	L17	M-018711- SPC24, ND	147841	SPC24	3466	14.974	5.564
50073	L18	M-018534- solute carri	148641	SLC35F3	4047	10.378	0.968
50073	L19	M-015777- hypothetic	147872	FLJ32658	4922	20.093	10.683
50073	L20	M-008998- ubiquitin-c	148581	UBE2U	4553	16.824	7.414
50073	L21	M-015690- dapper, an	147906	DACT3	5095	8.106	1.304
50073	L23	M-017983- sine oculis	147912	SIX5	5288	11.517	2.107
50073	M02	M-018971- thrombosp	145501	THSD3	4532	6.09	3.32
50073	M04	M-019320- chromoson	145497	C14orf166	5491	6.4287	2.9813
50073	M05	M-015714- proteasom	143471	PSMA8	5172	12.336	2.926
50073	M06	M-016298- chromoson	145483	C14orf44	5715	15.958	6.548
50073	M07	M-015874- chromoson	143501	C11orf40	5565	13.729	4.319
50073	M08	M-008320- zinc bindin	145482	ZADH1	4239	15.9	6.49
50073	M09	M-029916- X-ray radia	143570	XRRA1	5020	8.1673	1.2427
50073	M10	M-019149- abhydrolas	145447	ABHD12B	4251	16.208	6.798
50073	M11	M-016109- ubiquilin-li	143630	UBQLNL	4449	10.811	1.401
50073	M12	M-007563- solute carri	145389	SLC38A6	3337	16.332	6.922
50073	M13	M-015614- mucin 15,	143662	MUC15	3436	7.6542	1.7558
50073	M14	M-016882- chromoson	145376	C14orf50	3256	12.009	2.599
50073	M15	M-015721- family with	143684	FAM76B	3905	18.592	9.182
50073	M16	M-017631- proline rich	145270	PRIMA1	3927	14.77	5.36
50073	M17	M-018289- sestrin 3	143686	SESN3	3444	8.5656	0.8444
50073	M18	M-008739- serpin pept	145264	SERPINA12	4474	22.776	13.366
50073	M19	M-004644- piwi-like 4	143689	PIWIL4	4158	15.801	6.391
50073	M20	M-019261- goosecoid	145258	GSC	4807	10.838	1.428
50073	M21	M-026507- hypothetic	143872	FLJ32810	4580	10.284	0.874
50073	M23	M-016974- kelch repea	143879	KBTBD3	5323	11.215	1.805
50073	N02	M-016713- neuroblast	148545	NBPF4	2452	1.6313	7.7787
50073	N04	M-016712- transmemb	148534	TMEM56	5385	9.7493	0.3393
50073	N05	M-016766- zinc finger	147923	ZNF420	6233	12.354	2.944
50073	N06	M-018742- chromoson	148523	C1orf51	5810	15.06	5.65
50073	N07	M-016203- zinc finger	147929	ZNF565	6148	9.5316	0.1216
50073	N08	M-016306- PHD finger	148479	PHF13	3833	5.844	3.566
50073	N09	M-015351- NLR family,	147945	NLRP4	3895	5.3402	4.0698
50073	N10	M-021428- chromoson	148423	C1orf52	4678	9.4271	0.0171
50073	N11	M-019316- zinc finger	147947	ZNF542	3951	7.8714	1.5386
50073	N12	M-021615- sterile alph	148418	SAMD13	4152	29.552	20.142
50073	N13	M-015751- zinc finger	147948	ZNF582	3775	10.967	1.557
50073	N14	M-027670- hypothetic	148413	LOC14841	4621	10.604	1.194
50073	N15	M-016204- zinc finger	147949	ZNF583	3029	12.446	3.036
50073	N16	M-016711- sterile alph	148398	SAMD11	4494	11.682	2.272
50073	N17	M-021329- family with	147965	FAM98C	2449	19.232	9.822
50073	N18	M-015709- chromoson	148362	C1orf58	4580	16.07	6.66
50073	N19	M-005802- calpain 12	147968	CAPN12	3403	19.835	10.425
50073	N20	M-018529- chromoson	148345	C1orf127	4742	13.686	4.276
50073	N21	M-031082- dpy-19-like	147991	DPY19L3	4288	9.5616	0.1516
50073	N23	M-016205- tetratricop	148014	TTC9B	3231	6.9328	2.4772
50073	O02	M-008319- retinol deh	145226	RDH12	3951	9.3141	0.0959

50073	O04	M-030335- hypothetic	145216	LOC14521	3211	17.533	8.123
50073	O05	M-016672- CWF19-like	143884	CWF19L2	3514	13.005	3.595
50073	O06	M-022004- chromoson	145200	C14orf72	3265	9.0352	0.3748
50073	O07	M-015652- KDEL (Lys-	143888	KDELC2	3721	11.045	1.635
50073	O08	M-019319- beta 1,3-ga	145173	B3GALTL	4053	11.103	1.693
50073	O09	M-018470- layilin	143903	LAYN	3056	12.467	3.057
50073	O10	M-016033- family with	145165	FAM10A4	3685	5.2917	4.1183
50073	O11	M-026589- hypothetic	144097	LOC14409	3248	16.502	7.092
50073	O12	M-021705- heterogene	144983	RP11-78J2	3934	13.447	4.037
50073	O13	M-018008- pleckstrin	144100	PLEKHA7	3023	8.0715	1.3385
50073	O14	M-021584- hypothetic	144920	LOC14492	2449	20.008	10.598
50073	O15	M-016032- family with	144106	FAM10A5	4613	19.033	9.623
50073	O16	M-015653- chromoson	144811	C13orf31	3538	17.467	8.057
50073	O17	M-026785- SPT2, Supp	144108	SPTY2D1	4990	14.469	5.059
50073	O18	M-018966- chromoson	144809	C13orf30	4587	14.912	5.502
50073	O19	M-016796- transmem	144110	TMEM86A	5786	8.3477	1.0623
50073	O20	M-030181- hypothetic	144776	LOC14477	3142	5.2514	4.1586
50073	O21	M-015858- dynein hea	144132	DNHD1	5707	14.876	5.466
50073	O23	M-016677- prickle hon	144165	PRICKLE1	4293	11.857	2.447
50073	P02	M-010738- cAMP resp	148327	CREB3L4	3962	9.4902	0.0802
50073	P04	M-018765- chromoson	148304	C1orf74	4124	9.1416	0.2684
50073	P05	M-012833- toll-like rec	148022	TICAM1	2411	3.567	5.843
50073	P06	M-021522- synaptotag	148281	SYT6	2804	9.0585	0.3515
50073	P07	M-016206- chromoson	148046	C19orf23	3775	7.6291	1.7809
50073	P08	M-015736- zinc finger	148268	ZNF570	2984	8.7131	0.6969
50073	P09	M-007141- zinc and rir	148066	ZNRF4	3156	7.1926	2.2174
50073	P10	M-016710- zinc finger	148266	ZNF569	3727	5.1248	4.2852
50073	P11	M-023643- zinc finger	148103	ZNF599	4136	4.7389	4.6711
50073	P12	M-016019- zinc finger	148254	ZNF555	2831	3.8856	5.5244
50073	P13	M-016707- transmem	148109	TMEM162	4086	7.9785	1.4315
50073	P14	M-016709- hypothetic	148231	FLJ25328	3770	4.6419	4.7681
50073	P15	M-015654- cartilage in	148113	CILP2	4606	9.1403	0.2697
50073	P16	M-023898- ATPase, Cla	148229	ATP8B3	4478	3.5507	5.8593
50073	P17	M-015733- chromoson	148137	C19orf55	2813	8.1052	1.3048
50073	P18	M-016708- chromoson	148223	C19orf25	3256	4.7297	4.6803
50073	P19	M-031073- hypothetic	148145	LOC14814	3616	10.73	1.32
50073	P20	M-015352- zinc finger	148213	ZNF681	2455	11.65	2.24
50073	P21	M-015741- zinc finger	148156	ZNF558	4585	9.4656	0.0556
50073	P23	M-024001- zinc finger	148203	ZNF738	4904	16.945	7.535
				MAD	4288	9.40845	3.0562
				MAD3			9.1686
				MADc			4.523176
50073	C22				1983	9.3797	
50073	D22				1621	5.4904	
50073	E22				2782	5.9669	
50073	F22				2064	2.6647	
				mn	2112.5	5.875425	

		sd	486.1156	2.753501
50073	G22		4267	38.481
50073	H22		5158	44.416
50073	I22		3509	35.281
50073	J22		4165	39.64
		mn	4274.75	39.4545
		sd	677.891	3.786674
		3psSD		11.36002
		3ngSD		8.260504
		SumSD		19.62053
		DiffMn		33.57908
		SmovrDiff		0.584308
		1minus		0.415692

50073	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	1054	1.9924
50073	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	1227	1.304
50073	I03	D-001206-	siControl non-targeting			4363	7.4948
50073	J03	D-001206-	siControl non-targeting			4979	9.8012
50073	K03	D-001600-	siGLO RISC-free siRNA			7689	11.419
50073	L03	D-001600-	siGLO RISC-free siRNA			7205	12.491

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.336169	2430	8.2305	1.0795	-0.25646	2827	7.959	3.781	-0.85555
5.040164	2182	33.914	24.604	5.82925	1852	28.132	16.392	3.71274
-0.46738	3211	12.146	2.836	0.671316	3303	13.896	2.156	0.488918
-0.54421	3206	6.9245	2.3855	-0.56592	2234	6.4011	5.3389	-1.20834
-0.34875	1827	9.4143	0.1043	0.024039	1865	7.9357	3.8043	-0.86083
-0.94853	3413	11.075	1.765	0.417542	2597	15.364	3.624	0.821355
-0.77756	3097	5.5538	3.7562	-0.89071	2378	4.2473	7.4927	-1.69608
-0.67135	2985	7.5712	1.7388	-0.41268	2490	12.048	0.308	0.070428
0.828522	3068	12.777	3.467	0.820831	2344	12.969	1.229	0.278993
0.233586	2743	10.427	1.117	0.263998	2084	8.7332	3.0068	-0.68023
0.30986	3485	14.634	5.324	1.260848	2461	17.432	5.692	1.289665
0.509719	2446	17.048	7.738	1.832846	1802	19.478	7.738	1.752993
-1.19979	3264	6.9547	2.3553	-0.55876	2893	10.508	1.232	-0.27831
0.60169	3082	13.692	4.382	1.037641	2149	13.96	2.22	0.503411
-0.51284	2143	5.8796	3.4304	-0.81351	2221	9.05	2.69	-0.60849
1.331487	2476	17.569	8.259	1.956297	1916	15.136	3.396	0.769723
0.692113	1641	16.027	6.717	1.59092	1696	11.439	0.301	-0.06748
0.935084	2515	13.439	4.129	0.977693	3709	18.118	6.378	1.445013
-0.60821	4125	13.842	4.532	1.073184	4161	5.5516	6.1884	-1.40072
-1.14166	2624	4.7256	4.5844	-1.08695	4021	5.2475	6.4925	-1.46958
-0.13691	6170	9.6596	0.3496	0.082163	5498	16.479	4.739	1.073853
-1.02403	4383	9.6053	0.2953	0.069296	3788	13.015	1.275	0.28941
-1.0772	4475	4.514	4.796	-1.13709	4260	9.3897	2.3503	-0.53156
0.597711	4186	15.432	6.122	1.449935	4409	17.646	5.906	1.338126
-0.74093	2433	6.4529	2.8571	-0.67767	3057	6.9349	4.8051	-1.08746
-1.0462	3018	4.3738	4.9362	-1.17031	2596	6.8182	4.9218	-1.11389
0.118821	3124	5.8259	3.4841	-0.82623	3395	10.545	1.195	-0.26994
-0.27873	2161	6.4785	2.8315	-0.6716	2926	13.602	1.862	0.42234
0.2568	2403	7.6571	1.6529	-0.39233	2703	15.427	3.687	0.835621
0.355182	3173	10.715	1.405	0.33224	3209	14.117	2.377	0.538964
0.034036	2429	6.0107	3.2993	-0.78245	2490	13.133	1.393	0.316132
1.523166	2868	10.495	1.185	0.280111	3166	14.593	2.853	0.646757
-0.3277	1533	9.85	0.54	0.127278	2112	11.79	0.05	0.012002
1.003841	2707	10.417	1.107	0.261629	2818	12.065	0.325	0.074277
1.803279	1927	7.836	1.474	-0.34994	2394	10.401	1.339	-0.30254
0.986818	2719	9.4888	0.1788	0.041691	2343	7.4691	4.2709	-0.96649
1.772991	2966	15.88	6.57	1.556088	3741	12.163	0.423	0.09647
1.471212	3049	11.709	2.399	0.567769	3316	11.882	0.142	0.032836
3.717421	4015	17.21	7.9	1.871232	4732	18.111	6.371	1.443428
1.744471	3698	8.1395	1.1705	-0.27803	4545	9.659	2.081	-0.47057
1.088958	4841	8.49	0.82	-0.19497	5684	22.854	11.114	2.517507
0.465724	2359	4.8749	4.4351	-1.05157	2379	11.517	0.223	-0.04982
-0.98133	3617	1.6588	7.6512	-1.81363	4293	6.6853	5.0547	-1.14399
1.404887	4526	6.9377	2.3723	-0.56279	4680	18.504	6.764	1.532425
-0.71278	2409	5.2719	4.0381	-0.9575	2309	10.351	1.389	-0.31387
-0.07752	2450	4.0816	5.2284	-1.23955	2375	8.8421	2.8979	-0.65557

0.100073	2695	6.4564	2.8536	-0.67684	4228	19.371	7.631	1.728762
-0.54671	1908	7.5472	1.7628	-0.41837	3040	9.5724	2.1676	-0.49019
-0.23215	1917	6.4684	2.8416	-0.67399	3287	9.3398	2.4002	-0.54286
0.961614	2695	8.7941	0.5159	-0.12292	3273	16.59	4.85	1.098989
2.544794	2858	15.92	6.61	1.565566	3006	25.848	14.108	3.195515
1.919127	3188	8.5006	0.8094	-0.19246	4347	16.586	4.846	1.098083
1.131406	2677	19.014	9.704	2.298691	2820	19.929	8.189	1.855125
2.807662	2615	22.103	12.793	3.03063	3244	27.004	15.264	3.457298
-0.79565	2824	2.6912	6.6188	-1.569	4250	8.5176	3.2224	-0.72905
1.215197	2403	10.32	1.01	0.238645	3849	12.783	1.043	0.236873
0.884898	3718	10.57	1.26	0.297882	4516	10.452	1.288	-0.291
0.347223	3025	6.1818	3.1282	-0.7419	4693	8.3316	3.4084	-0.77117
1.335024	3754	6.4198	2.8902	-0.68551	4515	8.2614	3.4786	-0.78707
2.832424	3791	15.642	6.332	1.499694	5162	15.246	3.506	0.794633
0.005649	3583	8.3171	0.9929	-0.23594	3888	10.159	1.581	-0.35735
0.180084	4305	13.101	3.791	0.897603	4265	12.286	0.546	0.124324
-0.58204	4160	5.6731	3.6369	-0.86244	4840	9.0909	2.6491	-0.59922
-1.35563	3399	10.121	0.811	0.191491	3762	3.6151	8.1249	-1.83925
-1.30792	2878	8.3739	0.9361	-0.22248	3794	5.8513	5.8887	-1.33285
-0.19218	3396	10.718	1.408	0.332951	3964	12.008	0.268	0.061369
-0.96599	3010	9.6678	0.3578	0.084106	4327	10.238	1.502	-0.33946
-0.02055	3308	14.299	4.989	1.18147	3812	19.019	7.279	1.64905
-0.34621	2811	8.0754	1.2346	-0.29321	2776	11.635	0.105	-0.0231
-0.87866	3089	6.1832	3.1268	-0.74157	2922	8.5558	3.1842	-0.7204
0.556368	3132	8.3972	0.9128	-0.21696	3172	11.759	0.019	0.004982
0.18141	3185	16.295	6.985	1.654423	3686	18.014	6.274	1.421462
-0.18322	3889	10.954	1.644	0.388871	3513	8.0273	3.7127	-0.84008
-0.41472	2473	10.109	0.799	0.188648	2899	12.177	0.437	0.09964
-1.13503	2472	8.5761	0.7339	-0.17457	3177	2.9588	8.7812	-1.98787
0.658951	3981	13.941	4.631	1.096642	3643	18.364	6.624	1.500721
-0.48646	4439	10.002	0.692	0.163294	6544	13.432	1.692	0.383842
0.798897	4581	24.056	14.746	3.493394	5405	21.776	10.036	2.273388
2.378981	5985	28.822	19.512	4.622699	4358	11.886	0.146	0.033742
0.809951	2809	11.962	2.652	0.627717	3860	16.114	4.374	0.991196
3.000668	6570	24.764	15.454	3.661155	5851	18.869	7.129	1.615082
1.516534	5440	16.232	6.922	1.639495	6237	20.891	9.151	2.072975
0.247956	5308	14.732	5.422	1.284069	4153	15.916	4.176	0.946358
2.264018	4915	14.791	5.481	1.298049	4649	18.907	7.167	1.623687
-0.42303	4990	5.2305	4.0795	-0.96731	4993	11.416	0.324	-0.07269
0.668015	2653	9.8756	0.5656	0.133344	3580	14.302	2.562	0.580859
0.352308	2264	14.576	5.266	1.247105	2890	15.052	3.312	0.7507
0.885782	3369	12.467	3.157	0.747377	3493	19.697	7.957	1.802587
-0.1555	3168	11.995	2.685	0.635536	2715	10.866	0.874	-0.19724
0.222532	3051	8.3251	0.9849	-0.23405	2982	13.146	1.406	0.319076
0.851957	2764	7.8509	1.4591	-0.34641	2890	11.557	0.183	-0.04076
-0.2616	2816	6.6051	2.7049	-0.6416	4084	18.707	6.967	1.578396
0.730361	2109	17.876	8.566	2.029041	3198	25.078	13.338	3.021145

0.578476	3952	9.1346	0.1754	-0.04224	4148	22.372	10.632	2.408356
-0.93013	2392	3.0518	6.2582	-1.48356	2852	13.359	1.619	0.367311
2.918204	3579	12.601	3.291	0.779128	3852	24.688	12.948	2.932827
-0.24152	3166	3.1586	6.1514	-1.45825	4128	11.652	0.088	-0.01925
3.102367	3396	7.9505	1.3595	-0.32281	3819	34.119	22.379	5.06853
-1.08414	2868	3.2427	6.0673	-1.43832	4873	11.164	0.576	-0.12976
0.253262	5415	3.3426	5.9674	-1.41465	6979	15.575	3.835	0.869137
-0.81008	3156	15.304	5.994	1.419605	5509	6.8615	4.8785	-1.10408
-0.49015	3889	14.425	5.115	1.211326	5608	13.32	1.58	0.358479
-0.9128	3076	15.54	6.23	1.475525	5268	9.6621	2.0779	-0.46987
-1.79813	2870	7.9443	1.3657	-0.32428	3758	2.6344	9.1056	-2.06134
-1.51607	2928	14.344	5.034	1.192133	3449	6.0597	5.6803	-1.28566
-0.08873	3528	16.695	7.385	1.749203	2939	10.888	0.852	-0.19226
-1.31502	1897	9.5414	0.2314	0.054155	3354	8.6762	3.0638	-0.69314
-0.68115	3335	22.039	12.729	3.015465	3229	16.414	4.674	1.059133
0.363141	2753	23.538	14.228	3.370654	3933	12.942	1.202	0.272879
0.044648	2671	30.176	20.866	4.94353	3175	16.189	4.449	1.00818
-1.24418	2544	12.107	2.797	0.662075	2532	10.032	1.708	-0.38611
-0.8325	3801	18.206	8.896	2.107235	3310	11.269	0.471	-0.10598
-1.11788	2743	6.7444	2.5656	-0.6086	3537	7.5205	4.2195	-0.95485
-0.34466	2527	16.898	7.588	1.797304	2918	11.857	0.117	0.027175
-1.14814	2788	14.347	5.037	1.192843	3147	9.7871	1.9529	-0.44157
0.786295	3529	14.423	5.113	1.210852	3987	12.566	0.826	0.187732
0.021766	4707	15.764	6.454	1.528602	4497	14.632	2.892	0.655589
-0.46356	5027	14.223	4.913	1.163462	5847	11.493	0.247	-0.05526
0.643475	5737	21.335	12.025	2.848652	4991	19.195	7.455	1.688906
-0.93157	2070	7.0531	2.2569	-0.53545	2128	7.8477	3.8923	-0.88075
-0.63238	4472	7.0886	2.2214	-0.52704	5267	4.3099	7.4301	-1.68191
0.15068	4961	12.155	2.845	0.673448	5092	5.597	6.143	-1.39044
-0.45186	3938	4.1646	5.1454	-1.21988	4767	7.5729	4.1671	-0.94298
-0.98892	4063	6.0546	3.2554	-0.77204	5189	5.4153	6.3247	-1.43158
-0.53444	4570	8.7309	0.5791	-0.13789	3695	8.6604	3.0796	-0.69671
-0.08389	3672	15.033	5.723	1.355391	4806	12.027	0.287	0.065672
1.068176	2741	13.791	4.481	1.061099	3217	10.009	1.731	-0.39132
-0.78877	3155	5.4834	3.8266	-0.90739	3374	9.4843	2.2557	-0.51014
-0.00174	2766	6.6522	2.6578	-0.63044	3092	7.3739	4.3661	-0.98805
0.268296	2681	5.4084	3.9016	-0.92516	2531	16.199	4.459	1.010445
-0.64502	1777	4.2206	5.0894	-1.20661	2084	3.3589	8.3811	-1.89727
0.749595	3761	15.209	5.899	1.397095	3742	15.794	4.054	0.918731
-0.35954	3131	6.1642	3.1458	-0.74607	4517	10.516	1.224	-0.2765
-0.58024	3683	10.698	1.388	0.328212	4457	9.1317	2.6083	-0.58998
-1.2725	2700	8.8889	0.4211	-0.10046	3254	11.033	0.707	-0.15942
-0.89164	3249	3.7858	5.5242	-1.30964	3097	8.04	3.7	-0.83721
-1.0206	3351	4.8045	4.5055	-1.06825	4110	9.0998	2.6402	-0.59721
-0.9646	4193	3.8397	5.4703	-1.29686	5043	5.4928	6.2472	-1.41403
-0.1561	4009	6.8346	2.4754	-0.58722	6766	14.366	2.626	0.595352
-0.82808	4100	2.9512	6.3588	-1.50739	5871	9.317	2.423	-0.54802

-1.5898	5029	10.002	0.692	0.163294	5313	6.6817	5.0583	-1.1448
-0.67516	3882	5.0489	4.2611	-1.01034	4669	9.1026	2.6374	-0.59657
1.176286	4227	25.952	16.642	3.942652	4187	18.82	7.08	1.603985
-1.24694	4224	9.4697	0.1597	0.037166	4759	11.809	0.069	0.016305
-0.31371	3102	14.894	5.584	1.322455	2771	13.533	1.793	0.406714
-1.10468	3615	5.9474	3.3626	-0.79744	4883	12.554	0.814	0.185014
-0.71144	3126	8.9891	0.3209	-0.07671	3506	18.739	6.999	1.585642
0.935968	4015	19.776	10.466	2.479247	3772	18.399	6.659	1.508647
-1.07607	3244	10.018	0.708	0.167086	2811	10.779	0.961	-0.21694
-1.39498	2591	6.5612	2.7488	-0.652	2668	10.457	1.283	-0.28986
-1.43104	2860	6.049	3.261	-0.77337	2605	8.9443	2.7957	-0.63242
-0.35419	2802	8.6724	0.6376	-0.15175	2340	8.0769	3.6631	-0.82885
-1.1718	3242	3.2387	6.0713	-1.43927	2351	9.9107	1.8293	-0.41358
-0.4858	3454	7.8749	1.4351	-0.34072	3478	9.747	1.993	-0.45065
1.368408	5142	17.289	7.979	1.889951	4002	16.017	4.277	0.96923
0.285983	4237	12.485	3.175	0.751642	4628	13.872	2.132	0.483483
1.381452	3560	19.579	10.269	2.432567	2155	19.35	7.61	1.724007
-0.73058	5793	9.3043	0.0057	-0.00203	4568	12.172	0.432	0.098508
-0.76138	5036	11.577	2.267	0.536491	4613	12.703	0.963	0.218756
0.564327	5312	13.197	3.887	0.920351	3794	11.993	0.253	0.057973
-0.5487	3249	2.8009	6.5091	-1.54301	4597	5.6341	6.1059	-1.38204
-0.29531	3187	7.7189	1.5911	-0.37769	3053	8.7127	3.0273	-0.68487
0.32622	2924	9.9863	0.6763	0.159574	3424	11.332	0.408	-0.09171
1.39737	4377	14.188	4.878	1.155168	3890	12.596	0.856	0.194525
0.024131	3473	11.517	2.207	0.522274	3243	8.3256	3.4144	-0.77253
-0.77988	3164	6.4159	2.8941	-0.68643	3227	7.995	3.745	-0.8474
0.435877	4514	6.5352	2.7748	-0.65817	3800	6.5526	5.1874	-1.17404
-0.40088	4064	16.043	6.733	1.594711	3048	10.302	1.438	-0.32496
0.878487	4303	13.711	4.401	1.042143	2815	13.748	2.008	0.455402
1.286165	4669	17.841	8.531	2.020748	3319	12.504	0.764	0.173691
-0.2084	2982	12.173	2.863	0.677713	2713	8.8463	2.8937	-0.65462
0.914302	3740	7.6471	1.6629	-0.3947	3020	8.245	3.495	-0.79078
-1.0674	3159	6.9959	2.3141	-0.549	2455	6.1507	5.5893	-1.26505
0.034235	4510	11.796	2.486	0.588383	4264	12.219	0.479	0.109152
0.292173	3768	13.27	3.96	0.937648	3724	11.01	0.73	-0.16463
-0.14124	4678	12.27	2.96	0.700698	4301	12.09	0.35	0.079939
1.195078	5137	25.715	16.405	3.886495	3855	16.939	5.199	1.178022
0.084973	5118	8.0305	1.2795	-0.30385	4288	11.124	0.616	-0.13882
-0.07967	5625	13.831	4.521	1.070577	4701	9.6575	2.0825	-0.47091
-0.19257	5724	10.203	0.893	0.210921	5122	10.445	1.295	-0.29258
0.625788	5094	8.0094	1.3006	-0.30885	5525	9.991	1.749	-0.39539
-0.26337	4210	9.5724	0.2624	0.0615	5216	9.3942	2.3458	-0.53054
0.57516	4455	13.872	4.562	1.080292	5374	15.091	3.351	0.759532
-0.08661	4598	10.265	0.955	0.225612	4091	7.9198	3.8202	-0.86443
1.285502	4059	18.872	9.562	2.265044	5163	28.782	17.042	3.859936
0.016305	4052	9.0326	0.2774	-0.06641	6248	11.796	0.056	0.013361
0.001736	2565	9.7466	0.4366	0.102777	4264	10.999	0.741	-0.16712

0.429687	3065	19.837	10.527	2.493701	4222	15.846	4.106	0.930506
0.096448	3039	4.87	4.44	-1.05273	4417	8.3541	3.3859	-0.76608
0.61186	3058	14.814	5.504	1.303499	3758	20.144	8.404	1.903813
0.143826	2619	7.9038	1.4062	-0.33387	3537	19.112	7.372	1.67011
-0.83657	3330	11.051	1.741	0.411855	3841	15.152	3.412	0.773346
-0.20485	3564	9.3154	0.0054	0.000604	4674	16.003	4.263	0.96606
0.121784	4134	12.724	3.414	0.808273	4941	15.301	3.561	0.807088
-0.65194	2960	6.0135	3.2965	-0.78178	3548	14.91	3.17	0.718544
1.844622	5039	15.023	5.713	1.353022	6033	25.675	13.935	3.156339
-0.11546	3109	10.839	1.529	0.361622	4248	17.137	5.397	1.22286
-0.17579	4094	7.1324	2.1776	-0.51666	4890	11.431	0.309	-0.0693
-0.56411	4365	8.1558	1.1542	-0.27416	5381	15.796	4.056	0.919183
-0.23367	4119	6.6278	2.6822	-0.63622	5057	6.4465	5.2935	-1.19806
-1.09552	5091	9.6248	0.3148	0.073917	5759	6.9109	4.8291	-1.0929
-0.71886	4309	8.401	0.909	-0.21606	4396	12.534	0.794	0.180485
0.088887	4902	9.6083	0.2983	0.070007	3814	13.424	1.684	0.382031
-0.69906	4849	7.218	2.092	-0.49638	4503	10.437	1.303	-0.29439
-1.50073	4955	4.2583	5.0517	-1.19768	5137	8.7794	2.9606	-0.66977
-0.9638	3356	9.3564	0.0464	0.010319	4753	9.1732	2.5668	-0.58059
0.021346	4729	12.645	3.335	0.789554	4851	11.812	0.072	0.016984
-0.78859	4153	10.956	1.646	0.389345	4606	12.006	0.266	0.060917
-0.01978	4231	11.085	1.775	0.419912	4894	9.9714	1.7686	-0.39983
-0.45942	2817	6.8868	2.4232	-0.57485	3463	7.4791	4.2609	-0.96423
-0.78342	2606	11.589	2.279	0.539334	3363	10.021	1.719	-0.3886
-0.69357	2910	6.4605	2.8495	-0.67587	3334	11.428	0.312	-0.06997
-1.34088	4018	7.3171	1.9929	-0.47289	4191	6.2754	5.4646	-1.23681
0.27935	4948	12.631	3.321	0.786237	5578	15.669	3.929	0.890424
-1.01505	4152	7.0087	2.3013	-0.54597	5526	9.7358	2.0042	-0.45318
-0.96626	3401	5.4984	3.8116	-0.90384	4588	10.31	1.43	-0.32315
1.030592	5394	16.518	7.208	1.707263	5759	16.565	4.825	1.093328
-0.26863	4262	10.371	1.061	0.250729	5268	7.6879	4.0521	-0.91694
-0.56718	4779	8.5164	0.7936	-0.18872	4425	11.864	0.124	0.02876
-1.14673	3973	5.8142	3.4958	-0.82901	3670	2.4251	9.3149	-2.10873
-0.3298	5635	9.0683	0.2417	-0.05795	4595	12.492	0.752	0.170974
-0.67339	4653	5.9961	3.3139	-0.7859	4146	10.902	0.838	-0.18909
0.568085	5774	12.383	3.073	0.727473	5362	15.927	4.187	0.948849
-0.78775	3942	8.2953	1.0147	-0.24111	2980	11.007	0.733	-0.16531
-0.29569	5152	3.222	6.088	-1.44323	4514	10.722	1.018	-0.22985
-0.73954	5059	7.5904	1.7196	-0.40814	4174	12.698	0.958	0.217624
0.212141	4831	9.1906	0.1194	-0.02897	3917	14.067	2.327	0.527642
0.061207	5152	9.1615	0.1485	-0.03586	4546	13.792	2.052	0.465366
-0.39542	2714	8.9536	0.3564	-0.08512	3082	10.772	0.968	-0.21853
1.846612	2829	19.689	10.379	2.458632	2687	18.72	6.98	1.58134
0.27515	2786	7.3941	1.9159	-0.45465	2853	11.742	0.002	0.001132
-0.98737	3406	4.1691	5.1409	-1.21881	2935	8.075	3.665	-0.82928
-1.40851	3677	7.5061	1.8039	-0.42811	3360	6.4881	5.2519	-1.18864
1.659133	5185	8.4089	0.9011	-0.21419	5450	8.3486	3.3914	-0.76732

1.230452	2997	14.448	5.138	1.216775	3643	10.321	1.419	-0.32066
0.214352	5226	5.5874	3.7226	-0.88275	4665	11.447	0.293	-0.06567
2.362179	4951	13.209	3.899	0.923194	5311	13.99	2.25	0.510205
1.639456	5254	15.874	6.564	1.554667	6252	12.028	0.288	0.065899
-0.28795	4577	8.4335	0.8765	-0.20836	5704	12.482	0.742	0.168709
0.466166	3886	5.9701	3.3399	-0.79207	5213	6.292	5.448	-1.23305
-0.73365	3503	7.622	1.688	-0.40065	4802	7.7051	4.0349	-0.91305
-0.65877	2682	4.959	4.351	-1.03165	5611	4.705	7.035	-1.59244
0.647233	3716	11.598	2.288	0.541467	3589	9.8913	1.8487	-0.41797
1.447998	4560	10.57	1.26	0.297882	5609	11.268	0.472	-0.10621
0.955203	5109	8.9646	0.3454	-0.08252	5242	9.9962	1.7438	-0.39421
1.435175	3591	12.141	2.831	0.670131	3742	11.732	0.008	-0.00113
-0.2744	4865	9.1059	0.2041	-0.04904	5410	10.148	1.592	-0.35984
1.503269	4061	13.593	4.283	1.014183	4886	13.795	2.055	0.466046
0.310081	4768	7.4245	1.8855	-0.44745	5249	7.5443	4.1957	-0.94946
1.530683	2273	8.491	0.819	-0.19474	3059	11.769	0.029	0.007247
-0.38784	3302	6.9958	2.3142	-0.54903	2163	6.4263	5.3137	-1.20264
0.574939	2579	6.3591	2.9509	-0.69989	2808	11.004	0.736	-0.16599
2.030332	3807	10.848	1.538	0.363754	3304	8.5351	3.2049	-0.72509
1.185351	4062	12.777	3.467	0.820831	4097	12.033	0.293	0.067031
-0.18634	4233	8.7645	0.5455	-0.12993	3302	9.8728	1.8672	-0.42216
2.955346	6585	24.784	15.474	3.665894	5165	22.439	10.699	2.423528
1.413288	5606	11.452	2.142	0.506872	4752	15.025	3.285	0.744586
0.31605	3926	4.8905	4.4195	-1.04788	4416	7.7219	4.0181	-0.90924
0.19357	4084	6.7581	2.5519	-0.60535	4026	11.078	0.662	-0.14923
0.399399	3506	6.8169	2.4931	-0.59142	3301	9.3002	2.4398	-0.55183
-1.7194	2463	2.8015	6.5085	-1.54287	2099	5.2406	6.4994	-1.47115
0.075356	4511	11.439	2.129	0.503792	6315	20.317	8.577	1.942989
0.651213	4396	10.1	0.79	0.186515	6288	13.979	2.239	0.507714
1.249465	4612	7.4371	1.8729	-0.44446	5397	17.009	5.269	1.193874
0.027226	5172	7.4633	1.8467	-0.43825	6442	8.3204	3.4196	-0.77371
-0.78804	2810	3.1317	6.1783	-1.46463	3859	2.8505	8.8895	-2.0124
-0.89942	3374	7.2614	2.0486	-0.48609	5727	13.253	1.513	0.343307
0.004123	5190	9.3449	0.0349	0.007594	5954	13.168	1.428	0.324058
-0.33982	3300	6.0303	3.2797	-0.7778	5681	11.142	0.598	-0.13474
4.453408	3092	19.373	10.063	2.383756	5497	28.597	16.857	3.818042
0.34457	3322	8.4287	0.8813	-0.2095	4400	13.705	1.965	0.445665
0.264316	4725	12.571	3.261	0.77202	4769	12.12	0.38	0.086733
0.671552	4249	7.9313	1.3787	-0.32736	5642	9.252	2.488	-0.56274
0.502645	5125	4.3317	4.9783	-1.18029	6495	9.746	1.994	-0.45087
2.171826	3833	16.775	7.465	1.768159	3850	20.416	8.676	1.965408
1.472759	5182	15.477	6.167	1.460597	5664	18.291	6.551	1.48419
2.305139	4919	15.349	6.039	1.430268	3795	18.656	6.916	1.566847
0.945696	5957	8.7124	0.5976	-0.14228	5242	8.47	3.27	-0.73983
0.033859	5313	7.8675	1.4425	-0.34248	4307	12.422	0.682	0.155122
-0.54733	3853	7.1113	2.1987	-0.52166	3157	8.5207	3.2193	-0.72835
-0.02086	3915	6.1047	3.2053	-0.76017	4833	11.649	0.091	-0.01993

1.796205	4273	18.441	9.131	2.162918	4130	17.409	5.669	1.284456
0.795138	4206	17.808	8.498	2.012928	4590	15.882	4.142	0.938659
-0.08252	3593	7.292	2.018	-0.47884	4825	11.233	0.507	-0.11413
0.361814	4789	7.2458	2.0642	-0.48979	4744	15.831	4.091	0.927109
0.374637	4032	7.8373	1.4727	-0.34963	3964	7.3915	4.3485	-0.98406
0.676195	3119	8.8169	0.4931	-0.11752	4710	17.707	5.967	1.35194
-0.91015	2787	5.0592	4.2508	-1.0079	3156	8.7136	3.0264	-0.68467
1.568268	3816	11.137	1.827	0.432233	4322	11.199	0.541	-0.12183
0.892857	3069	12.773	3.463	0.819884	3696	21.834	10.094	2.286523
-0.29558	2536	10.213	0.903	0.213291	2612	12.289	0.549	0.125004
2.343387	4832	20.137	10.827	2.564786	4759	30.952	19.212	4.351345
2.12783	4100	13.707	4.397	1.041195	4677	14.881	3.141	0.711977
1.781613	4250	13.929	4.619	1.093798	4492	14.337	2.597	0.588785
1.118805	4476	11.148	1.838	0.434839	5131	12.882	1.142	0.259292
1.216745	4446	12.146	2.836	0.671316	4652	12.855	1.115	0.253177
-0.23451	5361	6.2302	3.0798	-0.73043	6086	6.3753	5.3647	-1.21419
-0.91906	3771	4.0573	5.2527	-1.2453	3759	7.0764	4.6636	-1.05542
1.208786	4403	15.853	6.543	1.549691	4987	16.603	4.863	1.101933
0.541334	3763	7.3877	1.9223	-0.45616	3465	6.6378	5.1022	-1.15474
0.018074	3694	3.059	6.251	-1.48185	2823	6.8367	4.9033	-1.1097
-0.059	4312	8.6039	0.7061	-0.16799	4745	6.8493	4.8907	-1.10685
-1.29145	2918	8.3276	0.9824	-0.23346	2813	12.798	1.058	0.240269
-0.07737	4641	8.3818	0.9282	-0.22061	4253	6.1839	5.5561	-1.25753
-0.39339	5094	11.602	2.292	0.542415	4972	10.177	1.563	-0.35327
-0.15373	2900	9.3103	0.0003	-0.0006	2907	16.546	4.806	1.089025
-0.48989	4716	13.147	3.837	0.908503	3291	12.914	1.174	0.266538
-0.94704	5141	15.367	6.057	1.434533	3821	14.342	2.602	0.589917
-1.03236	3107	7.8854	1.4246	-0.33823	3247	6.9911	4.7489	-1.07474
-1.22101	3215	7.465	1.845	-0.43785	2632	13.45	1.71	0.387919
-0.31614	3827	12.569	3.259	0.771546	2225	18.202	6.462	1.464036
-1.05381	4709	13.379	4.069	0.963476	2895	16.304	4.564	1.034223
-0.05928	4124	8.5839	0.7261	-0.17272	2349	11.707	0.033	-0.00679
-1.29505	3471	3.1691	6.1409	-1.45576	1966	9.9186	1.8214	-0.41179
-0.28813	3761	7.0726	2.2374	-0.53083	1944	16.872	5.132	1.16285
-1.03439	5135	7.2833	2.0267	-0.4809	3499	13.432	1.692	0.383842
0.292173	4234	11.266	1.956	0.4628	2395	17.035	5.295	1.199762
0.49557	4126	7.9254	1.3846	-0.32876	2196	23.953	12.213	2.766382
0.012635	3480	5.0862	4.2238	-1.00151	2766	10.774	0.966	-0.21808
1.666208	4679	9.6388	0.3288	0.077234	2995	13.289	1.549	0.351459
	3680	9.31285	2.85155		3859.5	11.737	2.9837	
			8.55465				8.9511	
			4.220294				4.415876	
2321	5.4287		2925	8.1026				
2893	13.93		3663	8.9817				
1423	4.6381		2755	10.744				
2222	11.521		2929	8.6036				
2214.75	8.87945		3068	9.107975				

605.0435	4.560065	404.872	1.148578		
		4507	44.753	3010	25.415
5074	44.974	4044	49.085		
5278	35.108	4458	36.294		
4956	44.431	4596	43.168		
5102.667	41.50433	4401.25	43.325		
162.9028	5.546037	244.9209	5.312764		
	16.63811		15.93829		
	13.68019		3.445735		
	30.3183		19.38403		
	32.62488		34.21703		
	0.9293		0.566502		
	0.0707		0.433498		

345	4.3478	951	2.2082
771	13.489	686	6.8513
2288	9.0035	4386	7.1135
3306	10.284	5626	15.286
6791	19.541	6410	16.771
6815	15.554	6511	19.121

y

y

y

y
y

y

y

y

y

y

y

y

y

					cell ct	% inf	AD
50074	A02	M-007146- ring finger	153830	RNF145	4303	14.478	0.122
50074	A04	M-007145- SH3 domai	153769	SH3RF2	2615	16.023	1.423
50074	A05	M-016528- chromosom	150135	C21orf129	3111	13.533	1.067
50074	A06	M-019471- PRELI doma	153768	PRELID2	4289	12.45	2.15
50074	A07	M-021431- chromosom	150142	C21orf121	4279	26.198	11.598
50074	A08	M-015305- family with	153745	FAM71B	2484	11.192	3.408
50074	A09	M-016529- chromosom	150147	C21orf128	3293	14.121	0.479
50074	A10	M-031957- protein pho	153743	PPP1R2P3	4598	13.636	0.964
50074	A11	M-016836- Na+/H+ exc	150159	NHEDC1	4201	15.211	0.611
50074	A12	M-015448- coiled-coil (	153733	CCDC112	3343	9.0039	5.5961
50074	A13	M-017648- T-complex	150160	CESK1	4295	22.98	8.38
50074	A14	M-019313- hypothetica	153684	LOC153684	3569	17.12	2.52
50074	A15	M-018044- XK, Kell blo	150165	XKR3	2745	8.8889	5.7111
50074	A16	M-017051- hypothetica	153657	FLJ25439	4114	8.9451	5.6549
50074	A17	M-008134- apoptosis-i	150209	AIFM3	3626	15.361	0.761
50074	A18	M-015447- family with	153643	FAM81B	2644	10.401	4.199
50074	A19	M-024547- LOC150223	150223	LOC150223	3203	11.083	3.517
50074	A20	M-024328- arylsulfatas	153642	ARSK	3486	17.785	3.185
50074	A21	M-017628- similar to h	150236	LOC150236	3988	15.12	0.52
50074	A23	M-016350- FLJ31568 p	150244	FLJ31568	2963	6.4124	8.1876
50074	B02	M-018038- outer dens	161753	ODF3L1	3965	10.618	3.982
50074	B04	M-016638- sprouty-rel	161742	SPRED1	4494	15.576	0.976
50074	B05	M-028608- hypothetica	153910	LOC153910	4378	14.344	0.256
50074	B06	M-008841- OTU domai	161725	OTUD7A	4114	9.3583	5.2417
50074	B07	M-018855- chromosom	154007	C6orf151	3805	12.431	2.169
50074	B08	M-015300- dyslexia su	161582	DYX1C1	4039	14.731	0.131
50074	B09	M-018546- CNKSR fam	154043	CNKSR3	6019	16.448	1.848
50074	B10	M-016748- TBC1 doma	161514	TBC1D21	4181	7.558	7.042
50074	B11	M-017094- retinoic aci	154064	RAET1L	5383	24.317	9.717
50074	B12	M-018516- chromosom	161502	C15orf26	4327	10.608	3.992
50074	B13	M-015449- sterile alph	154075	SAMD3	5213	10.551	4.049
50074	B14	M-019224- echinoderr	161436	EML5	4858	13.956	0.644
50074	B15	M-016494- hypothetica	154089	RP4-662A9	4826	9.1794	5.4206
50074	B16	M-017798- chromosom	161424	C14orf21	5778	9.6227	4.9773
50074	B17	M-007512- solute carri	154091	SLC2A12	4687	9.8784	4.7216
50074	B18	M-030311- chromosom	161394	C14orf174	6608	9.201	5.399
50074	B19	M-028605- hypothetica	154092	LOC154092	6547	8.7521	5.8479
50074	B20	M-021977- chromosom	161380	C14orf42	6084	13.494	1.106
50074	B21	M-010303- membrane	154141	MBOAT1	6091	14.349	0.251
50074	B23	M-015693- hepatoma (	154150	HDGFL1	6082	16.458	1.858
50074	C02	M-015446- butyrophili	153579	BTNL9	6231	12.887	1.713
50074	C04	M-032005- iroquois ho	153572	IRX2	5193	16.773	2.173
50074	C05	M-018678- chromosom	150248	C22orf15	4984	15.55	0.95
50074	C06	M-017934- chromosom	153571	C5orf38	5725	11.389	3.211
50074	C07	M-017718- HscB iron-s	150274	HSCB	5121	10.291	4.309
50074	C08	M-017054- MARVEL do	153562	MARVELD2	3838	7.999	6.601

50074	C09	M-018556- coiled-coil	150275	CCDC117	4801	6.9152	7.6848
50074	C10	M-024458- glucuronid	153561	GUSBP1	4264	9.0994	5.5006
50074	C11	M-016850- HORMA do	150280	HORMAD2	4737	5.1932	9.4068
50074	C12	M-017090- zinc finger,	153527	ZMAT2	2237	11.757	2.843
50074	C13	M-016517- chromoso	150291	C22orf27	3497	3.7461	10.8539
50074	C14	M-030346- chromoso	153514	C14orf81	5315	9.031	5.569
50074	C15	M-024568- hypothetic	150297	RP1-127L4	3507	13.345	1.255
50074	C16	M-031878- KIAA1909	153478	KIAA1909	4655	7.9699	6.6301
50074	C17	M-018332- ENTH dom	150350	ENTHD1	5282	5.4714	9.1286
50074	C18	M-015445- serum resp	153443	SRFBP1	4744	4.0683	10.5317
50074	C19	M-008922- DnaJ (Hsp4	150353	DNAJB7	5768	14.199	0.401
50074	C20	M-016745- transmem	153396	TMEM161	5302	8.9589	5.6411
50074	C21	M-031490- hypothetic	150356	RP4-756G2	6097	10.645	3.955
50074	C23	M-024578- meiosis de	150365	RP5-821D1	4237	4.1775	10.4225
50074	D02	M-019402- MAM dom	161357	MDGA2	5193	4.0632	10.5368
50074	D04	M-021969- transmem	161291	TMEM30B	4970	15.151	0.551
50074	D05	M-018545- poly(A)-spe	154197	PNLDC1	4483	10.306	4.294
50074	D06	M-008318- RAS (RAD a	161253	REM2	3446	3.4533	11.1467
50074	D07	M-007147- IBR domai	154214	IBRDC1	5930	11.231	3.369
50074	D08	M-031931- similar to	161247	LOC161247	4423	28.917	14.317
50074	D09	M-016746- T-cell lymp	154215	TCBA1	6126	12.569	2.031
50074	D10	M-018015- C-type lecti	161198	CLEC14A	6386	15.612	1.012
50074	D11	M-028649- hypothetic	154222	LOC154222	5059	8.8753	5.7247
50074	D12	M-016637- chromoso	161176	C14orf49	4270	5.9719	8.6281
50074	D13	M-018380- chromoso	154313	C6orf165	4884	29.648	15.048
50074	D14	M-018974- chromoso	161145	C14orf83	5913	19.28	4.68
50074	D15	M-016989- chromoso	154386	C6orf195	5868	15.133	0.533
50074	D16	M-018521- chromoso	161142	C14orf54	6500	14.677	0.077
50074	D17	M-024909- hypothetic	154449	LOC154449	5895	17.625	3.025
50074	D18	M-016122- stomatin (	161003	STOML3	7641	19.749	5.149
50074	D19	M-025090- chromoso	154467	C6orf129	6230	8.4751	6.1249
50074	D20	M-016742- coiled-coil	160857	CCDC122	7435	28.46	13.86
50074	D21	M-015403- Rap2-bindi	154661	RPIB9	5915	14.134	0.466
50074	D23	M-016990- hypothetic	154743	FLJ31818	3811	6.56	8.04
50074	E02	M-031934- similar to	153364	LOC153364	2733	11.636	2.964
50074	E04	M-017783- transmem	153339	TMEM167	4070	16.855	2.255
50074	E05	M-024579- family with	150368	FAM109B	4871	16.978	2.378
50074	E06	M-007347- similar to	153328	LOC153328	5379	15.282	0.682
50074	E07	M-018753- NFAT activ	150372	NFAM1	5944	15.898	1.298
50074	E08	M-016493- coiled-coil	153241	CCDC100	4149	12.389	2.211
50074	E09	M-009563- patatin-like	150379	PNPLA5	5037	15.823	1.223
50074	E10	M-015907- adult retin	153222	LOC153222	5939	17.427	2.827
50074	E11	M-032224- similar to	150383	LOC150383	6131	17.534	2.934
50074	E12	M-028439- serine PI K	153218	SPINK5L3	5961	26.858	12.258
50074	E13	M-009837- tubulin tyr	150465	TTL	4793	9.8268	4.7732
50074	E14	M-007551- solute carri	153201	SLC36A2	5939	18.421	3.821
50074	E15	M-018844- cytoskelet	150468	CKAP2L	6735	36.808	22.208

50074	E16	M-007337-	hypothetica	153129	FLJ90709	6171	15.54	0.94
50074	E17	M-016624-	COBW dom	150472	CBWD2	5157	14.505	0.095
50074	E18	M-008249-	DAB2 inter	153090	DAB2IP	5167	11.961	2.639
50074	E19	M-015660-	tektin 4	150483	TEKT4	5976	7.2122	7.3878
50074	E20	M-015444-	RasGEF dor	153020	RASGEF1B	7482	20.957	6.357
50074	E21	M-016518-	hypothetica	150538	FLJ32063	7438	21.484	6.884
50074	E23	M-027795-	hypothetica	150568	LOC150568	5930	36.863	22.263
50074	F02	M-018416-	coiled-coil	160777	CCDC60	5223	16.102	1.502
50074	F04	M-016858-	coiled-coil	160762	CCDC63	5897	20.892	6.292
50074	F05	M-027202-	hypothetica	154791	HSPC268	3154	20.26	5.66
50074	F06	M-007596-	solute carri	160728	SLC5A8	4746	19.258	4.658
50074	F07	M-015417-	angiomotir	154796	AMOT	4691	13.281	1.319
50074	F08	M-017364-	hypothetica	160518	MGC24039	4419	10.704	3.896
50074	F09	M-018539-	vitamin K e	154807	VKORC1L1	4900	16.918	2.318
50074	F10	M-016857-	intermedia	160492	IFLTD1	5739	22.687	8.087
50074	F11	M-017595-	angiomotir	154810	AMOTL1	1928	11.566	3.034
50074	F12	M-026918-	aldehyde d	160428	ALDH1L2	3360	12.381	2.219
50074	F13	M-029221-	hypothetica	154822	LOC154822	4106	7.9152	6.6848
50074	F14	M-016856-	chromosom	160419	C12orf50	4202	11.756	2.844
50074	F15	M-018861-	IQ motif an	154865	IQUB	3603	13.822	0.778
50074	F16	M-018618-	transmemb	160418	TMTC3	5217	17.961	3.361
50074	F17	M-016991-	potassium	154881	KCTD7	4396	9.8271	4.7729
50074	F18	M-016625-	dendritic ce	160365	DCAL1	4616	10.095	4.505
50074	F19	M-028939-	hypothetica	155006	LOC155006	3930	11.374	3.226
50074	F20	M-021369-	C-type lecti	160364	CLEC12A	5837	17.663	3.063
50074	F21	M-025497-	family with	155019	FAM10A7	4907	13.409	1.191
50074	F23	M-019213-	GTPase, IM	155038	GIMAP8	5545	9.3417	5.2583
50074	G02	M-015548-	chromosom	152992	C4orf23	5016	21.99	7.39
50074	G04	M-015547-	hypothetica	152940	FLJ25371	4703	12.737	1.863
50074	G05	M-022738-	SET and MY	150572	SMYD1	5165	34.618	20.018
50074	G06	M-018772-	protein pho	152926	PPM1K	4375	12.137	2.463
50074	G07	M-027789-	hypothetica	150577	LOC150577	5263	17.158	2.558
50074	G08	M-017948-	klotho beta	152831	KLB	3944	10.877	3.723
50074	G09	M-015472-	chromosom	150590	C2orf15	4581	18.38	3.78
50074	G10	M-018406-	chromosom	152816	C4orf26	6292	28.067	13.467
50074	G11	M-016519-	hypothetica	150596	FLJ32955	4645	31.367	16.767
50074	G12	M-021456-	THAP doma	152815	THAP6	4242	17.421	2.821
50074	G13	M-016520-	hypothetica	150622	FLJ30594	4070	19.214	4.614
50074	G14	M-017067-	janus kinas	152789	JAKMIP1	5291	24.759	10.159
50074	G15	M-016473-	otospiralin	150677	OTOS	5234	22.965	8.365
50074	G16	M-018552-	hypothetica	152766	MGC24125	3768	21.975	7.375
50074	G17	M-015502-	myeloma o	150678	MYEOV2	4868	16.044	1.444
50074	G18	M-015545-	hypothetica	152756	FLJ31659	4328	12.361	2.239
50074	G19	M-007264-	copper me	150684	COMMD1	6343	19.849	5.249
50074	G20	M-028346-	hypothetica	152742	LOC152742	5044	16.178	1.578
50074	G21	M-008551-	prominin 2	150696	PROM2	5507	25.277	10.677
50074	G23	M-023108-	ankyrin anc	150709	ANKAR	3995	20.551	5.951

50074	H02	M-016855- transmemb	160335	TMTC2	6322	15.074	0.474
50074	H04	M-018523- chromoson	160298	C11orf42	4778	10.109	4.491
50074	H05	M-017044- crystallin, g	155051	CRYGN	5381	15.926	1.326
50074	H06	M-008760- lactate deh	160287	LDHAL6A	5088	14.328	0.272
50074	H07	M-025363- zinc finger	155054	ZNF425	3323	15.919	1.319
50074	H08	M-016854- chromoson	160140	C11orf65	5046	17.36	2.76
50074	H09	M-016992- zinc finger	155061	ZNF746	4856	20.84	6.24
50074	H10	M-008877- expressed i	160065	PATE	5275	12.474	2.126
50074	H11	M-028869- FLJ45737 p	155063	FLJ45737	4796	12.114	2.486
50074	H12	M-018584- coiled-coil	159989	CCDC67	4924	23.883	9.283
50074	H13	M-025369- ATPase, H+	155066	ATP6V0E2	4043	11.897	2.703
50074	H14	M-007367- solute carri	159963	SLC5A12	3574	12.003	2.597
50074	H15	M-025400- similar to T	155100	LOC15510	5600	25.982	11.382
50074	H16	M-026312- chromoson	159686	C10orf80	5379	25.284	10.684
50074	H17	M-025281- archaemet	155185	AMZ1	5092	19.462	4.862
50074	H18	M-018526- chromoson	159491	C10orf64	5722	14.925	0.325
50074	H19	M-021320- Williams Be	155368	WBSCR27	4594	18.415	3.815
50074	H20	M-016496- transmemb	159371	TMEM20	6098	28.452	13.852
50074	H21	M-025253- vacuolar pr	155382	VPS37D	5608	17.101	2.501
50074	H23	M-017409- NOL1/NOP	155400	NSUN5B	5176	10.896	3.704
50074	I02	M-018879- zinc finger	152687	ZNF595	5083	9.5219	5.0781
50074	I04	M-015544- hypothetica	152641	FLJ30277	5792	21.202	6.602
50074	I05	M-022720- F-box prote	150726	FBXO41	3918	17.407	2.807
50074	I06	M-018771- sec1 family	152579	SCFD2	4324	11.702	2.898
50074	I07	M-016521- tetratricop	150737	TTC30B	4746	16.351	1.751
50074	I08	M-024202- NIPA-like d	152519	NPAL1	3788	16.156	1.556
50074	I09	M-010302- hypothetica	150763	LOC15076	4623	14.341	0.259
50074	I10	M-021465- nuclear tra	152518	NFXL1	5310	30.527	15.927
50074	I11	M-018384- KIAA1754-l	150771	KIAA1754L	2471	17.523	2.923
50074	I12	M-024058- SH3 domai	152503	SH3D19	3616	33.379	18.779
50074	I13	M-027928- FLJ41352 p	150776	FLJ41352	4161	33.309	18.709
50074	I14	M-018454- hypothetica	152485	LOC15248	5051	25.302	10.702
50074	I15	M-022647- family with	150946	FAM59B	4067	13.696	0.904
50074	I16	M-015543- chromoson	152405	C3orf30	4373	27.19	12.59
50074	I17	M-015635- hypothetica	150962	FLJ32312	4666	31.547	16.947
50074	I18	M-010688- immunoglo	152404	IGSF11	5631	12.698	1.902
50074	I19	M-016522- hypothetica	151009	FLJ38359	6457	24.609	10.009
50074	I20	M-019199- contactin 4	152330	CNTN4	5227	18.251	3.651
50074	I21	M-017363- septin 10	151011	SEPT10	5479	32.342	17.742
50074	I23	M-016151- hypothetica	151050	FLJ23861	5324	9.5229	5.0771
50074	J02	M-016853- ubiquitin sp	159195	USP54	4003	8.1939	6.4061
50074	J04	M-021458- RNA bindin	159163	RBMY1F	6201	18.755	4.155
50074	J05	M-028751- RNA bindin	155435	RBM33	5052	15.697	1.097
50074	J06	M-016594- family with	159091	FAM122C	4666	11.659	2.941
50074	J07	M-010689- anterior gra	155465	AGR3	4879	13.609	0.991
50074	J08	M-016085- family with	159090	FAM122B	4688	12.713	1.887
50074	J09	M-029312- hypothetica	157273	LOC15727	3871	8.1374	6.4626

50074	J10	M-016693- chromoson	159013	CXorf38	4836	10.753	3.847
50074	J11	M-029292- hypothetic	157278	LOC15727	3789	17.604	3.004
50074	J12	M-024783- H2B histon	158983	H2BFWT	4714	12.049	2.551
50074	J13	M-017036- phosphatid	157310	PEBP4	3269	13.888	0.712
50074	J14	M-017040- armadillo r	158947	ARMCX4	4600	10.326	4.274
50074	J15	M-025787- cell divisior	157313	CDCA2	5166	13.086	1.514
50074	J16	M-032247- ubiquitin s	158880	USP51	3667	2.9179	11.6821
50074	J17	M-018907- chromoson	157376	C8orf78	4452	11.321	3.279
50074	J18	M-016172- zinc finger,	158866	ZDHHC15	4380	19.68	5.08
50074	J19	M-019155- transmem	157378	TMEM65	6473	21.489	6.889
50074	J20	M-021328- cancer/tes	158852	CT45-2	6681	14.339	0.261
50074	J21	M-010008- retinol deh	157506	RDH10	5415	8.7535	5.8465
50074	J23	M-025934- family with	157530	FAM10A6	5351	7.7742	6.8258
50074	K02	M-028076- hypothetic	152274	LOC15227	5494	13.797	0.803
50074	K04	M-028077- FYVE, Rho	152273	FGD5	4155	18.556	3.956
50074	K05	M-008684- phospholip	151056	PLB1	2864	19.797	5.197
50074	K06	M-028143- hypothetic	152225	LOC15222	4192	23.497	8.897
50074	K07	M-007142- zinc finger,	151112	ZSWIM2	5439	18.165	3.565
50074	K08	M-017063- coiled-coil	152206	CCDC13	3713	25.236	10.636
50074	K09	M-027954- hypothetic	151121	LOC151121	4372	20.334	5.734
50074	K10	M-019317- nudix (nucl	152195	NUDT16P	3946	18.931	4.331
50074	K11	M-027967- hypothetic	151171	LOC151171	3732	11.254	3.346
50074	K12	M-010755- CKLF-like M	152189	CMTM8	3887	15.693	1.093
50074	K13	M-022974- hypothetic	151174	LOC15117	3536	16.431	1.831
50074	K14	M-017060- coiled-coil	152185	CCDC52	3286	12.203	2.397
50074	K15	M-022967- family with	151176	FAM132B	4324	13.784	0.816
50074	K16	M-017781- coiled-coil	152137	CCDC50	5017	20.949	6.349
50074	K17	M-016152- ADP-ribosy	151188	ARL6IP6	4439	15.431	0.831
50074	K18	M-018794- hypothetic	152100	MGC61571	4815	10.758	3.842
50074	K19	M-018481- family with	151194	FAM119A	6639	11.026	3.574
50074	K20	M-028086- zinc finger,	152098	ZCWPW2	5926	19.102	4.502
50074	K21	M-016153- cyclin Y-like	151195	CCNYL1	6146	7.3706	7.2294
50074	K23	M-015647- kelch-like 2	151230	KLHL23	5015	8.4546	6.1454
50074	L02	M-027188- diacylglyce	158835	DGAT2L4	6314	16.693	2.093
50074	L04	M-010304- diacylglyce	158833	DGAT2L3	5084	14.477	0.123
50074	L05	M-025925- ankyrin rep	157567	ANKRD46	3732	40.059	25.459
50074	L06	M-019273- melanoma	158809	MAGEB6	4048	14.6	0
50074	L07	M-025788- establishm	157570	ESCO2	4304	22.514	7.914
50074	L08	M-018527- chromoson	158801	CXorf42	4583	21.907	7.307
50074	L09	M-017447- F-box prote	157574	FBXO16	3874	11.874	2.726
50074	L10	M-017005- paired-like	158800	OTEX	4960	17.762	3.162
50074	L11	M-010690- family with	157638	FAM84B	3435	28.093	13.493
50074	L12	M-017018- RIB43A do	158787	RIBC1	3699	26.169	11.569
50074	L13	M-017967- chromoson	157657	C8orf37	4116	35.398	20.798
50074	L14	M-008446- hypothetic	158763	RP13-102H	4731	12.915	1.685
50074	L15	M-012873- vacuolar pr	157680	VPS13B	4132	24.637	10.037
50074	L16	M-017039- motile spe	158747	MOSPD2	4867	19.006	4.406

50074	L17	M-029254-	family with	157693	FAM87A	2605	17.927	3.327
50074	L18	M-031758-	family with	158724	FAM47A	4794	21.026	6.426
50074	L19	M-018027-	chromoso	157695	C8orf42	5613	21.824	7.224
50074	L20	M-017038-	hypothetic	158722	FLJ32742	5748	33.751	19.151
50074	L21	M-025827-	glutamate-	157697	ERICH1	6176	19.883	5.283
50074	L23	M-007613-	solute carri	157724	SLC7A13	4941	21.959	7.359
50074	M02	M-028190-	chromoso	152078	C3orf55	4478	8.084	6.516
50074	M04	M-016066-	chromoso	152065	C3orf22	3053	21.389	6.789
50074	M05	M-023104-	protein ph	151242	PPP1R1C	4548	13.171	1.429
50074	M06	M-015460-	fibronectin	152028	FNDC6	4190	17.685	3.085
50074	M07	M-016154-	shugoshin-	151246	SGOL2	3298	17.253	2.653
50074	M08	M-028084-	hypothetic	152024	LOC15202	4520	22.721	8.121
50074	M09	M-018770-	amyotroph	151254	ALS2CR11	2251	16.482	1.882
50074	M10	M-016824-	chromoso	152007	C9orf19	3943	20.314	5.714
50074	M11	M-007336-	hypothetic	151258	FLJ39822	3227	14.379	0.221
50074	M12	M-018789-	chromoso	152002	C3orf21	2773	11.323	3.277
50074	M13	M-016155-	hypothetic	151278	FLJ32447	3913	16.56	1.96
50074	M14	M-018391-	chromoso	151963	C3orf59	3663	9.4458	5.1542
50074	M15	M-007463-	solute carri	151295	SLC23A3	2825	22.053	7.453
50074	M16	M-015455-	coiled-coil	151903	CCDC12	3722	16.228	1.628
50074	M17	M-028016-	hypothetic	151300	LOC15130	5663	31.785	17.185
50074	M18	M-018893-	B and T ly	151888	BTLA	4898	21.641	7.041
50074	M19	M-027825-	myeloid-as	151325	MYADML	6176	21.454	6.854
50074	M20	M-018258-	coiled-coil	151887	CCDC80	5359	15.171	0.571
50074	M21	M-015929-	family with	151354	FAM84A	5363	16.782	2.182
50074	M23	M-015588-	family with	151393	FAM82A	5198	9.2536	5.3464
50074	N02	M-018774-	hypothetic	158696	FLJ30672	3398	15.774	1.174
50074	N04	M-017796-	fatty acid a	158584	FAAH2	2925	12.752	1.848
50074	N05	M-015923-	transmem	157753	TMEM74	2672	10.928	3.672
50074	N06	M-031531-	hypothetic	158572	LOC15857	3503	17.157	2.557
50074	N07	M-017034-	family with	157769	FAM91A1	3443	15.452	0.852
50074	N08	M-016772-	fragile X m	158521	FMR1NB	4230	12.979	1.621
50074	N09	M-018544-	chromoso	157777	C8orf45	3332	9.2137	5.3863
50074	N10	M-007148-	zinc finger	158506	ZNF645	3308	14.601	0.001
50074	N11	M-018542-	hypothetic	157807	MGC34646	2633	9.1531	5.4469
50074	N12	M-016593-	prune hom	158471	PRUNE2	3822	11.224	3.376
50074	N13	M-015925-	NK6 transc	157848	NKX6-3	3694	15.945	1.345
50074	N14	M-018284-	chromoso	158427	C9orf97	3776	10.805	3.795
50074	N15	M-016495-	RPE-spondi	157869	RPESP	4563	14.639	0.039
50074	N16	M-029606-	KIAA1958	158405	KIAA1958	4146	9.3825	5.2175
50074	N17	M-025989-	calmodulin	157922	CAMSAP1	3898	18.881	4.281
50074	N18	M-018530-	chromoso	158401	C9orf84	4271	14.282	0.318
50074	N19	M-018532-	chromoso	157927	C9orf62	3985	21.782	7.182
50074	N20	M-026189-	zinc finger	158399	ZNF483	5034	14.025	0.575
50074	N21	M-015926-	chromoso	157983	C9orf66	4286	9.8227	4.7773
50074	N23	M-029541-	chromoso	158035	C9orf14	5522	12.532	2.068
50074	O02	M-028116-	hypothetic	151877	LOC15187	3762	8.5327	6.0673

50074	O04	M-018977- developme	151871	DPPA2	2852	13.78	0.82
50074	O05	M-019401- growth diff	151449	GDF7	3919	13.243	1.357
50074	O06	M-017582- copine fam	151835	CPNE9	4065	13.53	1.07
50074	O07	M-016156- solute carri	151473	SLC16A14	3657	14.356	0.244
50074	O08	M-016744- leucine ric	151827	LRRC34	3533	23.917	9.317
50074	O09	M-018549- chromoso	151477	C2orf52	3804	21.504	6.904
50074	O10	M-018465- WD repeat	151790	WDR49	3611	14.567	0.033
50074	O11	M-028022- hypothetic	151484	LOC15148	4427	14.344	0.256
50074	O12	M-028144- hypothetic	151658	LOC15165	3115	16.95	2.35
50074	O13	M-016064- skin aspart	151516	SASP	3244	7.3366	7.2634
50074	O14	M-018853- EF-hand do	151651	EFHB	4091	12.784	1.816
50074	O15	M-007203- WD repeat	151525	WDSUB1	4261	28.303	13.703
50074	O16	M-015501- chromoso	151649	C3orf48	5268	25.494	10.894
50074	O17	M-006646- uridine ph	151531	UPP2	4613	10.666	3.934
50074	O18	M-015475- shugoshin-	151648	SGOL1	3461	7.7434	6.8566
50074	O19	M-015474- hypothetic	151534	LOC15153	7093	34.597	19.997
50074	O20	M-018777- family with	151647	FAM19A4	5637	15.629	1.029
50074	O21	M-015350- tetratricop	151613	TTC14	6744	16.34	1.74
50074	O23	M-007143- deltex 3-lik	151636	DTX3L	5683	10.523	4.077
50074	P02	M-029548- hypothetic	158381	LOC158381	4343	13.723	0.877
50074	P04	M-029552- hypothetic	158376	LOC15837	3529	12.383	2.217
50074	P05	M-015927- leucine ric	158038	LINGO2	2005	13.566	1.034
50074	P06	M-026111- KIAA2026	158358	KIAA2026	3541	12.68	1.92
50074	P07	M-016081- chromoso	158046	C9orf121	3087	7.5478	7.0522
50074	P08	M-017026- FRAS1 rela	158326	FREM1	2260	13.894	0.706
50074	P09	M-016767- chromoso	158055	C9orf163	2496	21.635	7.035
50074	P10	M-029616- chromoso	158314	C9orf44	4013	15.873	1.273
50074	P11	M-032232- lipocalin 6	158062	LCN6	2669	15.024	0.424
50074	P12	M-016747- chromoso	158297	C9orf138	2769	16.071	1.471
50074	P13	M-026203- olfactory r	158131	OR1Q1	3304	15.345	0.745
50074	P14	M-027289- family with	158293	FAM120AC	2094	6.9723	7.6277
50074	P15	M-016360- tubulin tyr	158135	TTLL11	3355	11.863	2.737
50074	P16	M-017031- tetratricop	158248	TTC16	4558	13.142	1.458
50074	P17	M-016768- RAS and EF	158158	RASEF	4274	15.746	1.146
50074	P18	M-017032- RNA (guani	158234	RG9MTD3	2667	12.111	2.489
50074	P19	M-009534- hydroxyste	158160	HSD17B7P	3948	11.93	2.67
50074	P20	M-029558- chromoso	158228	C9orf122	3121	9.3239	5.2761
50074	P21	M-016769- chromoso	158219	C9orf52	3585	7.5593	7.0407
50074	P23	M-017982- hypothetic	150759	LOC15075	4671	22.286	7.686
				MAD	4560.5	14.6005	3.688
				MAD3			11.064
				MADc			5.45824
50074	C22				5272	38.771	
50074	D22				6704	49.329	
50074	E22				6129	54.936	
50074	F22				5888	50.747	

					mn	5998.25	48.44575
					sd	592.951	6.875076
50074	G22					2445	11.779
50074	H22					3004	12.284
50074	I22					2722	11.866
50074	J22					3207	8.0449
					mn	2844.5	10.99348
					sd	332.3918	1.978038
					3psSD		5.934113
					3ngSD		20.62523
					SumSD		26.55934
					DiffMn		37.45228
					SmovrDiff		0.709152
					1minus		0.290848

50074	G03	M-003290-	polo-like ki	5347	PLK1 SMA	1113	22.911
50074	H03	M-003290-	polo-like ki	5347	PLK1 SMA	1350	10.074
50074	I03	D-001206-	siControl non-targetin			4270	18.103
50074	J03	D-001206-	siControl non-targetin			3728	10.756
50074	K03	D-001600-	siGLO RISC-free siRNA			6181	25.627
50074	L03	D-001600-	siGLO RISC-free siRNA			6591	27.31

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-0.02244	4576	13.265	1.545	0.29625	4193	9.2774	0.8826	-0.18716
0.260615	2121	7.6851	4.0349	-0.77437	1897	8.1708	1.9892	-0.42235
-0.19558	2369	11.186	0.534	-0.10265	2896	11.464	1.304	0.277569
-0.39399	3536	7.9468	3.7732	-0.72416	3768	14.278	4.118	0.875638
2.124769	2642	18.925	7.205	1.382243	3252	14.453	4.293	0.912831
-0.62447	3653	16.808	5.088	0.976051	3155	14.358	4.198	0.89264
-0.08785	3455	14.298	2.578	0.494453	3910	13.836	3.676	0.781698
-0.17671	4153	17.602	5.882	1.128397	4480	18.103	7.943	1.688578
0.111849	3019	13.448	1.728	0.331362	3886	15.697	5.537	1.177223
-1.02535	2807	16.316	4.596	0.88165	2890	6.8858	3.2742	-0.69545
1.535202	3280	28.902	17.182	3.296545	4080	23.039	12.879	2.737643
0.461596	2742	15.208	3.488	0.669056	2629	16.736	6.576	1.398045
-1.04642	3357	7.8344	3.8856	-0.74573	2379	8.1547	2.0053	-0.42577
-1.03612	4412	8.6582	3.0618	-0.58766	3688	7.7007	2.4593	-0.52226
0.139331	4188	11.772	0.052	0.009785	2797	11.369	1.209	0.257378
-0.76939	3154	14.933	3.213	0.616291	2406	12.095	1.935	0.411677
-0.64444	3951	8.8585	2.8615	-0.54923	2052	13.986	3.826	0.813578
0.58343	5542	15.716	3.996	0.766527	2875	13.913	3.753	0.798063
0.095177	4577	7.2537	4.4663	-0.85715	2015	10.025	0.135	-0.02827
-1.50014	3220	4.8137	6.9063	-1.32531	2742	9.7009	0.4591	-0.09715
-0.72963	4209	10.145	1.575	-0.30239	3269	3.4261	6.7339	-1.43075
0.178721	4683	18.065	6.345	1.217233	4279	12.106	1.946	0.414015
-0.04699	5435	14.351	2.631	0.504622	4893	8.6246	1.5354	-0.3259
-0.96042	3315	4.6456	7.0744	-1.35757	3627	4.6044	5.5556	-1.18033
-0.39747	2745	8.0146	3.7054	-0.71115	3650	7.0959	3.0641	-0.6508
0.023909	3326	10.583	1.137	-0.21835	3823	8.8412	1.3188	-0.27986
0.338479	4276	14.687	2.967	0.569091	3829	8.8274	1.3326	-0.2828
-1.29025	2621	10.263	1.457	-0.27975	3706	7.7442	2.4158	-0.51301
1.780153	3720	32.097	20.377	3.909575	4027	25.925	15.765	3.351015
-0.73146	4308	13.347	1.627	0.311983	3580	8.2123	1.9477	-0.41353
-0.74191	3934	15.125	3.405	0.653131	2761	7.0989	3.0611	-0.65016
-0.11808	4542	15.808	4.088	0.784179	3635	11.829	1.669	0.355143
-0.9932	4103	13.649	1.929	0.369928	3558	12.844	2.684	0.570865
-0.91198	3649	19.211	7.491	1.437118	5915	12.883	2.723	0.579154
-0.86513	4308	9.6797	2.0403	-0.39167	4266	8.0403	2.1197	-0.45008
-0.98924	4352	7.3529	4.3671	-0.83811	4469	7.1604	2.9996	-0.63709
-1.07148	4617	2.7724	8.9476	-1.71698	4401	7.0893	3.0707	-0.6522
-0.20272	5232	9.6713	2.0487	-0.39328	3811	8.1606	1.9994	-0.42451
-0.04608	5619	8.845	2.875	-0.55182	3544	11.512	1.352	0.28777
0.340311	5202	11.438	0.282	-0.0543	3399	11.209	1.049	0.223373
-0.31393	5933	11.748	0.028	0.005181	5755	6.0643	4.0957	-0.87005
0.398022	4866	13.152	1.432	0.274568	3222	5.3383	4.8217	-1.02435
0.173957	4750	15.874	4.154	0.796843	6025	8.2656	1.8944	-0.4022
-0.58838	4371	8.0073	3.7127	-0.71255	6166	6.2277	3.9323	-0.83532
-0.78954	3952	11.943	0.223	0.042595	5667	8.4877	1.6723	-0.35499
-1.20946	3164	13.496	1.776	0.340572	4613	6.6551	3.5049	-0.74448

-1.40802	3725	15.275	3.555	0.681912	5301	7.4137	2.7463	-0.58326
-1.00785	4350	13.287	1.567	0.300471	6229	12.233	2.073	0.441007
-1.7235	3647	13.957	2.237	0.429025	4920	4.5122	5.6478	-1.19992
-0.52096	2262	14.943	3.223	0.61821	2155	4.6404	5.5196	-1.17267
-1.98863	2173	4.4639	7.2561	-1.39243	2285	4.1575	6.0025	-1.27531
-1.02038	3299	10.549	1.171	-0.22487	3787	4.8323	5.3277	-1.13189
-0.23002	3672	17.947	6.227	1.194592	4113	7.1967	2.9633	-0.62938
-1.21479	3660	12.869	1.149	0.220269	4753	12.687	2.527	0.537497
-1.67254	4735	12.313	0.593	0.113588	4382	8.8544	1.3056	-0.27706
-1.9296	4976	7.496	4.224	-0.81066	4890	8.1391	2.0209	-0.42908
-0.07356	5081	12.458	0.738	0.141409	5549	13.516	3.356	0.713687
-1.03359	4665	11.211	0.509	-0.09785	6258	11.649	1.489	0.316887
-0.72468	5829	8.8523	2.8677	-0.55042	5147	11.172	1.012	0.215509
-1.90959	5558	8.3303	3.3897	-0.65058	3896	6.4682	3.6918	-0.78421
-1.93053	5894	4.6827	7.0373	-1.35045	4588	2.354	7.806	-1.65861
0.100857	5522	14.524	2.804	0.537816	5208	7.0469	3.1131	-0.66121
-0.78679	5529	5.8419	5.8781	-1.12803	4161	3.4847	6.6753	-1.4183
-2.04227	3303	7.2056	4.5144	-0.86638	3286	1.7346	8.4254	-1.79025
-0.61732	4538	12.561	0.841	0.161172	4701	4.6373	5.5227	-1.17333
2.622915	2984	26.173	14.453	2.772928	3289	18.334	8.174	1.737673
-0.37219	3497	15.642	3.922	0.752328	4877	9.268	0.892	-0.18915
0.185316	4591	31.932	20.212	3.877916	5302	11.411	1.251	0.266304
-1.04891	2122	13.713	1.993	0.382208	3306	3.6298	6.5302	-1.38746
-1.58084	3234	7.2356	4.4844	-0.86062	3150	3.3333	6.8267	-1.45048
2.756841	2999	34.812	23.092	4.430506	3709	10.38	0.22	0.047182
0.857328	3019	15.502	3.782	0.725466	4873	9.3987	0.7613	-0.16138
0.097559	2825	9.3097	2.4103	-0.46266	4121	9.6336	0.5264	-0.11145
0.014016	3786	14.474	2.754	0.528222	6186	9.3598	0.8002	-0.16964
0.554116	3447	12.765	1.045	0.200314	4206	6.4432	3.7168	-0.78952
0.943253	4435	15.829	4.109	0.788208	6022	12.803	2.643	0.562151
-1.12223	3418	6.5828	5.1372	-0.98587	4951	4.8071	5.3529	-1.13725
2.539188	4813	23.416	11.696	2.243938	5595	11.367	1.207	0.256953
-0.08547	4432	19.743	8.023	1.539194	3876	12.564	2.404	0.511355
-1.47309	4457	6.6861	5.0339	-0.96605	3288	5.292	4.868	-1.03419
-0.54312	3463	3.5807	8.1393	-1.56189	3060	3.1046	7.0554	-1.49908
0.413045	3491	8.88	2.84	-0.54511	2612	10.72	0.56	0.119444
0.43558	5463	13.088	1.368	0.262288	4590	12.68	2.52	0.536009
0.124857	4291	13.051	1.331	0.255189	4069	7.0042	3.1558	-0.67029
0.237714	3537	18.858	7.138	1.369387	6260	17.396	7.236	1.538317
-0.40517	2831	13.387	1.667	0.319658	3323	9.5697	0.5903	-0.12503
0.223973	3958	15.589	3.869	0.742159	4644	11.606	1.446	0.307748
0.517841	4755	17.182	5.462	1.047811	4441	10.763	0.603	0.128583
0.537444	3491	15.755	4.035	0.77401	4196	8.1268	2.0332	-0.4317
2.245687	3291	28.38	16.66	3.196388	4542	19.771	9.611	2.043084
-0.87459	3615	7.6349	4.0851	-0.78401	3483	7.0055	3.1545	-0.67001
0.699951	3526	14.209	2.489	0.477376	5027	10.066	0.094	-0.01955
4.068619	4214	24.205	12.485	2.395324	5699	25.18	15.02	3.192677

0.172125	4583	17.412	5.692	1.091941	6151	11.071	0.911	0.194043
-0.0175	3826	10.063	1.657	-0.31812	4704	6.7602	3.3998	-0.72215
-0.48358	3400	8.0294	3.6906	-0.70831	4428	5.3523	4.8077	-1.02137
-1.3536	5245	7.6072	4.1128	-0.78932	4564	2.6731	7.4869	-1.59079
1.16457	5865	15.891	4.171	0.800104	5621	10.639	0.479	0.102229
1.261121	6310	16.735	5.015	0.962044	5548	14.311	4.151	0.882651
4.078696	3526	26.858	15.138	2.90436	2920	27.329	17.169	3.649412
0.275089	4863	12.564	0.844	0.161748	5237	12.755	2.595	0.551949
1.152661	5434	19.746	8.026	1.539769	5013	17.814	7.654	1.627156
1.036873	3926	11.437	0.283	-0.05449	4836	17.639	7.479	1.589963
0.853297	5794	14.187	2.467	0.473155	6575	14.692	4.532	0.963627
-0.24174	3940	5.736	5.984	-1.14835	4701	7.4665	2.6935	-0.57203
-0.71387	3780	3.8889	7.8311	-1.50276	4599	7.98	2.18	-0.4629
0.424587	3224	16.222	4.502	0.863614	4471	15.366	5.206	1.106874
1.481522	3924	22.426	10.706	2.053985	4893	22.849	12.689	2.697262
-0.55595	2955	10.491	1.229	-0.236	3175	10.898	0.738	0.157275
-0.40663	3278	9.7926	1.9274	-0.37001	4123	10.017	0.143	-0.02997
-1.22481	3145	3.2114	8.5086	-1.63275	3266	5.1745	4.9855	-1.05916
-0.52114	3685	13.433	1.713	0.328484	4077	12.117	1.957	0.416353
-0.14263	3285	10.137	1.583	-0.30392	4315	13.465	3.305	0.702848
0.615675	3630	16.97	5.25	1.007134	5552	17.813	7.653	1.626943
-0.87453	3700	8.4324	3.2876	-0.63099	5237	10.483	0.323	0.069073
-0.82545	3433	7.3696	4.3504	-0.83491	5912	9.5568	0.6032	-0.12778
-0.59112	3775	6.8079	4.9121	-0.94268	4160	9.6154	0.5446	-0.11532
0.561078	5323	11.929	0.209	0.039909	4712	15.004	4.844	1.029937
-0.21829	4456	6.1041	5.6159	-1.07772	4313	9.6684	0.4916	-0.10406
-0.96346	4654	5.2213	6.4987	-1.24711	5571	7.3595	2.8005	-0.59477
1.353825	5015	17.149	5.429	1.041479	4920	11.565	1.405	0.299035
-0.34141	4134	12.748	1.028	0.197052	4577	9.3948	0.7652	-0.16221
3.667391	4070	25.971	14.251	2.73417	5220	25.594	15.434	3.280666
-0.45134	3920	15.867	4.147	0.795499	5328	10.83	0.67	0.142822
0.468558	3724	14.098	2.378	0.456079	4965	11.42	1.26	0.268217
-0.68218	2605	10.633	1.087	-0.20876	2701	4.4798	5.6802	-1.20681
0.692439	3107	11.136	0.584	-0.11224	4528	9.4302	0.7298	-0.15468
2.467187	4110	23.114	11.394	2.185993	5313	25.485	15.325	3.2575
3.071778	3353	11.423	0.297	-0.05718	4015	18.904	8.744	1.858817
0.516742	3075	8.3577	3.3623	-0.64532	4177	7.1104	3.0496	-0.64772
0.845236	2632	13.564	1.844	0.353619	4022	15.639	5.479	1.164896
1.861131	3885	17.349	5.629	1.079853	5029	21.754	11.594	2.464538
1.532454	3557	8.1529	3.5671	-0.68462	4345	13.487	3.327	0.707524
1.351077	2724	13.032	1.312	0.251544	3635	11.224	1.064	0.226561
0.264463	3895	9.7561	1.9639	-0.37701	4147	15.288	5.128	1.090297
-0.4103	3693	6.8779	4.8421	-0.92925	3941	8.5765	1.5835	-0.33612
0.961574	4644	6.2016	5.5184	-1.05902	5262	9.5401	0.6199	-0.13132
0.289013	4345	6.8124	4.9076	-0.94182	4210	9.7862	0.3738	-0.07902
1.956033	4816	12.189	0.469	0.089796	5913	21.935	11.775	2.503006
1.090187	4645	7.4058	4.3142	-0.82796	3905	15.186	5.026	1.068618

0.08675	4933	16.744	5.024	0.963771	5723	11.463	1.303	0.277356
-0.82288	3784	9.9894	1.7306	-0.33224	3881	3.8135	6.3465	-1.34842
0.242844	4358	19.229	7.509	1.440572	5902	10.945	0.785	0.167264
-0.04992	4254	13.54	1.82	0.349014	4746	7.9435	2.2165	-0.47066
0.241561	2837	11.103	0.617	-0.11858	2945	11.986	1.826	0.388511
0.505566	4403	18.26	6.54	1.254648	3102	10.155	0.005	-0.00064
1.143134	3953	21.579	9.859	1.89147	3899	17.62	7.46	1.585925
-0.38959	4842	14.209	2.489	0.477376	4510	9.9557	0.2043	-0.043
-0.45555	4108	11.003	0.717	-0.13776	3912	8.2311	1.9289	-0.40953
1.70064	3144	18.257	6.537	1.254072	2919	15.964	5.804	1.233969
-0.49531	3540	8.8983	2.8217	-0.5416	2864	10.161	0.001	0.000638
-0.47589	3372	13.642	1.922	0.368585	2907	9.2191	0.9409	-0.19955
2.085196	3744	23.424	11.704	2.245473	3017	19.987	9.827	2.088991
1.957316	3462	25.621	13.901	2.667015	3306	27.374	17.214	3.658976
0.890672	4443	13.482	1.762	0.337886	3604	16.315	6.155	1.308568
0.059451	4599	6.6754	5.0446	-0.96811	4193	9.7305	0.4295	-0.09086
0.698852	3667	12.817	1.097	0.210291	4102	19.625	9.465	2.012054
2.537723	5067	17.9	6.18	1.185574	3600	26.056	15.896	3.378857
0.458115	3630	8.3471	3.3729	-0.64736	3448	10.789	0.629	0.134109
-0.6787	4332	5.1939	6.5261	-1.25236	3959	15.029	4.869	1.03525
-0.93045	4790	7.7871	3.9329	-0.7548	5350	1.6822	8.4778	-1.80139
1.209456	5568	19.648	7.928	1.520966	4052	5.7502	4.4098	-0.9368
0.514177	3656	11.844	0.124	0.0236	3682	4.3998	5.7602	-1.22381
-0.53103	4270	11.663	0.057	-0.01113	3711	3.1528	7.0072	-1.48884
0.320708	4343	10.661	1.059	-0.20338	4218	4.0778	6.0822	-1.29225
0.284982	3629	15.679	3.959	0.759428	3432	5.0991	5.0609	-1.07519
-0.04754	3864	12.785	1.065	0.204151	3072	8.3659	1.7941	-0.38088
2.917882	4097	34.757	23.037	4.419953	4418	10.616	0.456	0.09734
0.535429	2247	22.207	10.487	2.011965	1908	2.044	8.116	-1.7245
3.440395	2600	29.923	18.203	3.492446	3321	11.262	1.102	0.234637
3.42757	2786	33.094	21.374	4.100871	3201	13.496	3.336	0.709437
1.960614	4440	24.144	12.424	2.38362	3572	8.7346	1.4254	-0.30252
-0.16571	4053	16.062	4.342	0.832914	3357	3.5746	6.5854	-1.39919
2.306513	5142	26.293	14.573	2.795952	3298	5.852	4.308	-0.91517
3.104755	4806	28.672	16.952	3.252415	3312	7.7899	2.3701	-0.5033
-0.34856	5113	15.412	3.692	0.708198	4567	4.7077	5.4523	-1.15837
1.83365	5812	19.288	7.568	1.451892	4095	8.8156	1.3444	-0.2853
0.668805	4489	16.908	5.188	0.995238	3654	7.2523	2.9077	-0.61756
3.250407	4717	27.009	15.289	2.933332	3891	13.698	3.538	0.752368
-0.93026	5604	9.5824	2.1376	-0.41034	4288	3.0317	7.1283	-1.51458
-1.17375	3524	2.8377	8.8823	-1.70445	3104	7.9897	2.1703	-0.46084
0.761143	4315	7.1842	4.5358	-0.87048	3974	12.783	2.623	0.5579
0.200889	3409	3.3148	8.4052	-1.61291	3120	10.449	0.289	0.061847
-0.53891	3876	8.0753	3.6447	-0.69951	3114	12.203	2.043	0.434631
-0.18165	3482	5.8874	5.8326	-1.1193	2992	16.243	6.083	1.293266
-0.34581	5901	10.659	1.061	-0.20377	3346	12.403	2.243	0.477138
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-0.7049	4256	9.7039	2.0161	-0.38702	3020	10.596	0.436	0.09309
0.550269	2577	9.0415	2.6785	-0.51412	2456	13.599	3.439	0.731328
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-0.13054	2765	3.0741	8.6459	-1.65909	2838	7.9281	2.2319	-0.47393
-0.78313	3245	8.7827	2.9373	-0.56378	3580	10.922	0.762	0.162376
-0.27747	3665	5.457	6.263	-1.20188	2808	13.426	3.266	0.694559
-2.14036	2083	1.1042	10.6158	-2.03706	2461	4.3072	5.8528	-1.24349
-0.60083	2411	8.9589	2.7611	-0.52997	2465	9.2495	0.9105	-0.19309
0.930611	4143	16.389	4.669	0.895656	2784	21.875	11.715	2.490254
1.262037	4127	15.071	3.351	0.64277	3898	15.829	5.669	1.205277
-0.04791	4364	8.1347	3.5853	-0.68811	4100	15.732	5.572	1.184661
-1.07122	4450	6.9213	4.7987	-0.92093	3737	6.9575	3.2025	-0.68021
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0.724684	2989	12.211	0.491	0.094017	3568	8.6883	1.4717	-0.31236
0.952047	2301	12.994	1.274	0.244252	2880	13.75	3.59	0.76342
1.629921	4310	19.35	7.63	1.463788	4383	14.579	4.419	0.93961
0.653049	4421	16.173	4.453	0.854212	3986	20.672	10.512	2.234577
1.948522	3489	13.672	1.952	0.374341	4139	22.88	12.72	2.70385
1.05043	3941	10.683	1.037	-0.19916	4034	16.039	5.879	1.249909
0.793388	4097	12.473	0.753	0.144287	3630	16.612	6.452	1.371691
-0.61311	4237	11.706	0.014	-0.00288	3581	10.165	0.005	0.001488
0.200156	3569	10.255	1.465	-0.28128	3171	14.16	4	0.850559
0.335365	3403	8.1105	3.6095	-0.69275	2899	13.384	3.224	0.685633
-0.43924	3797	7.9273	3.7927	-0.7279	2781	6.6882	3.4718	-0.73745
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1.163104	5704	17.742	6.022	1.155259	4808	18.989	8.829	1.876883
0.152155	4318	9.1478	2.5722	-0.49372	3290	17.447	7.287	1.549156
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4.664232	3954	29.818	18.098	3.4723	2515	12.684	2.524	0.536859
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0.579216	5388	9.0757	2.6443	-0.50756	4270	3.185	6.975	-1.482
2.471951	3938	17.649	5.929	1.137415	2576	9.1227	1.0373	-0.22004
2.119456	3996	18.969	7.249	1.390685	3733	12.483	2.323	0.49414
3.810294	3573	15.701	3.981	0.763649	3163	11.793	1.633	0.347492
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1.83878	4652	16.402	4.682	0.898151	3727	7.7811	2.3789	-0.50517
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0.609446	2926	10.868	0.852	-0.16367	2358	5.8524	4.3076	-0.91508
1.177211	5472	18.476	6.756	1.296092	5218	12.764	2.604	0.553862
1.323412	5283	14.424	2.704	0.518629	4788	11.404	1.244	0.264817
3.508549	4956	16.606	4.886	0.937293	5455	14.372	4.212	0.895616
0.967803	5416	12.592	0.872	0.16712	5450	11.67	1.51	0.321351
1.348145	3700	6.7838	4.9362	-0.94731	4460	8.9013	1.2587	-0.26709
-1.19388	4134	17.417	5.697	1.0929	5296	10.423	0.263	0.056321
1.243716	3522	19.903	8.183	1.569893	3241	12.866	2.706	0.575541
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1.487751	5368	17.884	6.164	1.182504	4366	15.506	5.346	1.136629
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1.046766	4165	10.372	1.348	-0.25883	3843	12.36	2.2	0.467999
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3.148359	5296	22.413	10.693	2.051491	4646	23.16	13	2.76336
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9.16E-05	6231	17.525	5.805	1.113622	3934	13.218	3.058	0.650352
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-0.3328	4409	8.3239	3.3961	-0.65181	3503	9.0779	1.0821	-0.22956
2.510425	4696	19.676	7.956	1.526338	3453	16.913	6.753	1.435663
1.99579	5179	16.412	4.692	0.900069	3957	18.676	8.516	1.81036
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1.288785	3972	12.462	0.742	0.142177	2561	11.011	0.851	0.181291
0.233134	5698	12.548	0.828	0.158678	3102	8.7685	1.3915	-0.29532
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0.269409	2929	10.106	1.614	-0.30987	2315	7.6458	2.5142	-0.53393
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-0.26721	4347	7.9825	3.7375	-0.71731	4552	11.094	0.934	0.198931
0.209866	2483	13.492	1.772	0.339805	3456	7.4942	2.6658	-0.56615
-0.4561	3096	6.7506	4.9694	-0.95368	2999	14.138	3.978	0.845883
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-0.96672	3995	4.6558	7.0642	-1.35561	3775	6.755	3.405	-0.72325
-1.29001	2242	5.4416	6.2784	-1.20484	2986	7.6356	2.5244	-0.53609
1.408055	3577	10.54	1.18	-0.2266	4190	13.365	3.205	0.681595
	4092.5	11.721	3.5215		3911	10.158	3.17915	
			10.5645				9.53745	
			5.21182				4.705142	
6979	54.936		5703	47.361				
5189	48.372		4881	40.791				
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5853	45.327		5754	43.865				

5786.75	50.005	5236.75	45.24125
860.1831	4.113779	578.9544	3.648384
2127	4.2313	2936	11.989
2496	5.9295	1991	15.269
2793	10.92	1689	1.3025
1975	8.1519	1989	10.86
2347.75	7.308175	2151.25	9.855125
368.736	2.893962	542.0679	6.000573
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	12.34134		10.94515
	21.02322		28.94687
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757	13.21	1156	9.6021
960	19.896	743	4.8452
4077	17.537	3787	4.9115
3625	6.9793	3198	13.977
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50075	A02	M-007258-	selenophos	168474	LOC16847	2811	1.174	10.586
50075	A04	M-012923-	GTPase, IM	170575	GIMAP1	3653	13.332	1.572
50075	A05	M-017606-	piggyBac tr	161779	PGBD4	3743	17.66	5.9
50075	A06	M-013167-	DEAH (Asp-	170506	DHX36	2565	9.3567	2.4033
50075	A07	M-004787-	exonucleas	161829	EXDL1	2168	8.3487	3.4113
50075	A08	M-008921-	C-type lecti	170482	CLEC4C	2019	6.7855	4.9745
50075	A09	M-018333-	fibrous she	161835	FSIP1	2200	10.955	0.805
50075	A10	M-014943-	single strar	170463	SSBP4	1979	12.936	1.176
50075	A11	M-016307-	zinc finger	161882	ZFPM1	2511	9.5978	2.1622
50075	A12	M-029639-	hypothetica	170425	LOC17042	2352	8.5884	3.1716
50075	A13	M-018713-	adenosine	161931	ADAD2	2541	6.4935	5.2665
50075	A14	M-026282-	PWWP dor	170394	PWWP2	2530	9.3281	2.4319
50075	A15	M-022498-	hypothetica	162073	LOC16207	2857	16.906	5.146
50075	A16	M-018497-	chromosor	170393	C10orf91	3504	17.637	5.877
50075	A17	M-019403-	TNT protei	162083	TNT	3196	11.702	0.058
50075	A18	M-016942-	oncoprotei	170392	OIT3	3185	13.155	1.395
50075	A19	M-007149-	zinc finger	162239	ZFP1	2723	8.6669	3.0931
50075	A20	M-008993-	fucosyltran	170384	FUT11	2107	9.2074	2.5526
50075	A21	M-016498-	ankyrin-rep	162282	ANKFN1	2594	8.7124	3.0476
50075	A23	M-007150-	ring finger	162333	RNF190	2090	4.7368	7.0232
50075	B02	M-007566-	solute carri	201266	SLC39A11	4938	5.5691	6.1909
50075	B04	M-016887-	leucine rich	201255	LRRC45	5075	5.931	5.829
50075	B05	M-015294-	glycoprotei	170589	GPHA2	4286	7.2329	4.5271
50075	B06	M-016829-	stimulated	201254	STRA13	3957	16.351	4.591
50075	B07	M-015295-	S100 calciu	170591	S100Z	4740	9.0717	2.6883
50075	B08	M-016501-	hypothetica	201252	FLJ23754	1575	4.254	7.506
50075	B09	M-021721-	COMM dor	170622	COMMD6	3751	15.009	3.249
50075	B10	M-018020-	chromosor	201243	C17orf74	2806	10.478	1.282
50075	B11	M-017500-	X antigen fa	170626	XAGE3	2473	10.675	1.085
50075	B12	M-031866-	solute carri	201232	SLC16A13	2733	5.7446	6.0154
50075	B13	M-017499-	X antigen fa	170627	XAGE5	2806	17.89	6.13
50075	B14	M-030940-	hypothetica	201229	LOC20122	3078	15.01	3.25
50075	B15	M-020742-	psoriasis su	170679	PSORS1C1	3738	22.525	10.765
50075	B16	M-017804-	sterile alph	201191	SAMD14	3182	17.033	5.273
50075	B17	M-020744-	psoriasis su	170680	PSORS1C2	2297	10.71	1.05
50075	B18	M-027281-	Rho GTPas	201176	ARHGAP27	3538	11.193	0.567
50075	B19	M-024693-	nudix (nucl	170685	NUDT10	2852	4.6283	7.1317
50075	B20	M-030897-	hypothetica	201175	LOC20117	3320	8.9458	2.8142
50075	B21	M-015309-	cytochrom	170712	COX7B2	3976	9.9095	1.8505
50075	B23	M-015418-	GS homeob	170825	GSH2	4224	14.276	2.516
50075	C02	M-026272-	chromosor	170371	C10orf128	6167	16.264	4.504
50075	C04	M-029627-	chromosor	170370	C10orf73	5861	10.971	0.789
50075	C05	M-016639-	hypothetica	162387	FLJ35773	5232	19.82	8.06
50075	C06	M-018498-	zinc finger,	170261	ZCCHC12	4894	22.742	10.982
50075	C07	M-027164-	schlafen fa	162394	SLFN5	4196	19.113	7.353
50075	C08	M-024910-	TFS2-M do	170082	MGC17403	3361	15.382	3.622

50075	C09	M-008648- N-acetylglu	162417	NAGS	4120	18.01	6.25
50075	C10	M-016941- Fanconi an	2187	FANCB	2602	13.566	1.806
50075	C11	M-018456- family with	162427	FAM134C	2415	20.041	8.281
50075	C12	M-016940- chromosom	170063	CXorf22	3473	19.292	7.532
50075	C13	M-016870- transmemb	162461	TMEM92	2383	18.296	6.536
50075	C14	M-016939- family with	170062	FAM47B	3005	13.478	1.718
50075	C15	M-006029- rhomboid,	162494	RHBDL3	2244	12.121	0.361
50075	C16	M-024685- spindlin far	169981	SPIN3	3569	24.769	13.009
50075	C17	M-007404- solute carri	162515	SLC16A11	2743	11.083	0.677
50075	C18	M-016938- family with	169966	FAM46D	2847	15.033	3.273
50075	C19	M-016871- F-box prote	162517	FBXO39	4000	11.4	0.36
50075	C20	M-019308- zinc finger	169841	ZNF169	4143	16.462	4.702
50075	C21	M-005928- intramemb	162540	IMP5	4287	10.404	1.356
50075	C23	M-018761- keratin 28	162605	KRT28	5084	17.093	5.333
50075	D02	M-017858- similar to C	201164	LOC201164	5400	2.2963	9.4637
50075	D04	M-018965- proline rich	201161	PRR6	4436	5.7484	6.0116
50075	D05	M-030681- KIAA1987 p	170951	KIAA1987	4718	5.2353	6.5247
50075	D06	M-016281- family with	201158	FAM18B2	4532	15.512	3.752
50075	D07	M-025083- KIAA1949	170954	KIAA1949	4158	22.126	10.366
50075	D08	M-016483- coiled-coil	201134	CCDC46	3197	3.7222	8.0378
50075	D09	M-031147- zinc finger	170958	ZNF525	3319	10.093	1.667
50075	D10	M-016500- mucin 20, c	200958	MUC20	2777	12.495	0.735
50075	D11	M-015370- zinc finger	170959	ZNF431	2324	18.675	6.915
50075	D12	M-018492- kelch doma	200942	KLHDC8B	2630	11.597	0.163
50075	D13	M-023904- ankyrin rep	170961	ANKRD24	3116	13.96	2.2
50075	D14	M-023542- F-box prote	200933	FBXO45	1966	5.0865	6.6735
50075	D15	M-012856- additional s	171023	ASXL1	2422	21.429	9.669
50075	D16	M-017960- organic sol	200931	OSTalpha	2168	11.808	0.048
50075	D17	M-028243- synaptopod	171024	SYNPO2	3009	14.988	3.228
50075	D18	M-018951- 5-hydroxyt	200909	HTR3D	2919	9.7636	1.9964
50075	D19	M-015420- sperm acro	171169	SPACA4	4177	18.171	6.411
50075	D20	M-009013- dihydrofola	200895	DHFRL1	4535	21.72	9.96
50075	D21	M-015334- NLR family,	171389	NLRP6	3610	15.623	3.863
50075	D23	M-015356- zinc finger	171392	ZNF675	5174	16.796	5.036
50075	E02	M-026193- hypothetica	169834	LOC169834	6671	7.4801	4.2799
50075	E04	M-015621- GLIS family	169792	GLIS3	4152	10.356	1.404
50075	E05	M-007151- zinc finger	162655	ZNF519	5136	9.1121	2.6479
50075	E06	M-018803- quiescin Q6	169714	QSOX2	5128	18.701	6.941
50075	E07	M-018519- chromosom	162681	C18orf54	5363	23.121	11.361
50075	E08	M-016610- chromosom	169693	C9orf71	2975	12.773	1.013
50075	E09	M-005145- transcriptio	162699	TCEB3C	2931	15.899	4.139
50075	E10	M-018648- olfactomed	169611	OLFML2A	2679	12.878	1.118
50075	E11	M-018517- zinc finger	162963	ZNF610	3554	19.865	8.105
50075	E12	M-019310- indoleamin	169355	INDOL1	3046	26.395	14.635
50075	E13	M-031845- zinc finger	162966	ZNF600	2366	21.429	9.669
50075	E14	M-018501- zinc finger	169270	ZNF596	2371	18.22	6.46
50075	E15	M-031142- zinc finger	162967	ZNF320	3032	10.818	0.942

50075	E16	M-025917- transmemb	169200	TMEM64	3922	10.836	0.924
50075	E17	M-027216- zinc finger	162968	ZNF497	3368	13.836	2.076
50075	E18	M-016021- hypothetica	169166	MGC39715	3622	21.535	9.775
50075	E19	M-016872- zinc finger	162972	ZNF550	4919	20.817	9.057
50075	E20	M-025842- collagen, ty	169044	COL22A1	4277	16.203	4.443
50075	E21	M-016217- zinc finger	162979	ZNF342	4934	12.931	1.171
50075	E23	M-004422- death effec	162989	DEDD2	5882	12.122	0.362
50075	F02	M-017365- ADP-ribosy	200894	ARL13B	5928	17.797	6.037
50075	F04	M-008689- lipase, mer	200879	LIPH	5244	14.359	2.599
50075	F05	M-018275- citrate lyas	171425	CLYBL	4881	9.5472	2.2128
50075	F06	M-016612- potassium	200845	KCTD6	4467	15.335	3.575
50075	F07	M-017931- family with	171482	FAM9A	3610	7.7008	4.0592
50075	F08	M-027219- FLJ42117 p	200844	FLJ42117	4067	21.957	10.197
50075	F09	M-031998- family with	171483	FAM9B	4313	11.871	0.111
50075	F10	M-017436- tigger trans	200765	TIGD1	3344	9.3301	2.4299
50075	F11	M-017776- family with	171484	FAM9C	3912	10.199	1.561
50075	F12	M-018590- sprouty-rel	200734	SPRED2	2929	11.779	0.019
50075	F13	M-017156- chromosom	171546	C14orf147	2552	12.539	0.779
50075	F14	M-022701- transmemb	200728	TMEM17	2763	11.003	0.757
50075	F15	M-015503- polymerase	171568	POLR3H	2664	14.264	2.504
50075	F16	M-017757- keratinocyt	200634	KRTCAP3	3151	7.2675	4.4925
50075	F17	M-019404- placenta-sp	191585	PLAC4	2704	15.57	3.81
50075	F18	M-018493- chromosom	200558	C2orf13	3289	14.472	2.712
50075	F19	M-015919- phosphogly	192111	PGAM5	3015	7.7612	3.9988
50075	F20	M-017802- ankyrin rep	200539	ANKRD23	2852	16.269	4.509
50075	F21	M-016388- UDP-GlcNA	192134	B3GNT6	3314	13.096	1.336
50075	F23	M-016491- HIG1 doma	192286	HIGD2A	4142	9.7537	2.0063
50075	G02	M-007529- solute carri	169026	SLC30A8	5470	8.0804	3.6796
50075	G04	M-018503- cyclic nucle	168975	CNBD1	5392	9.069	2.691
50075	G05	M-031223- hypothetica	162993	LOC162993	4655	13.448	1.688
50075	G06	M-018115- zinc finger	168850	ZNF800	4094	10.967	0.793
50075	G07	M-031219- olfactory re	162998	OR7D2	4625	17.276	5.516
50075	G08	M-021489- BMP bindir	168667	BMPER	4451	12.222	0.462
50075	G09	M-016640- zinc finger	163033	ZNF579	3128	6.8734	4.8866
50075	G10	M-009045- basic helix-	168620	BHLHB8	3196	21.777	10.017
50075	G11	M-015752- zinc finger	163049	ZNF791	3818	7.6742	4.0858
50075	G12	M-025367- zinc finger	168544	ZNF467	3887	11.86	0.1
50075	G13	M-016911- zinc finger	163050	ZNF564	3223	17.344	5.584
50075	G14	M-017612- GTPase, IM	168537	GIMAP7	2937	17.297	5.537
50075	G15	M-016641- zinc finger	163051	ZNF709	4360	14.151	2.391
50075	G16	M-017434- polycystic k	168507	PKD1L1	3781	15.234	3.474
50075	G17	M-017041- zinc finger	163059	ZNF433	4576	18.094	6.334
50075	G18	M-018049- hypothetica	168455	FLJ36031	3668	10.224	1.536
50075	G19	M-015908- zinc finger	163071	ZNF114	5280	12.803	1.043
50075	G20	M-021462- THAP doma	168451	THAP5	6116	12.181	0.421
50075	G21	M-016451- zinc finger	163081	ZNF567	4579	12.907	1.147
50075	G23	M-016452- zinc finger	163087	ZNF383	5159	8.6451	3.1149

50075	H02	M-016189- chromosom	200523	C2orf51	4474	13.098	1.338
50075	H04	M-018916- gastrokine	200504	GKN2	3969	11.262	0.498
50075	H05	M-021177- keratin 24	192666	KRT24	5672	6.3293	5.4307
50075	H06	M-022722- hypothetic	200424	MGC22014	4282	37.039	25.279
50075	H07	M-004640- eukaryotic	192669	EIF2C3	3581	6.8975	4.8625
50075	H08	M-016277- LOC20042	200420	LOC20042	4644	9.087	2.673
50075	H09	M-004641- eukaryotic	192670	EIF2C4	4379	17.721	5.961
50075	H10	M-016905- cellular rep	200407	CREG2	3500	10.229	1.531
50075	H11	M-016650- secretory c	192683	SCAMP5	2708	5.0222	6.7378
50075	H12	M-015978- hypothetic	200403	MGC26733	2699	16.376	4.616
50075	H13	M-008869- epidermal	195814	RDHE2	2296	10.105	1.655
50075	H14	M-016271- similar to	200383	LOC20038	2550	9.6863	2.0737
50075	H15	M-026175- chromosom	195827	C9orf21	2508	15.71	3.95
50075	H16	M-008849- forkhead b	200350	FOXD4L1	3105	8.5668	3.1932
50075	H17	M-016034- zinc finger	195828	ZNF367	3444	8.8269	2.9331
50075	H18	M-024577- hypothetic	200321	LOC200321	3774	18.521	6.761
50075	H19	M-026409- anthrax to	195977	ANTXRL	3511	12.105	0.345
50075	H20	M-016188- hypothetic	200317	FLJ23865	3737	7.8405	3.9195
50075	H21	M-016943- methyltran	196074	METT5D1	2826	8.351	3.409
50075	H23	M-026546- hypothetic	196264	LOC19626	2899	3.3115	8.4485
50075	I02	M-007155- ring finger	168433	RNF133	4209	10.192	1.568
50075	I04	M-015755- zinc finger	168417	ZNF679	4327	8.2274	3.5326
50075	I05	M-016453- zinc finger	163115	ZNF781	5263	16.625	4.865
50075	I06	M-019305- DEAD (Asp-	168400	DDX53	3812	13.694	1.934
50075	I07	M-016873- EP300 inte	163126	EID2	5019	16.338	4.578
50075	I08	M-016228- UDP-N-ace	168391	GALNTL5	3825	7.1111	4.6489
50075	I09	M-015753- hypothetic	163154	MGC24975	4783	14.97	3.21
50075	I10	M-021315- zinc finger	168374	ZNF92	4221	10.116	1.644
50075	I11	M-017009- leucine-ric	163175	LGI4	4483	19.853	8.093
50075	I12	M-021302- chromosom	168090	C6orf118	2677	27.269	15.509
50075	I13	M-016874- chromosom	163183	C19orf46	2725	7.4862	4.2738
50075	I14	M-028651- dapper, an	168002	DACT2	3224	14.702	2.942
50075	I15	M-018515- zinc finger	163227	ZNF100	3592	23.218	11.458
50075	I16	M-024703- taxilin beta	167838	TXLNB	4225	15.408	3.648
50075	I17	M-024000- similar to Z	163233	LOC16323	3454	8.8593	2.9007
50075	I18	M-018595- chromosom	167691	C6orf152	3653	9.2527	2.5073
50075	I19	M-016454- zinc finger	163255	ZNF540	5589	13.008	1.248
50075	I20	M-008433- protease, s	167681	PRSS35	5355	14.995	3.235
50075	I21	M-031846- DENN/MA	163259	DENND2C	6025	19.054	7.294
50075	I23	M-032238- guanylate	163351	GBP6	5428	22.642	10.882
50075	J02	M-018910- hypothetic	200261	LOC200261	4002	8.6707	3.0893
50075	J04	M-024178- chromosom	200232	C20orf106	4299	15.097	3.337
50075	J05	M-005877- IMP1 inner	196294	IMMP1L	3776	12.818	1.058
50075	J06	M-024096- hypothetic	200213	LOC20021	4369	17.35	5.59
50075	J07	M-031341- doublecort	196296	DCDC5	3857	11.382	0.378
50075	J08	M-021938- chromosom	200205	C1orf69	4254	13.164	1.404
50075	J09	M-026768- hypothetic	196337	LOC19633	4388	19.006	7.246

50075	J10	M-018885-	chromoson	200197	C1orf126	3382	13.276	1.516
50075	J11	M-017878-	keratin 78	196374	KRT78	3965	18.789	7.029
50075	J12	M-018947-	CREB regul	200186	CRTC2	3540	15.254	3.494
50075	J13	M-027083-	dynein, axo	196385	DNAH10	3305	15.34	3.58
50075	J14	M-017759-	keratinocy	200185	KRTCAP2	3626	10.811	0.949
50075	J15	M-027056-	antagonist	196394	AMN1	2783	11.427	0.333
50075	J16	M-016973-	schlafen-lik	200172	SLFNL1	3407	13.707	1.947
50075	J17	M-007156-	deltex 3 ho	196403	DTX3	3181	10.909	0.851
50075	J18	M-031973-	sperm asso	200162	SPAG17	4822	19.535	7.775
50075	J19	M-015794-	methyltran	196410	METTL7B	5145	10.612	1.148
50075	J20	M-010305-	phospholip	200150	PLD5	4586	9.9433	1.8167
50075	J21	M-027049-	hypothetica	196415	LOC196415	4275	8.8187	2.9413
50075	J23	M-020839-	coiled-coil	196441	CCDC131	4036	4.2864	7.4736
50075	K02	M-031905-	AASA9217	167555	UNQ9217	3951	9.0863	2.6737
50075	K04	M-015620-	zinc finger	167465	ZNF366	5425	9.0138	2.7462
50075	K05	M-021642-	phosphatid	163404	PAP2D	5834	17.415	5.655
50075	K06	M-018373-	Lix1 homol	167410	LIX1	4819	15.626	3.866
50075	K07	M-018510-	fibronectin	163479	FNDC7	4313	12.659	0.899
50075	K08	M-008425-	DCP2 deca	167227	DCP2	5250	14.267	2.507
50075	K09	M-016923-	DENN/MAI	163486	DENND1B	4912	26.608	14.848
50075	K10	M-018505-	PAP associa	167153	PAPD4	4635	18.252	6.492
50075	K11	M-018507-	tudor doma	163589	TDRD5	3852	22.17	10.41
50075	K12	M-017807-	UDP glycos	167127	UGT3A2	4157	17.08	5.32
50075	K13	M-016470-	torsin A int	163590	TOR1AIP2	3633	11.12	0.64
50075	K14	M-028685-	integral me	166994	LOC166994	4117	13.796	2.036
50075	K15	M-016387-	calmodulin	163688	CALML6	4607	15.52	3.76
50075	K16	M-015619-	cell divisior	166979	CDC20B	4386	11.696	0.064
50075	K17	M-016455-	chromoson	163747	C1orf177	4424	8.7703	2.9897
50075	K18	M-018775-	sphingomy	166929	SGMS2	5168	11.165	0.595
50075	K19	M-017737-	small prolir	163778	SPRR4	5225	15.12	3.36
50075	K20	M-016997-	hypothetica	166863	MGC27016	6496	21.059	9.299
50075	K21	M-031887-	ankyrin rep	163782	ANKRD38	5879	21.075	9.315
50075	K23	M-019156-	spindle ass	163786	SASS6	3498	8.3476	3.4124
50075	L02	M-016187-	Tctex1 dom	200132	TCTEX1D1	4474	9.0076	2.7524
50075	L04	M-021928-	chromoson	200095	C1orf67	5598	11.415	0.345
50075	L05	M-018829-	chromoson	196446	C12orf28	5282	13.044	1.284
50075	L06	M-016435-	hypothetica	200058	FLJ23867	5384	19.781	8.021
50075	L07	M-018495-	hypothetica	196463	LOC196463	5476	8.8386	2.9214
50075	L08	M-019364-	neuroblast	200030	NBPF11	4870	7.0431	4.7169
50075	L09	M-015825-	family with	196472	FAM71C	6570	15.342	3.582
50075	L10	M-021796-	coiled-coil	200014	CC2D1B	4446	11.876	0.116
50075	L11	M-015795-	chromoson	196477	C12orf12	4364	17.851	6.091
50075	L12	M-007348-	solute carri	200010	SLC5A9	3942	16.159	4.399
50075	L13	M-027344-	family with	196483	FAM86A	3291	9.8754	1.8846
50075	L14	M-021800-	CUB domai	200008	CDCP2	2742	10.795	0.965
50075	L15	M-016372-	chromoson	196500	C12orf53	5191	13.215	1.455
50075	L16	M-018651-	chromoson	199990	C1orf86	4197	10.031	1.729

50075	L17	M-018776-	DCP1 deca	196513	DCP1B	4451	11.256	0.504
50075	L18	M-009123-	cytochrom	199974	CYP4Z1	4249	9.5552	2.2048
50075	L19	M-027115-	AF-1 specif	196515	FLJ30092	4604	9.3397	2.4203
50075	L20	M-018940-	transmem	199964	TMEM61	2496	9.8558	1.9042
50075	L21	M-003867-	transmem	196527	TMEM16F	4972	9.7949	1.9651
50075	L23	M-026945-	AT rich inte	196528	ARID2	5078	9.8858	1.8742
50075	M02	M-018468-	Ras associa	166824	RASSF6	4664	5.3816	6.3784
50075	M04	M-017437-	tigger tran	166815	TIGD2	3524	9.336	2.424
50075	M05	M-016456-	chromoso	163859	C1orf55	2714	8.622	3.138
50075	M06	M-007154-	zinc finger	166793	ZNF509	4846	22.967	11.207
50075	M07	M-017181-	chromoso	163882	C1orf71	6604	16.172	4.412
50075	M08	M-007153-	tripartite	166655	TRIM60	6216	8.269	3.491
50075	M09	M-032035-	family with	163933	FAM43B	6071	7.2146	4.5454
50075	M10	M-024221-	G protein-	166647	GPR125	5993	6.7913	4.9687
50075	M11	M-009902-	peptidylpr	164022	PPIAL4	6069	11.155	0.605
50075	M12	M-015617-	Bardet-Bie	166379	BBS12	3996	19.77	8.01
50075	M13	M-021627-	HFM1, ATP	164045	HFM1	3117	9.5605	2.1995
50075	M14	M-008418-	spermatog	166378	SPATA5	3069	10.231	1.529
50075	M15	M-017182-	chromoso	164127	C1orf65	5416	15.214	3.454
50075	M16	M-032036-	kelch dom	166348	KLHDC6	4789	7.0161	4.7439
50075	M17	M-017589-	WAP four-	164237	WFDC13	3597	5.9494	5.8106
50075	M18	M-023495-	prickle ho	166336	PRICKLE2	4517	13.017	1.257
50075	M19	M-015754-	adenomat	164284	APCDD1L	4606	11.572	0.188
50075	M20	M-009047-	carbohydr	166012	CHST13	4864	14.679	2.919
50075	M21	M-017183-	chromoso	164312	C20orf75	4423	11.282	0.478
50075	M23	M-024287-	tubulin tyr	164395	TTLL9	3584	3.5993	8.1607
50075	N02	M-027481-	hypothetic	199899	LOC19989	4032	8.4573	3.3027
50075	N04	M-016433-	family with	199870	FAM76A	4083	12.172	0.412
50075	N05	M-016238-	similar to h	196549	LOC19654	5204	5.9185	5.8415
50075	N06	M-017007-	asparagine	199857	ALG14	4540	7.4009	4.3591
50075	N07	M-016150-	chromoso	196740	C10orf72	4190	9.4272	2.3328
50075	N08	M-010977-	late cornif	199834	LCE4A	3876	10.243	1.517
50075	N09	M-008470-	polyamine	196743	PAOX	4654	14.224	2.464
50075	N10	M-031132-	hypothetic	199800	LOC19980	5137	12.712	0.952
50075	N11	M-015799-	family with	196792	FAM24B	4823	9.2266	2.5334
50075	N12	M-010692-	family with	199786	FAM129C	4126	5.1381	6.6219
50075	N13	M-021957-	hypothetic	196913	LOC19691	3279	11.131	0.629
50075	N14	M-016244-	zinc finger	199777	ZNF626	5240	16.031	4.271
50075	N15	M-016412-	chromoso	196951	C15orf33	4647	5.7241	6.0359
50075	N16	M-017011-	U2 small n	199746	U2AF1L4	5529	3.9067	7.8533
50075	N17	M-019306-	chromoso	196968	C15orf51	3708	13.754	1.994
50075	N18	M-021459-	THAP dom	199745	THAP8	3982	6.5043	5.2557
50075	N19	M-022265-	hypothetic	196993	LOC19699	5413	12.895	1.135
50075	N20	M-004302-	cell adhesi	199731	CADM4	4371	5.9483	5.8117
50075	N21	M-022268-	GRAM do	196996	GRAMD2	4536	6.5917	5.1683
50075	N23	M-030411-	hypothetic	197003	MGC15885	3399	6.5313	5.2287
50075	O02	M-007152-	ring finger	165918	RNF168	5054	13.376	1.616

50075	O04	M-019311-	cardiomyo	165904	CMYA1	2438	12.551	0.791
50075	O05	M-018314-	coiled-coil	164592	CCDC116	4297	10.566	1.194
50075	O06	M-016875-	DnaJ (Hsp4	165721	DNAJB8	5759	16.982	5.222
50075	O07	M-018982-	calcium bir	164633	CABP7	4472	10.756	1.004
50075	O08	M-017186-	poly (ADP-r	165631	PARP15	3885	6.0489	5.7111
50075	O09	M-006052-	transmemb	164656	TMPRSS6	3009	9.0395	2.7205
50075	O10	M-015380-	DEAQ box p	165545	DQX1	4806	14.128	2.368
50075	O11	M-019144-	apolipopro	164668	APOBEC3H	2582	9.45	2.31
50075	O12	M-010967-	C-type lecti	165530	CLEC4F	3323	16.642	4.882
50075	O13	M-017184-	WBP2 N-te	164684	WBP2NL	3264	11.734	0.026
50075	O14	M-019140-	UBX domai	165324	UBXD4	3914	7.6392	4.1208
50075	O15	M-017857-	WD repeat	164781	WDR69	4310	22.831	11.071
50075	O16	M-018745-	complemer	165257	C1QL2	4826	15.893	4.133
50075	O17	M-027218-	LON peptid	164832	LONRF2	3178	7.5205	4.2395
50075	O18	M-018304-	KIAA1946	165215	KIAA1946	5365	11.892	0.132
50075	O19	M-016986-	coiled-coil	165055	CCDC138	5812	16.655	4.895
50075	O20	M-027280-	similar to R	165186	LOC16518€	5132	12.763	1.003
50075	O21	M-023118-	hypothetica	165057	FLJ39061	4560	8.0263	3.7337
50075	O23	M-017185-	hypothetica	165100	MGC35154	3146	8.932	2.828
50075	P02	M-019177-	gametoger	199720	GGN	5	40	28.24
50075	P04	M-023619-	hypothetica	199714	MGC35045	4691	8.8894	2.8706
50075	P05	M-022259-	lactase-like	197021	LCTL	2649	14.76	3
50075	P06	M-016890-	NLR family,	199713	NLRP7	2699	15.154	3.394
50075	P07	M-030657-	hypothetica	197187	MGC23284	4535	11.621	0.139
50075	P08	M-016432-	zinc finger	199704	ZNF585A	2848	9.691	2.069
50075	P09	M-016611-	transmemb	197196	TMEM148	4230	6.1229	5.6371
50075	P10	M-016415-	DAN doma	199699	DAND5	3663	10.893	0.867
50075	P11	M-008761-	lactate deh	197257	LDHD	2892	9.8893	1.8707
50075	P12	M-017826-	chromosom	199675	C19orf59	2216	13.538	1.778
50075	P13	M-018832-	zinc finger	197320	ZNF778	2351	21.182	9.422
50075	P14	M-016484-	tetratricop	199223	TTC21A	3315	7.632	4.128
50075	P15	M-017808-	hypothetica	197322	LOC197322	3692	6.6631	5.0969
50075	P16	M-018494-	DAZ intera	199221	DZIP1L	1824	6.0307	5.7293
50075	P17	M-017531-	WD repeat	197335	WDR90	2928	9.1872	2.5728
50075	P18	M-016413-	zinc finger	197407	ZNF553	2719	18.205	6.445
50075	P19	M-021344-	similar to R	197336	LOC19733€	2822	8.6109	3.1491
50075	P20	M-007157-	non-SMC e	197370	NSMCE1	3981	8.8671	2.8929
50075	P21	M-022614-	hypothetica	197350	LOC19735C	2904	11.433	0.327
50075	P23	M-008796-	NLR family,	197358	NLRC3	2047	6.8393	4.9207
					MAD	3946.5	11.7565	3.242
					MAD3			9.726
					MADc			4.79816
50075	C22					4627	47.439	
50075	D22					3571	42.733	
50075	E22					4167	50.204	
50075	F22					3721	45.364	
					mn	4021.5	46.435	

					sd	476.463	3.165713
50075	G22					2167	6.1375
50075	H22					1642	6.0901
50075	I22					2767	10.481
50075	J22					2196	5.4189
					mn	2193	7.031875
					sd	459.6238	2.322714
					3psSD		6.968141
					3ngSD		9.49714
					SumSD		16.46528
					DiffMn		39.40313
					SmovrDiff		0.417867
					1minus		0.582133
50075	G03	M-003290-	polo-like ki	5347	PLK1 SMA	682	11.584
50075	H03	M-003290-	polo-like ki	5347	PLK1 SMA	973	12.436
50075	I03	D-001206-	siControl non-targetin			4854	17.347
50075	J03	D-001206-	siControl non-targetin			2622	10.984
50075	K03	D-001600-	siGLO RISC-free siRNA			6496	24.092
50075	L03	D-001600-	siGLO RISC-free siRNA			6444	22.408

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-2.20553	2093	5.8767	3.6133	-0.8577	3767	7.433	3.407	-0.69304
0.328355	3956	12.968	3.478	0.825393	5875	22.502	11.662	2.373151
1.230367	3352	15.334	5.844	1.386953	4331	18.702	7.862	1.599939
-0.50015	2578	7.6416	1.8484	-0.4388	2600	11.538	0.698	0.14223
-0.71023	2201	8.6324	0.8576	-0.20364	3024	12.136	1.296	0.26391
-1.03602	2481	7.6582	1.8318	-0.43486	2889	11.423	0.583	0.118831
-0.16704	3535	11.089	1.599	0.379421	3048	18.602	7.762	1.579591
0.245823	2751	13.74	4.25	1.008624	3063	25.955	15.115	3.075757
-0.4499	3621	11.765	2.275	0.539866	3234	17.718	6.878	1.399718
-0.66027	3383	3.6063	5.8837	-1.39657	2205	8.5261	2.3139	-0.47062
-1.09688	2645	7.9395	1.5505	-0.3681	3079	8.4768	2.3632	-0.48065
-0.50611	3060	7.5163	1.9737	-0.46854	2495	16.834	5.994	1.219844
1.073224	3700	10.297	0.807	0.191443	3322	17.971	7.131	1.451197
1.225574	4393	8.2404	1.2496	-0.29668	4263	9.8288	1.0112	-0.20555
-0.01136	2895	8.532	0.958	-0.22747	3368	13.361	2.521	0.513169
0.291466	4670	12.484	2.994	0.710518	3468	14.937	4.097	0.833848
-0.64391	3018	7.5878	1.9022	-0.45157	2754	11.765	0.925	0.18842
-0.53127	1478	9.8782	0.3882	0.092043	2818	13.414	2.574	0.523953
-0.63443	2624	17.797	8.307	1.971536	4599	19.156	8.316	1.692318
-1.463	2902	7.6154	1.8746	-0.44502	2050	15.561	4.721	0.960818
-1.28954	4607	7.0979	2.3921	-0.56785	5737	10.528	0.312	-0.06328
-1.21411	6278	6.3555	3.1345	-0.74405	3628	5.237	5.603	-1.13988
-0.94278	4075	5.7423	3.7477	-0.8896	3568	10.006	0.834	-0.1695
0.957555	5299	12.399	2.909	0.690344	3785	17.384	6.544	1.331757
-0.55955	4515	4.4075	5.0825	-1.2064	3355	5.9911	4.8489	-0.98644
-1.56362	3312	3.2005	6.2895	-1.49288	1664	6.6106	4.2294	-0.86038
0.677864	4027	12.739	3.249	0.771041	3713	18.126	7.286	1.482736
-0.26646	3450	4.7826	4.7074	-1.11738	2942	15.058	4.218	0.858469
-0.2254	2643	5.4862	4.0038	-0.95038	1255	24.143	13.303	2.707057
-1.25296	2455	3.8289	5.6611	-1.34373	2638	8.3397	2.5003	-0.50855
1.278303	5059	13.422	3.932	0.933148	3493	29.259	18.419	3.748045
0.678072	4990	9.7996	0.3096	0.073387	3613	13.784	2.944	0.59924
2.244298	5523	14.919	5.429	1.288455	2882	13.602	2.762	0.562207
1.099692	6026	10.969	1.479	0.350939	3560	17.051	6.211	1.263999
-0.2181	3122	9.1288	0.3612	-0.08582	2489	13.941	3.101	0.631185
-0.11744	4913	9.9125	0.4225	0.100184	4139	10.993	0.153	0.031335
-1.48561	4300	11.395	1.905	0.452049	2786	5.5276	5.3124	-1.08075
-0.58579	3668	12.459	2.969	0.704584	3799	16.504	5.664	1.152697
-0.38494	4406	12.506	3.016	0.71574	4926	14.84	4	0.814111
0.525097	4834	11.46	1.97	0.467476	5864	14.905	4.065	0.827337
0.939423	4212	3.0152	6.4748	-1.53686	5642	14.286	3.446	0.701385
-0.16371	4333	0.90007	8.58993	-2.03888	5373	10.776	0.064	-0.01282
1.68054	4711	4.2242	5.2658	-1.24991	3736	13.597	2.757	0.561189
2.289523	5319	4.1173	5.3727	-1.27528	3946	11.759	0.919	0.187199
1.533192	5114	4.9276	4.5624	-1.08296	2961	9.5238	1.3162	-0.26761
0.755602	4283	4.5295	4.9605	-1.17745	2636	15.099	4.259	0.866812

1.303312	4844	6.3584	3.1316	-0.74337	3428	11.464	0.624	0.127173
0.377124	3613	3.1276	6.3624	-1.51018	1632	6.25	4.59	-0.93376
1.726599	3787	5.2284	4.2616	-1.01157	2544	10.574	0.266	-0.05392
1.570498	3482	4.4515	5.0385	-1.19596	2986	10.851	0.011	0.002442
1.362918	3295	4.4613	5.0287	-1.19364	2143	9.6127	1.2273	-0.24952
0.358783	4489	6.6384	2.8516	-0.67691	2803	10.275	0.565	-0.11476
0.075967	3277	6.5609	2.9291	-0.6953	1826	9.8576	0.9824	-0.19969
2.711977	3637	6.7363	2.7537	-0.65367	2094	18.529	7.689	1.564738
-0.14037	4262	6.2177	3.2723	-0.77676	1868	9.3148	1.5252	-0.31014
0.682866	3828	8.3072	1.1828	-0.28083	1795	9.805	1.035	-0.2104
-0.0743	3812	7.1616	2.3284	-0.55273	3733	6.2952	4.5448	-0.92456
0.980688	5435	9.6964	0.2064	0.048893	4961	9.1917	1.6483	-0.33519
-0.28188	5873	9.1946	0.2954	-0.07021	3904	7.582	3.258	-0.66272
1.112197	4722	18.149	8.659	2.055081	4606	15.241	4.401	0.895705
-1.97163	5162	4.2813	5.2087	-1.23636	4565	3.7021	7.1379	-1.45219
-1.25217	5493	7.1546	2.3354	-0.55439	5125	9.5415	1.2985	-0.26401
-1.3591	5958	8.006	1.484	-0.35232	4351	2.9878	7.8522	-1.59754
0.782696	6754	21.913	12.423	2.94845	4630	13.693	2.853	0.580723
2.161141	5901	18.387	8.897	2.11157	4290	9.627	1.213	-0.24661
-1.67445	4178	8.2815	1.2085	-0.28693	2772	3.5354	7.3046	-1.48611
-0.3467	5858	8.9109	0.5791	-0.13754	4516	11.492	0.652	0.13287
0.153913	6419	14.099	4.609	1.093831	4022	10.567	0.273	-0.05535
1.441907	4977	18.927	9.437	2.239736	2742	24.435	13.595	2.766472
-0.03324	3372	6.3167	3.1733	-0.75326	1934	9.7208	1.1192	-0.22753
0.459239	4932	8.1711	1.3189	-0.31313	3032	9.7625	1.0775	-0.21904
-1.39012	4988	3.2478	6.2422	-1.48165	2282	2.2349	8.6051	-1.75074
2.015877	6313	16.727	7.237	1.717576	3403	23.597	12.757	2.595959
0.010733	5656	11.97	2.48	0.588522	2282	12.445	1.605	0.326784
0.673487	6147	10.883	1.393	0.330528	3964	16.372	5.532	1.125838
-0.41535	6067	8.3402	1.1498	-0.27299	2906	11.356	0.516	0.105198
1.336867	6091	12.789	3.299	0.782908	4011	16.006	5.166	1.051365
2.076525	7396	24.486	14.996	3.559141	4360	17.087	6.247	1.271324
0.80583	5343	17.294	7.804	1.852151	4010	20.224	9.384	1.909631
1.050298	6132	24.119	14.629	3.472035	6177	25.805	14.965	3.045236
-0.89126	6362	5.8315	3.6585	-0.86842	6485	15.621	4.781	0.973027
-0.29188	4637	4.5288	4.9612	-1.17761	2891	8.1287	2.7113	-0.55148
-0.55113	4569	3.9177	5.5723	-1.32266	4334	10.083	0.757	-0.15383
1.447326	5647	6.7469	2.7431	-0.65116	4326	20.989	10.149	2.065291
2.368512	6079	5.7082	3.7818	-0.89769	3550	20.338	9.498	1.932827
0.211852	5448	7.5808	1.9092	-0.45324	2820	10.603	0.237	-0.04802
0.863352	5279	4.3758	5.1142	-1.21393	2750	15.527	4.687	0.9539
0.233735	3376	4.1469	5.3431	-1.26826	2834	21.348	10.508	2.138339
1.689919	4985	5.9579	3.5321	-0.83842	3023	10.023	0.817	-0.16604
3.050857	4646	12.118	2.628	0.62365	2813	29.897	19.057	3.877863
2.015877	4699	12.088	2.598	0.616529	3187	20.835	9.995	2.033955
1.347079	4925	6.0102	3.4798	-0.82601	3223	11.387	0.547	0.111505
-0.1956	5122	5.2714	4.2186	-1.00136	2995	12.654	1.814	0.369311

-0.19184	4605	5.1683	4.3217	-1.02583	2968	11.894	1.054	0.214668
0.433395	3840	4.6354	4.8546	-1.15231	2511	9.4783	1.3617	-0.27687
2.037969	5044	13.224	3.734	0.886154	3590	22.173	11.333	2.306208
1.888328	5328	11.205	1.715	0.406953	4136	19.802	8.962	1.823764
0.926709	5875	11.966	2.476	0.587573	3521	18.773	7.933	1.614386
0.244781	5614	7.8019	1.6881	-0.40076	3225	9.2093	1.6307	-0.33161
0.076175	5813	7.036	2.454	-0.58254	6469	14.608	3.768	0.766905
1.25892	5856	17.657	8.167	1.938307	5666	12.46	1.62	0.329836
0.542395	5439	11.951	2.461	0.584013	5169	11.008	0.168	0.034388
-0.46045	3630	8.0165	1.4735	-0.34982	3922	5.8899	4.9501	-1.00703
0.745807	5328	14.94	5.45	1.293439	4840	14.442	3.602	0.733127
-0.84526	4297	10.472	0.982	0.232979	3298	7.641	3.199	-0.65072
2.125919	5032	14.865	5.375	1.275638	4084	15.622	4.782	0.97323
0.023863	5449	12.131	2.641	0.626735	4636	8.9733	1.8667	-0.37963
-0.50569	4561	7.1914	2.2986	-0.54566	3673	23.822	12.982	2.641741
-0.3246	4235	9.6576	0.1676	0.039684	3314	9.0223	1.8177	-0.36966
0.004689	4379	11.076	1.586	0.376335	3234	5.3185	5.5215	-1.12329
0.163083	4395	12.332	2.842	0.674441	4036	9.1675	1.6725	-0.34011
-0.15704	4142	10.357	0.867	0.205684	2351	9.698	1.142	-0.23217
0.522596	4176	20.618	11.128	2.641088	2878	20.188	9.348	1.902306
-0.93557	6003	8.4958	0.9942	-0.23606	3343	6.6707	4.1693	-0.84815
0.794784	4982	16.038	6.548	1.554045	3184	13.222	2.382	0.484886
0.565946	5861	13.087	3.597	0.853637	4130	11.695	0.855	0.174176
-0.83267	5742	8.3595	1.1305	-0.26841	4317	5.9069	4.9331	-1.00357
0.940465	4033	17.307	7.817	1.855236	3224	13.555	2.715	0.552643
0.27917	4876	14.848	5.358	1.271603	5027	13.825	2.985	0.607582
-0.41741	5937	15.766	6.276	1.489487	4885	13.327	2.487	0.506251
-0.76615	4725	12.127	2.637	0.625786	5740	11.063	0.223	0.045579
-0.56011	5288	13.294	3.804	0.902768	5916	10.311	0.529	-0.10744
0.352531	3701	17.914	8.424	1.999305	4543	10.302	0.538	-0.10927
-0.16454	3766	7.3818	2.1082	-0.50047	4686	6.9996	3.8404	-0.78123
1.150337	4121	11.017	1.527	0.362332	5391	7.7908	3.0492	-0.62024
0.097016	3782	9.4923	0.0023	0.000451	4870	7.1253	3.7147	-0.75565
-1.0177	4313	7.4194	2.0706	-0.49154	4070	7.8133	3.0267	-0.61566
2.088405	3901	15.381	5.891	1.398108	4432	10.672	0.168	-0.03398
-0.85081	3423	10.926	1.436	0.340733	4474	13.299	2.459	0.500553
0.021571	3380	5.4142	4.0758	-0.96747	2416	5.0911	5.7489	-1.16957
1.164509	4385	15.507	6.017	1.428014	3667	11.699	0.859	0.17499
1.154713	2987	11.65	2.16	0.512572	3708	6.5534	4.2866	-0.87202
0.499045	4559	6.1198	3.3702	-0.8	4123	6.9124	3.9276	-0.79897
0.724757	5128	12.5	3.01	0.714316	3541	13.781	2.941	0.598629
1.320819	4607	9.4422	0.0478	-0.01144	4181	9.3997	1.4403	-0.29286
-0.31939	4797	9.7353	0.2453	0.058126	4422	5.9023	4.9377	-1.0045
0.218104	4987	10.227	0.737	0.174829	5163	10.304	0.536	-0.10886
0.088471	5310	16.591	7.101	1.685297	5462	11.553	0.713	0.145283
0.239779	3342	9.9042	0.4142	0.098214	4297	7.5169	3.3231	-0.67597
-0.64846	5743	11.806	2.316	0.549598	4359	6.5382	4.3018	-0.87511

0.279586	4495	6.9855	2.5045	-0.59453	4450	11.438	0.598	0.121883
-0.10306	3050	10.918	1.428	0.338835	3870	16.925	6.085	1.238361
-1.1311	3983	3.7409	5.7491	-1.36462	5431	10.992	0.152	0.031132
5.269207	3336	24.281	14.791	3.510485	3890	40.026	29.186	5.938881
-1.01268	4233	12.733	3.243	0.769617	5176	21.522	10.682	2.173744
-0.55636	4675	5.1551	4.3349	-1.02896	5057	17.58	6.74	1.371638
1.243081	3608	9.3404	0.1496	-0.0356	3061	16.629	5.789	1.178131
-0.31835	3108	9.3308	0.1592	-0.03788	3370	12.7	1.86	0.378671
-1.40352	2507	6.5417	2.9483	-0.69986	2574	15.385	4.545	0.925006
0.962765	3611	16.284	6.794	1.612432	3041	21.736	10.896	2.217288
-0.34419	3531	8.4962	0.9938	-0.23597	3638	12.974	2.134	0.434423
-0.43146	3927	11.332	1.842	0.437096	3093	22.729	11.889	2.419341
0.823962	3460	16.301	6.811	1.616466	3199	24.758	13.918	2.832195
-0.66478	2781	6.041	3.449	-0.8187	2238	9.6515	1.1885	-0.24163
-0.61057	4211	6.673	2.817	-0.6687	4091	10.144	0.696	-0.14142
1.409811	4844	21.243	11.753	2.789429	4680	30.128	19.288	3.924867
0.072632	4178	8.808	0.682	-0.16196	3581	10.332	0.508	-0.10316
-0.81615	4132	8.4221	1.0679	-0.25356	4794	13.058	2.218	0.451515
-0.70975	4550	8	1.49	-0.35374	4064	7.6772	3.1628	-0.64335
-1.76005	4104	9.2349	0.2551	-0.06064	3999	10.828	0.012	-0.00224
-0.32606	5282	9.7122	0.2222	0.052643	5452	19.699	8.859	1.802806
-0.73551	3877	9.8272	0.3372	0.079938	2996	14.119	3.279	0.667404
1.01466	5816	15.973	6.483	1.538617	5286	25.331	14.491	2.948788
0.403801	4423	8.9306	0.5594	-0.13287	4082	20.186	9.346	1.901899
0.954845	5101	17.016	7.526	1.786169	4185	22.843	12.003	2.442537
-0.96816	2960	10.405	0.915	0.217076	3568	12.584	1.744	0.355067
0.669736	4797	17.052	7.562	1.794713	3931	19.995	9.155	1.863035
-0.3419	4805	15.983	6.493	1.540991	4183	14.535	3.695	0.752051
1.687418	3980	15.025	5.535	1.313613	2846	10.014	0.826	-0.16787
3.23301	4155	26.835	17.345	4.116666	3507	31.965	21.125	4.298654
-0.88999	2261	9.1552	0.3348	-0.07956	2526	7.5218	3.3182	-0.67497
0.613881	2765	10.38	0.89	0.211143	2393	11.868	1.028	0.209378
2.388728	4205	10.654	1.164	0.276175	4043	13.653	2.813	0.572584
0.761021	5124	19.496	10.006	2.374786	4633	23.441	12.601	2.564216
-0.60381	2856	8.6134	0.8766	-0.20815	2760	6.8478	3.9922	-0.81212
-0.52183	3412	4.4549	5.0351	-1.19515	3057	8.8649	1.9751	-0.40168
0.260829	4126	12.312	2.822	0.669695	5361	7.6665	3.1735	-0.64553
0.674946	5003	15.191	5.701	1.353013	5315	14.374	3.534	0.719291
1.520896	4780	16.234	6.744	1.600564	5224	17.037	6.197	1.26115
2.268682	3306	18.603	9.113	2.162836	6341	22.315	11.475	2.335101
-0.64312	4956	7.3043	2.1857	-0.51886	4939	4.4543	6.3857	-1.29914
0.696204	3339	9.5538	0.0638	0.015048	4514	11.453	0.613	0.124935
0.221231	3733	11.144	1.654	0.392475	4666	11.595	0.755	0.153829
1.165759	4478	11.009	1.519	0.360433	4330	9.7921	1.0479	-0.21302
-0.07805	3070	10.782	1.292	0.306556	5129	10.684	0.156	-0.03154
0.293342	2776	9.2939	0.1961	-0.04664	4043	3.0918	7.7482	-1.57638
1.510892	3548	16.404	6.914	1.640913	4357	7.3445	3.4955	-0.71105

0.316684	3534	3.4522	6.0378	-1.43314	4042	3.9584	6.8816	-1.40004
1.465666	3224	20.192	10.702	2.539979	3883	6.4641	4.3759	-0.89019
0.728925	2557	14.314	4.824	1.144861	3068	7.0078	3.8322	-0.77956
0.746849	2563	11.627	2.137	0.507113	4127	11.437	0.597	0.121679
-0.19705	2944	11.719	2.229	0.528949	4055	8.2367	2.6033	-0.52951
-0.06867	2543	10.145	0.655	0.155366	3567	9.672	1.168	-0.23746
0.40651	3322	18.182	8.692	2.062914	3419	8.4235	2.4165	-0.4915
-0.17663	1763	3.7436	5.7464	-1.36398	3672	6.4815	4.3585	-0.88665
1.621142	4346	23.424	13.934	3.30708	4281	10.371	0.469	-0.09523
-0.23853	3867	8.7665	0.7235	-0.17181	4753	7.0692	3.7708	-0.76707
-0.37789	4241	12.898	3.408	0.808779	3877	2.992	7.848	-1.59668
-0.61228	4450	5.1685	4.3215	-1.02578	3662	4.26	6.58	-1.33867
-1.55687	5580	5.6989	3.7911	-0.8999	4444	2.2502	8.5898	-1.74762
-0.5565	2497	3.4842	6.0058	-1.42555	5208	5.2803	5.5597	-1.13107
-0.57161	2597	3.5811	5.9089	-1.40255	3271	3.3017	7.5383	-1.53367
1.179306	3351	6.3265	3.1635	-0.75094	4194	3.958	6.882	-1.40012
0.806455	3078	7.18	2.31	-0.54836	4965	3.1621	7.6779	-1.56207
0.188093	2924	2.736	6.754	-1.60313	4385	3.6488	7.1912	-1.46304
0.523221	2268	8.9947	0.4953	-0.11765	6139	8.9754	1.8646	-0.3792
3.095249	2911	14.943	5.453	1.294151	5275	13.668	2.828	0.575636
1.353748	2850	11.649	2.159	0.512334	5529	8.3198	2.5202	-0.5126
2.170311	3982	11.301	1.811	0.429738	4491	5.923	4.917	-1.00029
1.109488	2957	10.889	1.399	0.331952	4133	8.541	2.299	-0.46759
-0.13266	2455	5.2138	4.2762	-1.01503	4264	6.2617	4.5783	-0.93137
0.425059	3917	6.7399	2.7501	-0.65282	3223	7.7567	3.0833	-0.62718
0.784363	4303	12.619	3.129	0.74256	6053	16.075	5.235	1.065405
-0.01261	3700	7.9459	1.5441	-0.36658	6093	8.9283	1.9117	-0.38878
-0.62236	1722	4.3554	5.1346	-1.21877	5005	7.7522	3.0878	-0.62809
-0.12328	3518	10.404	0.914	0.216839	4924	7.5345	3.3055	-0.67239
0.700998	4356	12.879	3.389	0.80427	5109	8.945	1.895	-0.38539
1.938764	3407	14.441	4.951	1.175004	6382	22.422	11.582	2.356873
1.942099	2852	16.129	6.639	1.575643	5979	15.036	4.196	0.853993
-0.71046	1521	2.1696	7.3204	-1.73756	3464	4.2148	6.6252	-1.34787
-0.57291	2973	3.4645	6.0255	-1.43022	6319	15.05	4.21	0.856841
-0.07117	3349	8.5399	0.9501	-0.2256	5463	8.7498	2.0902	-0.4251
0.268332	3658	11.427	1.937	0.459644	4045	9.5674	1.2726	-0.25874
1.672412	4288	12.01	2.52	0.598016	5553	8.9141	1.9259	-0.39167
-0.60813	2496	9.4151	0.0749	-0.01787	5923	8.3573	2.4827	-0.50497
-0.98233	2397	7.0088	2.4812	-0.589	6023	7.737	3.103	-0.63119
0.747266	2946	10.862	1.372	0.325543	7130	15.961	5.121	1.042209
0.024905	2969	13.506	4.016	0.953085	5384	16.048	5.208	1.059911
1.270174	3182	14.645	5.155	1.223422	4746	12.979	2.139	0.435441
0.917539	2344	12.585	3.095	0.73449	2594	7.2089	3.6311	-0.73864
-0.39205	2386	9.6815	0.1915	0.045357	3363	8.1178	2.7222	-0.5537
-0.20039	2561	9.4885	0.0015	-0.00045	3578	12.521	1.681	0.342248
0.303971	3248	15.148	5.658	1.342807	6147	17.488	6.648	1.352918
-0.35962	3322	9.693	0.203	0.048086	3627	7.2512	3.5888	-0.73003

-0.10431	3463	8.7785	0.7115	-0.16897	4952	8.441	2.399	-0.48794
-0.45878	3798	16.403	6.913	1.640676	5552	9.0778	1.7622	-0.35836
-0.50369	3248	15.086	5.596	1.328091	5725	11.878	1.038	0.211413
-0.39613	2469	20.656	11.166	2.650107	2795	12.129	1.289	0.262485
-0.40882	4479	11.878	2.388	0.566687	4665	11.683	0.843	0.171735
-0.38988	5512	10.867	1.377	0.32673	5787	11.059	0.219	0.044765
-1.32861	4987	11.771	2.281	0.541291	6068	12.343	1.503	0.306029
-0.50446	2973	10.225	0.735	0.174354	6100	12.295	1.455	0.296262
-0.65327	2682	15.809	6.319	1.499692	3060	10.85	0.01	0.002238
2.336416	5003	24.265	14.775	3.506687	5398	22.193	11.353	2.310277
0.920249	3415	17.218	7.728	1.834112	5024	16.182	5.342	1.087177
-0.72684	4372	11.985	2.495	0.592083	5184	12.191	1.351	0.275101
-0.94659	3782	10.709	1.219	0.289229	5516	9.5178	1.3222	-0.26883
-1.03481	4307	13.281	3.791	0.899683	4641	7.4337	3.4063	-0.6929
-0.12536	4098	15.642	6.152	1.460056	5721	12.882	2.042	0.415703
1.670119	2740	18.577	9.087	2.156665	4203	11.754	0.914	0.186181
-0.45768	3257	7.6451	1.8449	-0.43797	3861	9.9197	0.9203	-0.18706
-0.31793	3152	17.449	7.959	1.888939	3599	14.448	3.608	0.734348
0.720589	3671	9.5614	0.0714	0.016852	4987	12.873	2.033	0.413872
-0.98796	3571	9.7452	0.2552	0.060476	5071	14.06	3.22	0.655399
-1.21028	2179	8.7655	0.7245	-0.17205	3387	4.2811	6.5589	-1.33438
0.262705	4880	12.234	2.744	0.651182	5696	8.8308	2.0092	-0.40862
-0.03845	4815	6.7913	2.6987	-0.64062	5011	6.805	4.035	-0.82083
0.609088	4377	11.675	2.185	0.518505	5216	10.755	0.085	-0.01709
-0.09889	4724	7.409	2.081	-0.49401	4224	10.133	0.707	-0.14365
-1.70007	3398	4.8852	4.6048	-1.09302	4881	6.1668	4.6732	-0.95068
-0.6876	5661	7.5782	1.9118	-0.45385	4944	6.4118	4.4282	-0.90083
0.086596	4538	7.4041	2.0859	-0.49517	4449	5.4169	5.4231	-1.10327
-1.21672	4626	4.2802	5.2098	-1.23662	6019	6.9281	3.9119	-0.79578
-0.90776	3482	7.668	1.822	-0.43254	4885	8.3316	2.5084	-0.5102
-0.48546	3499	2.4007	7.0893	-1.68271	4885	4.0532	6.7868	-1.38075
-0.31543	3094	11.054	1.564	0.371114	4917	12.345	1.505	0.306436
0.51426	3577	13.447	3.957	0.939082	4638	16.192	5.352	1.089212
0.199139	4092	11.779	2.289	0.543189	6175	12.713	1.873	0.381316
-0.52726	3487	11.356	1.866	0.442792	4850	15.835	4.995	1.016571
-1.37936	2470	1.9028	7.5872	-1.80088	3648	5.8662	4.9738	-1.01185
-0.13036	3193	9.5208	0.0308	0.007215	3739	18.534	7.694	1.565755
0.890862	3579	9.2763	0.2137	-0.05082	5006	13.044	2.204	0.448667
-1.25723	2772	11.688	2.198	0.521591	5390	19.647	8.807	1.792225
-1.636	3127	4.1573	5.3327	-1.26579	6238	12.744	1.904	0.387624
0.416305	1941	18.187	8.697	2.0641	3057	23.585	12.745	2.593517
-1.09463	2673	6.4347	3.0553	-0.72526	4414	7.5442	3.2958	-0.67042
0.237278	3467	12.374	2.884	0.68441	4586	22.372	11.532	2.346699
-1.21051	3390	5.7817	3.7083	-0.88024	3453	6.8636	3.9764	-0.8089
-1.07641	3262	6.5604	2.9296	-0.69542	4610	8.7636	2.0764	-0.4223
-1.089	1709	7.6068	1.8832	-0.44706	2973	9.519	1.321	-0.26859
0.337525	4388	9.7311	0.2411	0.057129	3760	4.6011	6.2389	-1.26927

0.165584	2305	8.026	1.464	-0.34757	3039	9.5426	1.2974	-0.26379
-0.24812	3358	4.6456	4.8444	-1.14989	3850	4.8571	5.9829	-1.21718
1.089063	4155	9.4344	0.0556	-0.01329	5781	7.9398	2.9002	-0.58992
-0.20852	3100	6.871	2.619	-0.6217	5274	4.7023	6.1377	-1.24868
-1.18954	3218	5.3449	4.1451	-0.98392	4165	6.1945	4.6455	-0.94505
-0.56626	2218	5.0947	4.3953	-1.0433	3607	8.234	2.606	-0.53006
0.494252	3062	6.3684	3.1216	-0.74099	5783	7.9543	2.8857	-0.58697
-0.48071	2301	3.9983	5.4917	-1.30353	3568	8.0157	2.8243	-0.57448
1.018203	1722	4.82	4.67	-1.1085	3092	5.4981	5.3419	-1.08675
-0.00469	1954	8.393	1.097	-0.26046	4138	5.3407	5.4993	-1.11878
-0.8581	3158	3.7049	5.7851	-1.37316	5560	6.9065	3.9335	-0.80017
2.308072	2332	11.407	1.917	0.454897	5488	19.843	9.003	1.832106
0.862101	2751	6.9429	2.5471	-0.60464	6770	18.656	7.816	1.590579
-0.88284	2240	6.7411	2.7489	-0.65253	4521	18.668	7.828	1.593021
0.02824	3402	10.729	1.239	0.293976	5685	19.402	8.562	1.742373
1.020912	3627	10.422	0.932	0.221111	6268	26.308	15.468	3.147585
0.209768	2496	11.058	1.568	0.372063	4166	15.963	5.123	1.042616
-0.77742	3966	7.9677	1.5223	-0.36141	5605	11.204	0.364	0.074269
-0.58866	2344	4.9488	4.5412	-1.07793	3916	13.994	3.154	0.64197
5.886319	2719	6.9511	2.5389	-0.60269	3723	2.0145	8.8255	-1.79558
-0.59754	3060	9.3137	0.1763	-0.04194	4682	3.994	6.846	-1.3928
0.625969	2018	5.1041	4.3859	-1.04107	5269	7.6865	3.1535	-0.64146
0.708084	2078	12.753	3.263	0.774364	4157	6.8078	4.0322	-0.82026
-0.02824	1721	6.8565	2.6335	-0.62514	5172	6.3805	4.4595	-0.9072
-0.43048	898	4.343	5.147	-1.22171	4387	1.6868	9.1532	-1.86226
-1.17412	2303	9.0317	0.4583	-0.10887	4375	1.5314	9.3086	-1.89388
-0.17996	1559	6.2861	3.2039	-0.76053	4056	4.8077	6.0323	-1.22723
-0.38915	1471	8.3617	1.1283	-0.26789	3933	4.8818	5.9582	-1.21215
0.371288	1578	10.963	1.473	0.349515	3906	8.8326	2.0074	-0.40826
1.964399	1892	15.751	6.261	1.485926	4497	13.898	3.058	0.622436
-0.8596	2548	7.5746	1.9154	-0.45471	5022	10.155	0.685	-0.13918
-1.06153	2062	5.4801	4.0099	-0.95183	4019	4.9764	5.8636	-1.1929
-1.19333	1928	4.3568	5.1332	-1.21844	2828	7.7086	3.1314	-0.63696
-0.53548	1241	7.6551	1.8349	-0.4356	2864	13.547	2.707	0.551016
1.343953	1397	6.9435	2.5465	-0.6045	2968	19.778	8.938	1.81888
-0.65558	2107	6.1224	3.3676	-0.79938	2371	11.135	0.295	0.060229
-0.60219	3420	9.269	0.221	-0.05255	4132	12.343	1.503	0.306029
-0.06742	2809	11.036	1.546	0.366841	3993	13.849	3.009	0.612466
-1.02481	2807	8.0513	1.4387	-0.34156	2295	9.6732	1.1668	-0.23721
	3774	9.4904	2.8468		4076	10.839	3.32065	
			8.5404				9.96195	
			4.213264				4.914562	
5049	50.485		5585	43.474				
6435	50.334		5339	54.392				
4737	45.303		4551	53.922				
6468	53.973		5863	53.045				
5672.25	50.02375		5334.5	51.20825				

908.8709	3.567962	564.4924	5.186295
2611	4.8257	2247	3.0263
3054	9.9214	2328	13.703
1358	8.542	2160	3.9352
2405	7.6507	2354	3.356
2357	7.73495	2272.25	6.005125
718.9414	2.152729	87.61421	5.14565
	6.458187		15.43695
	10.70389		15.55889
	17.16207		30.99583
3315.25	42.2888	3062.25	45.20313
	0.40583		0.685701
	0.59417		0.314299

699	12.876	899	4.3382
548	6.7518	929	19.268
4354	11.897	4466	16.749
3657	12.196	4052	6.0711
5301	11.47	7640	14.411
4453	11.812	7730	18.642

y

y

y

y

y
x debris c

y

y

y

y

y

y

y

y

					cell ct	% inf	AD
50076	A02	M-015469- spermatog	221178	SPATA13	1820	6.9231	2.3931
50076	A04	M-015468- EF-hand do	221154	EFHA1	1410	9.1489	4.6189
50076	A05	M-016502- hypothetic	201283	FLJ32065	894	5.7047	1.1747
50076	A06	M-017843- N-6 adenin	221143	N6AMT2	1308	9.1743	4.6443
50076	A07	M-018490- tripartite	201292	TRIM65	1274	12.323	7.793
50076	A08	M-031762- similar to h	221091	LOC221091	1380	12.029	7.499
50076	A09	M-022951- unc-13 ho	201294	UNC13D	1529	10.988	6.458
50076	A10	M-017861- ADP-ribosy	221079	ARL5B	1552	10.309	5.779
50076	A11	M-017410- RAD52 mo	201299	RDM1	1847	7.7423	3.2123
50076	A12	M-018822- NOL1/NOP	221078	NSUN6	1236	8.4951	3.9651
50076	A13	M-018953- spinster ho	201305	SPNS3	1662	7.5812	3.0512
50076	A14	M-007567- solute carri	221074	SLC39A12	1227	12.714	8.184
50076	A15	M-016503- F-box prote	201456	FBXO15	1521	7.1006	2.5706
50076	A16	M-026397- chromoso	221061	C10orf38	2503	5.0739	0.5439
50076	A17	M-018489- zinc finger	201514	ZNF584	645	12.093	7.563
50076	A18	M-016615- chromoso	221060	C10orf111	892	13.677	9.147
50076	A19	M-016504- zinc finger	201516	ZSCAN4	609	13.465	8.935
50076	A20	M-016194- chromoso	221044	C10orf49	1099	6.0965	1.5665
50076	A21	M-017859- STT3, subu	201595	STT3B	935	7.5936	3.0636
50076	A23	M-017812- dynein hea	201625	DNHD2	726	9.7796	5.2496
50076	B02	M-027182- similar to	388726	LOC38872	899	4.2269	0.3031
50076	B04	M-032074- hypothetic	388685	FLJ39739	1734	9.3426	4.8126
50076	B05	M-017625- copine II	221184	CPNE2	925	2.8108	1.7192
50076	B06	M-026285- placenta-s	219348	PLAC9	1982	1.4632	3.0668
50076	B07	M-030630- plasma kall	221191	Klkbl4	2176	3.3088	1.2212
50076	B08	M-016614- centrosom	220766	CEP170L	2988	4.6854	0.1554
50076	B09	M-008602- carboxyles	221223	CES7	1994	7.4223	2.8923
50076	B10	M-018398- hypothetic	253815	FLJ36335	1429	3.9888	0.5412
50076	B11	M-015470- chromoso	221241	C18orf20	2463	5.1563	0.6263
50076	B12	M-018973- hypothetic	220081	FLJ32682	2007	8.6697	4.1397
50076	B13	M-028586- chromoso	221261	C6orf184	2817	5.9638	1.4338
50076	B14	M-016759- bromodom	254065	BRWD3	1710	5.614	1.084
50076	B15	M-028587- chromoso	221262	C6orf185	2935	11.823	7.293
50076	B16	M-017081- leucine ric	254050	LRRC43	3563	12.349	7.819
50076	B17	M-031760- 5'-nucleoti	221294	NT5DC1	2009	5.7242	1.1942
50076	B18	M-025464- hypothetic	254048	FLJ25778	1150	14.174	9.644
50076	B19	M-016124- family with	221301	FAM26D	2847	18.932	14.402
50076	B20	M-032013- methionin	254042	MAP1D	2872	17.827	13.297
50076	B21	M-015894- chromoso	221302	C6orf113	2671	8.2366	3.7066
50076	B23	M-016125- chromoso	221322	C6orf170	1238	9.9354	5.4054
50076	C02	M-018746- coiled-coil	221016	CCDC7	4995	3.4434	1.0866
50076	C04	M-016264- RasGEF do	221002	RASGEF1A	3512	12.528	7.998
50076	C05	M-017946- 2'-phospho	201626	2'-PDE	3821	2.4077	2.1223
50076	C06	M-016310- zinc finger	220992	ZNF485	4909	6.8649	2.3349
50076	C07	M-016505- family with	201627	FAM116A	2472	5.2184	0.6884
50076	C08	M-019347- heterogen	220988	HNRPA3	2396	29.716	25.186

50076	C09	M-018488-	V-set and i	201633	VSIG9	4335	6.3899	1.8599
50076	C10	M-016622-	chromoson	220979	C10orf25	3592	5.6514	1.1214
50076	C11	M-028275-	hypothetica	201725	LOC201725	2274	3.9578	0.5722
50076	C12	M-026426-	family with	220965	FAM13C1	1686	4.4484	0.0816
50076	C13	M-007379-	solute carri	201780	SLC10A4	1735	8.5303	4.0003
50076	C14	M-019303-	solute carri	220963	SLC16A9	4251	8.5392	4.0092
50076	C15	M-017441-	tigger trans	201798	TIGD4	2316	3.2383	1.2917
50076	C16	M-019384-	zinc finger	220929	ZNF438	4884	10.217	5.687
50076	C17	M-016801-	transmemb	201799	TMEM154	2867	8.8594	4.3294
50076	C18	M-029775-	hypothetica	220906	LOC220906	1394	6.241	1.711
50076	C19	M-016613-	hypothetica	201824	MGC42157	2545	7.5049	2.9749
50076	C20	M-025998-	COBW dom	220869	CBWD5	2269	5.2446	0.7146
50076	C21	M-017827-	chromoson	201895	C4orf34	2288	10.49	5.96
50076	C23	M-016802-	hypothetica	201931	FLJ38482	1797	8.9594	4.4294
50076	D02	M-030268-	hypothetica	254028	LOC254028	3049	2.099	2.431
50076	D04	M-018388-	hypothetica	254013	MGC50559	2055	3.2117	1.3183
50076	D05	M-016126-	chromoson	221336	C6orf65	2830	0.91873	3.61127
50076	D06	M-003992-	aspartate b	253982	ASPHD1	1768	0.90498	3.62502
50076	D07	M-009064-	glutathione	221357	GSTA5	1481	2.0257	2.5043
50076	D08	M-017862-	potassium	253980	KCTD13	2936	2.6567	1.8733
50076	D09	M-025108-	tudor doma	221400	TDRD6	2437	4.2265	0.3035
50076	D10	M-021940-	hypothetica	253970	LOC253970	3517	6.7671	2.2371
50076	D11	M-016547-	spermatog	221409	SPATS1	2063	5.0412	0.5112
50076	D12	M-023212-	hypothetica	253962	LOC253962	2142	2.7544	1.7756
50076	D13	M-016757-	hypothetica	221416	MGC45491	1145	3.4934	1.0366
50076	D14	M-021937-	GTPase act	253959	GARNL1	1238	4.2003	0.3297
50076	D15	M-018694-	chromoson	221421	C6orf206	3892	5.2158	0.6858
50076	D16	M-017080-	YTH domai	253943	YTHDF3	1716	2.0396	2.4904
50076	D17	M-028716-	chromoson	221424	C6orf154	1722	1.1614	3.3686
50076	D18	M-007808-	angiopoieti	253935	ANGPTL5	2115	4.1608	0.3692
50076	D19	M-025095-	hypothetica	221442	LOC221442	1902	5.9411	1.4111
50076	D20	M-017079-	hypothetica	253868	FLJ30313	1316	3.2675	1.2625
50076	D21	M-015886-	chromoson	221443	C6orf130	2556	3.4038	1.1262
50076	D23	M-016448-	kinesin fam	221458	KIF6	2517	3.536	0.994
50076	E02	M-007160-	ring finger	220441	RNF152	4639	0.79759	3.73241
50076	E04	M-015467-	coiled-coil	220388	CCDC89	4004	0.37463	4.15537
50076	E05	M-016803-	RWD doma	201965	RWDD4A	2528	4.4304	0.0996
50076	E06	M-018051-	hypothetica	220382	MGC33846	4598	2.3488	2.1812
50076	E07	M-016804-	coiled-coil	201973	CCDC111	3095	1.1309	3.3991
50076	E08	M-017439-	tigger trans	220359	TIGD3	1711	2.0456	2.4844
50076	E09	M-015826-	transmemb	202018	TAPT1	2216	2.5722	1.9578
50076	E10	M-017894-	OAF homol	220323	OAF	3375	2.4889	2.0411
50076	E11	M-016805-	hypothetica	202020	FLJ39653	2277	3.3816	1.1484
50076	E12	M-015466-	hepatocyte	220296	HEPACAM	2242	1.1151	3.4149
50076	E13	M-028343-	hypothetica	202025	DKFZp667E	1378	4.8621	0.3321
50076	E14	M-026487-	OTU domai	220213	OTUD1	1276	2.8213	1.7087
50076	E15	M-024410-	hypothetica	202051	LOC202051	3142	3.7237	0.8063

50076	E16	M-009030- atonal hom	220202	ATOH7	3091	2.3617	2.1683
50076	E17	M-016895- DnaJ (Hsp4	202052	DNAJC18	3615	4.343	0.187
50076	E18	M-015595- docking pr	220164	DOK6	3366	2.0202	2.5098
50076	E19	M-018290- RAN bindin	202151	RANBP3L	3575	8.1678	3.6378
50076	E20	M-016630- coiled-coil	220136	CCDC11	2498	4.3235	0.2065
50076	E21	M-024602- hypothetic	202181	LOC202181	3756	5.0053	0.4753
50076	E23	M-018477- coiled-coil	202243	CCDC125	2331	8.2797	3.7497
50076	F02	M-021432- methionin	253827	MSRB3	1989	2.916	1.614
50076	F04	M-032207- LAG1 hom	253782	LASS6	5652	6.1571	1.6271
50076	F05	M-018752- chromoso	221468	C6orf128	1713	6.7717	2.2417
50076	F06	M-019181- WD repeat	253769	WDR27	2076	3.7572	0.7728
50076	F07	M-008431- FYVE, Rho	221472	FGD2	1622	1.6646	2.8654
50076	F08	M-026500- early B-cell	253738	EBF3	1831	2.8946	1.6354
50076	F09	M-015830- peptidase i	221476	PI16	3135	5.1356	0.6056
50076	F10	M-029678- family with	253725	FAM21C	3731	7.5851	3.0551
50076	F11	M-016129- chromoso	221477	C6orf89	3362	9.3992	4.8692
50076	F12	M-027225- chromoso	253714	C6orf167	1311	3.5088	1.0212
50076	F13	M-018747- chromoso	221481	C6orf81	1659	2.9536	1.5764
50076	F14	M-016661- ankyrin rep	253650	ANKRD18A	2782	4.2775	0.2525
50076	F15	M-017897- chromoso	221491	C6orf1	2815	0.42629	4.10371
50076	F16	M-023468- zinc finger	253639	ZNF620	2855	2.1716	2.3584
50076	F17	M-017941- LEM domai	221496	LEMD2	5028	7.8162	3.2862
50076	F18	M-017855- coiled-coil	253635	CCDC75	4776	7.2236	2.6936
50076	F19	M-016248- zinc finger	221504	ZBTB9	4055	10.234	5.704
50076	F20	M-028601- chromoso	253582	C6orf191	4063	8.1467	3.6167
50076	F21	M-018786- zinc finger	221527	ZBTB12	3022	11.35	6.82
50076	F23	M-016445- chromoso	221545	C6orf136	3783	3.5422	0.9878
50076	G02	M-015917- chromoso	220134	C18orf24	4921	1.1177	3.4123
50076	G04	M-018744- family with	220108	FAM124A	3599	4.3345	0.1955
50076	G05	M-018446- chromoso	202299	C5orf27	2565	1.4425	3.0875
50076	G06	M-032243- deleted in	220107	DLEU7	2719	2.0964	2.4336
50076	G07	M-016896- chromoso	202309	C5orf29	3114	1.0918	3.4382
50076	G08	M-015594- spermatid	220082	SPERT	2666	0.56264	3.96736
50076	G09	M-016373- cardiomyo	202333	CMYA5	2949	1.3564	3.1736
50076	G10	M-016302- leucine ric	220074	LRRC51	1878	2.2897	2.2403
50076	G11	M-016284- similar to R	202459	LOC20245	2007	0.79721	3.73279
50076	G12	M-016294- chromoso	220070	C11orf76	1058	0.56711	3.96289
50076	G13	M-018956- hypothetic	202500	RP11-444E	1771	2.3715	2.1585
50076	G14	M-010374- oral cancer	220064	ORAOV1	2210	0.36199	4.16801
50076	G15	M-016897- KH domain	202559	KHDRBS2	3282	0.76173	3.76827
50076	G16	M-018459- coiled-coil	220047	CCDC83	2944	3.3288	1.2012
50076	G17	M-016273- chromoso	202865	C7orf33	1670	4.5509	0.0209
50076	G18	M-007159- hypothetic	220042	FLJ25416	2856	2.8361	1.6939
50076	G19	M-016898- hypothetic	202915	MGC9712	2198	5.0045	0.4745
50076	G20	M-019405- glycerophо	220032	GDPD4	3535	5.3465	0.8165
50076	G21	M-016813- t-SNARE d	203062	TSNARE1	3424	17.231	12.701
50076	G23	M-025792- R3H domai	203069	R3HCC1	2524	5.2694	0.7394

50076	H02	M-016035-	cell adhesi	253559	CADM2	1455	1.4433	3.0867
50076	H04	M-010307-	lysocardioli	253558	LYCAT	1989	1.458	3.072
50076	H05	M-005291-	histone clu	221613	HIST1H2AA	2191	1.5974	2.9326
50076	H06	M-007350-	solute carri	253512	SLC25A30	1304	0.6135	3.9165
50076	H07	M-008121-	amine oxid	221656	AOF1	2231	0.62752	3.90248
50076	H08	M-023605-	zinc finger	253461	ZBTB38	2999	0.96699	3.56301
50076	H09	M-009788-	RNA bindin	221662	RBM24	1572	0.57252	3.95748
50076	H10	M-016984-	rapamycin-	253260	RICTOR	3258	1.5347	2.9953
50076	H11	M-007162-	ring finger	221687	RNF182	1471	0.47587	4.05413
50076	H12	M-018374-	hypothetic	253150	MGC14276	1845	0.59621	3.93379
50076	H13	M-025063-	phosphatas	221692	PHACTR1	1695	0.35398	4.17602
50076	H14	M-018415-	chromosom	253143	C22orf30	3017	1.1601	3.3699
50076	H15	M-028677-	hypothetic	221710	LOC22171	1993	0.45158	4.07842
50076	H16	M-018963-	HLA compl	253018	HCG27	1749	0.11435	4.41565
50076	H17	M-019304-	145 kDa nu	221711	NO145	1539	0.32489	4.20511
50076	H18	M-024084-	steroid 5 al	253017	SRD5A2L2	2841	0.24639	4.28361
50076	H19	M-016250-	chromosom	221718	C6orf218	1907	1.4158	3.1142
50076	H20	M-021499-	hypothetic	253012	LOC25301	2827	1.1319	3.3981
50076	H21	M-019365-	chromosom	221749	C6orf145	3191	1.7236	2.8064
50076	H23	M-028629-	hypothetic	221756	MGC39372	1603	0.93575	3.59425
50076	I02	M-016619-	chromosom	220004	C11orf66	4394	2.64	1.89
50076	I04	M-016374-	cytochrom	220002	CYBASC3	2099	0.71463	3.81537
50076	I05	M-027221-	tryptophan	203074	UNQ9391	3397	1.3541	3.1759
50076	I06	M-015593-	von Willeb	220001	VWCE	5201	1.9035	2.6265
50076	I07	M-005880-	HtrA serine	203100	HTRA4	2062	0.33948	4.19052
50076	I08	M-015592-	hypothetic	219995	MGC35295	2683	1.0809	3.4491
50076	I09	M-018487-	chromosom	203111	C8orf47	2461	1.4628	3.0672
50076	I10	M-018461-	placenta-sp	219990	PLAC1L	2169	1.1065	3.4235
50076	I11	M-016999-	leucine-rich	203190	LGI3	1865	2.4129	2.1171
50076	I12	M-015591-	FLJ36874 p	219988	FLJ36874	1304	1.227	3.303
50076	I13	M-026196-	chromosom	203197	C9orf91	1445	1.8685	2.6615
50076	I14	M-026664-	macrophag	219972	MPEG1	1911	1.5175	3.0125
50076	I15	M-013341-	chromosom	203228	C9orf72	2091	2.0564	2.4736
50076	I16	M-010306-	glycine-N-a	219970	GLYATL2	1670	1.7964	2.7336
50076	I17	M-018478-	chromosom	203238	C9orf93	1627	2.5814	1.9486
50076	I18	M-017842-	spermatog	219938	SPATA19	1743	6.0815	1.5515
50076	I19	M-021314-	chromosom	203245	C9orf90	1479	3.5159	1.0141
50076	I20	M-019072-	mitochond	219927	MRPL21	2291	3.2737	1.2563
50076	I21	M-017484-	chromosom	203259	C9orf25	1429	6.508	1.978
50076	I23	M-017801-	coiled-coil	203260	CCDC107	1663	4.0289	0.5011
50076	J02	M-016166-	fibronectin	252995	FNDC5	2115	1.5603	2.9697
50076	J04	M-017952-	syntaxin bi	252983	STXBP4	1930	4.5078	0.0222
50076	J05	M-017385-	zinc finger	221785	ZNF498	2300	3.5217	1.0083
50076	J06	M-016345-	nei like 2 (	252969	NEIL2	1924	0.88358	3.64642
50076	J07	M-017383-	chromosom	221786	C7orf38	2447	5.0674	0.5374
50076	J08	M-021304-	zinc finger	252884	ZNF396	2053	2.8251	1.7049
50076	J09	M-028811-	hypothetic	221806	FLJ14712	1443	0.693	3.837

50076	J10	M-021131- transmemb	252839	TMEM9	1012	2.668	1.862
50076	J11	M-025303- TWIST neig	221830	TWISTNB	2704	5.7322	1.2022
50076	J12	M-007987- interleukin	246778	IL27	1655	1.7523	2.7777
50076	J13	M-007163- Sp8 transcr	221833	SP8	1380	2.971	1.559
50076	J14	M-015701- sperm equa	246777	SPESP1	3558	6.127	1.597
50076	J15	M-018012- JAZF zinc fi	221895	JAZF1	2852	4.9088	0.3788
50076	J16	M-013602- DNA direct	246721	POLR2J2	1018	2.6523	1.8777
50076	J17	M-016181- chromoson	221908	C7orf47	1731	4.2172	0.3128
50076	J18	M-015764- chromoson	246705	C21orf94	1381	2.462	2.068
50076	J19	M-016251- glypican 2	221914	GPC2	1744	3.211	1.319
50076	J20	M-017000- chromoson	246704	C21orf93	1904	1.9958	2.5342
50076	J21	M-016785- chromoson	221927	C7orf27	2932	5.9004	1.3704
50076	J23	M-018964- sidekick ho	221935	SDK1	1272	6.2107	1.6807
50076	K02	M-017799- transmemb	219902	TMEM136	3971	2.4931	2.0369
50076	K04	M-015590- tubulin folc	219899	TBCEL	3533	5.2363	0.7063
50076	K05	M-018474- ankyrin rep	203286	ANKS6	3165	2.4645	2.0655
50076	K06	M-007555- solute carri	219855	SLC37A2	2016	2.5794	1.9506
50076	K07	M-016811- sushi doma	203328	SUSD3	2799	3.3941	1.1359
50076	K08	M-026532- hypothetica	219854	LOC21985	1832	5.2948	0.7648
50076	K09	M-007349- solute carri	203427	SLC25A43	1282	2.8861	1.6439
50076	K10	M-016600- hydroletha	219844	HYLS1	927	5.0701	0.5401
50076	K11	M-018780- chromoson	203429	CXorf50	2659	5.378	0.848
50076	K12	M-016656- chromoson	219833	C11orf45	2822	12.828	8.298
50076	K13	M-016899- zinc finger,	203430	ZCCHC5	1197	6.4327	1.9027
50076	K14	M-017071- chromoson	219793	C10orf27	2084	6.142	1.612
50076	K15	M-024786- Nik related	203447	NRK	3159	2.7224	1.8076
50076	K16	M-016664- pleckstrin h	219790	PLEKHK1	2424	4.8267	0.2967
50076	K17	M-018958- DEAD/H (A	203522	DDX26B	1411	7.725	3.195
50076	K18	M-015828- connexin4(	219770	CX40.1	2392	5.8528	1.3228
50076	K19	M-016030- zinc finger	203523	ZNF449	2416	4.553	0.023
50076	K20	M-016000- zinc finger	219749	ZNF25	3086	10.175	5.645
50076	K21	M-031593- hypothetica	203547	LOC203547	2607	8.9375	4.4075
50076	K23	M-018960- transmemb	203562	TMEM31	2109	6.4011	1.8711
50076	L02	M-015632- pellino hon	246330	PELI3	1490	0.73826	3.79174
50076	L04	M-015865- SH3 and cy	246329	STAC3	2506	3.7909	0.7391
50076	L05	M-008052- monocyte t	221938	MMD2	1856	3.3944	1.1356
50076	L06	M-008222- lactation el	246269	LACE1	1620	2.6543	1.8757
50076	L07	M-016837- diacylglyce	221955	DAGLB	1389	1.6559	2.8741
50076	L08	M-012595- ribonucleas	246243	RNASEH1	1895	3.0607	1.4693
50076	L09	M-021483- chromoson	221960	C7orf28B	2463	4.3443	0.1857
50076	L10	M-007418- solute carri	246213	SLC17A8	1637	1.6494	2.8806
50076	L11	M-018827- V-set and t	222008	VSTM2	1731	5.7192	1.1892
50076	L12	M-017012- growth arr	246176	GAS2L2	1537	5.4652	0.9352
50076	L13	M-007923- transmemb	222068	TMED4	1228	6.759	2.229
50076	L14	M-025055- chromoson	246126	CYorf15A	2492	8.0257	3.4957
50076	L15	M-016788- hypothetica	222161	DKFZp586I	2826	13.199	8.669
50076	L16	M-016967- cancer/test	246100	CTAG1A	4300	8.093	3.563

50076	L17	M-016789- chromoson	222166	C7orf41	2917	3.4967	1.0333
50076	L18	M-016263- ATPase, H+	245973	ATP6V1C2	2371	7.8026	3.2726
50076	L19	M-018053- proline ricl	222171	PRR15	1998	3.3534	1.1766
50076	L20	M-005105- ATPase, H+	245972	ATP6V0D2	1904	11.187	6.657
50076	L21	M-016790- hypothetic	222183	FLJ37078	1941	8.8614	4.3314
50076	L23	M-032240- round sper	222194	RSBN1L	2658	9.067	4.537
50076	M02	M-018463- trypsin don	219743	TYSND1	3235	4.4204	0.1096
50076	M04	M-016289- chromoson	219738	C10orf35	3987	7.3489	2.8189
50076	M05	M-032037- P antigen f	203569	PAGE2	3902	6.4326	1.9026
50076	M06	M-017070- storkhead l	219736	STOX1	2508	6.2201	1.6901
50076	M07	M-025053- chromodor	203611	CDY2B	1404	12.749	8.219
50076	M08	M-029749- hypothetic	219690	LOC21969	2751	5.8161	1.2861
50076	M09	M-023566- EPH recept	203806	EPHA6	1229	19.447	14.917
50076	M10	M-017744- armadillo r	219681	ARMC3	3073	5.7273	1.1973
50076	M11	M-026787- transmemk	203859	TMEM16E	2785	10.018	5.488
50076	M12	M-015999- chromoson	219670	C10orf63	2263	8.3959	3.8659
50076	M13	M-017860- LAG1 homo	204219	LASS3	1744	20.241	15.711
50076	M14	M-015827- chromoson	219654	C10orf56	2614	12.089	7.559
50076	M15	M-017829- protein dis	204474	PDILT	2342	7.2161	2.6861
50076	M16	M-017890- transmemk	219623	TMEM26	2887	7.9321	3.4021
50076	M17	M-009033- NLR family,	204801	NLRP11	2941	10.031	5.501
50076	M18	M-018457- chromoson	219621	C10orf107	2131	9.2914	4.7614
50076	M19	M-016900- solute carri	204962	SLC44A5	5101	7.9396	3.4096
50076	M20	M-007158- zinc finger	219578	ZNF804B	2751	11.123	6.593
50076	M21	M-017019- hypothetic	205147	FLJ38377	2829	6.4687	1.9387
50076	M23	M-017831- LOC205251	205251	LOC205251	1821	8.2372	3.7072
50076	N02	M-017614- defensin, b	245938	DEFB125	2480	0.72581	3.80419
50076	N04	M-017613- defensin, b	245936	DEFB123	2162	1.7114	2.8186
50076	N05	M-017566- KIAA1324-l	222223	KIAA1324L	1341	0.67114	3.85886
50076	N06	M-021506- defensin, b	245932	DEFB119	1833	3.928	0.602
50076	N07	M-016934- hypothetic	222229	DKFZp434	2808	2.0299	2.5001
50076	N08	M-016644- defensin, b	245909	DEFB106A	2837	1.5157	3.0143
50076	N09	M-016147- hypothetic	222234	MGC35361	2295	5.9695	1.4395
50076	N10	M-016609- defensin, b	245908	DEFB105A	3466	1.1252	3.4048
50076	N11	M-016001- F-box and l	222235	FBXL13	2386	1.0897	3.4403
50076	N12	M-016983- PRotein As	245812	MGC40499	2763	5.1031	0.5731
50076	N13	M-027347- N-acyl-pho	222236	NAPE-PLD	3983	8.0341	3.5041
50076	N14	M-015963- vestigial lik	245806	VGLL2	1577	0.50729	4.02271
50076	N15	M-016979- ataxin 7-lik	222255	ATXN7L1	3318	8.0772	3.5472
50076	N16	M-017287- membrane	245802	MS4A6E	2867	1.4998	3.0302
50076	N17	M-016980- hypothetic	222256	FLJ23834	4028	1.0924	3.4376
50076	N18	M-009141- speedy hor	245711	SPDYA	2164	1.6636	2.8664
50076	N19	M-016981- chromoson	222389	C10orf30	2395	1.9624	2.5676
50076	N20	M-016982- sema doma	223117	SEMA3D	3107	2.0921	2.4379
50076	N21	M-007164- ligand of nu	222484	LNX2	3266	1.4391	3.0909
50076	N23	M-018443- hypothetic	222521	FLJ25791	2538	0.35461	4.17539
50076	O02	M-017069- hypothetic	219557	MGC26647	3545	5.4725	0.9425

50076	O04	M-016056-	mediator o	219541	MED19	2746	5.7174	1.1874
50076	O05	M-018633-	hypothetica	205327	FLJ38973	2954	4.807	0.277
50076	O06	M-016670-	yippee-like	219539	YPEL4	2092	6.6444	2.1144
50076	O07	M-018471-	chromoson	205428	C3orf58	3306	6.8361	2.3061
50076	O08	M-015895-	GS homeob	219409	GSH1	3679	8.9698	4.4398
50076	O09	M-005946-	SUMO1/se	205564	SENP5	1832	6.8231	2.2931
50076	O10	M-017068-	polymerase	219404	POLR1C	2906	13.593	9.063
50076	O11	M-023709-	KIAA2018	205717	KIAA2018	1841	9.3427	4.8127
50076	O12	M-018895-	mitochond	219402	MTIF3	2732	7.5403	3.0103
50076	O13	M-009017-	hypothetica	205860	FLJ25801	1655	6.0423	1.5123
50076	O14	M-027224-	ATPase fam	219293	ATAD3C	1948	6.7248	2.1948
50076	O15	M-005878-	laeverin	206338	FLJ90650	1621	7.773	3.243
50076	O16	M-017021-	family with	219287	FAM123A	863	8.9224	4.3924
50076	O17	M-007550-	solute carri	206358	SLC36A1	867	4.4983	0.0317
50076	O18	M-008124-	dehydroge	207063	DHRSX	2072	1.8822	2.6478
50076	O19	M-024875-	chromoson	206412	C6orf163	2340	5.6838	1.1538
50076	O20	M-017020-	chromoson	206938	C9orf94	2901	1.7925	2.7375
50076	O21	M-024504-	KIAA1999	202149	KIAA1999	2489	2.0892	2.4408
50076	O23	M-017421-	SPANX fam	171489	SPANXE	2009	3.2354	1.2946
50076	P02	M-007165-	zinc and ri	223082	ZNRF2	1633	4.8377	0.3077
50076	P04	M-019302-	coiled-coil	223075	CCDC129	1402	6.4907	1.9607
50076	P05	M-008978-	heparan su	222537	HS3ST5	2045	8.4108	3.8808
50076	P06	M-018418-	hypothetica	222967	LOC222967	2302	6.0382	1.5082
50076	P07	M-018439-	regulatory	222546	RFXDC1	4442	9.5678	5.0378
50076	P08	M-007508-	solute carri	222962	SLC29A4	999	8.5085	3.9785
50076	P09	M-028593-	solute carri	222553	SLC35F1	1964	2.9532	1.5768
50076	P10	M-021312-	hypothetica	222950	FLJ37538	2851	9.751	5.221
50076	P11	M-025113-	family with	222584	FAM83B	3934	9.4814	4.9514
50076	P12	M-008437-	Fer3-like (	222894	FERD3L	3999	12.528	7.998
50076	P13	M-028712-	benzodiaza	222642	BZRPL1	2037	4.2219	0.3081
50076	P14	M-016401-	transmemb	222865	TMEM130	2086	6.8552	2.3252
50076	P15	M-018437-	unc-5 hom	222643	UNC5CL	3256	5.2211	0.6911
50076	P16	M-018430-	chromoson	222826	C6orf146	1449	4.6929	0.1629
50076	P17	M-018436-	potassium	222658	KCTD20	1668	7.9137	3.3837
50076	P18	M-025126-	chromoson	222698	C6orf194	3592	6.1247	1.5947
50076	P19	M-016935-	peroxisoma	222659	PXT1	3795	6.5349	2.0049
50076	P20	M-025080-	zinc finger	222696	ZSCAN23	2230	5.7399	1.2099
50076	P21	M-018911-	lipoma HM	222662	LHFPL5	1780	6.4607	1.9307
50076	P23	M-018371-	signal pept	222663	SCUBE3	1999	4.002	0.528
					MAD	2252.5	4.52935	2.5022
					MAD3			7.5066
					MADc			3.703256
50076	C22					1576	35.914	
50076	D22					2403	28.797	
50076	E22					1651	24.349	
50076	F22					3032	36.313	

					mn	2165.5	31.34325
					sd	687.8588	5.8021
50076	G22					722	4.1551
50076	H22					726	0.55096
50076	I22					387	10.853
50076	J22					602	6.9767
					mn	609.25	5.63394
					sd	158.9452	4.361393
					3psSD		17.4063
					3ngSD		13.08418
					SumSD		30.49048
					MeanDf		25.70931
					SumovrMn		1.18597
					1minus		-0.18597
50076	G03	M-003290-	polo-like ki	5347	PLK1 SMAR	452	1.5487
50076	H03	M-003290-	polo-like ki	5347	PLK1 SMAR	259	3.861
50076	I03	D-001206-	siControl non-targeting			3718	10.597
50076	J03	D-001206-	siControl non-targeting			988	7.5911
50076	K03	D-001600-	siGLO RISC-free siRNA			4962	19.025
50076	L03	D-001600-	siGLO RISC-free siRNA			3176	23.583

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.646391	1374	3.9301	2.3199	-0.58668	826	5.569	1.811	-0.4804
1.247429	544	10.662	4.412	1.113883	1100	3	4.38	-1.16103
0.317383	427	7.0258	0.7758	0.195333	341	8.2111	0.8311	0.219595
1.254288	718	7.2423	0.9923	0.250023	938	3.838	3.542	-0.93901
2.10454	394	11.929	5.679	1.433943	1300	8	0.62	0.163666
2.02515	651	11.982	5.732	1.447332	864	13.079	5.699	1.509295
1.744046	428	8.1776	1.9276	0.486292	723	3.5961	3.7839	-1.0031
1.560694	453	9.0508	2.8008	0.706873	853	11.137	3.757	0.994782
0.867601	558	11.649	5.399	1.363212	797	6.7754	0.6046	-0.16078
1.070882	538	14.684	8.434	2.129891	1157	4.8401	2.5399	-0.67352
0.824099	721	9.8474	3.5974	0.908105	1205	7.2199	0.1601	-0.04301
2.210123	795	25.409	19.159	4.839162	1214	6.7545	0.6255	-0.16632
0.694321	900	12.222	5.972	1.507959	1597	8.2655	0.8855	0.234008
0.147046	731	10.123	3.873	0.977725	1438	2.0862	5.2938	-1.40313
2.042432	453	20.751	14.501	3.662492	729	13.855	6.475	1.714888
2.470164	286	24.126	17.876	4.51506	655	6.2595	1.1205	-0.29746
2.412917	566	20.848	14.598	3.686995	711	11.111	3.731	0.987894
0.423182	1346	20.728	14.478	3.656682	1019	10.795	3.415	0.904173
0.827448	609	21.511	15.261	3.854477	516	18.411	11.031	2.921954
1.417739	611	27.823	21.573	5.448968	634	17.823	10.443	2.766169
-0.08167	960	1.1458	5.1042	-1.29003	562	4.4484	2.9316	-0.77729
1.299735	1454	0.61898	5.63102	-1.42311	814	6.8796	0.5004	-0.13317
-0.46406	1527	0.98232	5.26768	-1.33133	680	4.5588	2.8212	-0.74804
-0.82796	1769	0.28265	5.96735	-1.50807	1451	3.3081	4.0719	-1.0794
-0.32959	1354	1.1078	5.1422	-1.29963	2109	6.5434	0.8366	-0.22224
0.042139	1278	0.86072	5.38928	-1.36204	1216	2.0559	5.3241	-1.41116
0.781191	1369	2.2644	3.9856	-1.00746	819	9.6459	2.2659	0.599731
-0.14597	1473	1.0862	5.1638	-1.30509	1549	5.2937	2.0863	-0.55334
0.169297	1799	5.0028	1.2472	-0.3157	2521	14.637	7.257	1.922071
1.11803	1547	2.8442	3.4058	-0.86099	1969	6.1453	1.2347	-0.32772
0.387348	473	2.7484	3.5016	-0.88519	564	6.5603	0.8197	-0.21777
0.292891	1549	2.8405	3.4095	-0.86193	1272	2.044	5.336	-1.41431
1.969524	1603	6.7998	0.5498	0.138242	1230	6.0163	1.3637	-0.36189
2.111561	1481	2.7684	3.4816	-0.88014	2261	9.4206	2.0406	0.54004
0.322649	826	2.1792	4.0708	-1.02898	1393	6.2455	1.1345	-0.30117
2.60437	1147	6.1029	0.1471	-0.0378	1284	8.0997	0.7197	0.190081
3.889186	2076	7.2736	1.0236	0.25793	2654	12.547	5.167	1.368347
3.5908	1800	7.0556	0.8056	0.202861	1715	6.9388	0.4412	-0.11749
1.001079	1483	2.3601	3.8899	-0.98328	1440	6.5278	0.8522	-0.22638
1.45981	1287	4.5843	1.6657	-0.42142	1070	10	2.62	0.693546
-0.29324	2067	0.33866	5.91134	-1.49392	2282	4.0316	3.3484	-0.88772
2.159897	1258	3.9746	2.2754	-0.57544	1061	6.3148	1.0652	-0.28281
-0.57291	1699	2.2955	3.9545	-0.9996	1076	2.0446	5.3354	-1.41416
0.630675	4119	6.2879	0.0379	0.00893	3815	9.5413	2.1613	0.572018
0.186066	847	4.0142	2.2358	-0.56544	1191	5.4576	1.9224	-0.50992
6.801218	1378	24.165	17.915	4.524911	1205	16.266	8.886	2.353658

0.502409	1440	3.6806	2.5694	-0.64971	1477	4.6716	2.7084	-0.71816
0.30299	1738	3.7975	2.4525	-0.62018	1691	2.8977	4.4823	-1.18814
-0.15434	1041	8.3573	2.1073	0.531686	900	4.5556	2.8244	-0.74889
-0.02186	1529	5.4938	0.7562	-0.19167	2321	4.7824	2.5976	-0.6888
1.080387	1178	2.0374	4.2126	-1.0648	528	3.7879	3.5921	-0.95229
1.08279	2814	18.443	12.193	3.079462	4295	12.037	4.657	1.233228
-0.34863	810	8.0247	1.7747	0.447668	1330	9.3985	2.0185	0.534185
1.535851	2496	10.176	3.926	0.991113	2963	8.0324	0.6524	0.172251
1.169255	2351	10.208	3.958	0.999197	2831	10.385	3.005	0.795548
0.462201	998	17.234	10.984	2.774053	1647	3.5823	3.7977	-1.00676
0.803496	2768	6.6474	0.3974	0.099744	2112	4.4508	2.9292	-0.77666
0.193141	1904	4.8845	1.3655	-0.34559	1503	2.2621	5.1179	-1.35653
1.60957	1349	8.0059	1.7559	0.442918	1554	7.529	0.149	0.03888
1.196258	1824	10.746	4.496	1.135102	1561	4.9327	2.4473	-0.64898
-0.65627	3825	1.8562	4.3938	-1.11057	2460	2.8049	4.5751	-1.21272
-0.35581	2347	5.9651	0.2849	-0.07261	1693	13.703	6.323	1.674618
-0.97499	2468	1.2561	4.9939	-1.26217	2368	1.9848	5.3952	-1.43
-0.9787	1469	1.0892	5.1608	-1.30433	1466	3.5471	3.8329	-1.01608
-0.67607	2106	3.3713	2.8787	-0.72784	2065	6.0533	1.3267	-0.35209
-0.50568	1891	4.9709	1.2791	-0.32376	1492	3.8874	3.4926	-0.92592
-0.08178	1653	3.0853	3.1647	-0.80009	1953	5.7348	1.6452	-0.43647
0.604266	3248	5.8805	0.3695	-0.09398	3008	9.2753	1.8953	0.501544
0.138216	1204	7.0598	0.8098	0.203922	1318	6.0698	1.3102	-0.34772
-0.47929	2274	5.8927	0.3573	-0.0909	1035	5.8937	1.4863	-0.39438
-0.27974	665	2.8571	3.3929	-0.85773	524	8.5878	1.2078	0.319398
-0.08885	708	8.6158	2.3658	0.596987	549	5.6466	1.7334	-0.45984
0.185364	2428	6.4662	0.2162	0.053971	2612	7.0827	0.2973	-0.07936
-0.67231	1177	4.0782	2.1718	-0.54927	1085	6.2673	1.1127	-0.29539
-0.90946	1078	2.6902	3.5598	-0.89989	944	3.4958	3.8842	-1.02967
-0.09952	2052	3.9961	2.2539	-0.57001	1749	2.6301	4.7499	-1.25903
0.381219	1918	2.7112	3.5388	-0.89459	1740	4.1954	3.1846	-0.84432
-0.34074	836	4.067	2.183	-0.5521	780	3.4615	3.9185	-1.03876
-0.30394	1753	6.6743	0.4243	0.106539	1579	6.0798	1.3002	-0.34507
-0.26824	3025	6.0826	0.1674	-0.04293	1941	6.9037	0.4763	-0.12679
-1.0077	2837	2.7494	3.5006	-0.88494	1837	1.252	6.128	-1.62415
-1.12191	999	6.6066	0.3566	0.089438	663	4.5249	2.8551	-0.75703
-0.02672	1146	6.8935	0.6435	0.161912	841	2.0214	5.3586	-1.4203
-0.58882	1650	5.4545	0.7955	-0.2016	1459	1.5764	5.8036	-1.5382
-0.91769	1371	8.3151	2.0651	0.521026	1475	2.9831	4.3969	-1.16551
-0.67069	895	3.352	2.898	-0.73272	870	0.8046	6.5754	-1.74268
-0.52849	1400	5.1429	1.1071	-0.28031	1685	1.543	5.837	-1.54705
-0.55099	1729	5.5523	0.6977	-0.17689	1410	1.0638	6.3162	-1.67401
-0.30993	1603	6.7374	0.4874	0.122479	1095	1.9178	5.4622	-1.44775
-0.92196	928	9.375	3.125	0.78877	1191	1.7632	5.6168	-1.48871
0.089853	1299	4.9269	1.3231	-0.33488	452	7.0796	0.3004	-0.08018
-0.46123	1400	5.5	0.75	-0.1901	915	0.98361	6.39639	-1.69525
-0.21755	1096	7.938	1.688	0.425766	2084	2.6392	4.7408	-1.25662

-0.58534	1711	6.8381	0.5881	0.147917	1693	2.2445	5.1355	-1.36119
-0.05032	3077	11.862	5.612	1.417018	1979	5.0025	2.3775	-0.63049
-0.67755	3940	26.802	20.552	5.191051	1757	1.7644	5.6156	-1.48839
0.9825	2027	7.3014	1.0514	0.264953	2273	3.7835	3.5965	-0.95345
-0.05559	2926	8.7491	2.4991	0.63066	2187	3.9781	3.4019	-0.90189
0.128522	2037	5.891	0.359	-0.09133	2630	6.5019	0.8781	-0.23324
1.012717	2384	14.22	7.97	2.012679	905	5.1934	2.1866	-0.57991
-0.43566	2555	3.1703	3.0797	-0.77862	1673	3.945	3.435	-0.91066
0.439546	3499	6.8591	0.6091	0.153222	3501	8.5404	1.1604	0.30684
0.605508	358	5.0279	1.2221	-0.30936	767	10.691	3.311	0.876619
-0.20851	979	6.9459	0.6959	0.175149	1624	6.5887	0.7913	-0.21024
-0.77358	437	1.6018	4.6482	-1.17484	577	5.1993	2.1807	-0.57835
-0.44144	872	3.7844	2.4656	-0.62349	1064	3.0075	4.3725	-1.15904
0.163707	1221	9.4185	3.1685	0.799759	1449	9.2478	1.8678	0.494258
0.825152	1733	11.714	5.464	1.379631	2505	13.174	5.794	1.534464
1.315018	1011	15.826	9.576	2.418375	2192	12.637	5.257	1.392192
-0.27558	1147	5.7541	0.4959	-0.12591	666	4.6547	2.7253	-0.72264
-0.4255	830	3.7349	2.5151	-0.63599	1249	9.4476	2.0676	0.547193
-0.06801	1283	13.25	7	1.767644	1431	2.7254	4.6546	-1.23378
-1.10796	1409	2.4131	3.8369	-0.96989	1030	4.466	2.914	-0.77263
-0.63667	672	5.3571	0.8929	-0.2262	575	2.9565	4.4235	-1.17256
0.887557	2426	12.366	6.116	1.544335	3572	15.342	7.962	2.108854
0.727535	1523	10.243	3.993	1.008038	2415	6.6667	0.7133	-0.18958
1.540442	2479	15.732	9.482	2.394629	1819	7.4766	0.0966	0.024997
0.976803	1614	6.5056	0.2556	0.063924	1586	4.855	2.525	-0.66957
1.841798	1179	8.5666	2.3166	0.584558	2617	9.209	1.829	0.483979
-0.26656	1003	7.0788	0.8288	0.208721	1079	4.8193	2.5607	-0.67903
-0.92126	3128	0.86317	5.38683	-1.36143	1896	4.6941	2.6859	-0.7122
-0.05262	1716	3.3217	2.9283	-0.74037	1308	12.385	5.005	1.325427
-0.83355	1574	1.7154	4.5346	-1.14614	1792	10.1	2.72	0.72004
-0.65698	2650	9.5472	3.2972	0.83227	2598	15.512	8.132	2.153893
-0.92825	1503	3.1936	3.0564	-0.77273	1801	9.2726	1.8926	0.500829
-1.07114	1433	2.3029	3.9471	-0.99773	1572	9.2875	1.9075	0.504776
-0.8568	3059	7.4861	1.2361	0.31161	1280	15.469	8.089	2.142501
-0.60478	1576	1.9036	4.3464	-1.0986	1406	7.8236	0.4436	0.116931
-1.0078	1805	2.0499	4.2001	-1.06164	1622	6.5968	0.7832	-0.2081
-1.06993	1092	3.1136	3.1364	-0.79294	773	9.5731	2.1931	0.580443
-0.58269	1725	3.5942	2.6558	-0.67153	1397	9.0909	1.7109	0.452689
-1.12532	1470	2.585	3.665	-0.92647	1303	5.2187	2.1613	-0.57321
-1.01738	2279	3.3348	2.9152	-0.73706	2908	12.792	5.412	1.433257
-0.32419	2353	4.3774	1.8726	-0.47369	2352	6.1224	1.2576	-0.33378
0.005819	1007	2.7805	3.4695	-0.87708	1061	8.4826	1.1026	0.291526
-0.45723	1198	2.8381	3.4119	-0.86253	1554	9.7169	2.3369	0.618541
0.128306	1113	7.1878	0.9378	0.236256	1074	18.529	11.149	2.953216
0.220657	1737	4.0299	2.2201	-0.56147	2184	8.4249	1.0449	0.276239
3.42986	2550	20.353	14.103	3.561952	3105	24.928	17.548	4.648565
0.199838	1680	4.6429	1.6071	-0.40662	1772	8.2957	0.9157	0.242009

-0.83333	1485	3.0303	3.2197	-0.81398	1861	3.9764	3.4036	-0.90234
-0.82936	1491	5.0973	1.1527	-0.29183	2314	14.045	6.665	1.765227
-0.79172	1676	3.1623	3.0877	-0.78064	969	9.8039	2.4239	0.641591
-1.05741	1021	5.9745	0.2755	-0.07024	917	4.1439	3.2361	-0.85797
-1.05362	1228	2.1173	4.1327	-1.04462	1722	8.8269	1.4469	0.382745
-0.96195	1794	7.971	1.721	0.434102	1835	10.027	2.647	0.700699
-1.06847	1599	2.7517	3.4983	-0.88436	536	8.5821	1.2021	0.317888
-0.80865	1709	6.7291	0.4791	0.120383	2316	9.0242	1.6442	0.435018
-1.09457	788	2.7919	3.4581	-0.8742	591	9.9831	2.6031	0.689068
-1.06208	1193	8.4661	2.2161	0.559171	1408	8.6648	1.2848	0.339798
-1.12749	1323	6.5004	0.2504	0.06261	1012	11.067	3.687	0.976236
-0.90981	1757	10.985	4.735	1.195477	2301	14.342	6.962	1.843914
-1.10113	2144	6.3899	0.1399	0.034696	762	9.7113	2.3313	0.617058
-1.19219	908	8.4802	2.2302	0.562733	727	0.82531	6.55469	-1.73719
-1.13534	1015	2.8571	3.3929	-0.85773	1148	6.0976	1.2824	-0.34035
-1.15654	3158	12.223	5.973	1.508211	3483	12.547	5.167	1.368347
-0.84076	1585	2.1451	4.1049	-1.03759	1196	10.117	2.737	0.724544
-0.91742	2605	8.8676	2.6176	0.660595	2771	12.089	4.709	1.247005
-0.75764	2122	5.7964	0.4536	-0.11523	2890	11.592	4.212	1.11533
-0.97039	1355	2.952	3.298	-0.83376	1125	9.6889	2.3089	0.611123
-0.51019	3054	3.3071	2.9429	-0.74406	2691	4.5336	2.8464	-0.75472
-1.0301	1832	10.371	4.121	1.040373	1684	7.7791	0.3991	0.105141
-0.85742	1452	5.2342	1.0158	-0.25725	1779	12.591	5.211	1.380005
-0.70907	4766	15.401	9.151	2.311014	4425	11.593	4.213	1.115595
-1.1314	1439	5.6289	0.6211	-0.15754	1343	6.1802	1.1998	-0.31847
-0.93119	1695	13.392	7.142	1.803515	1881	11.111	3.731	0.987894
-0.82807	907	6.946	0.696	0.175174	1050	11.524	4.144	1.097314
-0.92428	1039	5.0048	1.2452	-0.3152	2178	8.1726	0.7926	0.209395
-0.57151	2008	9.7112	3.4612	0.873699	1637	12.156	4.776	1.264756
-0.89174	1068	10.674	4.424	1.116914	962	15.177	7.797	2.065139
-0.71852	1137	16.095	9.845	2.486327	1181	12.024	4.644	1.229784
-0.8133	1799	5.7254	0.5246	-0.13316	1564	13.235	5.855	1.550626
-0.66778	2360	16.229	9.979	2.520177	2379	14.04	6.66	1.763902
-0.73799	1846	9.0466	2.7966	0.705812	1508	7.626	0.246	0.064579
-0.52601	1363	11.299	5.049	1.274797	2190	10.228	2.848	0.753952
0.419131	1651	4.8455	1.4045	-0.35544	1149	6.2663	1.1137	-0.29566
-0.27366	1648	7.4636	1.2136	0.305927	522	14.176	6.796	1.799934
-0.33907	2991	10.465	4.215	1.064118	1999	9.3047	1.9247	0.509333
0.5343	1800	5.8889	0.3611	-0.09186	1501	8.5943	1.2143	0.32112
-0.13514	1423	5.8327	0.4173	-0.10606	1838	8.2699	0.8899	0.235174
-0.80174	1514	3.5667	2.6833	-0.67848	1351	3.4049	3.9751	-1.05376
-0.00582	2869	4.7752	1.4748	-0.3732	2258	9.256	1.876	0.496431
-0.2721	2037	5.6946	0.5554	-0.14095	1572	11.196	3.816	1.010414
-0.98448	2295	3.573	2.677	-0.67689	1237	4.1229	3.2571	-0.86353
0.145291	3111	7.9396	1.6896	0.42617	1214	6.2603	1.1197	-0.29725
-0.4602	1674	3.2258	3.0242	-0.7646	1672	5.5622	1.8178	-0.4822
-1.03594	2067	1.2095	5.0405	-1.27394	2262	3.9788	3.4012	-0.90171

-0.50263	1226	13.458	7.208	1.820188	1402	4.4223	2.9577	-0.78421
0.324809	2156	9.9258	3.6758	0.927909	3222	12.601	5.221	1.382654
-0.74989	1170	1.3675	4.8825	-1.23403	1854	6.5804	0.7996	-0.21244
-0.42081	949	1.7914	4.4586	-1.12694	1304	1.4571	5.9229	-1.56981
0.431418	2223	9.8965	3.6465	0.920508	2504	11.581	4.201	1.112415
0.102464	1771	3.3315	2.9185	-0.73789	2031	6.3516	1.0284	-0.27306
-0.50686	735	3.8095	2.4405	-0.61715	1101	3.6331	3.7469	-0.9933
-0.08429	1297	8.1727	1.9227	0.485054	1633	8.6957	1.3157	0.347985
-0.55825	1479	3.1778	3.0722	-0.77672	1533	4.8924	2.4876	-0.65966
-0.356	2058	7.9203	1.6703	0.421295	1520	4.0789	3.3011	-0.87519
-0.68414	1798	5.673	0.577	-0.1464	2199	7.2306	0.1494	-0.04018
0.370228	1433	4.6057	1.6443	-0.41602	2021	4.8986	2.4814	-0.65802
0.454019	652	6.9018	0.6518	0.164009	1029	5.2478	2.1322	-0.5655
-0.54985	1720	2.093	4.157	-1.05075	1430	4.1958	3.1842	-0.84422
0.1909	3090	8.6731	2.4231	0.611462	1052	16.255	8.875	2.350744
-0.55758	2162	3.9315	2.3185	-0.58633	782	5.4987	1.8813	-0.49903
-0.52655	2025	4.9383	1.3117	-0.332	1123	7.0347	0.3453	-0.09208
-0.30655	1933	4.2938	1.9562	-0.49481	1283	8.0281	0.6481	0.171111
0.206696	2023	6.7227	0.4727	0.118766	1018	9.2338	1.8538	0.490549
-0.44373	1646	5.164	1.086	-0.27498	529	9.2628	1.8828	0.498232
0.14602	757	10.04	3.79	0.956758	431	16.473	9.093	2.4085
0.229163	1978	7.9879	1.7379	0.438371	1586	12.169	4.789	1.2682
2.240906	2091	13.247	6.997	1.766887	1847	13.535	6.155	1.630108
0.513967	1542	9.4682	3.2182	0.812314	565	19.823	12.443	3.296048
0.435468	1711	9.6435	3.3935	0.856597	548	11.679	4.299	1.13838
-0.48794	3508	8.9225	2.6725	0.674463	3132	13.282	5.902	1.563078
0.080294	2569	4.1261	2.1239	-0.53717	1361	5.8046	1.5754	-0.41798
0.86293	1107	5.6007	0.6493	-0.16467	912	19.298	11.918	3.156955
0.357375	2793	5.7644	0.4856	-0.12331	1953	8.6534	1.2734	0.336778
0.006386	3703	10.937	4.687	1.183351	2270	13.524	6.144	1.627193
1.52451	3518	9.6362	3.3862	0.854753	1868	9.6895	2.3095	0.611282
1.190344	2388	7.0771	0.8271	0.208292	1822	10.154	2.774	0.734347
0.505434	2227	4.5802	1.6698	-0.42246	1426	7.3633	0.0167	-0.00502
-1.02372	1675	2.6866	3.5634	-0.9008	2066	1.8393	5.5407	-1.46855
-0.19941	2001	2.4988	3.7512	-0.94824	2199	6.2301	1.1499	-0.30525
-0.30647	2528	4.6282	1.6218	-0.41033	988	5.4656	1.9144	-0.5078
-0.50632	1611	1.1794	5.0706	-1.28154	1105	1.3575	6.0225	-1.5962
-0.77593	3160	3.3861	2.8639	-0.7241	1842	8.1433	0.7633	0.201632
-0.39658	1716	2.6807	3.5693	-0.90229	1085	2.8571	4.5229	-1.19889
-0.04997	2344	7.0392	0.7892	0.198718	1404	5.4131	1.9669	-0.52171
-0.77768	2603	5.2247	1.0253	-0.25965	1426	5.6101	1.7699	-0.46951
0.321298	2212	7.7306	1.4806	0.373374	1349	5.4855	1.8945	-0.50252
0.25271	1820	4.8352	1.4148	-0.35804	1351	8.9563	1.5763	0.417028
0.602078	1856	5.9267	0.3233	-0.08231	647	6.0278	1.3522	-0.35885
0.944129	1475	4.6102	1.6398	-0.41488	1524	3.6089	3.7711	-0.99971
2.341088	2913	5.5613	0.6887	-0.17462	1387	10.526	3.146	0.832904
0.962302	3305	6.475	0.225	0.056194	2211	4.1158	3.2642	-0.86541

-0.27885	1430	3.4965	2.7535	-0.69621	1206	9.2869	1.9069	0.504617
0.883884	1791	4.9135	1.3365	-0.33826	1695	6.8437	0.5363	-0.14268
-0.31754	2001	6.6467	0.3967	0.099567	1444	15.859	8.479	2.245827
1.797783	1355	8.8561	2.6061	0.65769	1157	17.373	9.993	2.646946
1.169795	2378	7.233	0.983	0.247674	1381	8.979	1.599	0.423042
1.225314	2155	12.436	6.186	1.562018	1647	7.4074	0.0274	0.006663
-0.02942	1268	5.5205	0.7295	-0.18493	1545	3.4304	3.9496	-1.047
0.761371	1677	4.4723	1.7777	-0.44971	1581	4.4276	2.9524	-0.7828
0.51394	1283	4.9883	1.2617	-0.31937	2292	6.7627	0.6173	-0.16414
0.456558	2901	6.8942	0.6442	0.162089	1963	6.9791	0.4009	-0.10681
2.219574	1132	7.4205	1.1705	0.295039	1451	6.0648	1.3152	-0.34904
0.347465	2880	2.8472	3.4028	-0.86023	1709	2.1065	5.2735	-1.39776
4.028252	1984	14.315	8.065	2.036677	875	13.6	6.22	1.647329
0.323486	2831	4.5214	1.7286	-0.43731	2224	3.0126	4.3674	-1.15769
1.482115	2413	9.5731	3.3231	0.838813	1813	11.031	3.651	0.966699
1.044095	1691	4.0213	2.2287	-0.56364	874	10.755	3.375	0.893575
4.242658	1583	25.079	18.829	4.755799	1633	21.127	13.747	3.64153
2.041352	2550	10.431	4.181	1.055529	1120	3.4821	3.8979	-1.0333
0.72551	2165	5.5889	0.6611	-0.16765	770	6.2338	1.1462	-0.30427
0.918854	1892	5.2326	1.0174	-0.25765	1938	6.5015	0.8785	-0.23335
1.485625	2818	9.2619	3.0119	0.7602	1664	8.6538	1.2738	0.336884
1.285909	1977	4.7547	1.4953	-0.37838	683	6.4422	0.9378	-0.24906
0.920879	4317	3.7294	2.5206	-0.63738	2464	5.8847	1.4953	-0.39676
1.780501	2482	14.222	7.972	2.013184	1082	9.7043	2.3243	0.615203
0.523688	3981	7.5107	1.2607	0.317825	2489	6.4283	0.9517	-0.25274
1.001241	1167	7.455	1.205	0.303754	679	15.169	7.789	2.063019
-1.02708	2312	9.083	2.833	0.715007	2003	2.7459	4.6341	-1.22835
-0.76094	1643	8.1558	1.9058	0.480785	2066	4.8403	2.5397	-0.67346
-1.04184	1164	8.677	2.427	0.612447	1134	4.7619	2.6181	-0.69423
-0.16238	1501	8.994	2.744	0.692525	1153	8.5863	1.2063	0.319001
-0.67493	3302	12.72	6.47	1.63376	3399	8.0612	0.6812	0.179881
-0.81378	1492	2.2788	3.9712	-1.00382	2343	7.0849	0.2951	-0.07878
0.388888	1161	11.886	5.636	1.423081	1797	7.4012	0.0212	0.005021
-0.91923	2720	5.2206	1.0294	-0.26068	4020	7.0647	0.3153	-0.08413
-0.92882	2449	8.1666	1.9166	0.483513	1909	8.2766	0.8966	0.236949
0.154931	1325	12.302	6.052	1.528168	1634	10.098	2.718	0.71951
0.946397	1018	9.0373	2.7873	0.703463	1573	9.6631	2.2831	0.604288
-1.08609	1330	9.8496	3.5996	0.90866	1690	12.012	4.632	1.226605
0.958035	2331	9.3522	3.1022	0.783011	1543	6.5457	0.8343	-0.22164
-0.81808	1771	5.4207	0.8293	-0.21014	2048	7.7148	0.3348	0.088106
-0.92809	4007	13.127	6.877	1.736573	2518	9.6108	2.2308	0.590431
-0.77385	1060	7.5472	1.2972	0.327045	764	8.1152	0.7352	0.194188
-0.69316	1215	6.2551	0.0051	0.000644	704	20.312	12.932	3.425604
-0.65814	1492	7.1716	0.9216	0.232164	1904	13.498	6.118	1.620305
-0.83447	2766	5.7845	0.4655	-0.11824	2988	5.1874	2.1926	-0.5815
-1.12732	1397	7.3729	1.1229	0.283015	2502	6.275	1.105	-0.29335
0.254681	983	10.682	4.432	1.118935	1321	4.6177	2.7623	-0.73244

0.320812	1101	10.263	4.013	1.01309	921	13.464	6.084	1.611297
0.074975	931	7.304	1.054	0.26561	1035	8.8889	1.5089	0.399171
0.571133	1222	7.6923	1.4423	0.363699	1736	9.3318	1.9518	0.516513
0.622898	1498	5.5407	0.7093	-0.17982	1473	7.332	0.048	-0.01331
1.199066	2509	8.9279	2.6779	0.675827	1234	13.047	5.667	1.500817
0.619387	1451	7.5121	1.2621	0.318178	1541	4.8021	2.5779	-0.68358
2.447481	2115	12.009	5.759	1.454152	1767	9.9038	2.5238	0.668059
1.299762	1504	6.25	0	-0.00064	892	5.8296	1.5504	-0.41136
0.813055	2476	5.6139	0.6361	-0.16133	1171	5.9778	1.4022	-0.37209
0.408546	1610	7.0186	0.7686	0.193514	770	11.688	4.308	1.140764
0.592843	1927	11.624	5.374	1.356896	929	5.3821	1.9979	-0.52992
0.875891	1296	13.117	6.867	1.734047	1181	9.6528	2.2728	0.601559
1.186267	1050	13.143	6.893	1.740615	931	6.9817	0.3983	-0.10612
-0.00838	1058	9.2628	3.0128	0.760427	525	20	12.62	3.342943
-0.71482	1952	3.6373	2.6127	-0.66065	1878	4.7391	2.6409	-0.70028
0.311739	2442	12.162	5.912	1.492802	2103	11.175	3.795	1.00485
-0.73904	2726	5.6126	0.6374	-0.16166	3131	7.6653	0.2853	0.074991
-0.65892	2061	6.1621	0.0879	-0.02285	2946	8.0448	0.6648	0.175536
-0.34941	1305	9.8851	3.6351	0.917628	1274	8.0063	0.6263	0.165336
0.083265	554	0.90253	5.34747	-1.35148	829	8.9264	1.5464	0.409107
0.529629	654	4.1284	2.1216	-0.53659	1291	9.5275	2.1475	0.568362
1.048118	1427	2.9432	3.3068	-0.83598	1081	7.9556	0.5756	0.151903
0.407439	2852	3.8569	2.3931	-0.60517	1312	12.271	4.891	1.295224
1.360546	3300	4.6667	1.5833	-0.40061	3338	7.7891	0.4091	0.107791
1.0745	944	2.9661	3.2839	-0.8302	1161	16.193	8.813	2.334317
-0.42561	1783	3.309	2.941	-0.74358	2068	9.9613	2.5813	0.683293
1.410016	2111	4.1686	2.0814	-0.52643	2968	11.422	4.042	1.07029
1.337215	2275	4.4835	1.7665	-0.44688	3289	9.8814	2.5014	0.662124
2.159897	1954	6.9601	0.7101	0.178736	1881	12.919	5.539	1.466905
-0.08302	2063	5.1381	1.1119	-0.28152	1599	6.4415	0.9385	-0.24924
0.628055	2333	7.7583	1.5083	0.380371	1849	8.2747	0.8947	0.236445
0.186795	1810	3.2044	3.0456	-0.77	2063	8.3374	0.9574	0.253057
0.044164	1676	10.143	3.893	0.982777	1046	7.1702	0.2098	-0.05618
0.913885	687	11.063	4.813	1.215181	1438	8.484	1.104	0.291897
0.430797	2640	11.136	4.886	1.233621	3253	10.882	3.502	0.927223
0.541564	2536	12.145	5.895	1.488507	1842	9.8806	2.5006	0.661912
0.326888	1994	7.7232	1.4732	0.371505	1967	6.7616	0.6184	-0.16443
0.521528	2089	10.388	4.138	1.044667	2232	10.753	3.373	0.893045
-0.1424	1432	7.4022	1.1522	0.290416	2197	8.8757	1.4957	0.395674
	1649	6.25255	2.67475		1496.5	7.38225	2.5503	
			8.02425				7.6509	
			3.95863				3.774444	

1910	33.77		834	18.825
1116	27.24		1466	22.442
1180	27.119		1222	17.758
1149	30.374		1502	22.437

1338.75	29.62575	1256	20.3655		
381.7289	3.146971	307.6015	2.434143		
821	1.5834			340	16.765
481	4.5738	405	8.3951		
751	1.9973			223	24.215
458	5.0218	541	7.9482		
627.75	3.294075	473	8.17165		
185.1907	1.754116	96.16652	0.316006		
	9.440914		7.30243		
	5.262347		0.948018		
	14.70326		8.250448		
	26.33168		12.19385		
	0.558387		0.676607		
	0.441613		0.323393		
242	2.8926	169	27.219		
203	5.9113	80	35		
1324	9.3656	1165	7.382		
2036	14.882	1146	5.0611		
3533	27.682	3247	9.1469		
3724	21.536	3181	8.9909		

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
y	

y

x toxic a,b,c

y

					cell ct	% inf	AD
50077	A02	M-007979- interleukin	282616	IL28A	704	5.8239	4.3161
50077	A04	M-017565- WAP four-	280664	WFDC10B	926	15.335	5.195
50077	A05	M-018030- chromoson	439940	C8orf15	510	11.176	1.036
50077	A06	M-017883- synovial sa	280660	SSX9	1146	12.565	2.425
50077	A07	M-027667- hypothetic	254099	LOC25409	1038	12.042	1.902
50077	A08	M-017415- synovial sa	280658	SSX7	518	6.7568	3.3832
50077	A09	M-026598- EH domain	254102	EHBP1L1	512	14.453	4.313
50077	A10	M-017420- synovial sa	280657	SSX6	586	8.0205	2.1195
50077	A11	M-017082- hypothetic	254122	FLJ30934	803	6.3512	3.7888
50077	A12	M-016555- chromoson	280636	C11orf31	437	7.0938	3.0462
50077	A13	M-017083- chromoson	254158	CXorf58	494	14.777	4.637
50077	A14	M-031764- ATP syntha	267020	ATP5L2	410	22.927	12.787
50077	A15	M-021948- F-box prot	254170	FBXO33	683	17.57	7.43
50077	A16	M-015665- D-amino a	267012	DAOA	914	15.208	5.068
50077	A17	M-016100- tubulin tyr	254173	TTLL10	572	21.154	11.014
50077	A18	M-007168- piggyBac tr	267002	PGBD2	836	16.388	6.248
50077	A19	M-017084- testis speci	254187	TSGA10IP	725	13.103	2.963
50077	A20	M-015440- nucleosom	266812	NAP1L5	708	17.797	7.657
50077	A21	M-016101- family with	254228	FAM26E	834	10.791	0.651
50077	A23	M-009088- bactericida	254240	BPIL2	812	7.1429	2.9971
50077	B02	M-018154- hypothetic	284033	LOC28403	2519	8.6145	1.5255
50077	B04	M-018233- chromoson	284029	C17orf44	1857	10.501	0.361
50077	B05	M-007980- interleukin	282617	IL28B	1792	8.5379	1.6021
50077	B06	M-023231- chromoson	284021	C17orf60	2726	4.9523	5.1877
50077	B07	M-007982- interleukin	282618	IL29	2042	10.48	0.34
50077	B08	M-018673- chromoson	284018	C17orf58	711	10.408	0.268
50077	B09	M-009008- aquaporin	282679	AQP11	1509	10.205	0.065
50077	B10	M-018976- vitelline m	284013	VMO1	2068	6.7215	3.4185
50077	B11	M-015667- WD repeat	282809	WDR51B	634	15.457	5.317
50077	B12	M-030827- hypothetic	284009	LOC28400	1159	6.9888	3.1512
50077	B13	M-025081- zinc finger	282890	ZNF311	3040	7.2039	2.9361
50077	B14	M-018235- hexosamin	284004	HEXDC	1603	8.1098	2.0302
50077	B15	M-018851- chromoson	282966	C10orf53	1586	14.061	3.921
50077	B16	M-021433- coiled-coil	284001	CCDC57	2010	6.6667	3.4733
50077	B17	M-027226- chromoson	282969	C10orf125	1554	7.0142	3.1258
50077	B18	M-022956- hypothetic	283999	LOC28399	1705	3.2845	6.8555
50077	B19	M-019299- chromoson	282973	C10orf39	873	9.3929	0.7471
50077	B20	M-022953- chromoson	283994	C17orf52	2062	8.9719	1.1681
50077	B21	M-029700- hypothetic	282980	LOC28298	1193	4.4426	5.6974
50077	B23	M-018342- biogenesis	282991	BLOC1S2	2458	2.8885	7.2515
50077	C02	M-019148- melanoma	266740	MAGEA2B	3357	6.7024	3.4376
50077	C04	M-015966- heparan su	266722	HS6ST3	2110	10.474	0.334
50077	C05	M-018740- cornichon	254263	CNIH2	1832	5.0764	5.0636
50077	C06	M-015877- bestrophin	266675	BEST4	2612	10.873	0.733
50077	C07	M-015758- chromoson	254268	C1orf62	1500	4.7333	5.4067
50077	C08	M-016633- orofacial cl	266553	OFCC1	543	18.785	8.645

50077	C09	M-023035-	hypothetica	254272	FLJ40244	1212	4.868	5.272
50077	C10	M-010739-	six transme	261729	STEAP2	702	9.5442	0.5958
50077	C11	M-031962-	phytanoyl-	254295	PHYHD1	1656	6.0386	4.1014
50077	C12	M-019323-	TIP41, TOR	261726	TIPRL	1678	3.9928	6.1472
50077	C13	M-029716-	hypothetica	254312	LOC254312	795	12.201	2.061
50077	C14	M-016809-	chromoson	260436	C4orf7	1106	15.19	5.05
50077	C15	M-017615-	minichrom	254394	MCM9	1339	12.621	2.481
50077	C16	M-016808-	PYD (pyrin	260434	PYDC1	1732	12.587	2.447
50077	C17	M-018375-	chromoson	254427	C10orf47	889	10.011	0.129
50077	C18	M-013551-	NOL1/NOP	260294	NSUN5C	930	15.376	5.236
50077	C19	M-007577-	solute carri	254428	SLC41A1	2021	10.886	0.746
50077	C20	M-009129-	cytochrom	260293	CYP4X1	2591	17.213	7.073
50077	C21	M-015759-	chromoson	254528	C16orf73	1965	7.5318	2.6082
50077	C23	M-016375-	1-acylglyce	254531	AGPAT7	3939	17.873	7.733
50077	D02	M-018939-	family with	283991	FAM100B	2975	4.0672	6.0728
50077	D04	M-022947-	tRNA splici	283989	TSEN54	2361	10.885	0.745
50077	D05	M-029656-	RNA bindin	282996	RBM20	2357	12.261	2.121
50077	D06	M-014638-	chromoson	283987	C17orf28	4071	9.0887	1.0513
50077	D07	M-026290-	family with	283008	FAM22A	3854	12.74	2.6
50077	D08	M-008932-	fatty acid d	283985	FADS6	1092	6.5018	3.6382
50077	D09	M-029744-	chromoson	283025	C10orf40	1178	5.1783	4.9617
50077	D10	M-018924-	chromoson	283982	C17orf54	2682	10.03	0.11
50077	D11	M-019300-	hypothetica	283031	LOC283031	2306	8.7598	1.3802
50077	D12	M-018238-	hypothetica	283971	MGC34761	1974	4.5086	5.6314
50077	D13	M-029757-	hypothetica	283050	LOC283050	1966	3.2045	6.9355
50077	D14	M-022581-	pyridoxal-d	283970	PDXDC2	2608	8.8957	1.2443
50077	D15	M-018344-	mohawk ho	283078	MKX	3268	8.5985	1.5415
50077	D16	M-030774-	hypothetica	283951	LOC283951	1931	3.6769	6.4631
50077	D17	M-027228-	FLJ46111 p	283102	FLJ46111	2416	9.4371	0.7029
50077	D18	M-022881-	hypothetica	283948	FLJ36208	1929	6.48	3.66
50077	D19	M-018057-	hypothetica	283127	FLJ37045	3393	5.7471	4.3929
50077	D20	M-022795-	hypothetica	283933	MGC46336	2974	4.4385	5.7015
50077	D21	M-026592-	hypothetica	283129	LOC283129	4803	11.264	1.124
50077	D23	M-007351-	solute carri	283130	SLC25A45	1142	1.7513	8.3887
50077	E02	M-008109-	interleukin	259307	IL4I1	2574	8.9744	1.1656
50077	E04	M-017800-	taste recep	259296	TAS2R50	994	2.9175	7.2225
50077	E05	M-018935-	nudix (nucl	254552	NUDT8	2346	9.5908	0.5492
50077	E06	M-017832-	taste recep	259295	TAS2R49	3145	10.556	0.416
50077	E07	M-019195-	lysozyme-li	254773	LYG2	2446	10.589	0.449
50077	E08	M-017805-	taste recep	259291	TAS2R45	3088	11.723	1.583
50077	E09	M-015760-	chromoson	254778	C8orf46	766	7.3107	2.8293
50077	E10	M-017825-	taste recep	259290	TAS2R44	3236	10.074	0.066
50077	E11	M-023685-	hypothetica	254808	LOC254808	1404	15.385	5.245
50077	E12	M-017779-	taste recep	259289	TAS2R43	2149	13.495	3.355
50077	E13	M-023654-	N-acetylate	254827	NAALADL2	911	7.0252	3.1148
50077	E14	M-017033-	family with	259282	FAM44A	3585	11.548	1.408
50077	E15	M-015761-	chromoson	254863	C17orf61	949	8.0084	2.1316

50077	E16	M-017481-	WAP four-c	259240	WFDC9	3778	12.785	2.645
50077	E17	M-018381-	zinc finger,	254887	ZDHHC23	1261	5.3925	4.7475
50077	E18	M-017480-	WAP four-c	259239	WFDC11	2578	10.667	0.527
50077	E19	M-018695-	keratin ass	254950	KRTAP15-1	1081	9.6207	0.5193
50077	E20	M-016265-	transmemb	259236	TMIE	4241	9.4317	0.7083
50077	E21	M-031946-	chromoson	254956	C9orf18	1399	3.6455	6.4945
50077	E23	M-015664-	REX1, RNA	254958	REXO1L1	1676	3.9379	6.2021
50077	F02	M-018124-	hypothetica	283932	LOC283932	2878	3.5789	6.5611
50077	F04	M-022678-	hypothetica	283922	LOC283922	2261	4.1575	5.9825
50077	F05	M-018326-	chromoson	283135	C11orf72	3820	8.4293	1.7107
50077	F06	M-030696-	hypothetica	283914	LOC283914	3482	7.1511	2.9889
50077	F07	M-029808-	hypothetica	283143	LOC283143	4175	10.587	0.447
50077	F08	M-030734-	hypothetica	283901	LOC283901	3531	8.1563	1.9837
50077	F09	M-010858-	B-cell CLL/l	283149	BCL9L	1470	0.7483	9.3917
50077	F10	M-003994-	coiled-coil	283899	CCDC95	2792	2.6862	7.4538
50077	F11	M-026523-	forkhead b	283150	FOXR1	4271	12.058	1.918
50077	F12	M-003990-	chromoson	283897	C16orf54	522	6.3218	3.8182
50077	F13	M-029810-	hypothetica	283152	LOC283152	1693	5.0797	5.0603
50077	F14	M-030608-	hypothetica	283887	LOC283887	2404	5.0333	5.1067
50077	F15	M-018321-	proline rich	283165	PRR10	2791	2.8305	7.3095
50077	F16	M-030680-	hypothetica	283876	FLJ39639	2070	3.0435	7.0965
50077	F17	M-018318-	chromoson	283171	C11orf44	5157	8.0085	2.1315
50077	F18	M-022877-	hypothetica	283871	LOC283871	2026	3.307	6.833
50077	F19	M-018316-	hypothetica	283176	FLJ90231	5616	7.7991	2.3409
50077	F20	M-009063-	chromoson	283870	C16orf79	2909	1.3407	8.7993
50077	F21	M-017923-	chromoson	283197	C11orf64	5849	8.6511	1.4889
50077	F23	M-008479-	procollager	283208	P4HA3	1440	0.34722	9.79278
50077	G02	M-017052-	Down synd	259234	DSCR10	1993	3.0105	7.1295
50077	G04	M-006519-	sodium lea	259232	NALCN	1975	15.747	5.607
50077	G05	M-023564-	hypothetica	255025	LOC255025	1142	13.748	3.608
50077	G06	M-019477-	sphingomy	259230	SGMS1	3629	7.9361	2.2039
50077	G07	M-018370-	MPV17 mit	255027	MPV17L	576	13.021	2.881
50077	G08	M-026318-	heat shock	259217	HSPA12A	2858	12.001	1.861
50077	G09	M-018801-	transmemb	255043	TMEM86B	4363	13.385	3.245
50077	G10	M-019226-	ALS2 C-terr	259173	ALS2CL	1186	3.7099	6.4301
50077	G11	M-015762-	hypothetica	255055	FLJ25378	3232	6.25	3.89
50077	G12	M-015625-	ankyrin rep	257629	ANKS4B	1668	8.9329	1.2071
50077	G13	M-015763-	chromoson	255057	C19orf26	1345	13.532	3.392
50077	G14	M-015573-	family with	257415	FAM133B	2337	11.767	1.627
50077	G15	M-016778-	tachykinin	255061	TAC4	2639	5.0019	5.1381
50077	G16	M-015572-	mitogen-ac	257397	MAP3K7IP3	2159	12.923	2.783
50077	G17	M-017863-	cancer susc	255082	CASC2	1905	15.328	5.188
50077	G18	M-028489-	hypothetica	257396	LOC257396	3851	5.0896	5.0504
50077	G19	M-019301-	coiled-coil	255101	CCDC108	3090	5.6958	4.4442
50077	G20	M-015876-	SH3 and PX	257364	SH3PX3	3690	8.8076	1.3324
50077	G21	M-018952-	transmemb	255104	TMCO4	2305	5.0325	5.1075
50077	G23	M-015942-	chromoson	255119	C4orf22	2877	3.1283	7.0117

50077	H02	M-030632- hypothetic	283867	LOC28386	1711	5.1432	4.9968
50077	H04	M-018244- chromoson	283860	C16orf81	1365	10.989	0.849
50077	H05	M-018432- phosphoglu	283209	PGM2L1	3517	16.434	6.294
50077	H06	M-030623- hypothetic	283854	LOC28385	2207	11.056	0.916
50077	H07	M-018305- hypothetic	283212	FLJ33790	4121	28.149	18.009
50077	H08	M-018232- exocyst co	283849	EXOC3L	2169	5.7169	4.4231
50077	H09	M-029918- hypothetic	283214	LOC28321	4861	13.68	3.54
50077	H10	M-008935- hypothetic	283848	FLJ37464	2143	8.4928	1.6472
50077	H11	M-026714- potassium	283219	KCTD21	1819	8.4662	1.6738
50077	H12	M-018247- coiled-coil	283847	CCDC79	1593	10.232	0.092
50077	H13	M-018066- hypothetic	283225	FLJ37266	1381	13.613	3.473
50077	H14	M-018249- NODAL mo	283820	NOMO2	2069	11.986	1.846
50077	H15	M-018303- EF-hand ca	283229	EFCAB4A	2270	12.555	2.415
50077	H16	M-031751- F-box and l	283807	FBXL22	1888	6.303	3.837
50077	H17	M-017925- transmem	283232	TMEM80	2848	11.482	1.342
50077	H18	M-018252- hypothetic	283796	FLJ35785	2606	8.9409	1.1991
50077	H19	M-026590- coiled-coil	283234	CCDC88B	3033	8.7043	1.4357
50077	H20	M-018880- hypothetic	283777	FLJ39743	3189	12.794	2.654
50077	H21	M-018302- tetratricop	283237	TTC9C	3055	5.1391	5.0009
50077	H23	M-007365- hypothetic	283238	MGC34821	2053	4.3838	5.7562
50077	I02	M-028408- hypothetic	257358	LOC25735	4851	8.39	1.75
50077	I04	M-021500- urotensin	257313	UTS2D	5377	12.479	2.339
50077	I05	M-030410- hypothetic	255177	LOC25517	2569	5.3328	4.8072
50077	I06	M-015875- kelch-like	257240	KLHL34	4122	7.3993	2.7407
50077	I07	M-018363- hypothetic	255180	FLJ38723	1525	7.6066	2.5334
50077	I08	M-015726- coiled-coil	257236	CCDC96	4090	11.198	1.058
50077	I09	M-010308- phospholip	255189	PLA2G4F	1945	5.0386	5.1014
50077	I10	M-007167- SNF2 histo	257218	SHPRH	2872	10.968	0.828
50077	I11	M-015943- chromoson	255193	C19orf34	1469	8.1007	2.0393
50077	I12	M-017055- Down synd	257203	DSCR9	3562	17.35	7.21
50077	I13	M-021616- mucolipin	255231	MCOLN2	979	7.763	2.377
50077	I14	M-019309- glutathion	257202	GPX6	2922	5.3046	4.8354
50077	I15	M-016103- leucine ric	255252	LRRC57	1016	13.78	3.64
50077	I16	M-018345- neuronal g	257194	NEGR1	4658	12.538	2.398
50077	I17	M-018362- cancer/tes	255313	RP6-166C1	1077	8.078	2.062
50077	I18	M-015571- chromoson	257169	C9orf43	3271	3.424	6.716
50077	I19	M-028155- chromoson	255330	C3orf46	1328	9.7139	0.4261
50077	I20	M-026520- ring finger	257160	RNF214	4650	12.28	2.14
50077	I21	M-018355- chromoson	255352	C10orf93	2295	7.7996	2.3404
50077	I23	M-015944- t-complex	255394	TCP11L2	1567	13.274	3.134
50077	J02	M-022336- golgi autoa	283768	GOLGA8G	3144	9.8919	0.2481
50077	J04	M-030486- hypothetic	283761	LOC283761	1593	11.174	1.034
50077	J05	M-018069- hypothetic	283241	LOC283241	3488	16.17	6.03
50077	J06	M-008599- phospholip	283748	PLA2G4D	1796	10.523	0.383
50077	J07	M-018296- REST corep	283248	RCOR2	3622	19.299	9.159
50077	J08	M-018254- family with	283742	FAM98B	2761	14.56	4.42
50077	J09	M-018300- chromoson	283254	C11orf77	3252	8.0873	2.0527

50077	J10	M-030428-	hypothetica	283731	LOC283731	1339	9.1113	1.0287
50077	J11	M-018298-	immunoglo	283284	IGSF22	2340	11.581	1.441
50077	J12	M-030371-	hypothetica	283697	LOC283697	1805	6.9806	3.1594
50077	J13	M-018288-	chromoson	283294	C11orf47	4349	15.866	5.726
50077	J14	M-018092-	chromoson	283687	C15orf37	1305	7.433	2.707
50077	J15	M-032016-	olfactory re	283297	OR10A4	4200	11.619	1.479
50077	J16	M-018970-	hypothetica	283685	FLJ36144	2417	12.702	2.562
50077	J17	M-027229-	olfactomec	283298	OLFML1	2480	11.331	1.191
50077	J18	M-030495-	hypothetica	283682	LOC283682	2258	9.4774	0.6626
50077	J19	M-018280-	chromoson	283303	C11orf36	1822	7.5741	2.5659
50077	J20	M-030425-	hypothetica	283677	LOC283677	2320	16.681	6.541
50077	J21	M-018260-	chromoson	283310	C12orf64	3340	16.976	6.836
50077	J23	M-030110-	hypothetica	283314	UNQ2963	4365	15.556	5.416
50077	K02	M-019286-	germinal ce	257144	GCET2	5086	16.103	5.963
50077	K04	M-009130-	Rho GTPase	257106	ARHGAP30	1828	7.2757	2.8643
50077	K05	M-015722-	zinc finger	255403	ZNF718	2078	9.8171	0.3229
50077	K06	M-015964-	chromoson	257103	C21orf86	4145	9.6984	0.4416
50077	K07	M-018016-	RasGEF dor	255426	RASGEF1C	1212	9.1584	0.9816
50077	K08	M-018347-	zinc finger	257101	ZNF683	4916	13.954	3.814
50077	K09	M-025119-	IBR domair	255488	IBRDC2	843	11.388	1.248
50077	K10	M-007166-	phosphatid	257068	PLCXD2	2439	12.71	2.57
50077	K11	M-016104-	ELMO/CED	255520	ELMOD2	1850	4.9189	5.2211
50077	K12	M-015570-	transmemb	257062	TMEM146	3320	16.777	6.637
50077	K13	M-017525-	histone clu	255626	HIST1H2BA	1518	7.7075	2.4325
50077	K14	M-015569-	D-2-hydrox	257054	D2HGDH	2852	14.481	4.341
50077	K15	M-018815-	collagen, ty	255631	COL24A1	2572	7.5039	2.6361
50077	K16	M-018349-	chromoson	257044	C1orf101	4924	9.4029	0.7371
50077	K17	M-022143-	hypothetica	255654	LOC255654	2216	8.7996	1.3404
50077	K18	M-017706-	FERM dom	257019	FRMD3	5591	12.645	2.505
50077	K19	M-032038-	zona pelluc	22917	ZP1	1632	12.194	2.054
50077	K20	M-015725-	placenta-sp	257000	PLAC2	3396	20.671	10.531
50077	K21	M-005989-	proprotein	255738	PCSK9	1395	5.5197	4.6203
50077	K23	M-027204-	nephronec	255743	NPNT	3202	6.3086	3.8314
50077	L02	M-018257-	transmemb	283673	TMEM84	1836	2.5054	7.6346
50077	L04	M-030407-	hypothetica	283663	LOC283663	1464	14.208	4.068
50077	L05	M-030069-	hypothetica	283331	LOC283331	2280	16.36	6.22
50077	L06	M-022248-	protogenin	283659	PRTG	2791	11.143	1.003
50077	L07	M-030070-	hypothetica	283332	LOC283332	3962	15.573	5.433
50077	L08	M-031913-	solute carri	283652	SLC24A5	395	9.3671	0.7729
50077	L09	M-018472-	Ras associa	283349	RASSF3	3649	18.827	8.687
50077	L10	M-018259-	chromoson	283651	C15orf21	1665	7.6276	2.5124
50077	L11	M-018273-	beta-1,4-N-	283358	B4GALNT3	3314	10.229	0.089
50077	L12	M-018263-	chromoson	283643	C14orf80	2108	23.292	13.152
50077	L13	M-030080-	ankyrin rep	283373	ANKRD52	4299	20.865	10.725
50077	L14	M-022012-	KIAA0284	283638	KIAA0284	2482	9.6293	0.5107
50077	L15	M-007364-	solute carri	283375	SLC39A5	2182	5.4079	4.7321
50077	L16	M-018433-	chromoson	283635	C14orf24	2171	5.7577	4.3823

50077	L17	M-027007-	SPRY doma	283377	SPRYD4	5615	16.26	6.12
50077	L18	M-007317-	chromoson	283600	C14orf68	1426	17.812	7.672
50077	L19	M-027093-	G protein-c	283383	GPR133	5766	18.176	8.036
50077	L20	M-018954-	chromoson	283598	C14orf177	1588	29.03	18.89
50077	L21	M-017746-	MORN repe	283385	MORN3	5436	20.309	10.169
50077	L23	M-030089-	hypothetica	283392	LOC283392	5096	15.463	5.323
50077	M02	M-018248-	serine inco	256987	SERINC5	4491	7.0808	3.0592
50077	M04	M-015568-	Sad1 and U	256979	SUNC1	4332	18.329	8.189
50077	M05	M-015945-	hypothetica	255758	MGC33212	2430	11.77	1.63
50077	M06	M-016261-	chromoson	256957	C17orf66	4786	7.9398	2.2002
50077	M07	M-018354-	chromoson	255762	C16orf65	1344	10.789	0.649
50077	M08	M-031728-	ankyrin rep	256949	ANKRD47	5383	14.713	4.573
50077	M09	M-023534-	chromoson	255798	C3orf43	3534	9.7906	0.3494
50077	M10	M-015724-	chromoson	256815	C10orf67	4291	11.279	1.139
50077	M11	M-023531-	succinate d	255812	SDHALP1	4911	21.482	11.342
50077	M12	M-019385-	WD repeat	256764	WDR72	1471	10.945	0.805
50077	M13	M-018790-	transmemb	255919	TMEM188	2299	17.747	7.607
50077	M14	M-016260-	MAP7 dom	256714	MAP7D2	3665	13.37	3.23
50077	M15	M-016105-	synaptotag	255928	SYT14	5475	24.986	14.846
50077	M16	M-015768-	MAM doma	256691	MAMDC2	2259	13.546	3.406
50077	M17	M-017990-	PAN3 polyA	255967	PAN3	3689	7.807	2.333
50077	M18	M-022211-	nuclear pro	256646	NUT	4570	24.814	14.674
50077	M19	M-024511-	ankyrin rep	256006	ANKRD31	3210	9.19	0.95
50077	M20	M-024917-	chromoson	256643	CXorf23	4692	15.793	5.653
50077	M21	M-030044-	hypothetica	256021	LOC256021	1190	15.042	4.902
50077	M23	M-016106-	zinc finger	256051	ZNF549	928	8.6207	1.5193
50077	N02	M-030321-	chromoson	283592	C14orf86	1776	3.7162	6.4238
50077	N04	M-021989-	hypothetica	283587	LOC283587	1868	3.7473	6.3927
50077	N05	M-030071-	hypothetica	283400	LOC283400	5769	11.752	1.612
50077	N06	M-030316-	hypothetica	283585	LOC283585	2746	6.8463	3.2937
50077	N07	M-026955-	hypothetica	283403	LOC283403	4773	13.032	2.892
50077	N08	M-017928-	chromoson	283579	C14orf178	2251	8.4851	1.6549
50077	N09	M-018068-	chromoson	283416	C12orf61	5116	18.471	8.331
50077	N10	M-021982-	transmemb	283578	TMED8	3003	15.951	5.811
50077	N11	M-018272-	dpy-19-like	283417	DPY19L2	4795	14.557	4.417
50077	N12	M-022054-	prospero h	283571	PROX2	1824	8.8268	1.3132
50077	N13	M-032040-	C-type lecti	283420	CLEC9A	4869	14.13	3.99
50077	N14	M-005743-	G protein-c	283554	GPR137C	3590	12.786	2.646
50077	N15	M-018912-	chromoson	283422	C12orf36	5842	18.726	8.586
50077	N16	M-030289-	hypothetica	283551	LOC283551	1672	5.9809	4.1591
50077	N17	M-017927-	growth arre	283431	GAS2L3	4484	19.67	9.53
50077	N18	M-030287-	hypothetica	283547	LOC283547	2188	9.6435	0.4965
50077	N19	M-030051-	hypothetica	283432	LOC283432	5185	21.311	11.171
50077	N20	M-018594-	solute carri	283537	SLC46A3	2140	11.215	1.075
50077	N21	M-032183-	hypothetica	283439	LOC283439	5117	23.568	13.428
50077	N23	M-018271-	myosin IH	283446	MYO1H	2104	10.456	0.316
50077	O02	M-015723-	LysM, puta	256586	LYSMD2	4283	6.9344	3.2056

50077	O04	M-017916- transcripti	256536	TCERG1L	2470	8.9879	1.1521
50077	O05	M-015765- hypothetic	256076	FLJ35880	2621	6.1045	4.0355
50077	O06	M-015767- transmem	256472	TMEM151	2560	4.0234	6.1166
50077	O07	M-015946- hypothetic	256130	MGC42090	2601	9.3426	0.7974
50077	O08	M-007362- major facili	256471	MFSD8	2944	5.3329	4.8071
50077	O09	M-029449- hemicentin	256158	HMCN2	804	9.5771	0.5629
50077	O10	M-015456- ST6 (alpha-	256435	ST6GALNA	4759	14.604	4.464
50077	O11	M-032039- similar to S	256227	MGC87042	1484	9.9057	0.2343
50077	O12	M-021430- sex comb c	256380	SCML4	2210	11.131	0.991
50077	O13	M-029531- coactivator	256280	CARM1L	1554	10.811	0.671
50077	O14	M-016258- chromoson	256369	C14orf48	4676	14.115	3.975
50077	O15	M-009076- nudix (nucl	256281	NUDT14	3052	11.861	1.721
50077	O16	M-015766- echinoderr	256364	EML3	2466	10.462	0.322
50077	O17	M-018469- pancreas s	256297	PTF1A	1678	8.2241	1.9159
50077	O18	M-006816- glycerol kir	256356	GK5	1855	26.954	16.814
50077	O19	M-016632- transcript	256302	MGC33894	1703	11.509	1.369
50077	O20	M-028819- ribosomal	256355	MGC27348	2117	9.1167	1.0233
50077	O21	M-015947- coiled-coil	256309	CCDC110	1895	20.369	10.229
50077	O23	M-018350- chromoson	256329	C11orf35	1030	22.136	11.996
50077	P02	M-018264- potassium	283518	KCNRG	1550	15.032	4.892
50077	P04	M-032242- similar to s	283514	LOC28351	1019	10.893	0.753
50077	P05	M-018270- chromoson	283450	C12orf51	4188	15.521	5.381
50077	P06	M-018266- hypothetic	283492	FLJ25694	2339	6.4558	3.6842
50077	P07	M-018269- chromoson	283461	C12orf40	4872	12.931	2.791
50077	P08	M-030231- olfactory re	283491	OR7E156P	2807	9.4051	0.7349
50077	P09	M-026987- glycosyltra	283464	GLT8D3	4805	16.857	6.717
50077	P10	M-021601- chromoson	283489	C13orf8	3361	16.067	5.927
50077	P11	M-016318- cutaneous	64693	CTAGE1	5826	17.92	7.78
50077	P12	M-018213- chromoson	283487	C13orf29	2990	8.3612	1.7788
50077	P13	M-015666- putative pr	282706	G30	3520	17.813	7.673
50077	P14	M-030190- hypothetic	283483	LOC28348	1856	3.3944	6.7456
50077	P15	M-019031- late cornifi	254910	LCE5A	4807	15.29	5.15
50077	P16	M-030189- hypothetic	283480	LOC28348	1790	12.626	2.486
50077	P17	M-017882- synovial sa	280659	SSX8	1898	10.959	0.819
50077	P18	M-005948- transmem	283471	TMPRSS12	3689	10.735	0.595
50077	P19	M-016426- neuropepti	256933	NPB	3752	13.753	3.613
50077	P20	M-008784- hypothetic	283470	FLJ34278	1872	13.088	2.948
50077	P21	M-031928- transmem	388730	TMEM81	1721	8.4834	1.6566
50077	P23	M-032078- FLJ45717 p	388759	FLJ45717	2334	5.9126	4.2274
				MAD	2275	10.1395	3.1553
				MAD3			9.4659
				MADc			4.669844
50077	C22				1488	38.239	
50077	D22				2258	21.391	
50077	E22				1637	26.634	
50077	F22				3696	28.95	
				mn	2269.75	28.8035	

					sd	1007.61	7.040407
50077	G22					472	6.5678
50077	H22					688	4.6512
50077	I22			370	10		
50077	J22					899	6.6741
					mn	686.3333	5.964367
					sd	213.5049	1.138477
					3psSD		21.12122
					3ngSD		3.415431
					SumSD		24.53665
					MeanDf		22.83913
					SumovrMn		1.074325
					1minus		-0.07433

50077	G03	M-003290-	polo-like ki	5347	PLK1 SMAF	237	13.08
50077	H03	M-003290-	polo-like ki	5347	PLK1 SMAF	105	27.619
50077	I03	D-001206-:	siControl non-targeting			1655	6.8882
50077	J03	D-001206-:	siControl non-targeting			883	10.646
50077	L03	D-001600-(	siGLO RISC-free siRNA			3482	16.198
50077	K03	D-001600-(	siGLO RISC-free siRNA			5260	14.068

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
-0.92414	870	8.046	0.946	0.169184	774	5.0388	2.6512	-0.52345
1.112564	342	19.006	11.906	2.123607	508	15.157	7.467	1.477174
0.221956	545	18.165	11.065	1.973637	443	8.3521	0.6621	0.131675
0.519396	564	13.298	6.198	1.105738	1439	5.8374	1.8526	-0.36554
0.407401	1052	4.5627	2.5373	-0.45197	871	5.1665	2.5235	-0.4982
-0.72437	720	11.389	4.289	0.765319	927	4.8544	2.8356	-0.55991
0.923693	804	7.9602	0.8602	0.153884	974	4.8255	2.8645	-0.56562
-0.45376	1124	11.388	4.288	0.76514	363	9.9174	2.2274	0.441174
-0.81123	545	11.376	4.276	0.763001	693	8.0808	0.3908	0.078032
-0.65221	599	8.8481	1.7481	0.312217	495	9.0909	1.4009	0.277754
0.993074	365	9.589	2.489	0.444337	275	13.091	5.401	1.068674
2.738314	299	31.773	24.673	4.40026	431	4.6404	3.0496	-0.60222
1.591167	278	24.82	17.72	3.160378	539	8.7199	1.0299	0.204398
1.085368	863	10.429	3.329	0.594128	854	11.827	4.137	0.818749
2.358644	329	13.678	6.578	1.173501	854	2.3419	5.3481	-1.05669
1.338053	405	15.062	7.962	1.4203	1126	12.167	4.477	0.885976
0.634604	830	6.3855	0.7145	-0.12692	598	13.88	6.19	1.224679
1.639776	493	11.765	4.665	0.832368	628	10.35	2.66	0.52671
0.139512	613	13.051	5.951	1.061692	369	21.409	13.719	2.71335
-0.64169	312	13.141	6.041	1.077741	425	13.176	5.486	1.08548
-0.32656	1394	0.7891	6.3109	-1.12489	1307	3.137	4.553	-0.89948
0.077412	1063	4.9859	2.1141	-0.3765	1121	3.2114	4.4786	-0.88477
-0.34297	1369	2.4836	4.6164	-0.82272	2206	7.5703	0.1197	-0.02291
-1.11079	1343	2.755	4.345	-0.77432	1736	4.3203	3.3697	-0.66551
0.072915	1166	4.3739	2.7261	-0.48564	1885	3.9788	3.7112	-0.73304
0.057497	765	2.4837	4.6163	-0.8227	948	3.7975	3.8925	-0.76888
0.014026	1109	4.5086	2.5914	-0.46162	1613	3.7198	3.9702	-0.78425
-0.73193	1452	1.7218	5.3782	-0.95857	2687	4.5032	3.1868	-0.62935
1.138689	568	11.092	3.992	0.712357	378	17.46	9.77	1.932534
-0.67469	824	2.7913	4.3087	-0.76785	419	7.8759	0.1859	0.037518
-0.62863	1205	1.0788	6.0212	-1.07323	1077	5.1068	2.5832	-0.51
-0.43464	1513	1.9828	5.1172	-0.91203	1757	4.667	3.023	-0.59696
0.83975	1224	5.3105	1.7895	-0.31862	1439	8.6866	0.9966	0.197814
-0.74367	1515	2.2442	4.8558	-0.86541	2401	2.7489	4.9411	-0.97622
-0.66925	830	1.6867	5.4133	-0.96483	1586	5.1072	2.5828	-0.50992
-1.46793	665	3.4586	3.6414	-0.64886	684	5.2632	2.4268	-0.47908
-0.15988	330	3.0303	4.0697	-0.72523	369	14.905	7.215	1.427347
-0.25003	1024	7.1289	0.0289	0.005644	2167	10.383	2.693	0.533235
-1.21993	834	2.6379	4.4621	-0.79521	1164	11.254	3.564	0.705453
-1.55273	2237	2.4586	4.6414	-0.82718	1749	6.0034	1.6866	-0.33272
-0.73602	3043	2.2018	4.8982	-0.87297	3064	3.9817	3.7083	-0.73246
0.07163	1918	8.6548	1.5548	0.277747	2338	3.9778	3.7122	-0.73323
-1.08421	1684	5.6413	1.4587	-0.25963	1976	4.9595	2.7305	-0.53913
0.157072	1779	6.2395	0.8605	-0.15296	4117	5.4166	2.2734	-0.44875
-1.15768	1441	7.2172	0.1172	0.02139	1906	5.6139	2.0761	-0.40974
1.851347	366	27.596	20.496	3.655404	740	12.432	4.742	0.938373

-1.12884	1037	7.9074	0.8074	0.144469	1767	6.0555	1.6345	-0.32242
-0.12748	532	13.534	6.434	1.147822	1045	4.4019	3.2881	-0.64938
-0.87817	1987	7.2471	0.1471	0.026722	2336	2.6969	4.9931	-0.9865
-1.31625	1402	12.197	5.097	0.909404	1633	16.534	8.844	1.749441
0.441449	444	14.64	7.54	1.345048	525	10.857	3.167	0.626956
1.081514	1279	15.637	8.537	1.522836	1944	5.1955	2.4945	-0.49246
0.531388	1402	10.913	3.813	0.680437	1600	5.1875	2.5025	-0.49405
0.524107	1463	10.731	3.631	0.647982	2070	2.8986	4.7914	-0.94662
-0.02752	799	15.895	8.795	1.568843	1357	5.4532	2.2368	-0.44151
1.121344	959	17.205	10.105	1.802447	1628	6.2039	1.4861	-0.29308
0.159855	1625	10.092	2.992	0.534034	1515	5.9406	1.7494	-0.34514
1.514719	3309	16.893	9.793	1.74681	3517	13.904	6.214	1.229424
-0.55841	1929	6.3245	0.7755	-0.1378	2584	3.9087	3.7813	-0.7469
1.656051	4221	8.9078	1.8078	0.322863	4398	13.256	5.566	1.101298
-1.30032	1546	1.3583	5.7417	-1.02339	1623	4.5595	3.1305	-0.61822
0.159641	976	4.7131	2.3869	-0.42515	1595	6.0188	1.6712	-0.32968
0.454298	1367	8.4857	1.3857	0.247593	1986	8.2075	0.5175	0.103084
-0.22502	3147	6.3553	0.7447	-0.13231	3902	5.1256	2.5644	-0.50628
0.556871	3957	6.0399	1.0601	-0.18855	4293	6.9881	0.7019	-0.13802
-0.77898	716	8.3799	1.2799	0.228726	801	11.361	3.671	0.72661
-1.06239	770	6.2338	0.8662	-0.15397	1273	3.9277	3.7623	-0.74314
-0.02345	1513	12.227	5.127	0.914754	2357	6.7883	0.9017	-0.17753
-0.29545	2622	8.3905	1.2905	0.230617	3184	5.1508	2.5392	-0.5013
-1.2058	1049	5.0524	2.0476	-0.36464	1074	4.0968	3.5932	-0.7097
-1.48506	1681	4.878	2.222	-0.39574	1421	3.3075	4.3825	-0.86577
-0.26635	1116	6.362	0.738	-0.13111	1281	2.498	5.192	-1.02583
-0.32999	2808	13.212	6.112	1.090402	3166	7.5174	0.1726	-0.03337
-1.3839	1171	5.38	1.72	-0.30623	1642	1.6443	6.0457	-1.19462
-0.15041	1991	12.104	5.004	0.89282	3223	9.4012	1.7112	0.339108
-0.78365	1520	12.961	5.861	1.045643	2059	2.0398	5.6502	-1.11642
-0.94059	2497	9.6115	2.5115	0.448349	3515	3.5277	4.1623	-0.82223
-1.22081	1986	6.7976	0.3024	-0.05343	1566	3.1928	4.4972	-0.88845
0.2408	4923	24.782	17.682	3.153602	5627	12.049	4.359	0.862644
-1.79625	1314	5.5556	1.5444	-0.27491	767	5.4759	2.2141	-0.43702
-0.24949	1194	1.1725	5.9275	-1.05652	1944	5.0926	2.5974	-0.51281
-1.54652	733	1.2278	5.8722	-1.04666	911	5.2689	2.4211	-0.47795
-0.1175	2284	3.0648	4.0352	-0.71908	3443	6.0122	1.6778	-0.33098
0.089189	2367	6.8019	0.2981	-0.05267	3479	6.065	1.625	-0.32054
0.096256	695	1.8705	5.2295	-0.93205	1350	7.7778	0.0878	0.018121
0.339091	3040	9.2763	2.1763	0.388575	3691	8.1279	0.4379	0.087345
-0.60576	744	2.957	4.143	-0.7383	779	4.4929	3.1971	-0.63139
-0.01403	1981	11.257	4.157	0.74178	3270	5.9021	1.7879	-0.35275
1.123271	658	13.678	6.578	1.173501	1854	10.68	2.99	0.591959
0.718546	2146	10.718	3.618	0.645664	1995	3.2581	4.4319	-0.87554
-0.6669	275	4	3.1	-0.55231	250	9.6	1.91	0.378416
0.301616	3706	23.314	16.214	2.891823	4613	10.514	2.824	0.559137
-0.45635	809	5.686	1.414	-0.25166	1069	8.232	0.542	0.107928

0.566507	4597	15.967	8.867	1.581683	4386	9.8723	2.1823	0.432256
-1.01652	661	4.6899	2.4101	-0.42929	1131	2.6525	5.0375	-0.99528
0.112959	1161	8.5271	1.4271	0.254975	1545	5.2427	2.4473	-0.48313
-0.1111	1265	9.4071	2.3071	0.4119	1257	3.4208	4.2692	-0.84337
-0.15157	3519	19.352	12.252	2.185307	5369	10.281	2.591	0.513067
-1.39062	589	8.1494	1.0494	0.187623	1017	4.9164	2.7736	-0.54765
-1.32801	1887	8.638	1.538	0.274752	1009	5.55	2.14	-0.42237
-1.40489	2511	0.71685	6.38315	-1.13777	1951	3.6904	3.9996	-0.79006
-1.28098	2392	2.2993	4.8007	-0.85559	1862	7.6262	0.0638	-0.01185
-0.36622	4248	3.2957	3.8043	-0.6779	3445	10.363	2.673	0.52928
-0.63994	2193	0.091199	7.008801	-1.24934	2616	6.6131	1.0769	-0.21217
0.095828	4951	6.6855	0.4145	-0.07342	5414	19.616	11.926	2.358829
-0.42468	1049	2.9552	4.1448	-0.73862	1132	12.279	4.589	0.908121
-2.01103	1254	0.39872	6.70128	-1.1945	1307	5.8914	1.7986	-0.35487
-1.59605	1990	1.2563	5.8437	-1.04158	1907	4.9292	2.7608	-0.54512
0.410827	3532	13.25	6.15	1.097178	4738	16.547	8.857	1.752011
-0.81752	246	8.1301	1.0301	0.184181	601	17.471	9.781	1.934709
-1.08351	605	4.6281	2.4719	-0.44031	977	8.4954	0.8054	0.160009
-1.09344	1217	2.2186	4.8814	-0.86998	1060	3.3962	4.2938	-0.84823
-1.56515	2374	2.8222	4.2778	-0.76234	2954	11.747	4.057	0.802931
-1.51954	1046	3.8241	3.2759	-0.58368	1791	3.6851	4.0049	-0.79111
-0.45633	4296	12.942	5.842	1.042255	5856	16.291	8.601	1.701394
-1.46311	1501	2.0653	5.0347	-0.89731	2395	2.5887	5.1013	-1.00789
-0.50117	5896	21.014	13.914	2.48168	5851	10.614	2.924	0.578909
-1.88417	2047	3.8105	3.2895	-0.5861	2130	0.75117	6.93883	-1.37122
-0.31873	4013	7.8993	0.7993	0.143024	6153	17.406	9.716	1.921857
-2.09692	647	9.5827	2.4827	0.443213	376	1.5957	6.0943	-1.20423
-1.5266	2285	6.477	0.623	-0.1106	2022	3.907	3.783	-0.74723
1.20079	2048	23.145	16.045	2.861687	1262	9.588	1.898	0.376043
0.772724	625	20	12.9	2.30086	244	12.705	5.015	0.992352
-0.47184	4426	16.064	8.964	1.59898	2379	7.9025	0.2125	0.042778
0.617044	231	40.693	33.593	5.990903	200	26	18.31	3.621106
0.398621	3557	14.76	7.66	1.366446	1410	6.7376	0.9524	-0.18755
0.694991	4053	23.341	16.241	2.896638	2639	7.6923	0.0023	0.001216
-1.37683	756	8.8624	1.7624	0.314767	444	4.955	2.735	-0.54002
-0.8329	1523	16.415	9.315	1.661571	1316	7.4468	0.2432	-0.04733
-0.25838	1109	12.894	5.794	1.033695	784	3.4439	4.2461	-0.8388
0.72647	653	24.655	17.555	3.130955	400	8.5	0.81	0.160918
0.348513	1297	14.958	7.858	1.401754	1545	8.6731	0.9831	0.195145
-1.10017	1633	9.553	2.453	0.437917	2000	3.6	4.09	-0.80793
0.596058	1715	15.627	8.527	1.521053	1588	11.398	3.708	0.733925
1.111065	855	17.193	10.093	1.800307	480	10.417	2.727	0.539957
-1.08139	2483	8.1353	1.0353	0.185108	3034	3.9222	3.7678	-0.74423
-0.95157	1341	12.081	4.981	0.888718	1159	5.3494	2.3406	-0.46203
-0.28521	2892	20.124	13.024	2.322972	2093	9.3645	1.6745	0.331852
-1.09361	1300	11.846	4.746	0.846812	1709	7.4312	0.2588	-0.05041
-1.50138	1343	4.8399	2.2601	-0.40254	858	3.4965	4.1935	-0.8284

-1.06991	1144	8.8287	1.7287	0.308758	873	3.3219	4.3681	-0.86292
0.181912	1119	17.784	10.684	1.905696	372	13.441	5.751	1.137878
1.347904	3700	17.946	10.846	1.934584	4323	10.826	3.136	0.620827
0.196259	1234	8.59	1.49	0.266192	1093	6.9533	0.7367	-0.1449
3.856553	2962	25.726	18.626	3.321939	2682	21.663	13.973	2.763572
-0.94706	1382	17.149	10.049	1.792461	661	9.8336	2.1436	0.424605
0.758162	5219	16.938	9.838	1.754834	4223	14.492	6.802	1.345687
-0.35262	1150	7.5652	0.4652	0.083446	782	6.266	1.424	-0.2808
-0.35832	1163	10.576	3.476	0.620342	1435	4.8084	2.8816	-0.569
0.019808	812	11.946	4.846	0.864645	437	7.5515	0.1385	-0.02662
0.743815	671	19.672	12.572	2.24237	268	14.179	6.489	1.283799
0.395409	469	15.139	8.039	1.434031	625	7.68	0.01	-0.00122
0.517255	1768	16.007	8.907	1.588815	830	11.205	3.515	0.695765
-0.82155	1007	8.0437	0.9437	0.168774	1244	8.3601	0.6701	0.133257
0.287483	1531	13.063	5.963	1.063832	1137	11.609	3.919	0.775645
-0.25667	1478	11.705	4.605	0.821669	1024	7.5195	0.1705	-0.03295
-0.30733	3466	16.33	9.23	1.646414	2012	12.326	4.636	0.917414
0.568434	1928	18.257	11.157	1.990043	1723	6.7324	0.9576	-0.18858
-1.07079	1731	8.3189	1.2189	0.217849	1279	1.9547	5.7353	-1.13325
-1.23253	1362	9.6182	2.5182	0.449544	864	8.4491	0.7591	0.150854
-0.37464	4957	4.3776	2.7224	-0.48498	5550	9.9279	2.2379	0.44325
0.50098	5124	10.792	3.692	0.65886	4939	16.603	8.913	1.763084
-1.02931	2243	1.9171	5.1829	-0.92374	1647	9.4718	1.7818	0.353068
-0.58679	6007	8.6066	1.5066	0.269152	4379	12.606	4.916	0.972777
-0.54239	1472	6.25	0.85	-0.15108	1062	11.676	3.986	0.788893
0.226667	3720	8.629	1.529	0.273147	3896	15.939	8.249	1.631795
-1.09231	1149	1.2185	5.8815	-1.04832	1047	8.1184	0.4284	0.085467
0.177415	1309	1.7571	5.3429	-0.95227	1116	7.7957	0.1057	0.021661
-0.43659	694	7.0605	0.0395	-0.00655	405	19.753	12.063	2.385918
1.544056	3916	9.6527	2.5527	0.455696	4346	22.918	15.228	3.011717
-0.5089	681	1.6153	5.4847	-0.97756	496	12.097	4.407	0.872135
-1.03535	2144	7.3694	0.2694	0.048531	2015	12.754	5.064	1.002041
0.779576	598	9.3645	2.2645	0.404303	606	22.277	14.587	2.884975
0.513615	3123	6.9805	0.1195	-0.02082	4411	20.721	13.031	2.577315
-0.44145	893	2.9115	4.1885	-0.74642	808	9.5297	1.8397	0.364516
-1.43806	3077	2.0799	5.0201	-0.89471	4075	6.6012	1.0888	-0.21452
-0.09114	1040	5.6731	1.4269	-0.25396	851	3.2902	4.3998	-0.86919
0.458366	4734	7.9003	0.8003	0.143202	4613	17.212	9.522	1.883498
-0.50107	2854	3.0834	4.0166	-0.71576	2905	11.945	4.255	0.842081
0.671222	1113	7.8167	0.7167	0.128295	1078	17.904	10.214	2.020324
-0.05302	1696	5.3066	1.7934	-0.31931	2096	2.2424	5.4476	-1.07637
0.221528	1344	4.6131	2.4869	-0.44298	1211	4.7069	2.9831	-0.58907
1.291371	5070	14.655	7.555	1.347722	4099	11.783	4.093	0.81005
0.082123	1261	5.0753	2.0247	-0.36056	387	3.6176	4.0724	-0.80445
1.961415	2768	13.295	6.195	1.105203	1816	5.6167	2.0733	-0.40918
0.946605	883	12.458	5.358	0.955946	373	6.9705	0.7195	-0.1415
-0.43946	2056	3.356	3.744	-0.66715	984	3.1504	4.5396	-0.89683

-0.22018	1241	5.2377	1.8623	-0.3316	601	4.1597	3.5303	-0.69727
0.308683	2052	7.7973	0.6973	0.124835	999	2.8028	4.8872	-0.96556
-0.67645	1707	5.7411	1.3589	-0.24183	946	2.1142	5.5758	-1.10171
1.226272	4613	14.979	7.879	1.405499	3891	10.846	3.156	0.624781
-0.57957	1320	10.985	3.885	0.693276	985	3.6548	4.0352	-0.7971
0.31682	4594	12.495	5.395	0.962544	4096	11.768	4.078	0.807084
0.548734	2233	12.091	4.991	0.890502	1260	3.8095	3.8805	-0.76651
0.255148	3573	7.2768	0.1768	0.032018	3113	8.8018	1.1118	0.220592
-0.14178	1518	3.5573	3.5427	-0.63126	991	4.2381	3.4519	-0.68177
-0.54935	2386	2.6823	4.4177	-0.78729	1751	1.3706	6.3194	-1.24874
1.400796	2473	10.352	3.252	0.580398	1134	10.67	2.98	0.589982
1.463968	3109	10.743	3.643	0.650122	2874	9.4294	1.7394	0.344684
1.159889	4291	10.114	3.014	0.537957	3993	10.118	2.428	0.480837
1.277023	5137	10.337	3.237	0.577723	5733	14.722	7.032	1.391163
-0.61325	1464	0.61475	6.48525	-1.15598	887	8.23	0.54	0.107533
-0.06904	1864	3.3262	3.7738	-0.67247	726	10.055	2.365	0.468381
-0.09446	3741	4.5175	2.5825	-0.46003	2941	5.5423	2.1477	-0.42389
-0.21009	619	3.8772	3.2228	-0.57421	452	19.469	11.779	2.329764
0.816837	3717	9.8197	2.7197	0.485476	3435	9.8108	2.1208	0.420096
0.267354	337	14.243	7.143	1.274253	180	28.333	20.643	4.082398
0.550447	1721	5.9268	1.1732	-0.20872	1141	12.007	4.317	0.85434
-1.11794	573	7.5044	0.4044	0.072604	360	9.7222	2.0322	0.402578
1.421354	3091	9.9644	2.8644	0.511279	1926	12.876	5.186	1.026163
-0.52079	591	15.228	8.128	1.449902	337	11.869	4.179	0.827054
0.929688	1229	12.856	5.756	1.026919	928	13.47	5.78	1.143612
-0.56439	1523	10.834	3.734	0.666349	1217	8.9565	1.2665	0.25118
-0.15774	3229	10.963	3.863	0.689353	3384	7.1217	0.5683	-0.11161
-0.28693	1465	6.4164	0.6836	-0.12141	1246	10.353	2.663	0.527303
0.536528	4984	17.516	10.416	1.857905	4515	11.008	3.318	0.656813
0.43995	1567	16.847	9.747	1.738607	498	17.47	9.78	1.934512
2.255215	1470	26.735	19.635	3.501867	1598	17.146	9.456	1.870449
-0.98928	1042	16.987	9.887	1.763572	762	21.129	13.439	2.657987
-0.82035	2829	6.9636	0.1364	-0.02383	2649	4.7188	2.9712	-0.58672
-1.63477	837	0.59737	6.50263	-1.15908	1189	8.2422	0.5522	0.109945
0.871228	942	0.42463	6.67537	-1.18988	947	13.728	6.038	1.194625
1.332057	1595	4.6395	2.4605	-0.43827	1625	11.692	4.002	0.792057
0.214889	1648	2.0024	5.0976	-0.90853	826	9.4431	1.7531	0.347393
1.163529	5391	13.764	6.664	1.188836	3426	12.201	4.511	0.892699
-0.1654	457	0.87527	6.22473	-1.10952	173	14.451	6.761	1.33758
1.860341	4857	14.742	7.642	1.363237	3514	14.57	6.88	1.361109
-0.5379	1117	1.2534	5.8466	-1.04209	645	6.6667	1.0233	-0.20157
0.019166	3419	4.6797	2.4203	-0.43111	2298	6.1358	1.5542	-0.30654
2.816475	829	6.2726	0.8274	-0.14705	722	8.3102	0.6202	0.12339
2.296758	2329	6.0541	1.0459	-0.18602	4678	16.567	8.877	1.755966
-0.10925	1683	7.4272	0.3272	0.058838	1585	9.9054	2.2154	0.438801
-1.01322	1248	5.4487	1.6513	-0.29397	1095	9.7717	2.0817	0.412365
-0.93832	865	1.2717	5.8283	-1.03883	950	9.2632	1.5732	0.311822

1.310643	4729	14.845	7.745	1.381604	4624	13.906	6.216	1.22982
1.642989	586	2.901	4.199	-0.74829	282	28.014	20.324	4.019324
1.720935	4237	10.668	3.568	0.636748	4756	6.3499	1.3401	-0.26421
4.04521	722	6.2327	0.8673	-0.15417	782	28.517	20.827	4.118779
2.177696	4905	12.457	5.357	0.955768	4958	13.493	5.803	1.148159
1.139974	4187	9.3384	2.2384	0.399649	4974	9.6301	1.9401	0.384367
-0.65499	3606	2.5513	4.5487	-0.81065	4238	9.4148	1.7248	0.341797
1.753699	2694	7.9807	0.8807	0.15754	3076	18.921	11.231	2.22141
0.349155	1572	1.4631	5.6369	-1.0047	819	4.2735	3.4165	-0.67477
-0.47104	2745	1.6029	5.4971	-0.97977	2771	3.8614	3.8286	-0.75625
0.139084	960	1.0417	6.0583	-1.07985	473	4.2283	3.4617	-0.6837
0.979369	4007	7.0377	0.0623	-0.01062	3985	12.472	4.782	0.946282
-0.07471	1694	2.8335	4.2665	-0.76033	1058	3.3081	4.3819	-0.86565
0.244012	3625	4.5241	2.5759	-0.45885	2597	4.5437	3.1463	-0.62134
2.428882	3710	7.655	0.555	0.09946	3011	12.587	4.897	0.96902
0.17249	1215	2.3868	4.7132	-0.83998	1190	1.1765	6.5135	-1.28712
1.629069	1164	4.9828	2.1172	-0.37706	1323	7.3318	0.3582	-0.07006
0.691779	3095	7.2698	0.1698	0.03077	3015	4.5108	3.1792	-0.62785
3.179228	4995	13.594	6.494	1.158522	3837	7.975	0.285	0.057113
0.729468	2226	8.3558	1.2558	0.224429	1697	4.1839	3.5061	-0.69248
-0.49948	2613	1.99	5.11	-0.91074	1787	2.0145	5.6755	-1.12143
3.142396	3918	11.383	4.283	0.764249	4674	6.3543	1.3357	-0.26334
-0.20333	1962	8.5117	1.4117	0.252229	1764	0.96372	6.72628	-1.32919
1.21064	4558	10.399	3.299	0.588779	4779	8.3072	0.6172	0.122797
1.049821	810	4.1975	2.9025	-0.51709	517	3.4816	4.2084	-0.83134
-0.32524	766	8.4856	1.3856	0.247575	1691	4.3761	3.3139	-0.65448
-1.37548	1068	0.74906	6.35094	-1.13203	2160	3.1481	4.5419	-0.89729
-1.36883	1207	1.4085	5.6915	-1.01444	1381	3.3309	4.3591	-0.86114
0.345301	3848	7.7703	0.6703	0.12002	5002	9.4362	1.7462	0.346029
-0.70521	1211	1.8167	5.2833	-0.94164	1468	3.7466	3.9434	-0.77895
0.6194	3656	6.7834	0.3166	-0.05597	3386	10.425	2.735	0.541539
-0.35427	1007	2.1847	4.9153	-0.87602	837	0.4779	7.2121	-1.42525
1.784107	3530	5.864	1.236	-0.21992	3562	8.0292	0.3392	0.06783
1.244474	2569	8.5636	1.4636	0.261484	1828	3.2823	4.4077	-0.87075
0.945963	3142	7.0656	0.0344	-0.00564	3708	8.1985	0.5085	0.101304
-0.2811	1102	5.1724	1.9276	-0.34325	1179	0.67854	7.01146	-1.38558
0.854525	3155	5.103	1.997	-0.35562	3120	5.0641	2.6259	-0.51844
0.566721	1547	6.2702	0.8298	-0.14748	1082	3.9741	3.7159	-0.73396
1.838712	4647	6.8001	0.2999	-0.05299	4321	8.8637	1.1737	0.232831
-0.89052	1763	1.418	5.682	-1.01274	497	1.2072	6.4828	-1.28105
2.04086	4008	13.473	6.373	1.136944	3918	16.794	9.104	1.800849
-0.10621	1518	5.4018	1.6982	-0.30234	907	0.77178	6.91822	-1.36714
2.392264	5344	10.741	3.641	0.649765	3439	6.3391	1.3509	-0.26635
0.230307	1448	4.0055	3.0945	-0.55133	997	3.009	4.681	-0.92479
2.875578	5032	9.8768	2.7768	0.495658	3948	7.1175	0.5725	-0.11244
0.067775	1368	3.655	3.445	-0.61383	1676	3.2816	4.4084	-0.87089
-0.68634	3316	3.7696	3.3304	-0.5934	3505	14.094	6.404	1.266992

-0.2466	2794	9.8425	2.7425	0.489542	1245	11.647	3.957	0.783159
-0.86405	1424	1.8258	5.2742	-0.94002	892	6.278	1.412	-0.27843
-1.3097	2423	4.9938	2.1062	-0.37509	884	5.6561	2.0339	-0.40139
-0.17065	1742	3.0425	4.0575	-0.72306	688	4.0698	3.6202	-0.71504
-1.02928	1537	2.7326	4.3674	-0.77832	526	10.456	2.766	0.547669
-0.12043	1155	4.1558	2.9442	-0.52453	304	12.829	5.139	1.01687
0.956028	4540	6.9383	0.1617	-0.02834	2488	14.831	7.141	1.412715
-0.05007	2032	3.7402	3.3598	-0.59864	472	4.8729	2.8171	-0.55625
0.21232	1596	2.4436	4.6564	-0.82985	1707	13.24	5.55	1.098135
0.143795	833	3.8415	3.2585	-0.58058	406	11.823	4.133	0.817959
0.851313	4051	6.0232	1.0768	-0.19153	1470	8.3673	0.6773	0.13468
0.368642	1544	3.6269	3.4731	-0.61884	1048	11.927	4.237	0.838522
0.06906	1589	4.2165	2.8835	-0.5137	589	6.2818	1.4082	-0.27768
-0.41016	1507	2.787	4.313	-0.76862	473	9.7252	2.0352	0.403171
3.600656	1355	6.3469	0.7531	-0.1338	909	14.741	7.051	1.39492
0.293265	1876	4.4776	2.6224	-0.46714	643	14.619	6.929	1.370798
-0.21902	1623	4.1898	2.9102	-0.51847	1061	8.4826	0.7926	0.157478
2.190544	1238	4.8465	2.2535	-0.40136	948	14.451	6.761	1.33758
2.568929	523	8.0306	0.9306	0.166438	300	22.333	14.643	2.896048
1.04768	690	1.5942	5.5058	-0.98132	1285	10.584	2.894	0.572977
0.161354	667	5.0975	2.0025	-0.3566	958	4.2797	3.4103	-0.67354
1.152394	3452	5.4171	1.6829	-0.29961	2990	10.268	2.578	0.510496
-0.78883	1725	1.4493	5.6507	-1.00716	534	5.0562	2.6338	-0.52001
0.597772	2923	11.427	4.327	0.772095	2250	9.2444	1.5544	0.308105
-0.15726	1354	1.8464	5.2536	-0.93635	792	4.5455	3.1445	-0.62098
1.438485	4007	6.1393	0.9607	-0.17082	3348	14.755	7.065	1.397688
1.269314	1838	9.2492	2.1492	0.383743	1389	8.7833	1.0933	0.216934
1.666116	3100	8.6452	1.5452	0.276035	2248	11.966	4.276	0.846233
-0.38081	1453	2.0647	5.0353	-0.89742	811	6.7818	0.9082	-0.17881
1.643203	1668	3.2374	3.8626	-0.6883	859	4.0745	3.6155	-0.71411
-1.4444	1803	2.6622	4.4378	-0.79087	738	1.084	6.606	-1.30541
1.102928	2231	4.7961	2.3039	-0.41035	2347	8.4789	0.7889	0.156746
0.532459	1350	1.9259	5.1741	-0.92217	1362	0.88106	6.80894	-1.34554
0.175488	1524	8.3333	1.2333	0.220416	953	3.3578	4.3322	-0.85582
0.12752	1376	3.9971	3.1029	-0.55283	1057	2.176	5.514	-1.08949
0.773795	2341	2.3921	4.7079	-0.83904	2216	2.5271	5.1629	-1.02007
0.631392	1677	5.6052	1.4948	-0.26607	1147	4.272	3.418	-0.67506
-0.35464	1194	1.7588	5.3412	-0.95197	1415	3.5336	4.1564	-0.82106
-0.90515	1058	2.8355	4.2645	-0.75997	1213	4.2869	3.4031	-0.67212
	1518	7.09725	3.78905		1399.5	7.68615	3.41725	
			11.36715				10.25175	
			5.607794				5.05753	
1718	34.109		1649	20.497				
2807	48.985		2280	27.588				
1519	35.945		1959	18.632				
2311	19.472		2345	18.806				
2088.75	34.62775		2058.25	21.38075				

585.1919	12.08072	320.7984	4.222793		
789	11.914	481	7.6923		
994	8.0483	335	11.045		
548	8.0292	602	11.296		
		377	8.7533	607	1.9769
777	9.3305	448.75	9.69665		
223.242	2.237397	119.1816	1.7591		
	36.24217		12.66838		
	6.712191		5.277299		
	42.95436		17.94568		
	25.29725		11.6841		
	1.697985		1.535906		
	-0.69799		-0.53591		

109	39.45	93	31.183
100	36	58	27.586
763	4.325	1271	8.812
1139	8.2529	1106	2.4412
2664	2.7778	3454	11.639
4291	10.114	3512	9.5957

x toxic a,b,c

x	toxic a,b,c

y

x toxic b,c

x toxic a,b,c

x	toxic a,b,c

						cell ct	% inf	AD
50078	A02	M-031922-	similar to R	284942	MGC70863	1260	5.7143	1.2743
50078	A04	M-023179-	dual specifi	285193	DUSP28	452	11.062	6.622
50078	A05	M-018978-	hypothetic	284034	FLJ34690	810	4.9383	0.4983
50078	A06	M-018799-	hypothetic	284131	FLJ35220	824	11.893	7.453
50078	A07	M-018229-	CMT1A du	284040	CDRT4	448	13.17	8.73
50078	A08	M-018854-	RANBP2-lik	285190	RGPD4	865	9.8266	5.3866
50078	A09	M-018980-	hypothetic	284047	FLJ36492	666	3.4535	0.9865
50078	A10	M-007335-	solute carri	285195	SLC9A9	1527	5.4355	0.9955
50078	A11	M-031748-	KIAA1267	284058	KIAA1267	367	20.708	16.268
50078	A12	M-028149-	hypothetic	285194	LOC285194	641	8.2683	3.8283
50078	A13	M-030894-	Similar to	284069	MGC34829	841	15.577	11.137
50078	A14	M-023180-	aquaporin	285192	AQP12B	382	10.995	6.555
50078	A15	M-023196-	hypothetic	284071	FLJ35848	863	5.562	1.122
50078	A16	M-022541-	plasminoge	285189	PLGLA1	1051	15.794	11.354
50078	A17	M-018230-	tubulin tyr	284076	TTLL6	719	15.021	10.581
50078	A18	M-027237-	RUN and F	285180	RUFY4	339	16.224	11.784
50078	A19	M-018180-	chromoson	284083	C17orf47	1203	6.3175	1.8775
50078	A20	M-018852-	chromoson	285175	C2orf21	449	4.0089	0.4311
50078	A21	M-018227-	hypothetic	284085	FLJ40504	210	14.286	9.846
50078	A23	M-021480-	phosphatid	284098	PIGW	243	9.8765	5.4365
50078	B02	M-017485-	stoned B/T	286749	SALF	1487	1.4122	3.0278
50078	B04	M-018486-	immunoglo	286676	ILDR1	1177	2.0391	2.4009
50078	B05	M-023260-	chromoson	285203	C3orf64	1821	7.8528	3.4128
50078	B06	M-018022-	BCL6 co-re	286554	BCORL2	1790	4.0223	0.4177
50078	B07	M-023570-	hypothetic	285205	LOC285205	1086	6.2615	1.8215
50078	B08	M-024797-	Ras-like GT	286526	LOC286526	499	4.8096	0.3696
50078	B09	M-032001-	F-box and	285231	FBXW12	575	8.3478	3.9078
50078	B10	M-018000-	melanoma	286514	MAGEB18	979	11.338	6.898
50078	B11	M-009016-	chromoson	285237	C3orf38	491	5.0916	0.6516
50078	B12	M-018026-	family with	286499	FAM133A	563	9.4139	4.9739
50078	B13	M-009120-	5-hydroxyt	285242	HTR3E	1550	6.1935	1.7535
50078	B14	M-018029-	hypothetic	286485	FLJ33610	860	5.5814	1.1414
50078	B15	M-018125-	zinc finger	285267	ZNF619	945	8.7831	4.3431
50078	B16	M-032228-	ubiquitin-c	286480	UBE2E4P	1246	5.7785	1.3385
50078	B17	M-032023-	zinc finger	285268	ZNF621	1579	13.743	9.303
50078	B18	M-031617-	ras-related	286472	RAC1P4	597	9.8827	5.4427
50078	B19	M-018128-	RAB, mem	285282	RABL3	1619	4.3237	0.1163
50078	B20	M-018043-	chromoson	286464	CXorf59	1546	18.693	14.253
50078	B21	M-028053-	hypothetic	285286	LOC285286	718	10.306	5.866
50078	B23	M-018007-	immunoglo	285313	IGSF10	385	16.623	12.183
50078	C02	M-018148-	family with	285172	FAM126B	738	0.67751	3.76249
50078	C04	M-018150-	hypothetic	285154	MGC34824	719	4.4506	0.0106
50078	C05	M-018802-	chromoson	284099	C17orf78	918	1.0893	3.3507
50078	C06	M-018849-	hypothetic	285150	FLJ33534	1394	0.71736	3.72264
50078	C07	M-030984-	hypothetic	284100	LOC284100	2235	1.0291	3.4109
50078	C08	M-022985-	isoamyl ace	285148	IAH1	1585	0.25237	4.18763

50078	C09	M-030876- hypothetica	284106	LOC284106	1504	1.2633	3.1767
50078	C10	M-018151- fibrous she	285135	FSIP2	968	1.6529	2.7871
50078	C11	M-018466- gasdermin	284110	GSDM1	1643	8.3384	3.8984
50078	C12	M-018153- DnaJ (Hsp4	285126	DNAJC5G	1676	3.9976	0.4424
50078	C13	M-007395- solute carri	284111	SLC13A5	1432	2.4441	1.9959
50078	C14	M-017660- hypothetica	285097	FLJ38379	1430	1.8182	2.6218
50078	C15	M-018245- transmemb	284114	TMEM102	2224	9.4874	5.0474
50078	C16	M-018155- hypothetica	285093	FLJ33590	2130	3.615	0.825
50078	C17	M-012807- polymerase	284119	PTRF	1568	1.4668	2.9732
50078	C18	M-018157- hypothetica	285051	FLJ40172	2944	5.8084	1.3684
50078	C19	M-031001- hypothetica	284121	LOC284121	2297	1.0884	3.3516
50078	C20	M-027824- hypothetica	285045	LOC285045	1655	0.96677	3.47323
50078	C21	M-031894- family with	284123	FAM27L	1721	3.835	0.605
50078	C23	M-007490- solute carri	284129	SLC26A11	2051	2.8279	1.6121
50078	D02	M-018045- Yip1 domai	286451	YIPF6	2477	0.8478	3.5922
50078	D04	M-031665- hypothetica	286442	LOC286442	3146	4.7044	0.2644
50078	D05	M-018126- chromosom	285315	C3orf33	1362	2.79	1.65
50078	D06	M-024784- H2B histon	286436	H2BFM	2670	2.0225	2.4175
50078	D07	M-018857- chromosom	285322	C3orf53	1492	4.2895	0.1505
50078	D08	M-031623- hypothetica	286411	LOC286411	958	0.41754	4.02246
50078	D09	M-023454- hypothetica	285326	LOC285326	1300	3.0769	1.3631
50078	D10	M-027287- ATPase, Cla	286410	ATP11C	2914	6.3487	1.9087
50078	D11	M-028111- coiled-coil (	285331	CCDC66	1480	3.4459	0.9941
50078	D12	M-032011- FOXD4-like	286380	FOXD4L2	1997	6.9104	2.4704
50078	D13	M-023575- solute carri	285335	SLC9A10	2237	9.4323	4.9923
50078	D14	M-018872- hypothetica	286359	LOC286359	1418	6.9817	2.5417
50078	D15	M-018121- chromosom	285343	C3orf23	1848	8.3874	3.9474
50078	D16	M-031930- chromosom	286343	C9orf150	2142	2.1008	2.3392
50078	D17	M-023477- hypothetica	285346	LOC285346	1982	6.3572	1.9172
50078	D18	M-015108- family with	286336	FAM78A	1774	2.5366	1.9034
50078	D19	M-018123- zinc finger	285349	ZNF660	2730	7.2527	2.8127
50078	D20	M-029586- chromosom	286333	C9orf109	1747	3.7779	0.6621
50078	D21	M-023699- phosducin-	285359	LOC285359	2274	13.852	9.412
50078	D23	M-019387- sulfatase m	285362	SUMF1	688	9.3023	4.8623
50078	E02	M-027823- hypothetica	285043	LOC285043	2175	2.2989	2.1411
50078	E04	M-027904- hypothetica	285033	LOC285033	1600	4.9375	0.4975
50078	E05	M-018992- glyceropho	284161	GDPD1	1625	2.8923	1.5477
50078	E06	M-031780- hypothetica	285025	FLJ39502	2009	3.783	0.657
50078	E07	M-018224- dynein, axo	284176	DNAHL1	1816	1.9824	2.4576
50078	E08	M-018848- hypothetica	285023	DKFZp451M	1791	3.5734	0.8666
50078	E09	M-018251- chromosom	284185	C17orf55	2256	7.3582	2.9182
50078	E10	M-022819- hypothetica	285016	hCG_19901	2477	2.3415	2.0985
50078	E11	M-018301- transmemb	284186	TMEM105	1308	4.5107	0.0707
50078	E12	M-027797- hypothetica	285000	LOC285000	1829	4.4833	0.0433
50078	E13	M-022983- meteorin, g	284207	METRNL	1455	6.4605	2.0205
50078	E14	M-007169- ring finger	284996	RNF149	2350	11.362	6.922
50078	E15	M-031009- hypothetica	284214	LOC284214	2328	11.942	7.502

50078	E16	M-018168-	hypothetica	284992	FLJ39660	2750	11.673	7.233
50078	E17	M-031018-	chromoson	284221	C18orf30	1795	4.7911	0.3511
50078	E18	M-022464-	acrosin-like	284967	bA395L14.	1941	9.119	4.679
50078	E19	M-023377-	chromoson	284222	C18orf58	2845	14.974	10.534
50078	E20	M-027342-	SH2 domai	284948	SH2D6	1485	12.121	7.681
50078	E21	M-031033-	hypothetica	284240	LOC28424	1858	7.6426	3.2026
50078	E23	M-018674-	hypothetica	284241	FLJ25715	1074	12.291	7.851
50078	F02	M-018548-	family with	286301	FAM27E3	2965	3.8786	0.5614
50078	F04	M-018048-	chromoson	286262	C9orf75	1967	1.9319	2.5081
50078	F05	M-018119-	RNA pseud	285367	RPUSD3	2092	0.71702	3.72298
50078	F06	M-026038-	chromoson	286257	C9orf142	3200	3.9062	0.5338
50078	F07	M-023444-	proline-rich	285368	PRRT3	1757	2.5043	1.9357
50078	F08	M-017773-	lipocalcin 1	286256	LCN12	2332	4.0309	0.4091
50078	F09	M-028074-	hypothetica	285375	LOC28537	1753	7.0736	2.6336
50078	F10	M-029522-	hypothetica	286238	LOC28623	1886	1.5907	2.8493
50078	F11	M-031948-	DPH3, KTI1	285381	DPH3	1118	0.71556	3.72444
50078	F12	M-026010-	hypothetica	286235	LOC28623	2870	4.5645	0.1245
50078	F13	M-032241-	family with	285386	FAM79B	2199	1.7281	2.7119
50078	F14	M-018013-	chromoson	286234	C9orf79	1983	6.0514	1.6114
50078	F15	M-018710-	hypothetica	285398	LOC28539	1648	0.91019	3.52981
50078	F16	M-026255-	chromoson	286207	C9orf117	1360	1.9853	2.4547
50078	F17	M-028114-	hypothetica	285401	LOC285401	1446	1.9364	2.5036
50078	F18	M-018050-	chromoson	286205	C9orf126	2968	9.2318	4.7918
50078	F19	M-028265-	hypothetica	285422	LOC28542	2454	7.5795	3.1395
50078	F20	M-018054-	crumbs hor	286204	CRB2	2654	7.272	2.832
50078	F21	M-024206-	WD repeat	285429	WDR21B	2835	4.6914	0.2514
50078	F23	M-024114-	cytochrom	285440	CYP4V2	1412	1.8414	2.5986
50078	G02	M-018194-	hypothetica	284944	FLJ37357	1906	1.1542	3.2858
50078	G04	M-031503-	hypothetica	284933	LOC28493	1667	4.5591	0.1191
50078	G05	M-027276-	potassium	284252	KCTD1	1124	2.669	1.771
50078	G06	M-031929-	hypothetica	284912	LOC28491	757	2.7741	1.6659
50078	G07	M-018222-	chromoson	284254	C18orf26	1484	2.5606	1.8794
50078	G08	M-019246-	SEC14-like	284904	SEC14L4	1210	1.3223	3.1177
50078	G09	M-018170-	family with	284257	FAM44C	1124	0.80071	3.63929
50078	G10	M-031457-	hypothetica	284898	LOC28489	1343	4.5421	0.1021
50078	G11	M-023427-	sialic acid b	284266	SIGLEC15	1176	2.381	2.059
50078	G12	M-031890-	hypothetica	284861	LOC284861	1279	4.1439	0.2961
50078	G13	M-010188-	zinc bindin	284273	ZADH2	761	6.8331	2.3931
50078	G14	M-019296-	hypothetica	284837	LOC28483	1562	2.6248	1.8152
50078	G15	M-031049-	hypothetica	284274	LOC28427	2149	3.49	0.95
50078	G16	M-019297-	chromoson	284836	C21orf125	625	0.64	3.8
50078	G17	M-018255-	hypothetica	284296	LOC28429	900	1.6667	2.7733
50078	G18	M-031382-	chromoson	284835	C21orf130	705	4.3972	0.0428
50078	G19	M-023621-	hypothetica	284297	LOC28429	1138	1.7575	2.6825
50078	G20	M-018688-	keratin ass	284827	KRTAP13-4	1509	1.4579	2.9821
50078	G21	M-023832-	zinc finger	284307	ZIK1	2621	4.4258	0.0142
50078	G23	M-018210-	zinc finger	284309	ZNF776	1883	5.948	1.508

50078	H02	M-029378- hypothetic	286186	LOC28618	2543	4.4042	0.0358
50078	H04	M-018052- family with	286183	FAM77D	1545	3.6246	0.8154
50078	H05	M-028300- hypothetic	285441	LOC285441	1789	4.0246	0.4154
50078	H06	M-029373- hypothetic	286177	LOC28617	1383	2.7477	1.6923
50078	H07	M-018858- hypothetic	285456	FLJ37673	1662	1.5644	2.8756
50078	H08	M-018733- hypothetic	286161	LOC286161	816	2.0833	2.3567
50078	H09	M-018504- cysteine-ric	285464	CRIPAK	1708	2.2248	2.2152
50078	H10	M-029344- hypothetic	286149	LOC28614	982	5.8045	1.3645
50078	H11	M-028326- hypothetic	285484	LOC28548	981	1.4271	3.0129
50078	H12	M-018930- dpy-19-like	286148	DPY19L4	1588	2.8967	1.5433
50078	H13	M-018805- docking pr	285489	DOK7	1534	3.455	0.985
50078	H14	M-029342- hypothetic	286144	LOC28614	1287	6.5268	2.0868
50078	H15	M-018114- hypothetic	285492	FLJ35424	1735	6.1095	1.6695
50078	H16	M-029334- hypothetic	286135	LOC28613	2301	3.4333	1.0067
50078	H17	M-008019- ring finger	285498	RNF212	939	4.4728	0.0328
50078	H18	M-018056- scavenger	286133	SCARA5	1210	3.4711	0.9689
50078	H19	M-024106- hypothetic	285501	LOC285501	2153	7.5708	3.1308
50078	H20	M-018062- zinc finger	286128	ZFP41	2111	2.2738	2.1662
50078	H21	M-031783- GPRIN fam	285513	GPRIN3	1358	11.635	7.195
50078	H23	M-018117- COX18 cyt	285521	COX18	1296	5.2469	0.8069
50078	I02	M-031369- hypothetic	284825	LOC28482	1252	3.6741	0.7659
50078	I04	M-018847- hypothetic	284805	FLJ33706	1392	4.7414	0.3014
50078	I05	M-018581- zinc finger	284312	ZSCAN1	1346	11.961	7.521
50078	I06	M-032042- similar to F	284802	MGC72104	276	9.4203	4.9803
50078	I07	M-023702- zinc finger	284323	ZNF780A	1063	2.0696	2.3704
50078	I08	M-031344- hypothetic	284801	LOC284801	1055	3.6967	0.7433
50078	I09	M-027230- chromoson	284325	C19orf54	1430	5.1049	0.6649
50078	I10	M-018843- chromoson	284800	C20orf91	645	19.07	14.63
50078	I11	M-018209- transmemb	284339	TMEM145	868	12.442	8.002
50078	I12	M-031342- hypothetic	284798	LOC28479	992	8.0645	3.6245
50078	I13	M-027232- DMC	284340	UNQ473	894	14.206	9.766
50078	I14	M-031339- hypothetic	284788	LOC28478	1821	11.642	7.202
50078	I15	M-032235- pleckstrin	284345	PHLDB3	1523	11.49	7.05
50078	I16	M-018839- hypothetic	284765	MGC34919	2333	9.5156	5.0756
50078	I17	M-017929- zinc finger	284346	ZNF575	2375	6.3579	1.9179
50078	I18	M-031322- signal-regu	284759	SIRPB2	1237	4.1229	0.3171
50078	I19	M-018677- LY6/PLAUR	284348	LYPD5	1821	6.8094	2.3694
50078	I20	M-018187- chromoson	284756	C20orf197	1319	8.3397	3.8997
50078	I21	M-031116- zinc finger	284349	ZNF283	1811	6.1844	1.7444
50078	I23	M-023860- hypothetic	284352	LOC28435	1364	3.6657	0.7743
50078	J02	M-018064- chromoson	286122	C8orf31	1247	0.72173	3.71827
50078	J03	D-001206-: siControl non-targeting			1487	0.4035	4.0365
50078	J04	M-025852- hypothetic	286114	LOC28611	2473	3.6393	0.8007
50078	J05	M-018859- Yip1 domai	285525	YIPF7	1727	3.1268	1.3132
50078	J06	M-029302- zinc finger	286101	ZNF252	1986	3.6254	0.8146
50078	J07	M-007170- ring finger	285533	RNF175	1461	2.6694	1.7706
50078	J08	M-018623- EF-hand do	286097	EFHA2	2374	2.1904	2.2496

50078	J09	M-028348-	hypothetica	285540	LOC285540	1133	0.97087	3.46913
50078	J10	M-025841-	hypothetica	286094	LOC286094	2050	1.4634	2.9766
50078	J11	M-028344-	hypothetica	285547	LOC285547	1872	2.0833	2.3567
50078	J12	M-027239-	family with	286077	FAM83H	1437	1.3222	3.1178
50078	J13	M-028345-	hypothetica	285548	LOC285548	1321	1.8168	2.6232
50078	J14	M-018065-	zinc finger	286075	ZNF707	2549	5.3354	0.8954
50078	J15	M-024218-	hypothetica	285550	LOC285550	2501	2.7189	1.7211
50078	J16	M-018070-	non-SMC e	286053	NSMCE2	1291	2.0914	2.3486
50078	J17	M-018031-	hypothetica	285555	MGC46496	2123	4.8516	0.4116
50078	J18	M-018072-	chromoson	439941	C8orf54	4059	2.6854	1.7546
50078	J19	M-028236-	hypothetica	285556	LOC285556	2197	0.95585	3.48415
50078	J20	M-018074-	XK, Kell blo	286046	XKR6	2749	8.5486	4.1086
50078	J21	M-018113-	NY-REN-7 a	285596	NY-REN-7	2380	2.563	1.877
50078	J23	M-018112-	ADP-ribosy	285598	ARL10	1913	5.1751	0.7351
50078	K02	M-031309-	hypothetica	284751	LOC284751	2228	5.2962	0.8562
50078	K03	D-001600-0	siGLO RISC-free siRNA			5365	6.3747	1.9347
50078	K04	M-031307-	hypothetica	284749	LOC284749	1527	4.7151	0.2751
50078	K05	M-027233-	NTPase, KA	284353	NKPD1	3779	6.9066	2.4666
50078	K06	M-018186-	zinc finger	284747	ZNF663	1373	2.3307	2.1093
50078	K07	M-027234-	tetra-pepti	284355	TPRX1	3175	2.9921	1.4479
50078	K08	M-031294-	proline rich	284739	PRR17	2465	0.93306	3.50694
50078	K09	M-018696-	likely ortho	284358	FLJ36070	2829	4.7367	0.2967
50078	K10	M-027677-	espin pseud	284729	ESPNP	2657	3.2367	1.2033
50078	K11	M-018698-	izumo sper	284359	IZUMO1	1190	5.7983	1.3583
50078	K12	M-032041-	solute carri	284723	SLC25A34	2621	5.5322	1.0922
50078	K13	M-018434-	hematopoi	284361	LOC284361	1186	8.2631	3.8231
50078	K14	M-018196-	family with	284716	FAM80A	2080	5.4808	1.0408
50078	K15	M-031135-	hypothetica	284365	MGC45922	1580	6.0759	1.6359
50078	K16	M-019409-	BTB (POZ) d	284697	BTBD8	2948	13.84	9.4
50078	K17	M-005920-	kallikrein-re	284366	KLK9	2177	7.1658	2.7258
50078	K18	M-019269-	zinc finger	284695	ZNF326	2658	3.3484	1.0916
50078	K19	M-023790-	sialic acid b	284367	SIGLECP3	1836	15.577	11.137
50078	K20	M-027594-	hypothetica	284688	RP11-297H	2012	10.686	6.246
50078	K21	M-018207-	hypothetica	284369	FLJ40235	801	6.9913	2.5513
50078	K23	M-032239-	zinc finger	284370	ZNF615	1733	6.4628	2.0228
50078	L02	M-018867-	chromoson	286032	C8orf79	2026	4.4916	0.0516
50078	L04	M-018067-	hypothetica	286023	FLJ40288	1863	2.6838	1.7562
50078	L05	M-018110-	chromoson	285600	C5orf36	2904	2.5138	1.9262
50078	L06	M-031761-	hypothetica	286016	tcag7.1015	3731	9.4613	5.0213
50078	L07	M-032227-	G protein-c	285601	GPR150	1647	1.3358	3.1042
50078	L08	M-028925-	hypothetica	286009	tcag7.929	3523	4.5416	0.1016
50078	L09	M-018520-	hypothetica	285603	FLJ39485	3043	1.5774	2.8626
50078	L10	M-018866-	hypothetica	286006	FLJ39575	2894	8.2585	3.8185
50078	L11	M-018032-	DTW doma	285605	DTWD2	2538	12.136	7.696
50078	L12	M-025421-	zinc finger	285989	ZNF789	3392	7.4292	2.9892
50078	L13	M-018109-	chromoson	285613	C5orf16	3978	4.0473	0.3927
50078	L14	M-028910-	hypothetica	285987	FLJ34048	2758	7.3967	2.9567

50078	L15	M-024519-	hypothetica	285622	RP5-964H1	2883	5.0989	0.6589
50078	L16	M-028876-	hypothetica	285972	LOC285972	2680	13.993	9.553
50078	L17	M-028404-	hypothetica	285626	LOC285626	2944	5.6046	1.1646
50078	L18	M-007171-	zinc finger	285971	ZNF775	3003	5.2614	0.8214
50078	L19	M-028405-	hypothetica	285629	LOC285629	3144	5.2481	0.8081
50078	L20	M-018084-	hypothetica	285970	FLJ36112	3199	14.004	9.564
50078	L21	M-018528-	hypothetica	285636	LOC285636	2453	9.8655	5.4255
50078	L23	M-028456-	hypothetica	285638	LOC285638	1816	6.0022	1.5622
50078	M02	M-018836-	chromosom	284680	C1orf111	2335	1.9272	2.5128
50078	M04	M-027567-	hypothetica	284661	LOC284661	2314	2.1175	2.3225
50078	M05	M-023804-	hypothetica	284371	LOC284371	3199	3.6574	0.7826
50078	M06	M-005325-	EPH recept	284656	EPHA10	2357	4.2851	0.1549
50078	M07	M-031149-	solute carri	284379	LOC284379	2117	0.66131	3.77869
50078	M08	M-018179-	R-spondin l	284654	RSPO1	1717	3.378	1.062
50078	M09	M-017981-	hypothetica	284382	MGC33407	1138	3.9543	0.4857
50078	M10	M-027695-	hypothetica	284628	LOC284628	2415	1.7805	2.6595
50078	M11	M-031222-	hypothetica	284385	LOC284385	1897	2.4249	2.0151
50078	M12	M-018171-	chromosom	284618	C1orf104	1847	2.7071	1.7329
50078	M13	M-031229-	zinc finger	284390	ZNF763	1943	2.7792	1.6608
50078	M14	M-018830-	cytochrom	284613	CYB561D1	1795	2.2841	2.1559
50078	M15	M-031230-	hypothetica	284391	FLJ14959	2300	7.0435	2.6035
50078	M16	M-022398-	neuroblast	284610	NBPF5	1645	1.8237	2.6163
50078	M17	M-031074-	hypothetica	284395	LOC284395	3721	5.9124	1.4724
50078	M18	M-031713-	hypothetica	284600	LOC284600	2466	4.9067	0.4667
50078	M19	M-031087-	hypothetica	284402	LOC284402	1885	1.1141	3.3259
50078	M20	M-031712-	family with	284593	FAM41C	1714	2.7421	1.6979
50078	M21	M-015354-	zinc finger	284406	ZNF545	2374	1.9377	2.5023
50078	M23	M-027236-	V-set and t	284415	VSTM1	674	0.89021	3.54979
50078	N02	M-018080-	hypothetica	285966	FLJ40722	1245	0.16064	4.27936
50078	N04	M-006320-	hypothetica	285962	FLJ40852	2939	0.20415	4.23585
50078	N05	M-007552-	solute carri	285641	SLC36A3	4304	2.3234	2.1166
50078	N06	M-019231-	Williams Be	285955	WBSCR19	2168	0.55351	3.88649
50078	N07	M-031966-	olfactory re	285659	OR2V2	3368	0.62352	3.81648
50078	N08	M-028822-	hypothetica	285941	LOC285941	3218	0.43505	4.00495
50078	N09	M-018107-	hypothetica	285668	FLJ37543	1427	1.6819	2.7581
50078	N10	M-025288-	hypothetica	285924	LOC285924	4536	5.6658	1.2258
50078	N11	M-017714-	ring finger	285671	RNF180	1892	2.1142	2.3258
50078	N12	M-018928-	hypothetica	285908	LOC285908	1372	0.87464	3.56536
50078	N13	M-018106-	P18SRP pro	285672	P18SRP	1035	0.96618	3.47382
50078	N14	M-018864-	hypothetica	285905	FLJ25037	2055	0.82725	3.61275
50078	N15	M-018860-	zinc finger	285676	ZNF454	2096	3.1489	1.2911
50078	N16	M-028753-	hypothetica	285889	LOC285889	3223	3.7853	0.6547
50078	N17	M-024606-	hypothetica	285679	LOC285679	2355	1.7834	2.6566
50078	N18	M-028750-	canopy 1 h	285888	CNPY1	2708	3.0281	1.4119
50078	N19	M-018091-	chromosom	285685	C5orf17	4243	4.9729	0.5329
50078	N20	M-018863-	hypothetica	285877	DKFZp564N	4503	2.4206	2.0194
50078	N21	M-018104-	hypothetica	285696	FLJ34047	2010	2.2388	2.2012

50078	N23	M-018102- RGM doma	285704	RGMB	2484	3.4219	1.0181
50078	O02	M-021842- hypothetica	284591	LOC284591	1327	3.0897	1.3503
50078	O04	M-027508- hypothetica	284581	LOC284581	826	5.3269	0.8869
50078	O05	M-018479- chromosom	284424	C19orf30	2884	5.2705	0.8305
50078	O06	M-018812- chromosom	284573	C1orf157	1776	1.6329	2.8071
50078	O07	M-007363- solute carri	284427	SLC25A41	1768	4.9208	0.4808
50078	O08	M-018169- neuroblasto	284565	NBPF15	1706	2.286	2.154
50078	O09	M-031245- NACHT and	284434	NWD1	736	5.9783	1.5383
50078	O10	M-027558- hypothetica	284551	LOC284551	1734	3.2872	1.1528
50078	O11	M-007361- solute carri	284439	SLC25A42	834	6.235	1.795
50078	O12	M-017971- solute carri	284525	SLC9A11	2001	4.6477	0.2077
50078	O13	M-018712- hypothetica	284440	MGC39821	1524	5.4462	1.0062
50078	O14	M-018167- hypothetica	284505	FLJ35487	1382	4.4863	0.0463
50078	O15	M-018435- zinc finger	284443	ZNF493	2245	14.967	10.527
50078	O16	M-021566- chromosom	284498	C1orf167	2681	6.9004	2.4604
50078	O17	M-018731- chromosom	284451	C19orf19	2553	3.0161	1.4239
50078	O18	M-018792- thioesteras	284486	THEM5	1570	10	5.56
50078	O19	M-018886- GLI-Kruppe	284459	HKR1	3282	5.3626	0.9226
50078	O20	M-021716- hypothetica	284485	FLJ36032	2055	8.7105	4.2705
50078	O21	M-019386- family with	284467	FAM19A3	1926	6.3863	1.9463
50078	O23	M-027616- hypothetica	284475	LOC284475	1481	8.1026	3.6626
50078	P02	M-027238- ribosomal p	285855	RPL7L1	1725	3.2464	1.1936
50078	P04	M-021501- triggering r	285852	TREML4	946	2.2199	2.2201
50078	P05	M-028550- hypothetica	285713	LOC285713	2030	6.601	2.161
50078	P06	M-009042- patatin-like	285848	PNPLA1	2140	1.5888	2.8512
50078	P07	M-028602- hypothetica	285733	LOC285733	2449	2.1233	2.3167
50078	P08	M-017661- hypothetica	285821	FLJ37940	1530	5.098	0.658
50078	P09	M-028603- hypothetica	285735	LOC285735	2017	5.1562	0.7162
50078	P10	M-018533- hypothetica	285800	MGC35308	1578	5.5767	1.1367
50078	P11	M-017921- hypothetica	285736	FLJ35700	2032	2.7067	1.7333
50078	P12	M-017944- cancer anti	285782	CAGE1	2264	12.323	7.883
50078	P13	M-028609- hypothetica	285740	LOC285740	1929	6.8429	2.4029
50078	P14	M-018087- hypothetica	285780	RP3-398D1	3083	7.9468	3.5068
50078	P15	M-018100- chromosom	285753	C6orf182	1821	6.5349	2.0949
50078	P16	M-028622- hypothetica	285768	LOC285768	2173	3.5435	0.8965
50078	P17	M-018093- hypothetica	285754	FLJ37396	1343	7.2971	2.8571
50078	P18	M-028620- hypothetica	285766	LOC285766	2155	2.9234	1.5166
50078	P19	M-009111- peptidylpro	285755	PPIL6	2686	5.2494	0.8094
50078	P20	M-018055- discoidin, C	285761	DCBLD1	3283	6.0311	1.5911
50078	P21	M-028591- hypothetica	285758	LOC285758	1304	1.4571	2.9829
50078	P23	M-018089- hypothetica	285759	FLJ34503	733	4.0928	0.3472
				MAD	1762.5	4.4382	2.2082
				MAD3			6.6246
				MADc			3.268136
50078	C22		1278	15.571			
50078	D22				1507	36.364	

50078	E22		1550	24.581
50078	F22		2087	31.433
		mn	1714.667	30.79267
		sd	323.1661	5.917541
50078	G22		288	4.5139
50078	H22		508	5.9055
50078	I22		215	4.6512
50078	J22		1124	3.4698
		mn	533.75	4.6351
		sd	412.7359	0.997796
		3psSD		17.75262
		3ngSD		2.993387
		SumSD		20.74601
		MeanDf		26.15757
		SumovrMn		0.793117
		1minus		0.206883

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.390467	709	1.5515	4.8985	-1.10691	660	4.8485	1.0415	-0.29105
2.026782	476	6.3025	0.1475	-0.03357	794	9.5718	3.6818	1.023645
0.153023	1003	10.169	3.719	0.839941	868	4.9539	0.9361	-0.26171
2.281056	623	9.4703	3.0203	0.682092	1543	1.9443	3.9457	-1.09941
2.671798	432	13.194	6.744	1.523343	534	5.9925	0.1025	0.027375
1.648769	646	11.92	5.47	1.235523	1065	5.8216	0.0684	-0.02019
-0.3013	684	8.9181	2.4681	0.55734	614	4.2345	1.6555	-0.46195
0.305159	624	8.8141	2.3641	0.533844	1572	2.6081	3.2819	-0.91465
4.978312	412	8.9806	2.5306	0.57146	332	18.675	12.785	3.55745
1.171952	946	8.1395	1.6895	0.38144	1191	5.1217	0.7683	-0.21501
3.408304	894	5.481	0.969	-0.21916	779	3.8511	2.0389	-0.56867
2.006281	535	5.0467	1.4033	-0.31728	995	5.8291	0.0609	-0.01811
0.343866	1302	2.765	3.685	-0.83276	890	2.0225	3.8675	-1.07764
3.474702	888	6.3063	0.1437	-0.03271	999	1.001	4.889	-1.36197
3.238176	422	10.427	3.977	0.898228	550	2	3.89	-1.08391
3.606276	258	10.465	4.015	0.906812	306	5.5556	0.3344	-0.09423
0.575037	847	10.744	4.294	0.969844	899	3.0033	2.8867	-0.80465
-0.13136	449	11.804	5.354	1.209317	577	9.3588	3.4688	0.964358
3.013277	319	18.182	11.732	2.650222	339	7.0796	1.1896	0.329961
1.664037	518	15.637	9.187	2.075261	265	3.0189	2.8711	-0.8003
-0.92591	1187	2.6116	3.8384	-0.86741	1492	0.67024	5.21976	-1.45403
-0.73409	993	2.6183	3.8317	-0.8659	933	2.8939	2.9961	-0.8351
1.044816	1384	5.5636	0.8864	-0.2005	1371	4.2305	1.6595	-0.46306
-0.12726	2070	2.8502	3.5998	-0.81351	888	3.2658	2.6242	-0.73158
0.557902	2363	2.2006	4.2494	-0.96026	2388	3.2663	2.6237	-0.73144
0.113643	768	3.3854	3.0646	-0.6926	584	1.5411	4.3489	-1.21164
1.196278	597	1.005	5.445	-1.23037	865	3.5838	2.3062	-0.64307
2.111234	1567	6.7645	0.3145	0.070803	2102	4.6622	1.2278	-0.3429
0.19993	737	3.7992	2.6508	-0.59911	1034	4.9323	0.9577	-0.26772
1.522489	320	5	1.45	-0.32783	280	14.286	8.396	2.335806
0.537095	852	2.5822	3.8678	-0.87405	1576	5.4569	0.4331	-0.12171
0.349802	1254	1.8341	4.6159	-1.04306	1259	2.9388	2.9512	-0.8226
1.329473	858	2.5641	3.8859	-0.87814	1590	3.8994	1.9906	-0.55522
0.410111	1595	1.2539	5.1961	-1.17414	1489	1.4775	4.4125	-1.22934
2.847128	1167	7.3693	0.9193	0.207438	2058	3.7415	2.1485	-0.59917
1.665934	747	7.6305	1.1805	0.266448	1463	7.5871	1.6971	0.471219
-0.03504	2016	6.4484	0.0016	-0.00061	3009	5.683	0.207	-0.05877
4.361752	772	14.378	7.928	1.79083	1592	9.7362	3.8462	1.069405
1.795458	338	4.4379	2.0121	-0.45482	1179	9.3299	3.4399	0.956314
3.728364	393	13.486	7.036	1.589311	569	16.696	10.806	3.006611
-1.15071	913	3.943	2.507	-0.56663	1000	2.5	3.39	-0.94474
0.003794	1134	8.4656	2.0156	0.455112	1216	5.3454	0.5446	-0.15274
-1.02471	1363	5.9428	0.5072	-0.11483	980	4.3878	1.5022	-0.41928
-1.13852	2022	1.3353	5.1147	-1.15575	1149	4.4386	1.4514	-0.40514
-1.04313	2666	0.97524	5.47476	-1.2371	1693	2.7761	3.1139	-0.86788
-1.2808	2099	2.1915	4.2585	-0.96232	2078	2.7911	3.0989	-0.86371

-0.97147	2135	2.1546	4.2954	-0.97066	2149	4.1415	1.7485	-0.48784
-0.85226	1665	5.6456	0.8044	-0.18198	1828	7.8228	1.9328	0.536825
1.193402	2902	15.989	9.539	2.154784	1626	7.3801	1.4901	0.413603
-0.13482	1349	9.192	2.742	0.619219	1960	9.7959	3.9059	1.086022
-0.61016	691	8.1042	1.6542	0.373465	537	11.918	6.028	1.676692
-0.80168	1324	4.9094	1.5406	-0.3483	1956	3.272	2.618	-0.72985
1.544979	3078	11.468	5.018	1.133408	3766	6.9304	1.0404	0.288432
-0.25189	2664	4.7673	1.6827	-0.3804	3250	1.4769	4.4131	-1.22951
-0.9092	1417	3.8814	2.5686	-0.58054	1300	5.1538	0.7362	-0.20607
0.41926	1374	1.0189	5.4311	-1.22723	1624	4.0025	1.8875	-0.52653
-1.02499	1512	5.2249	1.2251	-0.27702	2239	3.6623	2.2277	-0.62122
-1.0622	863	7.0684	0.6184	0.139459	994	9.1549	3.2649	0.907604
-0.18457	1030	2.7184	3.7316	-0.84328	1300	6.3077	0.4177	0.115108
-0.49273	1326	11.614	5.164	1.166392	1303	6.9839	1.0939	0.303323
-1.09861	1892	1.9556	4.4944	-1.01561	1298	2.7735	3.1165	-0.86861
0.081453	2844	6.5049	0.0549	0.012154	1616	7.4876	1.5976	0.443524
-0.50432	2761	4.1652	2.2848	-0.51643	2554	6.3038	0.4138	0.114023
-0.73917	2781	2.2654	4.1846	-0.94563	1928	1.7635	4.1265	-1.14973
-0.0455	1845	5.3659	1.0841	-0.24517	2404	9.5674	3.6774	1.02242
-1.23026	1291	2.866	3.584	-0.80994	1728	5.0347	0.8553	-0.23922
-0.41654	1365	3.5165	2.9335	-0.66298	1127	8.3407	2.4507	0.680978
0.584584	1822	5.2689	1.1811	-0.26708	2926	4.5796	1.3104	-0.36589
-0.30363	2550	3.098	3.352	-0.75753	2911	5.1529	0.7371	-0.20632
0.756456	1774	5.3551	1.0949	-0.24761	1711	4.9094	0.9806	-0.2741
1.528119	1827	4.5977	1.8523	-0.41872	2062	6.644	0.754	0.208715
0.778272	1310	6.1069	0.3431	-0.07776	1051	5.0428	0.8472	-0.23697
1.208395	3333	8.2208	1.7708	0.399807	2387	6.6611	0.7711	0.213475
-0.71521	3935	4.7014	1.7486	-0.39529	3985	3.5885	2.3015	-0.64176
0.587185	2264	4.7261	1.7239	-0.38971	2118	2.5496	3.3404	-0.93093
-0.58186	872	7.3394	0.8894	0.200683	1999	3.952	1.938	-0.54058
0.861194	2897	6.6275	0.1775	0.039852	2703	8.3241	2.4341	0.676358
-0.20204	2013	6.8554	0.4054	0.091339	2424	3.6304	2.2596	-0.6301
2.88048	2256	9.1312	2.6812	0.605483	2343	3.7559	2.1341	-0.59517
1.488341	727	14.443	7.993	1.805514	959	5.9437	0.0537	0.013792
-0.65459	1355	0.81181	5.63819	-1.27402	1206	1.8242	4.0658	-1.13284
0.152778	1461	4.6543	1.7957	-0.40593	1398	7.7969	1.9069	0.529616
-0.47302	864	0.5787	5.8713	-1.32668	1671	2.5733	3.3167	-0.92433
-0.20048	2007	0.89686	5.55314	-1.2548	1895	4.3272	1.5628	-0.43615
-0.75144	1561	2.4343	4.0157	-0.90747	1702	6.1692	0.2792	0.076558
-0.26462	1559	1.347	5.103	-1.15311	1982	3.4309	2.4591	-0.68563
0.893476	1353	1.4043	5.0457	-1.14016	2224	14.029	8.139	2.264272
-0.64156	1632	0.67402	5.77598	-1.30515	2730	4.2491	1.6409	-0.45789
0.022184	2110	1.5166	4.9334	-1.11479	2994	5.845	0.045	-0.01368
0.0138	1927	1.972	4.478	-1.01191	2700	7.1111	1.2211	0.338729
0.618793	750	0.93333	5.51667	-1.24656	455	18.022	12.132	3.375692
2.118578	2096	3.4828	2.9672	-0.67059	3155	4.2789	1.6111	-0.44959
2.296049	2167	2.8611	3.5889	-0.81105	2429	10.004	4.114	1.143945

2.213739	2031	2.6588	3.7912	-0.85675	3178	6.4821	0.5921	0.163651
0.107982	2159	0.23159	6.21841	-1.4051	1648	5.1578	0.7322	-0.20496
1.432254	2655	2.1469	4.3031	-0.9724	1684	3.8005	2.0895	-0.58275
3.223795	2268	5.4674	0.9826	-0.22224	3020	8.5762	2.6862	0.746528
2.35082	2438	1.0664	5.3836	-1.2165	2188	2.6508	3.2392	-0.90276
0.980498	2144	2.5653	3.8847	-0.87787	2932	3.4447	2.4453	-0.68179
2.402838	1670	2.2156	4.2344	-0.95688	1407	2.8429	3.0471	-0.84929
-0.17123	1515	0.19802	6.25198	-1.41268	2162	7.308	1.418	0.393534
-0.76689	2317	2.2874	4.1626	-0.94065	1206	9.8673	3.9773	1.105895
-1.13862	1241	0.88638	5.56362	-1.25717	921	4.5603	1.3297	-0.37127
-0.16278	1381	0.94135	5.50865	-1.24475	1455	4.1924	1.6976	-0.47367
-0.59174	1224	0.65359	5.79641	-1.30976	1007	6.6534	0.7634	0.211331
-0.12463	2333	1.5431	4.9069	-1.10881	1005	3.4826	2.4074	-0.67124
0.806392	1723	3.5403	2.9097	-0.6576	1004	4.1833	1.7067	-0.4762
-0.87129	1785	1.8487	4.6013	-1.03977	1375	5.8909	0.0009	-0.0009
-1.13907	1172	0.85324	5.59676	-1.26466	756	7.0106	1.1206	0.310755
0.038646	2428	0.9061	5.5439	-1.25272	1234	4.9433	0.9467	-0.26466
-0.82925	1285	1.1673	5.2827	-1.19371	968	4.5455	1.3445	-0.37539
0.493615	1175	2.383	4.067	-0.91906	380	8.4211	2.5311	0.703357
-1.07952	1350	1.037	5.413	-1.22314	2103	3.6614	2.2286	-0.62147
-0.75055	1175	3.234	3.216	-0.7268	611	6.5466	0.6566	0.181604
-0.76551	1301	0.8455	5.6045	-1.26641	752	2.1277	3.7623	-1.04836
1.466769	3230	5.9752	0.4748	-0.10751	3160	7.7215	1.8315	0.508629
0.96119	1929	7.154	0.704	0.158798	1954	9.0072	3.1172	0.866493
0.8671	2707	3.9158	2.5342	-0.57277	1523	4.2022	1.6878	-0.47094
0.077475	2284	4.2032	2.2468	-0.50784	1858	3.5522	2.3378	-0.65186
-0.79458	1158	3.3679	3.0821	-0.69655	958	1.7745	4.1155	-1.14667
-1.00485	1487	4.573	1.877	-0.4243	1595	0.81505	5.07495	-1.41373
0.036994	1011	5.3412	1.1088	-0.25075	886	1.0158	4.8742	-1.35785
-0.54135	2159	5.2802	1.1698	-0.26453	1403	2.851	3.039	-0.84704
-0.50919	925	3.2432	3.2068	-0.72472	436	4.3578	1.5322	-0.42763
-0.57452	2006	6.5304	0.0804	0.017915	1122	0.98039	4.90961	-1.36771
-0.95342	1114	5.386	1.064	-0.24063	841	1.1891	4.7009	-1.30961
-1.11302	1811	6.7918	0.3418	0.07697	754	0.79576	5.09424	-1.4191
0.031792	1298	8.2435	1.7935	0.404935	852	0.8216	5.0684	-1.4119
-0.62947	1072	10.541	4.091	0.923982	776	0.51546	5.37454	-1.49712
-0.09005	1012	11.561	5.111	1.154419	541	0.73937	5.15063	-1.43479
0.732803	308	20.779	14.329	3.236931	392	2.551	3.339	-0.93054
-0.55487	1297	11.642	5.192	1.172718	1055	1.6114	4.2786	-1.19207
-0.29013	951	10.41	3.96	0.894387	820	0.4878	5.4022	-1.50482
-1.16219	883	10.646	4.196	0.947704	1153	0.95403	4.93597	-1.37504
-0.84804	1214	12.191	5.741	1.296747	661	2.5719	3.3181	-0.92472
-0.01255	228	17.982	11.532	2.605038	421	1.6627	4.2273	-1.17779
-0.82025	1069	14.312	7.862	1.775919	949	1.5806	4.3094	-1.20064
-0.91193	1026	11.111	4.661	1.052755	1306	0.84227	5.04773	-1.40615
-0.00379	2716	12.555	6.105	1.378981	1692	1.0047	4.8853	-1.36094
0.461976	1057	12.867	6.417	1.449468	1612	4.0323	1.8577	-0.51823

-0.0104	1778	6.243	0.207	-0.04701	1072	3.6381	2.2519	-0.62795
-0.24895	1793	11.656	5.206	1.175881	1225	6.449	0.559	0.154438
-0.12656	1173	7.2464	0.7964	0.179673	1264	1.7405	4.1495	-1.15614
-0.51727	1392	6.4655	0.0155	0.003253	608	4.2763	1.6137	-0.45032
-0.87934	1751	8.2239	1.7739	0.400508	1085	0.92166	4.96834	-1.38405
-0.72056	1005	11.343	4.893	1.105168	595	3.6975	2.1925	-0.61142
-0.67727	1314	8.2953	1.8453	0.416638	1038	1.1561	4.7339	-1.3188
0.418067	582	22.68	16.23	3.666401	359	6.9638	1.0738	0.297729
-0.92135	639	13.615	7.165	1.618454	484	3.5124	2.3776	-0.66294
-0.47168	1384	10.983	4.533	1.023838	785	2.8025	3.0875	-0.86054
-0.30084	820	16.463	10.013	2.261869	595	7.2269	1.3369	0.370961
0.63908	1390	2.3022	4.1478	-0.93731	616	5.0325	0.8575	-0.23983
0.511392	946	14.376	7.926	1.790378	685	7.7372	1.8472	0.512999
-0.30748	2014	9.3843	2.9343	0.662663	2683	4.8453	1.0447	-0.29194
0.010587	1304	16.488	10.038	2.267517	915	3.6066	2.2834	-0.63672
-0.29592	994	10.966	4.516	1.019997	599	3.6728	2.2172	-0.6183
0.958528	1615	9.4118	2.9618	0.668876	1330	6.4662	0.5762	0.159226
-0.66227	2311	9.3899	2.9399	0.663928	1261	6.1856	0.2956	0.081123
2.202112	1103	7.0716	0.6216	0.140182	1092	3.022	2.868	-0.79944
0.24745	1722	7.259	0.809	0.182519	800	3	2.89	-0.80556
-0.2338	780	6.2821	0.1679	-0.03818	494	6.4777	0.5877	0.162427
0.092775	706	9.3484	2.8984	0.654552	496	7.6613	1.7713	0.491872
2.301863	1195	13.389	6.939	1.567397	988	9.919	4.029	1.120286
1.524447	262	25.954	19.504	4.406057	303	15.842	9.952	2.768906
-0.72476	1081	12.673	6.223	1.405639	781	16.645	10.755	2.992415
-0.22689	862	8.3527	1.9027	0.429606	1096	6.1131	0.2231	0.060943
0.204	1630	9.7546	3.3046	0.74632	828	4.8309	1.0591	-0.29595
4.477109	262	18.321	11.871	2.681625	230	23.043	17.153	4.773249
2.449041	648	14.506	8.056	1.819747	385	17.922	12.032	3.347858
1.109593	1305	13.103	6.653	1.502784	519	10.983	5.093	1.416442
2.988799	1002	10.08	3.63	0.819834	805	13.416	7.526	2.093648
2.204253	1252	10.463	4.013	0.906361	1996	20.641	14.751	4.104671
2.157744	904	11.836	5.386	1.216546	776	12.113	6.223	1.730968
1.553607	1488	4.7043	1.7457	-0.39463	2121	6.3178	0.4278	0.11792
0.587399	1587	6.3642	0.0858	-0.01963	1340	8.5075	2.6175	0.727406
-0.09648	1472	4.4158	2.0342	-0.45981	1229	9.9268	4.0368	1.122457
0.725551	1156	8.1315	1.6815	0.379633	1333	12.453	6.563	1.825605
1.1938	1434	9.6234	3.1734	0.71668	2595	5.6262	0.2638	-0.07458
0.534311	2625	11.048	4.598	1.038523	1771	8.3004	2.4104	0.669761
-0.23637	1455	6.6667	0.2167	0.048708	1565	8.754	2.864	0.796017
-1.13718	452	5.7522	0.6978	-0.15789	517	7.3501	1.4601	0.405252
-1.23456	833	3.6014	2.8486	-0.6438	649	9.8613	3.9713	1.104225
-0.24445	2200	9.2273	2.7773	0.627194	1901	4.1557	1.7343	-0.48388
-0.40127	1472	6.4538	0.0038	0.00061	1034	13.056	7.166	1.993445
-0.2487	1110	6.5766	0.1266	0.028353	912	11.732	5.842	1.62492
-0.54123	870	12.184	5.734	1.295166	858	15.035	9.145	2.544284
-0.68779	1004	1.2948	5.1552	-1.1649	982	9.8778	3.9878	1.108818

-1.06095	724	9.3923	2.9423	0.66447	836	18.182	12.292	3.420227
-0.91024	1502	3.5952	2.8548	-0.6452	837	5.6153	0.2747	-0.07762
-0.72056	1005	3.9801	2.4699	-0.55824	868	7.1429	1.2529	0.34758
-0.95345	1596	5.1378	1.3122	-0.2967	816	10.172	4.282	1.190706
-0.80211	1048	5.2481	1.2019	-0.27178	597	7.7052	1.8152	0.504092
0.27453	1483	7.35	0.9	0.203078	1340	12.015	6.125	1.703691
-0.52608	802	11.97	5.52	1.246819	564	28.014	22.124	6.156888
-0.71809	754	5.5703	0.8797	-0.19899	483	30.642	24.752	6.888371
0.126494	1643	9.9817	3.5317	0.797626	1307	10.176	4.286	1.19182
-0.53633	2048	4.248	2.202	-0.49772	1577	6.9753	1.0853	0.30093
-1.06555	1184	2.6182	3.8318	-0.86592	838	9.0692	3.1792	0.88375
1.25772	1130	10.885	4.435	1.001698	1955	14.936	9.046	2.516728
-0.57378	1117	6.7144	0.2644	0.059484	1276	4.9373	0.9527	-0.26633
0.22548	1321	12.036	5.586	1.26173	1083	11.634	5.744	1.597642
0.262535	1397	6.5855	0.1355	0.030363	2517	15.852	9.962	2.77169
0.59254	4060	9.3103	2.8603	0.645945	3314	10.35	4.46	1.240251
0.084727	609	8.5386	2.0886	0.471604	605	19.339	13.449	3.742269
0.755293	1783	6.7863	0.3363	0.075728	1839	9.8967	4.0067	1.114079
-0.64486	1371	4.5222	1.9278	-0.43577	564	8.8652	2.9752	0.826969
-0.44248	1742	2.9851	3.4649	-0.78303	1405	6.121	0.231	0.063142
-1.07252	1184	4.4764	1.9736	-0.44612	849	7.0671	1.1771	0.326481
0.091336	1774	5.2424	1.2076	-0.27307	1117	9.4897	3.5997	1.000793
-0.36764	1278	5.8685	0.5815	-0.13162	781	8.3227	2.4327	0.675968
0.41617	832	8.0529	1.6029	0.361876	384	23.958	18.068	5.027932
0.334747	1890	7.619	1.169	0.26385	961	11.759	5.869	1.632435
1.170361	1436	10.028	3.578	0.808086	1340	9.6269	3.7369	1.038982
0.31902	2280	8.9035	2.4535	0.554041	1304	7.362	1.472	0.408565
0.501111	2348	4.8552	1.5948	-0.36054	1378	10.377	4.487	1.247766
2.876808	1955	10.691	4.241	0.95787	701	12.268	6.378	1.774111
0.834604	2023	13.89	7.44	1.680582	1367	10.022	4.132	1.148955
-0.33346	1853	5.8824	0.5676	-0.12848	1496	6.6176	0.7276	0.201367
3.408304	1606	10.71	4.26	0.962162	1106	11.573	5.683	1.580664
1.911732	2447	3.1876	3.2624	-0.73728	1277	10.963	5.073	1.410875
0.78121	890	23.258	16.808	3.796982	904	13.274	7.384	2.054124
0.619497	1675	9.8507	3.4007	0.768031	2373	7.3746	1.4846	0.412072
0.01634	2760	5	1.45	-0.32783	1380	3.8406	2.0494	-0.57159
-0.53682	1530	2.1569	4.2931	-0.97014	1170	5.8974	0.0074	0.000905
-0.58884	2166	3.6473	2.8027	-0.63343	1609	4.8477	1.0423	-0.29127
1.536992	2575	10.214	3.764	0.850107	1830	4.8087	1.0813	-0.30213
-0.94929	1202	7.4043	0.9543	0.215345	862	4.8724	1.0176	-0.2844
0.031639	2253	5.2375	1.2125	-0.27417	1174	4.0886	1.8014	-0.50256
-0.87536	1549	2.4532	3.9968	-0.9032	1851	3.2415	2.6485	-0.73834
1.168954	1783	6.8985	0.4485	0.101076	1339	5.2278	0.6622	-0.18547
2.35541	1498	8.9453	2.4953	0.563485	1461	5.065	0.825	-0.23079
0.915201	1365	6.1538	0.2962	-0.06717	1582	7.4589	1.5689	0.435536
-0.11961	1951	2.3578	4.0922	-0.92475	862	4.1763	1.7137	-0.47815
0.905256	1141	7.4496	0.9996	0.225579	751	9.5872	3.6972	1.027932

0.202164	1156	8.3045	1.8545	0.418716	1299	4.7729	1.1171	-0.31209
2.923624	1806	10.631	4.181	0.944315	1199	5.8382	0.0518	-0.01557
0.356901	1013	6.614	0.164	0.036802	1095	2.7397	3.1503	-0.87802
0.251887	1668	5.2758	1.1742	-0.26552	1280	5.4688	0.4212	-0.11839
0.247817	2109	6.3063	0.1437	-0.03271	2345	2.6013	3.2887	-0.91654
2.92699	1165	8.5837	2.1337	0.481793	1670	6.4072	0.5172	0.142803
1.660671	1125	9.7778	3.3278	0.751562	772	7.2539	1.3639	0.378476
0.47856	1797	5.3979	1.0521	-0.23794	1379	1.7404	4.1496	-1.15616
-0.76833	999	5.6056	0.8444	-0.19101	1579	10.956	5.066	1.408926
-0.7101	1177	8.3263	1.8763	0.423642	1070	3.0841	2.8059	-0.78216
-0.23891	2096	6.9179	0.4679	0.105459	1236	9.2233	3.3333	0.926643
-0.04685	1274	7.9278	1.4778	0.333613	1908	7.2851	1.3951	0.38716
-1.15567	1565	3.7061	2.7439	-0.62015	1217	6.2449	0.3549	0.097629
-0.32441	809	8.0346	1.5846	0.357741	750	11.333	5.443	1.513861
-0.14807	555	11.351	4.901	1.106976	251	23.108	17.218	4.791341
-0.81322	1248	10.256	3.806	0.859596	936	7.6923	1.8023	0.500501
-0.61604	1025	15.512	9.062	2.047021	1090	10.917	5.027	1.398071
-0.52969	1830	7.3224	0.8724	0.196842	1279	9.6169	3.7269	1.036198
-0.50763	1126	12.966	6.516	1.471833	524	15.649	9.759	2.715186
-0.65912	610	11.639	5.189	1.17204	685	12.263	6.373	1.77272
0.797182	1846	15.168	8.718	1.969305	1775	10.648	4.758	1.323197
-0.8	971	5.8702	0.5798	-0.13124	397	8.3123	2.4223	0.673073
0.451083	2428	14.374	7.924	1.789926	1607	9.8942	4.0042	1.113383
0.143354	2651	12.41	5.96	1.346223	1056	6.0606	0.1706	0.04633
-1.01712	1496	7.8877	1.4377	0.324554	1005	6.3682	0.4782	0.131948
-0.51898	1875	10.88	4.43	1.000568	1461	7.8713	1.9813	0.550324
-0.76512	2343	7.5544	1.1044	0.249255	1451	8.9593	3.0693	0.853161
-1.08563	1349	4.3736	2.0764	-0.46934	1339	3.286	2.604	-0.72596
-1.30887	1071	3.1746	3.2754	-0.74022	1180	2.3729	3.5171	-0.98011
-1.29556	2651	5.1301	1.3199	-0.29844	1722	2.8455	3.0445	-0.84857
-0.6471	1210	12.479	6.029	1.361811	940	6.4894	0.5994	0.165683
-1.18866	1180	3.8983	2.5517	-0.57672	1104	6.4312	0.5412	0.149484
-1.16723	1347	3.1923	3.2577	-0.73622	1702	1.9389	3.9511	-1.10091
-1.2249	3774	9.1415	2.6915	0.60781	1912	1.9874	3.9026	-1.08741
-0.84339	898	4.1203	2.3297	-0.52657	781	4.8656	1.0244	-0.28629
0.375627	2580	15.349	8.899	2.010196	2117	8.6915	2.8015	0.778621
-0.71111	800	6.125	0.325	-0.07367	1702	3.7603	2.1297	-0.59394
-1.0904	1515	5.6106	0.8394	-0.18988	900	6.6667	0.7767	0.215033
-1.06239	885	7.0056	0.5556	0.125272	983	7.0193	1.1293	0.313177
-1.1049	1743	4.0734	2.3766	-0.53717	1857	3.4464	2.4436	-0.68131
-0.39451	1251	9.992	3.542	0.799953	1210	14.628	8.738	2.430999
-0.19978	2107	10.394	3.944	0.890772	1844	9.8156	3.9256	1.091505
-0.81233	1491	9.9262	3.4762	0.785088	1366	7.3206	1.4306	0.397041
-0.43147	1568	11.671	5.221	1.17927	1332	10.811	4.921	1.368567
0.16361	2090	5.9809	0.4691	-0.10623	1305	13.027	7.137	1.985373
-0.61735	1518	6.9829	0.5329	0.120143	1542	9.5331	3.6431	1.012873
-0.67298	831	10.59	4.14	0.935052	935	12.727	6.837	1.90187

-0.31097	2037	6.5292	0.0792	0.017644	2896	3.2804	2.6096	-0.72752
-0.41262	851	1.7626	4.6874	-1.05922	726	4.8209	1.0691	-0.29873
0.271929	549	4.1894	2.2606	-0.51096	345	8.6957	2.8057	0.77979
0.254671	1270	2.2835	4.1665	-0.94154	1074	2.8864	3.0036	-0.83718
-0.85838	1142	2.8021	3.6479	-0.82437	719	4.4506	1.4394	-0.4018
0.147668	1426	10.589	4.139	0.934826	1492	5.2949	0.5951	-0.1668
-0.65854	1190	7.8151	1.3651	0.308152	1014	4.4379	1.4521	-0.40534
0.471247	386	9.0674	2.6174	0.591069	350	14	8.11	2.2562
-0.35219	863	1.6222	4.8278	-1.09094	821	5.7247	0.1653	-0.04717
0.549794	697	7.3171	0.8671	0.195645	1064	3.7594	2.1306	-0.59419
0.064104	2144	6.1101	0.3399	-0.07704	2853	6.4844	0.5944	0.164291
0.308433	988	9.0081	2.5581	0.577672	1133	5.1192	0.7708	-0.2157
0.014718	1201	10.075	3.625	0.818704	657	2.8919	2.9981	-0.83565
3.221653	1037	20.54	14.09	3.182937	940	13.298	7.408	2.060804
0.753396	1608	10.634	4.184	0.944993	1652	5.9927	0.1027	0.027431
-0.43514	2224	3.5522	2.8978	-0.65491	1799	3.1128	2.7772	-0.77417
1.701826	1129	9.9203	3.4703	0.783755	755	6.3576	0.4676	0.128998
0.282852	1299	10.239	3.789	0.855755	1133	8.12	2.23	0.619548
1.307259	1552	1.7397	4.7103	-1.06439	894	5.5928	0.2972	-0.08388
0.596089	1363	9.4644	3.0144	0.680759	2798	10.65	4.76	1.323754
1.121251	1273	10.448	3.998	0.902972	1407	4.6198	1.2702	-0.35471
-0.36467	1796	5.0111	1.4389	-0.32532	1695	11.268	5.378	1.495769
-0.67877	1049	3.8132	2.6368	-0.59595	1311	0.91533	4.97467	-1.38582
0.661784	1380	3.1159	3.3341	-0.75348	2324	5.1635	0.7265	-0.20337
-0.87187	907	7.828	1.378	0.311067	1106	7.3237	1.4337	0.397904
-0.70832	2010	3.4328	3.0172	-0.68189	2031	9.0596	3.1696	0.881078
0.201889	1513	4.957	1.493	-0.33754	1078	6.308	0.418	0.115192
0.219697	2975	7.6639	1.2139	0.273993	1776	8.1644	2.2744	0.631906
0.348364	2343	5.0363	1.4137	-0.31963	1563	6.4619	0.5719	0.158029
-0.52981	2249	3.3793	3.0707	-0.69398	1838	5.2775	0.6125	-0.17164
2.412629	2702	9.3634	2.9134	0.657941	2393	12.16	6.27	1.74405
0.735802	1269	3.9401	2.5099	-0.56728	1342	7.6006	1.7106	0.474977
1.073578	1983	4.589	1.861	-0.42068	1913	3.8683	2.0217	-0.56388
0.641558	2109	6.9701	0.5201	0.117251	1048	6.6794	0.7894	0.218568
-0.27376	1493	5.3583	1.0917	-0.24688	1287	8.547	2.657	0.7384
0.87478	2220	3.6036	2.8464	-0.6433	1783	6.1133	0.2233	0.060999
-0.46351	2327	4.2544	2.1956	-0.49627	1522	3.2194	2.6706	-0.7445
0.248215	2479	4.5986	1.8514	-0.41851	2313	4.4099	1.4801	-0.41313
0.487403	2928	5.7377	0.7123	-0.16117	2763	6.1889	0.2989	0.082041
-0.91217	1229	4.882	1.568	-0.35449	1134	4.2328	1.6572	-0.46242
-0.10569	1515	11.683	5.233	1.181981	1291	6.1967	0.3067	0.084212
	1363	6.4511	2.9908		1227	5.89415	2.4275	
			8.9724				7.2825	
			4.426384				3.5927	
2262	36.87		1393	17.301				
2517	33.89		2472	20.267				

2550	28.235	3000	20.167		
2316	27.85	2558	28.694		
2411.25	31.71125	2355.75	21.60725		
143.507	4.410337	682.2426	4.920583		
		477	3.1447	274	16.423
436	10.55	362	3.8674		
462	7.5758			291	17.526
734	9.5368	803	10.212		
544	9.220867	547.3333	5.741367		
165.0576	1.51206	228.7582	3.888508		
	13.23101		14.76175		
	4.536181		11.66552		
	17.76719		26.42727		
	22.49038		15.86588		
	0.789991		1.665667		
	0.210009		-0.66567		

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

x toxic a,b,c

y

						cell ct	% inf	AD
50079	A02	M-028473-	hypothetica	340074	LOC340074	517	10.445	4.595
50079	A04	M-019388-	hypothetica	340069	LOC340069	553	11.573	5.723
50079	A05	M-016883-	tumor supp	286753	TUSC5	950	4.6316	1.2184
50079	A06	M-024333-	transmemb	340061	TMEM173	998	6.3126	0.4626
50079	A07	M-018918-	lin-9 homo	286826	LIN9	1466	8.2538	2.4038
50079	A08	M-007352-	solute carri	340024	SLC6A19	1181	6.3506	0.5006
50079	A09	M-007172-	tripartite m	286827	TRIM59	622	4.5016	1.3484
50079	A10	M-028274-	hypothetica	340017	LOC340017	1581	14.864	9.014
50079	A11	M-024229-	casein alph	286828	CSN1S2A	639	11.581	5.731
50079	A12	M-028328-	hypothetica	339988	LOC339988	439	5.2392	0.6108
50079	A13	M-017749-	keratin 6C	286887	KRT6C	956	2.9289	2.9211
50079	A14	M-009115-	N-acetyltra	339983	NAT8L	1343	10.276	4.426
50079	A15	M-007173-	tripartite m	287015	TRIM42	1534	4.3677	1.4823
50079	A16	M-007174-	tripartite m	339976	TRIML1	303	15.842	9.992
50079	A17	M-017884-	Rieske (Fe-	317671	RFESD	1321	5.4504	0.3996
50079	A18	M-009148-	transmemb	339967	TMPRSS11A	1268	7.4132	1.5632
50079	A19	M-015577-	kelch-like 1	317719	KLHL10	1346	10.475	4.625
50079	A20	M-019221-	hypothetica	339965	FLJ25770	478	10.042	4.192
50079	A21	M-021490-	dehydrogen	317749	DHRS4L2	248	22.177	16.327
50079	A23	M-017911-	ankyrin rep	317754	ANKRD21	556	10.072	4.222
50079	B02	M-019339-	RNA bindin	348093	RBPMS2	2224	5.8903	0.0403
50079	B04	M-018818-	hypothetica	348378	MGC52498	1861	6.7706	0.9206
50079	B05	M-024271-	hypothetica	340094	LOC340094	1079	4.0778	1.7722
50079	B06	M-018312-	CTAGE fam	340307	CTAGE6	2927	1.2641	4.5859
50079	B07	M-028501-	hypothetica	340107	LOC340107	1305	0.38314	5.46686
50079	B08	M-026465-	chromosom	340895	C10orf112	1558	3.1451	2.7049
50079	B09	M-028502-	hypothetica	340109	LOC340109	1819	6.0473	0.1973
50079	B10	M-017763-	chromosom	352909	C19orf51	2135	4.0749	1.7751
50079	B11	M-028504-	hypothetica	340113	LOC340113	1674	9.7372	3.8872
50079	B12	M-029803-	chromosom	349633	C11orf34	1361	5.3637	0.4863
50079	B13	M-010757-	solute carri	340146	SLC35D3	633	7.109	1.259
50079	B14	M-008688-	nicotinami	349565	NMNAT3	1091	3.0247	2.8253
50079	B15	M-027171-	hypothetica	340156	RP11-145H	1666	5.5222	0.3278
50079	B16	M-022178-	CXYorf1-re	349338	LOC349338	1266	6.3191	0.4691
50079	B17	M-018462-	triggering r	340205	TREML1	977	6.653	0.803
50079	B18	M-031739-	forkhead b	349334	FOXD4L4	1732	2.9446	2.9054
50079	B19	M-018017-	zinc finger	340252	ZNF680	1823	4.0592	1.7908
50079	B20	M-018871-	chromosom	349236	C9orf164	3742	5.0241	0.8259
50079	B21	M-025309-	chromosom	340277	C7orf46	1852	5.9935	0.1435
50079	B23	M-028865-	CTAGE fam	340311	CTAGE4	2093	6.259	0.409
50079	C02	M-009007-	testis serine	339906	TESSP2	1611	15.953	10.103
50079	C04	M-023472-	hypothetica	339903	LOC339903	3231	10.028	4.178
50079	C05	M-017933-	chromosom	317761	C14orf39	4224	15.412	9.562
50079	C06	M-023510-	glutamate	339896	GADL1	2639	14.854	9.004
50079	C07	M-019232-	histone clu	317772	HIST2H2AB	1813	16.657	10.807
50079	C08	M-028189-	hypothetica	339894	LOC339894	3142	19.287	13.437

50079	C09	M-018018-	DEAD (Asp	317781	DDX51	2213	13.24	7.39
50079	C10	M-017640-	chromoson	339883	C3orf35	2111	14.827	8.977
50079	C11	M-021942-	chromoson	319089	C14orf25	1359	9.4923	3.6423
50079	C12	M-028079-	hypothetic	339862	LOC33986	1516	12.929	7.079
50079	C13	M-018438-	zygote arre	326340	ZAR1	2164	10.675	4.825
t	C14	M-017970-	kyphoscoli	339855	KY	1350	20.222	14.372
50079	C15	M-031217-	egf-like mo	326342	EMR4	2645	12.628	6.778
50079	C16	M-018464-	coiled-coil	339834	CCDC36	2192	12.774	6.924
50079	C17	M-008933-	RAB37, me	326624	RAB37	2226	4.9416	0.9084
50079	C18	M-023658-	coiled-coil	339829	CCDC39	2456	9.6906	3.8406
50079	C19	M-017947-	serpin pep	327657	SERPINA9	1831	15.62	9.77
50079	C20	M-027890-	hypothetic	339822	LOC33982	3072	5.957	0.107
50079	C21	M-022600-	snail homo	333929	SNAI3	845	12.781	6.931
50079	C23	M-017914-	UBA domai	337867	UBAC2	2831	5.5104	0.3396
50079	D02	M-029304-	hypothetic	349196	LOC34919	4090	5.0367	0.8133
50079	D04	M-018870-	dpy-19-like	349152	DPY19L2P2	4056	10.799	4.949
50079	D05	M-028897-	nuclear env	340318	LOC34031	3363	5.62	0.23
50079	D06	M-018750-	gap junctio	349149	GJE1	2928	5.0546	0.7954
50079	D07	M-028923-	hypothetic	340340	LOC34034	3284	6.6382	0.7882
50079	D08	M-025374-	WD repeat	349136	WDR86	4489	12.586	6.736
50079	D09	M-018311-	tetraspani	340348	TSPAN33	3089	9.4529	3.6029
50079	D10	M-025321-	hypothetic	349114	LOC34911	3245	11.834	5.984
50079	D11	M-025456-	ATP/GTP bi	340351	AGBL3	1271	5.8222	0.0278
50079	D12	M-018833-	zinc finger	349075	ZNF713	2557	9.2296	3.3796
50079	D13	M-025859-	zinc finger	340385	ZNF517	2545	6.4833	0.6333
50079	D14	M-024488-	hypothetic	349035	MGC22265	3164	7.0796	1.2296
50079	D15	M-025811-	KIAA1875	340390	KIAA1875	3095	6.0743	0.2243
50079	D16	M-018906-	nucleopori	348995	NUP43	2071	12.265	6.415
50079	D17	M-017888-	R-spondin	340419	RSPO2	2209	5.0702	0.7798
50079	D18	M-024299-	ichthyin pr	348938	ICHTHYIN	2803	6.279	0.429
50079	D19	M-017866-	zinc finger,	340481	ZDHHC21	3593	5.1211	0.7289
50079	D20	M-007334-	solute carri	348932	SLC6A18	2425	3.6701	2.1799
50079	D21	M-026218-	hypothetic	340508	LOC34050	3816	5.3983	0.4517
50079	D23	M-029615-	hypothetic	340515	LOC34051	2804	2.6391	3.2109
50079	E02	M-023119-	KIAA2012	339809	LOC33980	3064	7.8655	2.0155
50079	E04	M-027850-	hypothetic	339807	LOC33980	2565	9.4347	3.5847
50079	E05	M-010966-	chondroiti	337876	CHSY-2	2966	8.7997	2.9497
50079	E06	M-027847-	hypothetic	339803	LOC33980	1532	7.5718	1.7218
50079	E07	M-017997-	keratin ass	337879	KRTAP8-1	3698	5.219	0.631
50079	E08	M-027976-	chromoson	339789	C2orf46	2409	6.3927	0.5427
50079	E09	M-017999-	keratin ass	337880	KRTAP11-1	3273	2.1998	3.6502
50079	E10	M-027975-	hypothetic	339788	LOC33978	2766	4.1938	1.6562
50079	E11	M-018593-	keratin ass	337882	KRTAP19-1	2291	3.9284	1.9216
50079	E12	M-017703-	chromoson	339779	C2orf53	2342	4.6968	1.1532
50079	E13	M-031262-	keratin ass	337959	KRTAP13-2	1292	4.9536	0.8964
50079	E14	M-019294-	espin-like	339768	ESPNL	2955	4.5347	1.3153
50079	E15	M-018680-	keratin ass	337960	KRTAP13-3	2565	4.3665	1.4835

50079	E16	M-022969- hypothetic	339766	LOC33976	3363	1.5462	4.3038
50079	E17	M-009143- keratin ass	337963	KRTAP23-1	2113	2.6503	3.1997
50079	E18	M-027940- hypothetic	339745	LOC33974	2543	2.1628	3.6872
50079	E19	M-017993- keratin ass	337967	KRTAP6-2	2620	2.5573	3.2927
50079	E20	M-022859- hypothetic	339692	LOC33969	3342	3.7403	2.1097
50079	E21	M-017979- keratin ass	337968	KRTAP6-3	4161	6.9214	1.0714
50079	E23	M-018579- keratin ass	337969	KRTAP19-2	3047	0.72202	5.12798
50079	F02	M-018717- hypothetic	348840	LOC34884	3034	2.8675	2.9825
50079	F04	M-018668- coiled-coil	348807	CCDC37	2280	3.2018	2.6482
50079	F05	M-024837- retrotrans	340526	RGAG4	2617	5.8082	0.0418
50079	F06	M-028142- hypothetic	348801	LOC34880	2620	3.6641	2.1859
50079	F07	M-024839- similar to p	340529	RP11-493K	2616	7.3012	1.4512
50079	F08	M-018933- WD repeat	348793	WDR53	2608	8.1288	2.2788
50079	F09	M-024823- KIAA2022	340533	KIAA2022	2261	3.7594	2.0906
50079	F10	M-018690- chromoso	348738	C2orf48	3474	2.5619	3.2881
50079	F11	M-024778- NGFRAP1-l	340542	NGFRAP1L	1449	4.0718	1.7782
50079	F12	M-018757- hypothetic	348654	FLJ40869	2878	11.883	6.033
50079	F13	M-018899- V-set and i	340547	VSIG1	1993	7.5765	1.7265
50079	F14	M-024639- chromoso	348645	C22orf34	3677	24.069	18.219
50079	F15	M-009099- ubiquitin-c	340561	UBE2DNL	3450	4.7536	1.0964
50079	F16	M-018945- family with	348487	FAM131C	2134	2.7179	3.1321
50079	F17	M-024771- spermidine	340562	SATL1	2406	4.6966	1.1534
50079	F18	M-022304- C219-react	348477	KIAA0268	4040	6.9307	1.0807
50079	F19	M-024944- hypothetic	340581	LOC34058	3479	4.599	1.251
50079	F20	M-014132- zinc finger	348327	ZNF530	4334	5.03	0.82
50079	F21	M-021418- lipoma HM	340596	LHFPL1	3719	3.1729	2.6771
50079	F23	M-031896- similar to	340602	LOC34060	1982	2.9768	2.8732
50079	G02	M-031497- hypothetic	339685	LOC33968	2661	1.8414	4.0086
50079	G04	M-031473- hypothetic	339674	LOC33967	2139	2.7583	3.0917
50079	G05	M-018572- keratin ass	337970	KRTAP19-3	1914	3.2393	2.6107
50079	G06	M-018448- chromoso	339669	C22orf33	1999	2.4512	3.3988
50079	G07	M-018564- keratin ass	337971	KRTAP19-4	1534	4.1069	1.7431
50079	G08	M-031462- solute carri	339665	SLC35E4	2021	3.0183	2.8317
50079	G09	M-018589- keratin ass	337972	KRTAP19-5	1942	2.6777	3.1723
50079	G10	M-024364- chromoso	339629	C21orf54	2527	3.0471	2.8029
50079	G11	M-018598- keratin ass	337973	KRTAP19-6	1045	6.7943	0.9443
50079	G12	M-031333- hypothetic	339593	LOC33959	1799	5.5586	0.2914
50079	G13	M-018601- keratin ass	337974	KRTAP19-7	1878	4.4728	1.3772
50079	G14	M-031302- hypothetic	339568	LOC33956	1933	6.208	0.358
50079	G15	M-018605- keratin ass	337975	KRTAP20-1	1868	5.8351	0.0149
50079	G16	M-027243- zinc finger	339559	ZNF642	2190	6.0731	0.2231
50079	G17	M-018607- keratin ass	337976	KRTAP20-2	2431	8.2271	2.3771
50079	G18	M-027464- hypothetic	339539	LOC33953	1411	10.135	4.285
50079	G19	M-018659- keratin ass	337977	KRTAP21-1	1683	6.2389	0.3889
50079	G20	M-027622- hypothetic	339535	LOC33953	2248	8.363	2.513
50079	G21	M-018617- keratin ass	337978	KRTAP21-2	1520	4.6053	1.2447
50079	G23	M-018663- keratin ass	337979	KRTAP22-1	3135	9.2185	3.3685

50079	H02	M-019314- selenoprot	348303	SELV	4420	14.344	8.494
50079	H04	M-031000- hypothetica	348262	LOC348262	2933	5.5574	0.2926
50079	H05	M-019363- cytochrome	340665	CYP26C1	1321	1.8168	4.0332
50079	H06	M-018781- family with	348235	FAM33A	2673	6.4347	0.5847
50079	H07	M-031756- von Willebr	340706	VWA2	1985	1.2594	4.5906
50079	H08	M-022609- hypothetica	348180	LOC348180	4080	2.9167	2.9333
50079	H09	M-027290- nanos hom	340719	NANOS1	2606	4.1059	1.7441
50079	H10	M-018779- secretory p	348174	LOC348174	3191	7.3018	1.4518
50079	H11	M-029973- otogelin	340990	OTOG	2786	3.6971	2.1529
50079	H12	M-022780- hypothetica	348162	LOC348162	1712	1.4603	4.3897
50079	H13	M-018628- doublecort	341019	DCDC1	2227	4.7598	1.0902
50079	H14	M-018702- acyl-CoA sy	348158	ACSM2	3109	6.6581	0.8081
50079	H15	M-027244- chromosom	341032	C11orf53	1028	7.7821	1.9321
50079	H16	M-018687- chromosom	348110	C15orf38	1973	1.0137	4.8363
50079	H17	M-031991- membrane	341116	MS4A10	1458	1.5775	4.2725
50079	H18	M-019312- ankyrin rep	348094	ANKDD1A	3596	4.5328	1.3172
50079	H19	M-029943- hephaestin	341208	HEPHL1	4315	3.0127	2.8373
50079	H20	M-018925- family with	348013	FAM70B	3043	3.5491	2.3009
50079	H21	M-031858- ovochymas	341277	OVCH2	2977	2.1834	3.6666
50079	H23	M-019444- ovochymas	341350	OVCH1	2365	3.4672	2.3828
50079	I02	M-022142- hypothetica	339531	MGC35030	1864	2.2532	3.5968
50079	I04	M-022138- hypothetica	339529	LOC339529	2915	5.8662	0.0162
50079	I05	M-017762- chromosom	338094	C1orf179	3012	5.4117	0.4383
50079	I06	M-027408- hypothetica	339524	LOC339524	1428	8.7535	2.9035
50079	I07	M-027145- S100 calciu	338324	S100A7A	2285	7.6586	1.8086
50079	I08	M-017922- chromosom	339512	C1orf110	2363	3.8934	1.9566
50079	I09	M-018458- high densit	338328	LOC338328	2346	6.5217	0.6717
50079	I10	M-005972- marapsin 2	339501	MPN2	1416	5.2966	0.5534
50079	I11	M-017844- interferon	338376	IFNE1	2556	7.7074	1.8574
50079	I12	M-018005- zinc finger	339500	ZNF678	2050	8.6829	2.8329
50079	I13	M-018225- RAB7B, me	338382	RAB7B	1978	9.6057	3.7557
50079	I14	M-018021- transcriptio	339488	TFAP2E	2134	5.8575	0.0075
50079	I15	M-026726- transmemb	338440	TMEM16J	2634	14.275	8.425
50079	I16	M-017915- zinc finger	339487	ZBTB8OS	1948	7.4435	1.5935
50079	I17	M-009140- potassium	338567	KCNK18	2971	13.06	7.21
50079	I18	M-032010- family with	339479	FAM5C	2994	7.1476	1.2976
50079	I19	M-029706- hypothetica	338588	LOC338588	1348	10.608	4.758
50079	I20	M-027548- chromosom	339476	C1orf99	2691	8.1011	2.2511
50079	I21	M-026399- ST8 alpha-N	338596	ST8SIA6	1550	6.5806	0.7306
50079	I23	M-026458- dual specifi	338599	DUPD1	2984	3.3847	2.4653
50079	J02	M-018922- EP400 N-te	347918	EP400NL	1661	2.4082	3.4418
50079	J04	M-018701- adhesion m	347902	AMIGO2	1989	8.9995	3.1495
50079	J05	M-032244- synaptotag	341359	SYT10	3455	5.0362	0.8138
50079	J06	M-018917- Parkinson d	347862	PDDC1	2315	4.4492	1.4008
50079	J07	M-018900- ankyrin rep	341405	ANKRD33	3467	4.4419	1.4081
50079	J08	M-012731- T-box 10	347853	TBX10	1521	2.8928	2.9572
50079	J09	M-018845- H1 histone	341567	H1FNT	1997	3.355	2.495

50079	J10	M-018445- otopetrin 3	347741	OTOP3	2555	4.775	1.075
50079	J11	M-021693- FRAS1 rela	341640	FREM2	1522	7.0302	1.1802
50079	J12	M-006790- thioredoxi	347736	TXNDC6	2107	7.7361	1.8861
50079	J13	M-021702- NIMA (nev	341676	NEK5	2286	6.4304	0.5804
50079	J14	M-017756- serine inco	347735	SERINC2	1903	5.3074	0.5426
50079	J15	M-030295- solute carri	341880	SLC35F4	2470	3.9271	1.9229
50079	J16	M-007543- solute carri	347734	SLC35B2	1586	5.2963	0.5537
50079	J17	M-027245- leucine ric	341883	LRRC9	4688	3.8396	2.0104
50079	J18	M-017790- tubulin, be	347733	TUBB2B	2468	4.2139	1.6361
50079	J19	M-019415- cytochrom	341947	COX8C	3256	9.5823	3.7323
50079	J20	M-008518- cation char	347732	CATSPER3	2456	5.3746	0.4754
50079	J21	M-018759- gliomedin	342035	GLDN	1586	4.6658	1.1842
50079	J23	M-018586- transmem	342125	TMC3	2799	2.5009	3.3491
50079	K02	M-027486- hypothetic	339468	LOC33946	2844	10.056	4.206
50079	K04	M-025223- hypothetic	339457	LOC33945	3980	8.0653	2.2153
50079	K05	M-029976- leucine zip	338645	LUZP2	3403	6.9351	1.0851
50079	K06	M-017847- transmem	339456	TMEM52	2591	5.5963	0.2537
50079	K07	M-027240- coiled-coil	338657	CCDC84	2827	9.2678	3.4178
50079	K08	M-031770- kelch-like 1	339451	KLHL17	2235	6.2192	0.3692
50079	K09	M-026534- hypothetic	338667	LOC33866	2946	6.5852	0.7352
50079	K10	M-021859- chromoso	339448	C1orf174	1761	4.3157	1.5343
50079	K11	M-026603- ankyrin rep	338692	ANKRD13D	3138	7.9031	2.0531
50079	K12	M-027459- hypothetic	339442	LOC33944	2835	10.547	4.697
50079	K13	M-026609- hypothetic	338694	LOC33869	3165	9.5735	3.7235
50079	K14	M-027242- ankyrin rep	339416	ANKRD45	3515	15.903	10.053
50079	K15	M-018873- ankyrin rep	338699	ANKRD42	4463	11.427	5.577
50079	K16	M-032216- C-type lecti	339390	CLEC4G	2528	6.0522	0.2022
50079	K17	M-017753- beta-1,4-N-	338707	B4GALNT4	4390	15.763	9.913
50079	K18	M-023895- ADAMTS-li	339366	ADAMTSL5	3383	4.3748	1.4752
50079	K19	M-030043- hypothetic	338758	LOC33875	2216	10.83	4.98
50079	K20	M-031124- nanos hom	339345	NANOS2	4137	12.424	6.574
50079	K21	M-018636- transmem	338773	TMEM119	2229	8.838	2.988
50079	K23	M-018041- keratin 6L	338785	KRT6L	2110	3.1754	2.6746
50079	L02	M-017738- leucine ric	347731	LRRTM3	2189	3.7917	2.0583
50079	L04	M-018328- leucine ric	347730	LRRTM1	2021	4.4532	1.3968
50079	L05	M-030385- formin 1	342184	FMN1	2969	3.5702	2.2798
50079	L06	M-027356- tubulin, be	347688	TUBB8	3027	3.634	2.216
50079	L07	M-019081- polycystic	342372	PKD1L3	2233	17.6	11.75
50079	L08	M-031575- RAB41, me	347517	RAB41	3973	9.036	3.186
50079	L09	M-027246- smoothelin	342527	SMTNL2	2838	2.4313	3.4187
50079	L10	M-010310- diacylglyce	347516	DGAT2L6	3481	12.64	6.79
50079	L11	M-031849- nascent po	342538	NACA2	2590	9.6911	3.8411
50079	L12	M-027251- LanC lantib	347404	LANCL3	3875	15.277	9.427
50079	L13	M-018754- keratin 27	342574	KRT27	2605	2.6871	3.1629
50079	L14	M-027250- inter-alpha	347365	ITIH5L	3366	9.8039	3.9539
50079	L15	M-027247- FLJ43826 p	342666	FLJ43826	2280	6.2281	0.3781
50079	L16	M-032218- zinc finger	347344	ZNF81	2612	3.5988	2.2512

50079	L17	M-027277-	SH3 and cy	342667	STAC2	1694	2.5384	3.3116
50079	L18	M-010459-	chromoson	347240	C9orf48	2988	14.424	8.574
50079	L19	M-023653-	hypothetic	342892	LOC34289	4129	8.1376	2.2876
50079	L20	M-031843-	RF(Arg-Phe	347148	P518	2645	4.7637	1.0863
50079	L21	M-008085-	syncollin	342898	SYCN	1653	14.217	8.367
50079	L23	M-023737-	zinc finger	342908	ZNF404	2321	10.513	4.663
50079	M02	M-023759-	hypothetic	339344	LOC33934	2604	1.8049	4.0451
50079	M04	M-017811-	zinc finger	339327	ZNF546	1332	3.7538	2.0962
50079	M05	M-027094-	hypothetic	338797	LOC33879	1663	4.089	1.761
50079	M06	M-023851-	zinc finger	339324	ZNF260	2057	1.7501	4.0999
50079	M07	M-017777-	hypothetic	338799	LOC33879	2320	2.6724	3.1776
50079	M08	M-023650-	hypothetic	339321	LOC339321	2230	1.9731	3.8769
50079	M09	M-030046-	hypothetic	338809	LOC33880	1707	1.8161	4.0339
50079	M10	M-023641-	zinc finger	339318	ZNF181	2757	4.2075	1.6425
50079	M11	M-017751-	family with	338811	FAM19A2	3082	4.575	1.275
50079	M12	M-031078-	hypothetic	339316	LOC33931	2990	5.1171	0.7329
50079	M13	M-030126-	organic ani	338821	LST-3TM12	1689	4.3813	1.4687
50079	M14	M-018756-	complexin	339302	CPLX4	3106	8.5641	2.7141
50079	M15	M-030234-	hypothetic	338862	LOC33886	3356	8.3731	2.5231
50079	M16	M-031011-	hypothetic	339290	LOC33929	3167	3.4417	2.4083
50079	M17	M-017782-	C1q and tu	338872	C1QTNF9	3364	3.5672	2.2828
50079	M18	M-023361-	hypothetic	339284	FLJ11822	3264	4.9326	0.9174
50079	M19	M-019112-	ceh-10 hon	338917	CHX10	3675	2.585	3.265
50079	M20	M-030975-	chromoson	339263	C17orf51	2377	2.8187	3.0313
50079	M21	M-022438-	WAS prote	339005	WHDC1L1	2648	4.2296	1.6204
50079	M23	M-032043-	protein exp	339010	POTE15	2944	2.2758	3.5742
50079	N02	M-029416-	FLJ43950 p	347127	FLJ43950	2787	2.4758	3.3742
50079	N04	M-005547-	G protein-c	347088	GPR144	3447	8.036	2.186
50079	N05	M-018901-	zinc finger	342926	ZNF677	3548	6.5953	0.7453
50079	N06	M-029388-	solute carri	347051	SLC10A5	4641	7.8647	2.0147
50079	N07	M-007175-	zinc finger	342945	ZSCAN22	3496	4.405	1.445
50079	N08	M-027249-	killer cell le	346689	KLRG2	3591	4.7341	1.1159
50079	N09	M-031277-	nanos hom	342977	NANOS3	2254	4.126	1.724
50079	N10	M-008440-	stimulated	346673	STRA8	1507	2.1234	3.7266
50079	N11	M-019462-	retinal deg	343035	RD3	2752	11.483	5.633
50079	N12	M-025447-	hypothetic	346653	LOC34665	1832	7.369	1.519
50079	N13	M-021570-	PRAME fan	343068	PRAMEF5	2383	3.441	2.409
50079	N14	M-004993-	monoacylg	346606	MOGAT3	2780	4.9281	0.9219
50079	N15	M-021571-	PRAME fan	343070	PRAMEF9	3326	5.5021	0.3479
50079	N16	M-028947-	guanine nu	346562	GNAT3	2453	3.0982	2.7518
50079	N17	M-021572-	PRAME fan	343071	PRAMEF10	2777	3.673	2.177
50079	N18	M-032046-	hypothetic	346547	FLJ42291	2779	6.4052	0.5552
50079	N19	M-021630-	coiled-coil	343099	CCDC18	4695	14.846	8.996
50079	N20	M-032047-	septin 14	346288	SEPT14	3894	6.7283	0.8783
50079	N21	M-027333-	potassium	343450	KCNT2	3602	2.5264	3.3236
50079	N23	M-032002-	BarH-like 2	343472	BARHL2	2291	3.1427	2.7073
50079	O02	M-023333-	ADP-ribosy	339231	ARL16	1865	1.1796	4.6704

50079	O04	M-030964- coiled-coil	339230	CCDC137	1734	5.6517	0.1983
50079	O05	M-030594- hypothetic	339047	LOC339047	1963	6.0112	0.1612
50079	O06	M-030963- hypothetic	339229	LOC33922	2110	4.1232	1.7268
50079	O07	M-018877- hypothetic	339059	FLJ40448	1869	4.9224	0.9276
50079	O08	M-009059- ectonucleo	339221	ENPP7	2222	3.6454	2.2046
50079	O09	M-017909- chromoson	317762	C14orf65	1621	3.0228	2.8272
50079	O10	M-030913- chromoson	339210	C17orf67	2224	7.2392	1.3892
50079	O11	M-018875- hypothetic	338999	FLJ36131	1798	8.3426	2.4926
50079	O12	M-017785- chromoson	339201	C17orf65	1421	2.3927	3.4573
50079	O13	M-018082- ATG9 autop	285973	ATG9B	1370	1.6788	4.1712
50079	O14	M-018908- methyltran	339175	METTL2A	2641	7.0049	1.1549
50079	O15	M-019295- hypothetic	286527	MGC39900	2380	11.555	5.705
50079	O16	M-021502- transmemb	339168	TMEM95	1099	8.0983	2.2483
50079	O17	M-032283- hypothetic	286087	LOC286087	2105	8.171	2.321
50079	O18	M-027241- family with	339145	FAM92B	2106	8.1671	2.3171
50079	O19	M-031925- keratin ass	388818	KRTAP26-1	3168	6.0606	0.2106
50079	O20	M-028161- RAB43, me	339122	RAB43	1735	9.2219	3.3719
50079	O21	M-027170- similar to P	388968	LOC38896	2676	3.438	2.412
50079	O23	M-032080- FLJ42986 p	389012	FLJ42986	1885	10.027	4.177
50079	P02	M-024856- EGF-like-dc	346007	EGFL11	1644	8.2117	2.3617
50079	P04	M-031759- transmemb	345757	TMEM157	1528	7.6571	1.8071
50079	P05	M-027201- transglutar	343641	TGM6	2405	17.547	11.697
50079	P06	M-030868- similar to A	345667	LOC345667	1868	5.2463	0.6037
50079	P07	M-032045- chromoson	343990	C2orf55	2343	8.4507	2.6007
50079	P08	M-028450- immunity-r	345611	IRGM	2253	8.1669	2.3169
50079	P09	M-022918- Nck-associ	344148	NAP5	1628	16.83	10.98
50079	P10	M-028432- BRCT doma	345499	BRCTD1	2787	11.446	5.596
50079	P11	M-027806- SH3 multip	344558	SH3MD4	2298	10.357	4.507
50079	P12	M-018524- hydroxyste	345275	HSD17B13	2463	6.5773	0.7273
50079	P13	M-005704- G protein-c	344561	GPR148	1732	5.0808	0.7692
50079	P14	M-007629- solute carri	345274	SLC10A6	3196	11.264	5.414
50079	P15	M-009146- sterile alph	344658	SAMD7	2540	7.4803	1.6303
50079	P16	M-027248- FLJ44691 p	345193	FLJ44691	2307	9.2328	3.3828
50079	P17	M-032044- arylacetam	344752	AADACL2	2433	7.1928	1.3428
50079	P18	M-019406- epidermis-	345062	ESSPL	2563	11.627	5.777
50079	P19	M-005697- G protein-c	344758	GPR149	2286	5.3806	0.4694
50079	P20	M-032025- osteocrin	344901	OSTN	1489	9.2008	3.3508
50079	P21	M-023574- transmemb	344805	TMPRSS7	1227	5.1345	0.7155
50079	P23	M-008055- progestin a	344838	PAQR9	1205	3.5685	2.2815
				MAD	2344.5	5.8463	2.28215
				MAD3			6.84645
				MADc			3.377582
50079	C22				497	19.92	
50079	D22				2512	18.432	
50079	E22		1963	32.756			
50079	F22				2113	20.681	
				mn	1707.333	19.67767	

				sd	1066.996	1.143916
50079	G22	466	11.159			
50079	H22				697	0.71736
50079	I22	251	19.124			
50079	J22				743	2.961
				mn	720	1.83918
				sd	32.52691	1.586493
				3psSD		3.431749
				3ngSD		4.759479
				SumSD		8.191228
				MeanDf		17.83849
				SumovrMn		0.459188
				1minus		0.540812

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
1.361536	542	6.0886	1.4614	-0.33106	974	6.6735	0.0535	0.012498
1.695503	436	14.22	6.67	1.516538	472	15.042	8.422	2.031599
-0.35964	621	14.654	7.104	1.61515	824	5.2184	1.4016	-0.33858
0.138057	446	14.35	6.8	1.546076	926	7.8834	1.2634	0.304415
0.712788	1078	8.7199	1.1699	0.266821	2296	5.0087	1.6113	-0.38917
0.149308	768	11.589	4.039	0.91873	1404	4.7009	1.9191	-0.46344
-0.39813	385	17.143	9.593	2.180694	449	15.367	8.747	2.110013
2.669869	1075	12.186	4.636	1.054379	937	10.993	4.373	1.054681
1.697871	672	15.774	8.224	1.869634	777	7.8507	1.2307	0.296526
-0.17974	464	16.164	8.614	1.958248	481	6.8607	0.2407	0.057664
-0.86375	920	6.1957	1.3543	-0.30672	510	7.0588	0.4388	0.105461
1.3115	860	16.977	9.427	2.142976	560	11.429	4.809	1.159876
-0.43777	1084	10.886	3.336	0.758996	709	4.5134	2.1066	-0.50868
2.959425	347	27.089	19.539	4.440596	295	8.8136	2.1936	0.528848
-0.11721	1030	13.689	6.139	1.395886	1238	3.231	3.389	-0.81809
0.463912	1085	12.811	5.261	1.196389	1110	10.631	4.011	0.96734
1.370418	1168	10.788	3.238	0.736729	977	9.1095	2.4895	0.600241
1.24222	383	18.016	10.466	2.379055	416	6.4904	0.1296	-0.03168
4.835027	391	17.136	9.586	2.179103	489	5.9305	0.6895	-0.16677
1.251102	226	20.354	12.804	2.910288	426	2.1127	4.5073	-1.0879
0.013027	1763	0.73738	6.81262	-1.54694	2469	5.3058	1.3142	-0.31749
0.273657	1973	2.6863	4.8637	-1.10412	1165	4.0343	2.5857	-0.62427
-0.5236	414	3.1401	4.4099	-1.00101	833	4.6819	1.9381	-0.46802
-1.35665	3535	0.42433	7.12567	-1.61807	2421	1.7761	4.8439	-1.16912
-1.61748	1610	0.68323	6.86677	-1.55925	884	3.5068	3.1132	-0.75154
-0.79974	1540	1.3636	6.1864	-1.40466	1364	1.0997	5.5203	-1.33231
0.05951	1059	1.7941	5.7559	-1.30684	799	7.5094	0.8894	0.214179
-0.52446	2162	3.2377	4.3123	-0.97883	2093	2.6756	3.9444	-0.95209
1.151978	1190	2.521	5.029	-1.14168	1705	6.6276	0.0076	0.001424
-0.14288	757	1.4531	6.0969	-1.38432	848	6.1321	0.4879	-0.11813
0.373847	570	2.6316	4.9184	-1.11655	393	6.6158	0.0042	-0.00142
-0.83539	492	5.4878	2.0622	-0.46757	573	9.5986	2.9786	0.718248
-0.09596	935	2.4599	5.0901	-1.15556	1028	6.9066	0.2866	0.068739
0.139982	1158	5.5268	2.0232	-0.45871	1004	7.4701	0.8501	0.204697
0.23884	325	3.3846	4.1654	-0.94545	533	3.94	2.68	-0.64702
-0.85911	1459	2.0562	5.4938	-1.24729	1797	5.5648	1.0552	-0.255
-0.52911	1797	2.1146	5.4354	-1.23402	1446	4.7718	1.8482	-0.44633
-0.24343	2251	2.1324	5.4176	-1.22997	1945	5.5013	1.1187	-0.27032
0.043581	1647	2.6715	4.8785	-1.10748	1740	7.8161	1.1961	0.288178
0.122188	1269	6.6194	0.9306	-0.21045	1291	8.2107	1.5907	0.383384
2.992289	1665	10.33	2.78	0.632663	1880	5.3723	1.2477	-0.30145
1.238075	1885	3.183	4.367	-0.99126	1766	5.0396	1.5804	-0.38172
2.832115	2196	3.1421	4.4079	-1.00055	3881	4.2257	2.3943	-0.57809
2.666908	1455	5.2921	2.2579	-0.51203	3561	7.8068	1.1868	0.285934
3.200722	1746	5.6701	1.8799	-0.42615	2400	4.25	2.37	-0.57223
3.979385	1858	14.747	7.197	1.636282	3939	11.018	4.398	1.060713

2.189051	1492	8.6461	1.0961	0.250052	2354	4.7579	1.8621	-0.44969
2.658914	786	17.939	10.389	2.361559	1303	10.361	3.741	0.902196
1.07947	1464	9.7678	2.2178	0.504922	1461	3.2854	3.3346	-0.80496
2.096974	1261	3.0928	4.4572	-1.01175	2014	3.8232	2.7968	-0.67521
1.429632	1548	13.63	6.08	1.38248	2338	3.8494	2.7706	-0.66888
4.256211	1014	22.88	15.33	3.484239	1368	7.6023	0.9823	0.236593
2.007857	1513	13.153	5.603	1.274098	2804	5.3495	1.2705	-0.30695
2.051083	1248	14.824	7.274	1.653777	1790	4.1341	2.4859	-0.60019
-0.26785	786	10.814	3.264	0.742637	1697	2.0625	4.5575	-1.10002
1.138181	1059	11.898	4.348	0.98894	2196	4.918	1.702	-0.41106
2.893697	1468	12.466	4.916	1.117999	2571	5.4842	1.1358	-0.27445
0.032775	2361	4.7861	2.7639	-0.62701	2663	3.8678	2.7522	-0.66444
2.053155	614	21.336	13.786	3.133416	581	17.9	11.28	2.72116
-0.09945	1820	8.8462	1.2962	0.295519	1206	5.2239	1.3961	-0.33725
-0.2397	3344	3.11	4.44	-1.00784	2604	8.1413	1.5213	0.36664
1.466345	2755	7.7314	0.1814	0.042217	1859	14.739	8.119	1.958493
-0.067	1659	2.7728	4.7772	-1.08446	1801	6.1632	0.4568	-0.11062
-0.2344	1182	5.5838	1.9662	-0.44575	2007	11.908	5.288	1.275447
0.234458	1290	9.2248	1.6748	0.381543	1128	17.287	10.667	2.573259
1.995422	2933	10.16	2.61	0.594037	4774	13.594	6.974	1.682234
1.067805	1636	6.7237	0.8263	-0.18675	2527	8.8643	2.2443	0.541081
1.772777	4098	14.959	7.409	1.684452	3881	18.629	12.009	2.897049
-0.00714	2201	5.8155	1.7345	-0.39311	1729	7.9237	1.3037	0.314139
1.001693	1793	3.5137	4.0363	-0.91612	1111	6.2106	0.4094	-0.09919
0.188596	2412	1.2438	6.3062	-1.43188	1641	8.897	2.277	0.548971
0.365143	3240	6.6975	0.8525	-0.1927	2896	8.3218	1.7018	0.41019
0.067504	2334	11.525	3.975	0.904188	3233	8.9391	2.3191	0.559128
1.900383	1975	13.823	6.273	1.426333	1599	15.697	9.077	2.189634
-0.22978	2008	9.0139	1.4639	0.333623	1447	10.85	4.23	1.020179
0.128109	2055	7.2019	0.3481	-0.07809	2647	9.8602	3.2402	0.781366
-0.21471	3081	5.2256	2.3244	-0.52714	2372	7.1669	0.5469	0.131543
-0.64431	2182	7.6535	0.1035	0.024517	712	6.882	0.262	0.062804
-0.13264	2471	6.3537	1.1963	-0.27082	2190	14.155	7.535	1.817589
-0.94956	1678	3.6949	3.8551	-0.87495	1348	4.3027	2.3173	-0.55951
0.597824	1819	5.4426	2.1074	-0.47784	1555	1.4791	5.1409	-1.24078
1.062417	2423	3.5493	4.0007	-0.90803	2097	5.4363	1.1837	-0.28601
0.874413	1497	6.2792	1.2708	-0.28775	2419	3.9272	2.6928	-0.65011
0.510868	784	8.4184	0.8684	0.198315	1289	1.9395	4.6805	-1.12969
-0.18572	2183	6.3216	1.2284	-0.27811	2859	0.7695	5.8505	-1.41198
0.161773	2586	7.3086	0.2414	-0.05385	2798	3.8242	2.7958	-0.67496
-1.07962	1981	4.7956	2.7544	-0.62485	3051	0.55719	6.06281	-1.46321
-0.48926	1852	6.1555	1.3945	-0.31585	1905	3.8845	2.7355	-0.66042
-0.56783	1458	4.4582	3.0918	-0.70151	1864	1.2876	5.3324	-1.28698
-0.34033	1167	8.826	1.276	0.290929	947	0.1056	6.5144	-1.57217
-0.2643	582	6.5292	1.0208	-0.23094	1723	2.0894	4.5306	-1.09353
-0.38833	1424	8.0056	0.4556	0.10452	790	5.1899	1.4301	-0.34546
-0.43812	2159	3.7981	3.7519	-0.8515	2080	1.25	5.37	-1.29605

-1.27313	2759	6.4154	1.1346	-0.2568	1879	0.42576	6.19424	-1.49492
-0.94624	2673	6.5844	0.9656	-0.2184	1067	2.9053	3.7147	-0.89667
-1.09057	2535	6.0355	1.5145	-0.34312	2681	1.5666	5.0534	-1.21966
-0.97377	2100	3.5714	3.9786	-0.90301	1353	2.1434	4.4766	-1.0805
-0.62352	2932	6.6508	0.8992	-0.20331	2128	1.7387	4.8813	-1.17814
0.318305	3023	5.4251	2.1249	-0.48181	2864	6.4944	0.1256	-0.03071
-1.51714	2076	2.2158	5.3342	-1.21102	1869	2.6752	3.9448	-0.95219
-0.88193	2648	3.3233	4.2267	-0.95938	2581	5.8892	0.7308	-0.17673
-0.78296	2074	7.8592	0.3092	0.071255	1966	5.3917	1.2283	-0.29677
-0.01128	3145	8.8712	1.3212	0.301199	3078	6.1404	0.4796	-0.11613
-0.64608	2276	6.5905	0.9595	-0.21702	1971	6.6464	0.0264	0.005959
0.430752	2586	11.524	3.974	0.903961	1909	7.7528	1.1328	0.272905
0.675779	1954	8.8025	1.2525	0.285589	2150	6.093	0.527	-0.12756
-0.61787	1330	6.6917	0.8583	-0.19402	1405	3.9146	2.7054	-0.65315
-0.97241	2103	7.1327	0.4173	-0.09382	1903	7.0415	0.4215	0.101287
-0.52538	1491	7.2435	0.3065	-0.06864	1473	5.3632	1.2568	-0.30364
1.787285	2230	10.628	3.078	0.700374	2262	5.7029	0.9171	-0.22168
0.51226	1549	11.879	4.329	0.984623	819	8.7912	2.1712	0.523444
5.395191	3033	19.651	12.101	2.750555	2204	8.3031	1.6831	0.405678
-0.32352	2360	9.4492	1.8992	0.432531	2404	2.5374	4.0826	-0.98544
-0.92622	1778	5.8493	1.7007	-0.38543	1360	3.5294	3.0906	-0.74609
-0.34039	1622	3.2676	4.2824	-0.97204	887	4.8478	1.7722	-0.428
0.321058	2446	6.5822	0.9678	-0.2189	2299	5.8286	0.7914	-0.19135
-0.36929	3064	8.8773	1.3273	0.302585	2237	7.1077	0.4877	0.117259
-0.24168	3310	7.9456	0.3956	0.090887	2986	6.7314	0.1114	0.026468
-0.79151	3993	10.343	2.793	0.635617	3863	9.9663	3.3463	0.806965
-0.84957	1748	6.0069	1.5431	-0.34962	1507	4.8441	1.7759	-0.42889
-1.18573	1731	5.9503	1.5997	-0.36248	2980	2.3154	4.3046	-1.039
-0.91426	1517	8.1081	0.5581	0.12781	2163	4.577	2.043	-0.49333
-0.77185	1149	13.142	5.592	1.271598	1172	6.8259	0.2059	0.049268
-1.00519	1758	6.0865	1.4635	-0.33153	1578	2.6616	3.9584	-0.95547
-0.51498	770	15.844	8.294	1.885539	1250	2	4.62	-1.1151
-0.83729	1931	7.6126	0.0626	0.015224	2471	2.9947	3.6253	-0.8751
-0.93813	1912	4.1841	3.3659	-0.76379	2027	3.0587	3.5613	-0.85966
-0.82876	2306	12.056	4.506	1.02484	2028	6.0651	0.5549	-0.13429
0.280674	900	13.444	5.894	1.340218	1477	8.5985	1.9785	0.47695
-0.08518	1210	16.529	8.979	2.041183	1793	7.2504	0.6304	0.151689
-0.40665	2088	14.128	6.578	1.495634	1095	7.2146	0.5946	0.143051
0.107088	1244	7.8778	0.3278	0.075482	1679	6.5515	0.0685	-0.01694
-0.00332	1243	6.9187	0.6313	-0.14244	701	9.7004	3.0804	0.74281
0.067149	1927	10.742	3.192	0.726277	1864	5.5258	1.0942	-0.26441
0.704883	1660	5.241	2.309	-0.52364	1591	9.1766	2.5566	0.616431
1.269755	707	11.598	4.048	0.920775	1008	8.5317	1.9117	0.460833
0.116237	936	7.4786	0.0714	-0.01522	805	5.5901	1.0299	-0.2489
0.745119	951	6.4143	1.1357	-0.25705	600	11	4.38	1.05637
-0.36742	1448	2.4862	5.0638	-1.14958	1611	5.7107	0.9093	-0.2198
0.998407	2042	6.3663	1.1837	-0.26796	1770	14.972	8.352	2.01471

2.515912	1791	7.426	0.124	-0.02718	1749	2.7444	3.8756	-0.93549
-0.08553	2414	13.795	6.245	1.419971	2130	7.9343	1.3143	0.316696
-1.19301	1318	10.243	2.693	0.612896	1580	6.7089	0.0889	0.021039
0.174207	1856	14.978	7.428	1.688769	1355	8.6347	2.0147	0.485684
-1.35804	918	7.2985	0.2515	-0.05615	1001	9.0909	2.4709	0.595754
-0.86737	3654	4.7619	2.7881	-0.6325	1263	4.2755	2.3445	-0.56608
-0.51528	1887	4.1865	3.3635	-0.76325	1187	9.604	2.984	0.719551
0.43093	1859	8.3378	0.7878	0.180001	2273	7.919	1.299	0.313005
-0.63631	1477	8.3277	0.7777	0.177707	994	8.7525	2.1325	0.514107
-1.29856	1879	7.3443	0.2057	-0.04574	504	7.5397	0.9197	0.221489
-0.32168	1373	10.051	2.501	0.56927	952	7.2479	0.6279	0.151086
0.240349	1698	10.483	2.933	0.667428	2010	16.169	9.549	2.303515
0.573132	666	7.0571	0.4929	-0.111	648	13.426	6.806	1.6417
-1.43079	1471	5.0306	2.5194	-0.57145	971	8.1359	1.5159	0.365337
-1.26386	887	5.5242	2.0258	-0.4593	864	7.9861	1.3661	0.329194
-0.38889	1306	15.391	7.841	1.78261	1462	8.7551	2.1351	0.514734
-0.83894	2339	9.4912	1.9412	0.442074	1799	12.34	5.72	1.379677
-0.68013	1439	4.1001	3.4499	-0.78288	1064	11.184	4.564	1.100764
-1.08447	3082	8.1116	0.5616	0.128605	2671	6.4021	0.2179	-0.05298
-0.70438	1224	4.4935	3.0565	-0.69349	1061	7.1631	0.5431	0.130626
-1.06381	1206	1.9071	5.6429	-1.28116	1623	2.711	3.909	-0.94355
0.005892	2584	10.178	2.628	0.598126	2891	9.1318	2.5118	0.605622
-0.12867	943	6.2566	1.2934	-0.29288	1630	11.902	5.282	1.273999
0.860734	723	6.9156	0.6344	-0.14315	429	17.949	11.329	2.732983
0.536567	659	9.8634	2.3134	0.526644	488	19.672	13.052	3.148698
-0.57819	1251	8.3933	0.8433	0.192612	1347	2.8211	3.7989	-0.91699
0.199966	1948	4.6715	2.8785	-0.65304	1296	6.713	0.093	0.022028
-0.16275	725	5.931	1.619	-0.36686	1088	8.2721	1.6521	0.398199
0.551015	979	10.93	3.38	0.768994	1567	10.976	4.356	1.050579
0.839832	1310	13.817	6.267	1.42497	1147	14.124	7.504	1.81011
1.113045	650	12.308	4.758	1.082099	528	8.5227	1.9027	0.458662
0.003316	1957	4.0879	3.4621	-0.78565	1189	9.7561	3.1361	0.756249
2.495483	1535	13.355	5.805	1.319995	943	18.134	11.514	2.777618
0.472883	1677	13.536	5.986	1.361122	1534	10.235	3.615	0.871795
2.135759	1104	6.7029	0.8471	-0.19148	461	16.703	10.083	2.432355
0.385276	2175	3.3563	4.1937	-0.95188	1449	9.5928	2.9728	0.716849
1.409796	749	7.8772	0.3272	0.075345	322	17.081	10.461	2.523557
0.667578	2790	8.9606	1.4106	0.321512	1813	8.9906	2.3706	0.571554
0.217404	1234	3.8898	3.6602	-0.83066	421	13.539	6.919	1.668964
-0.72881	3275	2.4427	5.1073	-1.15947	1152	8.3333	1.7133	0.412965
-1.01792	1018	4.5187	3.0313	-0.68776	1288	3.5714	3.0486	-0.73596
0.933567	1823	10.093	2.543	0.578813	1985	9.7733	3.1533	0.760399
-0.23985	1191	9.5718	2.0218	0.460387	2063	7.0286	0.4086	0.098174
-0.41364	1192	9.6477	2.0977	0.477633	912	6.5789	0.0411	-0.01033
-0.4158	1558	6.9961	0.5539	-0.12486	1253	5.1077	1.5123	-0.36529
-0.87444	1640	9.1463	1.5963	0.363707	628	10.032	3.412	0.822817
-0.7376	2437	4.0624	3.4876	-0.79144	1018	11.002	4.382	1.056852

-0.31718	2369	7.0072	0.5428	-0.12233	1507	6.5693	0.0507	-0.01264
0.350517	1354	20.679	13.129	2.984134	893	15.342	8.722	2.103981
0.559513	1928	14.73	7.18	1.632419	1105	11.131	4.511	1.087977
0.172934	1037	11.572	4.022	0.914867	350	7.7143	1.0943	0.263616
-0.15955	1733	7.79	0.24	0.055532	1256	7.0064	0.3864	0.092818
-0.56822	2153	5.5272	2.0228	-0.45862	879	6.1433	0.4767	-0.11543
-0.16284	978	7.6687	0.1187	0.02797	495	7.2727	0.6527	0.157069
-0.59412	3437	4.8589	2.6911	-0.61046	1621	3.2696	3.3504	-0.80877
-0.4833	1625	6.7077	0.8423	-0.19039	736	9.6467	3.0267	0.729854
1.106117	1945	12.751	5.201	1.182756	1193	10.981	4.361	1.051786
-0.13966	2694	8.5375	0.9875	0.225377	370	5.6757	0.9443	-0.22825
-0.34951	1136	10.035	2.485	0.565634	360	13.611	6.991	1.686336
-0.99047	1590	3.8994	3.6506	-0.82848	834	4.9161	1.7039	-0.41152
1.246365	2371	9.6162	2.0662	0.470476	2148	6.8901	0.2701	0.064758
0.656979	2490	5.4618	2.0882	-0.47348	1520	4.6711	1.9489	-0.47063
0.322361	3752	15.485	7.935	1.803968	2363	6.4325	0.1875	-0.04565
-0.07402	2371	5.3986	2.1514	-0.48784	1532	3.6554	2.9646	-0.71569
1.013003	1220	7.7869	0.2369	0.054828	441	14.966	8.346	2.013262
0.110404	2188	6.9927	0.5573	-0.12563	970	3.5052	3.1148	-0.75193
0.218766	2695	9.4991	1.9491	0.443869	1755	7.1225	0.5025	0.12083
-0.45316	1791	6.9235	0.6265	-0.14135	1569	6.1823	0.4377	-0.10602
0.608956	2045	6.0636	1.4864	-0.33674	1082	5.6377	0.9823	-0.23741
1.391735	1655	9.0634	1.5134	0.34487	1549	8.0697	1.4497	0.349365
1.103511	1755	10.94	3.39	0.771266	923	11.809	5.189	1.25156
2.977485	3025	17.322	9.772	2.221366	2114	10.927	4.307	1.038757
1.652277	1950	12.103	4.553	1.035519	1349	4.8184	1.8016	-0.43509
0.060961	1813	15.665	8.115	1.844867	1575	11.429	4.809	1.159876
2.936035	2273	11.791	4.241	0.964628	1524	10.892	4.272	1.030312
-0.43567	2388	7.1189	0.4311	-0.09695	1368	8.5526	1.9326	0.465876
1.475523	1806	20.432	12.882	2.928011	1897	17.765	11.145	2.688588
1.947458	3975	17.66	10.11	2.298165	3359	14.111	7.491	1.806973
0.885752	1573	16.275	8.725	1.983469	1617	14.348	7.728	1.864155
-0.79077	1634	9.4247	1.8747	0.426964	1421	10.274	3.654	0.881205
-0.6083	1788	8.3333	0.7833	0.178979	1981	1.4134	5.2066	-1.25663
-0.41245	953	1.6789	5.8711	-1.33301	1511	1.5884	5.0316	-1.2144
-0.67388	2041	5.8795	1.6705	-0.37857	2078	2.358	4.262	-1.02872
-0.655	2556	2.543	5.007	-1.13668	1217	0.98603	5.63397	-1.35974
3.479916	1180	20.085	12.535	2.849167	695	2.7338	3.8862	-0.93805
0.944374	3272	11.461	3.911	0.889646	1619	2.1001	4.5199	-1.09094
-1.01108	2292	7.2426	0.3074	-0.06885	1089	1.4692	5.1508	-1.24316
2.011409	2859	24.869	17.319	3.936174	2095	11.456	4.836	1.166391
1.138329	3099	17.877	10.327	2.347471	2605	5.7582	0.8618	-0.20834
2.792145	1858	10.28	2.73	0.621303	1378	3.8462	2.7738	-0.66966
-0.93534	1276	5.2508	2.2992	-0.52142	1517	2.1753	4.4447	-1.0728
1.171726	3145	24.356	16.806	3.819611	1820	5.7692	0.8508	-0.20569
0.113039	2415	27.246	19.696	4.476269	808	9.0347	2.4147	0.582194
-0.66542	1771	8.3004	0.7504	0.171504	1118	2.8623	3.7577	-0.90705

-0.97937	1315	12.776	5.226	1.188437	1016	2.8543	3.7657	-0.90898
2.539598	1367	12.143	4.593	1.044608	1505	3.3223	3.2977	-0.79606
0.678385	4394	16.158	8.608	1.956885	3748	6.3234	0.2966	-0.07197
-0.32053	1816	9.0859	1.5359	0.349983	1601	1.4366	5.1834	-1.25103
2.478311	1872	22.489	14.939	3.395397	2017	7.3872	0.7672	0.184695
1.381669	2300	17.913	10.363	2.355651	1893	5.1241	1.4959	-0.36133
-1.19654	2134	5.5764	1.9736	-0.44744	2015	1.1414	5.4786	-1.32225
-0.61953	1987	10.367	2.817	0.641071	1309	0.68755	5.93245	-1.43176
-0.52028	1993	10.788	3.238	0.736729	1129	1.24	5.38	-1.29846
-1.21276	1772	9.2551	1.7051	0.388428	1010	0.29703	6.32297	-1.52598
-0.9397	1021	9.1087	1.5587	0.355163	1407	1.7058	4.9142	-1.18608
-1.14674	2271	8.4104	0.8604	0.196497	1090	0.45872	6.16128	-1.48697
-1.19322	1594	15.37	7.82	1.777838	1082	0.83179	5.78821	-1.39695
-0.4852	2277	6.1924	1.3576	-0.30747	752	0.53191	6.08809	-1.46931
-0.37639	3487	8.546	0.996	0.227308	877	1.4823	5.1377	-1.24
-0.21589	2006	14.008	6.458	1.468368	2192	2.8741	3.7459	-0.9042
-0.43374	2142	12.979	5.429	1.234562	636	1.1006	5.5194	-1.3321
0.804658	2573	12.748	5.198	1.182075	667	1.3493	5.2707	-1.27209
0.748109	3628	17.999	10.449	2.375192	1402	3.6377	2.9823	-0.71996
-0.71193	2571	2.3726	5.1774	-1.17539	1295	1.39	5.23	-1.26227
-0.67477	3417	6.4969	1.0531	-0.23828	878	1.5945	5.0255	-1.21293
-0.27052	2835	5.1499	2.4001	-0.54434	1651	3.0285	3.5915	-0.86695
-0.96557	2537	5.7942	1.7558	-0.39795	1111	1.1701	5.4499	-1.31533
-0.89638	2325	4.5591	2.9909	-0.67858	1240	0.56452	6.05548	-1.46144
-0.47866	2177	4.5935	2.9565	-0.67077	1162	3.2702	3.3498	-0.80863
-1.05712	2015	7.6923	0.1423	0.033333	2013	3.3284	3.2916	-0.79459
-0.9979	2500	10.88	3.33	0.757633	2197	1.8662	4.7538	-1.14738
0.648304	3206	9.2639	1.7139	0.390427	1476	1.2873	5.3327	-1.28705
0.221756	2266	5.075	2.475	-0.56136	1898	1.7914	4.8286	-1.16543
0.597587	2775	8.7568	1.2068	0.275205	2213	3.1631	3.4569	-0.83447
-0.42673	3333	7.2007	0.3493	-0.07837	2822	7.2289	0.6089	0.146502
-0.32929	4627	7.0672	0.4828	-0.1087	3136	5.5804	1.0396	-0.25124
-0.50933	2747	4.4048	3.1452	-0.71364	1610	1.7391	4.8809	-1.17804
-1.10224	974	10.678	3.128	0.711735	861	4.6458	1.9742	-0.47673
1.668857	1779	6.0146	1.5354	-0.34787	2035	4.2752	2.3448	-0.56615
0.450825	1383	8.4599	0.9099	0.207745	905	3.0939	3.5261	-0.85117
-0.71214	2234	5.6849	1.8651	-0.42278	1483	4.1807	2.4393	-0.58895
-0.27185	3454	13.434	5.884	1.337946	2226	4.5373	2.0827	-0.50291
-0.10191	4195	7.056	0.494	-0.11125	2081	2.5469	4.0731	-0.98314
-0.81363	2937	3.4048	4.1452	-0.94086	1725	3.8261	2.7939	-0.67451
-0.64345	1866	5.4126	2.1374	-0.48465	1643	3.4693	3.1507	-0.76059
0.165473	2245	4.9443	2.6057	-0.59106	1634	4.7124	1.9076	-0.46066
2.664539	3179	12.583	5.033	1.144584	1543	13.351	6.731	1.623605
0.261134	2598	5.2733	2.2767	-0.51631	1591	9.5537	2.9337	0.707415
-0.98292	2838	3.8055	3.7445	-0.84981	2858	4.0938	2.5262	-0.60992
-0.80045	2902	6.8918	0.6582	-0.14855	2680	4.5896	2.0304	-0.49029
-1.38167	1314	0.91324	6.63676	-1.50699	998	10.321	3.701	0.892545

-0.05762	2077	3.6591	3.8909	-0.88308	2628	7.5723	0.9523	0.229355
0.048822	2091	1.5304	6.0196	-1.36676	1738	7.6525	1.0325	0.248705
-0.51016	2410	3.6929	3.8571	-0.8754	1771	10.615	3.995	0.963479
-0.27354	1519	2.2383	5.3117	-1.20591	1574	9.0851	2.4651	0.594354
-0.65162	2094	4.298	3.252	-0.73791	1739	7.8206	1.2006	0.289263
-0.83595	1398	2.432	5.118	-1.1619	1433	6.769	0.149	0.03554
0.412396	1646	6.3791	1.1709	-0.26505	1004	9.4622	2.8422	0.685339
0.739079	1641	3.4735	4.0765	-0.92525	774	11.628	5.008	1.20789
-1.02251	1329	1.2039	6.3461	-1.44094	1165	6.7811	0.1611	0.038459
-1.23387	609	1.8062	5.7438	-1.30409	813	10.947	4.327	1.043582
0.343026	2363	5.0783	2.4717	-0.56061	1894	7.9197	1.2997	0.313174
1.690174	2577	7.7222	0.1722	0.040127	1811	12.148	5.528	1.333352
0.666749	831	1.083	6.467	-1.46841	517	11.412	4.792	1.155775
0.688273	1932	2.8986	4.6514	-1.05588	1284	7.3988	0.7788	0.187494
0.687119	1069	5.4256	2.1244	-0.4817	1067	9.5595	2.9395	0.708815
0.063448	3054	2.0956	5.4544	-1.23833	2495	7.9359	1.3159	0.317082
0.999413	2095	6.5394	1.0106	-0.22863	1910	9.4241	2.8041	0.676146
-0.71302	2111	4.1213	3.4287	-0.77806	1478	5.0068	1.6132	-0.38963
1.237779	1253	6.3049	1.2451	-0.28191	1097	3.464	3.156	-0.76187
0.700323	846	16.785	9.235	2.09935	2230	12.422	5.802	1.399461
0.536123	907	15.987	8.437	1.918031	1276	11.207	4.587	1.106314
3.464224	1889	17.84	10.29	2.339064	1666	16.747	10.127	2.442971
-0.17764	2085	8.2494	0.6994	0.159915	1159	16.48	9.86	2.378551
0.771084	1471	21.414	13.864	3.151138	829	13.631	7.011	1.691162
0.68706	2316	11.01	3.46	0.787171	1100	11.455	4.835	1.166149
3.251942	1200	16.333	8.783	1.996648	1677	12.582	5.962	1.438065
1.657902	3069	11.795	4.245	0.965537	2707	13.373	6.753	1.628913
1.335482	1951	11.43	3.88	0.882602	1425	10.947	4.327	1.043582
0.216427	1990	7.8894	0.3394	0.078117	1995	14.135	7.515	1.812764
-0.22664	1591	6.2854	1.2646	-0.28634	1262	7.7655	1.1455	0.275969
1.604017	1954	10.133	2.583	0.587902	461	7.1584	0.5384	0.129492
0.483778	2308	5.6759	1.8741	-0.42483	1658	9.6502	3.0302	0.730698
1.00264	1884	8.0679	0.5179	0.118676	2015	11.861	5.241	1.264107
0.398658	2700	5.5556	1.9944	-0.45216	2813	12.264	5.644	1.36134
1.711491	1862	7.0892	0.4608	-0.1037	1912	10.46	3.84	0.926082
-0.13788	2015	5.7072	1.8428	-0.41772	1967	5.1856	1.4344	-0.34649
0.993166	1404	13.177	5.627	1.279551	1018	7.3674	0.7474	0.179918
-0.21074	705	11.064	3.514	0.799441	1483	7.2151	0.5951	0.143172
-0.67439	835	7.0659	0.4841	-0.109	1907	3.7231	2.8969	-0.69936
	1814.5	7.5456	2.9737		1509	6.6217	2.80045	
			8.9211				8.40135	
			4.401076				4.144666	
1372	39.359		1507	31.851				
2955	31.506		2195	42.597				
2237	27.045		2394	17.126				
2506	35.754		3806	43.221				
2267.5	33.416		2475.5	33.69875				

666.4305	5.323634	964.9775	12.21914				
406	2.2167	390	16.154				
		501	12.774	720	13.333	369	5.1491
393	5.0891						
513	4.6784	368	20.109				
437.3333	3.994733	419.6667	16.34567				
65.85084	1.553454	71.29049	3.671254				
	15.9709		36.65743				
	4.660363		11.01376				
	20.63126		47.67119				
	29.42127		17.35308				
	0.701236		2.747131				
	0.298764		-1.74713				

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

x	toxic b,c
x	toxic a,b,c
x	toxic a,b,c

y

y

x toxic b,c

x toxic a,b,c

y

x toxic b,c

y

x	toxic a,b

y

						cell ct	% inf	AD
50080	A02	M-031951-	chromoson	387119	C6orf204	916	6.5502	0.8202
50080	A04	M-032028-	forkhead b	387054	FOXD4L3	1167	5.7412	0.0112
50080	A05	M-018147-	hypothetic	353116	FLJ39378	1103	9.7915	4.0615
50080	A06	M-032209-	zinc finger	387032	ZKSCAN4	778	10.283	4.553
50080	A07	M-018129-	hypothetic	353117	FLJ39582	1070	9.4393	3.7093
50080	A08	M-031070-	hypothetic	386759	MGC9913	747	5.087	0.643
50080	A09	M-019023-	late cornifi	353139	LCE2A	372	12.903	7.173
50080	A10	M-031737-	solute carri	386757	SLC6A10P	2698	5.2261	0.5039
50080	A11	M-019024-	late cornifi	353140	LCE2C	583	9.434	3.704
50080	A12	M-031727-	adhesion m	386724	AMIGO3	427	4.6838	1.0462
50080	A13	M-019026-	late cornifi	353142	LCE3A	286	2.4476	3.2824
50080	A14	M-031734-	keratin ass	386683	KRTAP12-3	1008	7.7381	2.0081
50080	A15	M-019028-	late cornifi	353143	LCE3B	629	11.765	6.035
50080	A16	M-031544-	keratin ass	386681	KRTAP10-8	1384	19.22	13.49
50080	A17	M-019029-	late cornifi	353144	LCE3C	710	13.662	7.932
50080	A18	M-031733-	potassium	386618	KCTD4	699	14.02	8.29
50080	A19	M-018364-	hypothetic	353149	MGC51025	943	10.392	4.662
50080	A20	M-031732-	potassium	386617	KCTD8	561	11.23	5.5
50080	A21	M-009142-	ligand-gate	353174	LGICZ1	549	15.483	9.753
50080	A23	M-007374-	solute carri	353189	SLCO4C1	150	28	22.27
50080	B02	M-032151-	family with	400728	FAM87B	1308	1.4526	4.2774
50080	B04	M-032212-	eosinophil	400696	LOC40069	1008	4.0675	1.6625
50080	B05	M-032205-	neuropepti	387129	NPSR1	1653	7.7435	2.0135
50080	B06	M-032146-	FLJ46230 p	400679	FLJ46230	779	4.4929	1.2371
50080	B07	M-027181-	SLC7A5 pse	387254	IMAA	845	2.3669	3.3631
50080	B08	M-032149-	FLJ45684 l	400666	FLJ45684	761	5.2562	0.4738
50080	B09	M-031772-	hypothetic	387277	MGC45477	1598	2.3154	3.4146
50080	B10	M-032145-	FLJ44881	400661	FLJ44881	2054	13.096	7.366
50080	B11	M-032014-	zinc finger	387328	ZNF322B	1007	9.8312	4.1012
50080	B12	M-032147-	FLJ44313 p	400658	FLJ44313	1159	5.0043	0.7257
50080	B13	M-031738-	TATA box b	387332	TBPL2	1261	8.0888	2.3588
50080	B14	M-032144-	FLJ35767 p	400629	FLJ35767	466	11.588	5.858
50080	B15	M-027291-	NOL1/NOP	387338	NSUN4	974	5.3388	0.3912
50080	B16	M-032143-	FLJ46026 p	400627	FLJ46026	843	9.4899	3.7599
50080	B17	M-031911-	RAS-like, fa	387496	RASL11A	1363	8.2172	2.4872
50080	B18	M-032142-	FLJ46126 p	400597	FLJ46126	1553	16.098	10.368
50080	B19	M-027388-	G protein-c	387509	GPR153	1065	5.8216	0.0916
50080	B20	M-032139-	FLJ44815 p	400591	FLJ44815	2319	9.2281	3.4981
50080	B21	M-032201-	ubiquitin-c	387521	Kua	1392	2.8017	2.9283
50080	B23	M-032200-	ubiquitin-c	387522	Kua-UEV	1895	16.992	11.262
50080	C02	M-027974-	hypothetic	386597	LOC38659	1523	3.7426	1.9874
50080	C04	M-029350-	hypothetic	379034	FLJ10489	887	10.259	4.529
50080	C05	M-007176-	zinc finger	353274	ZNF445	1318	7.5114	1.7814
50080	C06	M-010758-	ring finger	378925	RNF148	952	9.2437	3.5137
50080	C07	M-017994-	synleurin	353281	SLRN	2280	10.263	4.533
50080	C08	M-027323-	NHL repeat	378884	NHLRC1	1631	5.3955	0.3345

50080	C09	M-018748- keratin 26	353288	KRT26	1062	11.77	6.04
50080	C10	M-031889- chromoso	378832	C21orf123	952	9.2437	3.5137
50080	C11	M-031742- chromoso	353289	C4orf11	666	12.763	7.033
50080	C12	M-027514- cation cha	378807	CATSPER4	1419	12.051	6.321
50080	C13	M-018782- regulator o	353299	RGSL1	783	14.815	9.085
50080	C14	M-028933- hypothetic	378805	FLJ43663	989	5.4601	0.2699
50080	C15	M-018949- ankyrin rep	353322	ANKRD37	813	24.846	19.116
50080	C16	M-019340- MORN rep	378464	MORN2	1358	9.352	3.622
50080	C17	M-018842- keratin ass	353323	KRTAP12-2	861	22.532	16.802
50080	C18	M-031736- tripartite m	378108	TRIM74	1179	11.45	5.72
50080	C19	M-018993- spermatog	353324	SPATA12	1653	11.252	5.522
50080	C20	M-027275- ectonucleo	377841	ENTPD8	2178	5.6933	0.0367
50080	C21	M-018837- keratin ass	353333	KRTAP10-1	1728	8.1019	2.3719
50080	C23	M-018565- zinc finger	353355	ZNF233	868	3.1106	2.6194
50080	D02	M-032138- FLJ35934 p	400579	FLJ35934	1157	0.17286	5.55714
50080	D04	M-032137- FLJ45200 p	400563	FLJ45200	1813	2.2063	3.5237
50080	D05	M-031741- chromoso	387597	C1orf32	2609	3.4879	2.2421
50080	D06	M-032136- FLJ45121 p	400556	FLJ45121	2067	3.0963	2.6337
50080	D07	M-031740- putative U	387601	LOC387601	1332	3.003	2.727
50080	D08	M-032134- FLJ27243 p	400539	FLJ27243	1176	2.551	3.179
50080	D09	M-031885- keratinocy	387628	KGFLP1	1458	2.332	3.398
50080	D10	M-032133- FLJ44674 p	400535	FLJ44674	1124	0.97865	4.75135
50080	D11	M-032220- hypothetic	387640	FLJ45187	1680	3.3333	2.3967
50080	D12	M-032132- FLJ45256 p	400511	FLJ45256	1226	7.2594	1.5294
50080	D13	M-032048- SH2 domai	387694	SH2D4B	2325	5.8495	0.1195
50080	D14	M-032131- IFMQ9370	400454	UNQ9370	1012	9.585	3.855
50080	D15	M-032051- chromoso	387695	C10orf99	1611	12.042	6.312
50080	D16	M-032129- hypothetic	400451	LOC400451	1185	10.97	5.24
50080	D17	M-031927- similar to R	387758	LOC38775	1785	5.6583	0.0717
50080	D18	M-032128- FLJ39531 p	400360	FLJ39531	257	12.451	6.721
50080	D19	M-032049- olfactory r	387772	UNQ6469	1800	3.2778	2.4522
50080	D20	M-032126- FLJ35695 p	400359	FLJ35695	1087	8.2797	2.5497
50080	D21	M-032053- C-type lecti	387836	CLEC2A	1471	7.6818	1.9518
50080	D23	M-031906- C-type lecti	387837	CLEC12B	1237	5.0121	0.7179
50080	E02	M-029301- hypothetic	377711	KIAA1833	1925	0.46753	5.26247
50080	E04	M-027325- carbonic a	377677	CA13	1701	1.6461	4.0839
50080	E05	M-004334- toll-like rec	353376	TICAM2	1774	2.3112	3.4188
50080	E06	M-027332- deubiquiti	377630	DUB3	2136	2.2472	3.4828
50080	E07	M-021393- polymeras	353497	POLN	3120	2.1154	3.6146
50080	E08	M-032009- testis serin	377047	TESSP5	2069	1.6916	4.0384
50080	E09	M-018645- bone morp	353500	BMP8A	1865	1.7694	3.9606
50080	E10	M-027274- kelch-like 3	377007	KLHL30	2427	1.5245	4.2055
50080	E11	M-013100- leukocyte i	353514	LILRA5	2288	1.9231	3.8069
50080	E12	M-031947- zinc finger	376940	ZC3H6	2213	7.3656	1.6356
50080	E13	M-009124- chromoso	359710	C20orf185	1656	3.3213	2.4087
50080	E14	M-010759- solute carri	376497	SLC27A1	1775	2.2535	3.4765
50080	E15	M-019315- family with	359845	FAM101B	1869	1.1771	4.5529

50080	E16	M-031564-	RAB15, me	376267	RAB15	1322	3.5552	2.1748
50080	E17	M-007177-	interferon	359948	IRF2BP2	1844	1.9523	3.7777
50080	E18	M-027337-	leucine rich	376132	LRRC10	1888	3.9195	1.8105
50080	E19	M-019293-	zinc finger	360023	ZBTB41	2419	2.4804	3.2496
50080	E20	M-027273-	deleted in	375940	FLJ46361	1891	5.1824	0.5476
50080	E21	M-027028-	homeobox	360030	LOC36003	3054	5.1081	0.6219
50080	E23	M-008989-	FK506 bind	360132	FKBP9L	1068	1.6854	4.0446
50080	F02	M-032123-	hypothetic	400242	FLJ45244	845	1.5385	4.1915
50080	F04	M-032122-	FLJ39779 p	400223	FLJ39779	803	6.9738	1.2438
50080	F05	M-032050-	overexpres	387882	OCC-1	990	4.6465	1.0835
50080	F06	M-032121-	FLJ42220 p	400207	FLJ42220	1871	6.6275	0.8975
50080	F07	M-031917-	SET domai	387893	SETD8	547	5.3016	0.4284
50080	F08	M-032120-	FLJ26443 p	400165	FLJ26443	1038	4.2389	1.4911
50080	F09	M-032055-	TIMM9	387990	UNQ9438	789	3.6755	2.0545
50080	F10	M-031901-	hypothetic	400120	LOC40012	1017	1.9666	3.7634
50080	F11	M-032052-	serpin pept	388007	SERPINA13	1552	4.317	1.413
50080	F12	M-032225-	FLJ46358 p	400110	FLJ46358	957	5.0157	0.7143
50080	F13	M-032057-	transmem	388021	TMEM179	1759	4.8891	0.8409
50080	F14	M-032118-	FLJ43808 p	400083	FLJ43808	1149	5.8312	0.1012
50080	F15	M-032054-	FLJ43339 p	388115	FLJ43339	1397	3.5791	2.1509
50080	F16	M-032115-	FLJ43486 p	400082	FLJ43486	694	6.6282	0.8982
50080	F17	M-032059-	tumor necr	388121	TNFAIP8L3	1085	4.1475	1.5825
50080	F18	M-032113-	FLJ42957 p	400077	FLJ42957	1950	5.4872	0.2428
50080	F19	M-032056-	similar to u	388165	FLJ43276	2436	7.225	1.495
50080	F20	M-032112-	FLJ40142 p	400073	FLJ40142	1547	8.7912	3.0612
50080	F21	M-032061-	FLJ42289 p	388182	FLJ42289	2194	4.0565	1.6735
50080	F23	M-032058-	QRWT581	388218	UNQ5810	1888	4.5551	1.1749
50080	G02	M-027279-	Similar to	375791	MGC59937	2628	1.5601	4.1699
50080	G04	M-010312-	patatin-like	375775	PNPLA7	1019	6.1825	0.4525
50080	G05	M-019463-	transmem	360200	TMPRSS9	1253	5.5866	0.1434
50080	G06	M-032130-	chromoson	375759	C9orf50	1709	4.9152	0.8148
50080	G07	M-019460-	glycosyltra	360203	GLT6D1	1360	1.3971	4.3329
50080	G08	M-029596-	chromoson	375757	C9orf119	1756	3.303	2.427
50080	G09	M-019445-	testis serin	360226	TESSP1	735	6.6667	0.9367
50080	G10	M-029572-	RAD26L hy	375748	LOC37574	913	3.6145	2.1155
50080	G11	M-031837-	ubiquitin s	373509	USP50	1578	6.5272	0.7972
50080	G12	M-010311-	protein pre	375743	PTAR1	1771	5.4207	0.3093
50080	G13	M-031434-	ubiquitin s	373856	USP41	964	8.5062	2.7762
50080	G14	M-029511-	aquaporin	375719	AQP7P1	1195	3.431	2.299
50080	G15	M-019355-	histone link	373861	HILS1	1725	1.1014	4.6286
50080	G16	M-029524-	CXYorf1-re	375690	FLJ00038	1180	3.8983	1.8317
50080	G17	M-019345-	dead end h	373863	DND1	1022	1.6634	4.0666
50080	G18	M-031850-	spermatog	375686	SPATC1	636	3.9308	1.7992
50080	G19	M-031977-	CMT1A du	374286	CDRT1	1320	3.0303	2.6997
50080	G20	M-032127-	cysteine ric	375616	CRIM2	1033	5.4211	0.3089
50080	G21	M-007912-	patched d	374308	PTCHD3	1382	1.809	3.921
50080	G23	M-031720-	NHL repeat	374354	NHLRC2	1209	3.8048	1.9252

50080	H02	M-032110-	hypothetic	400002	FLJ46363	1325	5.8113	0.0813
50080	H04	M-032108-	FLJ44874 p	399990	FLJ44874	347	21.614	15.884
50080	H05	M-030764-	similar to	388271	LOC388271	877	9.008	3.278
50080	H06	M-032106-	chromoson	399980	C11orf39	1128	6.6489	0.9189
50080	H07	M-032063-	chromoson	388289	C16orf47	941	11.477	5.747
50080	H08	M-032105-	FLJ45950 p	399975	FLJ45950	751	9.1877	3.4577
50080	H09	M-032000-	DTFT5783	388325	UNQ5783	1474	6.3094	0.5794
50080	H10	M-032202-	FLJ46266 p	399949	FLJ46266	1063	7.1496	1.4196
50080	H11	M-032060-	FLJ45455 p	388336	FLJ45455	738	9.2141	3.4841
50080	H12	M-032104-	FLJ45803 p	399948	FLJ45803	1165	4.8927	0.8373
50080	H13	M-032065-	chromoson	388341	C17orf76	1141	7.362	1.632
50080	H14	M-032221-	similar to e	399947	LOC399947	1114	9.7846	4.0546
50080	H15	M-031912-	transmem	388364	TMIGD1	1010	6.8317	1.1017
50080	H16	M-032103-	chromoson	399879	C11orf55	834	9.8321	4.1021
50080	H17	M-031999-	chemokine	388372	CCL4L2	837	5.8542	0.1242
50080	H18	M-032102-	hypothetic	399851	LOC399851	799	9.7622	4.0322
50080	H19	M-032062-	hypothetic	388387	FLJ31222	1276	5.2508	0.4792
50080	H20	M-032101-	forkhead b	399823	FOXI2	717	5.2999	0.4301
50080	H21	M-032067-	FLJ44861 p	388428	FLJ44861	1212	7.7558	2.0258
50080	H23	M-032064-	FLJ45910 p	388512	FLJ45910	789	4.1825	1.5475
50080	I02	M-031781-	lipoma HM	375612	LHFPL3	516	8.1395	2.4095
50080	I04	M-031941-	solute carri	375611	SLC26A5	477	12.998	7.268
50080	I05	M-031763-	UDP-N-ace	374378	GALNTL4	746	2.9491	2.7809
50080	I06	M-031848-	FLJ39237 p	375607	FLJ39237	1659	5.6661	0.0639
50080	I07	M-030031-	hypothetic	374383	DKFZp686	1432	7.4721	1.7421
50080	I08	M-029614-	olfactory re	375601	OR7E31P	1740	4.4253	1.3047
50080	I09	M-029985-	hypothetic	374387	DKFZp779	2650	5.8113	0.0813
50080	I10	M-028896-	tripartite	375593	TRIM73	1083	2.4007	3.3293
50080	I11	M-031722-	family with	374393	FAM111B	2065	6.4891	0.7591
50080	I12	M-027272-	von Willeb	375567	VWC2	910	3.956	1.774
50080	I13	M-032107-	similar to	374395	LOC374395	1931	9.5287	3.7987
50080	I14	M-031844-	gap junctio	375519	GJB7	1345	8.7732	3.0432
50080	I15	M-031765-	TBC1 doma	374403	TBC1D10C	1174	7.5809	1.8509
50080	I16	M-031972-	glucuronid	375513	GUSBL2	1167	6.4267	0.6967
50080	I17	M-028949-	DnaJ (Hsp4	374407	DNAJB13	809	2.3486	3.3814
50080	I18	M-031840-	chromoson	375484	C5orf25	1210	7.8512	2.1212
50080	I19	M-031766-	similar to	374408	MGC12965	1924	10.135	4.405
50080	I20	M-031608-	similar to	375449	LOC375449	1443	6.237	0.507
50080	I21	M-031886-	keratin 77	374454	KRT77	1422	6.7511	1.0211
50080	I23	M-027185-	protein ty	374462	PTPRQ	643	5.5988	0.1312
50080	J02	M-032099-	FLJ40536 p	399819	FLJ40536	772	1.1658	4.5642
50080	J04	M-032098-	FLJ45983 p	399717	FLJ45983	1423	3.3732	2.3568
50080	J05	M-032069-	regulator o	388531	RGS9BP	879	6.3709	0.6409
50080	J06	M-031768-	SHC (Src h	399694	SHC4	1038	6.0694	0.3394
50080	J07	M-032066-	keratinocy	388533	KRTDAP	282	5.3191	0.4109
50080	J08	M-031721-	hypothetic	399693	MGC50722	715	3.4965	2.2335
50080	J09	M-031968-	zinc finger	388536	ZNF790	1884	8.0149	2.2849

50080	J10	M-031755-	myosin XVI	399687	MYO18A	449	0.66815	5.06185
50080	J11	M-032071-	IGF-like fa	388555	IGFL3	950	7.0526	1.3226
50080	J12	M-027355-	HEAT repe	399671	HEATR4	611	2.946	2.784
50080	J13	M-032068-	FLJ45949 p	388560	FLJ45949	505	8.3168	2.5868
50080	J14	M-027354-	ribosomal	399670	MGC34774	710	5.7746	0.0446
50080	J15	M-032073-	zinc finger	388569	ZNF324B	1010	5.9406	0.2106
50080	J16	M-027353-	family with	399665	FAM102A	835	2.2754	3.4546
50080	J17	M-032070-	ring finger	388591	RNF207	251	8.7649	3.0349
50080	J18	M-031965-	ring finger	399664	RKHD1	1265	7.2727	1.5427
50080	J19	M-032075-	CD164 sial	388611	CD164L2	1051	12.559	6.829
50080	J20	M-027349-	zinc finger	399655	ZNF539	825	7.7576	2.0276
50080	J21	M-027465-	similar to	388625	LOC38862	1096	4.927	0.803
50080	J23	M-032072-	guanylate	388646	GBP7	615	6.1789	0.4489
50080	K02	M-031839-	chromoso	375444	C5orf34	2247	3.1598	2.5702
50080	K04	M-031838-	leucine ric	375387	LRRC33	1125	5.6889	0.0411
50080	K05	M-027253-	chromoso	374467	C12orf63	2257	7.798	2.068
50080	K06	M-027271-	FLJ44290 p	375347	FLJ44290	1576	3.9975	1.7325
50080	K07	M-027254-	chromoso	374470	C12orf42	1451	3.9283	1.8017
50080	K08	M-027270-	transmem	375346	TMEM110	1248	9.5353	3.8053
50080	K09	M-030336-	Similar to	374569	LOC37456	1783	5.4403	0.2897
50080	K10	M-031836-	chromoso	375341	C3orf62	1289	6.3615	0.6315
50080	K11	M-027255-	testis expr	374618	TEX9	1337	6.0583	0.3283
50080	K12	M-028099-	FLJ36157 p	375337	FLJ36157	1648	9.4053	3.6753
50080	K13	M-032114-	FLJ35171 p	374649	FLJ35171	618	10.68	4.95
50080	K14	M-027269-	lipoma HM	375323	LHFPL4	1513	6.9399	1.2099
50080	K15	M-031731-	golgi autoa	374650	FLJ40113	1350	9.7037	3.9737
50080	K16	M-032245-	aquaporin	375318	AQP12A	1891	13.696	7.966
50080	K17	M-022322-	kinesin fam	374654	KIF7	999	7.8078	2.0778
50080	K18	M-027268-	hypothetic	375307	MGC50811	1505	8.4385	2.7085
50080	K19	M-031888-	zinc finger	374655	ZNF710	1968	7.8252	2.0952
50080	K20	M-027336-	ceramide	375298	CERKL	1946	4.4707	1.2593
50080	K21	M-031786-	HD domain	374659	HDDC3	2047	7.2789	1.5489
50080	K23	M-032219-	hypothetic	374676	LOC37467	2283	9.5488	3.8188
50080	L02	M-027348-	hypothetic	399563	FLJ43806	831	1.3237	4.4063
50080	L04	M-031743-	solute carri	399512	SLC25A35	2407	8.6415	2.9115
50080	L05	M-032077-	hypothetic	388666	FLJ36116	1905	4.5669	1.1631
50080	L06	M-027563-	TTMB prot	399474	TTMB	862	5.5684	0.1616
50080	L07	M-032015-	family with	374666	FAM39DP	1341	4.8471	0.8829
50080	L08	M-028692-	chromoso	394263	C6orf205	956	3.0335	2.6965
50080	L09	M-018814-	kidney ass	353219	KAAG1	892	9.6413	3.9113
50080	L10	M-032096-	TPT1-like p	392490	FLJ44635	714	9.6639	3.9339
50080	L11	M-018840-	keratin ass	353332	KRTAP12-1	1166	3.6878	2.0422
50080	L12	M-028355-	deubiquiti	391622	DUB4	466	7.7253	1.9953
50080	L13	M-031735-	keratin ass	386684	KRTAP12-4	886	6.5463	0.8163
50080	L14	M-032097-	C1q and tu	390664	C1QTNF8	1392	7.3994	1.6694
50080	L15	M-031719-	keratin ass	386685	KRTAP10-1	738	3.6585	2.0715
50080	L16	M-031871-	similar to	390511	LOC390511	1354	7.9025	2.1725

50080	L17	M-031979-	keratin ass	386679	KRTAP10-2	748	4.4118	1.3182
50080	L18	M-031997-	G protein-c	390212	GPR152	1394	1.5065	4.2235
50080	L19	M-031501-	keratin ass	386672	KRTAP10-4	1070	4.6729	1.0571
50080	L20	M-031625-	ubiquitin-c	389898	UBE2NL	838	5.7279	0.0021
50080	L21	M-031541-	keratin ass	386680	KRTAP10-5	825	5.5758	0.1542
50080	L23	M-031525-	keratin ass	386676	KRTAP10-9	1244	6.9936	1.2636
50080	M02	M-027999-	hypothetic	375295	LOC37529	851	5.8754	0.1454
50080	M04	M-027267-	RNA bindin	375287	RBM43	1389	7.4874	1.7574
50080	M05	M-032181-	testis/pros	374739	TEPP	2558	5.6685	0.0615
50080	M06	M-031853-	family with	375260	FAM39B	2478	12.591	6.861
50080	M07	M-032109-	chromosom	374768	C17orf83	2260	3.8938	1.8362
50080	M08	M-027905-	ankyrin rep	375248	ANKRD36	3356	7.5089	1.7789
50080	M09	M-031787-	EF-hand ca	374786	EFCAB5	3972	11.631	5.901
50080	M10	M-027266-	hypothetic	375190	LOC37519	3097	16.468	10.738
50080	M11	M-032008-	chromosom	374864	C18orf34	2347	4.6442	1.0858
50080	M12	M-027358-	profilin fam	375189	PFN4	2118	8.593	2.863
50080	M13	M-032249-	ATPase, Cla	374868	ATP9B	2950	16.542	10.812
50080	M14	M-032119-	similar to p	375133	LOC37513	1931	3.2108	2.5192
50080	M15	M-027257-	chromosom	374872	C19orf35	2658	6.6215	0.8915
50080	M16	M-027329-	hypothetic	375127	FLJ26056	1165	11.931	6.201
50080	M17	M-027191-	hydroxyste	374875	HSD11B1L	2295	6.5795	0.8495
50080	M18	M-027278-	lipase, mer	149998	LIPI	1448	6.3536	0.6236
50080	M19	M-027331-	chromosom	374877	C19orf45	1185	18.734	13.004
50080	M20	M-027265-	FLJ44670 p	375096	FLJ44670	2843	7.5273	1.7973
50080	M21	M-031221-	zinc finger	374879	ZNF699	2227	14.549	8.819
50080	M23	M-027258-	FLJ44968 p	374887	FLJ44968	1822	8.562	2.832
50080	N02	M-031745-	zinc finger,	389874	ZCCHC13	1765	2.4363	3.2937
50080	N04	M-031910-	sperm acro	389852	SPACA5	2115	4.6336	1.0964
50080	N05	M-019016-	late cornifi	353133	LCE1C	3128	7.2251	1.4951
50080	N06	M-004847-	mitogen-ac	389840	MAP3K15	1900	1.5263	4.2037
50080	N07	M-019020-	late cornifi	353135	LCE1E	2176	3.2629	2.4671
50080	N08	M-032092-	family with	389835	FAM72A	1857	1.3463	4.3837
50080	N09	M-008071-	similar to p	387870	LOC38787	1099	2.5478	3.1822
50080	N10	M-031892-	MSFL2541	389812	UNQ2541	2425	4.3299	1.4001
50080	N11	M-027172-	similar to N	387927	LOC38792	1667	8.4583	2.7283
50080	N12	M-032095-	FLJ46082 p	389799	FLJ46082	1366	7.101	1.371
50080	N13	M-027173-	similar to e	388226	LOC38822	1545	5.5663	0.1637
50080	N14	M-031899-	immediate	389792	IER5L	1284	8.567	2.837
50080	N15	M-027174-	SH3-bindin	388228	SBK1	1787	3.8612	1.8688
50080	N16	M-032090-	FLJ44082 p	389762	FLJ44082	1475	5.4237	0.3063
50080	N17	M-019015-	late cornifi	353132	LCE1B	2165	6.1894	0.4594
50080	N18	M-027343-	v-maf musc	389692	MAFA	2465	4.9493	0.7807
50080	N19	M-031851-	chromosom	375704	C9orf165	3225	10.14	4.41
50080	N20	M-032087-	FLJ43860 p	389690	FLJ43860	2890	4.2215	1.5085
50080	N21	M-032222-	zinc finger	389114	ZNF662	996	9.8394	4.1094
50080	N23	M-031926-	chromosom	389119	C3orf54	790	6.2025	0.4725
50080	O02	M-027264-	family with	375061	FAM89A	1171	3.5013	2.2287

50080	O04	M-032125-	SFT2 doma	375035	SFT2D2	2796	5.4363	0.2937
50080	O05	M-031264-	hypothetic	374890	LOC37489	2329	0.90167	4.82833
50080	O06	M-027718-	platelet en	375033	PEAR1	2678	3.3607	2.3693
50080	O07	M-027259-	suprabasin	374897	SBSN	2456	0.9772	4.7528
50080	O08	M-031804-	SEC63 dom	374992	SEC63D1	1860	1.7204	4.0096
50080	O09	M-031096-	hypothetic	374899	DKFZp779	1345	2.2305	3.4995
50080	O10	M-032116-	chromoson	374987	C1orf118	1449	2.7605	2.9695
50080	O11	M-027357-	zinc finger	374900	ZNF568	817	5.3856	0.3444
50080	O12	M-031797-	family with	374986	FAM73A	928	2.8017	2.9283
50080	O13	M-031757-	UDP-GlcNA	374907	B3GNT8	1682	3.7455	1.9845
50080	O14	M-027321-	chromoson	374977	C1orf175	1094	5.3931	0.3369
50080	O15	M-027260-	IGF-like fan	374918	IGFL1	1068	4.6816	1.0484
50080	O16	M-027472-	LOC37497	374973	LOC37497	1060	8.4906	2.7606
50080	O17	M-032111-	hypothetic	374920	LOC37492	1348	1.3353	4.3947
50080	O18	M-032124-	coiled-coil	374969	CCDC23	2221	5.1328	0.5972
50080	O19	M-027261-	zinc finger	374928	ZNF773	2121	4.9033	0.8267
50080	O20	M-031793-	spermatog	374955	SPATA21	829	10.615	4.885
50080	O21	M-027262-	LOC14887	374939	MGC35434	446	4.7085	1.0215
50080	O23	M-027341-	chromoson	374946	C1orf187	309	11.65	5.92
50080	P02	M-031893-	RNA bindin	389677	RBM12B	2132	3.9869	1.7431
50080	P04	M-032091-	RPLK9433	389658	UNQ9433	804	5.4726	0.2574
50080	P05	M-031923-	IQ motif co	389123	IQCF2	1160	7.931	2.201
50080	P06	M-032085-	FLJ43582 p	389649	FLJ43582	3223	5.9572	0.2272
50080	P07	M-031907-	musculosk	389125	MUSTN1	462	11.688	5.958
50080	P08	M-032089-	XK, Kell blo	389610	XKR5	1333	3.976	1.754
50080	P09	M-031975-	vestigial lik	389136	VGLL3	1010	5.7426	0.0126
50080	P10	M-031909-	HWKM194	389558	UNQ1940	2682	9.0977	3.3677
50080	P11	M-032082-	FLJ46481 p	389197	FLJ46481	981	3.6697	2.0603
50080	P12	M-031753-	hypothetic	389458	LOC38945	1505	8.4385	2.7085
50080	P13	M-031897-	hypothetic	389199	LOC38919	1073	4.3802	1.3498
50080	P14	M-031936-	iodotyrosi	389434	IYD	1936	9.0393	3.3093
50080	P15	M-027163-	hypothetic	389203	LOC38920	3197	4.4417	1.2883
50080	P16	M-032083-	GDNF fami	389400	GFRAL	1557	5.3308	0.3992
50080	P17	M-032079-	coiled-coil	389206	CCDC4	840	9.881	4.151
50080	P18	M-032086-	AAAL3045	389383	RP3-510O8	3769	1.4062	4.3238
50080	P19	M-032084-	transmemb	389208	TMPRSS11	2634	4.2141	1.5159
50080	P20	M-031908-	surfactant	389376	SFTPG	1847	4.4396	1.2904
50080	P21	M-032081-	FLJ27505 p	389320	FLJ27505	395	5.8228	0.0928
50080	P23	M-031992-	similar to	389336	MGC23985	600	5.3333	0.3967
					MAD	1280	5.73455	2.2311
					MAD3			6.6933
					MADc			3.302028
50080	C22					1195	30.544	
50080	D22					725	21.241	
50080	E22					1002	11.577	
50080	F22					1289	28.239	
					mn	1052.75	22.90025	

			sd	249.0279	8.522485
50080	G22			114	9.6491
50080	H22			233	7.2961
50080	I22			327	5.8104
50080	J22			208	5.2885
			mn	220.5	7.011025
			sd	87.55379	1.953569
		Z score NT2 neg	3psSD		25.56746
			3ngSD		1.313097
			SumSD		26.88055
			MeanDf		17.83785
			SumovrMn		1.506939
			1minus		-0.50694

rZ	cell ct	% inf	AD	rZ	cell ct	% inf	AD	rZ
0.247015	1190	2.605	1.105	-0.33879	727	2.751	2.169	-0.73319
0.002014	423	8.5106	4.8006	1.469744	581	7.5731	2.6531	0.896305
1.228624	464	6.25	2.54	0.777455	355	6.4789	1.5589	0.526551
1.377472	341	8.5044	4.7944	1.467846	287	15.679	10.759	3.63547
1.121962	700	7	3.29	1.007136	769	8.8427	3.9227	1.325331
-0.19611	456	10.088	6.378	1.952809	340	7.0588	2.1388	0.722512
2.170923	222	30.18	26.47	8.105811	187	25.134	20.214	6.830525
-0.15398	851	7.168	3.458	1.058585	395	7.5949	2.6749	0.903672
1.120357	579	5.5268	1.8168	0.555981	803	11.706	6.786	2.292904
-0.31821	704	3.125	0.585	-0.17955	592	4.0541	0.8659	-0.29284
-0.99543	351	6.5527	2.8427	0.870154	194	10.309	5.389	1.820827
0.606763	984	1.2195	2.4905	-0.76309	877	4.7891	0.1309	-0.04447
1.826287	658	3.7994	0.0894	0.02698	423	2.8369	2.0831	-0.70416
4.08399	1112	6.9245	3.2145	0.984015	643	2.3328	2.5872	-0.87451
2.400782	605	6.6116	2.9016	0.888192	284	8.8028	3.8828	1.311848
2.5092	470	16.383	12.673	3.880599	274	13.869	8.949	3.02383
1.410482	617	7.9417	4.2317	1.295524	447	8.7248	3.8048	1.28549
1.664265	916	10.262	6.552	2.006095	589	5.9423	1.0223	0.345221
2.952261	453	16.336	12.626	3.866206	202	13.366	8.446	2.853855
6.742962	462	3.4632	0.2468	-0.07598	147	14.966	10.046	3.394531
-1.29676	1254	0.7177	2.9923	-0.91676	1067	2.5305	2.3895	-0.8077
-0.50486	789	1.3942	2.3158	-0.70959	684	0.5848	4.3352	-1.4652
0.608399	1062	4.1431	0.4331	0.132235	1264	0.23734	4.68266	-1.58261
-0.37603	768	1.1719	2.5381	-0.77767	1040	0.19231	4.72769	-1.59783
-1.01987	975	4.6154	0.9054	0.276873	1087	1.104	3.816	-1.28975
-0.14487	1093	0.45746	3.25254	-0.99646	762	0.26247	4.65753	-1.57412
-1.03547	1324	1.1329	2.5771	-0.78961	673	1.4859	3.4341	-1.1607
2.229372	1214	8.1549	4.4449	1.360814	1315	8.8973	3.9773	1.343782
1.240647	1413	4.2463	0.5363	0.163839	946	2.537	2.383	-0.80551
-0.22115	583	1.3722	2.3378	-0.71633	897	4.0134	0.9066	-0.3066
0.712971	1345	3.1227	0.5873	-0.18025	817	0.1224	4.7976	-1.62145
1.772683	859	5.1222	1.4122	0.432076	401	2.7431	2.1769	-0.73586
-0.11985	1234	3.9708	0.2608	0.07947	705	0.99291	3.92709	-1.32729
1.137286	1365	4.0293	0.3193	0.097385	496	5.4435	0.5235	0.176666
0.751856	1048	5.8206	2.1106	0.645955	1428	3.4314	1.4886	-0.50327
3.138511	1688	3.2583	0.4517	-0.13873	1339	4.4063	0.5137	-0.17383
0.026363	1190	3.1933	0.5167	-0.15863	571	5.6042	0.6842	0.23097
1.058001	1389	5.3996	1.6896	0.517027	1445	3.045	1.875	-0.63384
-0.8882	1410	5.9574	2.2474	0.687849	1000	3.9	1.02	-0.34492
3.409253	1163	9.8882	6.1782	1.891622	813	7.7491	2.8291	0.955779
-0.60325	1642	5.7247	2.0147	0.616586	1288	1.3199	3.6001	-1.21679
1.370203	460	11.739	8.029	2.458414	840	3.0952	1.8248	-0.61688
0.538109	1165	10.386	6.676	2.044069	863	2.5492	2.3708	-0.80138
1.062726	534	12.734	9.024	2.763124	488	1.0246	3.8954	-1.31658
1.371415	2141	7.3797	3.6697	1.123416	1365	1.3919	3.5281	-1.19246
-0.10268	2279	2.9399	0.7701	-0.23623	1932	0.05176	4.86824	-1.64532

1.827801	1614	8.9839	5.2739	1.614688	1140	4.0351	0.8849	-0.29926
1.062726	1106	5.6962	1.9862	0.607859	1109	0.99188	3.92812	-1.32764
2.128525	860	12.791	9.081	2.78058	556	4.3165	0.6035	-0.20417
1.9129	1188	8.3333	4.6233	1.415448	1452	1.8595	3.0605	-1.03445
2.749962	1511	7.4785	3.7685	1.153673	909	2.8603	2.0597	-0.69626
-0.08312	934	1.9272	1.7828	-0.54637	1211	1.3212	3.5988	-1.21635
5.787792	2199	13.37	9.66	2.957894	1578	7.0976	2.1776	0.735623
1.095524	1708	3.6885	0.0215	-0.00698	1563	1.9834	2.9366	-0.99258
5.08701	1600	7.9375	4.2275	1.294237	1530	4.6405	0.2795	-0.09469
1.730891	1004	2.7888	0.9212	-0.28251	1504	0.66489	4.25511	-1.43813
1.670928	2322	6.0724	2.3624	0.723067	2166	5.9095	0.9895	0.334138
-0.01249	2827	5.1645	1.4545	0.44503	2025	5.3827	0.4627	0.15612
0.716938	2181	7.3819	3.6719	1.12409	2764	7.3444	2.4244	0.819022
-0.79465	738	6.5041	2.7941	0.855271	1184	12.416	7.496	2.532829
-1.68433	1309	0.38197	3.32803	-1.01958	1685	1.6024	3.3176	-1.12133
-1.06851	1577	0.95117	2.75883	-0.84527	1488	1.6801	3.2399	-1.09507
-0.68038	3246	3.512	0.198	-0.06103	2830	2.4735	2.4465	-0.82696
-0.79898	2028	3.0572	0.6528	-0.20031	1500	1.6667	3.2533	-1.0996
-0.82723	1429	2.3793	1.3307	-0.40791	1534	1.8253	3.0947	-1.046
-0.96412	2694	3.3408	0.3692	-0.11346	1320	4.0152	0.9048	-0.30599
-1.03044	2748	1.4192	2.2908	-0.70194	1045	1.6268	3.2932	-1.11308
-1.4403	1346	3.3432	0.3668	-0.11273	1412	0.63739	4.28261	-1.44743
-0.7272	1001	4.3956	0.6856	0.209561	673	1.3373	3.5827	-1.21091
0.461792	996	10.04	6.33	1.93811	1243	3.3789	1.5411	-0.52101
0.034812	1452	2.135	1.575	-0.48273	1698	2.179	2.741	-0.92648
1.166086	1111	9.631	5.921	1.812857	597	1.1725	3.7475	-1.2666
1.910175	2613	15.729	12.019	3.680317	1616	5.6312	0.7112	0.240094
1.585526	1045	10.526	6.816	2.086943	726	5.0964	0.1764	0.059373
-0.02309	1698	5.1826	1.4726	0.450573	1256	2.0701	2.8499	-0.96328
2.034038	612	6.8627	3.1527	0.965089	371	5.1213	0.2013	0.067787
-0.74401	1882	3.2412	0.4688	-0.14396	677	4.2836	0.6364	-0.21529
0.770784	1754	8.3238	4.6138	1.412538	1154	4.9393	0.0193	0.006285
0.589713	1953	1.9457	1.7643	-0.5407	1897	7.6964	2.7764	0.937971
-0.21879	1620	3.4568	0.2532	-0.07794	1927	2.8542	2.0658	-0.69832
-1.59509	1099	0.36397	3.34603	-1.02509	1745	1.7765	3.1435	-1.0625
-1.23816	663	0.30166	3.40834	-1.04417	482	2.6971	2.2229	-0.7514
-1.03674	1245	0.40161	3.30839	-1.01356	1056	1.7992	3.1208	-1.05482
-1.05612	1755	1.1396	2.5704	-0.78756	1343	4.7655	0.1545	-0.05245
-1.09604	1453	1.0323	2.6777	-0.82042	1508	0.99469	3.92531	-1.32669
-1.22438	1916	0.26096	3.44904	-1.05664	955	0.62827	4.29173	-1.45051
-1.20082	2047	1.8564	1.8536	-0.56805	835	3.2335	1.6865	-0.57014
-1.27499	2115	1.2293	2.4807	-0.76009	1102	2.9946	1.9254	-0.65087
-1.15428	1676	0.59666	3.11334	-0.95383	1151	2.954	1.966	-0.66459
0.493954	1493	1.5405	2.1695	-0.66479	2075	4.0964	0.8236	-0.27855
-0.73084	947	2.6399	1.0701	-0.32811	1207	2.8998	2.0202	-0.68291
-1.05422	1630	4.0491	0.3391	0.103448	1387	4.9748	0.0548	0.018282
-1.3802	1733	3.2314	0.4786	-0.14697	1753	2.4529	2.4671	-0.83392

-0.66	1064	2.4436	1.2664	-0.38822	896	3.9062	1.0138	-0.34282
-1.14543	1447	0.13822	3.57178	-1.09422	1210	3.1405	1.7795	-0.60157
-0.54968	1493	2.8801	0.8299	-0.25455	1616	7.302	2.382	0.804694
-0.9855	2126	1.6463	2.0637	-0.63239	1970	5.8883	0.9683	0.326974
-0.16722	2092	2.6291	1.0809	-0.33141	1712	10.748	5.828	1.969175
-0.18972	1565	2.6198	1.0902	-0.33426	1439	8.2696	3.3496	1.131668
-1.22626	1335	2.0225	1.6875	-0.51718	1663	4.2093	0.7107	-0.2404
-1.27075	747	1.4726	2.2374	-0.68558	603	2.3217	2.5983	-0.87826
0.3753	836	3.3493	0.3607	-0.11086	825	3.2727	1.6473	-0.5569
-0.32951	743	1.0767	2.6333	-0.80682	1406	2.3471	2.5729	-0.86968
0.270425	1357	2.6529	1.0571	-0.32413	1438	2.0862	2.8338	-0.95784
-0.13112	578	2.5952	1.1148	-0.3418	611	6.383	1.463	0.494144
-0.45295	1069	2.9935	0.7165	-0.21982	445	5.618	0.698	0.235633
-0.62357	1129	1.5058	2.2042	-0.67542	1312	2.7439	2.1761	-0.73559
-1.1411	1154	2.253	1.457	-0.44659	577	5.5459	0.6259	0.211269
-0.4293	1452	2.4793	1.2307	-0.37729	1497	4.9432	0.0232	0.007603
-0.2177	507	0.78895	2.92105	-0.89494	382	4.712	0.208	-0.07052
-0.25604	1098	3.7341	0.0241	0.006982	1043	4.8897	0.0303	-0.01048
0.02927	833	5.6423	1.9323	0.591352	535	5.0467	0.1267	0.042578
-0.65277	987	3.6474	0.0626	-0.01957	775	2.7097	2.2103	-0.74715
0.270637	1440	3.6111	0.0989	-0.03069	662	5.287	0.367	0.123781
-0.48063	844	6.6351	2.9251	0.895389	385	5.1948	0.2748	0.092625
-0.07491	1238	4.4426	0.7326	0.223954	1125	0.88889	4.03111	-1.36244
0.451374	1641	3.9001	0.1901	0.057818	1210	3.6364	1.2836	-0.43399
0.925689	1752	10.103	6.393	1.957403	730	4.3836	0.5364	-0.1815
-0.50819	1240	4.1129	0.4029	0.122987	1532	7.8982	2.9782	1.006164
-0.35719	799	9.2616	5.5516	1.699732	1968	2.3882	2.5318	-0.85579
-1.26421	1729	0.4627	3.2473	-0.99486	1690	1.3609	3.5591	-1.20294
0.135659	634	1.2618	2.4482	-0.75014	475	4.4211	0.4989	-0.16883
-0.04481	786	2.4173	1.2927	-0.39628	854	3.63	1.29	-0.43616
-0.24814	594	1.3468	2.3632	-0.72411	1624	4.3103	0.6097	-0.20627
-1.31357	879	1.0239	2.6861	-0.82299	2031	3.1019	1.8181	-0.61461
-0.73638	494	3.6437	0.0663	-0.0207	828	1.6908	3.2292	-1.09146
0.282296	692	5.0578	1.3478	0.412354	532	4.3233	0.5967	-0.20187
-0.64204	855	6.0819	2.3719	0.725976	1298	3.3898	1.5302	-0.51733
0.240049	871	4.0184	0.3084	0.094047	1563	5.5022	0.5822	0.196502
-0.09505	770	4.6753	0.9653	0.295217	1141	4.908	0.012	-0.00429
0.839378	580	12.931	9.221	2.823454	1030	7.6699	2.7499	0.929016
-0.69762	789	8.4918	4.7818	1.463987	626	3.3546	1.5654	-0.52922
-1.40312	1755	12.251	8.541	2.61521	2223	11.876	6.956	2.350351
-0.5561	1657	8.0266	4.3166	1.321523	1270	4.9606	0.0406	0.013483
-1.23292	1160	6.0345	2.3245	0.71146	1535	5.2769	0.3569	0.120368
-0.54626	1043	5.3691	1.6591	0.507687	1135	6.5198	1.5998	0.540372
-0.81897	901	15.316	11.606	3.553839	913	9.4195	4.4995	1.520245
-0.09493	767	10.821	7.111	2.177284	854	4.918	0.002	-0.00091
-1.18883	1830	6.1749	2.4649	0.754456	1596	6.015	1.095	0.369788
-0.58441	1419	6.9063	3.1963	0.978441	1363	1.6141	3.3059	-1.11737

0.023243	255	4.3137	0.6037	0.18448	297	18.182	13.262	4.481289
4.808999	360	5.5556	1.8456	0.564801	440	18.182	13.262	4.481289
0.991345	1051	2.9496	0.7604	-0.23326	563	7.2824	2.3624	0.798071
0.276906	931	2.6853	1.0247	-0.3142	1907	7.3414	2.4214	0.818009
1.739068	733	3.6835	0.0265	-0.00851	1036	9.2664	4.3464	1.468509
1.045766	486	1.4403	2.2697	-0.69547	689	0.87083	4.04917	-1.36854
0.17409	1536	7.487	3.777	1.156276	1865	8.4718	3.5518	1.199996
0.42854	1127	3.638	0.072	-0.02245	1221	3.8493	1.0707	-0.36205
1.053762	1506	4.0505	0.3405	0.103877	1387	2.5234	2.3966	-0.8101
-0.25495	727	0.55021	3.15979	-0.96806	1295	3.5521	1.3679	-0.46248
0.492864	568	4.2254	0.5154	0.157439	909	4.9505	0.0305	0.01007
1.226534	461	13.883	10.173	3.114995	867	9.9193	4.9993	1.689139
0.332266	757	10.172	6.462	1.978534	1218	10.673	5.753	1.943831
1.240919	549	3.643	0.067	-0.02092	847	7.0838	2.1638	0.73096
0.036235	795	3.7736	0.0636	0.019079	1432	9.148	4.228	1.428499
1.21975	1049	8.8656	5.1556	1.57846	914	4.9234	0.0034	0.000912
-0.1465	383	7.8329	4.1229	1.262204	958	3.4447	1.4753	-0.49877
-0.13163	619	8.4006	4.6906	1.436058	1046	6.4054	1.4854	0.501713
0.612124	870	6.6667	2.9567	0.905066	681	4.5521	0.3679	-0.12456
-0.47003	798	4.386	0.676	0.206621	902	1.7738	3.1462	-1.06341
0.728325	184	8.1522	4.4422	1.359987	197	3.5533	1.3667	-0.46207
2.199694	206	7.2816	3.5716	1.093374	625	6.72	1.8	0.608024
-0.84356	485	3.5052	0.2048	-0.06312	236	8.4746	3.5546	1.200942
-0.02073	1112	5.2158	1.5058	0.46074	754	3.3156	1.6044	-0.5424
0.526207	413	15.496	11.786	3.608963	763	7.9948	3.0748	1.038807
-0.3965	495	11.919	8.209	2.513537	374	4.5455	0.3745	-0.12679
0.023243	1142	8.8441	5.1341	1.571876	1761	6.7007	1.7807	0.601502
-1.00964	608	12.829	9.119	2.792217	356	5.618	0.698	0.235633
0.228511	1701	13.345	9.635	2.950238	837	5.4958	0.5758	0.194339
-0.53862	423	20.095	16.385	5.017367	642	9.9688	5.0488	1.705866
1.149036	369	23.577	19.867	6.083699	738	12.195	7.275	2.458148
0.920238	442	13.348	9.638	2.951156	895	5.5866	0.6666	0.225022
0.559156	977	7.8813	4.1713	1.277027	1276	4.1536	0.7664	-0.25922
0.209614	399	22.306	18.596	5.694467	892	10.65	5.73	1.936058
-1.02542	547	14.077	10.367	3.174406	466	9.2275	4.3075	1.455364
0.641015	810	18.765	15.055	4.610066	1068	18.165	13.245	4.475545
1.332651	1368	19.079	15.369	4.706226	925	9.0811	4.1611	1.405892
0.152164	1823	10.971	7.261	2.223221	1392	7.0402	2.1202	0.716226
0.307856	823	9.9635	6.2535	1.914682	1048	5.916	0.996	0.336334
-0.04111	318	12.893	9.183	2.811817	443	6.5463	1.6263	0.549327
-1.38362	1140	0.087719	3.622281	-1.10969	796	7.9146	2.9946	1.011706
-0.71512	1017	2.0649	1.6451	-0.5042	510	3.5294	1.3906	-0.47015
0.192715	1292	2.322	1.388	-0.42546	941	3.8257	1.0943	-0.37002
0.101407	1167	2.6564	1.0536	-0.32305	1583	4.3588	0.5612	-0.18988
-0.12582	412	1.9417	1.7683	-0.54192	446	5.8296	0.9096	0.307138
-0.67778	487	3.9014	0.1914	0.058216	590	3.2203	1.6997	-0.5746
0.690591	1502	6.5912	2.8812	0.881945	675	5.1852	0.2652	0.08938

-1.53433	899	3.2258	0.4842	-0.14868	614	10.261	5.341	1.804607
0.399164	1214	7.084	3.374	1.03286	1246	3.8523	1.0677	-0.36104
-0.8445	787	4.4473	0.7373	0.225394	877	6.2714	1.3514	0.456432
0.782019	431	2.7842	0.9258	-0.28392	513	13.06	8.14	2.750451
0.012129	442	5.2036	1.4936	0.457004	743	10.229	5.309	1.793793
0.062401	592	6.25	2.54	0.777455	670	5.6716	0.7516	0.253746
-1.04758	443	4.7404	1.0304	0.315153	1180	5	0.08	0.026797
0.917724	356	3.0899	0.6201	-0.1903	609	9.3596	4.4396	1.500003
0.46582	999	1.5015	2.2085	-0.67673	1382	6.4399	1.5199	0.513372
2.066745	723	5.9474	2.2374	0.684786	1356	4.4985	0.4215	-0.14267
0.612669	873	4.4674	0.7574	0.231549	937	5.8698	0.9498	0.320722
-0.24456	811	8.1381	4.4281	1.355669	902	11.973	7.053	2.38313
0.134569	510	6.4706	2.7606	0.845012	951	7.1504	2.2304	0.753465
-0.77975	1126	1.2433	2.4667	-0.7558	1636	1.956	2.964	-1.00184
-0.01382	888	1.5766	2.1334	-0.65373	1032	6.2016	1.2816	0.432845
0.624904	1576	2.2843	1.4257	-0.43701	1947	3.0303	1.8897	-0.63881
-0.52606	1952	1.793	1.917	-0.58746	2195	2.1868	2.7332	-0.92385
-0.54701	623	1.6051	2.1049	-0.64501	2443	6.8768	1.9568	0.66101
1.151035	427	8.6651	4.9551	1.517059	1062	2.6365	2.2835	-0.77188
-0.08911	997	3.2096	0.5004	-0.15364	1706	0.87925	4.04075	-1.3657
0.189868	1076	2.4164	1.2936	-0.39655	1077	3.4355	1.4845	-0.50188
0.098046	470	2.9787	0.7313	-0.22435	777	6.9498	2.0298	0.685678
1.111665	965	2.7979	0.9121	-0.27972	1190	1.0084	3.9116	-1.32205
1.497701	730	3.9726	0.2626	0.080021	1183	1.6906	3.2294	-1.09152
0.365033	564	5.4965	1.7865	0.546702	1340	5.8209	0.9009	0.304198
1.202034	525	7.619	3.909	1.196699	1454	2.3384	2.5816	-0.87262
2.411079	811	9.3711	5.6611	1.733265	1353	2.6608	2.2592	-0.76367
0.627872	537	8.0074	4.2974	1.315644	2152	7.0167	2.0967	0.708285
0.818876	1157	5.5315	1.8215	0.557421	1628	2.2113	2.7087	-0.91557
0.633141	753	9.9602	6.2502	1.913672	1476	2.5068	2.4132	-0.81571
-0.38275	745	4.2953	0.5853	0.178845	1766	1.8686	3.0514	-1.03137
0.467697	1085	12.903	9.193	2.814879	2023	3.2625	1.6575	-0.56034
1.155123	1450	9.1034	5.3934	1.651284	1339	3.1367	1.7833	-0.60285
-1.3358	800	0.625	3.085	-0.94515	1455	3.5052	1.4148	-0.47833
0.880353	1554	3.9897	0.2797	0.085258	1733	6.8667	1.9467	0.657597
-0.35362	1092	0.7326	2.9774	-0.9122	2432	5.3043	0.3843	0.129627
-0.05032	915	0.54645	3.16355	-0.96921	2043	3.3774	1.5426	-0.52152
-0.26876	949	2.2129	1.4971	-0.45887	1512	10.053	5.133	1.734319
-0.818	1458	1.5775	2.1325	-0.65346	1147	1.2206	3.6994	-1.25035
1.183137	776	2.4485	1.2615	-0.38672	580	16.552	11.632	3.930476
1.189981	547	2.1938	1.5162	-0.46472	586	23.549	18.629	6.294918
-0.61985	1562	0.89629	2.81371	-0.86207	1870	3.4225	1.4975	-0.50628
0.602887	528	1.3258	2.3842	-0.73054	976	8.9139	3.9939	1.349391
0.245834	1210	1.157	2.553	-0.78223	1245	3.3735	1.5465	-0.52283
0.50419	1457	3.3631	0.3469	-0.10663	1467	3.7491	1.1709	-0.39591
-0.62872	1047	4.8711	1.1611	0.355179	1100	3.4545	1.4655	-0.49546
0.656551	1126	0.8881	2.8219	-0.86458	1229	5.3702	0.4502	0.151896

-0.40059	651	0.92166	2.78834	-0.8543	1269	5.2009	0.2809	0.094686
-1.28044	1012	2.2727	1.4373	-0.44056	1977	3.4901	1.4299	-0.48343
-0.32151	887	4.6223	0.9123	0.278986	1482	6.0729	1.1529	0.389354
-0.00201	1008	3.5714	0.1386	-0.04284	1695	5.3687	0.4487	0.151389
-0.04808	1489	5.7085	1.9985	0.611625	1200	5.8333	0.9133	0.308388
0.381296	1956	3.5276	0.1824	-0.05626	1233	7.4615	2.5415	0.858593
0.042656	1127	0.97604	2.73396	-0.83765	945	2.8571	2.0629	-0.69734
0.53084	559	0.35778	3.35222	-1.02699	849	5.1826	0.2626	0.088502
-0.02	1624	1.8473	1.8627	-0.57083	1630	5.0307	0.1107	0.037171
2.076436	1443	0.9009	2.8091	-0.86066	1678	11.561	6.641	2.243906
-0.55746	1514	0.7926	2.9174	-0.89383	1945	4.7301	0.1899	-0.06441
0.537352	2235	3.0872	0.6228	-0.19113	1606	6.538	1.618	0.546522
1.785706	1510	3.3775	0.3325	-0.10222	1717	5.0087	0.0887	0.029737
3.250563	2000	9.2	5.49	1.680867	1636	5.868	0.948	0.320114
-0.33021	705	2.8369	0.8731	-0.26778	1197	5.5138	0.5938	0.200422
0.865665	965	2.0725	1.6375	-0.50187	865	3.9306	0.9894	-0.33458
3.272973	2238	9.4727	5.7627	1.764379	2967	6.2353	1.3153	0.444233
-0.7643	1183	1.3525	2.3575	-0.72236	1212	3.1353	1.7847	-0.60333
0.268608	2203	2.3604	1.3496	-0.4137	2142	2.9412	1.9788	-0.66892
1.876559	986	1.3185	2.3915	-0.73277	903	5.0941	0.1741	0.058596
0.255888	1313	2.2087	1.5013	-0.46016	946	3.6998	1.2202	-0.41257
0.187476	1123	2.6714	1.0386	-0.31846	1407	5.6148	0.6948	0.234552
3.936808	875	7.0857	3.3757	1.033381	771	13.23	8.31	2.807898
0.542924	1274	3.2967	0.4133	-0.12697	1336	4.2665	0.6535	-0.22107
2.669405	2880	8.5417	4.8317	1.479268	3282	9.1408	4.2208	1.426066
0.856277	1814	4.8512	1.1412	0.349085	1459	3.9753	0.9447	-0.31947
-0.99886	2360	0.55085	3.15915	-0.96786	1788	3.8591	1.0609	-0.35874
-0.33342	2927	1.1616	2.5484	-0.78082	1563	6.206	1.286	0.434332
0.451404	1664	2.4639	1.2461	-0.38201	2562	14.481	9.561	3.230639
-1.27444	1348	1.0386	2.6714	-0.81849	1071	8.1232	3.2032	1.082196
-0.74852	1820	1.5385	2.1715	-0.6654	2001	5.1974	0.2774	0.093503
-1.32896	1241	1.2087	2.5013	-0.7664	882	8.5034	3.5834	1.210674
-0.96509	1068	0.37453	3.33547	-1.02186	865	9.1329	4.2129	1.423396
-0.42539	2509	3.2284	0.4816	-0.14788	1421	5.4187	0.4987	0.168285
0.824872	2198	3.3212	0.3888	-0.11946	1264	8.5443	3.6243	1.224495
0.413821	1968	2.439	1.271	-0.38963	1180	3.4746	1.4454	-0.48867
-0.05095	1503	5.3892	1.6792	0.513842	1140	8.4211	3.5011	1.182863
0.857791	673	3.1204	0.5896	-0.18096	1859	7.1544	2.2344	0.754817
-0.56733	1126	2.5755	1.1345	-0.34783	847	7.438	2.518	0.850652
-0.09414	454	1.7621	1.9479	-0.59693	772	3.6269	1.2931	-0.4372
0.137749	1258	4.6105	0.9005	0.275372	1409	4.8971	0.0229	-0.00797
-0.23781	1375	2.4	1.31	-0.40157	1450	5.1724	0.2524	0.085055
1.334165	1391	5.1042	1.3942	0.426564	2232	6.6308	1.7108	0.577881
-0.45822	1241	4.4319	0.7219	0.220678	2248	2.4911	2.4289	-0.82102
1.24313	1947	3.2357	0.4743	-0.14565	706	8.9235	4.0035	1.352635
0.141716	1070	7.8505	4.1405	1.267594	781	10.371	5.451	1.841778
-0.67633	992	1.0081	2.7019	-0.82783	1216	8.3882	3.4682	1.171746

-0.09032	999	2.002	1.708	-0.52346	1154	7.3657	2.4457	0.82622
-1.46361	991	0.50454	3.20546	-0.98204	1334	2.9985	1.9215	-0.64955
-0.71891	1055	2.5592	1.1508	-0.35282	1280	3.75	1.17	-0.39561
-1.44074	991	1.9173	1.7927	-0.5494	922	4.2299	0.6901	-0.23344
-1.21566	776	1.0309	2.6791	-0.82085	652	7.5153	2.5953	0.876773
-1.06118	452	0.66372	3.04628	-0.9333	670	8.0597	3.1397	1.060738
-0.90067	479	3.5491	0.1609	-0.04967	1129	4.783	0.137	-0.04653
-0.10568	604	2.4834	1.2266	-0.37603	849	8.1272	3.2072	1.083548
-0.8882	386	8.5492	4.8392	1.481565	852	12.559	7.639	2.581152
-0.60237	1224	4.2484	0.5384	0.164482	891	4.6016	0.3184	-0.10783
-0.10341	877	3.6488	0.0612	-0.01914	1384	6.2139	1.2939	0.437001
-0.31888	1080	4.4444	0.7344	0.224506	949	9.1675	4.2475	1.435089
0.834654	887	6.4262	2.7162	0.831415	1151	16.073	11.153	3.768611
-1.33229	823	5.5893	1.8793	0.575121	2400	5.9583	1.0383	0.350628
-0.18224	839	7.5089	3.7989	1.162982	1319	5.4587	0.5387	0.181802
-0.25174	1276	9.4044	5.6944	1.743463	2016	6.2996	1.3796	0.465961
1.478016	1363	10.271	6.561	2.008852	848	9.434	4.514	1.525145
-0.31073	480	12.917	9.207	2.819166	257	5.4475	0.5275	0.178017
1.79146	714	14.986	11.276	3.45278	378	11.905	6.985	2.360151
-0.52927	1232	0.32468	3.38532	-1.03712	1644	2.129	2.791	-0.94338
-0.07933	1535	1.3681	2.3419	-0.71758	745	3.2215	1.6985	-0.5742
0.665182	2053	3.6532	0.0568	-0.01779	1733	3.4045	1.5155	-0.51236
0.067428	1388	1.8732	1.8368	-0.5629	3840	4.375	0.545	-0.1844
1.802968	427	0.93677	2.77323	-0.84968	339	11.209	6.289	2.124957
-0.53257	620	1.9355	1.7745	-0.54382	552	6.5217	1.6017	0.541014
0.002438	1201	1.582	2.128	-0.65208	1044	3.4483	1.4717	-0.49756
1.01851	1847	3.4651	0.2449	-0.0754	3615	4.592	0.328	-0.11108
-0.62533	1812	3.4216	0.2884	-0.08872	2065	2.3729	2.5471	-0.86096
0.818876	1589	1.9509	1.7591	-0.53911	1434	7.2524	2.3324	0.787933
-0.41016	1959	10.975	7.265	2.224446	1568	3.5077	1.4123	-0.47748
1.000824	892	2.8027	0.9073	-0.27825	2246	5.1202	0.2002	0.067416
-0.39153	2037	5.2528	1.5428	0.472071	2453	3.139	1.781	-0.60208
-0.12227	1648	5.1578	1.4478	0.442978	1287	3.4188	1.5012	-0.50753
1.255728	589	7.3005	3.5905	1.099162	1167	5.3128	0.3928	0.132499
-1.31082	893	3.3595	0.3505	-0.10774	3045	2.2332	2.6868	-0.90817
-0.46046	2031	4.3328	0.6228	0.190329	2278	3.6874	1.2326	-0.41676
-0.39217	1804	4.7118	1.0018	0.306395	2684	5.924	1.004	0.339037
0.026726	565	11.858	8.148	2.494857	793	8.9533	4.0333	1.362706
-0.12152	322	6.8323	3.1223	0.955779	394	10.406	5.486	1.853605
	1058.5	3.7113	2.20635		1140.5	4.9207	1.9995	
			6.61905				5.9985	
			3.265398				2.95926	
1534	19.296		1487	25.286				
2439	25.256		1857	24.448				
2490	29.598		2130	31.221				
2068	28.143		1968	28.608				
2132.75	25.57325		1860.5	27.39075				

441.2523	4.557292	273.0696	3.122086
576	6.9444	506	4.9407
377	6.1008	407	5.4054
235	12.34	423	10.638
296	10.473	307	13.681
371	8.96455	410.75	8.666275
148.5283	2.941154	81.65119	4.224862
	13.67188		9.366258
	0.353412		7.949012
	14.02529		17.31527
	21.90025		23.31535
	0.640417		0.742655
	0.359583		0.257345

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

x	toxic a,b,c
y	

x toxic a,b

x	toxic a,b,c
x	toxic a,b,c
x	toxic a,b,c

x	toxic b,c
x	toxic a,b,c

x toxic a,b,c

Table S2 Potential False Negatives

Table S2. Wells Eliminated for Toxicity on Image Revi

50001.00	A13	M-003255-02	CHK1 checkpoint homolog (S. pom	1111.00
50001.00	B11	M-019847-01	coatomer protein complex, subuni	9276.00
50001.00	C13	M-006708-00	creatine kinase, mitochondrial 1B	1159.00
50001.00	I21	M-011426-01	A kinase (PRKA) anchor protein 1	8165.00
50001.00	K19	M-003000-01	v-akt murine thymoma viral oncog	207.00
50002.00	B18	M-008476-01	protein tyrosine phosphatase, rec	5795.00
50002.00	M09	M-004813-01	male germ cell-associated kinase	4117.00
50002.00	P02	M-004647-00	protein kinase N3	29941.00
50005.00	M15	M-020188-00	olfactory receptor, family 2, subfa	26211.00
50006.00	F09	M-003773-01	ELAV (embryonic lethal, abnormal	1994.00
50006.00	H06	M-004565-03	integrin, alpha V (vitronectin rece	3685.00
50006.00	H14	M-006983-01	inhibitor of growth family, membe	51147.00
50006.00	P19	M-009020-00	hairy and enhancer of split 7 (Dros	84667.00
50009.00	O23	M-012176-00	mesenchyme homeobox 2	4223.00
50009.00	P17	M-016508-00	SP140 nuclear body protein	11262.00
50010.00	F07	M-008651-00	amidohydrolase domain containin	51005.00
50010.00	I14	M-009599-01	S-adenosylhomocysteine hydrolas	191.00
50010.00	L04	M-009805-01	ectonucleotide pyrophosphatase/	59084.00
50010.00	P02	M-008125-01	dimethylglycine dehydrogenase	29958.00
50011.00	A07	M-008900-00	glycine amidinotransferase (L-argi	2628.00
50011.00	E05	M-008226-00	glucosamine (N-acetyl)-6-sulfatase	2799.00
50011.00	G21	M-011964-00	H2A histone family, member Y	9555.00
50011.00	I17	M-009823-01	homogentisate 1,2-dioxygenase (h	3081.00
50012.00	K02	M-004402-01	caspase 10, apoptosis-related cyst	843.00
50013.00	I07	M-019661-00	lactotransferrin	4057.00
50014.00	A02	M-020011-00	lipoprotein, Lp(a)	4018.00
50014.00	A07	M-009752-01	pyruvate dehydrogenase complex,	8050.00
50014.00	A23	M-009553-00	RAB36, member RAS oncogene fa	9609.00
50014.00	B02	M-011126-00	CD79b molecule, immunoglobulin-	974.00
50014.00	E10	M-004900-01	glucose phosphate isomerase	2821.00
50014.00	E18	M-009494-00	FK506 binding protein 1A, 12kDa	2280.00
50014.00	E20	M-009907-01	fatty acid amide hydrolase	2166.00
50014.00	F07	M-010020-00	cystatin A (stefin A)	1475.00
50014.00	G10	M-007880-01	chemokine (C-X-C motif) ligand 6 (	6372.00
50014.00	G14	M-003772-06	CASP8 and FADD-like apoptosis re	8837.00
50014.00	G19	M-008324-00	dual oxidase 2	50506.00
50014.00	H19	M-011298-01	immunoglobulin (CD79A) binding	3476.00
50014.00	P02	M-010216-01	serine peptidase inhibitor, Kunitz t	10653.00
50014.00	P05	M-008387-00	ral guanine nucleotide dissociation	23179.00
50014.00	P11	M-021066-00	serpin peptidase inhibitor, clade A	51156.00
50014.00	P13	M-015832-00	serpin peptidase inhibitor, clade A	5104.00
50014.00	P23	M-019684-00	serpin peptidase inhibitor, clade B	5268.00
50015.00	B13	M-003530-03	RAD51 homolog (RecA homolog, E	5888.00
50015.00	F21	M-017305-00	TRIAD3 protein	54476.00
50015.00	G05	M-006077-00	ubiquitin specific peptidase 29	57663.00

50015.00	K06	M-013642-00	anaphase promoting complex subu	29945.00
50015.00	N14	M-009469-01	kinesin family member 3C	3797.00
50015.00	O19	M-003281-04	menage a trois homolog 1, cyclin H	4331.00
50015.00	O20	M-006545-00	peroxisome biogenesis factor 10	5192.00
50015.00	P06	M-004959-01	kinesin heavy chain member 2A	3796.00
50015.00	P12	M-008252-01	kinesin family member 12	113220.00
50015.00	P14	M-003317-01	kinesin family member 11	3832.00
50016.00	A06	M-012316-00	KDEL (Lys-Asp-Glu-Leu) endoplasm	11015.00
50016.00	H17	M-017920-00	neutral sphingomyelinase (N-SMas	8439.00
50016.00	I04	M-006190-00	glutamate receptor, ionotropic, ka	2898.00
50016.00	N15	M-013710-00	secretogranin III	29106.00
50016.00	O12	M-017088-00	CD300c molecule	10871.00
50017.00	A05	M-004381-01	B-cell CLL/lymphoma 10	8915.00
50017.00	A23	M-011593-01	bone morphogenetic protein 8b (o	656.00
50017.00	I05	M-010206-01	CD36 molecule (thrombospondin r	948.00
50017.00	K12	M-011288-00	gonadotropin-releasing hormone 2	2797.00
50017.00	K20	M-020860-00	ghrelin/obestatin preprohormone	51738.00
50017.00	N21	M-013593-00	killer cell lectin-like receptor subfa	8302.00
50017.00	N23	M-011304-00	killer cell lectin-like receptor subfa	3824.00
50017.00	O04	M-013088-00	growth differentiation factor 1	2657.00
50017.00	P04	M-020015-00	CD180 molecule	4064.00
50017.00	P11	M-011718-00	lectin, galactoside-binding, soluble	3956.00
50017.00	P19	M-012491-00	C-type lectin domain family 2, mer	29121.00
50018.00	B10	M-010551-00	coiled-coil domain containing 6	8030.00
50018.00	D10	M-011622-00	collagen, type IX, alpha 1	1297.00
50018.00	K18	M-003401-02	estrogen receptor 1	2099.00
50018.00	P13	M-008096-00	tumor necrosis factor receptor sup	8764.00
50018.00	P19	M-005197-00	tumor necrosis factor receptor sup	7132.00
50018.00	P21	M-003934-00	tumor necrosis factor receptor sup	7133.00
50018.00	P23	M-004449-01	tumor necrosis factor receptor sup	8718.00
50019.00	I14	M-019674-00	nidogen 1	4811.00
50019.00	I16	M-019900-00	NHP2 non-histone chromosome pr	4809.00
50019.00	N04	M-007381-01	solute carrier family 11 (proton-co	4891.00
50019.00	O04	M-011034-00	fibrillin 1	2200.00
50019.00	O10	M-011270-00	FAT tumor suppressor homolog 2 (	2196.00
50021.00	G14	M-007879-01	chemokine (C-X-C motif) ligand 5	6374.00
50021.00	M19	M-020163-00	ceroid-lipofuscinosis, neuronal 5	1203.00
50021.00	O09	M-019513-00	clusterin	1191.00
50021.00	P17	M-016196-00	CD164 molecule, sialomucin	8763.00
50022.00	G12	M-011048-00	hemoglobin, delta	3045.00
50022.00	K10	M-028674-00	general transcription factor IIH, po	2968.00
50022.00	O07	M-012041-00	growth factor, augmenter of liver r	2671.00
50023.00	G14	M-009000-00	oligodendrocyte transcription fact	167826.00
50023.00	I20	M-018325-00	nuclear distribution gene C homolo	10726.00
50023.00	I21	M-004899-00	phosphatidic acid phosphatase typ	84513.00
50023.00	N05	M-026943-00	POU domain, class 6, transcription	5463.00
50024.00	G17	M-011157-00	ribosomal protein S29	6235.00

50024.00	I10	M-012599-00	slit homolog 1 (Drosophila)	6585.00
50024.00	N10	M-009552-02	X-box binding protein 1	7494.00
50024.00	P09	M-021117-00	RB1-inducible coiled-coil 1	9821.00
50047.00	A13	M-008795-00	ATP-binding cassette, sub-family A	21.00
50047.00	E17	M-012492-00	adaptor-related protein complex 2	160.00
50047.00	H15	M-011835-00	coatomer protein complex, subuni	1314.00
50047.00	I20	M-007817-00	complement component 4 binding	722.00
50047.00	J06	M-012999-00	defensin, alpha 1	1667.00
50047.00	K06	M-011597-00	betacellulin	685.00
50048.00	L11	M-005906-00	kallikrein 1	3816.00
50048.00	L14	M-011325-00	melanoma antigen family B, 1	4112.00
50048.00	O10	M-011676-00	glutathione peroxidase 4 (phospho	2879.00
50048.00	P02	M-010030-00	lymphocyte antigen 9	4063.00
50048.00	P05	M-017237-00	laminin, alpha 5	3911.00
50048.00	P07	M-013481-00	lysosomal-associated membrane p	3916.00
50049.00	A20	M-028956-00	postmeiotic segregation increased	5379.00
50049.00	C19	M-019919-00	myosin IE	4643.00
50049.00	J07	M-007748-00	acyl-CoA synthetase long-chain far	23305.00
50049.00	L04	M-006809-00	ADP-dependent glucokinase	83440.00
50049.00	L15	M-009002-00	acyl-Coenzyme A dehydrogenase f	28976.00
50049.00	L18	M-027136-00	asparagine-linked glycosylation 8 h	79053.00
50049.00	N08	M-010799-00	acyl-Coenzyme A binding domain c	64746.00
50049.00	O18	M-009401-00	N-ethylmaleimide-sensitive factor	4905.00
50049.00	O23	M-012726-00	metallothionein 1F	4494.00
50049.00	P09	M-021468-00	absent in melanoma 1-like	55057.00
50049.00	P17	M-020523-00	allantoicase	55821.00
50050.00	A20	M-008270-00	syndecan binding protein (syntenin)	
50050.00	C16	M-021405-00	SET binding factor 1	
50050.00	D10	M-011789-00	threonyl-tRNA synthetase	
50050.00	D11	M-007427-00	solute carrier family 1 (glial high affinity glutamate t	
50050.00	D16	M-010623-00	synaptophysin-like 1	
50050.00	E13	M-009261-00	proteasome (prosome, macropain) 26S subunit, ATF	
50050.00	E15	M-009484-00	proteasome (prosome, macropain) 26S subunit, ATF	
50050.00	E16	M-011891-00	ribosome binding protein 1 homolog 180kDa (dog)	
50050.00	E19	M-011363-00	proteasome (prosome, macropain) 26S subunit, nor	
50050.00	E20	M-013722-00	ribosomal protein S27a	
50050.00	E21	M-011364-00	proteasome (prosome, macropain) 26S subunit, nor	
50050.00	F12	M-012324-00	surfeit 5	SURF5
50050.00	F20	M-009862-00	sulfotransferase family, cytosolic,	SULT1C2
50050.00	F21	M-007600-00	solute carrier family 6 (neurotrans	SLC6A13
50050.00	F23	M-007610-00	solute carrier family 7 (cationic am	SLC7A1
50050.00	G21	M-019703-00	parvalbumin	PVALB
50050.00	J21	M-007422-00	solute carrier family 19 (folate trar	SLC19A1
50050.00	J23	M-007432-00	solute carrier family 20 (phosphate	SLC20A1
50050.00	P04	M-017377-00	SRY (sex determining region Y)-bo	SOX11
50050.00	P14	M-017520-00	sorting nexin 2	SNX2
50051.00	A19	M-010625-00	tetraspanin 4	7106.00

50051.00	C05	M-019747-00	tropomodulin 1	7111.00
50051.00	D04	M-011530-00	N-ethylmaleimide-sensitive factor	8775.00
50051.00	E15	M-028592-00	TSPY-like 1	7259.00
50051.00	G07	M-021218-00	tuftelin 1	7286.00
50051.00	M15	M-012773-00	zinc finger protein 16	7564.00
50052.00	E07	M-004286-00	procollagen-lysine, 2-oxoglutarate	8985.00
50052.00	I08	M-005076-00	palmitoyl-protein thioesterase 2	9374.00
50052.00	J07	M-020790-00	zinc finger protein 592	9640.00
50052.00	K11	M-005126-01	solute carrier family 16, member 3	9123.00
50052.00	K12	M-019851-00	elongation factor Tu GTP binding d	9343.00
50052.00	L12	M-017968-00	dedicator of cytokinesis 4	9732.00
50052.00	L16	M-021119-00	Vpr (HIV-1) binding protein	9730.00
50052.00	M14	M-015820-00	zinc finger and BTB domain contai	9278.00
50052.00	N20	M-020925-00	USP6 N-terminal like	9712.00
50053.00	A13	M-021122-00	Rho GTPase activating protein 11A	9824.00
50053.00	A18	M-020003-00	CTD (carboxy-terminal domain, RN	10217.00
50053.00	A19	M-009885-00	DnaJ (Hsp40) homolog, subfamily	9829.00
50053.00	A23	M-012968-00	KIAA0125	9834.00
50053.00	C08	M-012112-00	InaD-like (Drosophila)	10207.00
50053.00	C13	M-023203-00	pleckstrin homology domain conta	9842.00
50053.00	C23	M-018914-00	EPM2A (laforin) interacting protei	9852.00
50053.00	D04	M-020157-00	slowmo homolog 1 (Drosophila)	10650.00
50053.00	D12	M-017969-00	ATP synthase, H+ transporting, mit	10632.00
50053.00	E15	M-021249-00	proteasome (prosome, macropain	9861.00
50053.00	F08	M-008511-00	trans-golgi network protein 2	10618.00
50053.00	F11	M-020094-00	small nuclear RNA activating comp	10302.00
50053.00	G14	M-032208-00	splicing factor, arginine/serine-ric	10147.00
50053.00	G19	M-021230-00	TBC1 domain family, member 4	9882.00
50053.00	O13	M-003531-00	RNA binding motif protein 8A	9939.00
50053.00	P05	M-012732-00	translocase of outer mitochondrial	10452.00
50053.00	P06	M-013680-00	nuclear RNA export factor 1	10482.00
50053.00	P08	M-016219-00	PCI domain containing 1 (herpesvi	10480.00
50053.00	P12	M-007476-00	solute carrier family 25 (mitochon	10478.00
50053.00	P17	M-012992-00	sperm associated antigen 11B	10407.00
50053.00	P20	M-019123-00	component of oligomeric golgi cor	10466.00
50054.00	A18	M-006043-00	protease, serine, 23	11098.00
50054.00	A19	M-020158-00	adaptor-related protein complex 4	10717.00
50054.00	C15	M-012279-00	cell adhesion molecule with homo	10752.00
50054.00	G12	M-008872-00	leukocyte immunoglobulin-like rec	11025.00
50054.00	J07	M-008449-00	proline synthetase co-transcribed	11212.00
50054.00	J17	M-019671-00	PRA1 domain family, member 2	11230.00
50054.00	L20	M-020488-00	KIAA1009	22832.00
50054.00	N16	M-020293-00	coatomer protein complex, subuni	22818.00
50054.00	P04	M-019487-00	component of oligomeric golgi cor	22796.00
50054.00	P15	M-012393-00	DEAD (Asp-Glu-Ala-Asp) box polyp	11325.00
50055.00	D16	M-012845-00	protein O-fucosyltransferase 1	23509.00
50055.00	L07	M-014049-00	Dmx-like 2	23312.00

50055.00	L08	M-013104-00	coactosin-like 1 (Dictyostelium)	23406.00
50055.00	M10	M-031841-00	zinc finger, ZZ-type with EF-hand	23140.00
50055.00	N11	M-014051-00	tetratricopeptide repeat domain 2	23331.00
50057.00	I09	M-020546-00	sialic acid binding Ig-like lectin 7	27036.00
50057.00	M09	M-017649-00	trafficking protein particle comple	27095.00
50057.00	M20	M-017650-00	PRELI domain containing 1	27166.00
50057.00	O15	M-015461-00	structural maintenance of chromo	27127.00
50058.00	A18	M-006984-00	zinc finger protein 639	51193.00
50058.00	A20	M-021092-00	synovial sarcoma translocation ge	51188.00
50058.00	K20	M-020994-00	intraflagellar transport 52 homolo	51098.00
	N15	M-010207-00	archaemetzincins-2	51321.00
50059.00	O23	M-007940-00	interleukin 17D	53342.00
50059.00	P07	M-020288-00	ATP binding domain 1 family, me	54707.00
50059.00	P17	M-015498-00	chromosome 21 open reading fra	54073.00
50060.00	A19	M-004584-00	BCL6 co-repressor	54880.00
50060.00	A21	M-020741-00	testis expressed 10	54881.00
50060.00	O07	M-015366-00	transmembrane protein 70	54968.00
50060.00	O12	M-031212-00	hypothetical protein FLJ20581	54988.00
50060.00	P05	M-010039-00	nudix (nucleoside diphosphate lin	55190.00
50060.00	P07	M-007723-00	NAD synthetase 1	55191.00
50061.00	A06	M-016863-00	importin 9	55705.00
50061.00	A11	M-021333-00	La ribonucleoprotein domain famil	55323.00
50061.00	A12	M-030269-00	hypothetical protein FLJ10357	55701.00
50061.00	A13	M-021213-00	chromosome 4 open reading fram	55325.00
50061.00	A17	M-008473-00	lin-7 homolog C (C. elegans)	55327.00
50061.00	F08	M-013286-00	protocadherin gamma subfamily C	56098.00
50061.00	K07	M-007549-00	solute carrier family 35, member E	55508.00
50061.00	K08	M-020681-00	sphingomyelin phosphodiesterase	55627.00
50061.00	K12	M-021091-00	zinc finger, DHHC-type containing	55625.00
50061.00	K13	M-008358-00	elaC homolog 1 (E. coli)	55520.00
50061.00	K15	M-007012-00	tripartite motif-containing 36	55521.00
50061.00	K16	M-021071-00	THUMP domain containing 1	55623.00
50061.00	K18	M-015527-00	tetratricopeptide repeat domain 2	55622.00
50061.00	K20	M-009655-00	TRM1 tRNA methyltransferase 1 h	55621.00
50061.00	L05	M-017202-00	DEAD (Asp-Glu-Ala-Asp) box polyp	55794.00
50061.00	L09	M-015373-00	muscleblind-like 3 (Drosophila)	55796.00
50061.00	L11	M-008721-00	methyltransferase like 2B	55798.00
50061.00	L13	M-021246-00	calcium channel, voltage-depende	55799.00
50061.00	L16	M-020987-00	zinc finger protein 302	55900.00
50062.00	A09	M-010167-00	testis expressed 13A	56157.00
50062.00	A10	M-013200-00	T-box 20	57057.00
50062.00	A11	M-013487-00	testis expressed 12	56158.00
50062.00	A14	M-031983-00	phospholipid scramblase 2	57047.00
50062.00	E06	M-015289-00	bobby sox homolog (Drosophila)	56987.00
50062.00	F23	M-013847-00	KIAA1219	57148.00
50062.00	K05	M-006256-00	potassium channel, subfamily K, m	56660.00
50062.00	K09	M-015057-00	mucin 13, cell surface associated	56667.00

50062.00	K12	M-020414-00	chromosome 11 open reading fran	56935.00
50062.00	K13	M-020701-00	chromosome 11 open reading fran	56673.00
50062.00	K14	M-008550-00	carbonic anhydrase X	56934.00
50062.00	K15	M-020706-00	TMEM9 domain family, member B	56674.00
50062.00	K19	M-008980-00	achaete-scute complex homolog 3	56676.00
50062.00	K20	M-006041-00	signal peptide peptidase-like 2B	56928.00
50062.00	L02	M-019101-00	CCR4-NOT transcription complex, s	57472.00
50062.00	L05	M-024244-00	chromosome 20 open reading fran	57186.00
50062.00	L12	M-015488-00	hedgehog acyltransferase-like	57467.00
50062.00	L16	M-022880-00	TBC1 domain family, member 24	57465.00
50063.00	H02	M-006013-00	protease, serine, 22	64063.00
50063.00	K04	M-019159-00	sema domain, immunoglobulin do	57715.00
50063.00	K05	M-014129-00	zinc finger and BTB domain contai	57621.00
50063.00	K11	M-023134-00	KIAA1486 protein	57624.00
50063.00	K14	M-007340-00	solute carrier family 7 (cationic am	57709.00
50063.00	K18	M-023101-00	KIAA1604 protein	57703.00
50063.00	L04	M-013050-00	mitochondrial ribosomal protein S	63931.00
50063.00	L05	M-013978-00	tRNA methyltransferase 11 homol	60487.00
50063.00	L06	M-013917-00	chromosome 20 open reading fran	63930.00
50063.00	L08	M-013916-00	hepatocellular carcinoma antigen	63928.00
50063.00	L09	M-015916-00	phosphopantothenoylcysteine dec	60490.00
50063.00	L11	M-013979-00	NIF3 NGG1 interacting factor 3-like	60491.00
50063.00	L12	M-016168-00	cell death-inducing DFFA-like effec	63924.00
50064.00	K04	M-016323-00	family with sequence similarity 11	64773.00
50064.00	L04	M-014297-00	FAST kinase domains 3	79072.00
50064.00	L05	M-014256-00	chromosome 20 open reading fran	65992.00
50064.00	L06	M-008861-00	ELOVL family member 6, elongatio	79071.00
50064.00	L07	M-012884-00	mitochondrial ribosomal protein S	65993.00
50064.00	L09	M-014258-00	hypothetical protein MGC2752	65996.00
50064.00	L11	M-014261-00	leucine rich repeat containing 61	65999.00
50064.00	L12	M-016359-00	methyltransferase 10 domain cont	79066.00
50064.00	L13	M-023601-00	transmembrane protein 108	66000.00
50064.00	L14	M-014294-00	ATG9 autophagy related 9 homolo	79065.00
50065.00	K06	M-016135-00	chromosome 14 open reading fran	79686.00
50065.00	L02	M-014486-00	SET domain containing 6	79918.00
50065.00	L04	M-014485-00	MAGI family member, X-linked	79917.00
50065.00	L05	M-005339-00	NKF3 kinase family member	79834.00
50065.00	L06	M-004738-00	ATPase family, AAA domain contai	79915.00
50065.00	L07	M-007067-00	LON peptidase N-terminal domain	79836.00
50065.00	L08	M-008132-00	hypothetical protein FLJ22028	79912.00
50065.00	L10	M-014483-00	butyrophilin-like 8	79908.00
50065.00	L16	M-014479-00	hypothetical protein FLJ14154	79903.00
50065.00	L21	M-014447-00	zinc finger, DHHC-type containing	79844.00
50067.00	H16	M-018613-00	chromosome 12 open reading fran	84298.00
50067.00	M15	M-017950-00	yippee-like 3 (Drosophila)	83719.00
50072.00	H11	M-016793-00	chromosome 6 open reading fram	135398.00
50074.00	I10	M-021465-00	nuclear transcription factor, X-box	152518.00

50074.00	I16	M-015543-00	chromosome 3 open reading fram	152405.00
50075.00	E13	M-031845-00	zinc finger protein 600	162966.00
50076.00	A14	M-007567-00	solute carrier family 39 (zinc trans	221074.00
50076.00	A17	M-018489-00	zinc finger protein 584	201514.00
50076.00	A18	M-016615-00	chromosome 10 open reading fran	221060.00
50076.00	A19	M-016504-00	zinc finger and SCAN domain conta	201516.00
50076.00	A21	M-017859-00	STT3, subunit of the oligosaccharyl	201595.00
50076.00	A23	M-017812-00	dynein heavy chain domain 2	201625.00
50076.00	M09	M-023566-00	EPH receptor A6	203806.00
50077.00	A14	M-031764-00	ATP synthase, H+ transporting, mit	267020.00
50077.00	G07	M-018370-00	MPV17 mitochondrial membrane	255027.00
50077.00	K20	M-015725-00	placenta-specific 2	257000.00
50077.00	L20	M-018954-00	chromosome 14 open reading fran	283598.00
50077.00	O23	M-018350-00	chromosome 11 open reading fran	256329.00
50078.00	A11	M-031748-00	KIAA1267	284058.00
50078.00	A21	M-018227-00	hypothetical protein FLJ40504	284085.00
50078.00	B23	M-018007-00	immunoglobulin superfamily, mem	285313.00
50078.00	I06	M-032042-00	similar to FRG1 protein (FSHD regi	284802.00
50078.00	I10	M-018843-00	chromosome 20 open reading fran	284800.00
50078.00	I11	M-018209-00	transmembrane protein 145	284339.00
50078.00	I13	M-027232-00	DMC	284340.00
50078.00	I14	M-031339-00	hypothetical protein LOC284788	284788.00
50078.00	K21	M-018207-00	hypothetical protein FLJ40235	284369.00
50079.00	A09	M-007172-00	tripartite motif-containing 59	286827.00
50079.00	A16	M-007174-00	tripartite motif family-like 1	339976.00
50079.00	A21	M-021490-00	dehydrogenase/reductase (SDR fa	317749.00
50079.00	C10	M-017640-00	chromosome 3 open reading fram	339883.00
50079.00	C14	M-017970-00	kyphoscoliosis peptidase	339855.00
50079.00	C21	M-022600-00	snail homolog 3 (Drosophila)	333929.00
50079.00	I17	M-009140-00	potassium channel, subfamily K, m	338567.00
50079.00	J11	M-021693-00	FRAS1 related extracellular matrix	341640.00
50079.00	K19	M-030043-00	hypothetical protein LOC338758	338758.00
50079.00	L21	M-008085-00	syncollin	342898.00
50080.00	A09	M-019023-00	late cornified envelope 2A	353139.00
50080.00	A18	M-031733-00	potassium channel tetramerisatior	386618.00
50080.00	A21	M-009142-00	ligand-gated ion channel, zinc activ	353174.00
50080.00	A23	M-007374-00	solute carrier organic anion transp	353189.00
50080.00	C11	M-031742-00	chromosome 4 open reading fram	353289.00
50080.00	G15	M-019355-00	histone linker H1 domain, spermat	373861.00
50080.00	H04	M-032108-00	FLJ44874 protein	399990.00
50080.00	I13	M-032107-00	similar to RIKEN cDNA 1810059G2	374395.00
50080.00	I18	M-031840-00	chromosome 5 open reading fram	375484.00
50080.00	M06	M-031853-00	family with sequence similarity 39,	375260.00
50080.00	M19	M-027331-00	chromosome 19 open reading fran	374877.00
50080.00	O23	M-027341-00	chromosome 1 open reading fram	374946.00

ew	% inf	abs dev	robust Z	% inf	abs dev	robust Z	% inf
CHEK1	22.31	15.04	3.91	19.60	11.43	2.54	66.93
COPB2	29.52	22.25	5.78	20.61	12.44	2.77	31.51
CKMT1B	19.69	12.42	3.23	5.95	2.22	-0.49	24.97
AKAP1	15.37	8.10	2.11	5.36	2.81	-0.62	23.69
AKT1	15.20	7.93	2.06	18.40	10.23	2.28	11.20
PTPRJ	19.11	9.69	2.10	27.22	18.12	4.25	4.72
MAK	22.61	13.19	2.87	14.32	5.22	1.22	20.63
PKN3	32.26	22.84	4.96	37.50	28.40	6.66	5.68
OR2F1	14.22	7.00	1.73	18.35	10.15	2.16	40.56
ELAVL1	16.77	10.21	2.16	8.07	4.85	2.01	5.52
ITGAV	21.43	14.87	3.14	6.19	2.97	1.23	13.92
ING4	16.92	10.36	2.19	8.61	5.39	2.23	7.01
HES7	8.49	1.93	0.41	11.30	8.08	3.34	16.62
MEOX2	15.35	10.59	3.39	15.83	11.28	3.61	2.00
SP140	11.93	7.17	2.30	11.24	6.69	2.15	11.15
AMDHD2	7.59	4.78	2.37	7.22	5.05	2.94	3.99
AHCY	5.59	2.78	1.38	9.70	7.53	4.39	10.87
ENPP5	8.44	5.63	2.79	5.53	3.36	1.96	9.81
DMGDH	31.37	28.56	14.18	12.90	10.73	6.26	1.35
GATM	7.86	5.23	2.30	8.93	6.30	3.06	8.07
GNS	8.95	6.32	2.78	5.22	2.59	1.26	8.84
H2AFY	8.91	6.28	2.76	8.59	5.96	2.90	3.05
HGD	9.63	7.00	3.08	5.95	3.32	1.61	9.21
CASP10	9.27	4.43	1.13	9.09	5.65	2.15	17.15
LTF	10.36	6.61	2.21	6.91	4.42	2.18	6.67
LPA	3.51	1.13	-0.37	20.69	17.46	6.80	10.56
PDHX	10.08	5.44	1.80	8.37	5.14	2.00	13.43
RAB36	8.01	3.37	1.12	12.94	9.71	3.78	21.33
CD79B	16.45	11.81	3.90	11.74	8.51	3.32	13.33
GPI	14.19	9.55	3.16	12.37	9.14	3.56	16.76
FKBP1A	14.95	10.31	3.41	9.32	6.09	2.37	13.97
FAAH	12.31	7.67	2.53	9.75	6.52	2.54	11.58
CSTA	60.97	56.33	18.63	19.29	16.06	6.26	50.36
CXCL6	14.58	9.94	3.29	7.23	4.00	1.56	10.72
CFLAR	11.17	6.53	2.16	4.38	1.15	0.45	13.99
DUOX2	32.01	27.37	9.05	3.89	0.66	0.26	12.57
IGBP1	17.95	13.31	4.40	8.64	5.41	2.11	6.91
SPINT2	18.32	13.68	4.52	12.83	9.60	3.74	12.83
RGL1	5.18	0.54	0.18	17.35	14.12	5.50	15.56
SERPINA10	10.45	5.81	1.92	28.68	25.45	9.91	17.57
SERPINA5	3.11	1.53	-0.51	43.62	40.39	15.74	13.92
SERPINB5	2.56	2.08	-0.69	25.81	22.58	8.80	12.63
RAD51	12.70	7.75	2.58	4.22	0.15	0.05	21.47
TRIAD3	41.87	36.92	12.27	10.43	6.36	2.18	12.59
USP29	13.57	8.62	2.86	10.04	5.97	2.05	7.90

ANAPC4	12.06	7.11	2.36	8.06	3.99	1.37	14.31
KIF3C	11.29	6.34	2.10	10.18	6.11	2.10	6.74
MNAT1	13.80	8.85	2.94	19.26	15.19	5.21	15.63
PEX10	13.98	9.03	3.00	14.29	10.22	3.51	6.35
KIF2A	11.47	6.52	2.16	6.62	2.55	0.88	17.40
KIF12	15.85	10.90	3.62	16.07	12.00	4.12	26.96
KIF11	17.93	12.98	4.31	4.79	0.72	0.25	16.13
KDELR3	17.19	9.27	2.06	12.18	7.99	2.73	9.98
NSMAF	17.28	9.36	2.08	4.34	0.15	0.05	11.22
GRIK2	53.73	45.81	10.18	5.45	1.26	0.43	12.56
SCG3	60.68	52.76	11.73	19.15	14.96	5.10	4.75
CD300C	20.54	12.62	2.80	17.19	13.00	4.43	4.57
BCL10	2.58	1.25	-0.50	14.36	8.19	2.07	15.25
BMP8B	8.90	5.07	2.02	20.55	14.38	3.63	10.50
CD36	6.12	2.29	0.91	15.12	8.95	2.26	13.23
GNRH2	9.45	5.62	2.24	11.84	5.67	1.43	21.45
GHRL	10.42	6.59	2.63	7.73	1.56	0.39	14.21
KLRC4	19.58	15.75	6.28	14.41	8.24	2.08	9.10
KLRD1	14.37	10.54	4.20	3.19	2.98	-0.75	13.34
GDF1	7.47	3.64	1.45	23.04	16.87	4.26	19.76
CD180	10.97	7.14	2.85	11.77	5.60	1.41	15.33
LGALS1	9.07	5.24	2.09	15.66	9.49	2.39	19.62
CLEC2D	10.12	6.29	2.51	19.70	13.53	3.41	14.07
CCDC6	538.00	8.92	5.23	2.03	830.00	14.70	10.50
COL9A1	547.00	9.14	5.45	2.12	642.00	21.18	16.98
ESR1	1100.00	2.36	1.33	-0.52	2168.00	17.44	13.24
TNFRSF14	1678.00	2.98	0.71	-0.28	2012.00	13.62	9.42
TNFRSF1A	1368.00	3.80	0.11	0.04	1600.00	26.38	22.18
TNFRSF1B	828.00	7.25	3.56	1.38	1782.00	26.60	22.40
TNFRSF25	171.00	0.58	3.11	-1.21	250.00	35.20	31.00
NID1	2679.00	5.79	0.79	0.25	3826.00	16.49	6.87
NHP2L1	394.00	13.71	8.71	2.76	504.00	9.33	3.89
SLC11A2	3938.00	8.25	3.25	1.03	3496.00	10.58	4.41
FBN1	2917.00	12.10	7.10	2.25	3306.00	8.98	3.74
FAT2	2249.00	15.61	10.61	3.36	4257.00	9.56	3.98
CXCL5	3076.00	19.67	13.02	2.71	1694.00	7.44	3.23
CLN5	4082.00	22.17	15.52	3.23	2468.00	12.40	8.19
CLU	2276.00	24.96	18.31	3.81	1647.00	14.39	10.18
CD164	2010.00	4.88	1.77	-0.37	1749.00	12.41	8.20
HBD	1778.00	10.97	7.44	2.77	2132.00	8.68	5.15
GTF2H4	1312.00	10.67	7.14	2.66	1296.00	11.96	8.43
GFER	6155.00	16.65	13.12	4.89	1155.00	10.56	7.03
OLIG3	3133.00	13.18	7.86	2.43	1108.00	8.03	5.00
NUDC	2948.00	14.04	8.72	2.69	2978.00	5.74	2.71
PPAPDC1B	2534.00	16.10	10.78	3.33	2601.00	2.81	0.22
POU6F1	3124.00	6.02	0.70	0.22	3285.00	7.70	4.67
RPS29	174.00	41.38	36.69	11.80	132.00	8.33	6.54

SLIT1	1632.00	6.92	2.23	0.72	1067.00	7.69	5.90
XBP1	2137.00	12.17	7.48	2.40	1503.00	1.60	0.19
RB1CC1	938.00	12.79	8.10	2.61	840.00	2.02	0.23
ABCA3	1474.00	6.31	3.73	2.17	710.00	6.48	4.93
AP2A1	2034.00	1.67	0.91	-0.53	1612.00	5.71	4.16
COPA	64.00	12.50	9.92	5.77	67.00	5.97	4.42
C4BPA	3958.00	6.29	3.71	2.16	3270.00	5.38	3.83
DEFA1	2016.00	2.38	0.20	-0.11	1942.00	6.28	4.73
BTC	1901.00	8.52	5.94	3.46	2547.00	2.87	1.32
KLK1	2555.00	4.62	1.93	0.87	628.00	11.94	9.23
MAGEB1	3661.00	4.62	1.93	0.87	2400.00	7.92	5.21
GPX4	316.00	23.10	20.41	9.21	254.00	18.11	15.40
LY9	2411.00	8.38	5.69	2.57	13.00	76.92	74.21
LAMA5	717.00	9.34	6.65	3.00	308.00	18.51	15.80
LAMP1	1195.00	8.12	5.43	2.45	485.00	9.48	6.77
PMS2L1	1357.00	6.93	4.55	2.63	939.00	6.82	4.29
MYO1E	2344.00	7.59	5.21	3.01	1789.00	1.57	0.96
ACSL6	2000.00	7.40	5.02	2.90	1590.00	13.27	10.74
ADPGK	2796.00	6.37	3.99	2.30	3198.00	7.60	5.07
ACAD9	2183.00	2.57	0.19	0.11	2311.00	6.97	4.44
ALG8	2984.00	3.62	1.24	0.71	4040.00	7.85	5.32
ACBD3	1489.00	10.01	7.63	4.41	737.00	8.68	6.15
NSF	2098.00	8.20	5.82	3.36	2747.00	1.09	1.44
MT1F	2495.00	18.84	16.46	9.51	1273.00	3.46	0.93
AIM1L	3218.00	3.42	1.04	0.60	3813.00	7.58	5.05
ALLC	1859.00	15.12	12.74	7.36	2182.00	13.66	11.13
SDCBP	1960.00	5.26	3.90	3.07	2206.00	6.39	4.87
SBF1	1785.00	1.57	0.21	0.17	2722.00	4.70	3.18
TARS	882.00	0.45	0.91	-0.71	2014.00	4.32	2.80
SLC1A3	540.00	2.41	1.05	0.83	1101.00	5.27	3.75
SYPL1	772.00	1.55	0.19	0.15	1801.00	5.55	4.03
PSMC4	325.00	1.85	0.49	0.38	120.00	5.00	3.48
PSMC5	379.00	0.53	0.83	-0.66	425.00	5.65	4.13
RRBP1	1323.00	0.30	1.06	-0.83	1744.00	4.87	3.35
PSMD1	153.00	1.96	0.60	0.47	194.00	8.25	6.73
RPS27A	274.00	4.01	2.65	2.09	360.00	5.83	4.31
PSMD3	466.00	2.15	0.79	0.62	461.00	8.24	6.72
	453.00	0.22	1.14	-0.90	304.00	5.26	3.74
	2163.00	2.36	1.00	0.79	1595.00	5.27	3.75
	1422.00	5.49	4.13	3.25	1977.00	14.32	12.80
	1516.00	0.20	1.16	-0.92	1206.00	4.89	3.37
	1488.00	4.10	2.74	2.16	2118.00	4.25	2.73
	2560.00	6.76	5.40	4.26	1971.00	4.11	2.59
	1804.00	9.15	7.79	6.14	2491.00	8.71	7.19
	1283.00	3.98	2.62	2.06	1129.00	5.67	4.15
	1554.00	4.38	3.02	2.38	924.00	7.47	5.95
TSPAN4	606.00	12.38	8.79	4.99	865.00	9.71	6.91

TMOD1	4946.00	8.63	5.04	2.86	4065.00	4.82	2.02
NAPA	381.00	10.24	6.65	3.77	627.00	22.97	20.17
TSPYL1	759.00	8.83	5.24	2.97	1017.00	8.65	5.85
TUFT1	2383.00	7.39	3.80	2.15	2186.00	5.76	2.96
ZNF16	1005.00	7.76	4.17	2.37	347.00	12.68	9.88
PLOD3	1209.00	2.98	0.34	0.21	891.00	8.19	4.98
PPT2	1448.00	4.01	1.37	0.83	1371.00	8.83	5.62
ZNF592	1326.00	9.58	6.94	4.24	1034.00	7.54	4.33
SLC16A3	657.00	5.94	3.30	2.02	731.00	4.65	1.44
EFTUD2	986.00	5.17	2.53	1.55	635.00	8.03	4.82
DOCK4	1130.00	5.31	2.67	1.63	671.00	18.03	14.82
VPRBP	1322.00	3.03	0.39	0.24	1349.00	11.27	8.06
ZBTB22	2702.00	5.40	2.76	1.69	2195.00	8.75	5.54
USP6NL	367.00	28.61	25.97	15.89	524.00	9.54	6.33
ARHGAP11A	764.00	8.51	6.47	4.17	1059.00	1.13	0.76
CTDSPL	2857.00	6.90	4.86	3.13	1897.00	6.80	4.91
DNAJC6	403.00	10.42	8.38	5.40	1035.00	5.12	3.23
KIAA0125	687.00	2.91	0.87	0.56	479.00	5.64	3.75
INADL	4014.00	8.74	6.70	4.32	1907.00	6.66	4.77
PLEKHM1	3436.00	5.21	3.17	2.04	2714.00	6.26	4.37
EPM2AIP1	1985.00	8.16	6.12	3.95	1346.00	4.46	2.57
SLMO1	3382.00	6.68	4.64	2.99	2556.00	5.79	3.90
ATP5L	3339.00	7.01	4.97	3.20	2426.00	1.36	0.53
PSMD6	224.00	5.36	3.32	2.14	131.00	17.56	15.67
TGOLN2	632.00	3.48	1.44	0.93	564.00	14.89	13.00
SNAPC5	1374.00	1.24	0.80	-0.52	367.00	11.72	9.83
SFRS14	2005.00	8.23	6.19	3.99	2067.00	4.45	2.56
TBC1D4	2671.00	1.98	0.06	-0.03	2880.00	6.91	5.02
RBM8A	505.00	8.32	6.28	4.05	414.00	8.21	6.32
TOMM40	955.00	7.64	5.60	3.61	2219.00	5.68	3.79
NXF1	521.00	16.70	14.66	9.45	212.00	22.64	20.75
PCID1	479.00	6.89	4.85	3.13	469.00	8.32	6.43
SLC25A17	310.00	15.16	13.12	8.46	396.00	7.32	5.43
SPAG11B	2977.00	6.79	4.75	3.06	1495.00	6.09	4.20
COG5	2175.00	1.75	0.29	-0.19	1124.00	5.16	3.27
PRSS23	2189.00	6.85	3.77	2.16	2848.00	3.37	0.46
AP4B1	1388.00	7.49	4.41	2.52	1776.00	4.22	1.31
CHL1	4439.00	9.55	6.47	3.70	3394.00	4.66	1.75
LILRB3	3569.00	5.69	2.61	1.49	2704.00	9.17	6.26
PROSC	2697.00	7.08	4.00	2.29	1047.00	10.51	7.60
PRAF2	2340.00	4.40	1.32	0.75	1045.00	7.75	4.84
KIAA1009	4016.00	7.59	4.51	2.58	4123.00	10.94	8.03
COPZ1	486.00	10.29	7.21	4.12	290.00	10.00	7.09
COG2	3188.00	6.65	3.57	2.04	2676.00	4.56	1.65
DDX42	2142.00	5.04	1.96	1.12	1843.00	8.68	5.77
POFUT1	2866.00	6.91	4.46	3.24	3079.00	7.11	1.59
DMXL2	3437.00	6.75	4.30	3.12	2498.00	3.76	1.76

COTL1	1411.00	9.07	6.62	4.80	804.00	5.60	0.08
ZZEF1	3131.00	5.24	2.79	2.02	2421.00	0.70	4.82
TTC28	2364.00	7.53	5.08	3.69	2445.00	2.82	2.70
SIGLEC7	2483.00	7.17	2.65	0.87	1642.00	8.34	5.83
TRAPPC3	1533.00	11.81	7.29	2.38	1435.00	6.97	4.46
PRELID1	3433.00	12.21	7.69	2.51	2022.00	2.28	0.24
###############	1601.00	1.87	2.65	-0.87	2819.00	7.73	5.22
ZNF639	1877.00	12.52	7.53	2.54	1184.00	7.26	5.30
SS18L2	881.00	15.10	10.11	3.41	801.00	13.36	11.40
IFT52	4253.00	11.95	6.96	2.35	2121.00	3.35	1.39
AMZ2	4370.00	11.88	6.89	2.33	1965.00	1.12	0.84
IL17D	2297.00	14.80	9.77	2.09	2534.00	14.88	12.45
ATPBD1B	2545.00	14.62	9.59	2.05	1512.00	8.47	6.04
C21orf41	2448.00	14.95	9.92	2.12	1992.00	7.73	5.30
BCOR	351.00	9.97	6.66	2.12	348.00	8.05	4.65
TEX10	817.00	8.08	4.77	1.52	1452.00	17.42	14.02
TMEM70	4044.00	11.85	8.54	2.71	2967.00	8.09	4.69
FLJ20581	2120.00	10.09	6.78	2.16	1888.00	9.16	5.76
NUDT11	880.00	9.20	5.89	1.87	503.00	18.09	14.69
NADSYN1	2939.00	5.61	2.30	0.73	1676.00	14.80	11.40
IPO9	588.00	19.56	10.07	2.13	744.00	20.97	9.53
LARP6	468.00	40.17	30.69	6.49	420.00	24.05	12.61
FLJ10357	402.00	24.88	15.39	3.25	520.00	28.65	17.22
C4orf20	533.00	23.27	13.78	2.91	835.00	21.20	9.76
LIN7C	611.00	26.19	16.70	3.53	1094.00	23.04	11.60
PCDHGC4	2901.00	19.17	9.68	2.05	1797.00	25.54	14.11
SLC35E3	786.00	24.43	14.94	3.16	2182.00	25.30	13.86
SMPD4	323.00	36.22	26.74	5.65	1840.00	25.27	13.84
ZDHHC7	272.00	36.03	26.54	5.61	2040.00	23.33	11.90
ELAC1	320.00	27.19	17.70	3.74	1693.00	27.23	15.79
TRIM36	625.00	36.00	26.51	5.60	1530.00	23.14	11.70
THUMPD1	168.00	36.91	27.42	5.80	812.00	27.83	16.40
TTC27	418.00	37.80	28.31	5.98	2124.00	25.14	13.71
TRMT1	1063.00	19.10	9.61	2.03	3162.00	26.34	14.91
DDX28	2001.00	19.69	10.20	2.16	2188.00	23.45	12.01
MBNL3	556.00	28.06	18.57	3.93	622.00	32.48	21.04
METTL2B	1064.00	29.32	19.84	4.19	828.00	27.17	15.74
CACNA2D3	1492.00	21.38	11.90	2.51	1852.00	20.79	9.35
ZNF302	450.00	23.11	13.63	2.88	1212.00	21.29	9.85
TEX13A	876.00	23.74	13.43	2.73	1071.00	18.86	8.67
TBX20	1892.00	22.52	12.20	2.48	1298.00	22.34	12.15
TEX12	2703.00	23.31	12.99	2.65	1822.00	27.39	17.19
PLSCR2	749.00	26.04	15.72	3.20	1027.00	22.01	11.81
BBX	2270.00	18.72	8.40	1.71	1618.00	20.83	10.64
KIAA1219	4592.00	21.34	11.02	2.24	2761.00	23.43	13.24
KCNK12	2669.00	20.38	10.06	2.05	2241.00	23.43	13.23
MUC13	1763.00	21.04	10.73	2.18	2777.00	16.24	6.05

C11orf75	2142.00	30.72	20.40	4.15	2997.00	25.23	15.03
C11orf16	1052.00	32.41	22.10	4.50	901.00	27.86	17.67
CA10	1712.00	32.54	22.22	4.52	2676.00	21.56	11.37
TMEM9B	1050.00	31.62	21.30	4.34	1798.00	19.47	9.27
ASCL3	1474.00	30.26	19.94	4.06	2526.00	19.56	9.36
SPPL2B	2285.00	23.81	13.49	2.75	4269.00	12.81	2.62
CNOT6	4165.00	16.09	5.77	1.17	2911.00	26.42	16.22
C20orf74	3949.00	24.18	13.87	2.82	2806.00	26.52	16.32
HHATL	4240.00	20.09	9.78	1.99	3611.00	20.99	10.80
TBC1D24	2143.00	23.57	13.25	2.70	1897.00	23.30	13.11
PRSS22	3002.00	26.35	16.91	3.45	4360.00	12.48	2.52
SEMA4G	844.00	34.36	24.92	5.09	1654.00	20.74	10.78
ZBTB2	683.00	25.62	16.19	3.30	1689.00	16.05	6.08
KIAA1486	224.00	48.66	39.22	8.00	436.00	20.41	10.45
SLC7A14	694.00	19.60	10.16	2.07	3494.00	14.11	4.15
KIAA1604	276.00	32.25	22.81	4.65	347.00	31.12	21.16
MRPS14	4124.00	28.37	18.93	3.86	4100.00	20.49	10.53
TRMT11	3576.00	21.76	12.32	2.51	4372.00	14.43	4.47
C20orf51	4203.00	29.53	20.09	4.10	3352.00	21.69	11.73
LOC63928	3492.00	19.53	10.09	2.06	5036.00	17.75	7.79
PPCDC	2463.00	20.30	10.86	2.22	3550.00	16.37	6.41
NIF3L1	2422.00	24.07	14.63	2.99	4148.00	16.32	6.36
CIDEC	3538.00	20.04	10.60	2.16	3699.00	13.90	3.94
FAM113A	2659.00	20.23	9.66	2.19	1777.00	15.93	4.28
FASTKD3	3372.00	24.05	13.48	3.05	3173.00	26.35	14.70
C20orf116	4071.00	26.97	16.40	3.71	5622.00	21.93	10.29
ELOVL6	2654.00	20.61	10.04	2.27	4225.00	23.31	11.67
MRPS34	3013.00	23.33	12.76	2.89	4056.00	17.06	5.42
MGC2752	2845.00	22.32	11.75	2.66	2858.00	22.39	10.75
LRRC61	1078.00	29.13	18.56	4.20	1319.00	22.82	11.18
METT10D	2366.00	19.02	8.45	1.91	2471.00	20.88	9.24
TMEM108	1527.00	24.69	14.12	3.20	2174.00	17.16	5.51
ATG9A	2022.00	26.11	15.54	3.52	5052.00	30.48	18.84
C14orf139	2036.00	11.00	0.52	0.12	1876.00	19.56	9.85
SETD6	4157.00	19.75	9.27	2.06	3478.00	16.79	7.07
MAGIX	2860.00	23.88	13.40	2.98	2357.00	13.66	3.94
SGK269	4515.00	22.99	12.51	2.79	3744.00	15.04	5.32
ATAD5	4338.00	20.70	10.22	2.28	2216.00	21.48	11.76
LONRF3	2849.00	21.41	10.93	2.43	1595.00	26.40	16.68
FLJ22028	4175.00	23.88	13.40	2.98	3428.00	17.18	7.46
BTNL8	4552.00	20.56	10.08	2.24	2710.00	23.36	13.64
FLJ14154	1656.00	21.32	10.84	2.41	1245.00	20.24	10.52
ZDHHC11	1805.00	21.88	11.41	2.54	882.00	25.17	15.45
C12orf31	4752.00	35.82	16.98	2.44	4242.00	30.17	14.49
YPEL3	4652.00	27.06	8.22	1.18	3565.00	30.21	14.53
C6orf141	3904.00	23.03	11.42	2.28	3734.00	14.25	4.44
NFXL1	5310.00	30.53	15.93	2.92	4097.00	34.76	23.04

C3orf30	4373.00	27.19	12.59	2.31	5142.00	26.29	14.57
ZNF600	2366.00	21.43	9.67	2.02	4699.00	12.09	2.60
SLC39A12	1227.00	12.71	8.18	2.21	795.00	25.41	19.16
ZNF584	645.00	12.09	7.56	2.04	453.00	20.75	14.50
C10orf111	892.00	13.68	9.15	2.47	286.00	24.13	17.88
ZSCAN4	609.00	13.47	8.94	2.41	566.00	20.85	14.60
STT3B	935.00	7.59	3.06	0.83	609.00	21.51	15.26
DNHD2	726.00	9.78	5.25	1.42	611.00	27.82	21.57
EPHA6	1229.00	19.45	14.92	4.03	1984.00	14.32	8.07
ATP5L2	410.00	22.93	12.79	2.74	299.00	31.77	24.67
MPV17L	576.00	13.02	2.88	0.62	231.00	40.69	33.59
PLAC2	3396.00	20.67	10.53	2.26	1470.00	26.74	19.64
C14orf177	1588.00	29.03	18.89	4.05	722.00	6.23	0.87
C11orf35	1030.00	22.14	12.00	2.57	523.00	8.03	0.93
KIAA1267	367.00	20.71	16.27	4.98	412.00	8.98	2.53
FLJ40504	210.00	14.29	9.85	3.01	319.00	18.18	11.73
IGSF10	385.00	16.62	12.18	3.73	393.00	13.49	7.04
MGC72104	276.00	9.42	4.98	1.52	262.00	25.95	19.50
C20orf91	645.00	19.07	14.63	4.48	262.00	18.32	11.87
TMEM145	868.00	12.44	8.00	2.45	648.00	14.51	8.06
UNQ473	894.00	14.21	9.77	2.99	1002.00	10.08	3.63
LOC284788	1821.00	11.64	7.20	2.20	1252.00	10.46	4.01
FLJ40235	801.00	6.99	2.55	0.78	890.00	23.26	16.81
TRIM59	622.00	4.50	1.35	-0.40	385.00	17.14	9.59
TRIML1	303.00	15.84	9.99	2.96	347.00	27.09	19.54
DHRS4L2	248.00	22.18	16.33	4.84	391.00	17.14	9.59
C3orf35	2111.00	14.83	8.98	2.66	786.00	17.94	10.39
KY	1350.00	20.22	14.37	4.26	1014.00	22.88	15.33
SNAI3	845.00	12.78	6.93	2.05	614.00	21.34	13.79
KCNK18	2971.00	13.06	7.21	2.14	1104.00	6.70	0.85
FREM2	1522.00	7.03	1.18	0.35	1354.00	20.68	13.13
LOC338758	2216.00	10.83	4.98	1.48	1806.00	20.43	12.88
SYCN	1653.00	14.22	8.37	2.48	1872.00	22.49	14.94
LCE2A	372.00	12.90	7.17	2.17	222.00	30.18	26.47
KCTD4	699.00	14.02	8.29	2.51	470.00	16.38	12.67
LGICZ1	549.00	15.48	9.75	2.95	453.00	16.34	12.63
SLCO4C1	150.00	28.00	22.27	6.74	462.00	3.46	0.25
C4orf11	666.00	12.76	7.03	2.13	860.00	12.79	9.08
HILS1	1725.00	1.10	4.63	-1.40	1755.00	12.25	8.54
FLJ44874	347.00	21.61	15.88	4.81	360.00	5.56	1.85
LOC374395	1931.00	9.53	3.80	1.15	369.00	23.58	19.87
C5orf25	1210.00	7.85	2.12	0.64	810.00	18.77	15.06
FAM39B	2478.00	12.59	6.86	2.08	1443.00	0.90	2.81
C19orf45	1185.00	18.73	13.00	3.94	875.00	7.09	3.38
C1orf187	309.00	11.65	5.92	1.79	714.00	14.99	11.28

0.02
1.63
Roughly 1.6% of genes

abs dev	**robust Z**	
55.76	11.46	toxic a,b,c
20.34	4.18	toxic a,b,c
13.80	2.83	toxic a,b,c
12.52	2.57	toxic a,b
0.03	0.01	toxic a,b,c
4.81	-0.88	debris a,c
11.10	2.02	art b,c
3.85	-0.70	toxic a,b,c
30.09	5.48	toxic a,b,c
0.74	0.22	debris b
9.14	2.74	toxic a,b,c
2.23	0.67	debris b,c
11.84	3.55	b artifact
2.87	-0.75	toxic a,b,c
6.28	1.64	toxic a,b,c
1.31	0.70	toxic a,c
8.19	4.37	toxic a, artifact b
7.13	3.81	artifact a
1.33	-0.71	toxic a,b,c
4.48	1.74	toxic b,c
5.25	2.04	art a,b,c
0.54	-0.21	art. b,c
5.62	2.18	toxic b,c
13.74	5.08	art.b
3.11	1.26	txc a,b,c
6.48	2.21	toxic a,b,c
9.35	3.19	toxic a,b,c
17.25	5.89	toxic a,b,c
9.25	3.16	toxic a,b,c
12.68	4.33	toxic a,b,c
9.89	3.38	toxic a,b,c
7.50	2.56	toxic a,b,c
46.28	15.80	toxic a,b,c
6.64	2.27	toxic a
9.91	3.38	toxic a
8.49	2.90	toxic a,b
2.83	0.97	toxic a
8.75	2.99	toxic a,b
11.48	3.92	toxic a,b
13.49	4.60	toxic a,b
9.84	3.36	toxic a,b
8.55	2.92	toxic a,b
15.56	4.50	toxic a,b
6.68	1.96	debris b,c
1.99	0.62	debris b,c

8.40	2.45	toxic b,c			
0.83	0.29	toxic a,c			
9.72	2.83	toxic a,b			
0.44	0.18	toxic a,b			
11.49	3.34	toxic a,b,c			
21.05	6.07	toxic a,b,c			
10.22	2.97	toxic a,b,c			
6.14	2.21	toxic a,b,c			
7.38	2.65	art b,c			
8.72	3.13	toxic a			
0.91	0.33	toxic a,b,c			
0.73	0.26	toxic a,b,c			
9.45	2.69	toxic a,b			
4.70	1.34	toxic a,b,c			
7.43	2.12	toxic a,b			
15.65	4.45	toxic a,b			
8.41	2.39	debris B,c			
3.30	0.94	toxic a,b			
7.54	2.15	art a,b			
13.96	3.97	toxic a,b,c			
9.53	2.71	toxic a,b,c			
13.82	3.93	toxic a,b,c			
8.27	2.36	toxic a,b,c			
3.36	1729.00	0.95	0.36	x	toxic a,b,c
5.43	1148.00	4.20	1.57	x	toxic a,b
4.23	2117.00	8.01	2.99	x	tox a,art b,c
3.01	2955.00	5.60	2.09	x	toxic a,b
7.09	2348.00	8.57	3.20	x	toxic b,c
7.16	1297.00	22.83	8.52	x	toxic a,b
9.91	360.00	11.48	4.28	x	toxic a,b
5.50	3669.00	7.80	2.21	x	art. A,c
2.40	591.00	7.10	2.01	x	toxic a,b,c
2.95	5064.00	10.50	2.98	debris b,c	
2.26	3182.00	5.83	1.65	x	debris b,c
2.51	2267.00	4.81	1.36	x	debris b,c
1.01	2649.00	3.79	2.08	x	art b,c
2.57	2326.00	3.56	1.96	x	art a,c
3.19	1721.00	3.02	1.66	x	toxic b,c
2.57	2026.00	4.93	2.71	x	art a,c, tox b
2.01	1173.00	0.67	-0.24	x	tox a,c
3.29	1269.00	6.33	2.30	x	toxic a,b,c
2.74	1415.00	2.15	-0.78	x	toxic b,c
2.35	2200.00	0.38	-0.16	x	toxic b
1.28	3702.00	9.49	4.01	x	debris a,c
-0.10	2785.00	9.71	4.10	x	debris b,c
2.20	5310.00	5.28	2.23	x	debris a,b
4.36	99.00	9.27	4.90	x	toxic a,b,c

3.93	1896.00	4.96	2.62	x	toxic,b,c
-0.13	2547.00	3.94	2.08	x	debris b,c
0.16	1565.00	4.31	2.28	x	tox a,b,c
3.46	665.00	7.87	3.75	x	toxic a,b,c
2.92	1578.00	7.16	3.41	x	toxic b,c
3.10	43.00	6.64	3.16	x	toxic a,b,c
2.69	2579.00	2.34	1.11	x	debris a,b
3.32	1542.00	5.06	2.41	x	toxic b,c
0.92	747.00	7.51	3.58	x	toxic a,b,c
4.28	1590.00	10.35	3.96	x	toxic b,c
2.41	3399.00	7.42	2.84	x	debris a,b
7.14	621.00	1.56	0.60	x	toxic a,b,c
34.39	2101.00	1.46	0.56	x	toxic b
7.32	934.00	2.36	-0.90	x	toxic a,b,c
3.14	870.00	2.42	-0.93	x	toxic a,b,c
2.09	1251.00	0.24	0.15	x	toxic a,b,c
-0.47	2898.00	6.47	3.94	x	debris a,b
5.24	1573.00	2.04	1.24	x	toxic b,c,
2.47	2176.00	2.30	1.40	x	art a,c
2.16	1066.00	3.66	2.23	x	debris a,tox c
2.59	2594.00	3.47	2.12	x	debris a,c
3.00	907.00	2.47	1.51	x	toxic a,b,c
-0.70	1803.00	3.72	2.27	x	toxic a,b
0.45	1706.00	5.05	3.08	x	toxic b,c,
2.46	4399.00	5.50	3.35	x	debris a,b
5.42	1814.00	4.18	2.55	x	toxic a,c
3.74	2748.00	6.75	3.38	x	toxic a, art b
2.44	2181.00	10.20	5.12	x	debris a,c
2.15	1084.00	5.25	2.63	x	toxic a, c
2.88	1067.00	7.99	4.01	x	toxic a, b c
3.10	1435.00	4.84	2.43	x	toxic a,b,c
2.67	233.00	7.31	3.67	x	toxic a,b,c
3.17	497.00	6.12	3.07	x	toxic a,b,c
2.58	1848.00	6.37	3.19	x	toxic a,b,c
5.17	113.00	18.22	9.14	x	toxic a,b,c
3.31	411.00	12.23	6.13	x	toxic a,b,c
5.16	454.00	7.78	3.90	x	toxic a,b,c
2.87	336.00	6.50	3.26	x	toxic a,b,c
2.88	1230.00	7.22	3.62	x	toxic a,b,c
9.83	1389.00	5.21	2.61	x	toxic a,b,c
2.59	2077.00	4.80	2.41	x	toxic a,b
2.10	2259.00	0.71	-0.36	x	debris a
1.99	1995.00	4.04	2.02	x	tox b,c
5.52	2493.00	4.85	2.43	x	tox a, debris b,c
3.19	1771.00	0.72	-0.36	x	toxic a,b,c
4.57	3093.00	0.84	0.42	x	toxic a,b
4.43	739.00	1.10	0.62	x	toxic a,b,c

1.30	4134.00	6.54	3.68	x	art a,b
12.93	568.00	10.45	5.87	x	toxic a,b,c
3.75	824.00	2.06	1.16	x	toxic a,b,c
1.90	1599.00	8.49	4.77	x	toxic a,b
6.33	362.00	6.58	3.70	x	toxic a,b,c
2.83	688.00	6.70	2.98	x	toxic a,b,c
3.18	988.00	9.51	4.23	x	toxic a,b,c
2.46	832.00	10.42	4.64	x	toxic a,b,c
0.82	522.00	6.16	2.74	x	toxic a,b,c
2.73	734.00	11.81	5.25	x	toxic a,b,c
8.40	765.00	4.54	2.02	x	toxic a,b,c
4.57	846.00	8.78	3.91	x	toxic a,b,c
3.14	2933.00	4.56	2.03	x	debris a,b
3.59	235.00	8.02	3.57	x	toxic a,b,c
-0.49	1172.00	4.45	2.72	x	toxic a,b,c
3.17	2614.00	2.21	1.35	x	debris a,b
2.09	583.00	7.15	4.36	x	toxic a,b,c
2.42	437.00	6.01	3.67	x	toxic a,b,c
3.08	2173.00	0.62	-0.38	x	debris a
2.83	3403.00	1.68	1.03	x	debris a
1.66	1423.00	8.57	5.23	x	toxic a,b,c
2.52	3677.00	2.68	1.64	x	debris a
-0.34	2823.00	5.72	3.49	x	debris a
10.13	91.00	0.84	0.51	x	toxic a,b,c
8.40	253.00	4.65	2.84	x	toxic a,b,c
6.35	653.00	7.95	4.86	x	toxic a,b,c
1.65	1476.00	3.43	2.10	x	toxic c
3.24	2591.00	3.60	2.20	x	debris a,b
4.09	495.00	1.18	0.72	x	toxic a,b,c
2.45	2316.00	4.62	2.82	x	toxic a, art b,c
13.41	245.00	12.23	7.47	x	toxic a,b,c
4.15	808.00	0.02	0.01	x	toxic a,b,c
3.51	835.00	2.33	1.42	x	toxic a,b,c
2.71	3294.00	3.10	1.89	x	toxic b
2.11	1348.00	3.33	2.03	x	toxic b,c
0.24	3108.00	3.92	2.92	x	debris a,b
0.69	2068.00	4.77	3.55	x	toxic a,b
0.92	4863.00	2.91	2.17	x	art a,b
3.29	2723.00	2.70	2.01	debris a,b	
3.99	1678.00	0.62	-0.47	x	toxic b,c
2.54	1148.00	6.33	4.72	x	toxic b,c
4.22	4087.00	2.65	1.97	x	debris a,b
3.72	404.00	0.19	0.14	x	toxic a,b,c
0.87	2234.00	3.17	2.36	x	debris a,b
3.03	2179.00	10.19	7.59	x	toxic b
0.96	2494.00	5.98	3.69	x	debris a,b
0.35	4331.00	10.20	6.30	x	debris a

0.69	1297.00	6.58	4.06	x	toxic a,b,c
-0.21	2716.00	6.76	4.17	debris a.b	
0.18	2907.00	3.60	2.22	x	debris a,b
3.12	1599.00	6.82	2.86	x	art b
2.39	562.00	0.85	-0.36	x	debris b
-0.13	2045.00	4.87	2.04	x	debris b,c
2.79	2565.00	5.61	2.35	x	debris a,b
3.31	1413.00	5.38	1.50	x	debris a,b
7.12	1652.00	4.71	1.31	x	debris a,b
0.87	2496.00	15.64	4.35	x	debris a
-0.52	4413.00	16.72	4.65	x	debris a
5.56	2782.00	10.24	1.72	x	debris a,b
2.69	1942.00	3.35	-0.56	x	toxic b,c
2.37	997.00	3.49	-0.59	x	toxic b,c
1.67	467.00	5.14	3.09	x	toxic a,b,c
5.03	2354.00	4.87	2.92	x	toxic b
1.68	2906.00	3.95	2.37	x	debris a,b
2.07	2015.00	3.91	2.35	x	debris a,b
5.27	1572.00	8.42	5.05	x	toxic b,c
4.09	3194.00	9.16	5.50	x	toxic b
2.09	1964.00	20.06	0.79	x	toxic a,b,c
2.76	1220.00	21.84	0.57	x	toxic a,b,c
3.77	1056.00	16.43	0.41	x	toxic a,b,c
2.14	1143.00	13.22	0.70	x	toxic a,b,c
2.54	1086.00	12.29	0.79	x	toxic a,b,c
3.09	2968.00	12.47	0.22	X	toxic b
3.03	1550.00	26.97	1.31	x	toxic a,c
3.03	2015.00	20.70	0.84	x	toxic a,b
2.60	3197.00	18.80	0.70	x	toxic a
3.46	1660.00	20.90	0.85	x	toxic a,b,c
2.56	1475.00	28.88	1.45	x	toxic a,b,c
3.59	520.00	25.58	1.20	x	toxic a,b,c
3.00	1382.00	27.42	1.34	x	toxic a,c
3.26	1543.00	15.04	0.42	x	toxic a,c
2.63	1556.00	19.60	0.76	X	toxic a,c
4.60	549.00	30.24	1.55	x	toxic a,b,c
3.44	816.00	28.31	1.41	x	toxic a,b,c
2.05	2355.00	18.85	0.70	x	toxic a,b
2.16	969.00	20.74	0.84	x	toxic a,b
1.70	1692.00	12.00	3.02	x	toxic a,b,c
2.39	1862.00	5.32	1.34	x	toxic a,b,c
3.38	2532.00	16.37	4.12	X	toxic b, art a,b
2.32	648.00	1.90	0.48	x	toxic a,b,c
2.09	2558.00	9.55	2.40	X	toxic b
2.60	3109.00	4.73	1.19	x	debris a
2.60	3375.00	1.30	0.33	X	debris a,c
1.19	2822.00	9.08	2.28	X	toxic a

2.95	2594.00	10.03	2.52	X	debris b,c
3.47	1203.00	18.19	4.58	x	toxic a,b,c
2.23	2564.00	13.44	3.38	X	toxic a,debris c,a
1.82	1842.00	11.12	2.80	x	debris a,b,tox c
1.84	2646.00	10.98	2.76	X	toxic a
0.51	3663.00	12.46	3.14	X	debris c
3.19	1668.00	14.03	3.53	X	debris c
3.21	2263.00	13.83	3.48	X	debris c
2.12	1506.00	14.89	3.75	X	toxic c
2.57	1305.00	14.01	3.53	X	toxic b,c
0.59	4361.00	11.45	2.23	x	art a
2.51	2004.00	9.47	1.85	x	toxic a,b
1.42	2000.00	15.11	2.95	x	toxic a,b
2.43	1467.00	6.16	1.20	x	toxic a,b,c
0.97	4367.00	10.91	2.13	x	toxic a
4.93	786.00	7.64	1.49	x	toxic a,b,c
2.45	4989.00	9.05	1.77	X	debris a,b
1.04	3991.00	11.59	2.26	X	debris a,c
2.73	4053.00	15.26	2.98	X	debris a,c
1.81	3153.00	12.73	2.49	X	debris a,c
1.49	2461.00	11.87	2.32	X	debris a,c
1.48	3091.00	12.37	2.42	X	debris a,c
0.92	3287.00	17.38	3.39	X	debris a,c
0.98	2335.00	11.78	2.47	X	debris a,b
3.35	4646.00	8.87	1.86	X	debris a,b
2.34	4989.00	8.72	1.82	X	debris a,b
2.66	3738.00	12.81	2.68	X	debris a,b
1.23	4313.00	12.57	2.63		debris a,b
2.45	3702.00	12.05	2.52	X	debris a,b
2.55	1236.00	17.73	3.71	x	toxic a,b,c
2.11	2419.00	13.09	2.74		debris a,b
1.26	2159.00	14.11	2.95	X	toxic a
4.29	2561.00	16.57	3.47	X	debris a,b
2.48	1463.00	9.07	2.19	x	toxic b,c
1.78	3232.00	11.96	2.89	X	debris a,c
0.99	2879.00	13.17	3.18	x	debris a,c
1.34	3039.00	15.18	3.67	x	debris a,c
2.96	2608.00	8.19	1.98	X	debris a,c
4.20	2836.00	6.29	1.52	x	toxic b
1.88	3198.00	10.10	2.44	X	debris a,c
3.43	4257.00	6.28	1.52	X	debris a,c
2.65	2081.00	1.65	0.40	x	toxic ab
3.89	1095.00	1.26	0.30	x	toxic a,b,c
2.23	2861.00	9.86	1.84	x	debris a,b
2.24	5321.00	15.64	2.92	x	debris b
0.94	3102.00	12.04	2.01	x	debris a
4.42	4418.00	0.46	0.10	x	debris a

2.80	3298.00	4.31	-0.92	x	debris a
0.62	3187.00	10.00	2.03	x	debris c
4.84	1214.00	0.63	-0.17	x	toxic a,b,c
3.66	729.00	6.48	1.71	x	toxic a,b,c
4.52	655.00	1.12	-0.30	x	toxic a,b,c
3.69	711.00	3.73	0.99	x	toxic a,b,c
3.85	516.00	11.03	2.92	x	toxic a,b,c
5.45	634.00	10.44	2.77	x	toxic a,b,c
2.04	875.00	6.22	1.65	x	toxic a,b,c
4.40	431.00	3.05	-0.60	x	toxic a,b,c
5.99	200.00	18.31	3.62	x	toxic a,b,c
3.50	1598.00	9.46	1.87	x	toxic b,c
-0.15	782.00	20.83	4.12	x	toxic a,b,c
0.17	300.00	14.64	2.90	x	toxic a,b,c
0.57	332.00	12.79	3.56	x	toxic a,b,c
2.65	339.00	1.19	0.33	x	toxic a,b,c
1.59	569.00	10.81	3.01	x	toxic a,b,c
4.41	303.00	9.95	2.77	x	toxic a,b,c
2.68	230.00	17.15	4.77	x	toxic a,b,c
1.82	385.00	12.03	3.35	x	toxic a,b,c
0.82	805.00	7.53	2.09	x	toxic a,b,c
0.91	1996.00	14.75	4.10	x	toxic a,b,c
3.80	904.00	7.38	2.05	x	toxic a,b,c
2.18	449.00	8.75	2.11	x	toxic a,b,c
4.44	295.00	2.19	0.53	x	toxic a,b,c
2.18	489.00	0.69	-0.17	x	toxic a,b,c
2.36	1303.00	3.74	0.90	x	toxic b,c
3.48	1368.00	0.98	0.24	x	toxic a,b,c
3.13	581.00	11.28	2.72	x	toxic a,b,c
-0.19	461.00	10.08	2.43	x	toxic b,c
2.98	893.00	8.72	2.10	x	toxic a,b,c
2.93	1897.00	11.15	2.69	x	toxic b,c
3.40	2017.00	0.77	0.18	x	toxic a,b
8.11	187.00	20.21	6.83	x	toxic a,b,c
3.88	274.00	8.95	3.02	x	toxic a,b,c
3.87	202.00	8.45	2.85	x	toxic a,b,c
-0.08	147.00	10.05	3.39	x	toxic a,b,c
2.78	556.00	0.60	-0.20	x	toxic a,b,c
2.62	2223.00	6.96	2.35	x	toxic a,b
0.56	440.00	13.26	4.48	x	toxic a,b,c
6.08	738.00	7.28	2.46	x	toxic a,b,c
4.61	1068.00	13.25	4.48	x	toxic a,b,c
-0.86	1678.00	6.64	2.24	x	toxic b,c
1.03	771.00	8.31	2.81	x	toxic a,b,c
3.45	378.00	6.99	2.36	x	toxic a,b,c

screened were eliminated for toxicity.

Table S3. IFN-Enhancement scores for known dependency facto

Li et al Dependency F	Dharmacon ad	plt A robust	plt B robust Z	plt C robust Z	mean robust Z
ADAMTS4	12, k13	0.10	1.38	2.53	1.34
ALAD	20, B15	-1.07	-0.45	-0.03	-0.51
AP1GBP1	20, H15	0.92	0.42	0.57	0.64
AP3B1	19, B17	-0.85	0.19	-0.64	-0.43
APLP2	8, M13	-0.39	0.97	0.61	0.40
ARHGAP22	63, B21	-0.74	-1.43	-1.23	-1.13
ARHGEF10L	60, J15	0.84	-0.64	-0.40	-0.07
ARRDC2	57, M17	0.01	-0.54	1.41	0.30
BAGE2	68, H12	-1.10	-1.50	-0.36	-0.99
BCKDHA	10, A4	-1.33	0.18	-1.02	-0.72
BRF1	8, A4	-1.18	-0.76	0.05	-0.63
BRUNOL6	63, P9	0.25	-0.04	-0.13	0.03
C10orf112	79, B8	-0.80	-1.40	-1.33	-1.18
C14orf73	70, B11	-0.53	0.00	-1.54	-0.69
C19orf44	67, H17	-0.33	-0.47	-1.00	-0.60
C20orf20	60, H18	-0.91	-0.88	-0.38	-0.73
C21orf56	67, N7	-0.55	-1.31	-0.92	-0.93
CAMTA2	21, H19	-1.06	-0.37	0.14	-0.43
CASP4	12, I18	7.16	1.29	-0.61	2.61
CCDC8	67,E12	1.26	-0.44	0.93	0.58
CCNB2	21,L17	-0.62	-0.37	1.24	0.08
CCPG1	21, M10	-0.13	-0.10	0.83	0.20
CDC6	6,O4	-0.44	-0.35	0.31	-0.16
CDH1	6,O2	-0.02	0.73	0.92	0.54
CDKL5	1, A16	0.08	1.82	0.45	0.78
CHKA	1, A17	0.29	1.05	2.16	1.17
CHUK	1, A23	-0.58	0.21	-1.04	-0.47
CISH	21, K23	-1.12	-0.90	-0.55	-0.86
CLDN1	18, H12	-0.40	-1.02	-1.23	-0.88
CLSTN1	21, O7	-0.15	0.77	-0.46	0.05
CNOT1	55,E5	0.24	0.23	-0.43	0.01
CNOT2	19,A16	-0.13	0.52	-1.25	-0.29
CNOT3	8,F5	0.55	-0.30	-0.31	-0.02
CNOT6L	21,O21	0.24	0.80	-0.76	0.10
CSNK1A1L	2,G16	-0.51	-0.31	-0.10	-0.31
CTAGE6	79,B6	-1.36	-1.62	-1.17	-1.38
CTGF	6,C14	1.09	1.05	1.75	1.29
CTSF	10,L9	-0.75	-0.70	-0.41	-0.62
CX3CL1	17,O5	-1.17	0.38	-0.24	-0.34
CYBA	76,I4	-0.81	-0.13	1.55	0.20
CYP4A22	81,F15				#DIV/0!
DACT3	73,L21	-0.29	-0.21	0.17	-0.11
DBNDD1	64,P17	-0.60	0.15	-0.56	-0.34

DDX3X	47,J18	-0.14	-0.69	1.79	0.32
DEFA5	47,H20	-0.33	0.03	0.13	-0.06
DEFB126	66,L4	-0.78	0.29	0.47	-0.01
DGAT1	10,P21	-0.44	-0.07	0.45	-0.02
DHRS12	65,B7	-0.15	-0.24	0.81	0.14
DIO3	47,H6	-0.61	-0.70	-1.19	-0.83
DLGAP4	54,L12	-0.67	-0.89	-0.32	-0.63
DNAJB1	59,K21	1.01	0.54	0.32	0.62
DOCK3	21,N16	0.09	-0.82	0.07	-0.22
E2F2	21,L14	0.71	0.70	0.11	0.51
ERC2	21,J11	2.22	1.09	0.45	1.25
ERCC5	12,D18	0.46	1.75	0.25	0.82
ETF1	19,c6	-0.23	0.65	-0.74	-0.11
EWSR1	6,H9	-0.64	0.37	-0.81	-0.36
FAU	19, O8	2.61	0.45	1.16	1.41
FBLN5	21,B6	-0.86	-1.15	-0.67	-0.89
FBXO38	66, N23	-0.06	-1.37	-1.13	-0.85
FCGRT	17, F12	0.62	-0.69	-1.00	-0.36
FER1L3	57, A11	-0.43	-0.46	-0.63	-0.51
FLJ22659	66, A5	-0.42	-0.47	-1.40	-0.76
FLT4	1, J14	0.29	-0.53	1.98	0.58
FOXA2	8,P12	-0.53	0.14	-0.53	-0.31
FRMPD3	68,C7	0.18	-0.73	-1.11	-0.55
GNB2L1	22,O4	-0.42	-0.24	-0.90	-0.52
GNG8	69,B15	-1.39	-1.20	-0.83	-1.14
GPSN2	52,B15	-1.47	-1.14	-0.47	-1.03
GTF3A	8,H2	0.13	2.07	-0.70	0.50
GUCY1A2	11,E23	-0.59	1.40	-0.90	-0.03
HCCS	48,G18	0.06	0.45	1.47	0.66
HEATR1	60,D21	-0.85	-1.09	-0.34	-0.76
HIPK3	1,B20	-0.65	-0.25	0.06	-0.28
HRC	23,G7	-0.66	-0.02	-0.06	-0.25
HSD17B13	79,P12	0.22	0.08	1.81	0.70
HSPA1A	23,G21	-0.13	-1.00	-1.08	-0.74
IFITM3	23,M23	-1.14	-1.38	0.70	-0.61
IGSF11	74,I18	-0.35	0.71	-1.16	-0.27
ILVBL	54,I14	-0.38	1.04	1.90	0.85
IMP4	70,P8	-1.02	-1.18	-1.76	-1.32
IRF3	9,G13	-0.01	1.89	-0.05	0.61
ITGA7	17,L7	0.69	-0.81	-0.30	-0.14
KCNJ3	4,B20	-1.49	-1.04	-0.85	-1.13
KCNK3	19,N9	0.31	0.89	0.44	0.55
KIAA1166	61,L10	1.13	2.24	0.67	1.35
KRT4	19,E5	1.39	0.21	2.08	1.23
L1TD1	59,L7	-0.28	-0.77	0.07	-0.33
LOC285556	78,J19	-1.07	-0.87	0.88	-0.35
LOC285643	81,A4				#DIV/0!

LOC400451	80,D16	1.59	2.09	0.06	1.24
LTC4S	22,F16	-0.99	-0.30	-1.31	-0.87
MAP4	48,J18	0.61	-0.67	-0.90	-0.32
MAPK1	2,M18	1.38	-0.84	0.43	0.33
MARK3	2,I18	0.85	1.24	-0.22	0.62
MCHR2	4,H11	0.10	-0.61	-0.49	-0.33
MCM2	13,I19	1.20	0.83	0.70	0.91
MED12	18,N18	-1.32	-1.07	2.60	0.07
MGC13057	67,L6	-0.96	-1.23	-1.26	-1.15
MLLT1	23,J20	-1.33	-0.49	-0.37	-0.73
MLXIPL	8,E5	-0.82	-0.31	-0.77	-0.63
MRPL15	57,J17	1.37	-0.89	-0.41	0.02
MRPL38	64,B23	-1.38	0.31	-0.65	-0.57
MRPL48	59,E21	0.38	0.29	0.29	0.32
MTHFSD	64,I16	-0.67	-1.31	-0.69	-0.89
MYCL2	9,K18	-0.84	0.80	0.46	0.14
MYO3A	2,C6	-0.55	-1.11	-0.69	-0.78
MYO7B	49,C23	-0.90	-1.17	0.86	-0.40
NAALADL1	53,O4	-0.57	-0.88	-0.59	-0.68
NMT1	49, O7	-0.04	-0.76	-0.02	-0.27
NOC4L	64,L20	0.46	0.24	-0.59	0.04
NOL1	23,M6	-0.78	-0.69	-0.81	-0.76
NOL5A	53,L8	-0.92	-1.04	-0.25	-0.74
NOL6	64,F7	-0.83	-0.61	-0.84	-0.76
NOP5/NOP58	59,C7	-0.96	-0.95	-1.08	-1.00
NOS1AP	14,D23	-0.10	0.98	-0.99	-0.03
NUAK2	3,G21	-0.42	-0.58	0.00	-0.33
ORAOV1	76,G14	-1.13	-0.93	-0.57	-0.88
OSBP	7,O4	0.64	0.75	1.08	0.83
PARP11	62,B13	0.47	-0.06	0.36	0.25
PECR	11,H11	-0.01	-0.41	-0.25	-0.22
PEMT	53,J11	-0.54	-0.72	-0.72	-0.66
PGLYRP4	62, D5	-0.33	-0.45	-0.15	-0.31
PI4KA	2,P11	-0.64	0.04	-0.97	-0.52
PNO1	62,O16	-1.03	-1.43	-1.43	-1.30
POLR2J2	76,J16	-0.51	-0.62	-0.99	-0.71
PPIA	49,B21	-0.78	-1.02	-0.66	-0.82
PPP2R1A	16,E9	-0.38	-0.56	-0.74	-0.56
PPTC7	16,M23	0.95	0.39	0.16	0.50
PRKRIP1	65,G18	-0.37	0.31	-0.52	-0.19
PROX1	23,P18	-0.11	0.74	2.86	1.16
PRPF40A	61,G8	0.77	-0.65	-0.48	-0.12
PRPSAP2	2,F2	-1.17	-0.38	-1.08	-0.87
PSME1	14,L19	0.27	0.13	0.10	0.17
PTCD1	56,L5	-0.78	-0.36	-1.12	-0.75
PTHR1	5,I10	0.84	1.01	0.64	0.83
RAB10	24,H21	-1.18	-0.37	-0.22	-0.59

RAB11A	14,A13	-0.67	-0.53	1.06	-0.05
RABEPK	24,J21	-0.47	1.15	-0.58	0.03
RAC1	2,B8	-0.97	0.28	-1.65	-0.78
RBM22	61,C2	-1.09	-0.13	-0.47	-0.56
RBM9	55,B10	-1.43	-0.15	-0.37	-0.65
Rgr	5,G18	1.52	-0.24	0.79	0.69
RIPK2	3,A19	0.16	-0.26	-0.71	-0.27
RNF207	80,J17	0.92	-0.19	1.50	0.74
RNF31	15,D7	-1.01	-0.86	-1.30	-1.06
ROCK2	3,C7	-1.24	-0.49	-0.38	-0.70
RPS6KL1	3,E15	-0.48	-0.28	-0.76	-0.51
SH3TC1	59,E12	-0.79	0.36	-0.27	-0.23
SLC11A1	19,N6	-0.23	0.48	-0.69	-0.15
SLC6A8	19,H4	5.55	7.16	2.56	5.09
SMAD5	18,J18	-0.99	0.60	0.39	0.00
SMAD6	17,P2	-0.71	-0.66	-0.86	-0.74
SMARCD3	9,N9	0.57	-0.69	0.42	0.10
SMURF1	15,F9	-1.17	1.14	0.70	0.23
SMURF2	15,F11	-0.05	1.59	-0.07	0.49
SPDEF	9,P23	7.51	-1.44	0.62	2.23
SRFBP1	74,C18	-1.93	-0.81	-0.43	-1.06
STMN2	24,B11	-1.00	-0.52	-0.83	-0.79
STX2	19,H11	1.96	1.87	1.58	1.80
SURF1	11,H2	2.48	0.71	1.70	1.63
SUV420H1	58,I20	-0.14	-0.61	-0.41	-0.38
SUZ12	6,F20	-0.39	-0.27	-1.08	-0.58
TCOF1	19,F12	-0.81	-0.76	0.36	-0.41
TFAP2A	9,F8	-1.03	-0.05	-0.41	-0.50
TM6SF2	89,M12				#DIV/0!
TMEM142A	68,D9	0.09	0.15	-0.18	0.02
TOP1	12,B19	-0.51	-0.85	-0.64	-0.66
TPM4	19,E10	1.48	1.19	2.24	1.64
TRAPPC5	71,P12	-0.91	-0.35	-1.56	-0.94
TRIM42	79,A15	-0.44	0.76	-0.51	-0.06
TRIM62	60,N6	0.67	-1.08	-0.95	-0.46
TRRAP	11,D12	-0.69	-0.97	0.90	-0.25
TTTY5	7,M14	0.77	0.91	0.86	0.85
TWIST1	8,G2	-0.41	-0.30	-0.85	-0.52
UBA52	19,K7	1.03	0.91	0.01	0.65
USP11	15,C13	-0.90	-0.56	-1.33	-0.93
USP42	15,I5	-0.39	-0.93	0.14	-0.39
USP51	74,J16	-2.14	-2.04	-1.24	-1.81
VAMP1	50,F8	-0.07	1.14	0.31	0.46
WDR37	54,F20	0.18	-0.06	-0.64	-0.17
WDR43	55,K6	-0.53	-0.15	-0.47	-0.39
WIF1	3,E16	-0.10	-1.16	-0.78	-0.68
WWTR1	56,B19	-0.81	-0.10	0.69	-0.08

XBP1	24,N10	2.40	-0.13	2.08	1.45
XPNPEP1	12,G9	-0.10	-0.18	0.40	0.04
ZEB1	9,F20	0.02	-1.02	-0.80	-0.60
ZNF148	10,E23	-0.07	-0.34	-1.11	-0.51
ZNF346	56,C9	-1.23	-0.36	-0.35	-0.64
ZNF467	75,G12	0.02	-0.97	-1.17	-0.71
ZNF608	62,F14	-0.54	-0.80	-1.49	-0.94
ZNF767	65,D14	-1.06	-0.12	-0.12	-0.43
ZNRF2	76,P2	0.08	-1.35	0.41	-0.29

ors from Li, Brass et al 2009

Table S4 Top 120 HCV IEGs

ACSL6	acyl-CoA synthetase long-chain family member 6
ACTN2	actinin, alpha 2
ADAM30	ADAM metallopeptidase domain 30
AKAP8L	A kinase (PRKA) anchor protein 8-like
ALG10	asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltra
ANKFY1	ankyrin repeat and FYVE domain containing 1
APC2	adenomatosis polyposis coli 2
ASCL1	achaete-scute complex homolog 1 (Drosophila)
ASPA	aspartoacylase (Canavan disease)
BCHE	butyrylcholinesterase
C14ORF100	chromosome 14 open reading frame 100
CAPN6	calpain 6
CCL26	chemokine (C-C motif) ligand 26
CCRL1	chemokine (C-C motif) receptor-like 1
CDX2	caudal type homeobox transcription factor 2
CPA6	carboxypeptidase A6
CSF2	colony stimulating factor 2 (granulocyte-macrophage)
DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-relatec
DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
DMRT1	doublesex and mab-3 related transcription factor 1
DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein
DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
EDEM3	ER degradation enhancer, mannosidase alpha-like 3
EIF3S3	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
EIF4E	eukaryotic translation initiation factor 4E
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3
EPO	erythropoietin
ETV3	ets variant gene 3
FANCG	Fanconi anemia, complementation group G
FFAR2	free fatty acid receptor 2
FLJ25168	(C17orf69)
FLJ45235	(ANKRD45) ankyrin repeat domain-containing protein 45
FN1	fibronectin 1
FOXI1	forkhead box I1
GCKR	glucokinase (hexokinase 4) regulator
GCM1	glial cells missing homolog 1 (Drosophila)
GJB4	gap junction protein, beta 4
GUCY1B3	guanylate cyclase 1, soluble, beta 3
GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine este
HDGF2	(HDGFRP2) hepatoma-derived growth factor-related protein 2
HEY2	hairy/enhancer-of-split related with YRPW motif 2
HRH4	histamine receptor H4
HSFY1	heat shock transcription factor, Y-linked 1

HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1
HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
IFNAR1	interferon (alpha, beta and omega) receptor 1
IFNAR2	interferon (alpha, beta and omega) receptor 2
IFNGR1	interferon gamma receptor 1
IQGAP2	IQ motif containing GTPase activating protein 2
IRF7	interferon regulatory factor 7
ISGF3G / IRF9	interferon-stimulated transcription factor 3, gamma 48kDa
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 incl
JAK1	Janus kinase 1 (a protein tyrosine kinase)
KCNIP3	Kv channel interacting protein 3, calsenilin
KIAA1049	(TCF25) transcription factor 25 (basic helix-loop-helix)
KIAA1919	sodium-dependent glucose transporter 1
KIAA1944	(TMEM132D) transmembrane protein 132D
LIPG	lipase, endothelial
LOC113444	(C1orf212) chromosome 1 open reading frame 212
LOC51315	(KRCC1) lysine-rich coiled-coil 1
MAP2K4	mitogen-activated protein kinase kinase 4
MAP7	microtubule-associated protein 7
MCM7	minichromosome maintenance complex component 7
MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Droso
MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
MYOT	myotilin
MYST1	MYST histone acetyltransferase 1
NBEA	neurobeachin
NCAM2	neural cell adhesion molecule 2
NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
NLRP14	NLR family, pyrin domain containing 14
OTC	ornithine carbamoyltransferase
OTOP1	otopetrin 1
OTUB1	OTU domain, ubiquitin aldehyde binding 1
PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa
PAX5	paired box gene 5 (B-cell lineage specific activator)
PCDHB12	protocadherin beta 12
PCDHB14	protocadherin beta 14
PDIA2	protein disulfide isomerase family A, member 2
PEO1	progressive external ophthalmoplegia 1
PGD	phosphogluconate dehydrogenase
PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide bindi
POLS	polymerase (DNA directed) sigma
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
PRDM5	PR domain containing 5
PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285

RAB4B	RAB4B, member RAS oncogene family
RALA	v-ral simian leukemia viral oncogene homolog A (ras related)
RANBP2	RAN binding protein 2
RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1
RASGRF1	RAS (RAD and GEM)-like GTP-binding 1
REM1	RAS (RAD and GEM)-like GTP-binding 1
REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
RGPD5	RANBP2-like and GRIP domain containing 5
RNF32	ring finger protein 32
RNGTT	RNA guanylyltransferase and 5'-phosphatase
ROCK1	Rho-associated, coiled-coil containing protein kinase 1
S100A8	S100 calcium binding protein A8
SCG5	secretogranin V (7B2 protein)
SFRS11	splicing factor, arginine/serine-rich 11
SFRS15	splicing factor, arginine/serine-rich 15
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2
SMAD3	SMAD family member 3
SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein
ST14	suppression of tumorigenicity 14 (colon carcinoma)
STAT2	signal transducer and activator of transcription 2, 113kDa
SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1
TAFA5	(FAM19A5) family with sequence similarity 19 (chemokine (C-C motif)-lik
TAS2R5	taste receptor, type 2, member 5
TEAD3	TEA domain family member 3
TFB2M	transcription factor B2, mitochondrial
TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like l
THNSL1	threonine synthase-like 1
TM7SF3	transmembrane 7 superfamily member 3
TTC5	tetratricopeptide repeat domain 5
TYK2	tyrosine kinase 2
UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
ZBTB6	zinc finger and BTB domain containing 6
ZNF224	zinc finger protein 224
ZNF469	zinc finger protein 469

Percent of Hits Positive

Found in C,D, or E

ISG in Primary Human Hepatocytes	**ISG in some cell type**
no	no
no	no
no	no
no	no
no	no
PMC2808168	PMC2808168
no	no
no	no
no	no
no	no
no	no
no	no
no	no
PMC2947462	PMC2947462
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	PMC3409588
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no

no	no
no	no
no	no
no	no
no	PMC3409588
PMC2808168	PMC2808168
PMC2383932	
PMC2808168	PMC3409588
PMC2947462	
no	no
PMC2808168	PMC2808168
PMC2808168	PMC2808168
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
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no	no
no	no
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no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
PMC2383932	
PMC2808168	PMC3409588

PMC2947462	
PMC2947462	PMC2947462
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	PMC3409588
no	no
no	no
no	no
no	no
no	PMC3409588
no	no
no	no
PMC2808168 PMC2947462	PMC3409588
PMC2808168	PMC2808168
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
ISG in Primary Human Hepatocytes	**ISG in some cell type**
8.33	11.67

other identification as IFNα related gene	**related to HCV**
no	PMC3390353
no	no
no	no
no	no
no	no
PMC3409588	PMC3409588
no	no
no	PMC3409588
no	PMID:19486448
PMID:16628626	PMC3388175
no	no
no	no
	PMID: 22739041
no	no
no	no
no	no
no	no
no	no
PMID:21957149	PMID:18782589 PMID: 17684232
no	no
no	PMC3007131
no	no
no	PMC3199473
no	no
PMID:2254439	PMC3281608
no	no
PMC1472600	
no	no
no	no
PMC3409588	PMC3409588
no	no
no	no
no	PMID: 16820872
no	no
no	no
no	no
no	no
no	no
PMID:15840100	
no	no
no	no
no	no
no	no

no	PMID:22490666
no	
PMC3261326	PMC3261326
PMC3156775	PMC3156775
PMID:14996348	
PMC3409588	PMC3409588
no	no
PMC3409588	PMC3409588
PMC3261326	PMC3261326
PMID:22711689	PMID:22711689
PMC3390613	
PMC3261326	PMC3261326
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
PMC3261326	PMC3261326
PMC3261326	PMC3261326
no	no
PMC3427032	
no	no
no	no
no	no
no	no
PMC2836033	
no	no
no	PMID: 9850179
no	no
no	no
no	no
no	no
no	PMID: 20676096
no	no
no	no
no	PMC2808168
no	PMC3348056
PMC3409588	

PMC2947462	
no	no
no	PMC2668029
no	no
no	no
no	no
no	no
no	no
no	no
no	no
no	no
PMC3409588	PMC3409588
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no	no
no	no
no	no
PMC3409588	
no	no
no	no
PMC3261326	PMC3261326
no	PMC2701521
no	no
no	no
no	no
no	no
no	PMC2597299
no	no
no	no
no	no
PMC3261326	PMC3261326
no	no
no	no
no	no
no	no
other identification as IFN-α related gene	**related to HCV**
20.83	22.50
23.33	

related to a non-HCV virus	**other**
PMID: 16448567	PMC1175008
no	PMC3281001
PMC2723137	
no	
no	
PMC2780751	
no	
PMC3170792	
no	
no	
no	
PMC2211551	PMID:22226123
no	
PMC3071656	
no	
PMID:20124101	PMC2810293
PMID: 22661216	
no	
no	
PMC2967539	
no	
PMC3312915	
no	PMID:14578863
no	
PMC1472600	
no	PMID:18025162
PMC3233135	PMID:15299030
no	
no	
PMID: 16820872	
PMID 19701604	
no	
PMID 17454446	
no	
no	PMC2430169
PMC2803336	
no	
no	
no	PMID:21614010
no	

no	PMC2988069
PMC3347391	
no	
no	
no	
no	
no	
no	
no	
PMC303354	
no	
PMID:16703398	PMID:22784096
PMID: 21908553	
no	
no	
no	
no	
no	PMID:14567964
no	
PMC2836033	
no	
PMC2045388	PMID: 22457049
no	
no	
PMID:16507315	
no	
no	
no	
PMC3145673	

no PMC2839122, HCC
PMC3407688
no
no
no
no
no
no
PMID: 12408826
no

PMC2884103
PMC3027118
PMC2255568
PMC1091719

PMC3334515
PMC3351729
PMID: 22088470

no
no
no
no
PMC3037883
PMC3292548
PMC3127837
no
no

PMC374249
no
no
no
related to a non-HCV virus
25.83

Search method:

1. if had any (>1%) effect on HCV infection levels in Schoggins screen, inserted this
2. if detected as a hit in Barten or Zhao screens, inserted this
3. HCV + IFN: searched pubmed for articles using terms " gene + virus" and "gene + IFN"

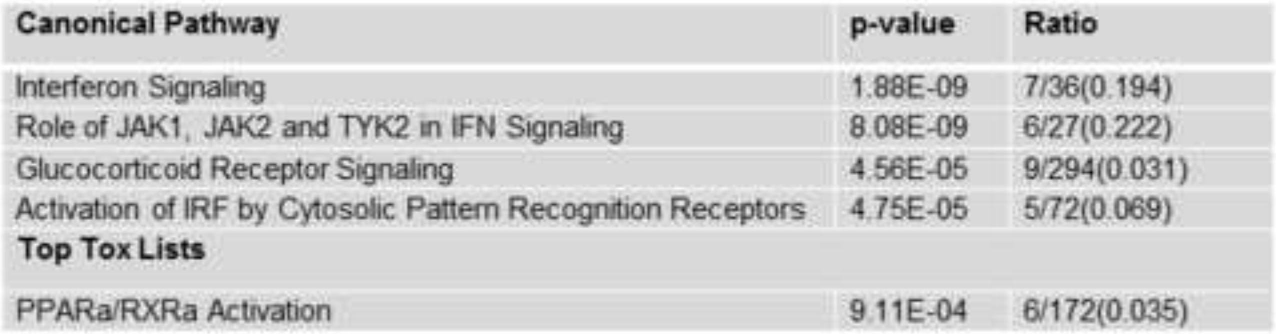
<u>How we defined "IFN alpha ISG in Primary Hepatocytes":</u>

identified in Lanford microarray Hepatology 2006; 43(5): 961-972 chimpanzee liver biopsies with fold-change >

identified in Sarasin-Filipowicz microarray PNAS 2008; 105(19): 7034-9 human liver biopsies 4h fold-change >2

2 at 4h, >4 at 8h, in liver
in liver from rapid responders

Table S5 IPA analysis



Canonical Pathway	p-value	Ratio
Interferon Signaling	1.88E-09	7/36(0.194)
Role of JAK1, JAK2 and TYK2 in IFN Signaling	8.08E-09	6/27(0.222)
Glucocorticoid Receptor Signaling	4.56E-05	9/294(0.031)
Activation of IRF by Cytosolic Pattern Recognition Receptors	4.75E-05	5/72(0.069)
Top Tox Lists		
PPARa/RXRa Activation	9.11E-04	6/172(0.035)

Table S5.

Table S6 Comparison of our HCV IEGs to Primary Hep

Lanford ISGs	Our IEGs
ABCB4	ACSL6
ABLIM3	ACTN2
ADFP	ADAM30
APOL3	AKAP8L
ARG2	ALG10
ARNTL	ANKFY1
BAZ1A	APC2
BAZ2A	ASCL1
BLZF1	ASPA
C10ORF18	BCHE
CASP7	C14ORF100
CCL2	CAPN6
CCND3	CCL26
CPT1A	CCRL1
CRP	CDX2
CTCFL	CPA6
CXCL11	CSF2
DDX3X	DCT
DLL1	DHX9
EIF2C2	DMRT1
ELF1	DPP4
FAM46C	DR1
FLJ39370	EDEM3
FLJ39739	EIF3S3
G6PC	EIF4E
GJA4	ENTPD3
GLRX	EPO
GMPR	ETV3
IFI27	FANCG
IL15RA	FFAR2
IL28RA	FLJ25168
IRS2	FLJ45235
JUNB	FN1
KIAA1217	FOXI1
KIAA1971	GCKR
LEPR	GCM1
LOC441168	GJB4
LRG1	GUCY1B3
MAB21L2	GZMA
MAP3K5	HDGF2
MAX	HEY2
MCL1	HRH4
MGC11324	HSFY1
MGC20410	HSP90AA1

reference:

Lanford RE, Guerra B, Lee H, Chavez D, Brasky
Hepatology. 2006 May;43(5):961-72.

NOD27
OGFR
PCTK2
PNRC1
PXK
RAB27A
SAA1
SAMHD1
SIPA1L2
SLC1A1
SLC25A28
SLC6A16
SSB1
TLR3
TRIM38
TRIM56
UPP2
ZC3HAV1
ZNF295
ZNF618

HSP90AB1
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1

REM1
REV3L
RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

atocyte ISG lists

KM, Bigger CB.

Sarasin ISGs	**Our IEGs**
ADM	ACSL6
AIM2	ACTN2
ANKRD22	ADAM30
APOBEC3A	AKAP8L
APOBEC3F	ALG10
APOBEC3G	ANKFY1
APOL6	APC2
ARHGEF3	ASCL1
ARNTL	ASPA
ATF3	BCHE
AXUD1	C14ORF100
BIRC4BP	CAPN6
BRDG1	CCL26
C17ORF27	CCRL1
C20ORF18	CDX2
C6ORF150	CPA6
C9ORF91	CSF2
CACNA1A	DCT
CCDC75	DHX9
CCL2	DMRT1
CCL8	DPP4
CD274	DR1
CD38	EDEM3
CD69	EIF3S3
CD80	EIF4E
CLEC2B	ENTPD3
CNP	EPO
CXCL10	ETV3
CXCL11	FANCG
DCP1A	FFAR2
DDX58	FLJ25168
DUSP5	FLJ45235
ECGF1	FN1
EIF2AK2	FOXI1
ELF1	GCKR
EPSTI1	GCM1
ETV7	GJB4
FAM46A	GUCY1B3
FANCA	GZMA
FCGR1A	HDGF2
FLJ10260	HEY2
FLJ11000	HRH4
FLJ20035	HSFY1
FLJ31033	HSP90AA1
FUT4	HSP90AB1

reference:

Sarasin-Filipowicz M, Oakeley EJ, Duong FH, C
Proc Natl Acad Sci U S A. 2008 May 13;105(19

G1P2
G1P3
GBP1
GBP4
GBP5
GMPR
GPR37
GTPBP1
HERC5
HERC6
HESX1
HPSE
IBRDC3
IFI16
IFI35
IFI44
IFI44L
IFIH1
IFIT1
IFIT2
IFIT3
IFIT5
IFRG28
IL15RA
IL1RN
INDO
IRF1
IRF7
ISG20
KIAA1404
KIAA1618
LAMP3
LGALS9
LGP2
LIPA
LOC129607
LOC389289
LOC400368
LOC440424
LOC441109
LOC441168
MAB21L2
MASTL
MCOLN2
MGC19764
MGC20410
MICB
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1
REM1

MLKL
MSX1
MT1M
MX1
MX2
NCF1
NCOA7
NEXN
NMI
NOD27
NRN1
NT5C3
OAS1
OAS2
OAS3
OASL
PARP12
PARP14
PARP9
PBEF1
PHF15
PLEKHA4
PLSCR1
PMAIP1
PML
PNPT1
PRIC285
PRKD2
RABGAP1L
RGS1
RP1-93h18.5
RSAD2
SAMD9
SAMD9L
SECTM1
SLC25A28
SMCHD1
SOCS1
SP100
SP110
SPTLC2
STAT1
TAGAP
TAP1
TDRD7
TFEC
TLR3
REV3L
RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

TLR7
TNFSF10
TNFSF13B
TRAFD1
TREX1
TRIM21
TRIM25
TRIM34
TRIM38
TRIM56
TSLP
USP18
ZC3HAV1
ZCCHC2
ZNF588

hristen V, Terracciano L, Filipowicz W, Heim MH
):7034-9. Epub 2008 May 8.

Feld ISGs	**Our IEGs**
AADAC	ACSL6
ABAT	ACTN2
ABCA8	ADAM30
ABCB1/ ABCB4	AKAP8L
ABCB10	ALG10
ABCB4	ANKFY1
ABCD3	APC2
ABCG2	ASCL1
ABHD2	ASPA
ABHD6	BCHE
ACAA1	C14ORF100
ACAA2	CAPN6
ACADM	CCL26
ACADSB	CCRL1
ACADVL	CDX2
ACMSD	CPA6
ACO1	CSF2
ACOX1	DCT
ACP1	DHX9
ACSL1	DMRT1
ACSL5	DPP4
ADAMTS9	DR1
ADAR	EDEM3
ADFP	EIF3S3
ADH6	EIF4E
ADRA1A	ENTPD3
AGMAT	EPO
AGXT	ETV3
AHCY	FANCG
AIM2	FFAR2
AKR1C3	FLJ25168
ALAS1	FLJ45235
ALB	FN1
ALDH3A2	FOXI1
ALDH5A1	GCKR
ALDH6A1	GCM1
ALDOB	GJB4
AMACR	GUCY1B3
AMN	GZMA
ANGPTL3	HDGF2
ANK3	HEY2
ANKFY1	HRH4
ANKRD15	HSFY1
ANKRD27	HSP90AA1
ANXA10	HSP90AB1

reference:

Feld JJ, Nanda S, Huang Y, Chen W, Cam M, Pu
Hepatology. 2007 Nov;46(5):1548-63.

liver bx ISG comparison of matched RRs pre a
RRon vs RRpre FC>1.5 p<0.001

ANXA8
APLP2
APOA5
APOB
APOBEC3A
APOL3
APOL6
APOM
APTX
AQP9
ARG1
ARHGEF7
ARL6IP
ARL6IP5
ARMC1
ARNTL
ASAH1
ATF6
ATP5G3
ATP5O
AZI2
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BAAT
BACH1
BBX
bioB
bioC
bioD
BIRC3
BIRC4BP
BLZF1
BNIP3
BTF3
BZW1 /// LOC151579
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C11orf32
C17orf27
C19orf22
C1orf151
C1orf169
C1orf85
C1S
C2
C21orf33
C2orf25
C5orf13
C5orf4
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
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KIAA1919
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MYST1
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OTUB1
PAFAH2
PAX5
PCDHB12
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PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
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RALA
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RASGRF1
REM1

C6orf62
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C8B
C8orf40
C9
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CA2
CACNG6
CALM1
CANX
CASP1
CAT
CBLL1
CBR1
CBX4
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CCND3
CCNG1
CCNT2
CCR1
CD36
CENTD1
CHN2
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CMAS
CNIH4
CNKSR3
CNP
COL6A2
COPG
COX5B
COX6C
COX7C
CPEB3
CPS1
CPT1A
CPT2
CRAMP1L
CREBL2
CRY1
CSK
CSRP2
CTBS
CTSB
CXCL11
REV3L
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ROCK1
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SCG5
SFRS11
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TEAD3
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TM7SF3
TTC5
TYK2
UCHL3
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CYP2C9
CYP2J2
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CYP3A43
CYP4A11
CYP4F3 /// CYP4F2
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DDX3Y
DDX58
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DHRS8
DMGDH
DNAJB9
DNAJC19
DTX1
DTX3L
DUSP1
E2IG5
ECGF1
ECM2
EEF2
EGR1
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EPSTI1
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GART
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GCLM
GCSH
Gene Symbol

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GLUD2
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GNMT
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GPHN
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HERPUD1
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HLA-F
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HMGCS2
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HPD
HPRT1
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HSPCB
HSPD1

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IFI44L
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IFIT2
IFIT3
IFIT5
IFITM1
IFITM2
IFNA4
IFRG28
IGF2
IGFBP2
IGH@ /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM
IGHA1 /// IGHA2 /// MGC27165
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IGKC /// IGKV1-5
IGKV1-5
IGKV1D-13
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IL18BP
IL6R
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INSR
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ISGF3G
ITGB1
ITIH2
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JAK1
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KIAA0564
KIAA0830
KIAA0841
KIAA1404
KIAA1447

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LAP3
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LDLR
LDLRAP1
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LOC91614
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LRRFIP2

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MGC20410
MGC35366
MGC46336
MGST3
MICB
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MIF
MINA
MMP14
MOBKL2B
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MRPS36
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MT1M
MTHFD1L
MTMR4
MTMR9
MTO1
MUCDHL
MX2
MYCBP
NAG
NAPE-PLD
NAT2
NBL1
NCK1
NCOA7
NDRG2
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NDUFA4
NDUFB4
NDUFB6
NDUFC1

NDUFS4
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NEK11
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NFIA
NFIL3
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NIPSNAP3A
NME7
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NT5C3
NT5E
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NUDT3
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OAS3
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OIT3
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PAK2
PANK1
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PARP12
PARP14
PARP9
PAX8
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PCBP2
PCK1
PCSK6
PCTP
PCYOX1
PDE3B
PDK4
PDLIM5
PDXK

PECI
PELO
PERP
PGM1
PGRMC1
PHF11
PHF3
PHYH
PIGR
PIK3AP1
PLEKHC1
PLSCR1
POLR2E
POLR2J
PON2
PPAP2B
PPID
PPM1A
PPP2R5C
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PRIC285
PRKAA1
PROS1
PROX1
PRRG4
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PSD3
PSMAL
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PXMP2
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RAPGEF2
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RBL2
RCL1
RCN1
RDX
RetSat
RGS5
RHEB
RHOBTB1
RHOBTB3
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RPS16
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RPS3A
RPS4X
RPS4Y1
RPS5
RPS9
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RSAD2
RTN2
RUTBC3
S100A14
SAMD9
SAMD9L
SAR1B
SAT
SBDS /// SBDSP
SCAP2
SCCPDH
SCD
SCHIP1
SCLY
SCO2
SCOTIN
SDC2
SDHC
SEC11L1
SEC23B
SECTM1
SELS
SELT
SERPINC1
SFN

SFRS7
SKP1A
SLAMF6
SLC10A1
SLC12A2
SLC15A3
SLC16A7
SLC17A5
SLC19A2
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SLC22A7
SLC25A28
SLC25A5
SLC31A1
SLC35A3
SLC37A4
SLC38A4
SLC39A5
SLC39A8
SLC3A1
SLC4A4
SLC7A8
SLCO1B1
SLCO1B3
SLCO2B1
SLICK
SMAD4
SMARCA1
SMARCA2
SMBP
SMCHD1
SN
SNX4
SNX5
SOD1
SORD
SORL1
SOX18
SP100
SP110
SP192
SPP1
SPP2
SQLE
SRCAP
ST13

ST3GAL6
STARD4
STAT1
STAT2
STAU
STEAP1
STEAP3
STK19
STK38L
SULT1E1
SUMO2
SVIL
TAGAP
TAP1
TAP2
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TBC1D22A
TBCA
TCP1
TDE1
TDO2
TFAM
TFPI
TGDS
THEM2
THOC2
THOC4
TINP1
TM9SF2
TMED10
TMED5
TMEM14B
TMEM38B
TMEM41B
TMEM59
TMEM64
TMEM70
TncRNA
TNFAIP3
TNIK
TNIP1
TOB1
TP53AP1
TP53INP1
TPARL
TRAFD1
TRIB1

TRIM14
TRIM22
TRIM25
TRIM35
TRIM68
TSPAN6
TTBK2
TTPA
TXN
TXNDC5
TXNIP
UAP1
UBE1L
UBE2D4
UBE2H
UBE2L6
UBL5
UBLCP1
UBXD2
UGP2
UGT3A1
UHMK1
UQCRC2
USP18
USP9Y
VNN1
WDR72
WIRE
XIST
XRCC5
YEATS2
ZCCHC2
ZF
ZFAND1
ZFYVE26
ZKSCAN1
ZNF533

usek SN, Schweigler LM, Theodore D, Zacks SL, Liang TJ, Fried MW.

nd on IFNa tx

He ISGs	**Our IEGs**
ARL5B	ACSL6
BAZ1A	ACTN2
BLZF1	ADAM30
BST2	AKAP8L
C1ORF38	ALG10
C3AR1	ANKFY1
CA7	APC2
CARHSP1	ASCL1
CASP1	ASPA
CCRL1	BCHE
CD38	C14ORF100
CD40	CAPN6
CD53	CCL26
CDC25B	CCRL1
CMPK2	CDX2
CSF2RB	CPA6
CTSO	CSF2
CTSS	DCT
CX3CL1	DHX9
CXCL10	DMRT1
CXCL9	DPP4
CYORF15A	DR1
CYP1B1	EDEM3
DDO	EIF3S3
DDX58	EIF4E
DDX60L	ENTPD3
DUOXA1	EPO
DUOXA2	ETV3
DUSP6	FANCG
EIF2AK2	FFAR2
EPSTI1	FLJ25168
ETV6	FLJ45235
EXT1	FN1
FAM111A	FOXI1
FAM26F	GCKR
FAM72B	GCM1
FLJ11171	GJB4
FLJ39639	GUCY1B3
FST	GZMA
GBP1	HDGF2
GBP2	HEY2
GCNT1	HRH4
GLB1	HSFY1
GMPR	HSP90AA1
GNB4	HSP90AB1

reference:

He XS, Nanda S, Ji X, Calderon-Rodriguez GM,
J Interferon Cytokine Res. 2010 May;30(5):31

Primary Human Hepatocyte ISGs after 6h IFN

HIST2H2AA3
HK2
HLA-DPA1
HLA-DQB1
HLA-DRB1
HLA-DRB4
HLA-E
HMCN2
IFI16
IFI30
IFI44L
IFI6
IFIH1
IFIT1
IFIT2
IFITM1
IL18BP
IL1RN
INDO
IRF2
IRF7
IRF8
ISG15
ISG20
JAK2
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LOC285194
LOC644151
LOC727820
LOC730054
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MX2
MXD1
MYC
NLRC5
NM1
NT5C3
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1
REM1

OAS1
OAS2
OAS3
OTUD4
PARP14
PLA1A
PLA2G2A
PLAUR
PLEK
PLEKHA4
PLSCR1
PML
PPM1K
PRIC285
PSMB10
PSMB8
RAB4B
RAB8B
RABGAP1L
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RASGRP3
RASSF5
RNF213
RNF34
RSAD2
RTP4
SAMD9L
SAMHD1
SDS
SELL
SLC15A3
SLC22A23
SOCS1
SP110
SRGN
STAT1
STAT2
TAP1
TAP2
TLR2
TMEM110
TMEM192
TMEM50A
TMEM86A
TNFSF10
TNFSF13B
TRAFD1

REV3L
RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

TRIM22
TRIM31
TRIM46
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UBD
UBE2D4
UBE2L6
USP18
VAMP5
VCAM1
WARS
WNT10B
XRN1
ZCCHC2
ZNF313
ZNFX1

Greenberg HB, Liang TJ.
1-20.

alpha

Lanford/Sarasin/Felds/He Composite Primary Hepatocyte ISG list

AADAC
ABAT
ABCA8
ABCB1/ ABCB4
ABCB10
ABCB4
ABCD3
ABCG2
ABHD2
ABHD6
ABLIM3
ACAA1
ACAA2
ACADM
ACADSB
ACADVL
ACMSD
ACO1
ACOX1
ACP1
ACSL1
ACSL5
ADAMTS9
ADAR
ADFP
ADH6
ADM
ADRA1A
AGMAT
AGXT
AHCY
AIM2
AKR1C3
ALAS1
ALB
ALDH3A2
ALDH5A1
ALDH6A1
ALDOB
AMACR
AMN
ANGPTL3
ANK3
ANKFY1

Our IEG Li

ACSL6
ACTN2
ADAM30
AKAP8L
ALG10
ANKFY1
APC2
ASCL1
ASPA
BCHE
C14ORF10
CAPN6
CCL26
CCRL1
CDX2
CPA6
CSF2
DCT
DHX9
DMRT1
DPP4
DR1
EDEM3
EIF3S3
EIF4E
ENTPD3
EPO
ETV3
FANCG
FFAR2
FLJ25168
FLJ45235
FN1
FOXI1
GCKR
GCM1
GJB4
GUCY1B3
GZMA
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HRH4
HSFY1
HSP90AA1

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ANKRD22
ANKRD27
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APOA5
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APOBEC3F
APOBEC3G
APOL3
APOL6
APOM
APTX
AQP9
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ARG2
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ARHGEF7
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ARL6IP
ARL6IP5
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ARNTL
ASAH1
ATF3
ATF6
ATP5G3
ATP5O
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BAZ1A
BAZ2A
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bioB
bioC
bioD
BIRC3
BIRC4BP
BLZF1
BNIP3
BRDG1
BST2

HSP90AB1
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
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MYST1
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NFATC2
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OTUB1
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PAX5
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PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
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RANBP2
RAPGEF1
RASGRF1

BTF3
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C10orf116
C10ORF18
C11orf32
C17ORF27
C19orf22
C1orf151
C1orf169
C1ORF38
C1orf85
C1S
C2
C20ORF18
C21orf33
C2orf25
C3AR1
C5orf13
C5orf4
C6ORF150
C6orf62
C7orf6
C8B
C8orf40
C9
C9ORF91
C9orf98
CA2
CA7
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CACNG6
CALM1
CANX
CARHSP1
CASP1
CASP7
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CBR1
CBX4
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CCND1
CCND3
CCNG1
CCNT2

REM1
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TEAD3
TFB2M
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THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

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CHN2
CIDEB
CKS1B
CLDN23
CLEC2B
CMAS
CMPK2
CNIH4
CNKSR3
CNP
COL6A2
COPG
COX5B
COX6C
COX7C
CPEB3
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CPT1A
CPT2
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CRY1
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CTSB
CTSO
CTSS
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CXCL10
CXCL11
CXCL14
CXCL9

CYORF15A
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CYP2C19 /// CYP2C9
CYP2C9
CYP2J2
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CYP3A43
CYP4A11
CYP4F3 /// CYP4F2
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DDX3Y
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EIF3S8

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FOXA3
FOXQ1
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FUBP1
FUT4
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G1P3
G6PC
GABPA
GADD45A
GALNACT-2
GAPDH
GART
GAS5
GBP1
GBP2
GBP4
GBP5
GCAT
GCLM
GCNT1
GCSH
Gene Symbol
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GLUD2
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GNB4
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GNMT
GNS
GOT1
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HERC4
HERC5
HERC6
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HSPA1A
HSPA1A /// HSPA1B
HSPA8
HSPC121
HSPCA
HSPCB

HSPD1
IBRDC3
ID1
IF
IFI16
IFI27
IFI30
IFI35
IFI44
IFI44L
IFI6
IFIH1
IFIT1
IFIT2
IFIT3
IFIT5
IFITM1
IFITM2
IFNA4
IFRG28
IGF2
IGFBP2
IGH@ /// IGHG1 /// IGHG2 /// IGHG3 /// IGHM
IGHA1 /// IGHA2 /// MGC27165
IGKC
IGKC /// IGKV1-5
IGKV1-5
IGKV1D-13
IGL@ /// IGLC1 /// IGLC2 /// IGLV3-25 /// IGLV2-14
IGL@ /// IGLC1 /// IGLC2 /// IGLV3-25 /// IGLV2-14 /// IGLJ3
IGLC2
IL13RA1
IL13RA2
IL15RA
IL17RB
IL18BP
IL1RN
IL28RA
IL6R
INDO
INSIG1
INSR
IQGAP2
IRF1
IRF2
IRF7
IRF8

IRS2
ISG15
ISG20
ISGF3G
ITGB1
ITIH2
JAG1
JAK1
JAK2
JUNB
KCTD2
KIAA0082
KIAA0226
KIAA0564
KIAA0830
KIAA0841
KIAA1217
KIAA1404
KIAA1447
KIAA1618
KIAA1971
KLC2L
KLF11
KLF3
KLF6
KLHDC2
KLHL17
KTN1 /// PDIA6
KYNU
LACTB2
LAMP3
LAP3
LBA1
LBP
LDB2
LDHA
LDLR
LDLRAP1
LEPR
LGALS9
LGP2
LGR4
LIFR
LIPA
LIPC
LITAF
LMO2

LOC100129349
LOC113386
LOC123876 /// ACSM2
LOC129607
LOC153222
LOC201895
LOC23117 /// DKFZp547E087 /// LOC348162 /// LOC440354 /// LOC613037
LOC253039
LOC283177
LOC283666
LOC283902
LOC285194
LOC286044
LOC286167
LOC389289
LOC389831
LOC391020
LOC400368
LOC440118
LOC440424
LOC441109
LOC441168
LOC63929
LOC644151
LOC727820
LOC730054
LOC91353
LOC91614
LOC93343
LONPL
LPA /// PLG
LRG1
LRP6
LRRC44
LRRFIP1
LRRFIP2
LSM5
LTB4DH
LYPLAL1
LYSMD3
MAB21L2
MAN2A1
MAOA
MAP2K1
MAP2K5
MAP3K5
MARCKS

MASTL
MAT2B
MAWBP
MAX
MBL2
MCEE
MCL1
MCOLN2
MEG3
MEST
MGC11324
MGC16028
MGC19764
MGC20410
MGC35366
MGC46336
MGST3
MICB
MID1IP1
MIF
MINA
MLKL
MMP14
MOBKL2B
MRPL37
MRPS36
MS4A4A
MS4A6A
MSX1
MT1F
MT1M
MTHFD1L
MTMR4
MTMR9
MTO1
MUCDHL
MX1
MX2
MXD1
MYC
MYCBP
NAG
NAPE-PLD
NAT2
NBL1
NCF1
NCK1

NCOA7
NDRG2
NDUFA3
NDUFA4
NDUFB4
NDUFB6
NDUFC1
NDUFS4
NEDD4L
NEK11
NET1
NEXN
NFE2L2
NFIA
NFIL3
NGFRAP1
NIPSNAP3A
NLRC5
NM1
NME7
NMI
NOD27
NP
NR1H4
NRN1
NT5C2L1
NT5C3
NT5E
NUDT21
NUDT3
NUMB
OAS1
OAS2
OAS3
OASL
OAZ1
OGFR
OIT3
OPTN
OSBPL8
OTUD4
OXA1L
PABPC1
PACS1
PAK2
PANK1
PAPOLA

PARP12
PARP14
PARP9
PAX8
PBEF1
PCBD1
PCBP2
PCK1
PCSK6
PCTK2
PCTP
PCYOX1
PDE3B
PDK4
PDLIM5
PDXK
PECI
PELO
PERP
PGM1
PGRMC1
PHF11
PHF15
PHF3
PHYH
PIGR
PIK3AP1
PLA1A
PLA2G2A
PLAUR
PLEK
PLEKHA4
PLEKHC1
PLSCR1
PMAIP1
PML
PNPT1
PNRC1
POLR2E
POLR2J
PON2
PPAP2B
PPID
PPM1A
PPM1K
PPP2R5C
PRDX4

PRIC285
PRKAA1
PRKD2
PROS1
PROX1
PRRG4
PSAT1
PSD3
PSMAL
PSMB10
PSMB8
PVRL3
PXK
PXMP2
RAB15
RAB2
RAB27A
RAB4B
RAB8B
RABGAP1L
RAP1GA1
RAPGEF2
RARA
RARRES3
RASGRP3
RASSF5
RBL2
RCL1
RCN1
RDX
RetSat
RGS1
RGS5
RHEB
RHOBTB1
RHOBTB3
RNF13
RNF130
RNF213
RNF34
RNH1
RP1-93h18.5
RPL11
RPL13
RPL13A /// LOC283340 /// LOC387930
RPL14
RPL15

RPL29
RPL3
RPL30
RPL4
RPL7A
RPS15A
RPS16
RPS27L
RPS3
RPS3A
RPS4X
RPS4Y1
RPS5
RPS9
RRBP1
RSAD2
RTN2
RTP4
RUTBC3
S100A14
SAA1
SAMD9
SAMD9L
SAMHD1
SAR1B
SAT
SBDS /// SBDSP
SCAP2
SCCPDH
SCD
SCHIP1
SCLY
SCO2
SCOTIN
SDC2
SDHC
SDS
SEC11L1
SEC23B
SECTM1
SELL
SELS
SELT
SERPINC1
SFN
SFRS7
SIPA1L2

SKP1A
SLAMF6
SLC10A1
SLC12A2
SLC15A3
SLC16A7
SLC17A5
SLC19A2
SLC1A1
SLC1A2
SLC22A23
SLC22A7
SLC25A28
SLC25A5
SLC31A1
SLC35A3
SLC37A4
SLC38A4
SLC39A5
SLC39A8
SLC3A1
SLC4A4
SLC6A16
SLC7A8
SLCO1B1
SLCO1B3
SLCO2B1
SLICK
SMAD4
SMARCA1
SMARCA2
SMBP
SMCHD1
SN
SNX4
SNX5
SOCS1
SOD1
SORD
SORL1
SOX18
SP100
SP110
SP192
SPP1
SPP2
SPTLC2

SQLE
SRCAP
SRGN
SSB1
ST13
ST3GAL6
STARD4
STAT1
STAT2
STAU
STEAP1
STEAP3
STK19
STK38L
SULT1E1
SUMO2
SVIL
TAGAP
TAP1
TAP2
TBC1D10B
TBC1D22A
TBCA
TCP1
TDE1
TDO2
TDRD7
TFAM
TFEC
TFPI
TGDS
THEM2
THOC2
THOC4
TINP1
TLR2
TLR3
TLR7
TM9SF2
TMED10
TMED5
TMEM110
TMEM14B
TMEM192
TMEM38B
TMEM41B
TMEM50A

TMEM59
TMEM64
TMEM70
TMEM86A
TncRNA
TNFAIP3
TNFSF10
TNFSF13B
TNIK
TNIP1
TOB1
TP53AP1
TP53INP1
TPARL
TRAFD1
TREX1
TRIB1
TRIM14
TRIM21
TRIM22
TRIM25
TRIM31
TRIM34
TRIM35
TRIM38
TRIM46
TRIM56
TRIM68
TSLP
TSPAN6
TTBK2
TTPA
TXN
TXNDC5
TXNIP
UAP1
UBD
UBE1L
UBE2D4
UBE2H
UBE2L6
UBL5
UBLCP1
UBXD2
UGP2
UGT3A1
UHMK1

UPP2
UQCRC2
USP18
USP9Y
VAMP5
VCAM1
VNN1
WARS
WDR72
WIRE
WNT10B
XIST
XRCC5
XRN1
YEATS2
ZC3HAV1
ZCCHC2
ZF
ZFAND1
ZFYVE26
ZKSCAN1
ZNF295
ZNF313
ZNF533
ZNF588
ZNF618
ZNFX1

st

List of Our IEGs that have been described as Primary Hepatocyte IFN alpha Stimulated

ANKFY1
CCRL1
IQGAP2
IRF7
ITGB1
)
JAK1
PRIC285=PDIP1
RAB4B
STAT2
SULT1E1

Percent of our IEGs that have been described as Primary Hepatocyte IFNa SGs

Genes

8.333333

Table S7. HCV IEG Screen Comparative Analysis

Schoggins' IEGs that inhibit to <76% Jc1	Fusco JFH1 IEGs
ADFP	ACSL6
AGPAT9	ACTN2
AIM2	ADAM30
ALDH1A1	AKAP8L
ANGPTL1	ALG10
APOBEC3G	ANKFY1
APOL1	APC2
APOL2	ASCL1
ARG2	ASPA
B2M	BCHE
BATF2	C14ORF100
BCL2L14	CAPN6
BLVRA	CCL26
BLZF1	CCRL1
C10orf10	CDX2
C15orf48	CPA6
C22orf28	CSF2
C4orf33	DCT
C5orf27	DHX9
C5orf39	DMRT1
CCDC109B	DPP4
CCDC92	DR1
CCL19	EDEM3
CCL2	EIF3S3
CCL5	EIF4E
CCL8	ENTPD3
CD69	EPO
CD80	ETV3
CEBPD	FANCG
CES1	FFAR2
CFB	FLJ25168
CMAH	FLJ45235
CNP	FN1
COMMD3	FOXI1
CREB3L3	GCKR
CRP	GCM1
CSDA	GJB4
CXCL9	GUCY1B3
CYP1B1	GZMA
DDIT4	HDGF2
DDX58	HEY2
DDX60	HRH4
DEFB1	HSFY1

DTX3L
DYNLT1
EIF2AK2
EPSTI1
ETV7
FAM125B
FAM70A
FBXO6
FLJ11286
FLJ39739
FUT4
G6PC
GBP2
GCH1
GEM
GK
GTPBP2
GZMB
HLA-G
HPSE
HSH2D
IFI35
IFI44
IFIH1
IFIT1
IFIT5
IFITM2
IFNGR1
IGFBP2
IL17RB
IMPA2
IRF1
IRF2
IRF7
IRF9
ISG15
JUNB
LAP3
LGALS3
LGALS9
LRG1
LY6E
MAB21L2
MAFB
MAP3K14
MKX
MOV10
HSP90AA1
HSP90AB1
IFNAR1
IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1

MS4A4A
MT1F
MT1H
MYD88
N4BP1
NAPA
NCF1
NOD2
NOS2A
NRN1
NT5C3
NUP50
OAS3
OASL
P2RY6
PABPC4
PARP12
PBEF1
PCTK2
PDGFRL
PDK1
PFKFB3
PI4K2B
PMM2
PNRC1
PRAME
PUS1
S100A8
SAT3
SECTM1
SERPINE1
SERPING1
SIRPA
SLC1A1
SLC25A28
SLFN5
SOCS1
SOCS2
STEAP4
THBD
TLR3
TMEM49
TMEM51
TNFAIP6
TNFSF10
TNFSF13B
TRIM14
RASGRF1
REM1
REV3L
RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

TRIM38
TYMP
UBA7
UPP2
USP18
VAMP5
VEGFC
WARS
XAF1

Bartenschlager Replicon IEGs

IRF1
IRF9
PSME2
PSMB9
RnaseL
IFITM1
IFITM3
IFIT3
TRIM14
NOS2

Fusco JFH1 IEGs

ACSL6
ACTN2
ADAM30
AKAP8L
ALG10
ANKFY1
APC2
ASCL1
ASPA
BCHE
C14ORF100
CAPN6
CCL26
CCRL1
CDX2
CPA6
CSF2
DCT
DHX9
DMRT1
DPP4
DR1
EDEM3
EIF3S3
EIF4E
ENTPD3
EPO
ETV3
FANCG
FFAR2
FLJ25168
FLJ45235
FN1
FOXI1
GCKR
GCM1
GJB4
GUCY1B3
GZMA
HDGF2
HEY2
HRH4
HSFY1
HSP90AA1
HSP90AB1
IFNAR1

IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1
REM1
REV3L

RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

Zhao replicon IEGs

ACSS2
AKR1C1
ANKRD30A
ASCC3L1
ASTL
ATP5C1
BACE1
C14orf177
C1orf55
CDC5L
COPB2
CORO1C
CORT
CTRB1
CTSK
DGCR2
EFTUD2
EIF3S10
ERH
GAB4
GALP
GBP5
GDI2
GPC4
GPR18
HCFC1
HNRPC
HNRPL
IFNAR1
IK
IRF9
JAK1
KIAA1604
LOC283587
LOC284393
LOC285658
LOC342994
LOC388460
LOC388532
LOC392742
LOC401155
LSM6
LSM7
LSM8
LYPD2
MEOX2

Fusco JFH1 IEGs

ACSL6
ACTN2
ADAM30
AKAP8L
ALG10
ANKFY1
APC2
ASCL1
ASPA
BCHE
C14ORF100
CAPN6
CCL26
CCRL1
CDX2
CPA6
CSF2
DCT
DHX9
DMRT1
DPP4
DR1
EDEM3
EIF3S3
EIF4E
ENTPD3
EPO
ETV3
FANCG
FFAR2
FLJ25168
FLJ45235
FN1
FOXI1
GCKR
GCM1
GJB4
GUCY1B3
GZMA
HDGF2
HEY2
HRH4
HSFY1
HSP90AA1
HSP90AB1
IFNAR1

MFAP1
MRPL10
MYOT
MYST1
NAP5
NHP2L1
PDCD5
PKD1L3
PPP2R2A
PRPF6
PRPF8
RBM22
RNF187
RP11-487F23.3
RPL10
RPL11
RPL14L
RPL17
RPL21
RPL32
RPL5
RPL7
RPL7P6
RUVBL1
RUVBL2
RWDD2
SART1
SF3A1
SF3A3
SF3B1
SF3B14
SF3B4
SF3B5
SMU1
SNRP70
SNRPD1
SON
STAT2
STK40
TAS2R50
TSGA10IP
TYK2
UBA52
WBP11
ZC3HAV1
ZFP64
ZMAT2

IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1
REM1
REV3L

RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

Notes:

hits found at all 3 prior IEG screens : IRF9
hits found in 2 of 3 prior IEG screens: IFIH1, IRF1, TRIM14

Hits from this combined list (Schoggins <76% + Zhao + Barten) that are found on Fusco list:

IFNAR1
IFNGR1
IRF7
JAK1
MYST1
MYOT
S100A8
STAT2
TYK2

7.5 % of our hits are previously described HCV IEGs

Schoggins Jc1	**Bartenschlager Replicon II**	**Zhao replicon IEGs**
ADFP	IRF1	ACSS2
AGPAT9	IRF9	AKR1C1
AIM2	PSME2	ANKRD30A
ALDH1A1	PSMB9	ASCC3L1
ANGPTL1	RnaseL	ASTL
APOBEC3G	IFITM1	ATP5C1
APOL1	IFITM3	BACE1
APOL2	IFIT3	C14orf177
ARG2	TRIM14	C1orf55
B2M	NOS2	CDC5L
BATF2		COPB2
BCL2L14		CORO1C
BLVRA		CORT
BLZF1		CTRB1
C10orf10		CTSK
C15orf48		DGCR2
C22orf28		EFTUD2
C4orf33		EIF3S10
C5orf27		ERH
C5orf39		GAB4
CCDC109B		GALP
CCDC92		GBP5
CCL19		GDI2
CCL2		GPC4
CCL5		GPR18
CCL8		HCFC1
CD69		HNRPC
CD80		HNRPL
CEBPD		IFNAR1
CES1		IK
CFB		IRF9
CMAH		JAK1
CNP		KIAA1604
COMMD3		LOC283587
CREB3L3		LOC284393
CRP		LOC285658
CSDA		LOC342994
CXCL9		LOC388460
CYP1B1		LOC388532
DDIT4		LOC392742
DDX58		LOC401155
DDX60		LSM6
DEFB1		LSM7
DTX3L		LSM8
DYNLT1		LYPD2
EIF2AK2		MEOX2

EPSTI1
ETV7
FAM125B
FAM70A
FBXO6
FLJ11286
FLJ39739
FUT4
G6PC
GBP2
GCH1
GEM
GK
GTPBP2
GZMB
HLA-G
HPSE
HSH2D
IFI35
IFI44
IFIH1
IFIT1
IFIT5
IFITM2
IFNGR1
IGFBP2
IL17RB
IMPA2
IRF1
IRF2
IRF7
IRF9
ISG15
JUNB
LAP3
LGALS3
LGALS9
LRG1
LY6E
MAB21L2
MAFB
MAP3K14
MKX
MOV10
MS4A4A
MT1F
MT1H
MFAP1
MRPL10
MYOT
MYST1
NAP5
NHP2L1
PDCD5
PKD1L3
PPP2R2A
PRPF6
PRPF8
RBM22
RNF187
RP11-487F23.3
RPL10
RPL11
RPL14L
RPL17
RPL21
RPL32
RPL5
RPL7
RPL7P6
RUVBL1
RUVBL2
RWDD2
SART1
SF3A1
SF3A3
SF3B1
SF3B14
SF3B4
SF3B5
SMU1
SNRP70
SNRPD1
SON
STAT2
STK40
TAS2R50
TSGA10IP
TYK2
UBA52
WBP11
ZC3HAV1
ZFP64
ZMAT2

MYD88
N4BP1
NAPA
NCF1
NOD2
NOS2A
NRN1
NT5C3
NUP50
OAS3
OASL
P2RY6
PABPC4
PARP12
PBEF1
PCTK2
PDGFRL
PDK1
PFKFB3
PI4K2B
PMM2
PNRC1
PRAME
PUS1
S100A8
SAT3
SECTM1
SERPINE1
SERPING1
SIRPA
SLC1A1
SLC25A28
SLFN5
SOCS1
SOCS2
STEAP4
THBD
TLR3
TMEM49
TMEM51
TNFAIP6
TNFSF10
TNFSF13B
TRIM14
TRIM38
TYMP
UBA7

	UPP2		
	USP18		
	VAMP5		
	VEGFC		
	WARS		
	XAF1		
Cells are formatted to identify duplicate values across lists			
No.common genes	6	3	7

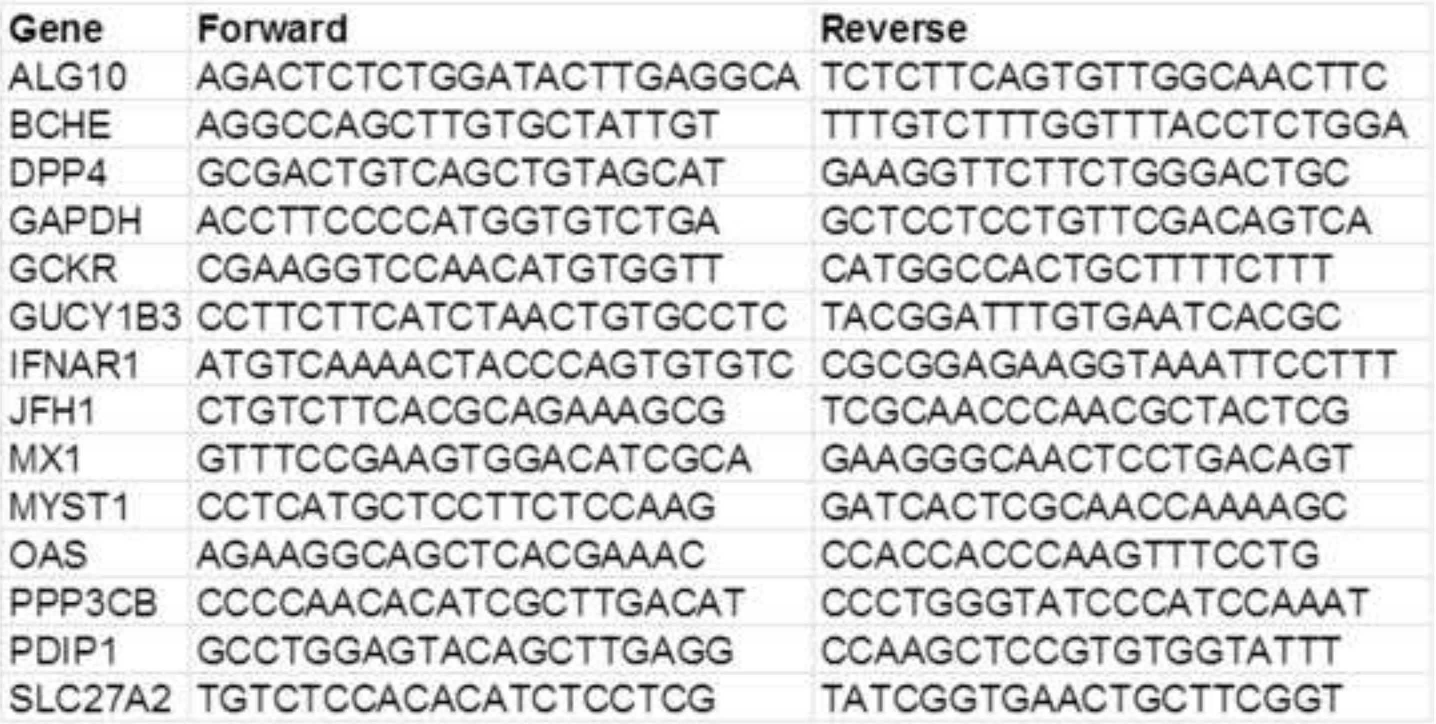
Fusco JFH1

ACSL6
ACTN2
ADAM30
AKAP8L
ALG10
ANKFY1
APC2
ASCL1
ASPA
BCHE
C14ORF100
CAPN6
CCL26
CCRL1
CDX2
CPA6
CSF2
DCT
DHX9
DMRT1
DPP4
DR1
EDEM3
EIF3S3
EIF4E
ENTPD3
EPO
ETV3
FANCG
FFAR2
FLJ25168
FLJ45235
FN1
FOXI1
GCKR
GCM1
GJB4
GUCY1B3
GZMA
HDGF2
HEY2
HRH4
HSFY1
HSP90AA1
HSP90AB1
IFNAR1

IFNAR2
IFNGR1
IQGAP2
IRF7
ISGF3G / IRF9
ITGB1
JAK1
KCNIP3
KIAA1049
KIAA1919
KIAA1944
LIPG
LOC113444
LOC51315
MAP2K4
MAP7
MCM7
MLL5
MYBL1
MYOT
MYST1
NBEA
NCAM2
NFATC2
NLRP14
OTC
OTOP1
OTUB1
PAFAH2
PAX5
PCDHB12
PCDHB14
PDIA2
PEO1
PGD
PLEKHA1
POLS
PPP3CB
PRDM5
PRIC285
RAB4B
RALA
RANBP2
RAPGEF1
RASGRF1
REM1
REV3L

RGPD5
RNF32
RNGTT
ROCK1
S100A8
SCG5
SFRS11
SFRS15
SLC27A2
SMAD3
SSX2IP
ST14
STAT2
SULT1E1
TAFA5
TAS2R5
TEAD3
TFB2M
TGFBR1
THNSL1
TM7SF3
TTC5
TYK2
UCHL3
ZBTB6
ZNF224
ZNF469

Table S8 Primers



Gene	Forward	Reverse
ALG10	AGACTCTCTGGATACTTGAGGCA	TCTCTTCAGTGTTGGCAACTTC
BCHE	AGGCCAGCTTGTGCTATTGT	TTTGTCTTTGGTTTACCTCTGGA
DPP4	GCGACTGTCAGCTGTAGCAT	GAAGGTTCTTCTGGGACTGC
GAPDH	ACCTTCCCCATGGTGTCTGA	GCTCCTCCTGTTCGACAGTCA
GCKR	CGAAGGTCCAACATGTGGTT	CATGGCCACTGCTTTTCTTT
GUCY1B3	CCTTCTTCATCTAACTGTGCCTC	TACGGATTTGTGAATCACGC
IFNAR1	ATGTCAAAACTACCCAGTGTGTC	CGCGGAGAAGGTAAATTCCTTT
JFH1	CTGTCTTCACGCAGAAAGCG	TCGCAACCCAACGCTACTCG
MX1	GTTTCCGAAGTGGACATCGCA	GAAGGGCAACTCCTGACAGT
MYST1	CCTCATGCTCCTTCTCCAAG	GATCACTCGCAACCAAAAGC
OAS	AGAAGGCAGCTCACGAAAC	CCACCACCCAAGTTTCCTG
PPP3CB	CCCCAACACATCGCTTGACAT	CCCTGGGTATCCCATCCAAAT
PDIP1	GCCTGGAGTACAGCTTGAGG	CCAAGCTCCGTGTGGTATTT
SLC27A2	TGTCTCCACACATCTCCTCG	TATCGGTGAACTGCTTCGGT

Table S8.

Table S9. Phenotype Knockdown Comparison

	Phenotype-FR	Fold mRNA	Fold protein
ALG10 si1	6.00	0.01	0.63
ALG10 si2	5.20	0.12	0.45
ALG10 si3	4.59	0.03	0.30
ALG10 si4	5.21	0.22	0.45
BCHE si1	4.78	0.04	0.52
BCHE si2	3.76	0.04	0.42
BCHE si3	6.76	0.03	0.41
BCHE si4	2.57	0.02	0.47
DPP4 si1	2.23	0.11	0.27
DPP4 si2	3.89	0.07	0.23
DPP4 si3	4.03	0.08	0.26
DPP4 si4	1.10	0.13	0.22
GCKR si1	4.34	0.11	n/a
GCKR si2	1.07	0.25	n/a
GCKR si3	4.10	0.06	n/a
GCKR si4	1.56	0.18	n/a
GUCY1B3 si1	5.61	0.12	0.79
GUCY1B3 si2	1.04	0.06	0.90
GUCY1B3 si3	3.33	0.12	0.58
GUCY1B3 si4	1.75	0.07	0.62
MYST1 si1	2.67	0.02	0.61
MYST1 si2	11.63	0.01	0.32
MYST1 si3	8.90	0.01	0.32
MYST1 si4	1.34	0.01	0.47
PPP3CB si1	3.68	0.06	0.59
PPP3CB si2	5.47	0.08	0.49
PPP3CB si3	1.84	0.09	0.68
PPP3CB si4	3.01	0.10	0.34
PDIP1 si1	10.87	0.09	0.53
PDIP1 si2	11.60	0.09	0.46
PDIP1 si3	6.39	0.32	0.81
PDIP1 si4	7.51	0.18	0.45
SLC27A2 si1	6.10	0.09	0.55
SLC27A2 si2	3.90	0.26	0.60
SLC27A2 si3	4.50	0.20	0.30
SLC27A2 si4	2.03	0.04	0.71

Table S10. Lifecycle Rescue S : the fold-rescue (p-value) for each siRNA that scored signific

	entry results				replication results	
	si1	si2	si3	si4	si1	si2
ALG10	1.6 (.001)			2.2 (.018)	1.6(.007)	1.9 (.000)
BCHE		1.7 (.002)				
DPP4	1.9 (.015)	1.7 (.002)	1.8 (.025)	1.6 (.001)		2.1 (.001)
GCKR	1.7 (.000)					
GUCY1B3	2.1 (.028)					
MYST1	2.2 (.031)			1.9 (.017)		
PPP3CB	2.7 (.002)	1.9 (.039)		1.9 (.001)		
PDIP1		1.6 (.022)		1.5 (.036)		1.3 (.042)
SLC27A2	2.0 (.004)	2.0 (.025)		2.8 (.000)		

Ranking by Rescue Scores

	entry results				
	si1	si2	si3	si4	entry rescue score
DPP4	1.9	1.7	1.8	1.6	7.0
SLC27A2	2	2.00		2.80	6.8
PPP3CB	2.7	1.90		1.90	6.5
MYST1	2.2			1.90	4.1
ALG10	1.6			2.2	3.8
PDIP1		1.60		1.50	3.1
GUCY1B3	2.1				2.1
BCHE		1.7			1.7
GCKR	1.7				1.7

entry effector group

	replication results				
	si1	si2	si3	si4	
ALG10	1.6	1.9	2		5.5
DPP4		2.1	2.6		4.7
PPP3CB			1.5		1.5
PDIP1		1.3			1.3
BCHE					0.0
GCKR					0.0
GUCY1B3					0.0
MYST1					0.0
SLC27A2					0.0

replication effector

	RNA production				
	si1	si2	si3	si4	RNA production rescue score
PDIP1	4.2	2.8	5.7	4.9	17.6
MYST1		4	3.2	1.6	8.8
ALG10	3.4	1.6		2.1	7.1
SLC27A2		1.7	2.6	1.8	6.1
PPP3CB	2.2	1.6			3.8
GUCY1B3	1.9				1.9
BCHE					0.0
DPP4					0.0

RNA prodcution effector

GCKR					0.0

	core production results				
	si1	si2	si3	si4	Translation rescue score
PDIP1	10.9	11.6	6.4	7.5	36.4
MYST1	2.7	11.6	8.9		23.2
ALG10	6	5.2	4.6	5.2	21.0
BCHE	4.8	3.8	6.8		15.4
SLC27A2	6.1	3.9	4.5		14.5
PPP3CB	3.7	5.5		3	12.2
DPP4	2.2	3.9	4		10.1
GUCY1B3	5.6		3.3		8.9
GCKR	4.3		4.1		8.4

translation effector group

	egress				
	si1	si2	si3	si4	Egress rescue score
ALG10	3	3		4	10.0
MYST1		5.1			5.1
PDIP1		4.7			4.7
BCHE	2.7				2.7
DPP4					0.0
GCKR					0.0
GUCY1B3					0.0
PPP3CB					0.0
SLC27A2					0.0

egress effector group

cantly in a given lifecycle assay is included. All significantly scoring siRNAs are summed below to yield the

		RNA production results				**production**
si3	**si4**	**si1**	**si2**	**si3**	**si4**	**si1**
2.0 (.002)		3.4 (.003)	1.6 (.014)		2.1 (.016)	6 (.003)
						4.8 (.001)
2.6 (.000)						2.2 (.000)
						4.3 (.012)
		1.9 (.047)				5.6 (.000)
			4.0 (.002)	3.2 (.001)	1.6 (.001)	2.7 (.003)
1.5 (.005)		2.2 (.04)	1.6 (.008)			3.7 (.013)
		4.2 (.000)	2.8 (.01)	5.7 (.001)	4.9 (.001)	10.9 (.000)
			1.7 (.045)	2.6 (.011)	1.8 (.044)	6.1 (.008)

rescue-score for each lifecycle step.

results		
si2	**si3**	**si4**
5.2 (.002)	4.6 (.001)	5.2 (.025)
3.8 (.002)	6.8 (.005)	
3.9 (.008)	4.0 (.009)	
	4.1 (.011)	
	3.3 (.020)	1.8 (.000)
11.6 (.003)	8.9 (.001)	
5.5 (.015)		3.0 (.005)
11.6 (.008)	6.4 (.002)	7.5 (.004)
3.9 (.021)	4.5 (.009)	

egress results			
si1	**si2**	**si3**	**si4**
3 (.001)	3 (.032)		4 (.024)
2.7 (.014)			
	5.1 (.019)		
4.7 (.029)			

Table S11. Non-HCV Viral Rescue Scores

	influenza virus results				
	si1	si2	si3	si4	influenza score sums
ALG10	1.62 (.000)	1.32 (.043)			2.94
BCHE	1.95 (.000)				1.95
DPP4			1.49 (.012)		1.49
GCKR		1.46 (.03)			1.46
GUCY1B	1.51 (.001)				1.51
MYST1		2.25 (.000)		1.62 (.028)	3.87
PPP3CB		1.51 (.005)	1.32 (.044)	1.45 (.006)	4.28
PDIP1			1.44 (.045)		1.44
SLC27A2			2.17 (.000)		2.17

Ranking by Rescue Scores

	influenza virus results				
	si1	si2	si3	si4	influenza rescue score
PPP3CB		1.51 (.005)	1.32 (.044)	1.45 (.006)	4.28
MYST1		2.25 (.000)		1.62 (.028)	3.87
ALG10	1.62 (.000)	1.32 (.043)			2.94
SLC27A2			2.17 (.000)		2.17
BCHE	1.95 (.000)				1.95
GUCY1B	1.51 (.001)				1.51
DPP4			1.49 (.012)		1.49
GCKR		1.46 (.03)			1.46
PDIP1			1.44 (.045)		1.44

	dengue virus results				
	si1	si2	si3	si4	dengue rescue score
PPP3CB		10.33 (0.01	11.47 (0.013)	6.89 (0.026)	28.69
PDIP1	14.71 (0.00	11.11 (0.01	2.78 (0.001)		28.59
ALG10	6.13 (.011)	4.04 (0.025)	10.89 (0.017)	5.07 (0.028)	26.13
MYST1		14.37 (0.006)		3.01 (0.000)	17.38
DPP4	1.99 (0.038)	10.86 (0.00	4.5 (0.007)		17.36
SLC27A2	4.46 (0.038)	3.91 (0.009)	2.82 (0.000)	3.58 (0.020)	14.77
BCHE	6.03 (0.004)	2.63 (0.017)	2.08 (0.046)	3.44 (0.029)	14.18
GCKR		4.10 (0.007)	3.41 (0.018)	2.26 (0.003)	9.77
GUCY1B3		3.38 (0.017)		4.43 (0.021)	7.81

	HCV results for comparison				
	si1	si2	si3	si4	HCV rescue score
PDIP1	10.9	11.6	6.4	7.5	36.4
MYST1	2.7	11.6	8.9		23.2
ALG10	6	5.2	4.6	5.2	21.0
BCHE	4.8	3.8	6.8		15.4
SLC27A2	6.1	3.9	4.5		14.5
PPP3CB	3.7	5.5		3	12.2

DPP4	2.2	3.9	4	10.1
GUCY1B3	5.6		3.3	8.9
GCKR	4.3		4.1	8.4

:fold-rescue (p-value) for each siRNA that scored significantly in a given viral assay is included.

dengue virus results

si1	si2	si3	si4	dengue score sums
6.13 (.011)	4.04 (0.025)	10.89 (0.017)	5.07 (0.028)	26.13
6.03 (0.004)	2.63 (0.017)	2.08 (0.046)	3.44 (0.029)	14.18
1.99 (0.038)	10.86 (0.009)	4.5 (0.007)		17.36
	4.10 (0.007)	3.41 (0.018)	2.26 (0.003)	9.77
	3.38 (0.017)		4.43 (0.021)	7.81
	14.37 (0.006)		3.01 (0.000)	17.38
	10.33 (0.016)	11.47 (0.013)	6.89 (0.026)	28.69
14.71 (0.009)	11.11 (0.019)	2.78 (0.001)		28.59
4.46 (0.038)	3.91 (0.009)	2.82 (0.000)	3.58 (0.020)	14.77

Influenza Virus IEG

Dengue Virus IEGs

HCV IEGs

All significantly scoring siRNAs are summed to yield rescue-score for each viral assay.

Figure S1. The HCV-IEG Screen Platform Detects the Release of Infectious HCV

To determine if our 48h screening assay encompassed late stage HCV lifecycle steps, we quantified both the infectious virions released and the percentage of cells that were scored as infected at 3 sequential time points. These studies revealed that during the timeframe of our assay there is a significant increase in the amount of infectious virions released . In addition, there was a marked elevation in the number of cells infected between 24 and 48h. These findings indicate that our assay encompasses the HCV viral lifecycle through infectious virion egress and an additional round of infection.

(A) A 96 well source plate was prepared by plating 10,000 Huh7.5.1 cells per well, then 24hr later infecting the cells with JFH1 (MOI = 1). At the indicated time points, viral supernatant was collected from the source plate well, and serially diluted (10x dilutions) then administered to a destination plate containing uninfected cells. The destination plate was then incubated for 48h post-inoculation, then fixed and stained to determine the percent infection. The X axis indicates fold dilution of supernatant collected at indicated times. The Y axis represents the percent infection determined by staining each replicate plate with anti –HCV core antibody and DNA stain. * indicates p<=.05 compared to 6H values.

(B) TCID50s of the viral supernant collected at 6, 24, and 48h post-infection in **(A).**

(C) Images of destination plates from (A, B). The time post-inoculation is indicated. Green and blue indicate HCV core and DNA staining, respectively. Percent infection of the destination plate is indicated.

(D) The kinetics of viral spread from cell to cell was assessed. Huh7.5.1 cells were plated in 96 well plates followed 12h later by inoculation with JFH1 in serial 2-fold dilutions. Cells were incubated for 9, 24, or 48h then fixed and stained for HCV core protein expression and cellular DNA, followed by imaging to assess the percentage of cells infected with HCV. X axis indicates fold dilution of inoculum, Y axis indicates percent infection at the indicated time post-inoculation. Values indicate mean +/-SEM, n=3. * indicates $p<=0.05$ when compared to 9H values. Arrows indicate percent infection for the viral dilution yielding an MOI of 1, the MOI used in the screen, and point to values of 4.9 and 47 percent infection at 24H and 48H, respectively. n=9.

(E) Images of plates from **(D),** neat viral inoculation at time indicated. Green and blue indicate HCV core and DNA staining, respectively. Percent infection of the destination plate is indicated.

Figure S2. Image Scoring Optimization Enhanced Sensitivity and Specificity for Rescue of Viral Infection from IFN-α. Custom analysis improves both sensitivity and accuracy of scoring for HCV infected cells. Algorithm: The algorithm used first segments the DAPI channel to pick up all the individual nuclei. A rough thresholding is performed for the entire DAPI image. The nuclear segmentation is then refined by adjusting the threshold on a per-object basis and dividing clustered nuclei. To score all cells in the GFP channel, the GFP image is smoothed and image background is calculated using smoothed image. Thresholding is performed for the GFP image using scaled image background. To score positive cells, the algorithm matches nuclear segmentation with GFP segmentation to find GFP positive nuclei. In order to remove the large circular debris in the GFP channel, the size and shape of all the objects identified are measured, and the objects with area and roundness above a given threshold are removed. Images represent cells infected with JFH1 HCV, stained with HCV core Ab, and imaged for 1000 ms in FITC channel.

(A) Raw image, where HCV-infected cells appear white in FITC channel.

(B) The raw image from **(A)** was scored using low threshold Metamorph parameters that captured all infected cells, but also scored reflected bubbles (black arrows). Scored pixels are indicated in green.

(C) Raw image **(A)** was scored using high threshold Metamorph parameters that did not capture artifact (black arrow). This method failed to detect multiple HCV positive cells (blue arrows).

(D) Custom analysis. enabled scoring of additional HCV positive cells (blue arrows), without capturing artifact (black arrow).

Figure S3. Select HCV-IEGs are Required for IFN-α's Suppression of an Established HCV Infection

(A). Huh7.5.1 cells were transfected with the indicated siRNAs for 72h, then infected with JFH1 for 48h, all in the absence of IFN-α .

(B) Huh7.5.1 cells were transfected with the indicated siRNAs, then infected with JFH1 (MOI of 1) and incubated for 24h. Cells were then treated with IFN-α (100 IU/ml) for 48h. Cells were stained for HCV core and DNA then imaged and analyzed for percent infection. Y axis values represent the fold rescue of HCV infection (percent infection, measured via HCV core staining) above the levels detected in cells transfected with non-targeting siRNA. X axis values represent individual siRNA duplex. siRNA targets are indicated in titles.

Figure S4. PDIP1 or BCHE overexpression does not inhibit HCV replication

We exogenously expressed PDIP1 to test its sufficiency as an IEG. PDIP1 exists in both long and short isoforms, both of which were targeted by all 4 siRNA sequences recovered in this screen[27]. Plasmids containing each isoform were transiently transfected into Huh7.5.1 cells for 24h, followed by JFH1 infection. Forty eight hours post-infection, we quantified the levels of intracellular JFH1 using qRT-PCR (**Fig. S4a,b**). These studies showed that neither the short nor long isoforms of PDIP1 were sufficient to decrease viral RNA production. Therefore, either the basal levels of PDIP1 are saturating, or PDIP1 acts in concert with, and/or elicits the actions of, additional IEGs to halt HCV. Expression of a second IEG, BCHE, in full length and truncated forms, yielded similar results (**Fig. S4c,d**).

(A) Huh7.5.1 cells were transiently transfected with the indicated vectors expressing PDIP1β (long isoform), or PDIP1α (short isoform). 24h following transfection, medium was replaced with fresh medium containing JFH1 (MOI = 1). Forty eight hours after infection RNA was isolated for qRT–PCR evaluation of PDIP1 levels and normalized to GAPDH.

(B) Huh7.5.1 cells were transiently transfected with the indicated vectors expressing BCHE (full length), or a truncated form of BCHE, then processed and evaluated for BCHE levels as in (A).

(C) qRT-PCR was performed to quantify the levels of JFH1, normalized to GAPDH, from (**A**).

(D) qRT-PCR was performed to quantify the levels of JFH1, normalized to GAPDH, from (**B**).

Y axes indicate mRNA fold change (arbitrary units), X axes indicate the transfected plasmid. Bars indicate the mean value +/- SEM, n=3 for all experiments.

Figure S5. IFN-α Inhibits HCV Entry

Prior to assessing the effects of IEG knockdown on HCV pseudoparticle (pp) entry, the inhibitory effect of IFN-α on HCVpp, compared to VSVpp, was evaluated. While fully infectious VSV is known to be IFN-α sensitive, to our knowledge only one study has assessed the IFN-α sensitivity of VSVpp entry [31]. This study, performed in human alveolar cells, detected inhibition of VSVpp entry when assessed 1.5h post-infection. In contrast, our assessment of VSVpp entry at 48h post infection in human hepatoma cells did not detect IFN-α mediated suppression of VSV entry. In our system, dose titration of IFN-α led to a modest decrease in HCVpp entry; this inhibition was specific for entry and not for subsequent steps required for ZSG reporter gene expression (transcription and translation), because treatment of cells subsequent to infection with HCVpps did not inhibit reporter expression. Entry pseudoparticles were constructed using JFH1 (HCV-E1 E2) or VSV (VSV-G) envelope, HIV gag-pol (PACS2), and a GFP reporter construct (pAGM).

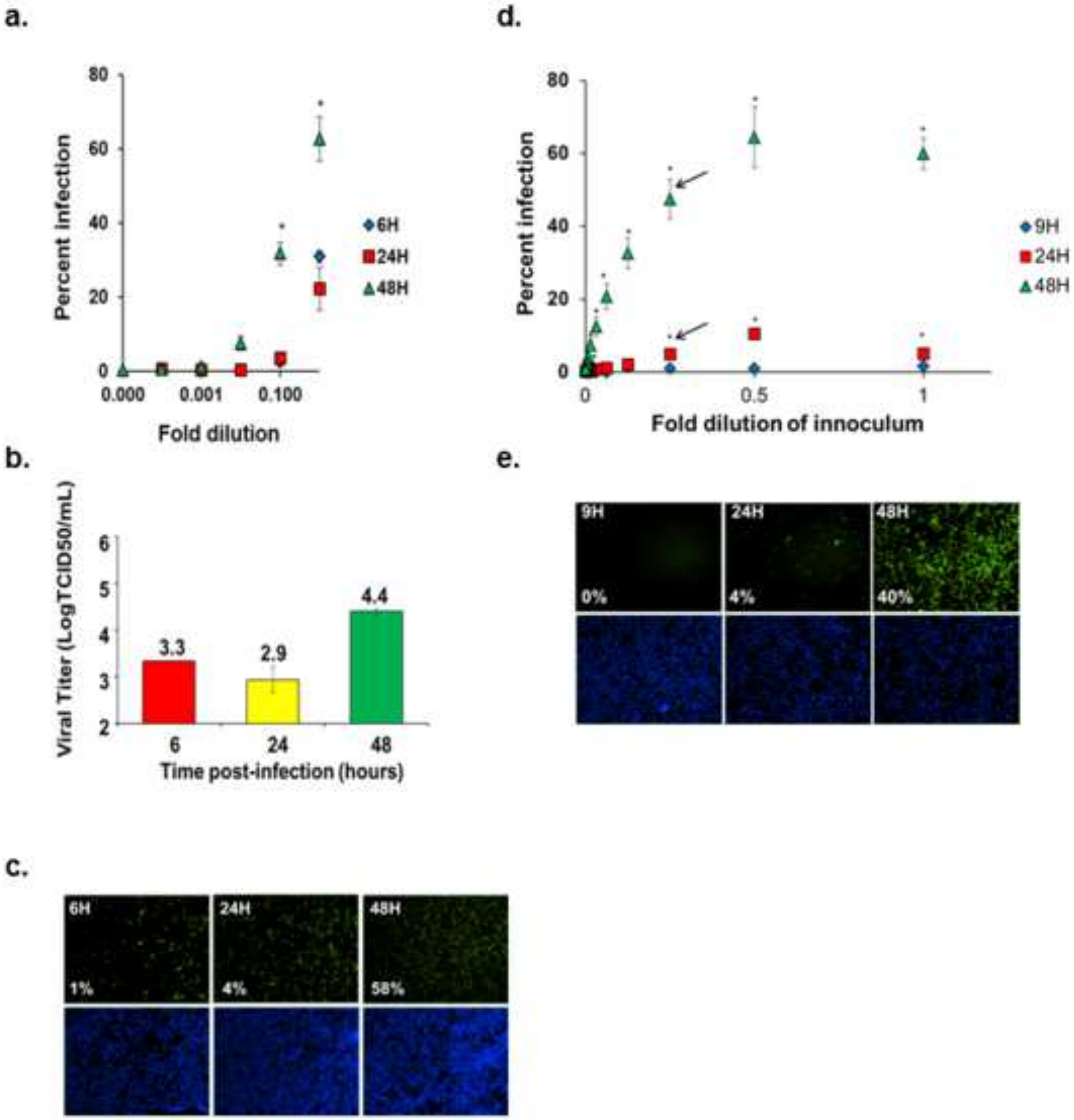
(A) HCVpp but not VSVpp are IFN-α sensitive. Cells were seeded then treated with IFN-α at the indicated concentration (X axis) for 24h, followed by removal of IFN-α and infection with pseudoparticles for 48h. Cells were then fixed, stained with Hoechst DNA stain, imaged for GFP and DNA, and scored for percent reporter-positive cells.

(B) IFN-α sensitivity is not due to impaired reporter transcription / translation. Post-entry treatment with IFN-α does not suppress HCV pseudoparticle signal production**.** Huh7.5.1 cells were seeded then infected with HCV pseudoparticles and incubated for one week to allow maximal protein expression to take place. Cells were then treated with IFN-α. X axis represents IFN-α dose, Y axis indicates percent reporter-positive cells.

(C) Corresponding images for **(A).** Images represent GFPpp reporter (green) in top row, and corresponding DNA stain (blue) in bottom row. From left to right, cells were infected with HCV-E1 E2 pp's, no IFN-α; HCV-E1 E2 pp's, 100 IU/ml IFN-α; VSVpp's, no IFN-α; VSVpp's, 100 IU/ml IFN-α.

Figure S6. Schematic of IFN Effector Groups Active at Each Step of the HCV Viral Lifecycle HCV lifecycle steps are outlined. The infectious HCV virion interacts with the cellular CD81, claudin, occludin, SRBP1 and LDL receptors, followed by clathrin mediated endocytosis and fusion within an acidic endosomal compartment. The positive sense single stranded RNA HCV genome is then released, and localized to the endoplasmic reticulum. Through interaction with host ribosomes, HCV +ssRNA is then translated into a single polyprotein (initial translation), followed by auto and cell-mediated cleavage to form 3 structural proteins (core, E1 and E2) and 7 non-structural proteins (the p7 ion channel, NS2, NS3, NS4A, NS4B, NS5A, and NS5B). The non-structural proteins form an HCV RNA replication complex, including the RNA polymerase NS5B, and transcribe – sense ssRNA from the +ssRNA HCV genome. This –ssRNA template is then used by the same replication complex for +ssRNA replication (initial replication). Freshly transcribed +ssRNA transcripts are then translated into additional HCV polyprotein (amplified translation) which is cleaved and used for 1) assembly of mature virions and 2) additional +ssRNA transcription (amplified replication). Mature virions are transported to the cell membrane and released. These fully infectious virions can then infect surrounding cells, representing secondary infection. Using assays for entry (pseudoparticles), replication (replicon), HCV core protein production (core IF), HCV RNA production (qRT-PCR) and egress (supernatant transfer), specific lifecycle steps rescued by each IEG knockdown were characterized. The IEG knockdowns that rescued each lifecycle step from IFN-α are indicated in boxes.

Fig S1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Percent infection
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60
40
20
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0.000
0.001
0.100
Fold dilution
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■24H
▲48H
b.
Viral Titer (LogTCID50/mL)
6
5
4
3
2
3.3
2.9
4.4
6
24
48
Time post-infection (hours)
c.
6H
24H
48H
1%
4%
58%
d.
Percent infection
80
60
40
20
0
0
0.5
1
Fold dilution of innoculum
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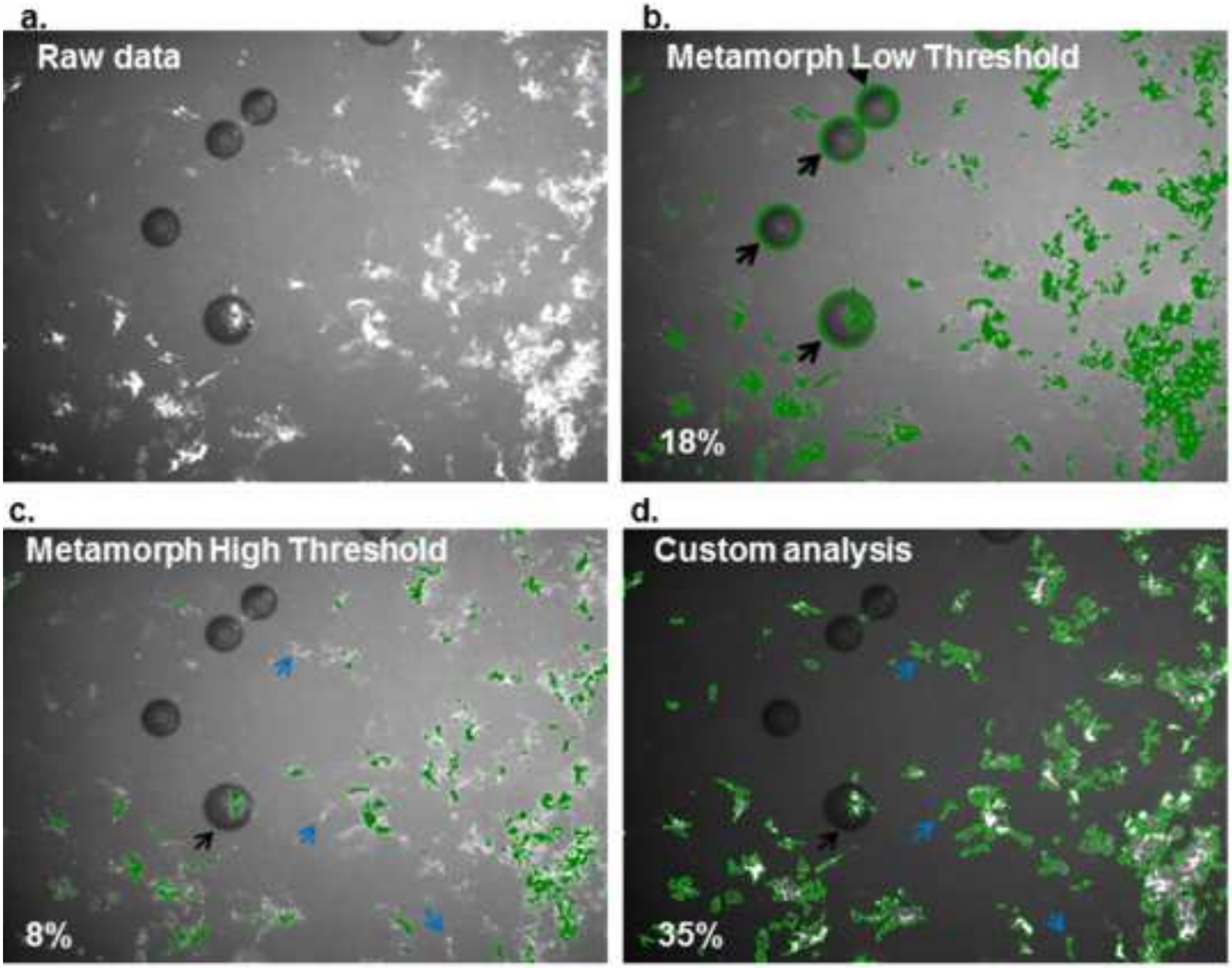
■24H
▲48H
e.
9H
24H
48H
0%
4%
40%

Fig.S1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c.
Metamorph High Threshold
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d.
Custom analysis
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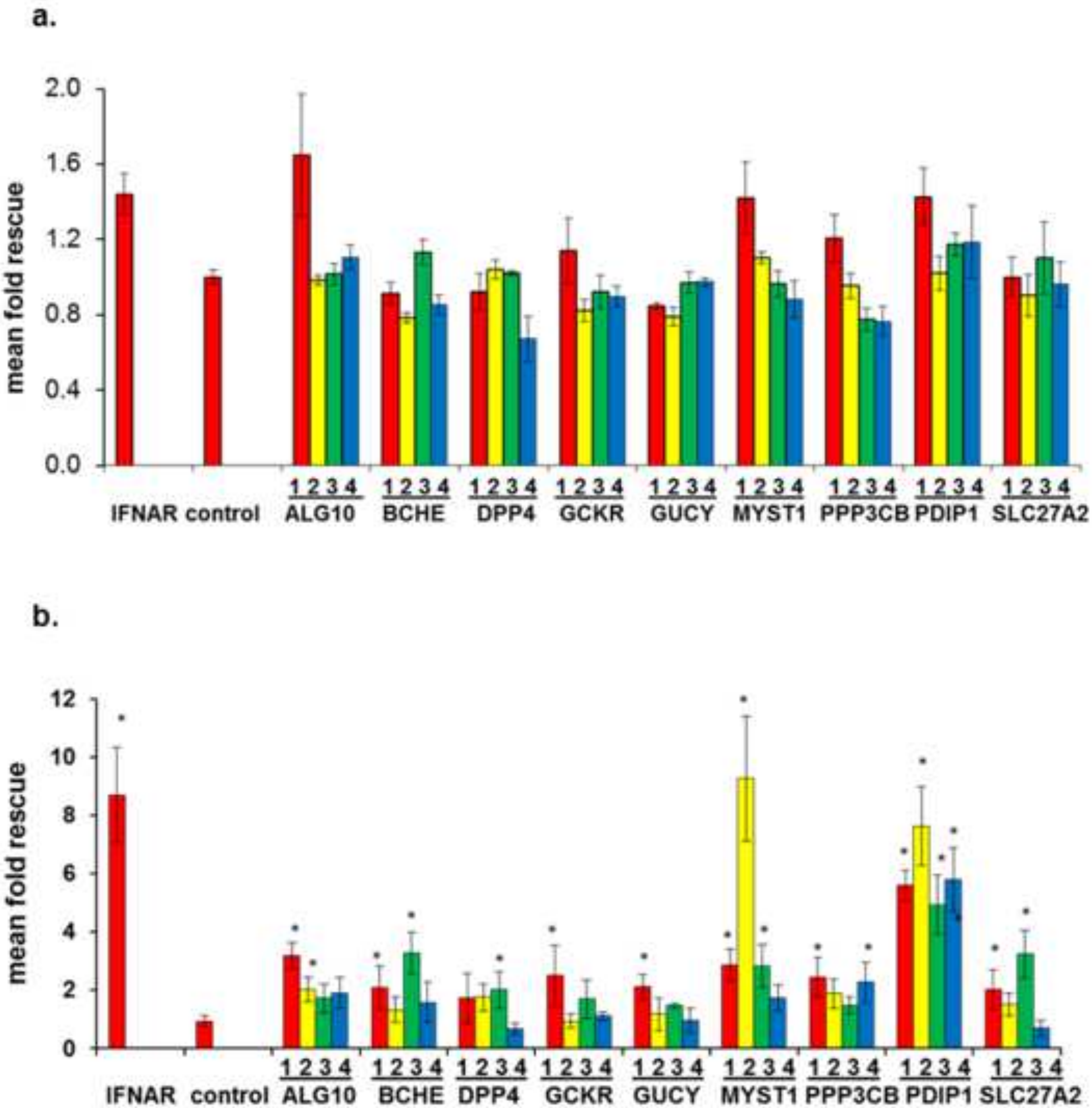
Fig. S2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mean fold rescue
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1.6
1.2
0.8
0.4
0.0
1 2 3 4
IFNAR
control
ALG10
BCHE
DPP4
GCKR
GUCY
MYST1
PPP3CB
PDIP1
SLC27A2
b.
mean fold rescue
12
10
8
6
4
2
0
*
1 2 3 4
IFNAR
control
ALG10
BCHE
DPP4
GCKR
GUCY
MYST1
PPP3CB
PDIP1
SLC27A2

Fig. S3

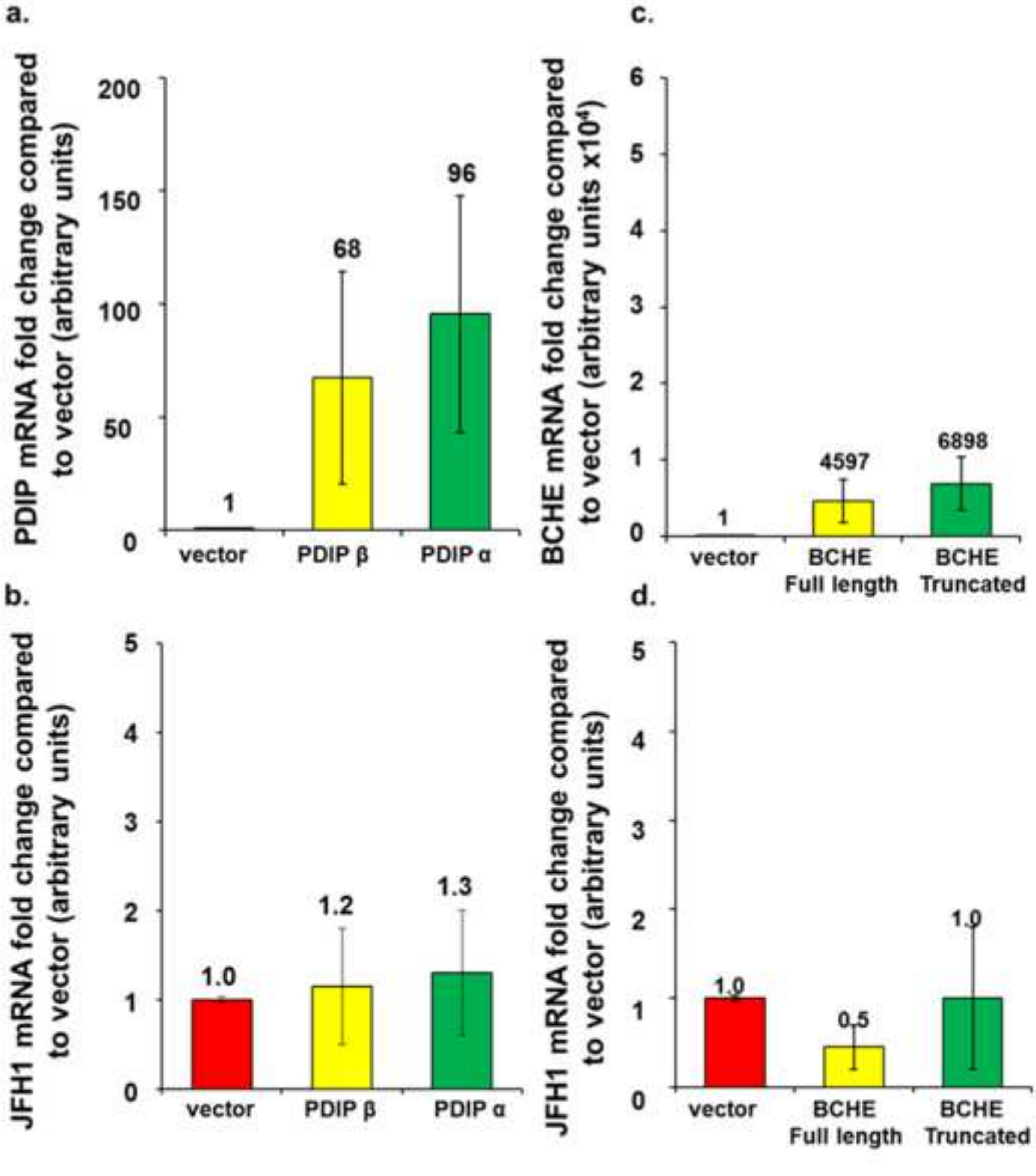
a.
PDIP mRNA fold change compared to vector (arbitrary units)
0
50
100
150
200
1
68
96
vector
PDIP β
PDIP α
b.
JFH1 mRNA fold change compared to vector (arbitrary units)
0
1
2
3
4
5
1.0
1.2
1.3
vector
PDIP β
PDIP α
c.
BCHE mRNA fold change compared to vector (arbitrary units x10⁴)
0
1
2
3
4
5
6
1
4597
6898
vector
BCHE Full length
BCHE Truncated
d.
JFH1 mRNA fold change compared to vector (arbitrary units)
0
1
2
3
4
5
1.0
0.5
1.0
vector
BCHE Full length
BCHE Truncated

Fig.S4

Fig S5

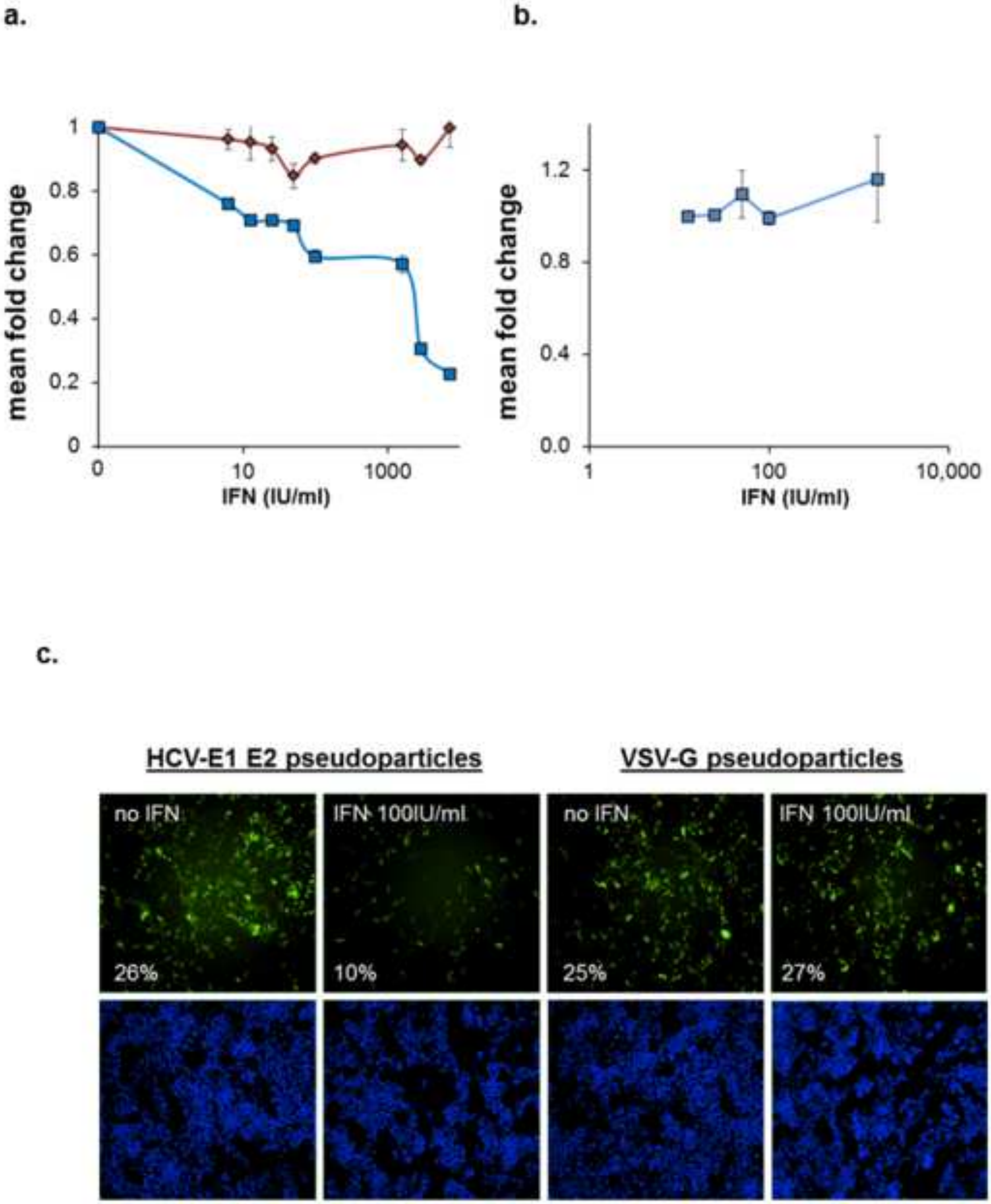
a.
b.
mean fold change
1
0.8
0.6
0.4
0.2
0
0
10
1000
IFN (IU/ml)
mean fold change
1.2
0.8
0.4
0.0
1
100
10,000
IFN (IU/ml)
c.
HCV-E1 E2 pseudoparticles
VSV-G pseudoparticles
no IFN
IFN 100IU/ml
no IFN
IFN 100IU/ml
26%
10%
25%
27%

Fig.S5

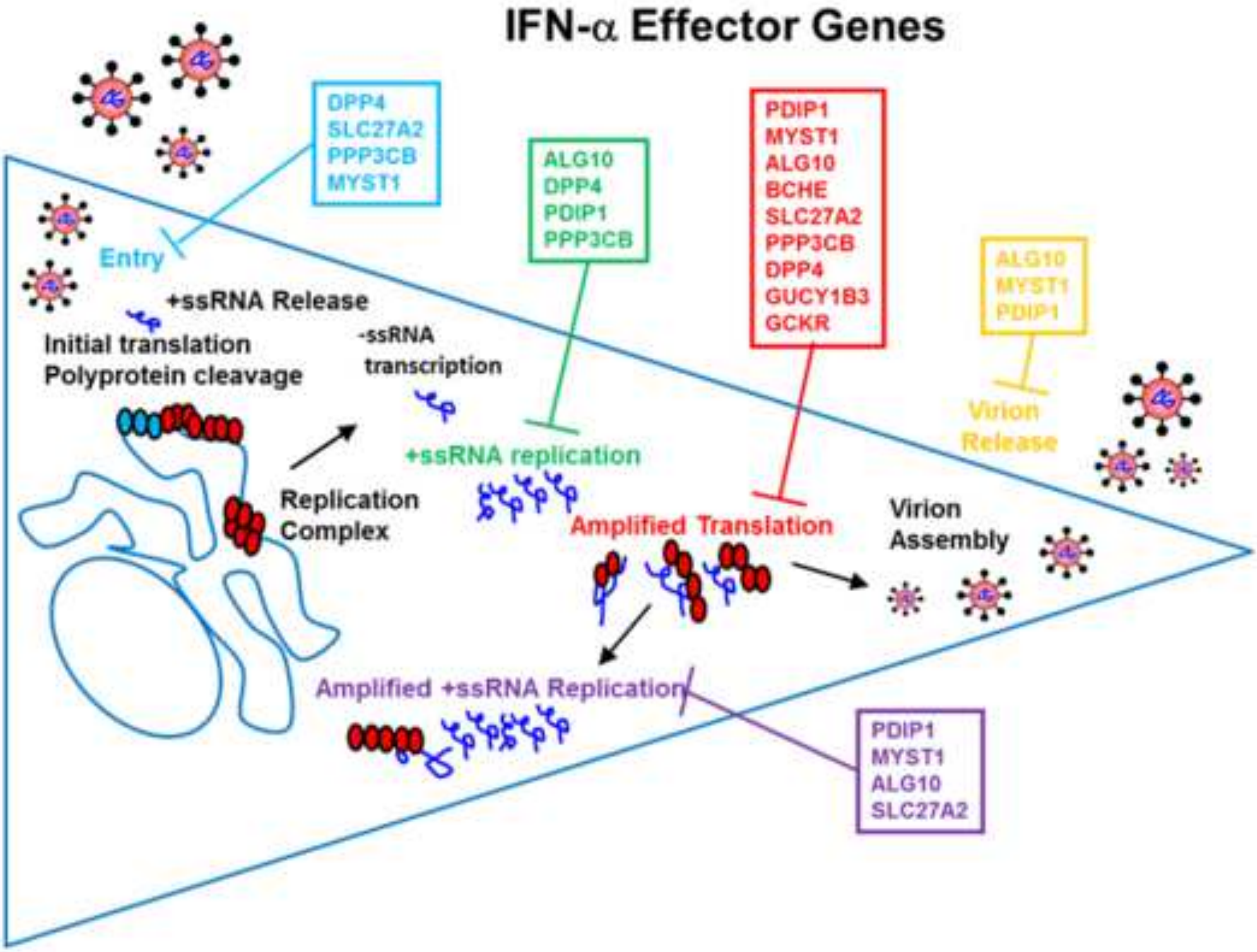
IFN-α Effector Genes
DPP4
SLC27A2
PPP3CB
MYST1
Entry
ALG10
DPP4
PDIP1
PPP3CB
PDIP1
MYST1
ALG10
BCHE
SLC27A2
PPP3CB
DPP4
GUCY1B3
GCKR
ALG10
MYST1
PDIP1
Virion
Release
+ssRNA Release
Initial translation
Polyprotein cleavage
-ssRNA
transcription
+ssRNA replication
Replication
Complex
Amplified Translation
Virion
Assembly
Amplified +ssRNA Replication
PDIP1
MYST1
ALG10
SLC27A2

Fig.S6