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Table 20 Genes with significant ChIP-on-CHIP bindings sites (MAT score p-value < 0.05) and significant siRNA expression values (p-value < 0.05)

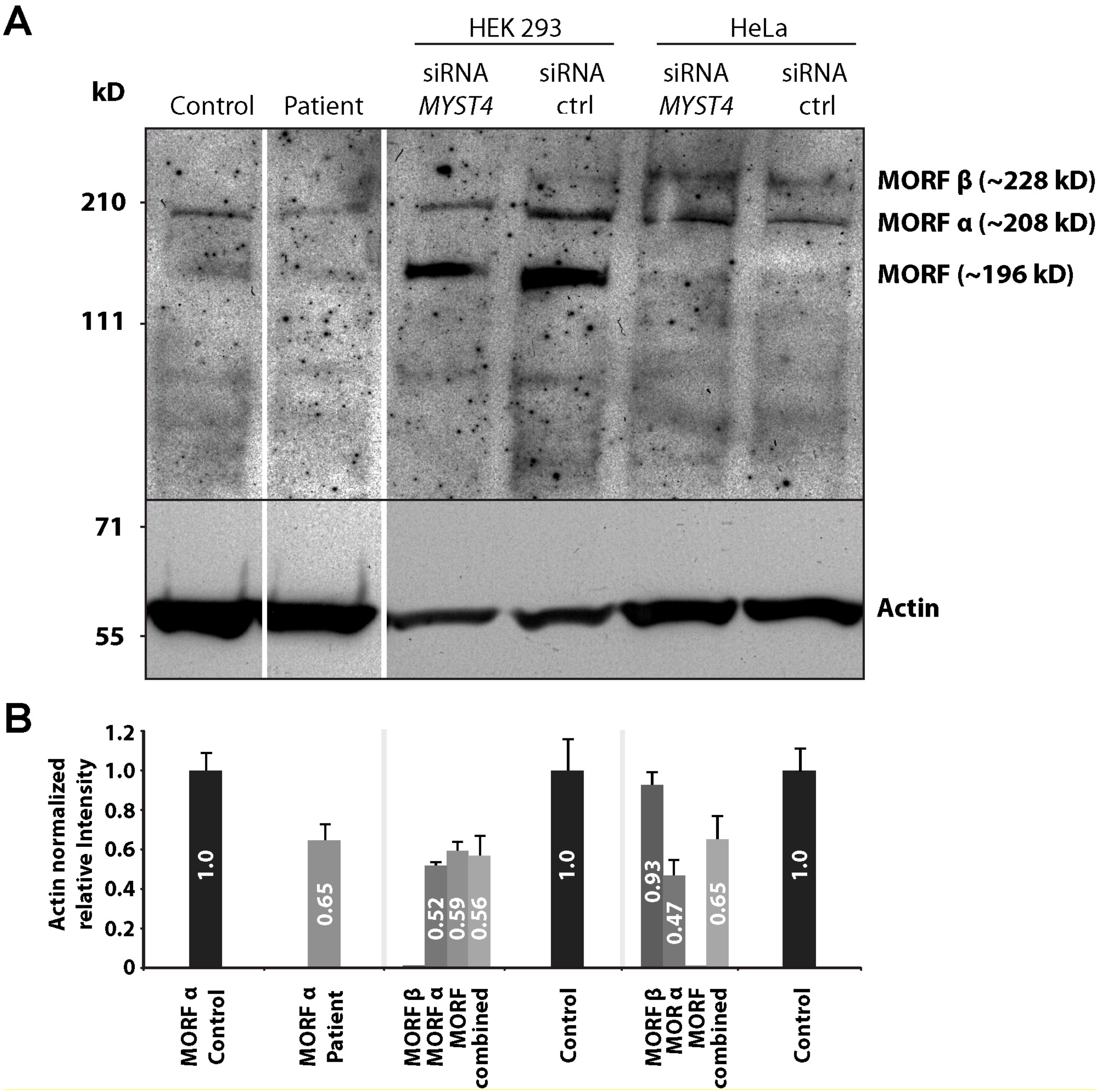
Table 21 KEGG pathways of significant differentially expressed genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < 0.05) (DAVID functional annotation)

Table 22 KEGG pathways of significant differentially expressed genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < 0.05) (Pathway Express calculation)

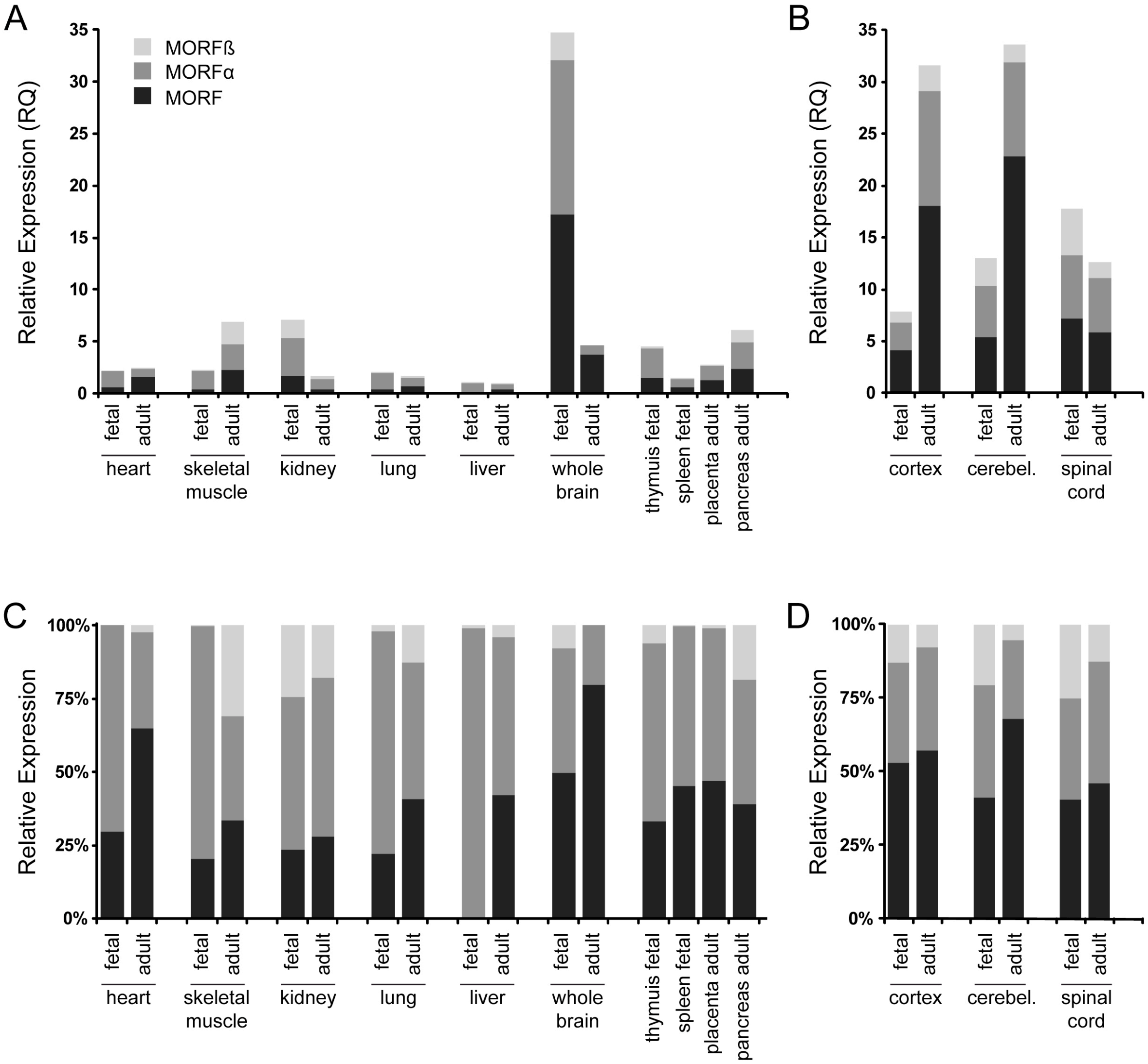
Table 23 Genes with ChIP-on-CHIP bindings sites (* region p-value < 0.05) and siRNA expression values of the KEGG MAPK signaling pathway

Table 24 Quantitative real-time PCR validation of genes with ChIP-on-CHIP bindings sites (region p-value < 0.05) and signififcant HEK & HeLA siRNA expression values and additional expression of patient versus 4 control lymphoblastoid cell lines values of the KEGG MAPK signaling pathway.

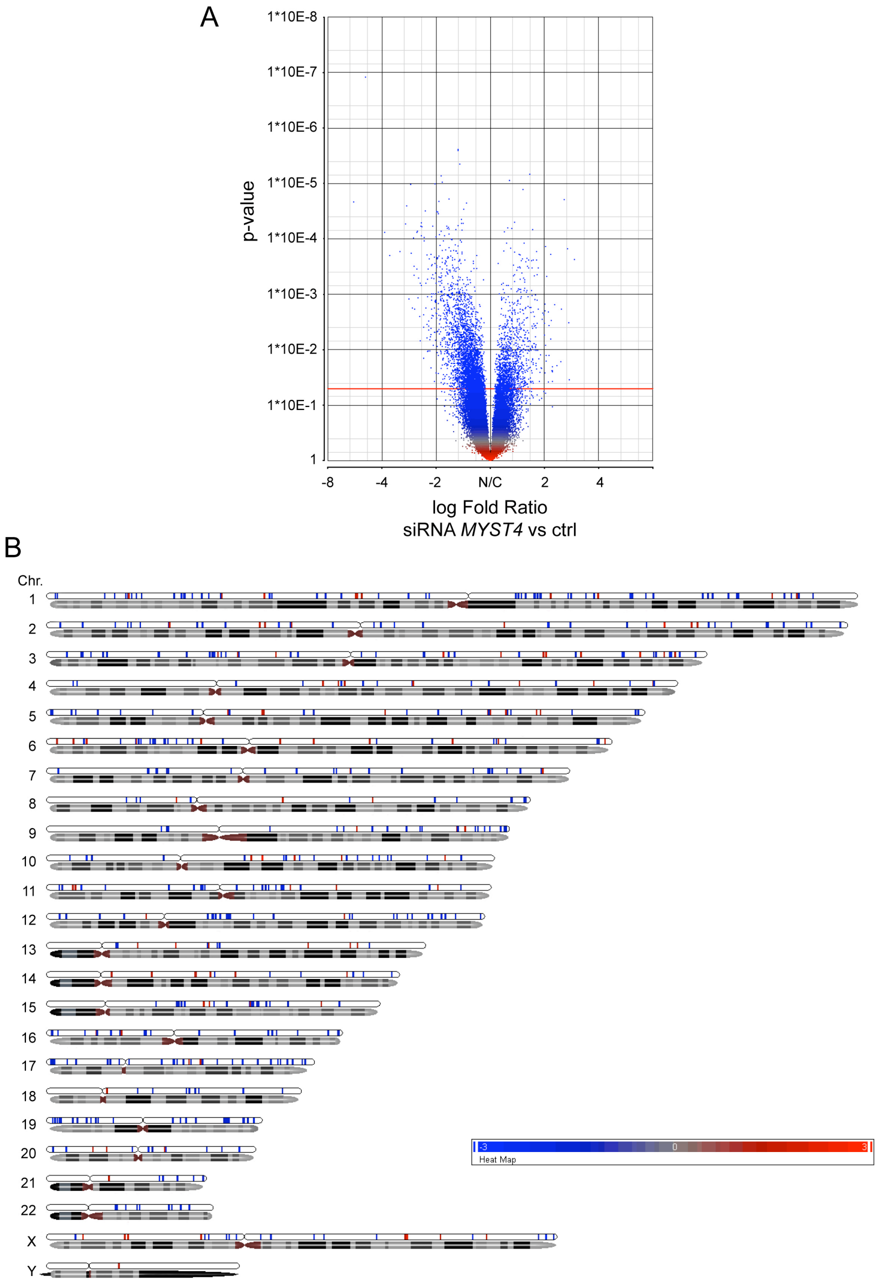
Table 25 Tissue expression pattern of significantly enriched genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < 0.05)



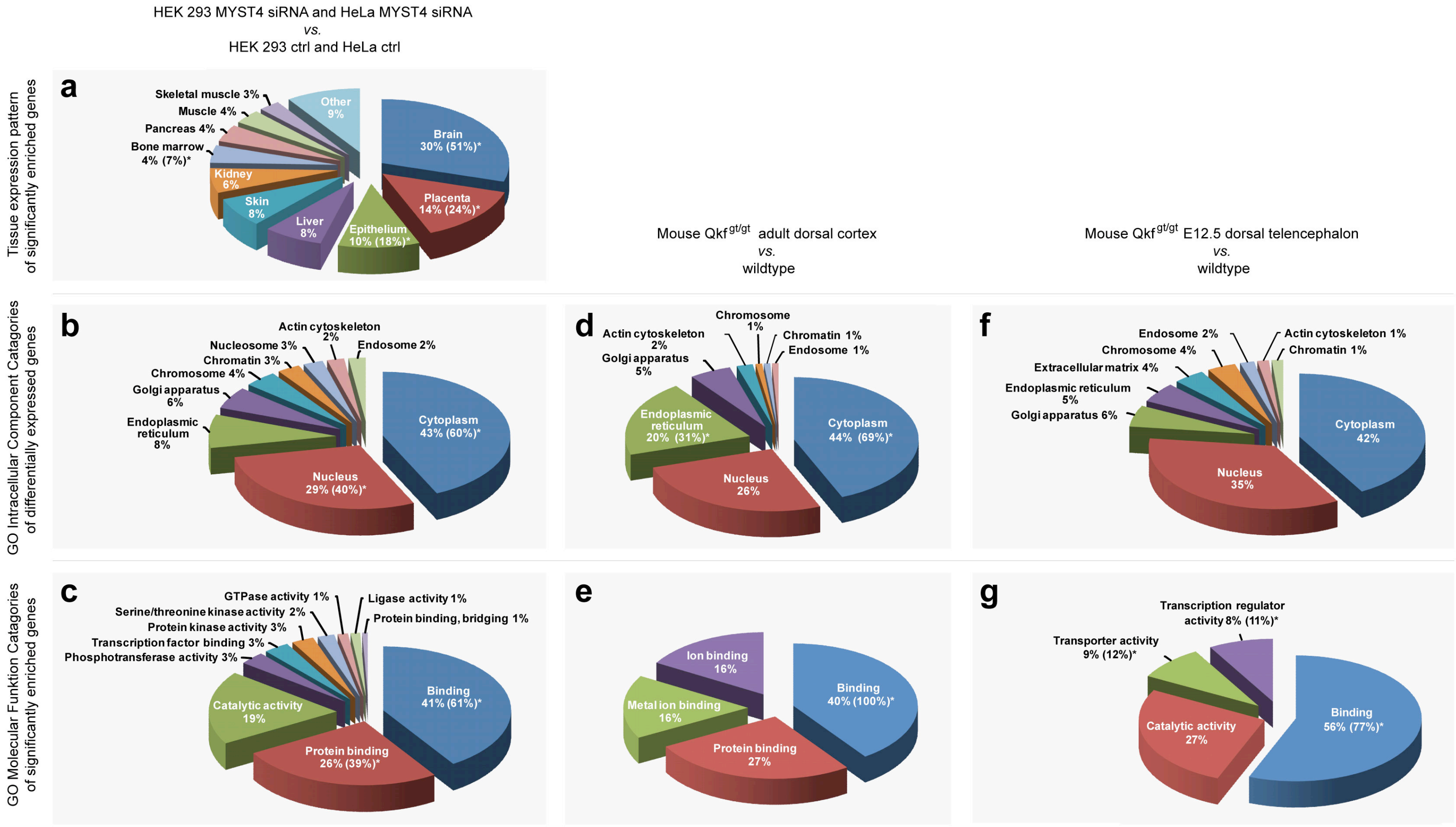
Supplemental Figure 1 Western blot analysis of MYST4. **(A)** Lymphoblastoid cell lines of the patient and a normal control in the first 2 lanes presenting mainly the MORF α isoform. Note the reduced protein band and the absence of a detectable fusionprotein. HEK 293 and HeLa cell lines after MYST4 specific siRNA and scrambled siRNA. Note the different pattern of MYST4 isoforms (MORF β, MORF α, and MORF). The lanes were run on the same gel but were contiguous. **(B)** Quantification of MYST4 isoforms normalized to the respective actin band. Note the significantly reduced protein levels in the patient, and after siRNA in HEK 293 and HeLa cell lines.



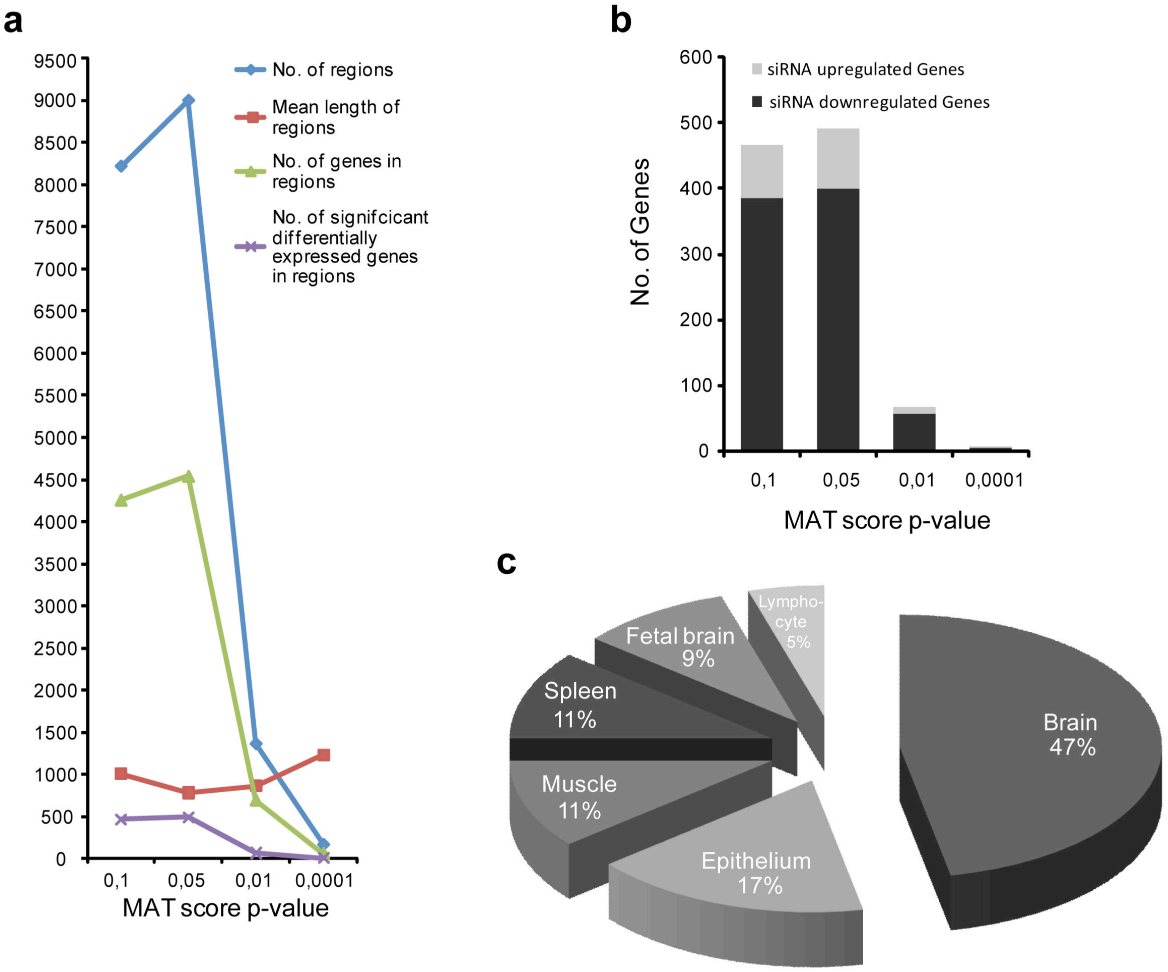
Supplemental Figure 2 Expression pattern of *MYST4* isoforms. **(A, B)** Relative expression levels of *MYST4* of all three isoforms. Note the highest expression levels in the fetal brain. Whereas in skeletal muscle expression levels increases up to 7fold from fetal to adult, whole brain expression levels decrease more than 7fold in adult brain. **(C, D)** The percentage of relative isoform expression is shown in relation to overall expression.



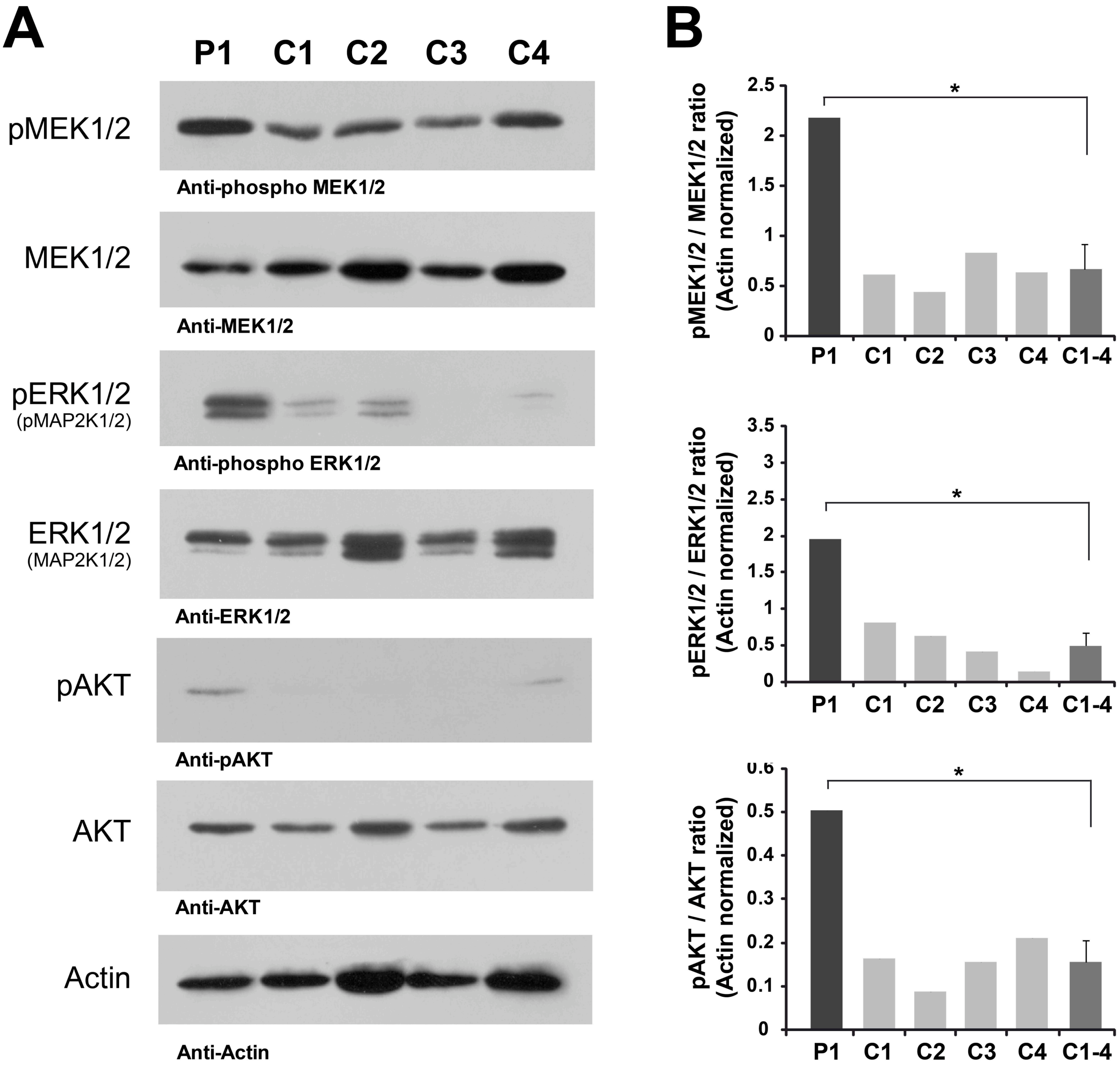
Supplemental Figure 3 Differentially expressed genes of HEK293/HeLa *Myst4* siRNA vs. controls. **(A)** Vulcano plot of differentially expressed genes. Each dot represents one gene. Note the red line marking p-value of 0.05. **(B)** Heat map and chromosomal location of significant differentially expressed genes (p-value < 0.05) with a fold change < - 1.5 oder > 1.5. Note significant higher count of downregulated genes.



Supplemental Figure 4 Summary of gene expression pattern and gene ontology (GO) of significant differentially expressed genes (p-value < 0.05). Tissue expression pattern and GO of intracellular component catagories and molecular function catagories of **(A-C)** HEK293/HeLa *MYST4* siRNA vs. controls, **(D, E)** mouse QKf$^{gt/gt}$ adult dorsal cortex and **(F, G)** mouse QKf$^{gt/gt}$ E12.5 dorsal telencephalon vs. controls. Note similar main categories for intracellular component and molecular function catagories.



Supplemental Figure 5 Results of the *MYST4* ChIP-CHIP analysis of HEK293/HeLa cell lines. **(A)** Length of the regions and number of genes identified by the MAT algorithm. Whereas the mean length of the regions is independent from the cut-off MAT score p-value, the number of genes rapidly decreases with higher significance. **(B)** The ratio of down- to up-regulated genes remains between 4:1 to 5:1 indicating transcriptional activation of genes by *MYST4*. **(C)** Tissue expression pattern (DAVID functional annotation of Uniprot tissues) of significantly enriched genes with CHIP binding sites-on-ChIP (MAT score p-value < 0.05) confirms importance of MYST4 regulation in brain development and function and muscle matching the phenotype in human and mouse.



Supplemental Figure 6 Biochemical characterization of MEK, ERK and AKT phosphorylation levels. **(A)** Increased MAPK signalling activity of the patient (P1) containing the MYST4 mutation compared to 4 control samples (C1-4). Cells were analyzed for the phosphorylation level of MEK/pMEK1/2 (MAP2K/pMAP2K1/2), ERK/pERK1/2 and AKT/pAKT. Total amounts of MEK, ERK and AKT and actin in cell lysates are shown and the specificity of the antibody is specified below each panel. **(B)** After normalization to Actin densitrometric analysis confirmed significant increased ratios of all three measured parameters (* t test $p < 0.05$).

Supplemental Tables

Table 1 Results of the ANOVA calculation ($p < 0.05$; FC < -1.5 or > 1.5) of HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl

Gene Symbol	Gene Title	Entrez Gene	Probeset ID	FDR-adjusted p-value	Ratio	Fold-Change
ARL5A	ADP-ribosylation factor-like 5A	26225	226617_at	2.16E-05	0.17	-5.75
ARL5A	ADP-ribosylation factor-like 5A	26225	218150_at	7.58E-05	0.26	-3.87
---	Transcribed locus	---	238431_at	2.00E-04	0.28	-3.62
---	Primary neuroblastoma cDNA, clone:Nbla11485	---	226520_at	1.70E-04	0.32	-3.17
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual tra	23169	209712_at	5.37E-05	0.34	-2.96
---	CDNA FLJ30090 fis, clone BNGH41000015	---	243176_at	2.52E-05	0.34	-2.91
MXD1	MAX dimerization protein 1	4084	226275_at	1.21E-03	0.35	-2.82
LCOR	ligand dependent nuclear receptor corepressor	84458	228454_at	1.81E-04	0.36	-2.74
CASP6	caspase 6, apoptosis-related cysteine peptidase	839	209790_s_at	1.75E-03	0.37	-2.71
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual tra	23169	209711_at	9.70E-05	0.38	-2.67
CDK6	cyclin-dependent kinase 6	1021	224851_at	4.51E-04	0.38	-2.65
CDK6	cyclin-dependent kinase 6	1021	224847_at	3.11E-04	0.38	-2.65
DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	9829	204720_s_at	1.84E-03	0.38	-2.63
---	CDNA FLJ30652 fis, clone DFNES2000011	---	224811_at	7.60E-05	0.39	-2.56
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	8760	212864_at	3.52E-04	0.39	-2.56
---	CDNA clone IMAGE:4819084	---	235456_at	7.26E-05	0.39	-2.53
SWAP70	SWAP-70 protein	23075	209307_at	1.17E-03	0.40	-2.52
CDK6	cyclin-dependent kinase 6	1021	224848_at	5.05E-04	0.40	-2.51
---	Transcribed locus	---	236350_at	2.52E-03	0.41	-2.47
CASP7	caspase 7, apoptosis-related cysteine peptidase	840	207181_s_at	6.37E-04	0.41	-2.45
---	Transcribed locus	---	228479_at	6.93E-03	0.41	-2.44
CENPO	centromere protein O	79172	226118_at	5.89E-05	0.41	-2.43
LOC149832	hypothetical protein LOC149832	149832	228456_s_at	8.87E-05	0.41	-2.42
FHL2	four and a half LIM domains 2	2274	202949_s_at	5.14E-05	0.41	-2.42
---	CDNA FLJ33585 fis, clone BRAMY2012163	---	1556194_a_at	6.87E-04	0.42	-2.40
CUGBP2	CUG triplet repeat, RNA binding protein 2	10659	202156_s_at	6.08E-05	0.42	-2.40
LOC731484	hypothetical LOC731484	730069	242539_at	2.33E-03	0.43	-2.35
---	Transcribed locus	---	230659_at	3.94E-03	0.43	-2.35
UBASH3B	ubiquitin associated and SH3 domain containing, B	84959	238462_at	1.42E-02	0.43	-2.34
TMEM64	transmembrane protein 64	169200	225972_at	1.07E-04	0.43	-2.33
HIST1H3H	histone cluster 1, H3h	8357	206110_at	9.48E-05	0.43	-2.33
WDR40A	WD repeat domain 40A	25853	224789_at	3.12E-05	0.44	-2.29
CETN2	centrin, EF-hand protein, 2	1069	209194_at	6.24E-04	0.44	-2.28
---	CDNA FLJ31919 fis, clone NT2RP7004964	---	214949_at	1.76E-03	0.44	-2.28
DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	349152	215143_at	3.53E-03	0.44	-2.25
ROD1	ROD1 regulator of differentiation 1 (S. pombe)	9991	214697_s_at	6.19E-03	0.44	-2.25
NLGN1	neuroligin 1	22871	205893_at	1.94E-04	0.45	-2.24
TMF1	TATA element modulatory factor 1	7110	214948_s_at	1.12E-03	0.45	-2.23
GOLM1	golgi membrane protein 1	51280	217771_at	5.30E-04	0.45	-2.22
CDK6	cyclin-dependent kinase 6	1021	235287_at	1.08E-02	0.45	-2.22
SAR1A	SAR1 gene homolog A (S. cerevisiae)	56681	201542_at	3.47E-04	0.45	-2.21
---	Transcribed locus	84901	229235_at	1.05E-02	0.45	-2.21
CRTAP	cartilage associated protein	10491	1555889_a_at	4.38E-03	0.46	-2.20
KIAA0368	KIAA0368	23392	212427_at	3.73E-03	0.46	-2.19
TRIOBP	TRIO and F-actin binding protein	11078	210276_s_at	2.32E-04	0.46	-2.18
CDH13	cadherin 13, H-cadherin (heart)	1012	204726_at	1.06E-02	0.46	-2.16
ROD1	ROD1 regulator of differentiation 1 (S. pombe)	9991	224617_at	6.61E-03	0.46	-2.16
---	Transcribed locus	---	235286_at	5.88E-03	0.46	-2.15
NUPL1	nucleoporin like 1	9818	204435_at	2.10E-02	0.47	-2.14
ROD1	ROD1 regulator of differentiation 1 (S. pombe)	9991	224618_at	4.16E-03	0.47	-2.14
C20orf177	chromosome 20 open reading frame 177	---	225313_at	1.89E-04	0.47	-2.13

CRTAP	cartilage associated protein	10491	1554464_a_at	5.32E-03	0.47	-2.13
LPP	LIM domain containing preferred translocation partner in lipoma	4026	202822_at	1.26E-03	0.47	-2.12
SNX1	sorting nexin 1	6642	213364_s_at	1.10E-03	0.47	-2.12
CCNYL1	Cyclin Y-like 1	151195	227280_s_at	1.86E-03	0.47	-2.12
ARHGAP1	Rho GTPase activating protein 1	392	202117_at	3.04E-04	0.47	-2.12
PEX19	peroxisomal biogenesis factor 19	5824	201707_at	2.70E-03	0.47	-2.11
NUBP1	nucleotide binding protein 1 (MinD homolog, E. coli)	4682	203978_at	5.08E-04	0.47	-2.11
DSC3	desmocollin 3	1825	206032_at	9.78E-04	0.47	-2.11
CUGBP2	CUG triplet repeat, RNA binding protein 2	10659	202158_s_at	2.41E-03	0.47	-2.11
TPM1	tropomyosin 1 (alpha)	7168	206117_at	2.93E-04	0.48	-2.10
WDR35	WD repeat domain 35	57539	226889_at	4.48E-04	0.48	-2.09
EPPK1	epiplakin 1	83481	232164_s_at	2.48E-03	0.48	-2.08
HAS2	hyaluronan synthase 2	3037	206432_at	8.32E-03	0.48	-2.07
CRIPT	cysteine-rich PDZ-binding protein	9419	218643_s_at	9.91E-04	0.48	-2.07
TMEM64	transmembrane protein 64	169200	225974_at	5.22E-04	0.48	-2.06
NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 intera	84901	217526_at	4.87E-03	0.49	-2.04
C14orf129	chromosome 14 open reading frame 129	51527	223239_at	2.13E-04	0.49	-2.04
PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	204897_at	3.72E-02	0.49	-2.04
BPGM	2,3-bisphosphoglycerate mutase	669	203502_at	1.75E-03	0.49	-2.04
---	CDNA clone IMAGE:3462401	---	228008_at	2.78E-04	0.49	-2.04
CCDC50	coiled-coil domain containing 50	152137	226713_at	4.82E-03	0.49	-2.03
BLCAP	bladder cancer associated protein	10904	201032_at	1.02E-05	0.49	-2.03
KDSR	3-ketodihydrosphingosine reductase	2531	229850_at	1.33E-03	0.49	-2.02
---	---	---	227921_at	1.26E-03	0.50	-2.02
CASP6	caspase 6, apoptosis-related cysteine peptidase	839	211464_x_at	1.40E-03	0.50	-2.01
SPIN3	spindlin family, member 3	169981	1555882_at	6.66E-03	0.50	-2.01
MGC16275	hypothetical protein MGC16275	85001	1558166_at	4.17E-04	0.50	-2.01
HP1BP3	heterochromatin protein 1, binding protein 3	50809	1554251_at	9.94E-04	0.50	-2.01
CYFIP2	cytoplasmic FMR1 interacting protein 2	26999	220999_s_at	2.59E-02	0.50	-2.01
GRPEL1	GrpE-like 1, mitochondrial (E. coli)	80273	212434_at	9.14E-05	0.50	-2.00
EPPK1	epiplakin 1	83481	232165_at	2.17E-03	0.50	-2.00
---	Transcribed locus	---	227959_at	6.23E-04	0.50	-2.00
DIDO1	death inducer-obliterator 1	11083	227335_at	1.32E-03	0.50	-2.00
RBM17	RNA binding motif protein 17	84991	224780_at	3.24E-04	0.50	-1.99
USP3	ubiquitin specific peptidase 3	9960	226652_at	3.19E-05	0.50	-1.99
LASP1	LIM and SH3 protein 1	3927	200618_at	3.04E-04	0.50	-1.98
ZNF805	zinc finger protein 805	390980	238436_s_at	2.69E-03	0.50	-1.98
---	CDNA FLJ41728 fis	---	227125_at	2.24E-03	0.51	-1.98
FN1	fibronectin 1	2335	211719_x_at	8.75E-03	0.51	-1.98
FBXO9	F-box protein 9	26268	212991_at	1.13E-02	0.51	-1.97
FKBP14	FK506 binding protein 14	55033	235311_at	4.76E-03	0.51	-1.97
C11orf59	chromosome 11 orf 59	55004	223009_at	2.20E-04	0.51	-1.97
IQCE	IQ motif containing E	23288	204202_at	2.32E-04	0.51	-1.97
TUBG1	tubulin, gamma 1	7283	201714_at	4.62E-03	0.51	-1.96
TBC1D24	TBC1 domain family, member 24	57465	227908_at	3.26E-05	0.51	-1.96
CCDC117	coiled-coil domain containing 117	150275	225644_at	2.21E-04	0.51	-1.96
GLO1	glyoxalase I	2739	200681_at	1.46E-03	0.51	-1.95
LYPD1	LY6/PLAUR domain containing 1	116372	212909_at	1.27E-02	0.51	-1.95
PLAGL2	pleiomorphic adenoma gene-like	5326	202925_s_at	1.85E-03	0.51	-1.94
MED8	mediator complex subunit 8	112950	213126_at	3.51E-05	0.51	-1.94
HLA-B	major histocompatibility complex, class I, B	4277	206247_at	9.22E-04	0.52	-1.94
VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	143187	236849_at	2.67E-02	0.52	-1.94
WDR68	WD repeat domain 68	10238	221744_at	4.85E-04	0.52	-1.94
CCDC50	coiled-coil domain containing 50	152137	228693_at	2.39E-03	0.52	-1.93
TPK1	thiamin pyrophosphokinase 1	27010	221218_s_at	5.88E-04	0.52	-1.93
GRHL1	grainyhead-like 1 (Drosophila)	29841	222830_at	2.10E-05	0.52	-1.93
---	CDNA FLJ42315 fis	---	230300_at	4.32E-03	0.52	-1.93
WDR68	WD repeat domain 68	10238	224748_at	2.06E-04	0.52	-1.92
---	CDNA FLJ37658 fis	---	226485_at	8.32E-05	0.52	-1.92
ACTA2	actin, alpha 2	59	200974_at	5.17E-03	0.52	-1.91
SSFA2	Sperm specific antigen 2	6744	229744_at	3.38E-03	0.52	-1.91

RAB11A	RAB11A, member RAS oncogene family	8766	200864_s_at	1.32E-04	0.52	-1.91
---	Transcribed locus	---	241879_at	5.02E-04	0.53	-1.90
C19orf56	chromosome 19 orf 56	51398	217780_at	6.93E-04	0.53	-1.90
CCDC25	coiled-coil domain containing 25	55246	218125_s_at	2.90E-03	0.53	-1.90
NLGN1	Neuroligin 1	22871	231361_at	3.21E-04	0.53	-1.90
C3orf10	chromosome 3 orf 10	55845	224575_at	1.26E-03	0.53	-1.89
CCDC50	coiled-coil domain containing 50	152137	235051_at	8.06E-03	0.53	-1.89
BCR	breakpoint cluster region	400892	226602_s_at	7.89E-03	0.53	-1.89
MXD1	MAX dimerization protein 1	4084	228846_at	1.05E-02	0.53	-1.89
C9orf58	chromosome 9 open reading frame 58	83543	223075_s_at	1.09E-03	0.53	-1.89
EDEM1	ER degradation enhancer, mannosidase alpha-like 1	9695	203279_at	8.90E-04	0.53	-1.89
SRI	sorcin	6717	208921_s_at	5.81E-04	0.53	-1.89
XRN1	5'-3' exoribonuclease 1	54464	225814_at	2.45E-03	0.53	-1.89
CRTAP	cartilage associated protein	10491	201380_at	8.06E-03	0.53	-1.89
LOC149832	Hypothetical protein LOC149832	149832	230502_s_at	4.72E-03	0.53	-1.89
NFATC2IP	nuclear factor of activated T-cells	84901	217527_s_at	7.30E-03	0.53	-1.88
---	CDNA clone IMAGE:6208446	---	221844_x_at	2.77E-03	0.53	-1.88
---	CDNA clone IMAGE:5277883	---	1558445_at	1.22E-03	0.53	-1.88
FKBP14	FK506 binding protein 14	55033	219390_at	7.32E-05	0.53	-1.88
HIST1H2AC	histone cluster 1, H2ac	8334	215071_s_at	1.32E-03	0.53	-1.88
TTC9	tetratricopeptide repeat domain 9	23508	213172_at	7.40E-06	0.53	-1.88
SLC25A14	solute carrier family 25 mem 14	9016	204587_at	4.93E-04	0.53	-1.87
---	Transcribed locus	---	243996_at	3.88E-02	0.53	-1.87
GNA11	guanine nucleotide binding protein (G protein), alpha 11	2767	213766_x_at	4.17E-04	0.53	-1.87
ZNF738	zinc finger protein 738	148203	229700_at	1.17E-02	0.53	-1.87
FN1	fibronectin 1	2335	210495_x_at	2.19E-02	0.53	-1.87
---	Transcribed locus	---	221973_at	1.11E-02	0.54	-1.87
FBXO9	F-box protein 9	26268	238472_at	3.93E-03	0.54	-1.87
CCNDBP1	cyclin D-type binding-protein 1	23582	223084_s_at	8.75E-04	0.54	-1.86
MAN2A1	mannosidase, alpha, class 2A, member 1	4124	226538_at	9.14E-04	0.54	-1.86
CAMSAP1	calmodulin regulated spectrin-associated protein 1	157922	212711_at	5.58E-04	0.54	-1.86
KDSR	3-ketodihydrosphingosine reductase	2531	1558279_a_at	1.05E-03	0.54	-1.86
ATAD2B	ATPase family, AAA domain containing 2B	54454	213387_at	6.36E-04	0.54	-1.86
MDH2	malate dehydrogenase 2, NAD (mitochondrial)	4191	213333_at	4.64E-04	0.54	-1.86
MAN2A1	mannosidase, alpha, class 2A, member 1	4124	235103_at	1.18E-03	0.54	-1.85
ECM2	extracellular matrix protein 2	1842	206101_at	1.90E-02	0.54	-1.85
CUGBP2	CUG triplet repeat, RNA BP 2	10659	202157_s_at	8.66E-03	0.54	-1.85
---	Clone IMAGE:111714 mRNA	---	228466_at	6.70E-03	0.54	-1.85
ARL8B	ADP-ribosylation factor-like 8B	55207	217852_s_at	9.57E-06	0.54	-1.85
USP6NL	USP6 N-terminal like	9712	238164_at	6.22E-03	0.54	-1.85
ZNF805	zinc finger protein 805	390980	235398_at	1.05E-03	0.54	-1.85
MED8	mediator complex subunit 8	112950	213127_s_at	1.62E-04	0.54	-1.85
GATAD2A	GATA zinc finger domain containing 2A	54815	222526_at	2.64E-04	0.54	-1.85
IFRD2	interferon-related developmental regulator 2	7866	209100_at	2.26E-04	0.54	-1.84
PPT1	palmitoyl-protein thioesterase 1	5538	200975_at	3.46E-04	0.54	-1.84
TMEM64	transmembrane protein 64	169200	242338_at	1.54E-02	0.54	-1.84
SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	60559	218817_at	1.45E-02	0.55	-1.83
FN1	fibronectin 1	2335	216442_x_at	3.40E-02	0.55	-1.83
CKAP4	cytoskeleton-associated protein 4	10970	200999_s_at	4.00E-03	0.55	-1.83
LOC100130506	hypothetical protein LOC100130506	---	236656_s_at	2.17E-03	0.55	-1.82
FN1	fibronectin 1	2335	212464_s_at	2.82E-02	0.55	-1.82
SUSD1	sushi domain containing 1	64420	226264_at	1.33E-03	0.55	-1.82
SLC25A37	solute carrier family 25, member 37	51312	226179_at	2.20E-03	0.55	-1.82
RPS15A	Ribosomal protein S15a	6210	235309_at	1.28E-03	0.55	-1.82
BMP2K	BMP2 inducible kinase	55589	59644_at	4.21E-02	0.55	-1.82
FIBIN	fin bud initiation factor	387758	226769_at	1.41E-02	0.55	-1.82
---	Transcribed locus	---	230728_at	1.08E-04	0.55	-1.81
VANGL1	vang-like 1	81839	219330_at	2.75E-03	0.55	-1.81
GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	2589	201724_s_at	7.45E-04	0.55	-1.81
ARHGAP26	Rho GTPase activating protein 26	23092	226576_at	1.61E-03	0.55	-1.81

PKD2	polycystic kidney disease 2	5311	203688_at	1.04E-03	0.55	-1.81
ITGB4	integrin, beta 4	3691	204990_s_at	5.95E-03	0.55	-1.81
AHI1	Abelson helper integration site 1	54806	221569_at	1.33E-03	0.55	-1.81
TP53INP1	tumor protein p53 inducible nuclear protein 1	94241	225912_at	6.49E-03	0.55	-1.80
KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	3768	207110_at	1.59E-03	0.56	-1.80
BTBD7	BTB (POZ) domain containing 7	55727	224945_at	2.27E-03	0.56	-1.80
GNA11	guanine nucleotide binding protein (G protein), alpha 11	2767	40562_at	1.94E-03	0.56	-1.80
C12orf44	chromosome 12 orf 44	60673	218214_at	8.84E-05	0.56	-1.80
SHISA2	shisa homolog 2	387914	230493_at	3.35E-02	0.56	-1.80
LPGAT1	lysophosphatidylglycerol acyltransferase 1	9926	202651_at	8.10E-04	0.56	-1.80
GNG12	guanine nucleotide binding protein (G protein), gamma 12	55970	212294_at	9.80E-04	0.56	-1.79
CKAP4	cytoskeleton-associated protein 4	10970	200998_s_at	4.02E-02	0.56	-1.79
---	Transcribed locus	---	242486_at	1.19E-02	0.56	-1.79
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	4329	221589_s_at	1.86E-02	0.56	-1.79
---	Transcribed locus	---	230399_at	1.55E-03	0.56	-1.79
NNT	nicotinamide nucleotide transhydrogenase	23530	238530_at	2.51E-03	0.56	-1.79
GALNAC4S-6ST	B cell RAG associated protein	51363	203066_at	2.68E-04	0.56	-1.79
---	CDNA clone IMAGE:5313062	---	234998_at	2.83E-04	0.56	-1.78
IDH1	isocitrate dehydrogenase 1	3417	1555037_a_at	1.08E-02	0.56	-1.78
RGS20	regulator of G-protein signaling	8601	210138_at	2.99E-02	0.56	-1.78
---	Transcribed locus	---	228925_at	6.05E-03	0.56	-1.78
CREBL2	cAMP responsive element binding protein-like 2	1389	201990_s_at	4.41E-03	0.56	-1.77
---	CDNA FLJ30652 fis	---	235000_at	4.62E-04	0.56	-1.77
SLU7	SLU7 splicing factor homolog	10569	227990_at	2.46E-04	0.56	-1.77
---	Transcribed locus	---	235685_at	3.82E-03	0.56	-1.77
---	Transcribed locus	---	239292_at	7.96E-03	0.56	-1.77
---	---	---	244107_at	2.78E-03	0.56	-1.77
ALMS1	Alstrom syndrome 1	7840	214221_at	7.26E-03	0.57	-1.77
DOCK4	dedicator of cytokinesis 4	9732	205003_at	1.78E-02	0.57	-1.77
KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	3768	232289_at	8.90E-03	0.57	-1.77
TRIOBP	TRIO and F-actin binding protein	11078	202795_x_at	1.60E-04	0.57	-1.77
GNA11	guanine nucleotide binding protein (G protein), alpha 11	2767	564_at	1.77E-03	0.57	-1.76
TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	6882	1558136_s_at	2.61E-04	0.57	-1.76
RABL2B	RAB, member of RAS oncogene family-like 2B	11159	219151_s_at	2.71E-03	0.57	-1.76
EEA1	early endosome antigen 1	8411	225885_at	2.11E-03	0.57	-1.75
HYPK	Huntingtin interacting protein K	25764	218680_x_at	3.24E-03	0.57	-1.75
NBPF14	neuroblastoma breakpoint family, member 14	400818	227926_s_at	3.17E-03	0.57	-1.75
SLC6A6	solute carrier family 6, member 6	6533	205920_at	1.03E-02	0.57	-1.75
KCTD12	potassium channel tetramerisation domain cont. 12	115207	212192_at	3.35E-03	0.57	-1.75
H2BFS	H2B histone family, member S	54145	208579_x_at	5.41E-03	0.57	-1.75
BTBD7	BTB (POZ) domain containing 7	55727	224943_at	2.88E-03	0.57	-1.75
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	3417	201193_at	1.79E-02	0.57	-1.75
BCAT2	branched chain aminotransferase 2, mitochondrial	587	203576_at	5.90E-05	0.57	-1.75
HIST1H2AI	histone cluster 1, H2ai	8969	207156_at	3.48E-04	0.57	-1.75
CAMSAP1	calmodulin regulated spectrin-associated protein 1	157922	212710_at	3.05E-04	0.57	-1.74
MTF1	metal-regulatory transcription factor 1	4520	227150_at	1.16E-02	0.57	-1.74
CSRP1	cysteine and glycine-rich prot. 1	1465	200621_at	4.94E-03	0.57	-1.74
MARCH5	membrane-associated ring finger (C3HC4) 5	54708	218582_at	3.91E-04	0.57	-1.74
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6391	215088_s_at	2.27E-03	0.57	-1.74
---	CDNA FLJ37917 fis	---	229460_at	1.28E-03	0.57	-1.74
SLC47A1	solute carrier family 47, mem. 1	55244	219525_at	1.92E-02	0.57	-1.74
KRT17	keratin 17	3872	205157_s_at	2.80E-02	0.57	-1.74
FAM105B	family with sequence similarity 105, member B	90268	229268_at	2.19E-03	0.58	-1.74
SLITRK5	SLIT and NTRK-like family, mem. 5	26050	214930_at	1.88E-03	0.58	-1.74
---	Transcribed locus	---	238700_at	9.96E-04	0.58	-1.74
LOC644617	hypothetical LOC644617	644617	221235_s_at	3.75E-03	0.58	-1.74
XRN1	5'-3' exoribonuclease 1	54464	233632_s_at	1.63E-03	0.58	-1.74
PCBP2	poly(rC) binding protein 2	5094	213263_s_at	1.06E-03	0.58	-1.74
MAGED2	melanoma antigen family D, 2	10916	208682_s_at	2.11E-03	0.58	-1.74
THSD4	thrombospondin, type I, domain containing 4	79875	222835_at	1.32E-02	0.58	-1.74

KIAA0999	KIAA0999 protein	23387	213034_at	2.87E-03	0.58	-1.74
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	5567	202742_s_at	1.41E-03	0.58	-1.74
NAV1	neuron navigator 1	89796	224772_at	1.02E-02	0.58	-1.74
C1orf19	chromosome 1 orf 19	116461	225399_at	2.90E-03	0.58	-1.74
ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2	91647	213057_at	2.26E-04	0.58	-1.73
SLC25A14	solute carrier family 25, mem. 14	9016	211855_s_at	4.09E-04	0.58	-1.73
CDK6	cyclin-dependent kinase 6	1021	243000_at	2.45E-03	0.58	-1.73
---	---	---	228443_s_at	1.09E-02	0.58	-1.73
HIST1H2BK	histone cluster 1, H2bk	85236	209806_at	1.27E-03	0.58	-1.73
SPATA18	spermatogenesis associated 18 homolog (rat)	132671	229331_at	7.59E-03	0.58	-1.73
NASP	nuclear autoantigenic sperm protein (histone-binding)	4678	201969_at	8.16E-03	0.58	-1.73
TRIOBP	TRIO and F-actin binding protein	11078	216210_x_at	6.41E-05	0.58	-1.73
ARGLU1	arginine and glutamate rich 1	55082	227448_at	2.19E-02	0.58	-1.73
GLCE	glucuronic acid epimerase	26035	213552_at	2.43E-03	0.58	-1.73
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6391	210131_x_at	1.48E-03	0.58	-1.73
EIF2C2	Eukaryotic translation initiation factor 2C, 2	27161	225569_at	4.11E-02	0.58	-1.73
ARID3B	AT rich interactive domain 3B	10620	218964_at	7.27E-03	0.58	-1.73
---	CDNA FLJ34899 fis, clone NT2NE2018594	---	226719_at	2.09E-04	0.58	-1.72
---	Transcribed locus	---	230918_at	1.83E-02	0.58	-1.72
TCTEX1D2 /// TM4SF19	transmembrane 4 L six family member 19 /// Tctex1 domain containing 2	255758	228606_at	4.83E-03	0.58	-1.72
PHKA1	phosphorylase kinase, alpha 1 (muscle)	5255	229876_at	8.18E-03	0.58	-1.72
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	2767	213944_x_at	4.36E-04	0.58	-1.72
---	CDNA clone IMAGE:6576427	---	228156_at	1.16E-02	0.58	-1.72
---	CDNA FLJ34038 fis, clone FCBBF2005645	---	244779_at	1.16E-02	0.58	-1.72
KIAA0999	KIAA0999 protein	23387	204156_at	1.97E-03	0.58	-1.72
CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	55450	218309_at	1.08E-02	0.58	-1.72
FAM130A1	family with sequence similarity 130, member A1	81566	221260_s_at	1.53E-03	0.58	-1.72
FAT3	FAT tumor suppressor homolog 3 (Drosophila)	120114	1558964_at	1.90E-02	0.58	-1.72
DUSP6	dual specificity phosphatase 6	1848	208892_s_at	9.10E-03	0.58	-1.72
SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-de	6715	204675_at	6.38E-04	0.58	-1.72
ICK	intestinal cell (MAK-like) kinase	22858	204569_at	5.18E-03	0.58	-1.71
MAN2A1	mannosidase, alpha, class 2A, member 1	4124	205105_at	1.46E-02	0.58	-1.71
---	CDNA clone IMAGE:3867353	---	240121_x_at	1.94E-03	0.58	-1.71
DSC3	desmocollin 3	1825	206033_s_at	1.06E-03	0.59	-1.71
TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	129685	1556178_x_at	2.22E-04	0.59	-1.71
---	Transcribed locus	---	241826_x_at	1.67E-03	0.59	-1.71
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	221	205640_at	1.61E-02	0.59	-1.71
SAPS2	SAPS domain family, member 2	9701	202792_s_at	5.43E-03	0.59	-1.70
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	2767	204248_at	8.40E-03	0.59	-1.70
ARID3A	AT rich interactive domain 3A (BRIGHT-like)	1820	205865_at	1.60E-03	0.59	-1.70
FASTK	Fas-activated serine/threonine kinase	10922	210975_x_at	6.21E-05	0.59	-1.70
VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	51652	222437_s_at	1.03E-03	0.59	-1.70
ZNF512	zinc finger protein 512	84450	225050_at	3.70E-04	0.59	-1.70
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	5567	202741_at	1.93E-05	0.59	-1.70
ENY2	enhancer of yellow 2 homolog (Drosophila)	56943	226776_at	1.23E-02	0.59	-1.70
ETNK1	ethanolamine kinase 1	55500	225290_at	6.24E-03	0.59	-1.70
ZNF805	zinc finger protein 805	390980	238437_at	8.55E-04	0.59	-1.70
---	Transcribed locus	---	236200_at	6.30E-03	0.59	-1.70
ETNK1	ethanolamine kinase 1	55500	226432_at	6.42E-03	0.59	-1.70
SAMM50	sorting and assembly machinery component 50 homolog	25813	201570_at	8.50E-04	0.59	-1.70
WIBG	within bgcn homolog (Drosophila)	84305	242304_at	6.60E-05	0.59	-1.70
LOC100130476	Similar to hCG2036711	---	243871_at	1.17E-02	0.59	-1.70
SLC38A9	solute carrier family 38, member 9	153129	235241_at	1.86E-03	0.59	-1.69
PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4	5303	204572_s_at	3.09E-02	0.59	-1.69
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	7088	228284_at	3.85E-03	0.59	-1.69
MACROD1	MACRO domain containing 1	28992	219188_s_at	1.66E-02	0.59	-1.69
SEC14L1	SEC14-like 1 (S. cerevisiae)	6397	202084_s_at	5.48E-03	0.59	-1.69
DVL3	dishevelled, dsh homolog 3	1857	201908_at	8.27E-05	0.59	-1.69

---	Transcribed locus	---	1559067_a_at	7.56E-04	0.59	-1.69
FAM120C	family with sequence similarity 120C	54954	229512_at	1.11E-03	0.59	-1.69
WDFY1	WD repeat and FYVE domain containing 1	57590	224800_at	1.44E-04	0.59	-1.69
BTBD7	BTB (POZ) domain containing 7	55727	1556000_s_at	3.30E-03	0.59	-1.69
XK	X-linked Kx blood group (McLeod syndrome)	7504	206698_at	5.15E-03	0.59	-1.69
ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	8728	209765_at	9.77E-03	0.59	-1.69
RQCD1	RCD1 required for cell differentiation1 homolog	9125	213179_at	5.16E-03	0.59	-1.69
ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	55723	218115_at	1.93E-03	0.59	-1.69
KIAA0895	KIAA0895 protein	23366	213424_at	1.99E-03	0.59	-1.68
GNB5	guanine nucleotide binding protein (G protein), beta 5	10681	207124_s_at	2.05E-03	0.59	-1.68
NISCH	nischarin	11188	201591_s_at	8.38E-04	0.59	-1.68
SAMM50	sorting and assembly machinery component 50 homolog (	25813	201569_s_at	1.76E-03	0.59	-1.68
SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	6533	228754_at	8.09E-03	0.59	-1.68
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	6634	202567_at	1.11E-03	0.59	-1.68
NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 intera	84901	212808_at	3.39E-02	0.59	-1.68
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6391	202004_x_at	1.75E-03	0.59	-1.68
CTPS	CTP synthase	1503	202613_at	2.17E-03	0.60	-1.68
HYPK	Huntingtin interacting protein K	25764	233746_x_at	4.17E-03	0.60	-1.68
KCTD12	potassium channel tetramerisation domain containing 12	115207	212188_at	4.45E-02	0.60	-1.68
CALCOCO2	calcium binding and coiled-coil domain 2	10241	210817_s_at	6.41E-03	0.60	-1.68
LYPLA1	lysophospholipase I	10434	203007_x_at	4.95E-03	0.60	-1.68
HDLBP	high density lipoprotein binding protein (vigilin)	3069	225012_at	8.07E-03	0.60	-1.68
C9orf125	chromosome 9 open reading frame 125	---	213386_at	3.93E-04	0.60	-1.68
KIAA0232	KIAA0232	9778	232366_at	1.57E-02	0.60	-1.67
GNB5	guanine nucleotide binding protein (G protein), beta 5	10681	204000_at	7.39E-03	0.60	-1.67
LOC645722	hypothetical LOC645722	645722	1555216_a_at	3.17E-03	0.60	-1.67
BTBD11	BTB (POZ) domain containing 11	121551	238692_at	3.72E-04	0.60	-1.67
SPIN3	spindlin family, member 3	169981	1555883_s_at	1.17E-03	0.60	-1.67
RBBP6	retinoblastoma binding protein 6	5930	1552329_at	6.73E-03	0.60	-1.67
GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	2589	201722_s_at	6.75E-04	0.60	-1.66
ERAP1	Endoplasmic reticulum aminopeptidase 1	51752	212580_at	1.31E-02	0.60	-1.66
SETD8	SET domain containing (lysine methyltransferase) 8	387893	225094_at	7.14E-04	0.60	-1.66
PPM1F	protein phosphatase 1F (PP2C domain containing)	9647	203063_at	2.05E-04	0.60	-1.66
VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	51652	217837_s_at	1.64E-04	0.60	-1.66
WDR68	WD repeat domain 68	10238	224730_at	1.96E-02	0.60	-1.66
---	Transcribed locus	---	214124_x_at	3.27E-03	0.60	-1.66
AKT2	v-akt murine thymoma viral oncogene homolog 2	208	226156_at	6.57E-03	0.60	-1.66
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa ///	642502	216591_s_at	4.59E-02	0.60	-1.66
PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	5717	208776_at	3.24E-02	0.60	-1.65
---	Transcribed locus	---	242965_at	3.98E-02	0.60	-1.65
EGLN3	egl nine homolog 3 (C. elegans)	112399	219232_s_at	1.19E-02	0.61	-1.65
C3orf63	chromosome 3 open reading frame 63	23272	209285_s_at	1.38E-02	0.61	-1.65
SGPL1	sphingosine-1-phosphate lyase 1	---	212321_at	9.69E-04	0.61	-1.65
---	CDNA FLJ13690 fis, clone PLACE2000097	---	232667_at	1.02E-04	0.61	-1.65
DYX1C1	dyslexia susceptibility 1 candidate 1	161582	235273_at	2.75E-02	0.61	-1.65
BBS1	Bardet-Biedl syndrome 1	10072	218567_x_at	1.32E-02	0.61	-1.65
KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	3768	208567_s_at	2.06E-03	0.61	-1.65
SDSL	serine dehydratase-like	113675	228274_at	1.77E-02	0.61	-1.65
KHDC1	KH homology domain cont. 1	387097	241024_at	1.75E-02	0.61	-1.65
---	CDNA clone IMAGE:6576427	---	242423_x_at	1.14E-03	0.61	-1.65
PDLIM5	PDZ and LIM domain 5	10611	212412_at	8.09E-04	0.61	-1.65
TAF8	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	129685	1556176_at	7.31E-04	0.61	-1.65
SEPN1	selenoprotein N, 1	57190	224659_at	2.62E-02	0.61	-1.65
RAP2C	RAP2C, member of RAS oncogene family	57826	218669_at	1.27E-02	0.61	-1.65
TOR1AIP1	torsin A interacting protein 1	26092	216100_s_at	6.09E-03	0.61	-1.64
KCTD16	potassium channel tetramerisation domain containing 16	57528	233234_at	2.64E-02	0.61	-1.64
---	CDNA FLJ13202 fis, clone NT2RP3004503	---	239050_s_at	4.52E-02	0.61	-1.64
RBM8A	RNA binding motif protein 8A	9939	213852_at	3.47E-03	0.61	-1.64
LOC650794	Similar to FRAS1 related extracellular matrix protein 2	650794	236837_x_at	3.93E-03	0.61	-1.64

SIPA1L1	Signal-induced proliferation-associated 1 like 1	26037	202254_at	4.40E-03	0.61	-1.64
CUGBP2	CUG triplet repeat, RNA binding protein 2	10659	227178_at	3.31E-03	0.61	-1.64
RUNX3	runt-related transcription factor 3	864	204197_s_at	4.99E-03	0.61	-1.64
PCGF2	polycomb group ring finger 2	7703	214239_x_at	2.26E-03	0.61	-1.64
ORAOV1	oral cancer overexpressed 1	220064	243531_at	1.02E-03	0.61	-1.64
CSNK1G1	casein kinase 1, gamma 1	53944	226888_at	4.17E-03	0.61	-1.64
SREBF2	sterol regulatory element binding transcription factor 2	---	201247_at	1.75E-02	0.61	-1.64
CCDC50	coiled-coil domain containing 50	152137	236831_at	1.13E-02	0.61	-1.63
PCBP2	poly(rC) binding protein 2	5094	213264_at	4.45E-03	0.61	-1.63
---	CDNA FLJ41633 fis, clone FCBBF3003435	---	238782_at	6.42E-03	0.61	-1.63
ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1994	227746_at	6.11E-04	0.61	-1.63
HIST3H2A	histone cluster 3, H2a	92815	221582_at	6.42E-03	0.61	-1.63
RBM8A	RNA binding motif protein 8A	9939	217856_at	8.88E-03	0.61	-1.63
PKP4	plakophilin 4	8502	214874_at	1.03E-04	0.61	-1.63
DCLK1	doublecortin-like kinase 1	9201	205399_at	1.50E-02	0.61	-1.63
MED19	mediator complex subunit 19	219541	226293_at	7.77E-04	0.61	-1.63
YIPF6	Yip1 domain family, member 6	286451	212342_at	2.19E-04	0.61	-1.63
---	CDNA FLJ13202 fis	---	233068_at	1.24E-02	0.62	-1.63
STX4	syntaxin 4	6810	229395_at	2.97E-04	0.62	-1.63
CNOT6	CCR4-NOT transcription complex, subunit 6	57472	217970_s_at	2.41E-04	0.62	-1.62
---	Transcribed locus	---	228254_at	9.68E-03	0.62	-1.62
---	CDNA FLJ42287 fis, clone TLIVE2005866	---	235924_at	3.94E-03	0.62	-1.62
---	Transcribed locus	---	230570_at	2.66E-03	0.62	-1.62
---	Transcribed locus	---	242051_at	3.96E-02	0.62	-1.62
DAZAP2	DAZ associated protein 2	9802	200794_x_at	7.14E-04	0.62	-1.62
FASTK	Fas-activated serine/threonine kinase	10922	214114_x_at	9.49E-04	0.62	-1.62
---	CDNA FLJ38461 fis, clone FEBRA2020977	---	243735_at	4.63E-02	0.62	-1.62
NNT	nicotinamide nucleotide transhydrogenase	23530	202784_s_at	1.03E-03	0.62	-1.62
LOC441453	similar to olfactory receptor, family 7, subfamily A, member 17	441453	217551_at	8.43E-03	0.62	-1.62
TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	6882	209358_at	9.76E-04	0.62	-1.62
C8orf32	chromosome 8 open reading frame 32	55093	219060_at	6.56E-03	0.62	-1.62
MIB2	mindbomb homolog 2 (Drosophila)	142678	226644_at	2.11E-03	0.62	-1.62
MEX3D	mex-3 homolog D (C. elegans)	399664	91816_f_at	8.20E-03	0.62	-1.62
TSPYL4	TSPY-like 4	23270	212928_at	1.31E-02	0.62	-1.62
SOCS2	suppressor of cytokine signaling 2	8835	203373_at	2.33E-03	0.62	-1.62
C18orf56	chromosome 18 open reading frame 56	494514	228989_at	2.34E-02	0.62	-1.62
SRI	sorcin	6717	208920_at	2.12E-03	0.62	-1.62
---	Transcribed locus	---	241114_s_at	4.75E-04	0.62	-1.62
TOB2	transducer of ERBB2, 2	10766	222243_s_at	1.22E-02	0.62	-1.62
PFAS	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	5198	213302_at	7.66E-03	0.62	-1.62
LETM1	Leucine zipper-EF-hand containing transmembrane protein 1	3954	222006_at	4.71E-03	0.62	-1.62
TMCC1	transmembrane and coiled-coil domain family 1	23023	213352_at	4.13E-02	0.62	-1.62
GJA1	gap junction protein, alpha 1, 43kDa	2697	201667_at	4.27E-03	0.62	-1.61
KIAA1632	KIAA1632	57724	228453_at	2.90E-02	0.62	-1.61
HINT3	histidine triad nucleotide binding protein 3	---	228697_at	3.24E-02	0.62	-1.61
RAP2C	RAP2C, member of RAS oncogene family	57826	218668_s_at	1.42E-02	0.62	-1.61
LOC400027	hypothetical gene supported by BC047417	400027	226413_at	2.53E-02	0.62	-1.61
EPPK1	epiplakin 1	83481	208156_x_at	4.43E-03	0.62	-1.61
BTBD2	BTB (POZ) domain containing 2	55643	207722_s_at	3.59E-02	0.62	-1.61
---	Transcribed locus	---	229029_at	2.46E-02	0.62	-1.61
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	25816	210260_s_at	3.31E-04	0.62	-1.61
NNT	nicotinamide nucleotide transhydrogenase	23530	202783_at	3.27E-04	0.62	-1.61
CROT	carnitine O-octanoyltransferase	54677	231102_at	5.00E-03	0.62	-1.61
PCSK6	proprotein convertase subtilisin/kexin type 6	5046	207414_s_at	7.68E-03	0.62	-1.61
C7orf41	chromosome 7 open reading frame 41	222166	226018_at	3.89E-03	0.62	-1.61
KIAA0101	KIAA0101	9768	202503_s_at	4.89E-03	0.62	-1.61
MAPK14	mitogen-activated protein kinase 14	1432	202530_at	5.15E-04	0.62	-1.61
C21orf51	chromosome 21 open reading frame 51	54065	228239_at	3.63E-03	0.62	-1.61
TPR	translocated promoter region (to activated MET oncogene)	7175	228709_at	1.68E-03	0.62	-1.61
PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	5287	204484_at	1.62E-04	0.62	-1.60

C16orf57	chromosome 16 open reading frame 57	79650	1554016_a_at	3.44E-03	0.62	-1.60
MED19	mediator complex subunit 19	219541	226300_at	5.36E-03	0.62	-1.60
FLJ11151	hypothetical protein FLJ11151	55313	218610_s_at	3.17E-02	0.63	-1.60
---	CDNA FLJ11723 fis, clone HEMBA1005314	---	227498_at	2.03E-02	0.63	-1.60
BUD13	BUD13 homolog (S. cerevisiae)	84811	224504_s_at	6.45E-04	0.63	-1.60
---	CDNA FLJ36977 fis, clone BRACE2006344	---	241808_at	5.79E-03	0.63	-1.60
PDCD6	programmed cell death 6 /// aryl-hydrocarbon receptor repressor	57491	229354_at	5.01E-03	0.63	-1.60
SH3KBP1	SH3-domain kinase binding protein 1	---	235692_at	1.35E-02	0.63	-1.60
CRTAP	cartilage associated protein	10491	227138_at	7.76E-03	0.63	-1.60
MYADM	myeloid-associated differentiation marker	91663	224920_x_at	1.25E-03	0.63	-1.60
PPP1R3E	protein phosphatase 1, regulatory (inhibitor) subunit 3E	90673	227412_at	1.75E-02	0.63	-1.60
SMAD6	SMAD family member 6	4091	207069_s_at	2.37E-02	0.63	-1.60
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	378938	224558_s_at	4.88E-02	0.63	-1.59
OSBPL3	oxysterol binding protein-like 3	26031	209627_s_at	1.25E-02	0.63	-1.59
EXT2	exostoses (multiple) 2	2132	202013_s_at	1.19E-03	0.63	-1.59
IFI44	interferon-induced protein 44	10561	214453_s_at	4.21E-02	0.63	-1.59
HAS2	Hyaluronan synthase 2	---	230372_at	1.60E-02	0.63	-1.59
NADSYN1	NAD synthetase 1	55191	232946_s_at	1.64E-03	0.63	-1.59
METAP1	methionyl aminopeptidase 1	23173	212673_at	1.02E-03	0.63	-1.59
MAGED2	melanoma antigen family D, 2	10916	213627_at	4.42E-03	0.63	-1.59
USP49	ubiquitin specific peptidase 49	---	229351_at	4.17E-02	0.63	-1.59
TSEN34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	79042	218132_s_at	2.76E-03	0.63	-1.59
LNPEP	leucyl/cystinyl aminopeptidase	4012	236728_at	1.49E-02	0.63	-1.59
MAML1	mastermind-like 1 (Drosophila)	9794	202360_at	3.72E-04	0.63	-1.59
LOC284356	hypothetical LOC284356	284356	1555842_at	2.60E-03	0.63	-1.59
LOC285535	hypothetical protein LOC285535	285535	229130_at	2.89E-03	0.63	-1.59
WDR68	WD repeat domain 68	10238	221745_at	4.35E-02	0.63	-1.58
KLHL24	kelch-like 24 (Drosophila)	54800	226158_at	4.08E-02	0.63	-1.58
FERMT1	fermitin family homolog 1 (Drosophila)	55612	218796_at	1.09E-02	0.63	-1.58
---	CDNA clone IMAGE:5301910	---	239503_at	6.96E-03	0.63	-1.58
DUSP6	dual specificity phosphatase 6	1848	208891_at	2.36E-02	0.63	-1.58
---	Transcribed locus	---	239236_at	3.47E-02	0.63	-1.58
SPRYD4	SPRY domain containing 4	283377	225616_at	2.53E-03	0.63	-1.58
SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-revers	6662	202936_s_at	3.47E-04	0.63	-1.58
TCEA2	transcription elongation factor A (SII), 2	6919	203919_at	4.03E-02	0.63	-1.58
SETD8	SET domain containing (lysine methyltransferase) 8	387893	225118_at	2.33E-04	0.63	-1.58
UNQ1887	signal peptide peptidase 3	121665	224639_at	3.72E-03	0.63	-1.58
LIMK1	LIM domain kinase 1	3984	204357_s_at	9.96E-03	0.63	-1.58
FAM126B	family with sequence similarity 126, member B	285172	1554178_a_at	1.92E-02	0.63	-1.58
---	MRNA full length insert cDNA clone EUROIMAGE 1674211	---	225543_at	7.96E-04	0.63	-1.58
---	CDNA: FLJ22542 fis, clone HSI00196	---	233820_at	9.62E-03	0.63	-1.58
PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	10197	200988_s_at	2.28E-02	0.63	-1.58
BACE1	beta-site APP-cleaving enzyme 1	23621	217904_s_at	1.61E-03	0.64	-1.57
NADSYN1	NAD synthetase 1	55191	218840_s_at	7.44E-03	0.64	-1.57
TPK1	thiamin pyrophosphokinase 1	27010	223686_at	8.47E-03	0.64	-1.57
TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	10245	203342_at	2.48E-03	0.64	-1.57
FAM101B	family with sequence similarity 101, member B	359845	226905_at	7.72E-03	0.64	-1.57
OPN3	opsin 3	23596	224392_s_at	1.77E-02	0.64	-1.57
SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-de	6715	211056_s_at	2.48E-03	0.64	-1.57
ACTR8	ARP8 actin-related protein 8 homolog (yeast)	93973	218658_s_at	3.03E-03	0.64	-1.57
DOCK5	Dedicator of cytokinesis 5	80005	230207_s_at	3.28E-02	0.64	-1.57
NKX2-2	NK2 homeobox 2	4821	206915_at	4.69E-03	0.64	-1.57
MGC5566	Hypothetical protein LOC100128040	79015	241759_at	4.57E-03	0.64	-1.57
DPY19L1	dpy-19-like 1 (C. elegans)	23333	212792_at	3.65E-03	0.64	-1.57
FOXA1	forkhead box A1	3169	204667_at	2.39E-02	0.64	-1.57
NPTX1	neuronal pentraxin I	4884	204684_at	2.88E-02	0.64	-1.57
PER2	period homolog 2 (Drosophila)	8864	205251_at	7.51E-03	0.64	-1.57
CDCA4	cell division cycle associated 4	55038	218399_s_at	1.82E-03	0.64	-1.57
---	CDNA FLJ30340 fis, clone BRACE2007411	---	226458_at	3.16E-03	0.64	-1.57
TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	7020	204654_s_at	5.95E-03	0.64	-1.57

C9orf116	chromosome 9 open reading frame 116	138162	221946_at	1.28E-02	0.64	-1.56
CPSF4	cleavage and polyadenylation specific factor 4, 30kDa	10898	206688_s_at	3.80E-03	0.64	-1.56
ZNF512	zinc finger protein 512	84450	1553218_a_at	1.56E-03	0.64	-1.56
BID	BH3 interacting domain death agonist	637	204493_at	3.86E-02	0.64	-1.56
HIST1H2BG	histone cluster 1, H2bg	8344	208527_x_at	5.87E-03	0.64	-1.56
HIST1H2BG	histone cluster 1, H2bg	8343	208490_x_at	4.93E-03	0.64	-1.56
SAR1A	SAR1 gene homolog A	56681	210790_s_at	9.95E-03	0.64	-1.56
---	---	---	227943_at	2.57E-02	0.64	-1.56
FLJ37453	hypothetical protein LOC729614	729614	227593_at	2.25E-02	0.64	-1.56
GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	8693	231832_at	1.37E-02	0.64	-1.56
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	817	231793_s_at	2.04E-03	0.64	-1.56
---	CDNA clone IMAGE:6576427	---	238109_at	2.03E-03	0.64	-1.56
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	501	213591_at	1.29E-04	0.64	-1.56
SOCS2	suppressor of cytokine signaling 2	8835	203372_s_at	2.89E-02	0.64	-1.56
MGC4172	short-chain dehydrogenase/reductase	79154	218756_s_at	2.86E-02	0.64	-1.56
FLJ44896	FLJ44896 protein	401166	236046_at	3.05E-02	0.64	-1.56
HOXA3	homeobox A3	3200	235521_at	1.53E-03	0.64	-1.56
CNOT6	CCR4-NOT transcription complex, subunit 6	57472	222476_at	3.83E-04	0.64	-1.56
---	Clone 24583 mRNA sequence	---	213686_at	1.29E-02	0.64	-1.56
DAZAP2	DAZ associated protein 2	9802	214334_x_at	1.55E-03	0.64	-1.56
TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	7020	204653_at	6.79E-05	0.64	-1.56
SETD8	SET domain containing (lysine methyltransferase) 8	387893	220200_s_at	6.53E-04	0.64	-1.56
TOR1AIP1	torsin A interacting protein 1	26092	212408_at	3.80E-03	0.64	-1.56
HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	138050	227564_at	7.30E-03	0.64	-1.55
CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	80777	238554_at	1.64E-04	0.64	-1.55
---	Transcribed locus	---	241950_at	2.84E-02	0.64	-1.55
FAM134A	family with sequence similarity 134, member A	79137	218037_at	3.09E-03	0.64	-1.55
RNFT2	ring finger protein, transmembrane 2	84900	221908_at	6.05E-03	0.64	-1.55
NBPF1	neuroblastoma breakpoint family, member 1	55672	236273_at	2.19E-03	0.64	-1.55
TUB	tubby homolog (mouse)	7275	228882_at	2.29E-02	0.64	-1.55
FLJ14213	protor-2	79899	219383_at	1.28E-03	0.64	-1.55
HPS3	Hermansky-Pudlak syndrome 3	84343	231121_at	1.06E-02	0.64	-1.55
PHLPPL	PH domain and leucine rich repeat protein phosphatase-like	23035	213407_at	3.13E-02	0.65	-1.55
ZFP36L1	zinc finger protein 36, C3H type-like 1	677	211965_at	1.04E-02	0.65	-1.55
BID	BH3 interacting domain death agonist	637	227143_s_at	1.20E-02	0.65	-1.55
PCGF2	polycomb group ring finger 2	7703	213551_x_at	1.86E-03	0.65	-1.55
C1orf151	chromosome 1 open reading frame 151	440574	228096_at	7.42E-03	0.65	-1.55
GNG12	guanine nucleotide binding protein (G protein), gamma 12	55970	222834_s_at	3.38E-02	0.65	-1.55
C9orf125	chromosome 9 open reading frame 125	84302	224458_at	2.27E-03	0.65	-1.55
PDLIM5	PDZ and LIM domain 5	10611	203243_s_at	1.07E-02	0.65	-1.55
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	817	228555_at	2.64E-02	0.65	-1.55
LOC728769	hypothetical protein LOC728769	728769	238039_at	4.70E-03	0.65	-1.55
PNPLA4	patatin-like phospholipase domain containing 4	8228	209740_s_at	3.53E-03	0.65	-1.55
IFNAR2	interferon (alpha, beta and omega) receptor 2	3455	204786_s_at	6.35E-03	0.65	-1.55
FAM64A	family with sequence similarity 64, member A	54478	221591_s_at	1.35E-02	0.65	-1.55
---	MRNA full length insert cDNA clone EUROIMAGE 898037	677778	228930_at	3.57E-02	0.65	-1.54
PHLDA1	pleckstrin homology-like domain, family A, member 1	22822	217996_at	4.78E-02	0.65	-1.54
SFRS14	Splicing factor, arginine/serine-rich 14	10147	212001_at	3.33E-02	0.65	-1.54
BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	60468	221234_s_at	1.02E-02	0.65	-1.54
RUNX3	runt-related transcription factor 3	864	204198_s_at	2.26E-02	0.65	-1.54
MAD2L1BP	MAD2L1 binding protein	9587	203094_at	1.65E-04	0.65	-1.54
---	Transcribed locus	---	225356_at	1.27E-03	0.65	-1.54
N4BP1	NEDD4 binding protein 1	9683	221867_at	1.50E-02	0.65	-1.54
---	Transcribed locus	---	235888_at	9.48E-04	0.65	-1.54
HDLBP	high density lipoprotein binding protein (vigilin)	3069	222916_s_at	4.81E-03	0.65	-1.54
SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	206358	213119_at	5.41E-03	0.65	-1.54
MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	55233	214812_s_at	4.03E-03	0.65	-1.54
IKZF4	IKAROS family zinc finger 4 (Eos)	64375	226759_at	3.36E-04	0.65	-1.54
BFSP1	beaded filament structural protein 1, filensin	631	206746_at	1.23E-02	0.65	-1.54
LYPLA1	lysophospholipase I	10434	212449_s_at	5.33E-03	0.65	-1.54

BCL7A	B-cell CLL/lymphoma 7A	605	203795_s_at	1.40E-03	0.65	-1.54
FERMT1	fermitin family homolog 1 (Drosophila)	55612	60474_at	2.25E-03	0.65	-1.54
RAB40B	RAB40B, member RAS oncogene family	10966	204547_at	9.09E-04	0.65	-1.54
RWDD4A	RWD domain containing 4A	201965	225574_at	9.42E-04	0.65	-1.54
ZNF185	zinc finger protein 185 (LIM domain)	7739	203585_at	2.33E-02	0.65	-1.54
IQCG	IQ motif containing G	84223	221185_s_at	6.00E-03	0.65	-1.54
SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	220963	227506_at	1.58E-03	0.65	-1.54
LOC388272	similar to RIKEN cDNA 4921524J17	388272	226608_at	4.14E-03	0.65	-1.53
PPIA	peptidylprolyl isomerase A (cyclophilin A)	5478	226336_at	2.68E-03	0.65	-1.53
IGF1R	insulin-like growth factor 1 receptor	3480	225330_at	2.66E-02	0.65	-1.53
DUSP6	dual specificity phosphatase 6	1848	208893_s_at	2.42E-02	0.65	-1.53
---	Transcribed locus	---	228955_at	2.30E-02	0.65	-1.53
NAV1	neuron navigator 1	89796	227584_at	4.76E-02	0.65	-1.53
TRIP13	thyroid hormone receptor interactor 13	9319	204033_at	4.26E-03	0.65	-1.53
C20orf11	chromosome 20 open reading frame 11	54994	225376_at	5.69E-03	0.65	-1.53
ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	517	208764_s_at	1.77E-03	0.65	-1.53
ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	2114	201328_at	1.09E-03	0.65	-1.53
BBS1	Bardet-Biedl syndrome 1	10072	232510_s_at	2.65E-02	0.65	-1.53
ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	23229	203264_s_at	7.34E-03	0.65	-1.53
DOCK5	Dedicator of cytokinesis 5	80005	230263_s_at	3.70E-02	0.65	-1.53
LOC100131989	hypothetical LOC100131989	---	235360_at	3.88E-03	0.65	-1.53
FLOT2	flotillin 2	2319	211299_s_at	9.55E-03	0.65	-1.53
JPH2	junctophilin 2	57158	229578_at	3.13E-02	0.66	-1.53
---	Transcribed locus	---	241726_at	2.13E-02	0.66	-1.53
DTX3L	deltex 3-like (Drosophila)	151636	225415_at	1.79E-03	0.66	-1.53
C14orf145	chromosome 14 open reading frame 145	145508	1557756_a_at	1.77E-02	0.66	-1.53
AACS	acetoacetyl-CoA synthetase	65985	218434_s_at	1.81E-04	0.66	-1.53
---	Transcribed locus	---	241815_at	1.56E-03	0.66	-1.53
FRMD8	FERM domain containing 8	83786	227964_at	3.13E-03	0.66	-1.52
DAZAP2	DAZ associated protein 2	9802	212595_s_at	1.73E-02	0.66	-1.52
HNT	neurotrimin	50863	227566_at	3.43E-02	0.66	-1.52
LOC25845	hypothetical LOC25845	25845	225458_at	3.80E-02	0.66	-1.52
LOC388272	Similar to RIKEN cDNA 4921524J17	388272	242555_at	1.48E-02	0.66	-1.52
CARHSP1	calcium regulated heat stable protein 1, 24kDa	23589	224910_at	9.59E-03	0.66	-1.52
CNPY3	canopy 3 homolog (zebrafish)	10695	1556389_at	3.22E-02	0.66	-1.52
---	Transcribed locus	---	239058_at	6.43E-04	0.66	-1.52
UBP1	upstream binding protein 1 (LBP-1a)	7342	218082_s_at	5.23E-03	0.66	-1.52
CANX	calnexin	821	238034_at	1.21E-02	0.66	-1.52
ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	55437	223266_at	6.40E-04	0.66	-1.52
LASS2	LAG1 homolog, ceramide synthase 2	29956	222212_s_at	1.26E-03	0.66	-1.52
LMNB2	lamin B2	84823	216952_s_at	3.83E-03	0.66	-1.52
C3orf64	chromosome 3 open reading frame 64	285203	221935_s_at	1.70E-02	0.66	-1.52
IGSF3	immunoglobulin superfamily, member 3	3321	202421_at	3.39E-02	0.66	-1.52
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	2633	231577_s_at	4.69E-03	0.66	-1.52
LOC729446	hypothetical LOC729446	729446	238043_at	4.63E-03	0.66	-1.52
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	25816	208296_x_at	1.18E-03	0.66	-1.52
FLOT2	flotillin 2	2319	201350_at	6.75E-04	0.66	-1.52
EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	440275	237145_at	5.84E-03	0.66	-1.52
STAM2	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	10254	242569_at	3.69E-02	0.66	-1.52
---	Transcribed locus	---	235015_at	4.42E-03	0.66	-1.52
IQCK	IQ motif containing K	124152	213392_at	6.97E-03	0.66	-1.52
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	817	224994_at	3.55E-02	0.66	-1.52
ZNF599	zinc finger protein 599	148103	243747_at	5.58E-04	0.66	-1.52
---	Transcribed locus	---	235581_at	2.93E-02	0.66	-1.52
SDC1	syndecan 1	6382	201286_at	4.09E-03	0.66	-1.52
POLI	polymerase (DNA directed) iota	11201	238992_at	4.59E-02	0.66	-1.52
KIAA0265	KIAA0265 protein	23008	209255_at	4.55E-03	0.66	-1.52
COL4A4	collagen, type IV, alpha 4	1286	214602_at	2.22E-02	0.66	-1.52
OSBPL6	oxysterol binding protein-like 6	---	236261_at	2.59E-02	0.66	-1.51

---	Transcribed locus	---	230795_at	5.83E-05	0.66	-1.51
RAB38	RAB38, member RAS oncogene family	23682	219412_at	1.11E-02	0.66	-1.51
RFC3	replication factor C (activator 1) 3, 38kDa	5983	204127_at	5.15E-03	0.66	-1.51
HIST1H2BH	histone cluster 1, H2bh	8345	208546_x_at	3.56E-03	0.66	-1.51
ABT1	activator of basal transcription 1	29777	218405_at	4.10E-03	0.66	-1.51
HIST1H2AE	histone cluster 1, H2ab	3012	214469_at	9.90E-03	0.66	-1.51
SLMAP	sarcolemma associated protein	7871	222924_at	1.80E-03	0.66	-1.51
ZNRF1	zinc and ring finger 1	84937	225962_at	1.84E-02	0.66	-1.51
PACS1	phosphofurin acidic cluster sorting protein 1	55690	224658_x_at	1.55E-02	0.66	-1.51
PAPPA	pregnancy-associated plasma protein A, pappalysin 1	5069	228128_x_at	1.75E-02	0.66	-1.51
ISG15	ISG15 ubiquitin-like modifier	9636	205483_s_at	7.25E-03	0.66	-1.51
PYGL	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	5836	202990_at	1.91E-03	0.66	-1.51
IGF1R	insulin-like growth factor 1 receptor	3480	203628_at	2.67E-02	0.66	-1.51
FZD6	frizzled homolog 6 (Drosophila)	8323	203987_at	1.35E-02	0.66	-1.51
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	81831	218888_s_at	8.16E-03	0.66	-1.51
LOC100130536	hypothetical protein LOC100130536	80863	230054_at	4.21E-02	0.66	-1.51
TEF	thyrotrophic embryonic factor	7008	225840_at	2.79E-03	0.66	-1.51
TMEM173	transmembrane protein 173	340061	224929_at	1.12E-02	0.66	-1.51
---	CDNA: FLJ23454 fis, clone HSI06959	---	232331_at	1.66E-02	0.66	-1.51
---	Transcribed locus	---	243023_at	3.43E-02	0.66	-1.51
WDR19	WD repeat domain 19	57728	232163_at	1.16E-02	0.66	-1.51
PPM1F	protein phosphatase 1F (PP2C domain containing)	9647	37384_at	2.42E-06	0.66	-1.51
FAF1	Fas (TNFRSF6) associated factor 1	11124	239749_at	2.16E-02	0.66	-1.51
NADK	NAD kinase	65220	208919_s_at	7.92E-04	0.66	-1.51
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinoca	10606	201013_s_at	4.72E-03	0.66	-1.51
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	2767	214679_x_at	1.35E-04	0.66	-1.51
Gcom1	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	145781	228568_at	2.59E-02	0.66	-1.51
---	Transcribed locus	---	238656_at	4.13E-02	0.66	-1.51
RGMB	RGM domain family, member B	285704	227340_s_at	1.89E-02	0.66	-1.51
---	CDNA clone IMAGE:4798227	---	242086_at	3.26E-04	0.66	-1.51
FASTK	Fas-activated serine/threonine kinase	10922	202676_x_at	2.52E-06	0.66	-1.51
---	CDNA FLJ33148 fis, clone UTERU2000238	---	238492_at	5.71E-04	0.66	-1.51
CALCOCO2	calcium binding and coiled-coil domain 2	10241	235076_at	7.87E-03	0.66	-1.51
C3orf10	chromosome 3 open reading frame 10	55845	224023_s_at	1.50E-03	0.66	-1.51
VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	51028	222478_at	2.30E-03	0.66	-1.50
SMC1A	structural maintenance of chromosomes 1A	8243	217555_at	9.54E-03	0.66	-1.50
---	CDNA FLJ34018 fis, clone FCBBF2002801	---	225896_at	2.32E-02	0.66	-1.50
---	CDNA clone IMAGE:5500261	---	227665_at	1.35E-02	0.66	-1.50
LOC158402	hypothetical protein LOC158402	158402	236769_at	1.57E-03	0.66	-1.50
---	CDNA FLJ33355 fis, clone BRACE2005151	---	242389_at	3.27E-02	0.67	-1.50
STOX1	storkhead box 1	219736	229378_at	9.22E-04	0.67	-1.50
ARIH2	ariadne homolog 2 (Drosophila)	10425	227932_at	9.60E-04	0.67	-1.50
PRDM16	PR domain containing 16	63976	232424_at	6.72E-03	0.67	-1.50
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	9050	219938_s_at	1.83E-03	0.67	-1.50
BCAN	brevican	63827	223632_s_at	1.20E-02	0.67	-1.50
---	CDNA FLJ33407 fis, clone BRACE2010535	---	205316_at	5.87E-03	0.67	-1.50
COL21A1	collagen, type XXI, alpha 1	81578	208096_s_at	3.32E-03	1.50	1.50
---	CDNA clone IMAGE:5298411	---	232242_at	5.60E-02	1.50	1.50
COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	10920	214260_at	6.28E-02	1.51	1.51
STK38L	serine/threonine kinase 38 like	23012	212572_at	7.16E-02	1.51	1.51
MAP2K6	mitogen-activated protein kinase kinase 6	5608	205699_at	3.36E-02	1.51	1.51
AP1S3	adaptor-related protein complex 1, sigma 3 subunit	130340	1555731_a_at	2.77E-01	1.51	1.51
RBM47	RNA binding motif protein 47	54502	218035_s_at	3.76E-02	1.51	1.51
CSNK1A1	casein kinase 1, alpha 1	1452	206562_s_at	1.86E-02	1.51	1.51
MCAM	melanoma cell adhesion molecule	4162	209087_x_at	1.91E-03	1.51	1.51
DCBLD1	discoidin, CUB and LCCL domain containing 1	285761	226609_at	6.47E-02	1.51	1.51
SPTLC1	serine palmitoyltransferase, long chain base subunit 1	10558	202277_at	2.31E-04	1.51	1.51
---	Transcribed locus	---	241404_at	1.24E-01	1.51	1.51
RHEB	Ras homolog enriched in brain	6009	201453_x_at	3.10E-02	1.52	1.52

RCAN2	regulator of calcineurin 2	10231	203498_at	1.94E-03	1.52	1.52
TMEM65	transmembrane protein 65	157378	241342_at	3.18E-03	1.52	1.52
CLIP4	CAP-GLY domain containing linker protein family, member 4	79745	226425_at	4.65E-02	1.52	1.52
FAM18B	family with sequence similarity 18, member B	51030	218446_s_at	1.29E-05	1.52	1.52
PCGF5	polycomb group ring finger 5	84333	229194_at	2.48E-02	1.52	1.52
ANKRD40	ankyrin repeat domain 40	91369	227064_at	6.71E-03	1.52	1.52
MANEA	mannosidase, endo-alpha	79694	219003_s_at	1.11E-02	1.52	1.52
TMTC2	transmembrane and tetratricopeptide repeat containing 2	160335	235775_at	2.68E-02	1.52	1.52
SPTLC1	serine palmitoyltransferase, long chain base subunit 1	10558	202278_s_at	7.04E-03	1.52	1.52
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	6319	211708_s_at	1.63E-01	1.52	1.52
FAM44A	family with sequence similarity 44, member A	259282	235009_at	4.39E-01	1.52	1.52
CLASP2	cytoplasmic linker associated protein 2	23122	212308_at	1.89E-02	1.53	1.53
FAM73A	family with sequence similarity 73, member A	374986	235125_x_at	5.08E-04	1.53	1.53
LRP12	low density lipoprotein-related protein 12	29967	220254_at	3.32E-02	1.53	1.53
KIAA0256	KIAA0256 gene product	9728	212450_at	2.25E-03	1.53	1.53
PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	5516	201375_s_at	2.21E-02	1.53	1.53
ZNF529	Zinc finger protein 529	57711	215307_at	4.58E-02	1.53	1.53
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	51109	217775_s_at	4.42E-03	1.53	1.53
---	Transcribed locus	---	228084_at	1.93E-02	1.53	1.53
---	CDNA FLJ33091 fis, clone TRACH2000660	---	232687_at	4.07E-02	1.53	1.53
DICER1	dicer 1, ribonuclease type III	23405	206061_s_at	8.17E-02	1.53	1.53
GPM6B	glycoprotein M6B	2824	209167_at	2.69E-01	1.53	1.53
SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	114134	1552695_a_at	1.73E-01	1.53	1.53
FAM152A	family with sequence similarity 152, member A	51029	222936_s_at	1.29E-02	1.54	1.54
CYBRD1	cytochrome b reductase 1	79901	222453_at	9.60E-03	1.54	1.54
---	---	---	237571_at	3.57E-03	1.54	1.54
RHEB	Ras homolog enriched in brain	6009	213404_s_at	3.66E-02	1.54	1.54
NEU1	sialidase 1 (lysosomal sialidase)	4758	208926_at	7.03E-03	1.54	1.54
PNRC2	proline-rich nuclear receptor coactivator 2	55629	217779_s_at	4.55E-03	1.54	1.54
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	3309	230031_at	2.88E-03	1.54	1.54
NMD3	NMD3 homolog (S. cerevisiae)	51068	218036_x_at	8.52E-04	1.54	1.54
MCAM	melanoma cell adhesion molecule	4162	211340_s_at	1.20E-04	1.54	1.54
IFRD1	interferon-related developmental regulator 1	3475	202147_s_at	4.40E-02	1.54	1.54
KLHL2	kelch-like 2, Mayven (Drosophila)	11275	219157_at	7.83E-04	1.55	1.55
MAP2K6	mitogen-activated protein kinase kinase 6	5608	205698_s_at	3.91E-02	1.55	1.55
TMTC2	Transmembrane and tetratricopeptide repeat containing 2	160335	228574_at	5.95E-04	1.55	1.55
RWDD2B	RWD domain containing 2B	10069	222614_at	6.16E-03	1.55	1.55
SEC24A	SEC24 related gene family, member A (S. cerevisiae)	10802	212900_at	9.92E-03	1.55	1.55
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	3936	208885_at	3.61E-02	1.55	1.55
RC3H2	ring finger and CCCH-type zinc finger domains 2	54542	238421_at	3.13E-02	1.55	1.55
FILIP1	filamin A interacting protein 1	27145	231945_at	5.54E-04	1.56	1.56
TMEM100	transmembrane protein 100	55273	219230_at	8.07E-03	1.56	1.56
SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	10924	213624_at	7.84E-04	1.56	1.56
CSNK1A1	casein kinase 1, alpha 1	1452	213086_s_at	5.40E-03	1.56	1.56
RPAP3	RNA polymerase II associated protein 3	79657	1557984_s_at	3.23E-02	1.56	1.56
---	Transcribed locus	---	225950_at	4.13E-02	1.56	1.56
DLAT	dihydrolipoamide S-acetyltransferase	1737	213149_at	2.37E-02	1.56	1.56
LOC387763	hypothetical LOC387763	387763	227099_s_at	6.90E-02	1.56	1.56
HK2	hexokinase 2	3099	202934_at	7.35E-02	1.56	1.56
BMP2K	BMP2 inducible kinase	55589	226853_at	3.88E-02	1.56	1.56
TMED5	Transmembrane emp24 protein transport domain containing 5	50999	242263_at	6.19E-03	1.56	1.56
MBNL2	muscleblind-like 2 (Drosophila)	10150	205018_s_at	5.48E-02	1.56	1.56
FGD6	FYVE, RhoGEF and PH domain containing 6	55785	219901_at	3.83E-02	1.56	1.56
EIF5A2	eukaryotic translation initiation factor 5A2	56648	235296_at	4.43E-02	1.57	1.57
ZBTB41	zinc finger and BTB domain containing 41	360023	226962_at	5.28E-03	1.57	1.57
KCNK1	potassium channel, subfamily K, member 1	3775	204679_at	2.54E-02	1.57	1.57
MCAM	melanoma cell adhesion molecule	4162	210869_s_at	5.37E-02	1.57	1.57
---	CDNA FLJ39602 fis, clone SKNSH2005061	---	226550_at	1.80E-03	1.57	1.57
RC3H2	ring finger and CCCH-type zinc finger domains 2	54542	225813_at	2.58E-04	1.57	1.57
CDH1	cadherin 1, type 1, E-cadherin (epithelial)	999	201131_s_at	3.91E-02	1.58	1.58

CLNS1A	chloride channel, nucleotide-sensitive, 1A	1207	209143_s_at	9.38E-02	1.58	1.58
LRP12	low density lipoprotein-related protein 12	29967	220253_s_at	4.79E-03	1.58	1.58
PGGT1B	Protein geranylgeranyltransferase type I, beta subunit	5229	242844_at	1.02E-02	1.58	1.58
TK1	thymidine kinase 1, soluble	7083	202338_at	1.71E-03	1.58	1.58
PDK4	pyruvate dehydrogenase kinase, isozyme 4	5166	225207_at	2.10E-01	1.58	1.58
IL1RAP	interleukin 1 receptor accessory protein	3556	205227_at	2.30E-02	1.58	1.58
ERO1LB	ERO1-like beta (S. cerevisiae)	56605	231944_at	1.77E-02	1.58	1.58
KLHL28	kelch-like 28 (Drosophila)	54813	235727_at	2.73E-03	1.58	1.58
GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1	2560	207010_at	4.22E-02	1.59	1.59
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	2820	225447_at	9.07E-02	1.59	1.59
SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	54557	228745_at	9.11E-04	1.59	1.59
SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	23657	209921_at	1.32E-01	1.59	1.59
UNKL	unkempt homolog (Drosophila)-like	64718	229908_s_at	1.46E-02	1.59	1.59
MAPK8	mitogen-activated protein kinase 8	5599	226048_at	1.57E-02	1.59	1.59
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	6319	211162_x_at	1.17E-01	1.59	1.59
---	Transcribed locus	---	241699_at	1.93E-02	1.59	1.59
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	30061	223044_at	6.89E-02	1.59	1.59
EGF	epidermal growth factor (beta-urogastrone)	1950	206254_at	8.48E-04	1.60	1.60
SFTPH	surfactant associated protein H	253970	228979_at	8.24E-02	1.60	1.60
---	CDNA FLJ39602 fis, clone SKNSH2005061	---	1558105_a_at	8.79E-03	1.60	1.60
SPPL2A	signal peptide peptidase-like 2A	84888	226353_at	2.24E-04	1.60	1.60
TK1	thymidine kinase 1, soluble	7083	1554408_a_at	1.17E-02	1.61	1.61
RNF13	ring finger protein 13	11342	201779_s_at	3.13E-04	1.61	1.61
GCLM	glutamate-cysteine ligase, modifier subunit	2730	236140_at	6.37E-03	1.61	1.61
FGF7	fibroblast growth factor 7	2252	1554741_s_at	2.66E-03	1.61	1.61
STK38L	serine/threonine kinase 38 like	23012	212565_at	4.05E-02	1.61	1.61
SEC24A	SEC24 related gene family, member A (S. cerevisiae)	10802	244841_at	1.15E-02	1.61	1.61
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	51109	217776_at	4.48E-03	1.61	1.61
FGF2	fibroblast growth factor 2 (basic)	2247	204422_s_at	2.46E-02	1.61	1.61
KCNK1	potassium channel, subfamily K, member 1	3775	204678_s_at	4.19E-02	1.61	1.61
---	Transcribed locus	---	228603_at	6.14E-03	1.62	1.62
RHEB	Ras homolog enriched in brain	6009	201452_at	1.25E-01	1.62	1.62
INHBE	inhibin, beta E	83729	210587_at	2.41E-01	1.62	1.62
SNAP91	synaptosomal-associated protein, 91kDa homolog (mouse)	9892	204953_at	7.02E-03	1.62	1.62
MIPOL1	mirror-image polydactyly 1	145282	244246_at	4.67E-02	1.62	1.62
SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	8671	203908_at	1.16E-01	1.62	1.62
---	CDNA FLJ30669 fis, clone FCBBF1000684	---	230764_at	2.23E-02	1.62	1.62
RNF13	ring finger protein 13	11342	201780_s_at	1.10E-03	1.62	1.62
MBNL2	muscleblind-like 2 (Drosophila)	10150	203640_at	1.64E-03	1.63	1.63
ANKRD43	ankyrin repeat domain 43	134548	230238_at	1.03E-02	1.63	1.63
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	9497	207604_s_at	3.40E-02	1.63	1.63
ANXA1	annexin A1	301	201012_at	1.54E-02	1.63	1.63
---	Transcribed locus	---	235585_at	3.31E-04	1.63	1.63
SPTBN1	spectrin, beta, non-erythrocytic 1	6711	226342_at	4.95E-03	1.64	1.64
FAM3C	family with sequence similarity 3, member C	10447	201889_at	2.42E-04	1.64	1.64
---	Clone 25028 mRNA sequence	---	227027_at	8.66E-03	1.64	1.64
C6orf120	chromosome 6 open reading frame 120	387263	221786_at	1.06E-02	1.64	1.64
TDG	thymine-DNA glycosylase	6996	203743_s_at	2.12E-02	1.64	1.64
CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1	260293	227702_at	6.96E-03	1.65	1.65
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	7035	210664_s_at	5.56E-02	1.65	1.65
ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	6785	219532_at	6.89E-06	1.65	1.65
ENOPH1	enolase-phosphatase 1	58478	217956_s_at	1.72E-03	1.66	1.66
RABGAP1L	RAB GTPase activating protein 1-like	9910	213982_s_at	7.51E-02	1.66	1.66
PURA	purine-rich element binding protein A	5813	204020_at	7.05E-03	1.66	1.66
DICER1	dicer 1, ribonuclease type III	23405	212888_at	9.57E-03	1.67	1.67
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	7035	210665_at	3.69E-02	1.67	1.67
LONRF1	LON peptidase N-terminal domain and ring finger 1	91694	226038_at	2.06E-02	1.67	1.67
LOC492311	similar to bovine IgA regulatory protein	492311	226977_at	3.27E-02	1.67	1.67
PPID	Peptidylprolyl isomerase D (cyclophilin D)	5481	228469_at	9.44E-02	1.68	1.68
ANK3	ankyrin 3, node of Ranvier (ankyrin G)	288	206385_s_at	1.73E-03	1.68	1.68

HSPB8	heat shock 22kDa protein 8	26353	221667_s_at	1.03E-02	1.68	1.68
COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	10920	202142_at	3.74E-02	1.68	1.68
SLMO2	slowmo homolog 2 (Drosophila)	51012	217851_s_at	3.86E-02	1.68	1.68
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	51232	202551_s_at	2.11E-03	1.69	1.69
MOXD1	monooxygenase, DBH-like 1	26002	1554474_a_at	6.48E-02	1.69	1.69
SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	23657	207528_s_at	2.37E-02	1.69	1.69
MAGT1	magnesium transporter 1	---	210596_at	5.04E-02	1.69	1.69
KLRC1	killer cell lectin-like receptor subfamily C, member 1	3821	206785_s_at	8.60E-04	1.69	1.69
NCOA2	nuclear receptor coactivator 2	10499	205732_s_at	2.46E-04	1.69	1.69
COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	10920	202141_s_at	5.63E-02	1.69	1.69
NAP1L1	nucleosome assembly protein 1-like 1	4673	208753_s_at	1.66E-02	1.70	1.70
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	5532	209817_at	1.05E-03	1.70	1.70
CSNK1A1	casein kinase 1, alpha 1	1452	208866_at	3.36E-04	1.70	1.70
TACC1	transforming, acidic coiled-coil containing protein 1	6867	1554690_a_at	3.72E-03	1.70	1.70
TCEAL7	transcription elongation factor A (SII)-like 7	56849	227705_at	2.65E-02	1.71	1.71
TMED5	transmembrane emp24 protein transport domain containing 5	50999	202194_at	8.93E-03	1.71	1.71
UBA3	ubiquitin-like modifier activating enzyme 3	9039	209115_at	8.52E-03	1.71	1.71
KIAA0256	KIAA0256 gene product	9728	212451_at	3.70E-02	1.71	1.71
C10orf46	chromosome 10 open reading frame 46	143384	227257_s_at	6.82E-02	1.71	1.71
MAGT1	magnesium transporter 1	728866	221553_at	4.14E-03	1.72	1.72
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	51232	202552_s_at	6.82E-05	1.72	1.72
RAB21	RAB21, member RAS oncogene family	23011	203885_at	9.05E-03	1.72	1.72
RHEB	Ras homolog enriched in brain	6009	1555780_a_at	1.54E-02	1.72	1.72
ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	55102	226684_at	1.44E-02	1.72	1.72
H2AFY	H2A histone family, member Y	9555	214500_at	2.43E-04	1.73	1.73
ELL2	elongation factor, RNA polymerase II, 2	22936	226982_at	1.73E-02	1.73	1.73
BCAT1	branched chain aminotransferase 1, cytosolic	586	214452_at	7.38E-02	1.73	1.73
C10orf46	chromosome 10 open reading frame 46	143384	225192_at	1.86E-02	1.73	1.73
CSNK1A1	casein kinase 1, alpha 1	1452	208867_s_at	2.08E-03	1.73	1.73
PHTF2	putative homeodomain transcription factor 2	57157	217097_s_at	3.97E-02	1.74	1.74
DEF8	differentially expressed in FDCP 8 homolog (mouse)	54849	219646_at	7.82E-03	1.74	1.74
SYTL5	synaptotagmin-like 5	---	242093_at	3.43E-03	1.74	1.74
CRIM1	Cysteine rich transmembrane BMP regulator 1 (chordin-like)	51232	228496_s_at	4.66E-04	1.75	1.75
GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	59345	223487_x_at	9.92E-03	1.75	1.75
CLDND1	claudin domain containing 1	56650	1554149_at	3.78E-03	1.75	1.75
SLC39A10	solute carrier family 39 (zinc transporter), member 10	57181	225295_at	2.49E-03	1.75	1.75
ASPH	aspartate beta-hydroxylase	444	209135_at	7.76E-03	1.76	1.76
LOC221710	Hypothetical protein LOC221710	221710	227124_at	1.24E-03	1.77	1.77
RHEB	Ras homolog enriched in brain	6009	213409_s_at	5.90E-03	1.78	1.78
B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	8702	210540_s_at	1.03E-03	1.78	1.78
LOC493869	similar to RIKEN cDNA 2310016C16	493869	227628_at	8.65E-03	1.78	1.78
C21orf91	chromosome 21 open reading frame 91	54149	226109_at	3.63E-03	1.78	1.78
CSNK1A1	casein kinase 1, alpha 1	1452	208865_at	9.02E-03	1.78	1.78
SFXN4	sideroflexin 4	119559	229236_s_at	8.14E-03	1.79	1.79
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium der	5176	202283_at	1.76E-02	1.79	1.79
---	CDNA clone IMAGE:5296106	---	1556834_at	1.95E-02	1.79	1.79
ZNF238	zinc finger protein 238	10472	212774_at	1.03E-02	1.80	1.80
GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	59345	225710_at	3.98E-03	1.80	1.80
---	Transcribed locus	---	234986_at	2.41E-04	1.80	1.80
MAPK8	mitogen-activated protein kinase 8	5599	226046_at	2.20E-02	1.81	1.81
KLHL28	kelch-like 28 (Drosophila)	54813	228328_at	1.68E-04	1.81	1.81
MEGF10	multiple EGF-like-domains 10	84466	232523_at	1.26E-03	1.82	1.82
---	CDNA: FLJ22522 fis, clone HRC12491	---	227095_at	3.36E-03	1.82	1.82
ZMAT3	zinc finger, matrin type 3	64393	1555609_a_at	6.54E-02	1.82	1.82
LOC493869	Similar to RIKEN cDNA 2310016C16	493869	228141_at	4.46E-04	1.82	1.82
CLDND1	claudin domain containing 1	56650	208925_at	1.02E-02	1.84	1.84
CHRNA9	cholinergic receptor, nicotinic, alpha 9	55584	221107_at	1.86E-03	1.85	1.85
NTS	neurotensin	4922	206291_at	3.33E-04	1.85	1.85
SFXN4	sideroflexin 4	119559	225143_at	1.45E-02	1.86	1.86

RAB8B	RAB8B, member RAS oncogene family	51762	222846_at	8.11E-02	1.87	1.87
RAB21	RAB21, member RAS oncogene family	23011	226268_at	3.76E-02	1.88	1.88
---	Transcribed locus, weakly similar to NP_608540.1 CG2839 CG2839-PA [Drosophila me	---	239329_at	2.56E-02	1.89	1.89
FAM49B	family with sequence similarity 49, member B	51571	217916_s_at	1.24E-02	1.90	1.90
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	3845	214352_s_at	2.11E-02	1.92	1.92
RAB8B	RAB8B, member RAS oncogene family	51762	226633_at	2.15E-02	1.93	1.93
F2RL2	coagulation factor II (thrombin) receptor-like 2	2151	230147_at	7.60E-02	1.93	1.93
RBM24	RNA binding motif protein 24	221662	235004_at	2.86E-03	1.95	1.95
CLCN4	chloride channel 4	1183	214769_at	2.19E-03	1.96	1.96
CCL20	chemokine (C-C motif) ligand 20	6364	205476_at	5.72E-02	1.98	1.98
C8orf4	chromosome 8 open reading frame 4	56892	218541_s_at	2.32E-03	1.98	1.98
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	3845	204009_s_at	5.43E-03	2.00	2.00
---	Transcribed locus	---	229167_at	3.34E-03	2.00	2.00
TNFRSF9	tumor necrosis factor receptor superfamily, member 9	3604	207536_s_at	2.59E-02	2.01	2.01
TACC1	transforming, acidic coiled-coil containing protein 1	6867	217437_s_at	1.51E-03	2.01	2.01
KLHL15	kelch-like 15 (Drosophila)	80311	226370_at	1.99E-03	2.02	2.02
SELT	selenoprotein T	51714	217811_at	1.37E-04	2.03	2.03
PHTF2	putative homeodomain transcription factor 2	57157	209780_at	8.30E-03	2.03	2.03
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	9497	210286_s_at	6.15E-02	2.03	2.03
ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	8754	202381_at	1.59E-02	2.04	2.04
GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	51809	218313_s_at	1.26E-02	2.05	2.05
NHLRC3	NHL repeat containing 3	387921	227040_at	4.78E-04	2.05	2.05
IMPACT	Impact homolog (mouse)	55364	218637_at	3.81E-02	2.11	2.11
AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chrom	9949	1553219_a_at	2.07E-03	2.11	2.11
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	7035	209676_at	1.26E-02	2.12	2.12
AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chrom	9949	204976_s_at	3.61E-03	2.12	2.12
ASPH	aspartate beta-hydroxylase	444	210896_s_at	6.45E-03	2.16	2.16
TACC1	transforming, acidic coiled-coil containing protein 1	6867	200911_s_at	1.89E-04	2.17	2.17
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	9497	209884_s_at	2.99E-03	2.18	2.18
GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	51809	222587_s_at	2.38E-02	2.20	2.20
HMOX1	heme oxygenase (decycling) 1	3162	203665_at	3.73E-02	2.21	2.21
ZMAT3	zinc finger, matrin type 3	64393	219628_at	2.37E-02	2.21	2.21
ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	8754	1555326_a_at	2.47E-02	2.22	2.22
---	CDNA clone IMAGE:5261213	---	225725_at	2.00E-02	2.22	2.22
PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	5806	206157_at	1.06E-01	2.22	2.22
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	7035	213258_at	1.54E-03	2.28	2.28
---	CDNA clone IMAGE:5261213	---	227221_at	1.95E-02	2.34	2.34
ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	23204	211935_at	1.62E-02	2.47	2.47
AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chrom	9949	226421_at	1.86E-03	2.48	2.48
LUM	lumican	4060	201744_s_at	1.95E-05	2.57	2.57
REEP3	receptor accessory protein 3	221035	225785_at	1.50E-04	2.68	2.68
REEP3	receptor accessory protein 3	221035	235016_at	3.28E-03	2.73	2.73
---	CDNA clone IMAGE:5261213	---	228315_at	3.51E-02	2.75	2.75
TAC1	tachykinin, precursor 1	6863	206552_s_at	2.33E-04	2.94	2.94

Table 2 Results of the ANOVA calculation of Mouse Qkf$^{gt/gt}$ adult dorsal cortex vs. wildtype ($p < 0.05$; FC < -1.5 or > 1.5)

Gene Symbol	Gene Title	Entrez Gene	Probeset ID	p-value	FDR-adjusted p-value	Fold-Change
---	---	---	1447258_at	3.52E-07	1.59E-03	-5.82
Myst4	MYST histone acetyltransferase monocytic leukemia 4	54169	1423508_at	1.01E-08	1.14E-04	-5.54
D14Ertd725e	DNA segment, Chr 14, ERATO Doi 725, expressed	52524	1439980_at	2.94E-07	1.48E-03	-4.91
Ctxn3	cortexin 3	629147	1438059_at	6.79E-09	1.02E-04	-3.68
Myl1	myosin, light polypeptide 1	17901	1452651_a_at	2.12E-05	4.35E-02	-2.66
Alas2	aminolevulinic acid synthase 2, erythroid	11656	1451675_a_at	3.85E-02	1.00E+00	-2.52

6030427F01Rik	RIKEN cDNA 6030427F01 gene	97411	1458931_at	3.63E-02	1.00E+00	-2.38
Ugt8a	UDP galactosyltransferase 8A	22239	1419064_a_at	2.87E-03	9.66E-01	-2.31
Gpr103	G protein-coupled receptor 103	229214	1457048_at	1.27E-05	2.72E-02	-2.31
9030218A15Rik	RIKEN cDNA 9030218A15 gene	77662	1432790_at	2.89E-02	1.00E+00	-2.28
Rab40c	Rab40c, member RAS oncogene family	224624	1424332_at	1.58E-02	1.00E+00	-2.22
Lgi3	leucine-rich repeat LGI family, member 3	213469	1436238_at	1.46E-03	6.84E-01	-2.14
Cd24a	CD24a antigen	12484	1416034_at	2.62E-03	9.61E-01	-2.08
Rorb	RAR-related orphan receptor beta	225998	1425162_at	4.24E-02	1.00E+00	-2.03
4931433A01Rik	RIKEN cDNA 4931433A01 gene	78933	1438158_at	3.48E-04	2.75E-01	-2.00
2900073C17Rik	RIKEN cDNA 2900073C17 gene	73020	1454301_at	4.80E-03	1.00E+00	-1.98
Gabra3	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	14396	1421263_at	1.07E-03	5.62E-01	-1.98
6430550H21Rik	RIKEN cDNA 6430550H21 gene	245386	1437137_at	2.43E-02	1.00E+00	-1.97
Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	16490	1422197_at	2.67E-04	2.33E-01	-1.97
Hrasls	HRAS-like suppressor	27281	1422919_at	2.36E-02	1.00E+00	-1.95
4833410I11Rik	RIKEN cDNA 4833410I11 gene	74612	1432836_at	9.32E-05	1.26E-01	-1.92
---	Transcribed locus, weakly similar to XP_001474741.1 PREDICTED: hypothetical prot	---	1446809_at	8.38E-05	1.18E-01	-1.91
---	Transcribed locus	---	1447473_at	4.92E-02	1.00E+00	-1.90
Etv5	ets variant gene 5	104156	1420998_at	8.42E-03	1.00E+00	-1.89
Edil3	EGF-like repeats and discoidin I-like domains 3	13612	1425622_at	6.23E-03	1.00E+00	-1.87
Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	14586	1423007_a_at	1.05E-04	1.32E-01	-1.86
Ifih1	interferon induced with helicase C domain 1	71586	1426276_at	4.55E-03	1.00E+00	-1.86
---	Transcribed locus	---	1457137_at	1.57E-06	5.43E-03	-1.84
Olfml1	olfactomedin-like 1	244198	1455663_at	9.70E-03	1.00E+00	-1.84
Opa1	optic atrophy 1 homolog (human)	100046	1418768_at	1.18E-02	1.00E+00	-1.83
Zbtb43	zinc finger and BTB domain containing 43	71834	1431127_at	6.90E-03	1.00E+00	-1.81
Foxn3	forkhead box N3	71375	1453094_at	3.07E-03	9.87E-01	-1.80
Pde10a	phosphodiesterase 10A	23984	1419389_at	1.02E-02	1.00E+00	-1.77
---	Transcribed locus	---	1443268_at	1.25E-04	1.49E-01	-1.77
Tacc1	transforming, acidic coiled-coil containing protein 1	320165	1429591_at	4.91E-02	1.00E+00	-1.77
Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	16497	1454043_a_at	2.57E-02	1.00E+00	-1.76
Mtf2	Metal response element binding transcription factor 2	17765	1445151_at	2.20E-04	2.06E-01	-1.76
Rnf39	Ring finger protein 39	386454	1441793_at	1.19E-02	1.00E+00	-1.76
Coro1c	coronin, actin binding protein 1C	23790	1417752_at	1.72E-02	1.00E+00	-1.75
Pcnx	pecanex homolog (Drosophila)	54604	1419049_at	3.26E-03	1.00E+00	-1.74
Syt1	synaptotagmin I	20979	1421990_at	4.94E-02	1.00E+00	-1.74
LOC665506	similar to T-cell receptor beta-2 chain C region	665506	1425854_x_at	1.25E-05	2.72E-02	-1.74
Mobp	myelin-associated oligodendrocytic basic protein	17433	1450088_a_at	4.13E-02	1.00E+00	-1.73
Col4a3bp	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	68018	1420383_a_at	1.71E-02	1.00E+00	-1.71
Il12a	interleukin 12a	16159	1425454_a_at	1.15E-04	1.40E-01	-1.70
---	Transcribed locus, strongly similar to NP_080291.1 zinc finger, matrin type 5 [M	---	1436141_at	5.61E-04	3.72E-01	-1.69
B930006L02Rik	RIKEN cDNA B930006L02 gene	319604	1454950_at	4.19E-05	6.99E-02	-1.68
Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	56194	1420917_at	1.34E-02	1.00E+00	-1.68
Prg4	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone pro	96875	1449824_at	3.17E-02	1.00E+00	-1.67
Tnnt2	troponin T2, cardiac	21956	1424967_x_at	1.47E-02	1.00E+00	-1.67
E130009J12Rik	RIKEN cDNA E130009J12 gene	381107	1439575_at	4.90E-04	3.40E-01	-1.67
Slc25a27	solute carrier family 25, member 27	74011	1454230_a_at	1.39E-02	1.00E+00	-1.65
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type	19058	1450368_a_at	1.66E-02	1.00E+00	-1.64
Nfe2l3	nuclear factor, erythroid derived 2, like 3	18025	1417520_at	9.46E-03	1.00E+00	-1.64
Ufsp1	UFM1-specific peptidase 1	70240	1447822_x_at	3.74E-04	2.81E-01	-1.63
Immt	inner membrane protein, mitochondrial	76614	1429533_at	1.42E-02	1.00E+00	-1.63
Tmtc4	transmembrane and tetratricopeptide repeat containing 4	70551	1432360_a_at	1.90E-02	1.00E+00	-1.63
Pxmp4	peroxisomal membrane protein 4	59038	1422780_at	3.29E-02	1.00E+00	-1.63
Cd24a	CD24a antigen	12484	1448182_a_at	2.46E-02	1.00E+00	-1.63
Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	17879	1427520_a_at	3.55E-02	1.00E+00	-1.63
5730414N17Rik	RIKEN cDNA 5730414N17 gene	70524	1429899_at	2.03E-03	8.56E-01	-1.62
Pcdh9	protocadherin 9	211712	1458269_at	1.07E-02	1.00E+00	-1.62
Ptger3	prostaglandin E receptor 3 (subtype EP3)	19218	1450344_a_at	9.32E-03	1.00E+00	-1.62
Carhsp1	calcium regulated heat stable protein 1	100046	1415976_a_at	1.01E-02	1.00E+00	-1.62
Klhdc8a	kelch domain containing 8A	213417	1441940_x_at	6.96E-03	1.00E+00	-1.61

Pibf1	progesterone immunomodulatory binding factor 1	52023	1430698_a_at	2.75E-02	1.00E+00	-1.61
Pdxdc1	pyridoxal-dependent decarboxylase domain containing 1	94184	1436372_a_at	1.81E-02	1.00E+00	-1.61
Map2k5	mitogen-activated protein kinase kinase 5	23938	1453712_a_at	3.79E-02	1.00E+00	-1.60
---	Transcribed locus	---	1456781_at	4.77E-02	1.00E+00	-1.60
---	Transcribed locus	---	1444238_at	1.36E-04	1.56E-01	-1.60
Ranbp3l	RAN binding protein 3-like	223332	1455707_at	2.44E-02	1.00E+00	-1.60
Epb4.1l2	erythrocyte protein band 4.1-like 2	13822	1433492_at	5.39E-04	3.68E-01	-1.60
Sprn	shadow of prion protein	212518	1459019_at	2.63E-02	1.00E+00	-1.59
Plekha7	pleckstrin homology domain containing, family A member 7	233765	1455343_at	3.60E-02	1.00E+00	-1.59
Frmd4b	FERM domain containing 4B	232288	1426594_at	2.95E-02	1.00E+00	-1.59
Tnfsf12	tumor necrosis factor (ligand) superfamily, member 12	100048	1452440_at	1.82E-06	5.87E-03	-1.59
Zfp296	zinc finger protein 296	63872	1449231_at	4.19E-07	1.72E-03	-1.58
Ifngr2	interferon gamma receptor 2	15980	1423557_at	2.97E-02	1.00E+00	-1.58
Ltb4dh	leukotriene B4 12-hydroxydehydrogenase	67103	1417777_at	4.90E-02	1.00E+00	-1.58
---	---	---	1459834_x_at	1.40E-02	1.00E+00	-1.58
Mr1	major histocompatibility complex, class I-related	15064	1421899_a_at	2.25E-02	1.00E+00	-1.57
---	---	---	1449781_at	2.14E-03	8.66E-01	-1.57
Serinc1	serine incorporator 1	56442	1437513_a_at	4.09E-02	1.00E+00	-1.57
Dtna	dystrobrevin alpha	13527	1419223_a_at	1.65E-02	1.00E+00	-1.56
Tle6	transducin-like enhancer of split 6, homolog of Drosophila E(spl)	114606	1448727_at	7.93E-03	1.00E+00	-1.56
---	---	---	1457847_at	3.60E-02	1.00E+00	-1.55
Gm967	gene model 967, (NCBI)	381217	1447475_at	8.99E-03	1.00E+00	-1.55
Rab3c	RAB3C, member RAS oncogene family	100044	1449494_at	1.14E-02	1.00E+00	-1.55
Kcnq3	potassium voltage-gated channel, subfamily Q, member 3	110862	1458421_at	2.12E-03	8.66E-01	-1.54
4930429B21Rik	RIKEN cDNA 4930429B21 gene	67576	1420580_at	2.71E-03	9.65E-01	-1.54
1110051M20Rik	RIKEN cDNA 1110051M20 gene	228356	1447229_x_at	1.12E-02	1.00E+00	-1.54
Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	11440	1450427_at	2.23E-04	2.06E-01	-1.53
---	---	---	1457483_at	1.05E-02	1.00E+00	-1.52
Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	229776	1436913_at	3.62E-02	1.00E+00	-1.52
Nkrf	NF-kappaB repressing factor	77286	1441325_at	1.34E-02	1.00E+00	-1.52
---	Transcribed locus	---	1440550_at	1.92E-03	8.25E-01	-1.52
Pibf1	progesterone immunomodulatory binding factor 1	52023	1431618_a_at	9.99E-03	1.00E+00	-1.52
Rerg	RAS-like, estrogen-regulated, growth-inhibitor	232441	1451236_at	1.50E-02	1.00E+00	-1.51
EG331480	predicted gene, EG331480	331480	1440060_at	4.27E-03	1.00E+00	-1.51
Apol11b	apolipoprotein L 11b	328563	1457307_at	2.01E-02	1.00E+00	-1.51
Cenpa	centromere protein A	12615	1450842_a_at	1.03E-02	1.00E+00	-1.51
Slc39a6	solute carrier family 39 (metal ion transporter), member 6	106957	1447893_x_at	3.89E-02	1.00E+00	-1.51
Ppm1d	protein phosphatase 1D magnesium-dependent, delta isoform	53892	1449092_at	4.34E-02	1.00E+00	-1.51
Tcea2	transcription elongation factor A (SII), 2	21400	1440791_x_at	1.07E-02	1.00E+00	-1.51
Cln8	ceroid-lipofuscinosis, neuronal 8	26889	1455745_at	9.16E-03	1.00E+00	-1.50
Ankrd10	ankyrin repeat domain 10	102334	1429304_at	2.28E-02	1.00E+00	-1.49
4930524O07Rik	RIKEN cDNA 4930524O07 gene	406209	1439134_s_at	1.72E-04	1.85E-01	-1.49
Numbl	numb-like	18223	1416491_at	3.52E-03	1.00E+00	1.50
Bmpr1a	bone morphogenetic protein receptor, type 1A	12166	1425493_at	9.54E-02	1.00E+00	1.50
Padi2	peptidyl arginine deiminase, type II	18600	1418252_at	4.54E-02	1.00E+00	1.50
---	Transcribed locus	---	1438880_at	3.91E-03	1.00E+00	1.50
Wnt10a	wingless related MMTV integration site 10a	22409	1460657_at	1.69E-02	1.00E+00	1.50
St5	suppression of tumorigenicity 5	76954	1428372_at	4.76E-02	1.00E+00	1.50
---	Transcribed locus	---	1439678_at	2.78E-02	1.00E+00	1.50
---	Transcribed locus	---	1444069_at	1.81E-02	1.00E+00	1.50
Ifnar2	interferon (alpha and beta) receptor 2	15976	1440169_x_at	9.00E-03	1.00E+00	1.50
---	Transcribed locus	---	1443075_at	2.36E-02	1.00E+00	1.50
OTTMUSG00000010657	predicted gene, OTTMUSG00000010657	666532	1451477_at	1.69E-04	1.85E-01	1.50
Gigyf2	GRB10 interacting GYF protein 2	227331	1451397_at	4.64E-02	1.00E+00	1.50
Ablim3	actin binding LIM protein family, member 3	319713	1434013_at	4.15E-02	1.00E+00	1.51
---	---	---	1446504_at	4.27E-02	1.00E+00	1.51
A230071A22Rik	RIKEN cDNA A230071A22 gene	320380	1442168_at	2.43E-02	1.00E+00	1.51
Gpc6	glypican 6	23888	1441438_at	2.13E-03	8.66E-01	1.51
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	16801	1421164_a_at	7.32E-02	1.00E+00	1.51

Smoc2	SPARC related modular calcium binding 2	64074	1415935_at	6.52E-02	1.00E+00	1.51
Cth	cystathionase (cystathionine gamma-lyase)	107869	1426243_at	3.34E-02	1.00E+00	1.51
---	Transcribed locus	---	1440563_at	1.03E-01	1.00E+00	1.51
---	---	---	1440650_at	5.84E-02	1.00E+00	1.51
---	Transcribed locus	---	1435858_at	3.63E-02	1.00E+00	1.51
---	Transcribed locus, strongly similar to NP_002237.1 potassium channel, subfamily	---	1456813_at	9.22E-03	1.00E+00	1.51
Ptpn11	protein tyrosine phosphatase, non-receptor type 11	19247	1427699_a_at	3.66E-02	1.00E+00	1.52
Spag5	sperm associated antigen 5	54141	1433892_at	1.06E-02	1.00E+00	1.52
---	Transcribed locus	---	1456979_at	1.01E-01	1.00E+00	1.52
Hr	hairless	15460	1435950_at	2.92E-02	1.00E+00	1.52
---	---	---	1459388_at	1.17E-02	1.00E+00	1.52
Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	14813	1449245_at	4.26E-02	1.00E+00	1.52
Gmeb2	glucocorticoid modulatory element binding protein 2	229004	1454818_at	6.39E-02	1.00E+00	1.52
Klhl20	kelch-like 20 (Drosophila)	226541	1454994_at	1.50E-02	1.00E+00	1.52
Plxnb2	plexin B2	140570	1416683_at	3.34E-03	1.00E+00	1.52
Smoc2	SPARC related modular calcium binding 2	64074	1431362_a_at	3.35E-02	1.00E+00	1.53
Morn1	MORN repeat containing 1	76866	1433180_at	6.42E-02	1.00E+00	1.53
Trhr	thyrotropin releasing hormone receptor	22045	1449571_at	7.41E-02	1.00E+00	1.53
Jun	Jun oncogene	16476	1417409_at	3.84E-02	1.00E+00	1.53
2900076A13Rik	RIKEN cDNA 2900076A13 gene	73002	1458869_at	4.94E-02	1.00E+00	1.53
---	Transcribed locus	---	1445204_at	5.03E-02	1.00E+00	1.53
Tekt1	tektin 1	21689	1432075_a_at	1.97E-02	1.00E+00	1.53
Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	16494	1456954_at	6.39E-02	1.00E+00	1.53
Daam2	dishevelled associated activator of morphogenesis 2	76441	1430247_at	2.21E-03	8.80E-01	1.53
Ckap4	cytoskeleton-associated protein 4	216197	1452181_at	2.47E-03	9.34E-01	1.53
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	17684	1421267_a_at	2.51E-02	1.00E+00	1.53
N4bp2	NEDD4 binding protein 2	333789	1434394_at	4.19E-02	1.00E+00	1.53
Arpc2	Actin related protein 2/3 complex, subunit 2	76709	1442295_at	4.72E-02	1.00E+00	1.54
Sh3rf1	SH3 domain containing ring finger 1	59009	1421271_at	3.27E-02	1.00E+00	1.54
Tuba8	tubulin, alpha 8	53857	1446771_at	7.64E-02	1.00E+00	1.54
1300012G16Rik	RIKEN cDNA 1300012G16 gene	71772	1423426_at	1.85E-02	1.00E+00	1.54
---	Transcribed locus	---	1440621_at	2.78E-02	1.00E+00	1.54
Alcam	activated leukocyte cell adhesion molecule	11658	1443086_at	6.94E-02	1.00E+00	1.54
Itch	itchy, E3 ubiquitin protein ligase	16396	1431316_at	2.78E-02	1.00E+00	1.54
Cgnl1	cingulin-like 1	68178	1452309_at	6.24E-02	1.00E+00	1.54
Vps39	vacuolar protein sorting 39 (yeast)	269338	1425474_a_at	9.46E-05	1.26E-01	1.54
Bat2	HLA-B associated transcript 2	53761	1422799_at	7.02E-03	1.00E+00	1.55
6030400A10Rik	RIKEN cDNA 6030400A10 gene	77069	1433203_at	4.26E-02	1.00E+00	1.55
---	---	---	1456717_at	9.67E-02	1.00E+00	1.55
Itgb5	integrin beta 5	16419	1417533_a_at	6.56E-03	1.00E+00	1.55
Flt1	FMS-like tyrosine kinase 1	14254	1440926_at	7.39E-02	1.00E+00	1.55
Dab2ip	disabled homolog 2 (Drosophila) interacting protein	69601	1441170_a_at	7.04E-03	1.00E+00	1.55
Asah3l	N-acylsphingosine amidohydrolase 3-like	230379	1451355_at	2.32E-02	1.00E+00	1.55
---	---	---	1445338_at	5.63E-02	1.00E+00	1.56
---	Transcribed locus	---	1442622_at	4.83E-02	1.00E+00	1.56
Pbx2	pre B-cell leukemia transcription factor 2	18515	1418894_s_at	1.83E-02	1.00E+00	1.56
Gpr153	G protein-coupled receptor 153	100129	1426973_at	2.78E-03	9.65E-01	1.56
---	Transcribed locus	---	1443095_at	6.81E-02	1.00E+00	1.56
2610024B07Rik	RIKEN cDNA 2610024B07 gene	269987	1429556_at	4.87E-02	1.00E+00	1.56
Zmym6	zinc finger, MYM-type 6	100177	1434193_at	3.48E-03	1.00E+00	1.57
---	Transcribed locus	---	1439236_at	4.40E-02	1.00E+00	1.57
Crkrs	Cdc2-related kinase, arginine/serine-rich	69131	1438831_at	5.86E-03	1.00E+00	1.57
Scel	sciellin	64929	1422837_at	1.42E-02	1.00E+00	1.57
D930050J11	hypothetical D930050J11	414326	1457484_at	5.90E-04	3.85E-01	1.57
---	Transcribed locus	---	1455624_at	9.81E-02	1.00E+00	1.58
Bcl2l11	BCL2-like 11 (apoptosis facilitator)	12125	1456005_a_at	5.28E-02	1.00E+00	1.58
Unc5a	unc-5 homolog A (C. elegans)	107448	1434095_at	3.20E-02	1.00E+00	1.58
C79242	expressed sequence C79242	98068	1442494_at	7.85E-02	1.00E+00	1.58
Nav2	neuron navigator 2	78286	1441353_at	1.35E-02	1.00E+00	1.58
---	---	---	1442593_at	8.11E-03	1.00E+00	1.58
Grid2	glutamate receptor, ionotropic, delta 2	14804	1421436_at	6.82E-03	1.00E+00	1.59

Flt1	FMS-like tyrosine kinase 1	14254	1454037_a_at	3.19E-02	1.00E+00	1.59
Zfhx4	zinc finger homeodomain 4	80892	1421433_at	1.00E-01	1.00E+00	1.59
---	Transcribed locus, strongly similar to NP_009049.2 triple functional domain (PTP	---	1446593_at	4.74E-02	1.00E+00	1.59
Pcdhb15	protocadherin beta 15	93886	1443421_s_at	4.37E-03	1.00E+00	1.60
---	---	---	1447204_at	?	1.23E-07	1.60
Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	17134	1448916_at	2.06E-04	2.06E-01	1.60
Eef2k	eukaryotic elongation factor-2 kinase	13631	1449013_at	1.58E-02	1.00E+00	1.60
Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	58801	1418203_at	6.64E-03	1.00E+00	1.60
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	12862	1417607_at	9.88E-04	5.44E-01	1.60
Col23a1	collagen, type XXIII, alpha 1	237759	1440911_at	1.60E-02	1.00E+00	1.60
---	---	---	X00686_M_at	8.89E-02	1.00E+00	1.60
March2	membrane-associated ring finger (C3HC4) 2	224703	1439540_at	1.46E-02	1.00E+00	1.61
6430537K16Rik	RIKEN cDNA 6430537K16 gene	320480	1438878_at	7.66E-02	1.00E+00	1.61
ENSMUSG00000074462	predicted gene, ENSMUSG00000074462	100038748	1444174_at	2.27E-02	1.00E+00	1.61
Rad18	RAD18 homolog (S. cerevisiae)	58186	1443954_at	3.85E-02	1.00E+00	1.61
Pik3r6	phosphoinositide-3-kinase, regulatory subunit 6	104709	1437956_at	4.10E-03	1.00E+00	1.61
Flna	filamin, alpha	192176	1426677_at	1.65E-02	1.00E+00	1.61
Neurl	neuralized-like homolog (Drosophila)	18011	1456854_at	4.53E-02	1.00E+00	1.61
Dpp6	dipeptidylpeptidase 6	13483	1439748_at	6.60E-02	1.00E+00	1.61
Rhoc	ras homolog gene family, member C	11853	1448605_at	4.54E-02	1.00E+00	1.61
Slc4a2	solute carrier family 4 (anion exchanger), member 2	20535	1416637_at	3.16E-02	1.00E+00	1.62
AI853363	expressed sequence AI853363	98471	1442887_at	4.15E-03	1.00E+00	1.62
Mapt	microtubule-associated protein tau	17762	1455028_at	7.94E-02	1.00E+00	1.62
Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	108012	1460036_at	2.24E-02	1.00E+00	1.62
Gnb4	guanine nucleotide binding protein (G protein), beta 4	14696	1419469_at	1.57E-02	1.00E+00	1.62
---	---	---	1443335_at	6.88E-06	1.83E-02	1.62
---	---	---	1440033_at	5.38E-02	1.00E+00	1.62
Epb4.1	erythrocyte protein band 4.1	269587	1444150_at	1.99E-02	1.00E+00	1.62
Htr7	5-hydroxytryptamine (serotonin) receptor 7	15566	1435332_at	2.01E-02	1.00E+00	1.62
Coro1a	coronin, actin binding protein 1A	12721	1435288_at	1.46E-03	6.84E-01	1.63
Doc2b	double C2, beta	13447	1420667_at	4.68E-02	1.00E+00	1.63
Wdr90	WD repeat domain 90	106618	1426767_at	3.13E-02	1.00E+00	1.63
Rgs6	regulator of G-protein signaling 6	50779	1452399_at	1.88E-02	1.00E+00	1.63
Tuba8	tubulin, alpha 8	53857	1419518_at	2.18E-02	1.00E+00	1.63
Tbc1d1	TBC1 domain family, member 1	57915	1447016_at	8.31E-02	1.00E+00	1.63
Inpp5a	inositol polyphosphate-5-phosphatase A	212111	1433605_at	1.38E-03	6.78E-01	1.63
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	12293	1441608_at	8.16E-02	1.00E+00	1.64
Plxna3	plexin A3	18846	1420996_at	2.14E-02	1.00E+00	1.64
A630057N01Rik	RIKEN cDNA A630057N01 gene	320057	1456345_at	9.40E-02	1.00E+00	1.65
---	---	---	1440052_at	2.40E-02	1.00E+00	1.65
Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	14809	1418784_at	1.89E-02	1.00E+00	1.65
---	Transcribed locus, moderately similar to NP_571986.1 acidic nuclear phosphoprote	---	1441666_at	7.31E-07	2.75E-03	1.65
Zfp438	zinc finger protein 438	240186	1457059_at	4.38E-02	1.00E+00	1.65
---	Transcribed locus	---	1446150_at	9.40E-02	1.00E+00	1.65
---	---	---	1447580_at	2.07E-02	1.00E+00	1.65
Sfmbt2	Scm-like with four mbt domains 2	353282	1434353_at	1.17E-02	1.00E+00	1.66
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	18719	1421834_at	5.59E-02	1.00E+00	1.66
Antxr1	anthrax toxin receptor 1	69538	1431995_at	2.73E-04	2.33E-01	1.66
Satb1	special AT-rich sequence binding protein 1	20230	1439449_at	1.07E-02	1.00E+00	1.66
Lmna	lamin A	16905	1457670_s_at	2.47E-02	1.00E+00	1.66
D430042O09Rik	RIKEN cDNA D430042O09 gene	233865	1435366_at	5.31E-02	1.00E+00	1.67
4932441J04Rik	RIKEN cDNA 4932441J04 gene	319216	1436563_at	2.61E-02	1.00E+00	1.67
Tln1	talin 1	21894	1457782_at	5.00E-02	1.00E+00	1.67
---	---	---	1447706_at	5.63E-02	1.00E+00	1.67
Rrm1	ribonucleotide reductase M1	20133	1415878_at	7.12E-04	4.34E-01	1.68
Oplah	5-oxoprolinase (ATP-hydrolysing)	75475	1424359_at	4.49E-02	1.00E+00	1.68
Figf	C-fos induced growth factor	14205	1438954_x_at	1.89E-02	1.00E+00	1.68
---	---	---	1457022_at	4.64E-02	1.00E+00	1.68
Gpr56	G protein-coupled receptor 56	14766	1433485_x_at	5.07E-03	1.00E+00	1.68
---	Transcribed locus	---	1456864_at	4.69E-02	1.00E+00	1.69

---	Transcribed locus	---	1443325_at	3.28E-02	1.00E+00	1.69
Hrh1	histamine receptor H1	15465	1438494_at	3.54E-03	1.00E+00	1.70
---	Transcribed locus	---	1445032_at	9.28E-02	1.00E+00	1.70
Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	22083	1442240_at	3.90E-02	1.00E+00	1.70
Oaf	OAF homolog (Drosophila)	102644	1424086_at	1.87E-04	1.94E-01	1.71
---	Transcribed locus	---	1442224_at	1.67E-02	1.00E+00	1.71
Rgs16	regulator of G-protein signaling 16	19734	1426037_a_at	4.07E-02	1.00E+00	1.72
RP23-143A14.5	candidate tumor suppressor OVCA2	246257	1437350_at	1.61E-03	7.23E-01	1.72
Tcap	titin-cap	21393	1423145_a_at	8.95E-06	2.24E-02	1.72
5730411F24Rik	RIKEN cDNA 5730411F24 gene	70507	1430470_at	2.20E-04	2.06E-01	1.73
---	---	---	1447454_at	3.38E-02	1.00E+00	1.73
Rassf3	Ras association (RalGDS/AF-6) domain family member 3	192678	1448546_at	7.10E-02	1.00E+00	1.73
---	Transcribed locus	---	1457279_at	5.09E-03	1.00E+00	1.74
Fbxl11	F-box and leucine-rich repeat protein 11	225876	1435329_at	7.55E-02	1.00E+00	1.74
---	---	---	1441498_at	3.90E-02	1.00E+00	1.74
Trio	Triple functional domain (PTPRF interacting)	223435	1457492_at	8.55E-03	1.00E+00	1.74
B930096F20Rik	RIKEN cDNA B930096F20 gene	319332	1442418_at	7.93E-03	1.00E+00	1.74
2610018G03Rik	RIKEN cDNA 2610018G03 gene	70415	1419033_at	2.16E-02	1.00E+00	1.74
Lrfn1	leucine rich repeat and fibronectin type III domain containing 1	80749	1444669_at	5.08E-05	7.91E-02	1.75
---	---	---	1446641_at	4.18E-02	1.00E+00	1.75
Trpm3	transient receptor potential cation channel, subfamily M, member 3	226025	1456923_at	8.03E-02	1.00E+00	1.75
Tenc1	tensin like C1 domain-containing phosphatase	209039	1452264_at	9.61E-02	1.00E+00	1.75
A330043J11Rik	RIKEN cDNA A330043J11 gene	320261	1440018_at	8.11E-03	1.00E+00	1.75
Pde4a	phosphodiesterase 4A, cAMP specific	18577	1421535_a_at	1.87E-02	1.00E+00	1.76
Lgr5	leucine rich repeat containing G protein coupled receptor 5	14160	1450988_at	5.52E-04	3.71E-01	1.76
Myo5c	myosin VC	208943	1424933_at	1.15E-03	5.97E-01	1.76
Fgf22	fibroblast growth factor 22	67112	1460296_a_at	1.51E-02	1.00E+00	1.77
Tifa	TRAF-interacting protein with forkhead-associated domain	637082	1426501_a_at	8.53E-02	1.00E+00	1.77
Pcdh21	protocadherin 21	170677	1418304_at	1.07E-02	1.00E+00	1.77
Macf1	Microtubule-actin crosslinking factor 1	11426	1439582_at	4.02E-03	1.00E+00	1.78
AU018740	expressed sequence AU018740	98528	1441354_at	3.90E-03	1.00E+00	1.79
Fancd2	Fanconi anemia, complementation group D2	211651	1438339_at	5.60E-06	1.69E-02	1.79
---	---	---	1441437_at	3.35E-03	1.00E+00	1.79
Dtx1	deltex 1 homolog (Drosophila)	14357	1458643_at	6.23E-03	1.00E+00	1.79
Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	12287	1425812_a_at	3.58E-04	2.78E-01	1.79
---	---	---	1445200_at	2.34E-02	1.00E+00	1.80
Mxra7	matrix-remodelling associated 7	67622	1440975_at	1.58E-07	8.91E-04	1.80
---	Transcribed locus	---	1445689_at	5.92E-02	1.00E+00	1.80
C130051F05Rik	RIKEN cDNA C130051F05 gene	320348	1459433_at	1.84E-02	1.00E+00	1.80
6330406I15Rik	RIKEN cDNA 6330406I15 gene	70717	1426937_at	1.36E-02	1.00E+00	1.80
Cdt1	chromatin licensing and DNA replication factor 1	67177	1424143_a_at	1.91E-02	1.00E+00	1.81
Slc14a1	solute carrier family 14 (urea transporter), member 1	108052	1428114_at	1.44E-03	6.84E-01	1.81
Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	223864	1438590_at	2.90E-03	9.68E-01	1.81
LOC552902	hypothetical LOC552902	552902	1456659_at	6.70E-06	1.83E-02	1.81
Hhatl	hedgehog acyltransferase-like	74770	1424553_at	7.00E-04	4.32E-01	1.82
Wnt7a	wingless-related MMTV integration site 7A	22421	1423367_at	8.49E-04	4.97E-01	1.84
---	---	---	1457317_at	2.42E-03	9.34E-01	1.84
Bean	brain expressed, associated with Nedd4	65115	1452451_at	7.84E-03	1.00E+00	1.85
Hspa8	heat shock protein 8	666031	1431182_at	1.57E-02	1.00E+00	1.85
Oprk1	opioid receptor, kappa 1	18387	1451813_at	6.60E-03	1.00E+00	1.86
---	Transcribed locus	---	1447612_x_at	2.01E-02	1.00E+00	1.89
---	---	---	1446943_at	6.01E-03	1.00E+00	1.90
Tor1b	torsin family 1, member B	30934	1417819_at	1.24E-03	6.30E-01	1.91
Col11a1	collagen, type XI, alpha 1	12814	1449154_at	1.57E-02	1.00E+00	1.91
Pth2r	parathyroid hormone 2 receptor	213527	1452129_at	6.14E-04	3.90E-01	1.92
Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	244672	1453688_at	2.36E-02	1.00E+00	1.93
Zfhx4	zinc finger homeodomain 4	80892	1437556_at	8.30E-03	1.00E+00	1.94
Extl1	exostoses (multiple)-like 1	56219	1423305_at	1.02E-03	5.54E-01	1.95
Myh7b	myosin, heavy chain 7B, cardiac muscle, beta	668940	1444305_at	7.82E-04	4.70E-01	1.95
Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7	20361	1422040_at	1.82E-02	1.00E+00	1.97

4930546H06Rik	RIKEN cDNA 4930546H06 gene	75202	1453713_s_at	5.74E-03	1.00E+00	1.99
Adam33	a disintegrin and metallopeptidase domain 33	110751	1451904_a_at	8.38E-05	1.18E-01	2.01
---	Transcribed locus	---	1446514_at	6.83E-04	4.28E-01	2.02
---	Transcribed locus	---	1439632_at	3.21E-02	1.00E+00	2.03
Spryd3	SPRY domain containing 3	223918	1452323_at	8.71E-02	1.00E+00	2.03
Vps54	vacuolar protein sorting 54 (yeast)	245944	1456810_at	2.74E-04	2.33E-01	2.05
Sgce	sarcoglycan, epsilon	20392	1443518_at	4.41E-02	1.00E+00	2.07
Npas1	neuronal PAS domain protein 1	18142	1420801_at	1.86E-02	1.00E+00	2.07
Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	20355	1419328_at	3.40E-05	6.39E-02	2.08
Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	72198	1447517_at	9.55E-02	1.00E+00	2.09
Pctk1	PCTAIRE-motif protein kinase 1	18555	1443296_at	2.46E-03	9.34E-01	2.10
Gh	growth hormone	14599	1437522_x_at	4.90E-02	1.00E+00	2.20
Col11a1	collagen, type XI, alpha 1	12814	1418599_at	5.17E-03	1.00E+00	2.33
2310047B19Rik	RIKEN cDNA 2310047B19 gene	66962	1452201_at	7.49E-02	1.00E+00	2.35
6330514A18Rik	RIKEN cDNA 6330514A18 gene	216166	1434984_at	7.23E-05	1.09E-01	2.41
Gh	growth hormone	14599	1460613_x_at	9.66E-02	1.00E+00	2.46
RP23-296G23.1	novel protein similar to odorant binding protein Ib Obp1b	236874	1449597_at	1.02E-01	1.00E+00	2.49
Igk-C	immunoglobulin kappa chain, constant region	628498	1427660_x_at	7.36E-02	1.00E+00	2.50
Gh	growth hormone	14599	1456595_x_at	6.47E-02	1.00E+00	2.57
Ngp	neutrophilic granule protein	18054	1418722_at	7.18E-02	1.00E+00	2.83
Cartpt	CART prepropeptide	27220	1422825_at	4.66E-05	7.50E-02	3.10
---	Transcribed locus	---	1456053_at	3.44E-04	2.75E-01	3.60
S100a8	S100 calcium binding protein A8 (calgranulin A)	20201	1419394_s_at	6.23E-02	1.00E+00	3.90
S100a9	S100 calcium binding protein A9 (calgranulin B)	20202	1448756_at	8.18E-02	1.00E+00	4.11

Table 3 Results of the ANOVA calculation of Mouse $Qkf^{gt/gt}$ E12.5 dorsal telencephalon vs wildtype ($p < 0.05$; FC < -1.5 or > 1.5)

Gene Symbol	Gene Title	Entrez Gene	ID	p-value	FDR-adjusted p-value	Fold-Change
Myst4	MYST histone acetyltransferase monocytic leukemia 4	54169	1447758_x_at	5.83E-09	3.76E-05	-5.17
Jakmip1	janus kinase and microtubule interacting protein 1	76071	1441317_x_at	2.10E-07	4.12E-04	-4.25
---	Transcribed locus	---	1455528_at	1.19E-08	5.53E-05	-3.85
---	Transcribed locus	---	1436633_at	6.57E-08	1.74E-04	-2.88
---	Transcribed locus	---	1441670_at	2.47E-02	8.91E-01	-2.81
Tmod3	Tropomodulin 3	50875	1455708_at	4.90E-07	7.13E-04	-2.55
---	---	---	1459322_at	3.65E-06	3.10E-03	-2.46
---	Transcribed locus, weakly similar to XP_851502.1 PREDICTED: similar to Retroviru	---	1447014_at	6.16E-06	4.41E-03	-2.42
Nrk	Nik related kinase	27206	1450079_at	6.41E-06	4.52E-03	-2.35
Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	53623	1434728_at	1.29E-05	7.99E-03	-2.34
Gpr123	G protein-coupled receptor 123	52389	1459750_s_at	3.15E-03	3.24E-01	-2.28
---	Transcribed locus	---	1444530_at	2.65E-03	2.90E-01	-2.23
Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	12287	1439612_at	5.95E-04	1.16E-01	-2.21
3110006E14Rik	RIKEN cDNA 3110006E14 gene	76980	1452779_at	3.49E-08	1.12E-04	-2.21
Kif20b	kinesin family member 20B	240641	1449612_x_at	7.75E-04	1.37E-01	-2.20
Ccdc80	coiled-coil domain containing 80	67896	1424186_at	5.00E-03	4.28E-01	-2.19
Ppbp	pro-platelet basic protein	57349	1418480_at	3.72E-02	1.00E+00	-2.16
Chl1	cell adhesion molecule with homology to L1CAM	12661	1435190_at	2.81E-04	7.05E-02	-2.15
Tbx18	T-box18	76365	1449871_at	1.23E-08	5.53E-05	-2.14
Otx2	orthodenticle homolog 2 (Drosophila)	18424	1425926_a_at	2.86E-02	9.32E-01	-2.12
Mgll	monoglyceride lipase	23945	1453836_a_at	4.36E-08	1.31E-04	-2.11
---	Transcribed locus	---	1420287_at	5.75E-05	2.18E-02	-2.09
Fbxo32	F-box protein 32	67731	1448747_at	4.67E-02	1.00E+00	-2.08
9130024F11Rik	RIKEN cDNA 9130024F11 gene	78900	1453245_at	9.38E-03	5.94E-01	-2.07
---	---	---	1457041_at	8.06E-03	5.47E-01	-2.05
2900046L07Rik	RIKEN cDNA 2900046L07 gene	73027	1432944_at	9.36E-03	5.94E-01	-2.05

Cyb5d2	cytochrome b5 domain containing 2	192986	1444065_at	2.30E-04	6.12E-02	-2.05
---	Transcribed locus, moderately similar to NP_891550.1 ADAM metallopeptidase with	---	1446346_at	1.49E-03	2.05E-01	-2.03
4632404H22Rik	RIKEN cDNA 4632404H22 gene	78755	1452682_at	2.51E-05	1.27E-02	-2.02
Uck2	uridine-cytidine kinase 2	80914	1439741_x_at	3.29E-07	5.94E-04	-2.02
2810442I21Rik	RIKEN cDNA 2810442I21 gene	72735	1439112_at	5.37E-06	4.03E-03	-1.99
Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	21835	1422973_a_at	1.53E-03	2.07E-01	-1.99
Huwe1	HECT, UBA and WWE domain containing 1	59026	1448056_at	1.18E-04	3.71E-02	-1.98
Cntnap2	contactin associated protein-like 2	66797	1437782_at	1.36E-02	7.06E-01	-1.98
Lmo7	LIM domain only 7	380928	1455056_at	5.07E-06	3.95E-03	-1.97
Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	12289	1427974_s_at	3.43E-05	1.56E-02	-1.96
---	Transcribed locus	---	1457743_at	1.73E-04	5.03E-02	-1.96
Fzd6	frizzled homolog 6 (Drosophila)	14368	1417301_at	1.04E-02	6.24E-01	-1.95
---	---	---	1457533_at	1.39E-05	8.25E-03	-1.95
Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	24014	1426603_at	2.46E-02	8.90E-01	-1.95
---	Transcribed locus	---	1458298_at	8.31E-03	5.58E-01	-1.95
Ugcg	UDP-glucose ceramide glucosyltransferase	22234	1439863_at	2.72E-04	6.90E-02	-1.94
5730410E15Rik	RIKEN cDNA 5730410E15 gene	319613	1438667_at	3.71E-06	3.10E-03	-1.93
Prkce	protein kinase C, epsilon	18754	1449956_at	8.47E-03	5.66E-01	-1.93
Socs6	suppressor of cytokine signaling 6	54607	1452764_at	1.44E-02	7.20E-01	-1.93
---	---	---	1459017_at	2.18E-02	8.57E-01	-1.92
Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	546336	1441441_at	1.87E-04	5.25E-02	-1.92
Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	58233	1418592_at	1.81E-04	5.18E-02	-1.92
Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	19085	1434325_x_at	1.88E-07	3.86E-04	-1.92
Rhobtb3	Rho-related BTB domain containing 3	73296	1429661_at	7.02E-03	5.12E-01	-1.92
Plcb1	phospholipase C, beta 1	18795	1425781_a_at	4.47E-02	1.00E+00	-1.91
Htra1	HtrA serine peptidase 1	56213	1416749_at	2.06E-02	8.32E-01	-1.91
---	---	---	1446318_at	1.10E-02	6.40E-01	-1.91
Ndrg1	N-myc downstream regulated gene 1	17988	1456174_x_at	3.13E-02	9.71E-01	-1.91
Smtn	smoothelin	29856	1452469_a_at	6.70E-05	2.40E-02	-1.91
Hivep3	human immunodeficiency virus type I enhancer binding protein 3	16656	1458802_at	1.20E-02	6.66E-01	-1.90
Psd	pleckstrin and Sec7 domain containing	73728	1435780_at	1.15E-02	6.55E-01	-1.90
---	---	---	1445892_at	9.82E-07	1.30E-03	-1.90
---	Transcribed locus	---	1458555_at	2.34E-02	8.77E-01	-1.90
A830039N20Rik	RIKEN cDNA A830039N20 gene	268723	1455554_at	8.07E-04	1.39E-01	-1.89
---	Transcribed locus	---	1434025_at	1.93E-02	8.05E-01	-1.88
6720454L07Rik	RIKEN cDNA 6720454L07 gene	77887	1454557_at	7.20E-05	2.50E-02	-1.87
Lpar2	lysophosphatidic acid receptor 2	53978	1420576_at	3.91E-02	1.00E+00	-1.87
---	Transcribed locus	---	1442867_at	4.83E-02	1.00E+00	-1.87
Snrpn	small nuclear ribonucleoprotein N	20646	1455890_x_at	2.36E-04	6.19E-02	-1.87
Arpp21	cyclic AMP-regulated phosphoprotein, 21	74100	1442121_at	5.54E-04	1.12E-01	-1.86
Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	16536	1451595_a_at	6.74E-06	4.60E-03	-1.86
2810030E01Rik	RIKEN cDNA 2810030E01 gene	72668	1430580_at	2.90E-04	7.17E-02	-1.86
---	Transcribed locus	---	1444384_at	1.68E-02	7.66E-01	-1.86
Dsp	desmoplakin	109620	1435494_s_at	1.70E-04	5.02E-02	-1.86
---	Transcribed locus	---	1457104_at	1.00E-05	6.54E-03	-1.85
---	Transcribed locus	---	1437896_at	3.49E-07	6.05E-04	-1.85
---	---	---	1456570_at	1.17E-02	6.58E-01	-1.85
Sox7	SRY-box containing gene 7	20680	1416564_at	6.43E-04	1.20E-01	-1.85
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	20474	1425767_a_at	2.35E-03	2.72E-01	-1.85
---	Transcribed locus	---	1447609_at	4.29E-05	1.78E-02	-1.85
Rai14	Retinoic acid induced 14	75646	1444777_at	2.51E-02	8.97E-01	-1.85
Gpr155	G protein-coupled receptor 155	68526	1452353_at	1.48E-05	8.56E-03	-1.84
Ppnr	per-pentamer repeat gene	26930	1420747_at	6.75E-04	1.24E-01	-1.84
2900083I11Rik	RIKEN cDNA 2900083I11 gene	58212	1421472_at	9.91E-03	6.10E-01	-1.84
Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	229731	1427483_at	1.17E-05	7.40E-03	-1.83
Aph1b	anterior pharynx defective 1b homolog (C. elegans)	208117	1435793_at	3.23E-03	3.27E-01	-1.83
Pif1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	208084	1438149_at	1.13E-07	2.68E-04	-1.83
Kctd4	potassium channel tetramerisation domain containing 4	67516	1420537_at	2.46E-02	8.90E-01	-1.83

Syngr1	synaptogyrin 1	20972	1434661_at	7.99E-03	5.44E-01	-1.82
Vstm2a	V-set and transmembrane domain containing 2A	211739	1452065_at	1.57E-03	2.09E-01	-1.82
Gpc6	glypican 6	23888	1419688_at	1.95E-04	5.43E-02	-1.82
1110018F16Rik	RIKEN cDNA 1110018F16 gene	68594	1429468_at	9.33E-03	5.94E-01	-1.82
Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	73094	1425181_at	2.44E-03	2.78E-01	-1.82
Rtn4ip1	reticulon 4 interacting protein 1	170728	1417668_at	7.88E-03	5.37E-01	-1.81
Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	17132	1447849_s_at	4.48E-03	3.95E-01	-1.81
Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	11306	1419931_at	1.16E-02	6.56E-01	-1.80
---	---	---	1440651_at	8.90E-05	3.00E-02	-1.80
Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	229706	1436137_at	2.18E-02	8.59E-01	-1.80
---	Transcribed locus	---	1443364_at	9.61E-03	6.00E-01	-1.80
Pfkp	Phosphofructokinase, platelet	56421	1437759_at	1.03E-02	6.23E-01	-1.79
Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	74559	1441891_x_at	2.92E-02	9.39E-01	-1.79
RP23-100C5.8	ProSAPiP1 protein	241638	1441963_at	1.18E-02	6.63E-01	-1.79
---	---	---	1443312_at	1.06E-03	1.68E-01	-1.78
---	Transcribed locus	---	1436844_at	1.25E-04	3.88E-02	-1.78
Kcnt1	potassium channel, subfamily T, member 1	227632	1439486_at	9.65E-03	6.00E-01	-1.78
Zfp69	zinc finger protein 69	381549	1458274_at	2.30E-05	1.22E-02	-1.78
Gabrb2	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 2	14401	1428205_x_at	5.72E-04	1.13E-01	-1.78
5530601H04Rik	RIKEN cDNA 5530601H04 gene	71445	1438893_at	1.99E-04	5.49E-02	-1.78
---	Transcribed locus	---	1445638_at	1.88E-02	7.94E-01	-1.77
---	---	---	1456900_at	2.71E-04	6.90E-02	-1.77
---	---	---	1459608_at	1.63E-05	8.88E-03	-1.77
Hivep2	human immunodeficiency virus type I enhancer binding protein 2	15273	1422018_at	1.03E-02	6.22E-01	-1.77
Thada	thyroid adenoma associated	240174	1443884_at	8.09E-07	1.11E-03	-1.77
---	Transcribed locus	---	1444136_at	2.36E-04	6.19E-02	-1.76
Arg2	arginase type II	11847	1418847_at	4.70E-02	1.00E+00	-1.76
Itga5	integrin alpha 5 (fibronectin receptor alpha)	16402	1423267_s_at	8.51E-03	5.67E-01	-1.76
Aldh1l2	aldehyde dehydrogenase 1 family, member L2	216188	1436119_at	7.39E-03	5.20E-01	-1.76
Ap3m2	adaptor-related protein complex 3, mu 2 subunit	64933	1448751_at	7.14E-03	5.15E-01	-1.76
Gatad2a	GATA zinc finger domain containing 2A	234366	1445239_at	2.26E-02	8.67E-01	-1.75
Ilf3	interleukin enhancer binding factor 3	16201	1422546_at	1.81E-06	1.90E-03	-1.75
---	Transcribed locus	---	1440655_at	1.36E-02	7.06E-01	-1.75
Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	12929	1421954_at	2.07E-02	8.32E-01	-1.75
Arnt	aryl hydrocarbon receptor nuclear translocator	11863	1437042_at	1.21E-02	6.66E-01	-1.74
Csnk2a1	casein kinase 2, alpha 1 polypeptide	12995	1419035_s_at	3.55E-02	1.00E+00	-1.74
---	---	---	1441547_at	3.64E-02	1.00E+00	-1.74
---	Transcribed locus	---	1457883_at	6.92E-03	5.09E-01	-1.74
Cdc7	cell division cycle 7 (S. cerevisiae)	12545	1426021_a_at	1.13E-03	1.73E-01	-1.74
Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	77097	1443123_at	3.64E-02	1.00E+00	-1.73
Ttll4	tubulin tyrosine ligase-like family, member 4	67534	1436249_at	4.91E-04	1.04E-01	-1.73
Sult4a1	sulfotransferase family 4A, member 1	29859	1433714_at	1.54E-03	2.07E-01	-1.72
Pik3ip1	phosphoinositide-3-kinase interacting protein 1	216505	1428332_at	9.58E-03	6.00E-01	-1.72
Zfp804a	zinc finger protein 804A	241514	1443036_at	7.51E-04	1.34E-01	-1.72
Ric3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	320360	1445553_at	5.12E-03	4.34E-01	-1.72
C330019G07Rik	RIKEN cDNA C330019G07 gene	215476	1434218_at	1.09E-02	6.38E-01	-1.71
---	Transcribed locus, strongly similar to XP_222254.4 PREDICTED: similar to autism	---	1434029_at	1.93E-03	2.39E-01	-1.71
Pskh1	protein serine kinase H1	244631	1433522_at	3.15E-05	1.47E-02	-1.71
Cyr61	cysteine rich protein 61	16007	1416039_x_at	2.20E-03	2.60E-01	-1.71
Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	13340	1447748_x_at	3.49E-02	1.00E+00	-1.70
Itga1	integrin alpha 1	109700	1455251_at	3.67E-05	1.61E-02	-1.70
Aph1b	anterior pharynx defective 1b homolog (C. elegans)	208117	1456500_at	3.69E-05	1.61E-02	-1.70
---	---	---	1459485_at	4.27E-02	1.00E+00	-1.70
---	---	---	1446897_at	3.75E-02	1.00E+00	-1.69
2810043O03Rik	RIKEN cDNA 2810043O03 gene	72697	1430195_at	6.42E-04	1.20E-01	-1.69
D430015B01Rik	RIKEN cDNA D430015B01 gene	58909	1456611_at	1.17E-02	6.58E-01	-1.69
---	---	---	1439412_at	9.66E-03	6.00E-01	-1.69

---	Transcribed locus	---	1444143_at	3.82E-02	1.00E+00	-1.69
Dclk3	doublecortin-like kinase 3	245038	1436532_at	2.95E-05	1.43E-02	-1.69
St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	20444	1421892_at	4.74E-02	1.00E+00	-1.69
Srprb	signal recognition particle receptor, B subunit	20818	1421012_at	2.91E-04	7.17E-02	-1.69
Smc2	Structural maintenance of chromosomes 2	14211	1458479_at	1.96E-02	8.13E-01	-1.69
Nckipsd	NCK interacting protein with SH3 domain	80987	1418975_at	2.40E-02	8.82E-01	-1.69
Sh2b2	SH2B adaptor protein 2	23921	1450718_at	1.46E-02	7.23E-01	-1.69
Edg5	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	14739	1428176_at	9.27E-06	6.15E-03	-1.68
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	18053	1454903_at	4.53E-02	1.00E+00	-1.68
---	Transcribed locus	---	1438310_at	6.12E-03	4.76E-01	-1.68
---	Transcribed locus	---	1436463_at	1.83E-02	7.91E-01	-1.68
Creb1	cAMP responsive element binding protein 1	12912	1423402_at	4.33E-03	3.89E-01	-1.68
Tyms	Thymidylate synthase	22171	1438690_at	2.02E-03	2.46E-01	-1.68
---	Transcribed locus	---	1440371_at	3.29E-06	2.97E-03	-1.68
Vwa1	von Willebrand factor A domain containing 1	246228	1426399_at	1.19E-02	6.64E-01	-1.68
Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	321022	1440332_at	2.73E-03	2.97E-01	-1.68
---	Transcribed locus	---	1440946_at	5.87E-03	4.63E-01	-1.68
Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	19087	1427414_at	2.31E-04	6.12E-02	-1.68
Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	16502	1456944_at	3.88E-06	3.18E-03	-1.68
---	---	---	1440570_at	4.72E-02	1.00E+00	-1.68
Arhgap6	Rho GTPase activating protein 6	11856	1451867_x_at	4.80E-02	1.00E+00	-1.68
Klhl5	kelch-like 5 (Drosophila)	71778	1444486_at	5.34E-06	4.03E-03	-1.68
Klf15	Kruppel-like factor 15	66277	1448181_at	3.38E-02	9.94E-01	-1.67
Gria4	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	14802	1436772_at	9.99E-03	6.11E-01	-1.67
---	---	---	1430605_at	3.09E-03	3.20E-01	-1.67
Cntn1	contactin 1	12805	1449563_at	7.53E-04	1.34E-01	-1.67
Rgs7bp	regulator of G-protein signalling 7 binding protein	52882	1436876_at	3.63E-04	8.35E-02	-1.66
Letmd1	LETM1 domain containing 1	68614	1437116_at	1.92E-03	2.39E-01	-1.66
Tmem25	transmembrane protein 25	71687	1436644_x_at	2.52E-02	8.98E-01	-1.66
4930525F21Rik	RIKEN cDNA 4930525F21 gene	75823	1438642_at	1.53E-02	7.38E-01	-1.66
Mmp15	matrix metallopeptidase 15	17388	1422597_at	3.56E-03	3.46E-01	-1.66
E030016H06Rik	RIKEN cDNA E030016H06 gene	402722	1440443_at	1.02E-02	6.17E-01	-1.66
Cplx2	complexin 2	12890	1421477_at	2.17E-04	5.96E-02	-1.66
Cplx1	complexin 1	12889	1448832_a_at	3.09E-05	1.47E-02	-1.65
Mta3	metastasis associated 3	116871	1421402_at	1.64E-03	2.14E-01	-1.65
Fcho1	FCH domain only 1	74015	1428575_at	7.23E-03	5.17E-01	-1.65
Sdf4	stromal cell derived factor 4	20318	1448367_at	1.05E-02	6.24E-01	-1.65
Clstn2	calsyntenin 2	64085	1422158_at	3.34E-02	9.88E-01	-1.65
Btbd7	BTB (POZ) domain containing 7	238386	1442061_at	1.40E-06	1.65E-03	-1.64
Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	207212	1433682_at	1.19E-02	6.64E-01	-1.64
Zcchc11	zinc finger, CCHC domain containing 11	230594	1439631_at	8.07E-04	1.39E-01	-1.64
Slitrk4	SLIT and NTRK-like family, member 4	245446	1437744_at	1.61E-02	7.56E-01	-1.64
Sh3gl2	SH3-domain GRB2-like 2	20404	1418792_at	3.46E-02	1.00E+00	-1.64
Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	269209	1434733_at	7.49E-03	5.24E-01	-1.64
C77370	expressed sequence C77370	245555	1440910_at	1.63E-05	8.88E-03	-1.64
Abhd6	abhydrolase domain containing 6	66082	1419104_at	2.57E-02	9.06E-01	-1.64
Tcf12	Transcription factor 12	21406	1446294_at	1.31E-03	1.90E-01	-1.64
---	Transcribed locus	---	1436260_at	3.91E-03	3.64E-01	-1.64
---	---	---	1444005_at	1.52E-03	2.07E-01	-1.64
Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	11441	1440681_at	3.61E-02	1.00E+00	-1.64
Ezh1	enhancer of zeste homolog 1 (Drosophila)	14055	1449023_a_at	7.51E-04	1.34E-01	-1.63
Slc35a2	solute carrier family 35 (UDP-galactose transporter), member A2	22232	1457024_x_at	4.61E-07	6.92E-04	-1.63
Kcnip4	Kv channel interacting protein 4	80334	1437631_at	2.98E-04	7.26E-02	-1.63
Pitpna	phosphatidylinositol transfer protein, alpha	18738	1423282_at	2.34E-05	1.22E-02	-1.63
2610204M08Rik	RIKEN cDNA 2610204M08 gene	70435	1436216_s_at	2.12E-02	8.43E-01	-1.63
Nr3c1	nuclear receptor subfamily 3, group C, member 1	14815	1457635_s_at	1.64E-02	7.63E-01	-1.63
Ptprj	protein tyrosine phosphatase, receptor type, J	19271	1425452_s_at	5.58E-03	4.53E-01	-1.63
---	Transcribed locus	---	1445575_at	1.49E-02	7.30E-01	-1.62

Psma1	proteasome (prosome, macropain) subunit, alpha type 1	26440	1436769_at	1.46E-03	2.02E-01	-1.62
Cadm2	cell adhesion molecule 2	239857	1435146_s_at	2.14E-02	8.45E-01	-1.62
Ttc9c	tetratricopeptide repeat domain 9C	70387	1432245_s_at	1.31E-02	6.89E-01	-1.61
Camk1d	calcium/calmodulin-dependent protein kinase ID	227541	1452050_at	4.96E-04	1.04E-01	-1.61
Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	67733	1449953_at	3.60E-03	3.46E-01	-1.61
Ppp1r14b	Protein phosphatase 1, regulatory (inhibitor) subunit 14B	18938	1436716_at	4.01E-06	3.23E-03	-1.61
Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	231642	1455673_at	2.24E-02	8.65E-01	-1.60
Josd3	Josephin domain containing 3	75316	1442289_at	1.56E-02	7.44E-01	-1.60
---	Transcribed locus	---	1439596_at	1.14E-02	6.51E-01	-1.60
B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	14421	1418655_at	3.82E-02	1.00E+00	-1.60
Scn2b	sodium channel, voltage-gated, type II, beta	72821	1436134_at	8.20E-03	5.53E-01	-1.60
Guf1	GUF1 GTPase homolog (S. cerevisiae)	231279	1455163_at	8.46E-03	5.66E-01	-1.60
Fgf1	fibroblast growth factor 1	14164	1423136_at	1.20E-03	1.79E-01	-1.60
Epha10	Eph receptor A10	230735	1436093_at	5.53E-03	4.50E-01	-1.60
Grb14	growth factor receptor bound protein 14	50915	1417673_at	4.83E-05	1.96E-02	-1.60
Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	19049	1451331_at	4.49E-03	3.95E-01	-1.60
Aldh16a1	aldehyde dehydrogenase 16 family, member A1	69748	1447372_at	2.84E-02	9.30E-01	-1.60
Gfm1	G elongation factor, mitochondrial 1	28030	1448381_at	9.73E-04	1.58E-01	-1.59
D230040A04Rik	RIKEN cDNA D230040A04 gene	414113	1442151_at	6.87E-03	5.09E-01	-1.59
---	---	---	1440123_at	7.73E-08	1.94E-04	-1.59
C77805	expressed sequence C77805	97592	1445490_at	3.12E-02	9.70E-01	-1.59
---	---	---	1440701_at	4.38E-04	9.59E-02	-1.59
Zswim4	zinc finger, SWIM domain containing 4	212168	1436710_at	3.99E-02	1.00E+00	-1.59
Usp32	ubiquitin specific peptidase 32	237898	1459857_at	1.24E-02	6.69E-01	-1.59
Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	16500	1423180_at	4.04E-03	3.72E-01	-1.59
Ank3	ankyrin 3, epithelial	11735	1425202_a_at	1.54E-03	2.07E-01	-1.59
---	Transcribed locus	---	1447279_at	3.61E-04	8.35E-02	-1.59
Ifnar2	interferon (alpha and beta) receptor 2	15976	1440169_x_at	2.52E-03	2.82E-01	-1.59
Abi1	abl-interactor 1	11308	1438506_s_at	4.52E-03	3.95E-01	-1.59
Usp14	Ubiquitin specific peptidase 14	59025	1437714_x_at	2.10E-02	8.39E-01	-1.59
Pcdh8	protocadherin 8	18530	1447825_x_at	7.23E-03	5.17E-01	-1.59
---	Transcribed locus, strongly similar to NP_081035.1 mitochondrial ribosomal prote	---	1459856_at	1.72E-02	7.73E-01	-1.59
Bcor	Bcl6 interacting corepressor	71458	1452910_at	6.22E-05	2.31E-02	-1.59
Adamts3	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin ty	330119	1441693_at	9.70E-03	6.01E-01	-1.58
Rab32	RAB32, member RAS oncogene family	67844	1416527_at	6.84E-03	5.08E-01	-1.58
Malt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	240354	1456429_at	3.80E-02	1.00E+00	-1.58
Gpr85	G protein-coupled receptor 85	64450	1424897_at	1.37E-04	4.21E-02	-1.58
Rtn4rl2	reticulon 4 receptor-like 2	269295	1439573_at	3.26E-02	9.84E-01	-1.58
---	---	---	1447136_at	2.61E-02	9.09E-01	-1.58
Slco3a1	solute carrier organic anion transporter family, member 3a1	108116	1418030_at	1.96E-02	8.13E-01	-1.58
Cnot6l	CCR4-NOT transcription complex, subunit 6-like	231464	1451723_at	3.88E-04	8.75E-02	-1.58
Chst11	carbohydrate sulfotransferase 11	218194	1456606_a_at	6.96E-03	5.09E-01	-1.58
Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	108100	1435128_at	3.25E-03	3.28E-01	-1.58
Dtl	denticleless homolog (Drosophila)	76843	1443864_at	1.20E-02	6.66E-01	-1.58
Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	232889	1436712_at	3.24E-03	3.27E-01	-1.58
Pold3	Polymerase (DNA-directed), delta 3, accessory subunit	67967	1459647_at	1.54E-02	7.38E-01	-1.57
Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	18974	1431440_at	2.76E-02	9.21E-01	-1.57
Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	21886	1436244_a_at	3.50E-02	1.00E+00	-1.57
Lpgat1	Lysophosphatidylglycerol acyltransferase 1	226856	1457961_at	1.06E-03	1.68E-01	-1.57
---	Transcribed locus, strongly similar to XP_001480950.1 PREDICTED: similar to ribo	---	1458629_at	7.82E-03	5.34E-01	-1.57
Wdr33	WD repeat domain 33	74320	1453322_at	3.30E-02	9.84E-01	-1.57
5830474E16Rik	RIKEN cDNA 5830474E16 gene	76094	1433110_at	1.13E-02	6.49E-01	-1.57
Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	14802	1440891_at	2.89E-02	9.38E-01	-1.57
AU021128	expressed sequence AU021128	99209	1457575_at	3.39E-04	7.97E-02	-1.57
Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	17957	1423173_at	1.52E-05	8.67E-03	-1.56
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	65962	1428954_at	3.28E-02	9.84E-01	-1.56
March7	membrane-associated ring finger (C3HC4) 7	57438	1458690_at	1.25E-02	6.71E-01	-1.56

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Clec14a	C-type lectin domain family 14, member a	66864	1419468_at	1.50E-02	7.30E-01	-1.56
3110001A13Rik	RIKEN cDNA 3110001A13 gene	66540	1416893_at	2.29E-03	2.67E-01	-1.56
Cplx1	complexin 1	12889	1417746_at	8.04E-03	5.46E-01	-1.56
---	---	---	1442375_at	1.42E-02	7.13E-01	-1.56
Agbl5	ATP/GTP binding protein-like 5	231093	1439465_x_at	1.93E-02	8.06E-01	-1.56
Kcnt2	Potassium channel, subfamily T, member 2	240776	1459971_at	1.18E-02	6.63E-01	-1.56
Kpnb1	karyopherin (importin) beta 1	16211	1451967_x_at	6.21E-03	4.80E-01	-1.56
BC062127	cDNA sequence BC062127	331188	1445274_at	2.44E-02	8.89E-01	-1.56
Ttll11	tubulin tyrosine ligase-like family, member 11	74410	1430064_at	6.19E-03	4.80E-01	-1.55
---	---	---	1446461_at	2.98E-03	3.16E-01	-1.55
Rnf11	ring finger protein 11	29864	1426405_at	2.67E-02	9.18E-01	-1.55
Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	14538	1425503_at	2.11E-02	8.40E-01	-1.55
4933417O08Rik	RIKEN cDNA 4933417O08 gene	71146	1439546_at	4.37E-02	1.00E+00	-1.55
2610020C07Rik	RIKEN cDNA 2610020C07 gene	69918	1430618_at	2.23E-04	5.98E-02	-1.55
Vldlr	very low density lipoprotein receptor	22359	1438258_at	1.22E-02	6.66E-01	-1.55
Aak1	AP2 associated kinase 1	269774	1435038_s_at	1.10E-03	1.72E-01	-1.55
---	Transcribed locus	---	1448037_at	1.35E-03	1.94E-01	-1.55
Zfp57	zinc finger protein 57	22715	1450929_at	2.61E-02	9.09E-01	-1.55
Cntnap2	contactin associated protein-like 2	66797	1450758_at	2.45E-02	8.89E-01	-1.55
Rai14	retinoic acid induced 14	75646	1417401_at	2.80E-02	9.24E-01	-1.55
---	---	---	1446094_at	2.38E-02	8.81E-01	-1.55
---	Transcribed locus	---	1439621_at	2.00E-02	8.19E-01	-1.55
Ets2	E26 avian leukemia oncogene 2, 3' domain	23872	1416268_at	1.79E-02	7.89E-01	-1.55
---	Transcribed locus, weakly similar to NP_001041402.1 hypothetical protein LOC4991	---	1440628_at	1.61E-03	2.12E-01	-1.55
3110039C02Rik	RIKEN cDNA 3110039C02 gene	73127	1430952_at	1.78E-02	7.87E-01	-1.54
---	Transcribed locus	---	1446200_at	3.92E-03	3.64E-01	-1.54
Wdr22	WD repeat domain 22	320808	1455702_at	4.95E-02	1.00E+00	-1.54
Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	26570	1443536_at	2.77E-02	9.22E-01	-1.54
Wapal	wings apart-like homolog (Drosophila)	218914	1442426_at	3.91E-03	3.64E-01	-1.54
2610012C04Rik	RIKEN cDNA 2610012C04 gene	70299	1432606_at	1.52E-02	7.35E-01	-1.54
Akap13	A kinase (PRKA) anchor protein 13	75547	1430185_at	3.47E-02	1.00E+00	-1.54
Mybl2	myeloblastosis oncogene-like 2	17865	1454946_at	1.54E-03	2.07E-01	-1.54
Ccdc18	coiled-coil domain containing 18	73254	1453600_at	1.22E-02	6.66E-01	-1.54
---	Transcribed locus, moderately similar to XP_001234258.1 PREDICTED: similar to ba	---	1445679_at	5.93E-03	4.67E-01	-1.54
Rai14	retinoic acid induced 14	75646	1441030_at	1.84E-02	7.92E-01	-1.54
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	53945	1417061_at	1.42E-02	7.13E-01	-1.53
C730026J16	hypothetical protein C730026J16	331006	1434687_at	1.05E-02	6.24E-01	-1.53
Ccnjl	cyclin J-like	380694	1456168_at	1.54E-02	7.38E-01	-1.53
BC010304	cDNA sequence BC010304	218236	1439120_at	1.57E-03	2.09E-01	-1.53
Tyw1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	100929	1426781_at	2.71E-02	9.18E-01	-1.53
BC032203	cDNA sequence BC032203	210982	1435545_at	1.44E-02	7.18E-01	-1.53
---	Transcribed locus, moderately similar to XP_001479965.1 PREDICTED: hypothetical	---	1442605_at	1.18E-02	6.63E-01	-1.53
Foxd1	forkhead box D1	15229	1418876_at	3.09E-02	9.65E-01	-1.53
Prkca	protein kinase C, alpha	18750	1450945_at	3.23E-02	9.79E-01	-1.53
---	Transcribed locus	---	1441334_at	5.60E-03	4.54E-01	-1.53
Hspbap1	Hspb associated protein 1	66667	1441900_x_at	6.53E-03	4.94E-01	-1.53
38231	septin 4	18952	1455422_x_at	1.08E-02	6.34E-01	-1.53
Hnrph1	Heterogeneous nuclear ribonucleoprotein H1	59013	1437267_x_at	1.54E-03	2.07E-01	-1.53
8430436O14Rik	RIKEN cDNA 8430436O14 gene	71506	1452761_a_at	2.07E-02	8.32E-01	-1.53
Sox21	SRY-box containing gene 21	223227	1451835_at	3.01E-05	1.44E-02	-1.53
C78704	expressed sequence C78704	97868	1458862_at	4.96E-02	1.00E+00	-1.53
AW413774	expressed sequence AW413774	106046	1435576_at	6.10E-04	1.17E-01	-1.53
---	---	---	1458382_a_at	3.32E-02	9.84E-01	-1.52
Wnt5b	wingless-related MMTV integration site 5B	22419	1439373_x_at	1.71E-03	2.18E-01	-1.52
Hivep3	human immunodeficiency virus type I enhancer binding protein 3	16656	1439660_at	6.41E-03	4.87E-01	-1.52
Slc12a9	solute carrier family 12 (potassium/chloride transporters), member 9	83704	1442599_at	2.62E-02	9.09E-01	-1.52
0610037D15Rik	RIKEN cDNA 0610037D15 gene	68394	1453639_s_at	1.27E-02	6.76E-01	-1.52

Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	56322	1448518_at	4.09E-02	1.00E+00	-1.52
Efs	Embryonal Fyn-associated substrate	13644	1438114_x_at	3.77E-02	1.00E+00	-1.52
Rimbp2	RIMS binding protein 2	231760	1441625_at	1.28E-02	6.80E-01	-1.52
Mipol1	mirror-image polydactyly gene 1 homolog (human)	73490	1435671_at	5.54E-04	1.12E-01	-1.52
6430514L14Rik	RIKEN cDNA 6430514L14 gene	76886	1425213_at	3.83E-02	1.00E+00	-1.52
Coro1c	Coronin, actin binding protein 1C	23790	1419911_at	1.32E-02	6.90E-01	-1.51
---	Transcribed locus	---	1442996_x_at	3.38E-03	3.34E-01	-1.51
Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	71704	1424250_a_at	4.11E-02	1.00E+00	-1.51
Kap	kidney androgen regulated protein	16483	1415968_a_at	1.40E-02	7.10E-01	-1.51
---	---	---	1454454_at	4.68E-02	1.00E+00	-1.51
Neurl	neuralized-like homolog (Drosophila)	18011	1460343_at	3.31E-02	9.84E-01	-1.51
4930506M07Rik	RIKEN cDNA 4930506M07 gene	71653	1429055_at	4.41E-02	1.00E+00	-1.51
Pif1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	208084	1436738_at	4.28E-03	3.85E-01	-1.51
2010317E24Rik	RIKEN cDNA 2010317E24 gene	72080	1438615_x_at	2.73E-02	9.18E-01	-1.51
Tmem209	Transmembrane protein 209	72649	1445660_at	1.75E-02	7.78E-01	-1.51
Dleu2	deleted in lymphocytic leukemia, 2	328425	1427411_s_at	1.06E-02	6.30E-01	-1.51
Ralyl	RALY RNA binding protein-like	76897	1454715_at	1.82E-02	7.91E-01	-1.51
Sfmbt1	Scm-like with four mbt domains 1	54650	1455412_at	1.34E-05	8.08E-03	-1.51
Myrip	myosin VIIA and Rab interacting protein	245049	1460601_at	1.12E-02	6.47E-01	-1.50
Arpp21	cyclic AMP-regulated phosphoprotein, 21	74100	1424248_at	1.78E-03	2.25E-01	-1.50
---	---	---	1446732_at	1.72E-02	7.73E-01	-1.50
Unkl	unkempt-like (Drosophila)	74154	1428565_at	5.47E-05	2.13E-02	-1.50
D3Ertd751e	DNA segment, Chr 3, ERATO Doi 751, expressed	73852	1454225_s_at	2.10E-02	8.39E-01	-1.50
Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	28113	1437166_at	9.35E-04	1.53E-01	-1.50
Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	14402	1435021_at	3.52E-06	3.05E-03	-1.50
---	---	---	1447257_at	3.28E-02	9.84E-01	-1.50
Nono	non-POU-domain-containing, octamer binding protein	53610	1447160_at	4.53E-02	1.00E+00	-1.50
Lyst	lysosomal trafficking regulator	17101	1421384_at	4.83E-02	1.00E+00	1.50
Inha	inhibin alpha	16322	1422728_at	1.67E-02	7.66E-01	1.50
2310061C15Rik	RIKEN cDNA 2310061C15 gene	66531	1427922_at	5.24E-04	1.07E-01	1.50
Tep1	telomerase associated protein 1	21745	1418196_at	1.26E-03	1.85E-01	1.50
---	---	---	1446570_at	2.11E-02	8.40E-01	1.50
Mknk1	MAP kinase-interacting serine/threonine kinase 1	17346	1417631_at	7.03E-03	5.12E-01	1.51
Gm2a	GM2 ganglioside activator protein	14667	1416188_at	3.69E-02	1.00E+00	1.51
Nfya	nuclear transcription factor-Y alpha	18044	1422082_a_at	3.08E-02	9.63E-01	1.51
Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	13685	1417562_at	1.15E-02	6.55E-01	1.51
---	---	---	1460144_at	3.85E-02	1.00E+00	1.51
Adam17	a disintegrin and metallopeptidase domain 17	11491	1421857_at	1.19E-02	6.64E-01	1.51
---	---	---	1440650_at	4.72E-02	1.00E+00	1.52
Dusp26	dual specificity phosphatase 26 (putative)	66959	1425848_a_at	3.64E-03	3.48E-01	1.52
---	---	---	1441177_at	2.71E-02	9.18E-01	1.52
Nid2	nidogen 2	18074	1423516_a_at	4.07E-03	3.73E-01	1.52
Prdm5	PR domain containing 5	70779	1442740_at	1.88E-02	7.94E-01	1.52
Kif2c	kinesin family member 2C	73804	1454221_a_at	2.61E-03	2.87E-01	1.52
Rad18	RAD18 homolog (S. cerevisiae)	58186	1423318_at	2.36E-02	8.78E-01	1.52
Ccdc24	coiled-coil domain containing 24	381546	1456905_at	3.71E-04	8.50E-02	1.53
Tmpo	thymopoietin	21917	1421237_at	4.02E-05	1.68E-02	1.53
Samd8	sterile alpha motif domain containing 8	67630	1434402_at	2.53E-06	2.48E-03	1.53
Pml	promyelocytic leukemia	18854	1448757_at	4.13E-02	1.00E+00	1.53
2810004I08Rik	RIKEN cDNA 2810004I08 gene	69932	1453534_at	3.16E-05	1.47E-02	1.53
Sorcs2	sortilin-related VPS10 domain containing receptor 2	81840	1419358_at	2.41E-02	8.85E-01	1.54
Serf1	small EDRK-rich factor 1	20365	1449509_at	5.19E-04	1.07E-01	1.54
2310068G24Rik	RIKEN cDNA 2310068G24 gene	70185	1433023_at	5.82E-03	4.62E-01	1.54
Hspg2	perlecan (heparan sulfate proteoglycan 2)	15530	1418670_s_at	2.24E-02	8.65E-01	1.54
Mmp11	matrix metallopeptidase 11	17385	1417234_at	1.22E-02	6.66E-01	1.54
---	Transcribed locus	---	1445612_at	3.78E-02	1.00E+00	1.54
Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	216616	1427183_at	3.51E-03	3.44E-01	1.54
Tpbg	trophoblast glycoprotein	21983	1423312_at	2.97E-02	9.48E-01	1.54

Gstm1	glutathione S-transferase, mu 1	14862	1425627_x_at	6.85E-03	5.08E-01	1.54
Igf1r	insulin-like growth factor I receptor	16001	1452108_at	5.80E-03	4.61E-01	1.54
Ctsh	cathepsin H	13036	1418365_at	6.63E-03	4.98E-01	1.54
Tgm2	transglutaminase 2, C polypeptide	21817	1417500_a_at	8.95E-03	5.84E-01	1.55
Mamdc4	MAM domain containing 4	381352	1440333_at	1.20E-06	1.51E-03	1.55
Rims1	regulating synaptic membrane exocytosis 1	116837	1438305_at	1.86E-02	7.94E-01	1.55
Adora1	adenosine A1 receptor	11539	1435495_at	1.38E-02	7.07E-01	1.55
Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	29820	1425212_a_at	1.04E-02	6.24E-01	1.55
C79407	expressed sequence C79407	217653	1443668_x_at	6.87E-05	2.43E-02	1.55
---	Transcribed locus	---	1444761_at	1.14E-03	1.73E-01	1.55
Rybp	RING1 and YY1 binding protein	56353	1421111_at	4.29E-02	1.00E+00	1.55
Anxa6	annexin A6	11749	1415818_at	1.92E-02	8.03E-01	1.55
---	Transcribed locus	---	1440675_at	3.84E-02	1.00E+00	1.55
Klf9	Kruppel-like factor 9	16601	1422264_s_at	3.39E-02	9.94E-01	1.55
---	Transcribed locus	---	1446121_at	9.10E-05	3.03E-02	1.56
Lyrm1	LYR motif containing 1	73919	1431774_a_at	2.72E-02	9.18E-01	1.56
Rps17	Ribosomal protein S17	20068	1438501_at	7.29E-05	2.51E-02	1.56
C330023M02Rik	RIKEN cDNA C330023M02 gene	231713	1433766_at	3.26E-02	9.84E-01	1.56
Atad2b	ATPase family, AAA domain containing 2B	320817	1446719_at	7.45E-04	1.34E-01	1.56
Lepre1	leprecan 1	56401	1452752_at	6.94E-09	3.91E-05	1.56
Tnfsf12	tumor necrosis factor (ligand) superfamily, member 12	619441	1452440_at	1.44E-06	1.65E-03	1.56
Abhd6	abhydrolase domain containing 6	66082	1419103_a_at	3.18E-04	7.63E-02	1.56
Zfp64	zinc finger protein 64	22722	1430117_a_at	3.90E-02	1.00E+00	1.56
Reep4	receptor accessory protein 4	72549	1428478_at	1.07E-03	1.69E-01	1.56
Nup160	nucleoporin 160	59015	1444892_at	3.57E-03	3.46E-01	1.57
Slc35b2	solute carrier family 35, member B2	73836	1423927_at	4.83E-02	1.00E+00	1.57
D3Wsu106e	DNA segment, Chr 3, Wayne State University 106, expressed	28011	1457626_at	2.17E-02	8.56E-01	1.57
Rdh18	retinol dehydrogenase 18	380674	1445728_at	1.88E-02	7.94E-01	1.57
Exosc5	exosome component 5	27998	1417167_at	2.22E-04	5.98E-02	1.57
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	20317	1416168_at	8.84E-03	5.80E-01	1.58
Endod1	endonuclease domain containing 1	71946	1426540_at	4.49E-02	1.00E+00	1.58
---	Transcribed locus	---	1443307_at	2.89E-03	3.11E-01	1.58
---	Transcribed locus	---	1441628_at	3.08E-03	3.19E-01	1.58
Bdh2	3-hydroxybutyrate dehydrogenase, type 2	69772	1453011_at	1.24E-02	6.69E-01	1.58
Fa2h	fatty acid 2-hydroxylase	338521	1426960_a_at	3.10E-04	7.47E-02	1.58
Samd8	sterile alpha motif domain containing 8	67630	1458408_at	2.29E-02	8.67E-01	1.59
Psrc1	proline/serine-rich coiled-coil 1	56742	1425416_s_at	3.31E-02	9.84E-01	1.59
---	---	---	1440958_at	8.40E-04	1.41E-01	1.59
---	---	---	1459563_x_at	2.49E-04	6.49E-02	1.59
Clcn6	chloride channel 6	26372	1422314_at	3.77E-02	1.00E+00	1.59
Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	56274	1418513_at	1.37E-02	7.06E-01	1.59
Camk1	calcium/calmodulin-dependent protein kinase I	52163	1417605_s_at	3.21E-02	9.78E-01	1.59
---	---	---	1447119_at	3.78E-03	3.58E-01	1.59
Ttc9	tetratricopeptide repeat domain 9	69480	1455649_at	1.88E-02	7.94E-01	1.59
Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	19679	1419757_at	4.64E-03	4.03E-01	1.59
Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	19766	1439273_at	3.56E-03	3.46E-01	1.59
6330500D04Rik	RIKEN cDNA 6330500D04 gene	193385	1458202_at	2.70E-02	9.18E-01	1.59
Ccdc49	coiled-coil domain containing 49	67480	1428759_s_at	1.08E-02	6.34E-01	1.59
Ptprd	protein tyrosine phosphatase, receptor type, D	19266	1444492_at	3.12E-02	9.70E-01	1.60
Apcdd1	Adenomatosis polyposis coli down-regulated 1	494504	1443639_at	1.64E-02	7.63E-01	1.60
Snhg7	Small nucleolar RNA host gene (non-protein coding) 7	72091	1447484_x_at	7.17E-03	5.15E-01	1.60
Zkscan1	zinc finger with KRAB and SCAN domains 1	74570	1447944_at	1.52E-06	1.67E-03	1.60
Creb3l4	cAMP responsive element binding protein 3-like 4	78284	1424218_a_at	3.11E-02	9.69E-01	1.60
9030624J02Rik	RIKEN cDNA 9030624J02 gene	71517	1432304_a_at	1.77E-02	7.86E-01	1.60
Fhl2	four and a half LIM domains 2	14200	1419184_a_at	2.99E-02	9.52E-01	1.60
Cpne8	copine VIII	66871	1430520_at	1.63E-03	2.13E-01	1.61
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	23964	1420718_at	1.31E-02	6.89E-01	1.61
Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	67092	1423569_at	3.73E-02	1.00E+00	1.61

Qars	glutaminyl-tRNA synthetase	97541	1456213_x_at	2.05E-02	8.31E-01	1.61
Ifi35	interferon-induced protein 35	70110	1459151_x_at	3.20E-03	3.26E-01	1.62
Nkain1	Na+/K+ transporting ATPase interacting 1	67149	1419651_at	1.12E-03	1.73E-01	1.62
Nfkbil2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-lik	72749	1428661_at	1.60E-05	8.88E-03	1.62
EG328825	ribosomal protein L11	1000405	1448773_at	3.52E-02	1.00E+00	1.62
Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	20528	1415958_at	3.88E-02	1.00E+00	1.62
Gimap4	GTPase, IMAP family member 4	107526	1424375_s_at	4.77E-02	1.00E+00	1.62
1700027J05Rik	RIKEN cDNA 1700027J05 gene	69440	1436140_at	4.17E-02	1.00E+00	1.63
---	---	---	1443191_at	7.89E-03	5.37E-01	1.63
Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	23972	1434510_at	2.83E-03	3.06E-01	1.63
Foxj1	forkhead box J1	15223	1425291_at	2.56E-02	9.04E-01	1.63
Cblb	Casitas B-lineage lymphoma b	208650	1437304_at	8.52E-03	5.67E-01	1.64
---	Transcribed locus	---	1435409_at	4.24E-02	1.00E+00	1.64
Zbed3	zinc finger, BED domain containing 3	72114	1452088_at	3.16E-02	9.71E-01	1.64
Nhedc2	Na+/H+ exchanger domain containing 2	97086	1439995_at	2.49E-02	8.95E-01	1.65
5830405M20Rik	RIKEN cDNA 5830405M20 gene	74749	1431221_at	1.04E-04	3.39E-02	1.65
Troap	trophinin associated protein	78733	1453370_at	5.34E-05	2.11E-02	1.65
0610037L13Rik	RIKEN cDNA 0610037L13 gene	74098	1429879_at	3.02E-03	3.16E-01	1.65
Slc39a6	solute carrier family 39 (metal ion transporter), member 6	106957	1424675_at	2.01E-02	8.24E-01	1.65
---	Transcribed locus	---	1458640_at	4.60E-04	1.00E-01	1.65
Olfml1	olfactomedin-like 1	244198	1455663_at	2.24E-02	8.65E-01	1.65
LOC674761 Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	140781 674761	1448553_at	3.19E-02	9.75E-01	1.66
Cep250	centrosomal protein 250	16328	1421512_at	1.92E-02	8.03E-01	1.66
Atp13a4	ATPase type 13A4	224079	1438707_at	2.10E-02	8.38E-01	1.67
Jmjd4	jumonji domain containing 4	194952	1435915_at	1.38E-02	7.07E-01	1.67
1700012H17Rik	RIKEN cDNA 1700012H17 gene	242297	1440359_at	1.44E-02	7.19E-01	1.67
Heatr6	HEAT repeat containing 6	217026	1424687_at	3.24E-04	7.74E-02	1.67
Nalcn	sodium leak channel, non-selective	675405	1448083_at	3.78E-05	1.64E-02	1.67
Zdhhc14	zinc finger, DHHC domain containing 14	224454	1438151_x_at	1.45E-03	2.02E-01	1.67
Thap2	THAP domain containing, apoptosis associated protein 2	66816	1421177_at	1.24E-03	1.84E-01	1.68
Frzb	frizzled-related protein	20378	1448424_at	2.73E-02	9.18E-01	1.68
Csdc2	cold shock domain containing C2, RNA binding	105859	1437841_x_at	1.39E-03	1.97E-01	1.68
Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	77951	1430452_at	3.93E-03	3.64E-01	1.68
Unc13c	unc-13 homolog C (C. elegans)	208898	1455304_at	4.90E-04	1.04E-01	1.68
Rad18	RAD18 homolog (S. cerevisiae)	58186	1451928_a_at	6.62E-05	2.40E-02	1.68
Etnk1	ethanolamine kinase 1	75320	1433515_s_at	1.17E-02	6.58E-01	1.68
Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	28169	1433818_at	5.35E-03	4.43E-01	1.68
Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	319924	1455369_at	8.56E-03	5.68E-01	1.68
Scn2a1	sodium channel, voltage-gated, type II, alpha 1	110876	1445259_at	2.26E-03	2.65E-01	1.69
Zfp64	zinc finger protein 64	22722	1438140_a_at	3.73E-03	3.55E-01	1.69
Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	98660	1452308_a_at	5.08E-04	1.06E-01	1.69
Atf6	activating transcription factor 6	226641	1456021_at	1.71E-03	2.18E-01	1.69
Plp1	proteolipid protein (myelin) 1	18823	1425467_a_at	3.76E-02	1.00E+00	1.69
Ephb4	Eph receptor B4	13846	1449845_a_at	2.54E-02	9.01E-01	1.69
Sae1	SUMO1 activating enzyme subunit 1	56459	1430022_at	6.35E-07	8.95E-04	1.70
Hic1	hypermethylated in cancer 1	15248	1449226_at	2.82E-02	9.26E-01	1.70
Cpne8	copine VIII	66871	1430521_s_at	3.54E-04	8.28E-02	1.70
---	---	---	1440425_at	1.68E-02	7.66E-01	1.70
Spata6	spermatogenesis associated 6	67946	1418650_at	1.39E-04	4.23E-02	1.70
---	Transcribed locus	---	1443626_at	1.06E-03	1.68E-01	1.70
Col6a2	collagen, type VI, alpha 2	12834	1426947_x_at	4.40E-03	3.91E-01	1.70
Dlg7	discs, large homolog 7 (Drosophila)	218977	1438811_at	7.67E-04	1.36E-01	1.70
Clec1b	C-type lectin domain family 1, member b	56760	1421182_at	2.29E-02	8.67E-01	1.71
4833424O15Rik	RIKEN cDNA 4833424O15 gene	75769	1429249_at	6.94E-03	5.09E-01	1.71
Klhl25	kelch-like 25 (Drosophila)	207952	1425192_at	9.19E-03	5.91E-01	1.71
Rad51l1	RAD51-like 1 (S. cerevisiae)	19363	1421430_at	1.48E-03	2.04E-01	1.71
EG544888	predicted gene, EG544888	544888	1436685_at	5.11E-04	1.06E-01	1.72
---	Transcribed locus	---	1456952_at	6.77E-04	1.24E-01	1.72

Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	239273	1443870_at	5.46E-03	4.47E-01	1.72
6330416G13Rik	RIKEN cDNA 6330416G13 gene	230279	1426315_a_at	7.48E-03	5.24E-01	1.72
Osbpl3	oxysterol binding protein-like 3	71720	1438724_at	9.33E-03	5.94E-01	1.72
Rnf20	ring finger protein 20	109331	1452361_at	1.95E-08	8.00E-05	1.72
---	Transcribed locus	---	1440374_at	1.49E-02	7.30E-01	1.72
S100a1	S100 calcium binding protein A1	20193	1419814_s_at	6.21E-04	1.18E-01	1.72
A230106D06Rik	RIKEN cDNA A230106D06 gene	232785	1434857_at	5.45E-03	4.47E-01	1.73
Ankrd13d	ankyrin repeat domain 13 family, member D	68423	1452965_at	3.25E-02	9.83E-01	1.73
Nfasc	neurofascin	269116	1456068_at	1.24E-02	6.69E-01	1.73
Man1c1	mannosidase, alpha, class 1C, member 1	230815	1436193_at	1.42E-04	4.28E-02	1.73
---	Transcribed locus	---	1458669_at	2.92E-02	9.39E-01	1.73
9130005N14Rik	RIKEN cDNA 9130005N14 gene	68303	1448648_at	1.13E-03	1.73E-01	1.74
D4Wsu114e	DNA segment, Chr 4, Wayne State University 114, expressed	28010	1417120_at	6.24E-03	4.81E-01	1.74
---	Transcribed locus	---	1459747_at	4.50E-02	1.00E+00	1.74
---	CDNA clone IMAGE:5029795	---	1427600_at	1.66E-03	2.16E-01	1.74
Trp53rk	transformation related protein 53 regulating kinase	381406	1419682_a_at	2.92E-02	9.39E-01	1.74
BB187676	expressed sequence BB187676	103517	1455716_at	5.17E-03	4.37E-01	1.74
Gfpt2	glutamine fructose-6-phosphate transaminase 2	14584	1418753_at	7.73E-03	5.30E-01	1.74
2810003C17Rik	RIKEN cDNA 2810003C17 gene	108897	1424263_at	2.60E-03	2.87E-01	1.74
Sipa1l1	signal-induced proliferation-associated 1 like 1	217692	1440647_at	3.29E-03	3.29E-01	1.75
Emp2	epithelial membrane protein 2	13731	1433670_at	1.49E-02	7.30E-01	1.75
Cd59a	CD59a antigen	12509	1429830_a_at	2.23E-02	8.65E-01	1.75
Cryl1	crystallin, lambda 1	68631	1447112_s_at	1.21E-02	6.66E-01	1.75
Rai1	retinoic acid induced 1	19377	1420454_at	4.30E-04	9.50E-02	1.75
Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	98660	1427465_at	1.58E-02	7.47E-01	1.75
D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	52897	1456149_at	5.46E-03	4.47E-01	1.75
2310061F22Rik	RIKEN cDNA 2310061F22 gene	234839	1428350_at	7.73E-03	5.30E-01	1.75
Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	16492	1438613_at	6.60E-06	4.58E-03	1.76
---	Transcribed locus	---	1419836_at	4.67E-02	1.00E+00	1.76
Ascl1	achaete-scute complex homolog 1 (Drosophila)	17172	1450164_at	2.18E-03	2.59E-01	1.76
Rhcg	Rhesus blood group-associated C glycoprotein	56315	1417362_at	3.03E-03	3.16E-01	1.76
Kif20b	kinesin family member 20B	240641	1440924_at	8.07E-04	1.39E-01	1.76
Etv5	ets variant gene 5	104156	1428142_at	2.45E-02	8.90E-01	1.77
4931406H21Rik	RIKEN cDNA 4931406H21 gene	77592	1432572_at	4.89E-04	1.04E-01	1.77
Wif1	Wnt inhibitory factor 1	24117	1425425_a_at	2.96E-03	3.15E-01	1.77
Etv1	ets variant gene 1	14009	1450684_at	1.77E-02	7.84E-01	1.78
Coro7	coronin 7	78885	1428150_at	1.32E-02	6.92E-01	1.78
Lpar4	lysophosphatidic acid receptor 4	78134	1452424_at	2.51E-03	2.82E-01	1.78
Apex2	apurinic/apyrimidinic endonuclease 2	77622	1425954_a_at	1.45E-02	7.22E-01	1.78
Gm1060	gene model 1060, (NCBI)	381738	1455279_at	1.84E-04	5.21E-02	1.78
Cotl1	coactosin-like 1 (Dictyostelium)	72042	1416001_a_at	4.91E-03	4.22E-01	1.79
Dach2	dachshund 2 (Drosophila)	93837	1449823_at	5.62E-03	4.55E-01	1.79
Trf	transferrin	22041	1425546_a_at	1.48E-02	7.28E-01	1.79
Rasgrp1	RAS guanyl releasing protein 1	19419	1434295_at	4.59E-02	1.00E+00	1.79
1190002F15Rik	RIKEN cDNA 1190002F15 gene	381822	1441757_at	2.13E-08	8.00E-05	1.80
Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	13418	1420501_at	1.14E-03	1.73E-01	1.80
Syt5	synaptotagmin V	53420	1422531_at	1.20E-03	1.79E-01	1.80
Stat4	signal transducer and activator of transcription 4	20849	1448713_at	2.03E-03	2.47E-01	1.80
Lgi4	leucine-rich repeat LGI family, member 4	243914	1434121_at	7.31E-03	5.18E-01	1.81
Bnc2	basonuclin 2	242509	1438861_at	3.08E-02	9.63E-01	1.81
Cd248	CD248 antigen, endosialin	70445	1417439_at	4.02E-04	8.97E-02	1.82
Gna12	guanine nucleotide binding protein, alpha 12	14673	1421026_at	2.08E-02	8.33E-01	1.83
Nfia	Nuclear factor I/A	18027	1446742_at	7.16E-04	1.30E-01	1.83
Ankle1	ankyrin repeat and LEM domain containing 1	234396	1443978_at	1.46E-03	2.02E-01	1.83
Ankrd34a	ankyrin repeat domain 34A	545554	1435809_at	2.35E-05	1.22E-02	1.84
Ftl2	ferritin light chain 2	14325	1422301_at	5.88E-04	1.15E-01	1.85
Adk	adenosine kinase	11534	1449641_at	5.64E-05	2.16E-02	1.86
Clec14a	C-type lectin domain family 14, member a	66864	1419467_at	7.98E-04	1.39E-01	1.86

Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	17218	1459658_at	1.61E-03	2.12E-01	1.87
Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	114644	1438377_x_at	1.32E-04	4.07E-02	1.87
AA407175	expressed sequence AA407175	105070	1459578_at	3.65E-02	1.00E+00	1.88
Plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding specif	231999	1436128_at	2.80E-06	2.58E-03	1.88
Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	74519	1424677_at	1.54E-03	2.07E-01	1.88
Xaf1	XIAP associated factor 1	327959	1443621_at	7.36E-03	5.20E-01	1.89
Omg	oligodendrocyte myelin glycoprotein	18377	1418212_at	6.50E-08	1.74E-04	1.89
---	Transcribed locus	---	1444052_at	1.62E-03	2.12E-01	1.89
Nptx2	neuronal pentraxin 2	53324	1420720_at	5.04E-04	1.06E-01	1.90
Lmcd1	LIM and cysteine-rich domains 1	30937	1424596_s_at	4.61E-03	4.02E-01	1.90
Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	73181	1454369_a_at	3.50E-02	1.00E+00	1.91
2810039B14Rik	RIKEN cDNA 2810039B14 gene	72665	1453248_at	6.70E-05	2.40E-02	1.91
1110065P19Rik	RIKEN cDNA 1110065P19 gene	68919	1452893_s_at	4.68E-03	4.06E-01	1.91
E2f4	E2F transcription factor 4	104394	1451480_at	3.47E-02	1.00E+00	1.92
Ccnjl	cyclin J-like	380694	1459978_x_at	2.15E-03	2.58E-01	1.92
Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	98660	1434893_at	6.00E-03	4.71E-01	1.93
Ears2	glutamyl-tRNA synthetase 2 (mitochondrial)(putative)	67417	1451471_at	4.29E-04	9.50E-02	1.94
Hif3a	hypoxia inducible factor 3, alpha subunit	53417	1425428_at	2.52E-06	2.48E-03	1.94
Rab3a	RAB3A, member RAS oncogene family	19339	1459980_x_at	1.01E-03	1.64E-01	1.94
6330406I15Rik	RIKEN cDNA 6330406I15 gene	70717	1452244_at	5.52E-05	2.13E-02	1.95
Epb4.1	erythrocyte protein band 4.1	269587	1430369_at	5.55E-06	4.10E-03	1.96
Sncaip	synuclein, alpha interacting protein (synphilin)	67847	1430463_a_at	1.26E-06	1.54E-03	1.96
Sox3	SRY-box containing gene 3	20675	1450485_at	3.49E-03	3.43E-01	1.97
2610016C23Rik	RIKEN cDNA 2610016C23 gene	71804	1432013_a_at	3.03E-03	3.16E-01	1.98
Rps6kl1	ribosomal protein S6 kinase-like 1	238323	1426466_s_at	1.16E-02	6.56E-01	2.00
Rps17	ribosomal protein S17	665772	1438502_x_at	2.77E-06	2.58E-03	2.00
2900075N08Rik	RIKEN cDNA 2900075N08 gene	72991	1453756_at	1.93E-03	2.39E-01	2.00
Pitpnm1	phosphatidylinositol membrane-associated 1	18739	1438854_x_at	8.55E-04	1.43E-01	2.01
EG666892	predicted gene, EG666892	666892	1447550_at	4.23E-03	3.83E-01	2.02
Inhba	inhibin beta-A	16323	1422053_at	3.38E-04	7.97E-02	2.04
Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	22290	1422247_a_at	3.17E-02	9.73E-01	2.04
A930037G23Rik	RIKEN cDNA A930037G23 gene	320678	1454628_at	1.20E-03	1.79E-01	2.05
Marcks	Myristoylated alanine rich protein kinase C substrate	17118	1430311_at	1.07E-04	3.49E-02	2.05
Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	223864	1424471_at	2.67E-05	1.33E-02	2.05
Msrb3	methionine sulfoxide reductase B3	320183	1439151_at	1.72E-04	5.02E-02	2.05
Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	14802	1435722_at	4.02E-05	1.68E-02	2.07
Hdlbp	high density lipoprotein (HDL) binding protein	110611	1415988_at	1.86E-02	7.94E-01	2.08
Bmp7	bone morphogenetic protein 7	12162	1432410_a_at	1.81E-04	5.18E-02	2.10
Etv5	ets variant gene 5	104156	1450082_s_at	4.50E-03	3.95E-01	2.11
Tmem179b	transmembrane protein 179B	67706	1455874_at	6.14E-04	1.17E-01	2.11
Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	69706	1427506_at	1.12E-04	3.57E-02	2.14
3300002P09Rik	RIKEN cDNA 3300002P09 gene	70246	1453863_at	8.72E-05	2.96E-02	2.16
Rpusd2	RNA pseudouridylate synthase domain containing 2	271842	1453138_at	1.06E-05	6.84E-03	2.16
---	---	---	1459817_at	1.04E-06	1.34E-03	2.19
Fgf17	fibroblast growth factor 17	14171	1421523_at	2.59E-02	9.09E-01	2.20
---	---	---	1458823_at	1.09E-04	3.50E-02	2.20
Fkrp	fukutin related protein	243853	1437536_at	1.98E-02	8.15E-01	2.22
---	Transcribed locus	---	1459072_at	1.42E-02	7.13E-01	2.22
Arsg	arylsulfatase G	74008	1452277_at	6.13E-03	4.76E-01	2.24
Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	30957	1416437_a_at	8.24E-04	1.40E-01	2.24
Comtd1	catechol-O-methyltransferase domain containing 1	69156	1428635_at	4.00E-07	6.44E-04	2.25
Gem	GTP binding protein (gene overexpressed in skeletal muscle)	14579	1426063_a_at	1.79E-06	1.90E-03	2.27
---	Transcribed locus	---	1446982_at	5.99E-04	1.16E-01	2.28
Grm1	glutamate receptor, metabotropic 1	14816	1425700_at	5.85E-06	4.26E-03	2.31
Tekt2	tektin 2	24084	1418484_at	2.95E-04	7.24E-02	2.31
Ccnb1	Cyclin B1	268697	1419944_at	6.07E-04	1.17E-01	2.40
---	Transcribed locus	---	1456820_at	4.66E-04	1.01E-01	2.48
Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	77219	1429474_at	4.58E-05	1.88E-02	2.48

Zfp618	zinc fingerprotein 618	72701	1453247_at	1.43E-05	8.37E-03	2.52
Troap	trophinin associated protein	78733	1433790_at	1.31E-03	1.90E-01	2.56
Hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	15497	1460232_s_at	2.31E-06	2.37E-03	2.57
---	Transcribed locus, weakly similar to NP_001034645.1 RAD54 homolog B [Mus musculu	---	1447488_at	3.49E-05	1.57E-02	2.62
Ptk7	PTK7 protein tyrosine kinase 7	71461	1452589_at	5.95E-04	1.16E-01	2.62
Grb10	growth factor receptor bound protein 10	14783	1425457_a_at	5.26E-05	2.11E-02	2.78
Ipo7	importin 7	233726	1458165_at	3.02E-08	1.05E-04	2.85
Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	80879	1449005_at	2.81E-05	1.38E-02	2.91
Nelf	nasal embryonic LHRH factor	56876	1439398_x_at	3.63E-07	6.07E-04	3.06
2610021K21Rik	RIKEN cDNA 2610021K21 gene	78767	1431667_s_at	4.41E-07	6.85E-04	3.06
Gfap	glial fibrillary acidic protein	14580	1426508_at	3.40E-06	3.01E-03	3.62
Ptchd1	patched domain containing 1	211612	1457649_x_at	1.51E-07	3.25E-04	5.86

Table 4 Tissue expression pattern of significantly enriched genes (HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl [p < 0.05; FC < -1.5 or > 1.5])

Uniprot-Term	Observed genes	%	p-value*	Benjamini*
Brain	227	29.7	6.20E-08	4.60E-05
Placenta	108	14.1	8.70E-06	3.30E-03
Epithelium	79	10.3	5.30E-05	1.30E-02
Liver	58	7.6	1.50E-02	7.10E-01
Skin	57	7.5	3.00E-03	3.60E-01
Kidney	48	6.3	6.50E-03	5.00E-01
Bone marrow	34	4.5	5.80E-05	1.10E-02
Pancreas	33	4.3	1.40E-02	7.20E-01
Muscle	27	3.5	4.10E-02	8.30E-01
Skeletal muscle	21	2.7	1.50E-02	6.40E-01
Other:				
T-cell	14	1.8	2.70E-02	7.50E-01
Platelet	14	1.8	3.70E-02	8.30E-01
Fetal kidney	10	1.3	6.20E-03	5.40E-01
Fibroblast	8	1.0	2.40E-02	7.60E-01
Urinary bladder	8	1.0	4.60E-02	8.50E-01
Foreskin	6	0.8	1.50E-02	6.70E-01
Aortic endothelium	4	0.5	2.00E-02	7.20E-01
Endometrial tumor	4	0.5	2.50E-02	7.50E-01
Uterus endothel	4	0.5	3.90E-02	8.30E-01

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of Uniprot tissue expression

Table 5 GO intracellular component catagories of significantly enriched genes (HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl [p < 0.05; FC < -1.5 or > 1.5])

GO-Term	Observed genes	%	p-value*	Benjamini*
Cytoplasm	238	43.0	2,0E-7	5,7E-5
Nucleus	160	28.9	1,6E-2	4,3E-1
Endoplasmic reticulum	47	8.5	2,6E-5	2,5E-3
Golgi apparatus	31	5.6	9,9E-3	3,1E-1
Chromosome	23	4.2	2,4E-3	9,9E-2
Chromatin	16	2.9	6,4E-4	3,6E-2
Nucleosome	14	2.5	1,5E-7	6,7E-5
Actin cytoskeleton	12	2.2	1,6E-2	9,5E-2
Endosome	12	2.2	3,1E-2	6,3E-1

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 6 GO molecular funktion catagories of significantly enriched genes (HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl [p < 0.05; FC < -1.5 or > 1.5])

GO-Term	Observed genes	%	p-value*	Benjamini*
Binding	403	40.8	1.00E-06	1.50E-03
Protein binding	256	25.9	1.10E-07	3.00E-04
Catalytic activity	184	18.6	4.50E-02	1.00E+00
Phosphotransferase activity	32	3.2	4.30E-02	1.00E+00
Transcription factor binding	32	3.2	4.60E-02	1.00E+00
Protein kinase activity	28	2.8	4.30E-02	1.00E+00
Serine/threonine kinase activity	21	2.1	2.60E-02	1.00E+00
GTPase activity	13	1.3	1.50E-02	1.00E+00
Ligase activity	12	1.2	4.60E-02	1.00E+00
Protein binding, bridging	7	0.7	3.50E-02	1.00E+00

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 7 GO intracellular component catagories of differentially expressed genes

(Mouse Qkf$^{gt/gt}$ adult dorsal cortex vs. wildtype [FC < -1.5 or > 1.5])

GO-Term	**Observed genes**	**%**	**p-value***	**Benjamini***
Cytoplasm	104	43.7	1.05E-06	2.06E-04
Nucleus	63	26.5	6.37E-02	8.73E-01
Endoplasmic reticulum	47	19.7	2,6E-5	2,5E-3
Golgi apparatus	13	5.5	6.90E-02	8.74E-01
Actin cytoskeleton	5	2.1	2.90E-01	9.99E-01
Chromosome	2	0.8	9.89E-01	1.00
Chromatin	2	0.8	8.88E-01	1.00
Endosome	2	0.8	8.88E-01	1.00

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 8 GO molecular funktion catagories of significantly enriched genes

(Mouse Qkf$^{gt/gt}$ adult dorsal cortex vs. wildtype [p < 0.05; FC < -1.5 or > 1.5])

GO-Term	**Observed genes**	**%**	**p-value***	**Benjamini***
Binding	39	40.2	1.9E-6	5,0E-3
Protein binding	26	26.8	1.3E-4	1,6E-1
Metal ion binding	16	16.5	1.9E-2	1,0E0
Ion binding	16	16.5	2.3E-2	1,0E0

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 9 GO intracellular component catagories of differentially expressed genes

(Mouse Qkfgt/gt E12.5 dorsal telencephalon vs wildtype [FC < -1.5 or > 1.5])

GO-Term	**Observed genes**	**%**	**p-value***	**Benjamini***
Cytoplasm	114	43.7	2.76E-02	9.13E-01
Nucleus	96	26.5	1.30E-03	6.41E-01
Golgi apparatus	15	19.7	1.51E-01	9.96E-01
Endoplasmic reticulum	14	5.5	5.06E-01	1.00E+00
Extracellular matrix	11	2.1	3.67E-02	9.13E-01
Chromosome	10	0.8	1.64E-01	1.00
Endosome	5	0.8	3.54E-01	1.00
Actin cytoskeleton	4		7.32E-01	1.00
Chromatin	4	0.8	5.81E-01	1.00

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 10 GO molecular funktion catagories of significantly enriched genes

(Mouse Qkfgt/gt E12.5 dorsal telencephalon vs wildtype [FC < -1.5 or > 1.5])

GO-Term	Observed genes	%	p-value*	Benjamini*
Binding	337	56.1	3.45E-07	6.21E-06
Catalytic activity	161	26.8	3.51E-02	1.49E-01
Transporter activity	53	8.8	2.00E-03	1.78E-02
Transcription regulator activity	50	8.3	2.54E-03	1.51E-02

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of GO Molecular Function Catagories

Table 11 KEGG pathways of significantly enriched genes (HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl [p < 0.05; FC < -1.5 or > 1.5]) (* significant corrected gamma p-value < 0.05, Pathway Express calculation)

KEGG pathway name	Rank	Impact factor	No. genes in pathway	No. input genes in pathway	% Pathwaygenes in input	p-value			
						uncorrected	corrected	gamma	corrected gamma
Phosphatidylinositol signaling system*	1	48.9	77	2	2.6	4.63E-02	4.63E-02	2.81E-20	2.81E-20
Circadian rhythm*	2	22.8	13	1	7.7	5.64E-02	5.64E-02	2.95E-09	2.95E-09
Insulin signaling pathway*	3	20.3	138	9	6.5	9.71E-09	9.71E-09	3.20E-08	3.20E-08
MAPK signaling pathway*	4	19.9	265	11	4.2	2.49E-08	2.49E-08	4.94E-08	4.94E-08
Wnt signaling pathway*	5	19.4	148	9	6.1	1.81E-08	1.81E-08	7.56E-08	7.56E-08
Melanoma*	6	19.3	71	7	9.9	2.90E-08	2.90E-08	8.82E-08	8.82E-08
Apoptosis*	7	18.0	84	7	8.3	9.43E-08	9.43E-08	2.93E-07	2.93E-07
Regulation of actin cytoskeleton*	8	17.1	211	9	4.3	3.47E-07	3.47E-07	6.94E-07	6.94E-07
GnRH signaling pathway*	9	16.8	97	7	7.2	2.55E-07	2.55E-07	9.11E-07	9.11E-07
Glioma*	10	16.1	64	6	9.4	4.03E-07	4.03E-07	1.71E-06	1.71E-06
Glycan structures - biosynthesis 1*	11	14.6	122	7	5.7	1.22E-06	1.22E-06	6.90E-06	6.90E-06
Colorectal cancer*	12	14.4	84	6	7.1	2.03E-06	2.03E-06	8.74E-06	8.74E-06
Gap junction*	13	14.2	96	5	5.2	6.30E-05	6.30E-05	1.06E-05	1.06E-05
Cell Communication*	14	14.2	138	7	5.1	1.96E-06	1.96E-06	1.08E-05	1.08E-05
Adherens junction*	15	13.8	75	2	2.7	4.41E-02	4.41E-02	1.51E-05	1.51E-05
Pancreatic cancer*	16	12.5	73	5	6.8	1.86E-05	1.86E-05	5.17E-05	5.17E-05
Focal adhesion*	17	12.5	199	7	3.5	2.85E-05	2.85E-05	5.22E-05	5.22E-05
Fc epsilon RI signaling pathway*	18	12.4	77	5	6.5	2.26E-05	2.26E-05	5.31E-05	5.31E-05
ErbB signaling pathway*	19	12.1	87	5	5.7	4.35E-05	4.35E-05	7.11E-05	7.11E-05
Endometrial cancer*	20	11.8	52	4	7.7	8.47E-05	8.47E-05	9.89E-05	9.89E-05
Prostate cancer*	21	11.6	89	5	5.6	4.59E-05	4.59E-05	1.11E-04	1.11E-04
Long-term potentiation*	22	11.6	69	4	5.8	2.55E-04	2.55E-04	1.17E-04	1.17E-04
Non-small cell lung cancer*	23	11.5	54	4	7.4	9.82E-05	9.82E-05	1.24E-04	1.24E-04
Melanogenesis*	24	11.4	101	5	5.0	8.47E-05	8.47E-05	1.33E-04	1.33E-04
Toll-like receptor signaling pathway*	25	10.8	102	5	4.9	9.30E-05	9.30E-05	2.41E-04	2.41E-04

Calcium signaling pathway*	26	10.7	175	6	3.4	1.28E-04	1.28E-04	2.53E-04	2.53E-04
Long-term depression*	27	10.7	76	4	5.3	3.70E-04	3.70E-04	2.74E-04	2.74E-04
Natural killer cell mediated cytotoxicity*	28	10.6	131	5	3.8	2.24E-04	2.24E-04	2.80E-04	2.80E-04
VEGF signaling pathway*	29	10.3	71	4	5.6	2.70E-04	2.70E-04	3.87E-04	3.87E-04
Thyroid cancer*	30	9.4	29	3	10.3	2.87E-04	2.87E-04	8.71E-04	8.71E-04
Neurodegenerative Diseases*	31	9.2	30	3	10.0	3.18E-04	3.18E-04	1.02E-03	1.02E-03
Bladder cancer*	32	9.0	42	3	7.1	8.65E-04	8.65E-04	1.28E-03	1.28E-03
ECM-receptor interaction*	33	8.9	87	4	4.6	5.92E-04	5.92E-04	1.33E-03	1.33E-03
Small cell lung cancer*	34	8.8	87	4	4.6	6.18E-04	6.18E-04	1.46E-03	1.46E-03
Notch signaling pathway*	35	8.4	46	3	6.5	1.13E-03	1.13E-03	2.19E-03	2.19E-03
Cytokine-cytokine receptor interaction*	36	8.2	259	6	2.3	1.00E-03	1.00E-03	2.43E-03	2.43E-03
Renal cell carcinoma*	37	8.0	69	3	4.3	3.62E-03	3.62E-03	2.98E-03	2.98E-03
Basal cell carcinoma*	38	7.9	55	2	3.6	2.42E-02	2.42E-02	3.44E-03	3.44E-03
p53 signaling pathway*	39	7.8	68	3	4.4	3.48E-03	3.48E-03	3.64E-03	3.64E-03
B cell receptor signaling pathway*	40	7.7	64	3	4.7	2.93E-03	2.93E-03	3.82E-03	3.82E-03
Dorso-ventral axis formation*	41	7.6	28	2	7.1	6.41E-03	6.41E-03	4.28E-03	4.28E-03
Hedgehog signaling pathway*	42	7.6	57	3	5.3	1.90E-03	1.90E-03	4.49E-03	4.49E-03
Alzheimer''s disease*	43	7.5	22	2	9.1	4.28E-03	4.28E-03	4.60E-03	4.60E-03
Chronic myeloid leukemia*	44	7.5	76	3	3.9	4.75E-03	4.75E-03	4.65E-03	4.65E-03
Jak-STAT signaling pathway*	45	7.2	153	4	2.6	4.88E-03	4.88E-03	6.04E-03	6.04E-03
T cell receptor signaling pathway*	46	7.2	93	3	3.2	8.31E-03	8.31E-03	6.29E-03	6.29E-03
TGF-beta signaling pathway*	47	7.2	89	3	3.4	6.92E-03	6.92E-03	6.38E-03	6.38E-03
Prion diseases*	48	6.3	1	1	100.0	4.45E-03	4.45E-03	1.34E-02	1.34E-02
Antigen processing and presentation*	49	6.2	88	3	3.4	5.11E-03	5.11E-03	1.50E-02	1.50E-02
Type II diabetes mellitus*	50	5.8	44	2	4.5	1.51E-02	1.51E-02	2.03E-02	2.03E-02
Glycan structures - degradation*	51	5.7	30	2	6.7	7.87E-03	7.87E-03	2.17E-02	2.17E-02
Tight junction*	52	5.7	135	3	2.2	2.21E-02	2.21E-02	2.28E-02	2.28E-02
Axon guidance*	53	5.6	128	3	2.3	1.96E-02	1.96E-02	2.34E-02	2.34E-02
Acute myeloid leukemia*	54	5.6	57	2	3.5	2.67E-02	2.67E-02	2.52E-02	2.52E-02

SNARE interactions in vesicular transport*	55	5.5	38	2	5.3	1.18E-02	1.18E-02	2.73E-02	2.73E-02
Nucleotide excision repair*	56	5.3	43	2	4.7	1.51E-02	1.51E-02	3.17E-02	3.17E-02
Cell adhesion molecules (CAMs)*	57	5.2	133	3	2.3	1.92E-02	1.92E-02	3.40E-02	3.40E-02
mTOR signaling pathway*	58	5.1	51	2	3.9	2.01E-02	2.01E-02	3.74E-02	3.74E-02
Vibrio cholerae infection*	59	5.0	59	2	3.4	2.85E-02	2.85E-02	4.15E-02	4.15E-02
Epithelial cell signaling in Helicobacter pylori infection	60	4.7	69	2	2.9	3.80E-02	3.80E-02	5.32E-02	5.32E-02
Adipocytokine signaling pathway	61	4.4	72	2	2.8	4.10E-02	4.10E-02	6.85E-02	6.85E-02
Dentatorubropallidoluysian atrophy (DRPLA)	62	4.2	15	1	6.7	6.06E-02	6.06E-02	7.67E-02	7.67E-02
Maturity onset diabetes of the young	63	4.2	25	1	4.0	9.36E-02	9.36E-02	7.92E-02	7.92E-02
Olfactory transduction	64	4.0	383	2	0.5	9.18E-02	9.18E-02	9.32E-02	9.32E-02
Taste transduction	65	3.6	53	1	1.9	1.86E-01	1.86E-01	1.21E-01	1.21E-01
Cell cycle	66	3.6	112	2	1.8	8.91E-02	8.91E-02	1.24E-01	1.24E-01
Renin-angiotensin system	67	3.5	17	1	5.9	7.31E-02	7.31E-02	1.33E-01	1.33E-01
Neuroactive ligand-receptor interaction	69	3.4	254	3	1.2	1.02E-01	1.02E-01	1.52E-01	1.52E-01
Proteasome	70	3.3	22	1	4.5	9.36E-02	9.36E-02	1.56E-01	1.56E-01
Biosynthesis of unsaturated fatty acids	71	3.2	23	1	4.3	9.76E-02	9.76E-02	1.66E-01	1.66E-01
Mismatch repair	72	3.2	22	1	4.5	9.36E-02	9.36E-02	1.66E-01	1.66E-01
Huntington''s disease	73	3.2	30	1	3.3	1.25E-01	1.25E-01	1.66E-01	1.66E-01
Base excision repair	74	2.9	33	1	3.0	1.37E-01	1.37E-01	2.09E-01	2.09E-01
DNA replication	75	2.8	35	1	2.9	1.45E-01	1.45E-01	2.30E-01	2.30E-01
Complement and coagulation cascades	76	2.6	69	1	1.4	2.65E-01	2.65E-01	2.60E-01	2.60E-01
Pathogenic Escherichia coli infection	77	2.5	51	1	2.0	1.97E-01	1.97E-01	2.80E-01	2.80E-01
Glycan structures - biosynthesis 2	78	2.4	63	1	1.6	2.45E-01	2.45E-01	3.02E-01	3.02E-01
Ribosome	79	2.4	91	1	1.1	2.65E-01	2.65E-01	3.13E-01	3.13E-01
PPAR signaling pathway	80	2.3	69	1	1.4	2.62E-01	2.62E-01	3.41E-01	3.41E-01
Leukocyte transendothelial migration	81	1.8	116	1	0.9	4.02E-01	4.02E-01	4.52E-01	4.52E-01
Ubiquitin mediated proteolysis	82	1.8	130	1	0.8	4.36E-01	4.36E-01	4.58E-01	4.58E-01

Table 12 KEGG pathways of significantly enriched genes

(HEK 293 *MYST4* siRNA and HeLa *MYST4* siRNA *vs* HEK 293 ctrl and HeLa ctrl [p < 0.05; FC < -1.5 or > 1.5])

(* significant corrected gamma p-value < 0.05, DAVID functional annotation)

KEGG pathway name	p-value	Fold enrichment
Melanoma*	2.75E-03	4.86
Insulin signaling pathway*	5.98E-03	3.22
Apoptosis*	7.30E-03	3.99
Glioma*	7.48E-03	4.79
Wnt signaling pathway*	1.20E-02	2.85
GnRH signaling pathway*	1.24E-02	3.57
Colorectal cancer*	3.01E-02	3.38
Regulation of actin cytoskeleton*	3.11E-02	2.24
Glycan structures - biosynthesis 1*	3.65E-02	2.79
MAPK signaling pathway*	3.92E-02	2.03
Cell Communication	6.07E-02	2.46
Pancreatic cancer	6.29E-02	3.28
Fc epsilon RI signaling pathway	6.55E-02	3.24
Endometrial cancer	8.33E-02	3.83
Non-small cell lung cancer	9.12E-02	3.68
ErbB signaling pathway	9.75E-02	2.82
Prostate cancer	1.04E-01	2.75
Thyroid cancer	1.06E-01	5.32
Focal adhesion	1.15E-01	1.93
Gap junction	1.32E-01	2.52
O-Glycan biosynthesis	1.41E-01	4.49
Melanogenesis	1.43E-01	2.44
Long-term potentiation	1.50E-01	2.95
Toll-like receptor signaling pathway	1.59E-01	2.35

VEGF signaling pathway	1.80E-01	2.70
Neurodegenerative Diseases	1.92E-01	3.68
Bladder cancer	1.99E-01	3.59
Long-term depression	2.01E-01	2.55
Notch signaling pathway	2.53E-01	3.06
Small cell lung cancer	2.67E-01	2.20
ECM-receptor interaction	2.73E-01	2.18
Natural killer cell mediated cytotoxicity	2.76E-01	1.86
Calcium signaling pathway	2.89E-01	1.65
Hedgehog signaling pathway	3.30E-01	2.52
B cell receptor signaling pathway	3.90E-01	2.21
Renal cell carcinoma	4.05E-01	2.14
p53 signaling pathway	4.12E-01	2.11
Alzheimer's disease	4.43E-01	3.42
Dorso-ventral axis formation	4.43E-01	3.42
Chronic myeloid leukemia	4.55E-01	1.94
Olfactory transduction	4.55E-01	3.30
Glycan structures - degradation	4.77E-01	3.09
Antigen processing and presentation	4.96E-01	1.80
TGF-beta signaling pathway	5.59E-01	1.60
SNARE interactions in vesicular transport	5.68E-01	2.39
T cell receptor signaling pathway	5.83E-01	1.53
Type II diabetes mellitus	6.11E-01	2.13
Jak-STAT signaling pathway	6.14E-01	1.26
Cytokine-cytokine receptor interaction	6.17E-01	1.12
mTOR signaling pathway	6.57E-01	1.88
Acute myeloid leukemia	6.85E-01	1.74
Basal cell carcinoma	6.91E-01	1.71

Table 13 KEGG pathways of significantly enriched genes (Mouse $Qkf^{gt/gt}$ adult dorsal cortex vs. wildtype [$p < 0.05$; FC < -1.5 or > 1.5])

(* significant corrected gamma p-value < 0.05, Pathway Express calculation)

		Impact	No. genes	No. input genes	% Pathwaygenes	p-value			
KEGG pathway name	**Rank**	**factor**	**in pathway**	**in pathway**	**in input**	**uncorrected**	**corrected**	**gamma**	**corrected gamma**
Neuroactive ligand-receptor interaction*	1	27.1	256	11	4.3	5.80E-12	5.80E-12	4.93E-11	4.93E-11
MAPK signaling pathway*	2	21.5	258	9	3.5	9.84E-09	9.84E-09	1.08E-08	1.08E-08
Calcium signaling pathway*	3	17.9	185	7	3.8	1.71E-07	1.71E-07	3.10E-07	3.10E-07
Axon guidance*	4	17.0	128	6	4.7	6.12E-07	6.12E-07	7.58E-07	7.58E-07
Focal adhesion*	5	15.8	192	6	3.1	5.72E-06	5.72E-06	2.34E-06	2.34E-06
Cytokine-cytokine receptor interaction*	6	12.1	242	6	2.5	1.66E-05	1.66E-05	7.29E-05	7.29E-05
Jak-STAT signaling pathway*	7	11.9	151	5	3.3	2.06E-05	2.06E-05	9.04E-05	9.04E-05
Long-term potentiation*	8	11.2	66	3	4.5	5.35E-04	5.35E-04	1.65E-04	1.65E-04
Natural killer cell mediated cytotoxicity*	9	10.4	127	4	3.2	1.66E-04	1.66E-04	3.40E-04	3.40E-04
Wnt signaling pathway*	10	10.3	145	4	2.8	4.18E-04	4.18E-04	3.71E-04	3.71E-04
Renal cell carcinoma*	11	8.7	69	3	4.3	6.10E-04	6.10E-04	1.60E-03	1.60E-03
Basal cell carcinoma*	12	8.6	55	1	1.8	1.26E-01	1.26E-01	1.74E-03	1.74E-03
Type II diabetes mellitus*	13	8.3	46	1	2.2	1.04E-01	1.04E-01	2.32E-03	2.32E-03
Toll-like receptor signaling pathway*	14	7.9	101	3	3.0	1.61E-03	1.61E-03	3.33E-03	3.33E-03
Melanoma*	15	7.8	71	1	1.4	1.57E-01	1.57E-01	3.46E-03	3.46E-03
Tight junction*	16	7.7	135	3	2.2	3.75E-03	3.75E-03	4.03E-03	4.03E-03
Notch signaling pathway*	17	7.2	47	2	4.3	4.93E-03	4.93E-03	6.24E-03	6.24E-03
Regulation of actin cytoskeleton*	18	6.7	206	3	1.5	1.23E-02	1.23E-02	9.36E-03	9.36E-03
ECM-receptor interaction*	19	6.0	84	2	2.4	1.63E-02	1.63E-02	1.79E-02	1.79E-02
B cell receptor signaling pathway*	20	5.9	66	2	3.0	1.13E-02	1.13E-02	1.88E-02	1.88E-02
p53 signaling pathway*	21	5.5	65	2	3.1	1.03E-02	1.03E-02	2.67E-02	2.67E-02
Gap junction*	22	5.4	92	2	2.2	1.87E-02	1.87E-02	2.85E-02	2.85E-02
T cell receptor signaling pathway*	23	5.3	105	2	1.9	2.16E-02	2.16E-02	3.25E-02	3.25E-02

Cell Communication	24	4.6	130	2	1.5	3.25E-02	3.25E-02	5.57E-02	5.57E-02
Leukocyte transendothelial migration	25	4.5	115	2	1.7	2.90E-02	2.90E-02	5.97E-02	5.97E-02
TGF-beta signaling pathway	26	4.3	89	1	1.1	1.87E-01	1.87E-01	6.93E-02	6.93E-02
Dentatorubropallidoluysian atrophy (DRPLA)	27	4.2	15	1	6.7	3.59E-02	3.59E-02	7.54E-02	7.54E-02
Melanogenesis	28	4.1	98	1	1.0	2.13E-01	2.13E-01	8.77E-02	8.77E-02
Alzheimer''s disease	29	3.9	23	1	4.3	5.22E-02	5.22E-02	9.82E-02	9.82E-02
VEGF signaling pathway	30	3.8	72	1	1.4	1.61E-01	1.61E-01	1.10E-01	1.10E-01
Taste transduction	31	3.7	60	1	1.7	6.83E-02	6.83E-02	1.12E-01	1.12E-01
Neurodegenerative Diseases	32	3.6	29	1	3.4	6.83E-02	6.83E-02	1.21E-01	1.21E-01
Colorectal cancer	33	3.5	84	1	1.2	1.85E-01	1.85E-01	1.36E-01	1.36E-01
Allograft rejection	34	3.4	65	1	1.5	9.07E-02	9.07E-02	1.46E-01	1.46E-01
Bladder cancer	35	3.3	42	1	2.4	9.52E-02	9.52E-02	1.53E-01	1.53E-01
Type I diabetes mellitus	36	3.3	70	1	1.4	1.02E-01	1.02E-01	1.60E-01	1.60E-01
Hedgehog signaling pathway	37	3.2	53	1	1.9	1.19E-01	1.19E-01	1.69E-01	1.69E-01
Apoptosis	38	3.2	81	1	1.2	1.79E-01	1.79E-01	1.75E-01	1.75E-01
mTOR signaling pathway	39	3.2	52	1	1.9	1.15E-01	1.15E-01	1.76E-01	1.76E-01
Cell adhesion molecules (CAMs)	40	3.1	157	1	0.6	2.69E-01	2.69E-01	1.79E-01	1.79E-01
Antigen processing and presentation	41	3.0	99	1	1.0	1.53E-01	1.53E-01	2.03E-01	2.03E-01
Pancreatic cancer	42	2.8	73	1	1.4	1.61E-01	1.61E-01	2.27E-01	2.27E-01
Adipocytokine signaling pathway	43	2.8	71	1	1.4	1.57E-01	1.57E-01	2.40E-01	2.40E-01
Long-term depression	44	2.7	76	1	1.3	1.67E-01	1.67E-01	2.43E-01	2.43E-01
Chronic myeloid leukemia	45	2.7	77	1	1.3	1.67E-01	1.67E-01	2.51E-01	2.51E-01
Hematopoietic cell lineage	46	2.7	85	1	1.2	1.83E-01	1.83E-01	2.55E-01	2.55E-01
ErbB signaling pathway	47	2.6	87	1	1.1	1.87E-01	1.87E-01	2.71E-01	2.71E-01
Glycan structures - biosynthesis 1	48	2.6	117	1	0.9	2.43E-01	2.43E-01	2.73E-01	2.73E-01
GnRH signaling pathway	49	2.5	95	1	1.1	2.05E-01	2.05E-01	2.89E-01	2.89E-01
Cell cycle	50	2.4	109	1	0.9	2.32E-01	2.32E-01	3.16E-01	3.16E-01
Ubiquitin mediated proteolysis	51	2.2	132	1	0.8	2.70E-01	2.70E-01	3.49E-01	3.49E-01

Table 14 KEGG pathways of significantly enriched genes (Mouse Qkf$^{gt/gt}$ adult dorsal cortex vs. wildtype [$p < 0.05$; FC < -1.5 or > 1.5])

(* significant corrected gamma p-value < 0.05, DAVID functional annotation)

KEGG pathway name	**p-value**	**Fold enrichment**
Neuroactive ligand-receptor interaction*	4.45E-03	3.01
Axon guidance*	2.12E-02	3.66
Calcium signaling pathway*	2.21E-02	3.10
MAPK signaling pathway*	3.90E-02	2.44
Focal adhesion	9.57E-02	2.41
Jak-STAT signaling pathway	1.27E-01	2.53
Long-term potentiation	1.91E-01	3.66
Cytokine-cytokine receptor interaction	1.93E-01	1.91
Natural killer cell mediated cytotoxicity	2.06E-01	2.50
Renal cell carcinoma	2.15E-01	3.40
Wnt signaling pathway	2.81E-01	2.12
Toll-like receptor signaling pathway	3.75E-01	2.26
Notch signaling pathway	4.48E-01	3.35
Tight junction	5.02E-01	1.76
B cell receptor signaling pathway	5.57E-01	2.44
p53 signaling pathway	5.69E-01	2.37
ECM-receptor interaction	6.63E-01	1.83
Gap junction	6.89E-01	1.71
T cell receptor signaling pathway	7.05E-01	1.64
Regulation of actin cytoskeleton	7.50E-01	1.12
Leukocyte transendothelial migration	7.76E-01	1.34
Cell Communication	8.19E-01	1.17

Table 15 KEGG pathways of significantly enriched genes (Mouse Qkf$^{gt/gt}$ E12.5 dorsal telencephalon vs wildtype [$p < 0.05$; FC < -1.5 or >1.5]) (* significant corrected gamma p-value < 0.05, Pathway Express calculation)

KEGG pathway name	Rank	Impact factor	No. genes in pathway	No. input genes in pathway	% Pathwaygenes in input	p-value uncorrected	p-value corrected	p-value gamma	p-value corrected gamma
Phosphatidylinositol signaling system*	1	21.9	70	2	2.9	3.06E-02	3.06E-02	6.92E-09	6.92E-09
MAPK signaling pathway*	2	21.7	258	11	4.3	4.37E-09	4.37E-09	8.70E-09	8.70E-09
Insulin signaling pathway*	3	21.0	137	9	6.6	2.68E-09	2.68E-09	1.60E-08	1.60E-08
Adherens junction*	4	17.1	74	4	5.4	1.92E-04	1.92E-04	6.77E-07	6.77E-07
Melanogenesis*	5	14.9	98	6	6.1	2.34E-06	2.34E-06	5.35E-06	5.35E-06
Type II diabetes mellitus*	6	13.7	46	4	8.7	2.85E-05	2.85E-05	1.62E-05	1.62E-05
Wnt signaling pathway*	7	13.6	145	6	4.1	2.15E-05	2.15E-05	1.77E-05	1.77E-05
Focal adhesion*	8	11.3	192	6	3.1	8.70E-05	8.70E-05	1.59E-04	1.59E-04
Long-term depression*	9	11.1	76	4	5.3	2.13E-04	2.13E-04	1.83E-04	1.83E-04
Regulation of actin cytoskeleton*	10	10.6	206	6	2.9	1.23E-04	1.23E-04	2.83E-04	2.83E-04
Basal cell carcinoma*	11	10.5	55	3	5.5	1.30E-03	1.30E-03	3.13E-04	3.13E-04
Long-term potentiation*	12	10.0	66	3	4.5	2.11E-03	2.11E-03	5.11E-04	5.11E-04
Neurodegenerative Diseases*	13	9.9	29	3	10.3	1.95E-04	1.95E-04	5.69E-04	5.69E-04
Cytokine-cytokine receptor interaction*	14	9.6	242	6	2.5	2.41E-04	2.41E-04	7.30E-04	7.30E-04
Calcium signaling pathway*	15	9.5	185	5	2.7	5.28E-04	5.28E-04	8.12E-04	8.12E-04
T cell receptor signaling pathway*	16	9.4	105	4	3.8	4.85E-04	4.85E-04	8.57E-04	8.57E-04
Tight junction*	17	9.3	135	4	3.0	1.60E-03	1.60E-03	9.28E-04	9.28E-04
Base excision repair*	18	9.2	36	3	8.3	2.62E-04	2.62E-04	1.06E-03	1.06E-03
ErbB signaling pathway*	19	9.1	87	4	4.6	3.44E-04	3.44E-04	1.10E-03	1.10E-03
DNA replication*	20	9.0	34	3	8.8	3.15E-04	3.15E-04	1.23E-03	1.23E-03
Melanoma*	21	8.6	71	3	4.2	2.60E-03	2.60E-03	1.82E-03	1.82E-03
Cell cycle*	22	8.2	109	4	3.7	8.51E-04	8.51E-04	2.56E-03	2.56E-03
Hedgehog signaling pathway*	23	7.8	53	3	5.7	1.11E-03	1.11E-03	3.62E-03	3.62E-03

TGF-beta signaling pathway*	24	7.5	89	3	3.4	4.50E-03	4.50E-03	4.65E-03	4.65E-03
GnRH signaling pathway*	25	7.5	95	3	3.2	5.96E-03	5.96E-03	4.78E-03	4.78E-03
Glycan structures - biosynthesis 2*	26	7.5	58	3	5.2	1.44E-03	1.44E-03	4.90E-03	4.90E-03
Gap junction*	27	7.4	92	2	2.2	4.46E-02	4.46E-02	4.99E-03	4.99E-03
Apoptosis*	28	7.4	81	3	3.7	3.93E-03	3.93E-03	5.24E-03	5.24E-03
Ubiquitin mediated proteolysis*	29	7.4	132	4	3.0	1.64E-03	1.64E-03	5.24E-03	5.24E-03
Neuroactive ligand-receptor interaction*	30	7.2	256	5	2.0	1.93E-03	1.93E-03	5.88E-03	5.88E-03
Prostate cancer*	31	7.1	88	3	3.4	4.96E-03	4.96E-03	6.87E-03	6.87E-03
ECM-receptor interaction*	32	6.9	84	3	3.6	3.80E-03	3.80E-03	8.22E-03	8.22E-03
Jak-STAT signaling pathway*	33	6.5	151	3	2.0	1.65E-02	1.65E-02	1.12E-02	1.12E-02
Hematopoietic cell lineage*	34	6.5	85	3	3.5	4.21E-03	4.21E-03	1.18E-02	1.18E-02
Natural killer cell mediated cytotoxicity*	35	6.3	127	3	2.4	9.88E-03	9.88E-03	1.29E-02	1.29E-02
Homologous recombination*	36	6.3	26	2	7.7	4.61E-03	4.61E-03	1.33E-02	1.33E-02
Taste transduction*	37	6.2	60	2	3.3	5.71E-03	5.71E-03	1.41E-02	1.41E-02
Huntington''s disease*	38	6.2	28	2	7.1	5.33E-03	5.33E-03	1.46E-02	1.46E-02
Renal cell carcinoma*	39	6.0	69	2	2.9	2.91E-02	2.91E-02	1.74E-02	1.74E-02
VEGF signaling pathway*	40	5.7	72	2	2.8	3.23E-02	3.23E-02	2.20E-02	2.20E-02
Glioma*	41	5.7	65	2	3.1	2.52E-02	2.52E-02	2.32E-02	2.32E-02
Cell adhesion molecules (CAMs)*	42	5.6	157	3	1.9	1.38E-02	1.38E-02	2.42E-02	2.42E-02
Dentatorubropallidoluysian atrophy (DRPLA)*	43	5.5	15	1	6.7	5.70E-02	5.70E-02	2.58E-02	2.58E-02
Nucleotide excision repair*	44	5.4	41	2	4.9	1.12E-02	1.12E-02	2.94E-02	2.94E-02
Acute myeloid leukemia*	45	5.3	58	2	3.4	2.09E-02	2.09E-02	3.14E-02	3.14E-02
Notch signaling pathway	46	4.7	47	1	2.1	1.55E-01	1.55E-01	5.30E-02	5.30E-02
Axon guidance	47	4.7	128	2	1.6	8.70E-02	8.70E-02	5.39E-02	5.39E-02
B cell receptor signaling pathway	48	4.6	66	2	3.0	2.75E-02	2.75E-02	5.72E-02	5.72E-02
Antigen processing and presentation	49	4.4	99	2	2.0	2.91E-02	2.91E-02	6.42E-02	6.42E-02
Chronic myeloid leukemia	50	4.3	77	2	2.6	3.48E-02	3.48E-02	7.12E-02	7.12E-02
Toll-like receptor signaling pathway	51	4.3	101	2	2.0	5.32E-02	5.32E-02	7.31E-02	7.31E-02

Fc epsilon RI signaling pathway	52	4.3	78	2	2.6	3.74E-02	3.74E-02	7.42E-02	7.42E-02
Colorectal cancer	53	4.1	84	2	2.4	4.27E-02	4.27E-02	8.19E-02	8.19E-02
Leukocyte transendothelial migration	54	4.1	115	2	1.7	6.78E-02	6.78E-02	8.23E-02	8.23E-02
Complement and coagulation cascades	55	4.1	71	1	1.4	2.28E-01	2.28E-01	8.36E-02	8.36E-02
Non-small cell lung cancer	56	4.0	54	1	1.9	1.87E-01	1.87E-01	8.81E-02	8.81E-02
Ribosome	57	4.0	92	2	2.2	4.46E-02	4.46E-02	9.10E-02	9.10E-02
Parkinson''s disease	58	3.7	21	1	4.8	7.53E-02	7.53E-02	1.17E-01	1.17E-01
Glycan structures - biosynthesis 1	59	3.6	117	2	1.7	7.33E-02	7.33E-02	1.28E-01	1.28E-01
Mismatch repair	60	3.5	20	1	5.0	7.53E-02	7.53E-02	1.39E-01	1.39E-01
mTOR signaling pathway	61	3.4	52	1	1.9	1.78E-01	1.78E-01	1.43E-01	1.43E-01
Dorso-ventral axis formation	62	3.2	26	1	3.8	9.68E-02	9.68E-02	1.70E-01	1.70E-01
Proteasome	63	3.1	31	1	3.2	1.14E-01	1.14E-01	1.87E-01	1.87E-01
ABC transporters	64	2.9	41	1	2.4	1.48E-01	1.48E-01	2.11E-01	2.11E-01
p53 signaling pathway	65	2.9	65	1	1.5	2.19E-01	2.19E-01	2.19E-01	2.19E-01
Adipocytokine signaling pathway	66	2.3	71	1	1.4	2.40E-01	2.40E-01	3.21E-01	3.21E-01
Cell Communication	67	2.0	130	1	0.8	3.66E-01	3.66E-01	4.15E-01	4.15E-01

Table 16 KEGG pathways of significantly enriched genes (Mouse Qkf$^{gt/gt}$ E12.5 dorsal telencephalon vs wildtype [$p < 0.05$; FC < -1.5 or >1.5]) (* significant corrected gamma p-value < 0.05, DAVID functional annotation)

KEGG pathway name	p-value	Fold enrichment
MAPK signaling pathway*	3.15E-04	1.77
Insulin signaling pathway*	2.18E-03	1.94
Type II diabetes mellitus*	7.64E-03	2.59
Pancreatic cancer*	1.43E-02	2.08
Glycolysis / Gluconeogenesis*	1.81E-02	2.29
Colorectal cancer*	1.96E-02	1.94

Wnt signaling pathway*	2.28E-02	1.65
Acute myeloid leukemia*	3.27E-02	2.09
Fc epsilon RI signaling pathway*	3.91E-02	1.88
Cell cycle*	3.91E-02	1.69
GnRH signaling pathway*	3.97E-02	1.77
Glutamate metabolism	5.18E-02	2.53
Carbon fixation	5.39E-02	2.83
Pentose phosphate pathway	7.32E-02	2.60
Toll-like receptor signaling pathway	8.15E-02	1.60
Chronic myeloid leukemia	8.53E-02	1.71
Endometrial cancer	9.14E-02	1.91
Cyanoamino acid metabolism	9.86E-02	5.42
Prostate cancer	9.90E-02	1.62

Table 17 Chromatin immunoprecipitation statistics

MAT score p-value cutoff	No. of regions	MAT score range	Average region		No. of genes in regions	No. of Genes with ANOVA expression p-value <.05			
			p-value	length (bps)		total	downregulated	upregulated	Ratio down/up-regulated
0.1	8222	8.6 - 98.6	2.64E-02	1008	4257	466	386	80	4.8
0.05	9003	8.6 - 98.6	2.80E-02	783	4540	467	378	89	4.3
0.01	1366	13.1 - 98.6	4.59E-03	863	689	67	56	11	5.1
0.0001	169	27.0 - 98.6	2.26E-05	1230	58	5	4	1	4.0

Table 18 KEGG pathways of enriched genes with ChIP-on-CHIP bindings sites

(* significant corrected gamma p-value < 0.05, Pathway Express calculation)

		Impact	No. genes	% Pathwaygenes	p-value			
KEGG pathway name	**Rank**	**factor**	**in pathway**	**in input**	**uncorrected**	**corrected**	**gamma**	**corrected gamma**
Phosphatidylinositol signaling system*	1	37.6	77	2.6	4.16E-01	4.16E-01	1.75E-15	1.75E-15
Circadian rhythm*	2	27.2	13	7.7	2.15E-01	2.15E-01	4.18E-11	4.18E-11
Gap junction*	3	6.6	96	2.1	5.19E-01	5.19E-01	1.00E-02	1.00E-02
Basal cell carcinoma*	4	6.4	55	5.5	7.72E-02	7.72E-02	1.23E-02	1.23E-02
Thyroid cancer*	5	6.1	29	6.9	9.91E-02	9.91E-02	1.62E-02	1.62E-02
mTOR signaling pathway*	6	5.6	51	7.8	1.25E-02	1.25E-02	2.46E-02	2.46E-02
MAPK signaling pathway*	7	5.5	265	3.0	1.14E-01	1.14E-01	2.69E-02	2.69E-02
Regulation of actin cytoskeleton*	8	5.1	211	1.9	5.27E-01	5.27E-01	3.80E-02	3.80E-02
Long-term depression*	9	5.1	76	1.3	7.57E-01	7.57E-01	3.85E-02	3.85E-02
Focal adhesion*	10	5.0	199	3.0	1.57E-01	1.57E-01	4.13E-02	4.13E-02
Small cell lung cancer	11	4.4	87	4.6	7.68E-02	7.68E-02	6.38E-02	6.38E-02
Long-term potentiation	12	4.3	69	1.4	7.23E-01	7.23E-01	6.93E-02	6.93E-02
Apoptosis	13	4.3	84	3.6	2.01E-01	2.01E-01	7.42E-02	7.42E-02
GnRH signaling pathway	14	4.1	97	4.1	1.04E-01	1.04E-01	8.26E-02	8.26E-02
Wnt signaling pathway	15	4.1	148	2.7	2.82E-01	2.82E-01	8.65E-02	8.65E-02
Pancreatic cancer	16	3.8	73	4.1	1.51E-01	1.51E-01	1.05E-01	1.05E-01
T cell receptor signaling pathway	17	3.8	93	1.1	8.23E-01	8.23E-01	1.06E-01	1.06E-01
Complement and coagulation cascades	18	3.7	69	1.4	7.23E-01	7.23E-01	1.13E-01	1.13E-01
Hedgehog signaling pathway	19	3.7	57	5.3	8.06E-02	8.06E-02	1.19E-01	1.19E-01
Maturity onset diabetes of the young	20	3.4	25	4.0	3.36E-01	3.36E-01	1.49E-01	1.49E-01
Homologous recombination	21	3.4	27	7.4	8.77E-02	8.77E-02	1.51E-01	1.51E-01
Dentatorubropallidoluysian atrophy	22	3.3	15	6.7	2.29E-01	2.29E-01	1.63E-01	1.63E-01

(DRPLA)								
Calcium signaling pathway	23	3.2	175	1.1	8.33E-01	8.33E-01	1.67E-01	1.67E-01
Axon guidance	24	3.2	128	1.6	6.86E-01	6.86E-01	1.71E-01	1.71E-01
Toll-like receptor signaling pathway	25	3.2	102	2.0	5.63E-01	5.63E-01	1.76E-01	1.76E-01
Antigen processing and presentation	26	3.0	88	2.3	4.22E-01	4.22E-01	2.01E-01	2.01E-01
Base excision repair	27	3.0	33	6.1	1.23E-01	1.23E-01	2.05E-01	2.05E-01
Chronic myeloid leukemia	28	2.9	76	2.6	4.09E-01	4.09E-01	2.11E-01	2.11E-01
Alzheimer''s disease	29	2.9	22	4.5	3.36E-01	3.36E-01	2.18E-01	2.18E-01
Insulin signaling pathway	30	2.8	138	2.9	2.42E-01	2.42E-01	2.27E-01	2.27E-01
Endometrial cancer	31	2.7	52	3.8	2.48E-01	2.48E-01	2.40E-01	2.40E-01
Melanoma	32	2.7	71	1.4	7.33E-01	7.33E-01	2.44E-01	2.44E-01
Acute myeloid leukemia	33	2.7	57	1.8	6.54E-01	6.54E-01	2.45E-01	2.45E-01
Neurodegenerative Diseases	34	2.6	30	3.3	4.27E-01	4.27E-01	2.60E-01	2.60E-01
Colorectal cancer	35	2.6	84	3.6	2.01E-01	2.01E-01	2.62E-01	2.62E-01
Taste transduction	36	2.6	53	1.9	5.75E-01	5.75E-01	2.76E-01	2.76E-01
Fc epsilon RI signaling pathway	37	2.5	77	2.6	4.09E-01	4.09E-01	2.80E-01	2.80E-01
ECM-receptor interaction	38	2.4	87	2.3	4.72E-01	4.72E-01	2.99E-01	2.99E-01
p53 signaling pathway	39	2.4	68	2.9	3.57E-01	3.57E-01	3.02E-01	3.02E-01
Melanogenesis	40	2.4	101	2.0	5.52E-01	5.52E-01	3.17E-01	3.17E-01
Tight junction	41	2.3	135	2.2	4.49E-01	4.49E-01	3.22E-01	3.22E-01
Non-small cell lung cancer	42	2.3	54	1.9	6.34E-01	6.34E-01	3.39E-01	3.39E-01
Prostate cancer	43	2.2	89	1.1	8.06E-01	8.06E-01	3.50E-01	3.50E-01
Epithelial cell signaling in Helicobacter pylori infection	44	2.2	69	1.4	7.23E-01	7.23E-01	3.60E-01	3.60E-01
B cell receptor signaling pathway	45	2.2	64	1.6	6.96E-01	6.96E-01	3.61E-01	3.61E-01
Glioma	46	2.2	64	1.6	6.96E-01	6.96E-01	3.61E-01	3.61E-01
Vibrio cholerae infection	47	2.2	59	1.7	6.66E-01	6.66E-01	3.65E-01	3.65E-01
VEGF signaling pathway	48	2.1	71	1.4	7.28E-01	7.28E-01	3.72E-01	3.72E-01
ErbB signaling pathway	49	2.1	87	2.3	4.78E-01	4.78E-01	3.73E-01	3.73E-01
TGF-beta signaling pathway	50	2.1	89	2.2	4.78E-01	4.78E-01	3.78E-01	3.78E-01
Renal cell carcinoma	51	2.1	69	2.9	3.64E-01	3.64E-01	3.86E-01	3.86E-01

Cell Communication	52	2.0	138	2.2	4.34E-01	4.34E-01	3.95E-01	3.95E-01
Glycan structures - biosynthesis 1	53	2.0	122	2.5	3.90E-01	3.90E-01	3.96E-01	3.96E-01
Cell cycle	54	2.0	112	2.7	3.40E-01	3.40E-01	4.00E-01	4.00E-01
Mismatch repair	55	2.0	22	4.5	3.36E-01	3.36E-01	4.08E-01	4.08E-01
Ubiquitin mediated proteolysis	56	1.9	130	2.3	4.20E-01	4.20E-01	4.33E-01	4.33E-01
Regulation of autophagy	57	1.8	30	3.3	4.06E-01	4.06E-01	4.50E-01	4.50E-01
Huntington''s disease	58	1.8	30	3.3	4.27E-01	4.27E-01	4.69E-01	4.69E-01
Cell adhesion molecules (CAMs)	59	1.7	133	0.8	9.06E-01	9.06E-01	4.83E-01	4.83E-01
Notch signaling pathway	60	1.7	46	2.2	5.75E-01	5.75E-01	4.90E-01	4.90E-01
Glycan structures - degradation	61	1.7	30	3.3	4.27E-01	4.27E-01	4.96E-01	4.96E-01
ABC transporters	62	1.7	44	2.3	5.50E-01	5.50E-01	5.04E-01	5.04E-01
Basal transcription factors	63	1.7	34	2.9	4.38E-01	4.38E-01	5.04E-01	5.04E-01
DNA replication	64	1.6	35	2.9	4.78E-01	4.78E-01	5.12E-01	5.12E-01
Olfactory transduction	65	1.6	383	0.3	8.80E-01	8.80E-01	5.15E-01	5.15E-01
Bladder cancer	66	1.5	42	2.4	5.42E-01	5.42E-01	5.47E-01	5.47E-01
Nucleotide excision repair	67	1.5	43	2.3	5.42E-01	5.42E-01	5.53E-01	5.53E-01
Adipocytokine signaling pathway	68	1.5	72	1.4	7.38E-01	7.38E-01	5.54E-01	5.54E-01
Cytokine-cytokine receptor interaction	69	1.4	259	0.8	9.51E-01	9.51E-01	5.82E-01	5.82E-01
Jak-STAT signaling pathway	70	1.3	153	0.7	9.42E-01	9.42E-01	6.39E-01	6.39E-01
Adherens junction	71	1.2	75	1.3	7.52E-01	7.52E-01	6.70E-01	6.70E-01
Neuroactive ligand-receptor interaction	72	0.9	254	0.4	9.91E-01	9.91E-01	7.84E-01	7.84E-01

Table 19 KEGG pathways of enriched genes with ChIP-on-CHIP bindings sites

(* significant corrected gamma p-value < 0.05, DAVID functional annotation)

KEGG pathway name	p-value	Fold enrichment
Thyroid cancer*	4.21E-03	11.78
MAPK signaling pathway*	3.81E-02	2.46
GnRH signaling pathway	1.09E-01	3.38
mTOR signaling pathway	1.30E-01	4.68
Basal cell carcinoma	1.51E-01	4.26
Hedgehog signaling pathway	1.56E-01	4.18
Focal adhesion	2.29E-01	2.00
Apoptosis	2.78E-01	2.84
Wnt signaling pathway	2.85E-01	2.11
Small cell lung cancer	2.92E-01	2.74
Cell cycle	4.13E-01	2.09
Ubiquitin mediated proteolysis	4.85E-01	1.82
Insulin signaling pathway	4.97E-01	1.78
Regulation of actin cytoskeleton	4.97E-01	1.49
Cell Communication	5.05E-01	1.75
p53 signaling pathway	5.73E-01	2.34
Pancreatic cancer	5.99E-01	2.18
Phosphatidylinositol signaling system	6.14E-01	2.09
Antigen processing and presentation	6.33E-01	1.99
Colorectal cancer	6.56E-01	1.87
ECM-receptor interaction	6.69E-01	1.81
TGF-beta signaling pathway	6.77E-01	1.77
Gap junction	6.97E-01	1.67
Melanogenesis	7.08E-01	1.62
Glycan structures - biosynthesis 1	7.79E-01	1.33
Tight junction	8.11E-01	1.20

Axon guidance	8.11E-01	1.20
Calcium signaling pathway	8.90E-01	0.91
Cytokine-cytokine receptor interaction	9.62E-01	0.62

Table 20 Genes with significant ChIP-on-CHIP bindings sites (MAT score p-value < 0.05) and significant siRNA expression values (p-value < 0.05)

		ChIP-on-CHIP enriched region					Expression	
Gene symbol	**Gene Name**	**Chromosome region**	**Length(bps)**	**Probes in region**	**p-value**	**MAT-score**	**Fold change**	**p-value**
---	---	chr19:63521299-63522196	898	20	2.72E-02	10.24	-1.43	5.48E-04
---	Transcribed locus	chr9:3479548-3480181	634	18	4.59E-02	8.82	1.33	2.29E-03
---	Transcribed locus	chr16:28864493-28864984	492	15	1.17E-02	12.60	-2.21	1.05E-02
---	Homo sapiens, clone IMAGE:5479947, mRNA	chr8:145085116-145085724	609	17	2.58E-02	10.38	-1.11	1.43E-02
---	CDNA clone IMAGE:4332981	chr12:47603351-47604092	742	21	2.60E-02	10.37	-1.23	3.96E-02
---	Transcribed locus	chr2:112529429-112530022	594	17	4.91E-02	8.65	1.42	4.06E-02
ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	chr7:150376929-150377531	603	18	4.00E-02	9.21	-1.38	4.88E-02
ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	chr3:185212808-185213413	606	13	4.75E-02	8.74	-1.47	8.75E-03
ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	chr6:30647281-30647924	644	18	4.24E-02	9.04	-1.20	1.73E-02
ACTR3	ARP3 actin-related protein 3 homolog (yeast)	chr2:114362478-114362934	457	14	2.61E-02	10.35	1.14	3.68E-03
AES	amino-terminal enhancer of split	chr19:3009424-3010085	662	14	1.41E-02	12.10	-1.20	2.11E-02
AKAP10	A kinase (PRKA) anchor protein 10	chr17:19821926-19822573	648	18	2.79E-02	10.18	1.12	4.73E-02
AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19:45477316-45477991	676	17	3.55E-02	9.50	-1.66	6.57E-03
ALAS1	aminolevulinate, delta-, synthase 1	chr3:52204906-52205313	408	12	4.10E-02	9.13	1.20	6.60E-03
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	chr11:67530404-67531257	854	22	1.78E-02	11.47	-1.71	1.61E-02
ALDH9A1	aldehyde dehydrogenase 9 family, member A1	chr1:163936862-163937734	873	21	9.00E-03	13.44	-1.27	2.18E-03
ALOX12B	arachidonate 12-lipoxygenase, 12R type	chr17:7933112-7933835	724	21	2.54E-02	10.44	-1.18	3.26E-02

ALPK1	alpha-kinase 1	chr4:113513483-113514005	523	15	1.61E-02	11.73	1.13	1.72E-02
AMACR	alpha-methylacyl-CoA racemase	chr5:34020360-34022353	1994	56	5.27E-05	29.56	-1.36	1.84E-02
AMH	anti-Mullerian hormone	chr19:2192702-2193213	512	14	3.98E-02	9.21	-1.26	2.78E-02
ANG	angiogenin, ribonuclease, RNase A family, 5	chr14:20228545-20229508	964	24	3.06E-03	16.68	1.28	3.44E-02
ANK1	ankyrin 1, erythrocytic	chr8:41647698-41649099	1402	40	8.79E-06	41.12	-1.16	2.94E-02
AP2A2	adaptor-related protein complex 2, alpha 2 subunit	chr11:915038-915635	598	17	4.96E-02	8.62	-1.21	4.18E-02
AP2B1	adaptor-related protein complex 2, beta 1 subunit	chr17:31085753-31086520	768	21	3.38E-02	9.64	-1.20	4.32E-02
APOL6	apolipoprotein L, 6	chr22:34371577-34371986	410	12	4.18E-02	9.07	-1.14	3.78E-02
ARMCX3	armadillo repeat containing, X-linked 3	chrX:100763565-100764333	769	20	2.07E-02	11.03	1.24	1.18E-02
ARMCX5	armadillo repeat containing, X-linked 5	chrX:101742631-101743333	703	20	3.78E-02	9.35	-1.29	1.63E-02
ARMCX6	armadillo repeat containing, X-linked 6	chrX:100763565-100764333	769	20	2.07E-02	11.03	1.16	4.26E-02
ARS2	arsenate resistance protein 2	chr7:100321185-100321782	598	16	4.88E-02	8.66	-1.17	4.46E-02
ASPH	aspartate beta-hydroxylase	chr8:62768744-62769635	892	25	4.25E-02	9.03	1.76	7.76E-03
ATP5SL	ATP5S-like	chr19:46640298-46640900	603	17	4.42E-02	8.93	-1.19	1.24E-02
ATXN3	ataxin 3	chr14:91046325-91046944	620	14	3.80E-02	9.33	1.30	1.21E-02
BATF2	basic leucine zipper transcription factor, ATF-like 2	chr11:64526945-64527591	647	14	3.62E-02	9.45	-1.17	2.15E-03
BBS1	Bardet-Biedl syndrome 1	chr11:66001170-66002216	1047	23	3.67E-02	9.42	-1.65	1.32E-02
BCL7B	B-cell CLL/lymphoma 7B	chr7:72609968-72610430	463	13	2.57E-02	10.40	-1.23	3.96E-02
BCR	breakpoint cluster region	chr22:21314999-21316082	1084	30	5.68E-03	14.82	-1.89	7.89E-03
BIRC2	baculoviral IAP repeat-containing 2	chr11:101713286-101714107	822	21	2.61E-02	10.35	-1.39	9.73E-03
BOLA2	PI-3-kinase-related kinase SMG-1 pseudogene	chr16:30010897-30011606	710	21	2.57E-02	10.40	-1.39	1.97E-03
BRWD1	bromodomain and WD repeat domain containing 1	chr21:39476423-39477062	640	19	4.02E-02	9.19	1.42	5.20E-03
BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	chr10:124890732-124891580	849	24	1.55E-02	11.83	-1.20	4.74E-02
C11orf59	chromosome 11 open reading frame 59	chr11:71496038-71496774	737	20	3.31E-02	9.71	-1.97	2.20E-04
C12orf44	chromosome 12 open reading frame 44	chr12:50746915-50747244	330	10	4.08E-02	9.14	-1.80	8.84E-05
C14orf179	chromosome 14 open reading frame 179	chr14:75517201-75517968	768	21	3.47E-02	9.56	-1.26	6.76E-03
C14orf45	chromosome 14 open reading frame 45	chr14:73620058-73620795	738	20	2.40E-02	10.59	-1.48	1.88E-03

C16orf13	chromosome 16 open reading frame 13	chr16:630613-631244	632	19	3.97E-02	9.22	-1.10	3.01E-02
C16orf14	chromosome 16 open reading frame 14	chr16:630613-631244	632	19	3.97E-02	9.22	-1.26	3.37E-02
C17orf49	chromosome 17 open reading frame 49	chr17:6866071-6866773	703	20	2.15E-02	10.91	-1.24	1.82E-02
C17orf56	chromosome 17 open reading frame 56	chr17:76816170-76816794	625	11	6.38E-03	14.52	-1.26	1.80E-02
C17orf62	chromosome 17 open reading frame 62	chr17:77995382-77996060	679	19	2.65E-02	10.30	-1.21	6.66E-03
C19orf29	chromosome 19 open reading frame 29	chr19:3564582-3565297	716	21	1.80E-02	11.45	-1.35	1.18E-02
C19orf56	chromosome 19 open reading frame 56	chr19:12636672-12637411	740	21	3.62E-02	9.46	-1.90	6.93E-04
C1orf128	chromosome 1 open reading frame 128	chr1:23990487-23992341	1855	52	1.42E-02	12.07	-1.43	2.08E-03
C1orf151	chromosome 1 open reading frame 151	chr1:19795551-19796133	583	17	4.40E-02	8.95	-1.55	7.42E-03
C1orf41	chromosome 1 open reading frame 41	chr1:54187151-54188076	926	26	3.52E-02	9.52	-1.34	2.99E-02
C1orf85	chromosome 1 open reading frame 85	chr1:154575759-154576395	637	18	4.80E-02	8.71	1.26	4.66E-02
C1orf93	chromosome 1 open reading frame 93	chr1:2507581-2508229	649	13	4.55E-02	8.84	-1.35	6.49E-03
C20orf11	chromosome 20 open reading frame 11	chr20:61040111-61041023	913	19	1.03E-02	13.01	-1.53	5.69E-03
C20orf27	chromosome 20 open reading frame 27	chr20:3709279-3710018	740	21	2.52E-02	10.46	-1.24	4.75E-02
C21orf34	chromosome 21 open reading frame 34	chr21:16366745-16367817	1073	27	2.27E-02	10.74	-1.14	1.54E-02
C22orf29	chromosome 22 open reading frame 29	chr22:18219907-18221515	1609	43	1.89E-02	11.32	-1.24	4.64E-02
C2orf46	chromosome 2 open reading frame 46	chr2:8390478-8391324	847	23	4.01E-03	15.86	-1.15	4.34E-02
C3orf64	chromosome 3 open reading frame 64	chr3:69106575-69107162	588	17	2.42E-02	10.57	-1.52	1.70E-02
C7orf20	chromosome 7 open reading frame 20	chr7:884201-884700	500	14	3.63E-02	9.45	-1.19	4.38E-02
C8orf55	chromosome 8 open reading frame 55	chr8:143804973-143805700	728	21	2.91E-02	10.05	-1.19	4.76E-02
C9orf105	chromosome 9 open reading	chr9:37772786-37773562	777	22	2.07E-02	11.03	-1.48	7.90E-03
C9orf116	chromosome 9 open reading frame 116	chr9:137538759-137539616	858	19	1.75E-02	11.51	-1.56	1.28E-02
C9orf3	chromosome 9 open reading frame 3	chr9:96525359-96525942	584	15	3.71E-02	9.39	1.15	4.66E-02
CA5B	carbonic anhydrase VB, mitochondrial	chrX:15676938-15677753	816	21	1.22E-02	12.48	-1.19	1.51E-02
CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	chr3:50349280-50350005	726	20	2.37E-02	10.62	-1.30	3.65E-02
CALML4	Calmodulin-like 4	chr15:66288414-66289018	605	15	5.00E-02	8.60	1.17	4.56E-02
CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	chr1:20688719-20689657	939	24	3.95E-02	9.23	-1.72	1.08E-02
CAMSAP1	calmodulin regulated spectrin-associated protein 1	chr9:137921384-137922022	639	19	2.08E-02	11.02	-1.86	5.58E-04

CARD8	caspase recruitment domain family, member 8	chr19:53236277-53236755	479	14	9.09E-03	13.41	-1.41	1.34E-02
CARHSP1	calcium regulated heat stable protein 1, 24kDa	chr16:8859452-8860167	716	15	2.06E-02	11.05	-1.52	9.59E-03
CASP7	caspase 7, apoptosis-related cysteine peptidase	chr10:115496691-115497319	629	12	3.37E-02	9.66	-2.45	6.37E-04
CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	chr12:52964079-52965329	1251	34	5.14E-03	15.06	-1.28	3.06E-02
CCDC144A	coiled-coil domain containing 144A	chr17:18469524-18469960	437	10	4.48E-02	8.90	1.15	6.32E-03
CCDC151	coiled-coil domain containing 151	chr19:11388319-11388799	481	14	3.56E-02	9.49	-1.22	3.04E-02
CCDC21	coiled-coil domain containing 21	chr1:26387639-26388361	723	21	1.20E-02	12.51	-1.41	7.17E-03
CCDC92	coiled-coil domain containing 92	chr12:122993965-122994738	774	18	4.18E-02	9.07	-1.35	2.22E-02
CCPG1	cell cycle progression 1	chr15:53579153-53579773	621	13	2.54E-02	10.44	1.30	5.36E-03
CIRBP	cold inducible RNA binding protein	chr19:1213533-1214142	610	13	4.72E-02	8.75	-1.30	8.86E-03
CKS1B	CDC28 protein kinase regulatory subunit 1B	chr1:153235172-153235507	336	10	3.84E-02	9.30	-1.33	1.88E-02
CLCN4	chloride channel 4	chrX:10082570-10083296	727	14	3.88E-02	9.28	1.96	2.19E-03
CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	chr15:66288414-66289018	605	15	5.00E-02	8.60	-1.48	1.91E-02
CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation	chr8:1720507-1721887	1381	39	2.64E-05	31.95	1.42	3.23E-02
COL5A1	collagen, type V, alpha 1	chr9:136667457-136668266	810	20	1.69E-02	11.61	-1.42	4.23E-03
COL7A1	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and rec	chr3:48575558-48576147	590	10	1.11E-02	12.75	-1.30	5.31E-03
CPEB4	cytoplasmic polyadenylation element binding protein 4	chr5:173242841-173243553	713	20	2.25E-02	10.77	1.32	4.16E-02
CPNE2	copine II	chr16:55682495-55683490	996	28	1.71E-02	11.56	-1.35	1.83E-02
CPSF1	cleavage and polyadenylation specific factor 1, 160kDa	chr8:145618685-145619351	667	18	3.31E-02	9.71	-1.29	2.07E-02
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	chr2:36437937-36438570	634	18	2.74E-02	10.22	1.72	6.82E-05
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	chr16:83407036-83407630	595	10	4.34E-02	8.98	-1.28	2.70E-02
CSK	c-src tyrosine kinase	chr15:72852306-72853347	1042	29	4.34E-02	8.98	-1.27	3.28E-02
CTDSP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas	chr2:218912808-218913629	822	18	2.27E-02	10.74	-1.25	1.99E-02
CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas	chr12:56533895-56534239	345	10	4.40E-02	8.95	-1.35	1.33E-02

CUGBP1	CUG triplet repeat, RNA binding protein 1	chr11:47477131-47477758	628	18	3.11E-02	9.87	-1.45	2.87E-03
CYB561D1	cytochrome b-561 domain containing 1	chr1:109832219-109832915	697	20	3.98E-02	9.21	-1.30	2.37E-02
CYFIP2	cytoplasmic FMR1 interacting protein 2	chr5:156667251-156667956	706	19	1.41E-02	12.08	-2.01	2.59E-02
DAZAP1	DAZ associated protein 1	chr19:1350720-1351402	683	19	2.88E-02	10.08	-1.45	8.31E-03
DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	chr16:88625558-88627275	1718	40	1.93E-04	25.48	-1.41	1.81E-02
DGKZ	diacylglycerol kinase, zeta 104kDa	chr11:46312509-46312965	457	14	1.16E-02	12.62	-1.42	1.54E-03
DHRS4	dehydrogenase/reductase (SDR family) member 4	chr14:23607994-23608887	894	25	2.36E-02	10.64	-1.33	2.76E-02
DHRS9	dehydrogenase/reductase (SDR family) member 9	chr2:169633720-169634333	614	18	4.32E-02	8.99	1.10	2.80E-02
DHRSX	dehydrogenase/reductase (SDR family) X-linked	chrX:2429121-2429928	808	23	5.96E-03	14.69	1.17	4.27E-02
DIDO1	death inducer-obliterator 1	chr20:61040111-61041023	913	19	1.03E-02	13.01	-2.00	1.32E-03
DKFZp434K191	POM121-like protein	chr22:22970633-22971548	916	19	3.41E-03	16.35	1.10	8.32E-03
DLG3	discs, large homolog 3 (neuroendocrine-dlg, Drosophila)	chrX:69560127-69560719	593	15	4.03E-02	9.18	-1.38	2.68E-02
DLGAP3	discs, large (Drosophila) homolog-associated protein 3	chr1:35221821-35222627	807	22	6.82E-03	14.30	-1.11	4.77E-02
DSC1	desmocollin 1	chr18:27001111-27001506	396	11	4.88E-02	8.66	1.44	4.78E-03
DYNLRB1	dynein, light chain, roadblock-type 1	chr20:32597202-32597568	367	11	3.16E-02	9.82	-1.15	4.15E-02
DYX1C1	dyslexia susceptibility 1 candidate 1	chr15:53579153-53579773	621	13	2.54E-02	10.44	-1.65	2.75E-02
EIF2C2	Eukaryotic translation initiation factor 2C, 2	chr8:141640667-141641604	938	26	2.26E-02	10.76	-1.73	4.11E-02
EIF3F	eukaryotic translation initiation factor 3, subunit F	chr2:58324176-58325154	979	25	7.06E-03	14.20	-1.25	2.97E-02
ELK1	ELK1, member of ETS oncogene family	chrX:47379659-47380243	585	14	4.84E-02	8.68	-1.23	3.72E-02
ELL2	elongation factor, RNA polymerase II, 2	chr5:95322519-95323146	628	18	4.06E-02	9.16	1.73	1.73E-02
EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	chr16:1771029-1771916	888	24	1.21E-02	12.51	-1.20	4.54E-02
EP400NL	EP400 N-terminal like	chr12:131130788-131131922	1135	31	4.80E-03	15.30	-1.36	1.80E-02
EPB41	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	chr1:29083808-29084958	1151	24	1.63E-02	11.70	-1.20	3.61E-02
EPHA4	EPH receptor A4	chr2:222142938-222144085	1148	25	1.27E-03	19.45	-1.29	1.99E-02
EPOR	erythropoietin receptor	chr19:11388319-11388799	481	14	3.56E-02	9.49	1.31	3.18E-02

EPPK1	epiplakin 1	chr8:145023818-145024397	580	16	4.72E-02	8.75	-1.61	4.43E-03
EPS8L1	EPS8-like 1	chr19:60282965-60283865	901	18	1.99E-02	11.16	-1.30	5.17E-03
ETHE1	ethylmalonic encephalopathy 1	chr19:48728591-48729301	711	20	2.89E-02	10.07	-1.33	1.36E-02
EXT2	exostoses (multiple) 2	chr11:44085944-44086674	731	20	3.70E-02	9.40	-1.59	1.19E-03
FABP5	fatty acid binding protein 5	chr7:151770436-151771145	710	20	2.06E-02	11.05	-1.39	4.29E-02
FAM111A	family with sequence similarity 111, member A	chr11:58668736-58669545	810	19	2.90E-02	10.06	-1.44	2.10E-02
FAM120C	family with sequence similarity 120C	chrX:54225005-54226319	1315	35	6.97E-03	14.24	-1.69	1.11E-03
FAM130A1	family with sequence similarity 130, member A1	chr12:49761995-49763016	1022	29	3.79E-02	9.34	-1.72	1.53E-03
FAM135A	family with sequence similarity 135, member A	chr6:71333497-71334072	576	17	1.52E-02	11.87	1.38	1.82E-02
FAM26B	family with sequence similarity 26, member B	chr10:105197126-105197847	722	21	2.18E-02	10.87	-1.22	9.35E-03
FAM41C	ribosomal protein L23a pseudogene 7	chr2:114107786-114108391	606	18	1.18E-02	12.56	-1.36	5.00E-02
FAM49B	family with sequence similarity 49, member B	chr8:130951421-130952038	618	10	1.09E-02	12.80	1.90	1.24E-02
FAM54B	family with sequence similarity 54, member B	chr1:25998481-25999536	1056	23	2.08E-02	11.01	-1.26	1.64E-02
FAM83H	family with sequence similarity 83, member H	chr8:144889408-144890269	862	24	6.22E-03	14.60	-1.37	4.13E-03
FAM96B	family with sequence similarity 96, member B	chr16:65511887-65512495	609	13	4.84E-02	8.69	-1.18	3.38E-02
FBXO4	F-box protein 4	chr5:41958702-41959391	690	17	2.87E-02	10.09	-1.41	3.39E-03
FBXO44	F-box protein 44	chr1:11646630-11647267	638	17	3.05E-02	9.93	-1.28	6.94E-03
FBXO9	F-box protein 9	chr6:53033483-53034247	765	22	2.68E-02	10.27	-1.97	1.13E-02
FHL3	four and a half LIM domains 3	chr1:38237132-38238176	1045	30	2.47E-02	10.52	-1.25	3.38E-02
FKBP7	FK506 binding protein 7	chr2:179058343-179059053	711	20	2.69E-02	10.27	1.47	2.28E-02
FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	chr1:153235172-153235507	336	10	3.84E-02	9.30	-1.36	7.92E-03
FLJ14213	protor-2	chr11:36427468-36428084	617	14	4.20E-02	9.06	-1.55	1.28E-03
FLJ20323	hypothetical protein FLJ20323	chr7:7570844-7571752	909	24	1.04E-02	12.94	-1.45	3.16E-02
FLJ22795	hypothetical protein FLJ22795	chr15:80590524-80592178	1655	45	1.63E-02	11.71	-1.21	5.21E-03
FLJ40296	FLJ40296 protein	chr13:56632612-56633637	1026	28	1.75E-02	11.52	1.22	1.40E-03
FLJ45224	FLJ45224 protein	chr9:138999924-139000612	689	19	2.85E-02	10.11	-1.10	5.90E-03
FMNL3	formin-like 3	chr12:48387328-48388141	814	20	4.20E-02	9.06	-1.35	2.17E-03
FNDC3B	fibronectin type III domain containing 3B	chr3:173307762-173308394	633	18	1.21E-02	12.49	1.44	6.07E-03
FOXP1	forkhead box P1	chr3:71627633-71628246	614	10	4.79E-02	8.71	-1.15	2.68E-02
FRAG1	FGF receptor activating protein 1	chr11:3786962-3787655	694	16	3.37E-02	9.66	-1.20	3.66E-03

FRMPD2	FERM and PDZ domain containing 2	chr10:48481913-48482546	634	16	2.79E-02	10.17	1.09	1.43E-02
FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	chr8:33449492-33450285	794	23	1.49E-02	11.93	-1.38	4.43E-03
FXYD5	FXYD domain containing ion transport regulator 5	chr19:40316142-40316876	735	21	3.14E-02	9.83	-1.34	4.00E-02
FZD8	frizzled homolog 8 (Drosophila)	chr10:35970414-35971005	592	16	4.11E-02	9.12	-1.34	4.40E-02
FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	chr19:3473887-3475032	1146	32	1.01E-02	13.05	-1.45	1.76E-02
GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	chr12:88441911-88442499	589	17	3.67E-02	9.42	-1.56	1.37E-02
GCHFR	GTP cyclohydrolase I feedback regulator	chr15:38847179-38848158	980	27	4.16E-02	9.09	-1.23	1.67E-03
GGT1	gamma-glutamyltransferase 1	chr22:22970633-22971548	916	19	3.41E-03	16.35	-1.10	1.75E-02
GLCE	glucuronic acid epimerase	chr15:67240878-67241760	883	25	3.04E-02	9.94	-1.73	2.43E-03
GLI2	GLI-Kruppel family member GLI2	chr2:121263980-121265182	1203	30	7.83E-03	13.89	-1.29	4.14E-03
GLOD4	glyoxalase domain containing 4	chr17:598746-599975	1230	35	1.93E-04	25.44	-1.19	4.32E-02
GLTPD1	glycolipid transfer protein domain containing 1	chr1:1255119-1255802	684	15	1.61E-02	11.73	-1.25	1.84E-02
GLTSCR2	glioma tumor suppressor candidate region gene 2	chr19:52937741-52938468	728	21	3.72E-02	9.38	-1.27	3.61E-02
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	chr19:3073208-3073852	645	18	4.44E-02	8.92	-1.87	4.17E-04
GOLGA6	golgi autoantigen, golgin subfamily a, 6	chr15:73410005-73410589	585	17	1.90E-02	11.29	-1.09	3.80E-02
GPHN	gephyrin	chr14:66043488-66044135	648	18	2.44E-02	10.53	-1.47	7.34E-03
GRHL1	grainyhead-like 1 (Drosophila)	chr2:10006148-10006679	532	16	2.41E-02	10.57	-1.93	2.10E-05
GRIK2	glutamate receptor, ionotropic, kainate 2	chr6:101945922-101946827	906	24	1.85E-02	11.36	1.40	3.44E-02
GSTZ1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	chr14:76858171-76858810	640	18	3.42E-02	9.60	-1.37	2.32E-02
GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	chr19:6331296-6331922	627	18	4.29E-02	9.01	-1.15	4.59E-02
H2BFS	H2B histone family, member S	chr6:26308019-26308606	588	17	4.56E-02	8.84	-1.75	5.41E-03
HBA1	hemoglobin, alpha 1	chr16:149514-150672	1159	33	3.73E-03	16.05	-1.33	4.43E-02
HCCA2	HCCA2 protein	chr11:1463024-1464509	1486	38	1.09E-02	12.82	-1.24	3.46E-02
HCRTR2	hypocretin (orexin) receptor 2	chr6:55146553-55147261	709	20	4.30E-02	9.00	-1.18	4.10E-02
HDAC3	histone deacetylase 3	chr5:140978477-140979173	697	19	4.03E-02	9.18	-1.32	6.63E-03

HES2	hairy and enhancer of split 2 (Drosophila)	chr1:6401463-6402361	899	23	2.93E-02	10.04	-1.20	4.91E-02
HIPK1	homeodomain interacting protein kinase 1	chr1:114318915-114319679	765	22	2.35E-02	10.65	-1.21	2.45E-02
HIST1H2BC	histone cluster 1, H2bg	chr6:26308019-26308606	588	17	4.56E-02	8.84	-1.56	5.87E-03
HIST1H2BH	histone cluster 1, H2bh	chr6:26308019-26308606	588	17	4.56E-02	8.84	-1.51	3.56E-03
HLA-DOA	major histocompatibility complex, class II, DO alpha	chr6:33085180-33085968	789	21	6.64E-03	14.36	1.27	4.85E-02
HLF	hepatic leukemia factor	chr17:50752704-50753707	1004	27	1.30E-02	12.33	-1.27	1.97E-02
HN1	hematological and neurological expressed 1	chr17:70637652-70638321	670	19	1.92E-02	11.26	-1.41	4.78E-03
HN1L	hematological and neurological expressed 1-like	chr16:1771029-1771916	888	24	1.21E-02	12.51	-1.22	4.77E-02
HNRNPA3P2	NDRG family member 3	chr20:34840873-34841680	808	22	1.58E-02	11.79	-1.29	3.85E-02
HNRNPF	heterogeneous nuclear ribonucleoprotein F	chr10:43223774-43224383	610	16	3.88E-02	9.27	-1.38	1.26E-02
HOXA3	homeobox A3	chr7:27128586-27129257	672	18	3.46E-02	9.57	-1.56	1.53E-03
HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	chr17:37953731-37954366	636	17	3.31E-02	9.70	-1.16	4.46E-02
HSF1	heat shock transcription factor 1	chr8:145480690-145481506	817	23	1.10E-02	12.78	-1.26	7.93E-03
HSPA1A	heat shock 70kDa protein 1A	chr6:31904789-31905394	606	17	4.72E-02	8.75	1.23	3.92E-02
HSPA4	Heat shock 70kDa protein 4	chr5:132414615-132415282	668	17	4.95E-02	8.62	-1.35	2.99E-02
HYOU1	hypoxia up-regulated 1	chr11:118287230-118288100	871	21	2.36E-02	10.64	-1.31	4.65E-02
HYPK	Huntingtin interacting protein K	chr15:41875012-41875624	613	12	4.69E-02	8.77	-1.75	3.24E-03
ICK	intestinal cell (MAK-like) kinase	chr6:52967559-52968234	676	16	2.47E-02	10.51	-1.71	5.18E-03
IDS	iduronate 2-sulfatase (Hunter syndrome)	chrX:148426001-148427098	1098	27	3.75E-02	9.36	-1.15	3.88E-02
IFNA16	interferon, alpha 16	chr9:21328142-21328734	593	17	4.50E-02	8.88	1.10	4.73E-02
IFRD2	interferon-related developmental regulator 2	chr3:50349280-50350005	726	20	2.37E-02	10.62	-1.84	2.26E-04
IGF2	insulin-like growth factor 2 (somatomedin A)	chr11:2123693-2124397	705	19	1.30E-02	12.31	-1.37	4.92E-03
IGHA1	immunoglobulin heavy constant alpha 1	chr14:106190798-106191390	593	17	1.58E-04	26.37	-1.20	1.97E-02
IGSF3	immunoglobulin superfamily, member 3	chr1:117012160-117013103	944	21	7.25E-03	14.12	-1.52	3.39E-02
IHPK1	inositol hexaphosphate kinase 1	chr3:49740434-49740865	432	13	4.73E-02	8.74	-1.27	2.23E-02
IMAA	solute carrier family 7	chr16:21443421-21444257	837	24	1.21E-02	12.50	-1.26	2.06E-02
INOC1	INO80 complex homolog 1 (S. cerevisiae)	chr15:38834427-38835394	968	24	2.08E-02	11.01	-1.16	4.70E-02
IRX5	iroquois homeobox 5	chr16:53521889-53522936	1048	24	2.73E-02	10.23	-1.17	4.81E-02
ITGB4	integrin, beta 4	chr17:71228920-71229583	664	19	8.70E-03	13.56	-1.81	5.95E-03

JPH2	junctophilin 2	chr20:42248774-42249377	604	16	4.80E-02	8.71	-1.53	3.13E-02
KAP2.1B	keratin associated protein 2.1B	chr17:36469261-36469990	730	21	3.38E-02	9.64	1.15	1.26E-03
KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	chr1:6017649-6018326	678	19	3.83E-02	9.31	-1.30	1.09E-03
KCNJ12	potassium inwardly-rectifying channel, subfamily J, member 12	chr17:21215558-21216694	1137	31	3.92E-02	9.25	-1.80	1.59E-03
KIAA0226	KIAA0226	chr3:198954376-198954954	579	16	2.85E-02	10.12	-1.17	1.04E-02
KIAA0323	KIAA0323	chr14:23970284-23971023	740	20	2.95E-02	10.02	-1.20	4.19E-02
KIAA0515	KIAA0515	chr9:133343651-133344404	754	21	2.31E-02	10.71	-1.39	1.77E-02
KIAA1545	KIAA1545 protein	chr12:131649613-131650431	819	23	1.85E-03	18.41	-1.18	4.23E-02
KIAA1920	KIAA1920 protein	chr15:81906637-81907723	1087	30	1.35E-02	12.21	-1.12	3.79E-03
KLK8	kallikrein-related peptidase 8	chr19:56195229-56195833	605	14	3.22E-02	9.77	1.19	3.27E-02
KRT17	keratin 17	chr17:37035091-37036189	1099	31	7.18E-03	14.15	-1.74	2.80E-02
LASS3	LAG1 homolog, ceramide synthase 3	chr15:98914126-98916197	2072	54	2.06E-02	11.05	-1.25	5.57E-03
LASS6	LAG1 homolog, ceramide synthase 6	chr2:169018286-169019171	886	25	2.95E-02	10.02	1.44	2.53E-02
LETM1	Leucine zipper-EF-hand containing transmembrane protein 1	chr4:1833808-1834462	655	19	2.48E-02	10.50	-1.62	4.71E-03
LIN37	lin-37 homolog (C. elegans)	chr19:40914258-40915100	843	23	2.95E-02	10.02	1.15	8.68E-03
LIN52	lin-52 homolog (C. elegans)	chr14:73620058-73620795	738	20	2.40E-02	10.59	-1.50	7.20E-03
LL22NC03-5H6.5	hypothetical protein FLJ20699	chr22:45070226-45070868	643	17	4.93E-02	8.63	-1.25	1.87E-02
LOC100130536	hypothetical protein LOC100130536	chr6:32231013-32231625	613	12	2.95E-02	10.02	-1.51	4.21E-02
LOC100134082	hypothetical protein LOC100134082	chr7:150439809-150440608	800	23	1.32E-02	12.27	1.15	2.14E-02
LOC100134365	hypothetical protein LOC100134365	chr2:96350334-96351010	677	14	3.33E-02	9.68	-1.35	3.37E-02
LOC116236	hypothetical protein LOC116236	chr17:24923347-24924293	947	26	4.30E-02	9.01	-1.28	4.43E-02
LOC149478	Hypothetical protein LOC149478	chr1:45037848-45038818	971	23	1.32E-02	12.28	-1.29	1.58E-02
LOC165186	similar to RIKEN cDNA 4632412N22 gene	chr2:29102890-29103516	627	17	2.58E-02	10.38	-1.24	3.98E-02
LOC257407	hypothetical protein LOC257407	chr2:231625240-231625927	688	19	3.29E-02	9.73	-1.26	5.20E-03
LOC645722	hypothetical LOC645722	chr16:21443421-21444257	837	24	1.21E-02	12.50	-1.67	3.17E-03
LOC90835	hypothetical protein LOC90835	chr16:30680003-30681320	1318	38	1.99E-02	11.16	-1.32	5.50E-03

LOC96610	hypothetical gene LOC96610	chr22:21314999-21316082	1084	30	5.68E-03	14.82	-1.14	3.59E-02
LPHN1	latrophilin 1	chr19:14177197-14177822	626	17	2.77E-02	10.19	-1.34	1.24E-03
LRRC42	leucine rich repeat containing 42	chr1:54187151-54188076	926	26	3.52E-02	9.52	-1.26	1.68E-02
LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr6:31873223-31873813	591	15	1.39E-02	12.13	-1.30	4.45E-03
LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	chr19:2284096-2284801	706	20	3.59E-02	9.47	-1.29	1.45E-02
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	chr21:46427939-46428777	839	24	1.85E-02	11.36	-1.27	2.52E-02
LYRM4	LYR motif containing 4	chr6:5058191-5058805	615	11	1.09E-02	12.81	-1.25	4.54E-02
MAF1	MAF1 homolog (S. cerevisiae)	chr8:145236676-145237756	1081	31	1.06E-02	12.91	-1.26	4.99E-02
MAML1	mastermind-like 1 (Drosophila)	chr5:179151418-179152044	627	18	2.55E-02	10.42	-1.59	3.72E-04
MAN1A2	mannosidase, alpha, class 1A, member 2	chr1:117708311-117709028	718	18	3.70E-02	9.40	1.44	1.33E-02
MAP2K3	mitogen-activated protein kinase kinase 3	chr17:21125336-21126121	786	22	1.29E-02	12.35	-1.43	1.41E-02
MARK2	MAP/microtubule affinity-regulating kinase 2	chr11:63361188-63361777	590	17	4.19E-02	9.06	-1.44	2.08E-02
MARVELD1	MARVEL domain containing 1	chr10:99457283-99458063	781	16	4.96E-02	8.62	-1.16	2.67E-02
MAX	MYC associated factor X	chr14:64638099-64638744	646	17	2.66E-02	10.29	-1.22	4.23E-02
MBD4	methyl-CpG binding domain protein 4	chr3:130605571-130606335	765	19	1.49E-02	11.93	-1.13	2.19E-02
MDFIC	MyoD family inhibitor domain containing	chr7:114350422-114351021	600	16	3.22E-02	9.77	-1.42	1.73E-02
MED8	mediator complex subunit 8	chr1:43624511-43625205	695	19	2.45E-02	10.53	-1.94	3.51E-05
MEF2A	myocyte enhancer factor 2A	chr15:97984549-97985224	676	13	4.70E-02	8.76	1.40	6.67E-03
MGC26718	Similar to ankyrin repeat domain 20A	chr9:43127294-43127905	612	18	7.43E-03	14.00	-1.37	3.37E-02
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	chr10:103527007-103527730	724	20	3.01E-02	9.96	-1.37	2.11E-02
MIER2	mesoderm induction early response 1, family member 2	chr19:285785-286849	1065	30	1.81E-02	11.43	-1.16	2.28E-02
MIPEP	mitochondrial intermediate peptidase	chr13:23374949-23375551	603	17	3.64E-02	9.44	-1.26	2.71E-02
MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	chr7:104491675-104492274	600	17	4.97E-02	8.62	-1.28	4.50E-02
MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	chr17:34112617-34113218	602	12	3.91E-02	9.26	-1.42	2.09E-02
MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)	chr10:99248522-99249142	621	18	3.92E-02	9.25	-1.30	4.51E-03

MRAS	muscle RAS oncogene homolog	chr3:139568666-139569273	608	12	3.98E-02	9.22	-1.13	4.60E-02
MT1P2	metallothionein 1 pseudogene 2	chr16:55208329-55209139	811	23	9.55E-03	13.25	-1.48	4.65E-02
MTCH1	mitochondrial carrier homolog 1 (C. elegans)	chr6:37056152-37057270	1119	31	6.52E-03	14.44	-1.29	4.73E-02
MTF1	metal-regulatory transcription factor 1	chr1:38043540-38044329	790	21	2.95E-02	10.02	-1.74	1.16E-02
MTIF3	mitochondrial translational initiation factor 3	chr13:26922013-26922774	762	22	2.70E-02	10.26	-1.27	4.22E-02
MTMR14	myotubularin related protein 14	chr3:9713473-9714562	1090	30	1.35E-02	12.21	-1.42	2.35E-03
NADK	NAD kinase	chr1:1672800-1673524	725	20	3.81E-02	9.32	-1.51	7.92E-04
NADSYN1	NAD synthetase 1	chr11:70842164-70842873	710	16	1.50E-02	11.92	-1.59	1.64E-03
NAE1	NEDD8 activating enzyme E1 subunit 1	chr16:65396396-65397082	687	14	3.15E-02	9.83	-1.25	1.85E-02
NBEAL2	neurobeachin-like 2	chr3:47019876-47020869	994	28	1.96E-02	11.21	-1.30	1.15E-02
NBL1	neuroblastoma, suppression of tumorigenicity 1	chr1:19854128-19854805	678	19	4.08E-02	9.14	-1.18	3.94E-02
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	chr9:32544740-32545447	708	16	2.75E-02	10.21	1.20	1.46E-02
NEU1	sialidase 1 (lysosomal sialidase)	chr6:31957923-31958571	649	14	2.43E-02	10.55	1.54	7.03E-03
NF2	neurofibromin 2 (merlin)	chr22:28416029-28416944	916	26	1.03E-02	13.01	1.18	4.46E-02
NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 intera	chr16:28864493-28864984	492	15	1.17E-02	12.60	-2.04	4.87E-03
NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	chr22:40420241-40421025	785	21	1.17E-02	12.60	-1.27	1.14E-02
NICN1	nicolin 1	chr3:49431748-49432626	879	24	7.19E-03	14.14	-1.43	8.61E-03
NKAPL	NFKB activating protein-like	chr6:28343442-28344021	580	11	4.98E-02	8.61	1.15	1.15E-02
NKX2-2	NK2 homeobox 2	chr20:21448581-21449168	588	17	4.53E-02	8.86	-1.57	4.69E-03
NLGN1	neuroligin 1	chr3:174596786-174597597	812	22	4.19E-02	9.07	-2.24	1.94E-04
NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)	chr15:32428549-32429144	596	11	4.03E-02	9.18	-1.29	1.39E-02
NPTX1	neuronal pentraxin I	chr17:76063261-76063975	715	21	3.16E-02	9.81	-1.57	2.88E-02
NRBP2	nuclear receptor binding protein 2	chr8:144975741-144976440	700	20	4.28E-02	9.01	-1.36	4.13E-02
NTAN1	N-terminal asparagine amidase	chr16:15057646-15058360	715	13	2.96E-02	10.00	-1.33	6.84E-03
NTS	neurotensin	chr12:84785307-84785959	653	15	4.84E-02	8.68	1.85	3.33E-04
NUBPL	nucleotide binding protein-like	chr14:31100312-31100984	673	20	3.68E-02	9.41	1.37	2.14E-03
NUP62	nucleoporin 62kDa	chr19:55104196-55105310	1115	31	3.80E-03	16.01	-1.22	4.24E-02
NUPL1	nucleoporin like 1	chr13:24772560-24773277	718	21	2.68E-02	10.28	-2.14	2.10E-02

NY-SAR-48	sarcoma antigen NY-SAR-48	chr19:17051260-17052031	772	23	1.41E-02	12.07	-1.28	3.40E-02
P53AIP1	p53-regulated apoptosis-inducing protein 1	chr11:128313396-128314982	1587	39	2.55E-02	10.42	-1.26	3.88E-02
PACS2	phosphofurin acidic cluster sorting protein 2	chr14:104955252-104956344	1093	31	4.22E-02	9.05	-1.25	1.99E-02
PAIP1	poly(A) binding protein interacting protein 1	chr5:43593177-43593578	402	11	2.98E-02	9.98	-1.39	6.95E-03
PALLD	palladin, cytoskeletal associated protein	chr4:169652048-169652657	610	18	3.55E-02	9.50	1.27	3.75E-02
PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	chr13:27759284-27759992	709	20	1.44E-02	12.03	-1.47	2.65E-03
PAQR6	progestin and adipoQ receptor family member VI	chr1:154487009-154487782	774	21	2.04E-02	11.09	-1.18	3.29E-02
PARC	p53-associated parkin-like cytoplasmic protein	chr6:43254307-43254904	598	17	4.91E-02	8.65	-1.44	4.41E-02
PARG	poly (ADP-ribose) glycohydrolase	chr10:51040679-51041426	748	20	2.96E-02	10.00	-1.19	3.93E-02
PARN	poly(A)-specific ribonuclease (deadenylation nuclease)	chr16:14634061-14634823	763	20	2.66E-02	10.30	-1.41	2.28E-03
PASK	PAS domain containing serine/threonine kinase	chr2:241696676-241697459	784	19	2.84E-02	10.13	-1.46	2.98E-03
PBX2	pre-B-cell leukemia homeobox 2	chr6:32267659-32268304	646	18	4.34E-02	8.98	-1.34	3.79E-02
PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	chr1:153180437-153181227	791	23	2.00E-02	11.13	1.37	4.43E-04
PCDHGA4	protocadherin gamma subfamily A, 4	chr5:140836142-140836762	621	18	2.60E-02	10.36	-1.21	1.40E-02
PCGF2	polycomb group ring finger 2	chr17:34149858-34150241	384	11	3.79E-02	9.34	-1.64	2.26E-03
PDCD6	programmed cell death 6	chr5:496137-497075	939	23	3.82E-02	9.32	-1.60	5.01E-03
PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosoph	chr19:10422186-10423026	841	24	2.82E-02	10.15	-1.45	2.49E-02
PDLIM7	PDZ and LIM domain 7 (enigma)	chr5:176856106-176856845	740	20	2.58E-02	10.39	-1.42	4.21E-02
PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	chr21:43975767-43976452	686	19	1.93E-02	11.24	-1.48	2.46E-03
PER2	period homolog 2 (Drosophila)	chr2:238805772-238806708	937	27	1.61E-02	11.73	-1.57	7.51E-03
PGPEP1	pyroglutamyl-peptidase I	chr19:18335500-18336115	616	15	1.80E-02	11.44	-1.34	9.50E-03
PHB2	prohibitin 2	chr12:6955515-6955847	333	10	4.72E-02	8.75	-1.39	2.73E-03
PHF15	PHD finger protein 15	chr5:133886247-133886960	714	17	4.19E-02	9.06	-1.34	4.57E-02
PHF19	PHD finger protein 19	chr9:122679739-122680405	667	19	4.16E-02	9.08	-1.32	2.00E-02
PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	chr22:19420189-19421470	1282	36	1.99E-02	11.15	-1.24	4.83E-02
PITPNB	phosphatidylinositol transfer protein, beta	chr22:26530651-26531809	1159	29	1.19E-02	12.54	-1.14	3.90E-02
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	chr6:122968010-122968655	646	18	2.83E-02	10.14	-1.24	4.96E-02

PKLR	pyruvate kinase, liver and RBC	chr1:153544954-153545760	807	24	8.72E-03	13.55	1.27	1.76E-02
PKN2	protein kinase N2	chr1:88921921-88922569	649	17	1.87E-02	11.34	1.37	1.88E-03
PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specif	chr7:30029353-30029697	345	10	3.56E-02	9.50	-1.28	3.89E-02
PLEKHJ1	pleckstrin homology domain containing, family J member 1	chr19:2192702-2193213	512	14	3.98E-02	9.21	-1.25	2.16E-02
PLEKHM1	pleckstrin homology domain containing, family M (with RUN domain) member 1	chr17:40863963-40864831	869	24	9.97E-03	13.10	-1.42	1.33E-03
PLXNA2	plexin A2	chr1:206269955-206270571	617	18	4.67E-02	8.77	-1.34	2.69E-02
PMEPA1	prostate transmembrane protein, androgen induced 1	chr20:55632837-55633711	875	18	2.46E-02	10.52	1.20	4.89E-02
PMF1	polyamine-modulated factor 1	chr1:154480125-154480743	619	17	4.51E-02	8.87	-1.23	4.99E-02
PMP22	peripheral myelin protein 22	chr17:15106972-15107576	605	16	4.18E-02	9.07	1.32	6.97E-03
PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	chr2:190352357-190352799	443	13	2.59E-02	10.37	-1.21	8.21E-03
POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	chr19:55612791-55613421	631	17	1.25E-02	12.42	-1.24	1.66E-02
POMT2	protein-O-mannosyltransferase 2	chr14:76858171-76858810	640	18	3.42E-02	9.60	-1.35	1.80E-03
PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	chr2:27454708-27455594	887	25	1.40E-02	12.11	-1.23	4.46E-02
PPP1R16A	protein phosphatase 1, regulatory (inhibitor) subunit 16A	chr8:145689073-145690100	1028	29	9.03E-03	13.43	-1.38	4.41E-02
PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	chr12:53267161-53267937	777	22	2.80E-02	10.17	1.38	2.00E-02
PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7	chr2:241773955-241774416	462	13	1.89E-02	11.31	-1.30	3.54E-03
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	chr10:74861293-74861781	489	14	4.98E-02	8.61	-1.15	1.05E-03
PRB4	proline-rich protein BstNI subfamily 4	chr12:11315987-11316653	667	17	1.70E-02	11.59	-1.23	8.86E-03
PRKX	protein kinase, X-linked	chrX:3643072-3643939	868	25	2.88E-02	10.09	-1.37	3.83E-02
PRR3	proline rich 3	chr6:30647281-30647924	644	18	4.24E-02	9.04	-1.25	2.58E-02
PSD4	pleckstrin and Sec7 domain containing 4	chr2:113656853-113657470	618	17	4.58E-02	8.82	-1.27	3.15E-02
PSG6	pregnancy specific beta-1-glycoprotein 6	chr19:47936219-47936932	714	19	1.12E-02	12.74	-1.24	4.19E-02
PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	chr20:1042710-1043933	1224	26	7.34E-03	14.06	-1.34	3.34E-03

PTPN9	protein tyrosine phosphatase, non-receptor type 9	chr15:73658034-73658643	610	17	4.35E-02	8.97	-1.34	1.07E-02
PUS1	pseudouridylate synthase 1	chr12:130972616-130973331	716	19	2.09E-02	10.99	-1.43	3.90E-03
RAB11FIP1	RAB11 family interacting protein 1 (class I)	chr8:37880028-37880658	631	18	2.34E-02	10.67	-1.33	3.44E-02
RABL2A	RAB, member of RAS oncogene family-like 2B	chr2:114067514-114068154	641	18	6.79E-03	14.32	-1.76	2.71E-03
RBM34	RNA binding motif protein 34	chr1:233561217-233561978	762	22	2.33E-02	10.68	-1.30	6.19E-03
RBMX	RNA binding motif protein, X-linked	chr1:89231135-89231729	595	17	8.77E-03	13.52	-1.43	2.54E-03
RET	ret proto-oncogene	chr10:42882970-42883618	649	19	4.02E-02	9.19	-1.32	2.08E-02
RIC8B	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	chr12:105690731-105691825	1095	21	2.48E-02	10.50	-1.23	1.30E-02
RIMS3	regulating synaptic membrane exocytosis 3	chr1:40906955-40907620	666	13	4.22E-02	9.05	1.28	2.11E-02
RNF130	ring finger protein 130	chr5:179429330-179430298	969	28	1.45E-02	12.01	-1.24	1.03E-02
RNF4	ring finger protein 4	chr4:2434247-2434858	612	11	4.18E-02	9.08	-1.22	4.53E-02
ROGDI	rogdi homolog (Drosophila)	chr16:4791708-4792452	745	16	2.06E-02	11.05	-1.34	5.73E-03
RPH3AL	rabphilin 3A-like (without C2 domains)	chr17:205518-206383	866	24	2.35E-02	10.65	-1.37	2.19E-02
RPL23AP7	ribosomal protein L23a pseudogene 7	chr2:114107786-114108391	606	18	1.18E-02	12.56	1.14	3.74E-02
RRAD	Ras-related associated with diabetes	chr16:65511887-65512495	609	13	4.84E-02	8.69	1.09	3.57E-02
RTKN2	rhotekin 2	chr10:63700883-63701519	637	15	3.33E-02	9.69	-1.25	2.96E-02
RUSC1	RUN and SH3 domain containing 1	chr1:153544954-153545760	807	24	8.72E-03	13.55	-1.22	2.29E-02
S100A2	S100 calcium binding protein A2	chr1:151805027-151805620	594	17	4.36E-02	8.97	-1.28	1.31E-02
S100A6	S100 calcium binding protein A6	chr1:151780267-151780901	635	18	3.67E-02	9.42	-1.24	2.54E-02
SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	chr11:120671784-120672676	893	22	1.19E-02	12.54	1.23	8.51E-03
SCAMP2	secretory carrier membrane protein 2	chr15:72927060-72927436	377	11	4.54E-02	8.85	-1.40	3.79E-03
SCUBE3	signal peptide, CUB domain, EGF-like 3	chr6:35283668-35284284	617	13	4.87E-02	8.66	1.15	3.36E-02
SEP6	septin 6	chrX:118710317-118711084	768	21	3.70E-02	9.39	-1.20	3.96E-02
SEC24C	SEC24 related gene family, member C (S. cerevisiae)	chr10:75211361-75211997	637	18	4.27E-02	9.02	-1.36	8.40E-03
SEC31A	SEC31 homolog A (S. cerevisiae)	chr4:84038500-84038897	398	12	4.16E-02	9.09	-1.49	1.78E-02
SEPN1	selenoprotein N, 1	chr1:25998481-25999536	1056	23	2.08E-02	11.01	-1.65	2.62E-02
SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1	chr1:172150579-172151126	548	16	1.15E-02	12.64	-1.09	4.97E-02

SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium der	chr17:1617045-1617673	629	13	2.43E-02	10.55	1.79	1.76E-02
SFXN5	sideroflexin 5	chr2:73155884-73156529	646	17	4.11E-02	9.12	-1.27	7.84E-03
SH3GL3	SH3-domain GRB2-like 3	chr15:81906637-81907723	1087	30	1.35E-02	12.21	-1.26	1.96E-02
SHKBP1	SH3KBP1 binding protein 1	chr19:45775297-45776450	1154	25	2.63E-02	10.33	-1.37	1.26E-02
SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), membe	chr2:218912808-218913629	822	18	2.27E-02	10.74	-1.11	1.50E-02
SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	chr10:118990614-118991611	998	28	1.95E-02	11.21	1.47	4.31E-02
SLC25A29	solute carrier family 25, member 29	chr14:99840206-99840823	618	14	4.26E-02	9.03	-1.38	3.23E-02
SLC35C2	solute carrier family 35, member C2	chr20:44418389-44419073	685	19	2.36E-02	10.65	-1.18	3.34E-02
SLC39A7	solute carrier family 39 (zinc transporter), member 7	chr6:33282072-33283030	959	27	1.25E-02	12.42	1.16	4.88E-02
SLC47A1	solute carrier family 47, member 1	chr17:19378654-19379036	383	11	3.87E-02	9.29	-1.74	1.92E-02
SLC47A2	solute carrier family 47, member 2	chr17:19586597-19587223	627	18	1.78E-02	11.47	-1.17	3.39E-02
SMAD4	SMAD family member 4	chr18:46825439-46825879	441	13	2.25E-02	10.77	-1.23	4.19E-02
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	chr22:22454226-22455278	1053	22	2.61E-02	10.36	-1.38	1.37E-02
SMG5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	chr1:154487009-154487782	774	21	2.04E-02	11.09	-1.25	3.50E-02
SNAP29	synaptosomal-associated protein, 29kDa	chr22:19536882-19538018	1137	28	3.04E-02	9.94	1.14	3.60E-02
SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	chr9:138390303-138391225	923	25	2.05E-02	11.07	-1.23	4.39E-02
SOLH	small optic lobes homolog (Drosophila)	chr16:513148-513704	557	16	1.75E-02	11.52	-1.19	5.34E-03
SPAG9	sperm associated antigen 9	chr17:46554359-46554974	616	17	2.99E-02	9.97	1.28	8.87E-06
SPPL2A	signal peptide peptidase-like 2A	chr15:48847262-48847740	479	14	4.67E-02	8.77	1.60	2.24E-04
SPRR2B	small proline-rich protein 2B	chr1:151283148-151283966	819	20	6.85E-03	14.29	-1.21	2.90E-02
SPTLC2	serine palmitoyltransferase, long chain base subunit 2	chr14:77151995-77152873	879	24	3.71E-02	9.38	1.32	3.46E-02
SRF	serum response factor (c-fos serum response element-binding transcription factor	chr6:43254307-43254904	598	17	4.91E-02	8.65	-1.35	1.22E-02
SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	chr20:60199335-60200021	687	14	3.40E-02	9.62	-1.30	2.54E-02
SSH2	slingshot homolog 2 (Drosophila)	chr17:24971940-24972524	585	16	3.41E-02	9.61	1.37	2.47E-02

SSNA1	Sjogren syndrome nuclear autoantigen 1	chr9:139198410-139199135	726	16	3.27E-03	16.48	-1.25	4.62E-02
ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	chr7:132416760-132417375	616	17	4.76E-02	8.73	-1.21	3.74E-03
STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	chr19:15431622-15432188	567	17	2.30E-02	10.71	-1.24	2.39E-02
STK38L	serine/threonine kinase 38 like	chr12:27287796-27288488	693	15	2.91E-02	10.06	1.61	4.05E-02
STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	chr2:168705880-168706465	586	10	4.00E-02	9.20	-1.25	2.01E-02
STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	chr15:72282238-72282918	681	21	1.59E-02	11.77	-1.29	3.97E-02
SUFU	suppressor of fused homolog (Drosophila)	chr10:104253614-104254402	789	20	8.47E-03	13.65	-1.24	3.82E-02
SWAP70	SWAP-70 protein	chr11:9642678-9643364	687	19	4.04E-02	9.17	-2.52	1.17E-03
TACC1	transforming, acidic coiled-coil containing protein 1	chr8:38764731-38765396	666	18	4.16E-02	9.08	2.17	1.89E-04
TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	chr6:34966439-34967042	604	17	4.66E-02	8.78	-1.76	2.61E-04
TAPBP	TAP binding protein (tapasin)	chr6:33364418-33365021	604	17	3.91E-02	9.25	-1.45	2.19E-02
TAPT1	transmembrane anterior posterior transformation 1	chr4:15836795-15837381	587	11	4.86E-02	8.67	1.19	1.51E-02
TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	chr5:179230943-179231655	713	19	2.74E-02	10.22	-1.15	3.64E-02
TGFB1I1	transforming growth factor beta 1 induced transcript 1	chr16:31399465-31400083	619	18	3.59E-02	9.47	-1.24	1.26E-02
TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	chr17:842885-843759	875	25	9.67E-05	26.97	-1.37	3.06E-03
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	chr14:23770763-23771413	651	18	3.38E-02	9.65	-1.25	2.06E-02
TK1	thymidine kinase 1, soluble	chr17:73698536-73699085	550	16	4.05E-02	9.16	1.61	1.17E-02
TLN1	talin 1	chr9:35717827-35718943	1117	32	2.04E-02	11.08	-1.37	1.08E-03
TMBIM1	transmembrane BAX inhibitor motif containing 1	chr2:218848629-218849264	636	18	2.69E-02	10.27	1.28	3.84E-02
TMCO3	transmembrane and coiled-coil domains 3	chr13:113186325-113186964	640	18	3.67E-02	9.42	1.24	1.93E-02
TMED9	transmembrane emp24 protein transport domain containing 9	chr5:176951293-176951960	668	15	4.26E-02	9.03	1.26	2.47E-02
TMEM173	transmembrane protein 173	chr5:138841211-138842141	931	25	1.87E-02	11.34	-1.51	1.12E-02
TMEM65	transmembrane protein 65	chr8:125457617-125458344	728	21	2.41E-02	10.58	1.52	3.18E-03
TMEM97	transmembrane protein 97	chr17:23667778-23668371	594	16	2.74E-02	10.22	-1.24	2.63E-02

TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	chr17:23682629-23683276	648	19	3.82E-02	9.31	-1.24	2.26E-02
TNIK	TRAF2 and NCK interacting kinase	chr3:172660066-172661004	939	26	1.09E-02	12.81	-1.30	2.32E-02
TOM1L2	target of myb1-like 2 (chicken)	chr17:17686351-17686891	541	10	4.16E-02	9.09	-1.35	3.38E-03
TOP1MT	topoisomerase (DNA) I, mitochondrial	chr8:144493117-144494071	955	28	3.87E-04	23.17	-1.35	3.92E-02
TOP3A	topoisomerase (DNA) III alpha	chr17:18161093-18161866	774	22	2.31E-02	10.70	-1.31	3.81E-02
TPM3	tropomyosin 3	chr1:152437989-152438670	682	20	2.87E-02	10.09	-1.43	1.24E-02
TRAF7	TNF receptor-associated factor 7	chr16:2153924-2155961	2038	41	1.35E-02	12.22	-1.34	2.18E-02
TRIP13	thyroid hormone receptor interactor 13	chr5:935878-936321	444	13	2.03E-02	11.09	-1.53	4.26E-03
TRPV2	transient receptor potential cation channel, subfamily V, member 2	chr17:16225806-16226766	961	27	2.91E-03	16.86	1.22	5.83E-03
TSC2	tuberous sclerosis 2	chr16:2033822-2034521	700	19	4.06E-02	9.16	-1.31	1.19E-02
TSPAN9	tetraspanin 9	chr12:3061426-3062099	674	19	1.74E-02	11.53	1.12	3.51E-02
TST	thiosulfate sulfurtransferase (rhodanese)	chr22:35751118-35751864	747	19	1.86E-02	11.35	-1.50	1.22E-02
TTLL4	tubulin tyrosine ligase-like family, member 4	chr2:219276437-219277053	617	18	4.83E-02	8.69	-1.16	1.35E-02
TYSND1	trypsin domain containing 1	chr10:71555676-71556508	833	21	4.13E-03	15.76	-1.47	5.31E-03
UBTF	upstream binding transcription factor, RNA polymerase I	chr17:39653911-39654711	801	21	4.30E-02	9.01	-1.44	2.49E-03
ULK1	unc-51-like kinase 1 (C. elegans)	chr12:130972616-130973331	716	19	2.09E-02	10.99	-1.29	3.39E-02
UNKL	unkempt homolog (Drosophila)-like	chr16:1423178-1424111	934	26	2.01E-02	11.12	1.59	1.46E-02
USP22	ubiquitin specific peptidase 22	chr17:19586597-19587223	627	18	1.78E-02	11.47	-1.21	2.56E-02
USP32	ubiquitin specific peptidase 32	chr17:4972856-4974634	1779	43	5.06E-03	15.13	1.32	3.15E-02
USP36	Ubiquitin specific peptidase 36	chr17:74347504-74348321	818	22	9.10E-03	13.41	-1.45	2.41E-03
USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	chr17:4972856-4974634	1779	43	5.06E-03	15.13	1.30	6.05E-03
UXT	ubiquitously-expressed transcript	chrX:47379659-47380243	585	14	4.84E-02	8.68	-1.27	8.27E-03
VAC14	Vac14	chr16:69391591-69392483	893	19	2.50E-02	10.49	-1.22	5.17E-03
VANGL1	vang-like 1 (van gogh, Drosophila)	chr1:115992088-115992703	616	17	2.06E-02	11.05	-1.81	2.75E-03
VEGFB	vascular endothelial growth factor B	chr11:63766169-63766785	617	14	4.52E-02	8.86	-1.26	5.04E-03
VIL1	villin 1	chr2:218912808-218913629	822	18	2.27E-02	10.74	1.07	2.47E-02
VPS36	vacuolar protein sorting 36 homolog (S. cerevisiae)	chr13:51877880-51878511	632	16	3.59E-02	9.47	-1.50	2.30E-03
VPS39	vacuolar protein sorting 39 homolog (S.	chr15:40238358-40239008	651	18	2.52E-02	10.46	-1.46	1.96E-03

	cerevisiae)							
VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	chr17:570253-571431	1179	31	4.32E-03	15.62	-1.16	3.03E-03
VWA3B	von Willebrand factor A domain containing 3B	chr2:98223803-98224721	919	26	2.89E-02	10.07	-1.12	2.94E-02
WDFY3	WD repeat and FYVE domain containing 3	chr4:85824461-85825032	572	16	4.54E-02	8.85	1.26	4.62E-02
WDR40A	WD repeat domain 40A	chr9:34123161-34124296	1136	28	4.46E-03	15.53	-2.29	3.12E-05
WDR90	WD repeat domain 90	chr16:668843-669823	981	28	2.85E-02	10.12	-1.32	5.00E-02
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	chr8:38252033-38252654	622	17	1.52E-02	11.87	1.19	3.65E-02
WWC3	WWC family member 3	chrX:9937799-9938561	763	22	3.25E-02	9.76	-1.49	3.87E-02
YPEL3	yippee-like 3 (Drosophila)	chr16:30010897-30011606	710	21	2.57E-02	10.40	1.49	1.00E-02
YRDC	yrdC domain containing (E. coli)	chr1:38043540-38044329	790	21	2.95E-02	10.02	-1.24	3.07E-02
ZBTB46	zinc finger and BTB domain containing 46	chr20:61939064-61939688	625	18	1.31E-02	12.30	-1.22	2.52E-02
ZCCHC11	zinc finger, CCHC domain containing 11	chr1:52791972-52792951	980	21	1.43E-02	12.04	-1.22	3.74E-02
ZFP62	zinc finger protein 62 homolog (mouse)	chr5:180166655-180167242	588	17	4.13E-02	9.11	-1.28	1.06E-02
ZFYVE20	zinc finger, FYVE domain containing 20	chr3:15114623-15115664	1042	26	1.89E-02	11.29	1.17	4.75E-02
ZMYM6	zinc finger, MYM-type 6	chr1:35221821-35222627	807	22	6.82E-03	14.30	-1.28	2.38E-02
ZMYND19	zinc finger, MYND-type containing 19	chr9:139600149-139600529	381	12	3.33E-02	9.68	-1.39	3.75E-03
ZNF14	zinc finger protein 14	chr19:19710590-19711211	622	15	4.95E-02	8.63	-1.26	3.47E-02
ZNF17	zinc finger protein 17	chr19:62560067-62560690	624	18	2.94E-02	10.03	-1.32	1.40E-02
ZNF179	zinc finger protein 179	chr17:19257280-19257644	365	11	4.60E-02	8.82	-1.12	4.15E-02
ZNF195	zinc finger protein 195	chr11:3361858-3362874	1017	29	1.76E-05	33.10	-1.24	2.48E-02
ZNF22	zinc finger protein 22 (KOX 15)	chr10:44811437-44812134	698	20	2.89E-02	10.07	1.17	2.89E-02
ZNF341	zinc finger protein 341	chr20:31779141-31779703	563	12	1.04E-02	12.96	-1.38	3.94E-02
ZNF367	zinc finger protein 367	chr9:98187198-98187787	590	17	4.57E-02	8.83	-1.28	2.74E-02
ZNF497	zinc finger protein 497	chr19:63571478-63573071	1594	45	5.52E-03	14.87	-1.27	3.85E-03
ZNF512	zinc finger protein 512	chr2:27659376-27660055	680	19	3.31E-02	9.71	-1.70	3.70E-04
ZNF569	zinc finger protein 569	chr19:42655543-42656153	611	17	4.36E-02	8.97	-1.22	4.83E-02
ZNF618	zinc finger protein 618	chr9:115853382-115854466	1085	30	1.39E-02	12.14	-1.42	2.62E-02
ZNF701	zinc finger protein 701	chr19:57748937-57749582	646	18	2.84E-02	10.13	-1.22	3.10E-02
ZNF76	zinc finger protein 76 (expressed in testis)	chr6:35368367-35368985	619	17	4.65E-02	8.78	-1.32	2.31E-03
ZSWIM3	zinc finger, SWIM-type containing 3	chr20:43949291-43949833	543	16	3.72E-02	9.38	-1.32	1.73E-03

Table 21 KEGG pathways of significant differentially expressed genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < 0.05) (* significant corrected gamma p-value < 0.05, DAVID functional annotation)

KEGG pathway name	p-value	Fold enrichment
Thyroid cancer*	5.73E-03	10.58
MAPK signaling pathway*	2.41E-02	2.48
Focal adhesion	1.37E-01	2.15
GnRH signaling pathway	1.38E-01	3.04
mTOR signaling pathway	1.55E-01	4.20
Arachidonic acid metabolism	1.75E-01	3.90
Basal cell carcinoma	1.80E-01	3.83
Hedgehog signaling pathway	1.85E-01	3.76
Heparan sulfate biosynthesis	2.53E-01	6.80
Nicotinate and nicotinamide metabolism	2.84E-01	5.95
Apoptosis	3.22E-01	2.55
Alzheimer's disease	3.22E-01	5.10
Small cell lung cancer	3.38E-01	2.46
Regulation of actin cytoskeleton	3.40E-01	1.67
Wnt signaling pathway	3.45E-01	1.89
Propanoate metabolism	3.77E-01	4.20
Melanogenesis	3.93E-01	2.19
Glutathione metabolism	4.19E-01	3.66
Bladder cancer	4.27E-01	3.57
Histidine metabolism	4.35E-01	3.48
Valine, leucine and isoleucine degradation	4.58E-01	3.25
Cell cycle	4.69E-01	1.88
Glycerolipid metabolism	5.02E-01	2.86
Ubiquitin mediated proteolysis	5.43E-01	1.64

Tyrosine metabolism	5.55E-01	2.46
Insulin signaling pathway	5.56E-01	1.60
Cell Communication	5.64E-01	1.58
Glycolysis / Gluconeogenesis	5.67E-01	2.38
p53 signaling pathway	6.13E-01	2.10
Metabolism of xenobiotics by cytochrome P450	6.13E-01	2.10
Pancreatic cancer	6.40E-01	1.96
Chronic myeloid leukemia	6.45E-01	1.93
Phosphatidylinositol signaling system	6.55E-01	1.88
Antigen processing and presentation	6.74E-01	1.79
Colorectal cancer	6.96E-01	1.68
ECM-receptor interaction	7.08E-01	1.62
TGF-beta signaling pathway	7.17E-01	1.59
Gap junction	7.36E-01	1.50
Glycan structures - biosynthesis 1	8.15E-01	1.19
Tight junction	8.44E-01	1.08
Axon guidance	8.44E-01	1.08
Purine metabolism	8.71E-01	0.99
Calcium signaling pathway	9.15E-01	0.82
Cytokine-cytokine receptor interaction	9.74E-01	0.56

Table 22 KEGG pathways of significant differentially expressed genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < 0.05) (* significant corrected gamma p-value < 0.05, Pathway Express calculation)

KEGG pathway name	Rank	Impact factor	No. genes in pathway	% Pathwaygenes in input	p-value			
					uncorrected	corrected	gamma	corrected gamma
Phosphatidylinositol signaling system*	1	42.5	76	1.3	8.34E-01	8.34E-01	1.51E-17	1.51E-17
Circadian rhythm*	2	26.8	13	7.7	2.47E-01	2.47E-01	6.46E-11	6.46E-11
Antigen processing and presentation*	3	25.9	89	5.6	3.72E-02	3.72E-02	1.45E-10	1.45E-10
MAPK signaling pathway*	4	6.0	272	4.0	4.82E-02	4.82E-02	1.72E-02	1.72E-02
Pathways in cancer*	5	6.0	330	3.9	4.39E-02	4.39E-02	1.74E-02	1.74E-02
Basal cell carcinoma*	6	5.9	55	5.5	1.31E-01	1.31E-01	1.90E-02	1.90E-02
Gap junction*	7	5.6	96	2.1	6.42E-01	6.42E-01	2.34E-02	2.34E-02
Thyroid cancer*	8	5.6	29	6.9	1.46E-01	1.46E-01	2.45E-02	2.45E-02
Apoptosis*	9	5.2	89	5.6	5.48E-02	5.48E-02	3.45E-02	3.45E-02
Regulation of actin cytoskeleton*	10	5.1	217	2.8	3.53E-01	3.53E-01	3.73E-02	3.73E-02
Small cell lung cancer*	11	4.8	86	5.8	5.06E-02	5.06E-02	4.60E-02	4.60E-02
mTOR signaling pathway	12	4.6	52	7.7	2.89E-02	2.89E-02	5.70E-02	5.70E-02
Focal adhesion	13	4.1	203	3.0	3.20E-01	3.20E-01	8.22E-02	8.22E-02
Bladder cancer	14	4.1	42	4.8	2.56E-01	2.56E-01	8.29E-02	8.29E-02
Maturity onset diabetes of the young	15	4.1	24	8.3	8.51E-02	8.51E-02	8.56E-02	8.56E-02
Long-term depression	16	4.1	75	1.3	8.26E-01	8.26E-01	8.67E-02	8.67E-02
Wnt signaling pathway	17	4.0	152	3.3	2.68E-01	2.68E-01	9.49E-02	9.49E-02
Complement and coagulation cascades	18	3.9	69	1.4	7.95E-01	7.95E-01	1.02E-01	1.02E-01
Long-term potentiation	19	3.5	73	4.1	2.30E-01	2.30E-01	1.41E-01	1.41E-01
GnRH signaling pathway	20	3.3	103	3.9	2.00E-01	2.00E-01	1.57E-01	1.57E-01
Calcium signaling pathway	21	3.2	182	1.6	7.78E-01	7.78E-01	1.66E-01	1.66E-01
Systemic lupus erythematosus	22	3.2	144	3.5	1.15E-01	1.15E-01	1.71E-01	1.71E-01
Hedgehog signaling pathway	23	3.2	57	5.3	1.31E-01	1.31E-01	1.72E-01	1.72E-01

Axon guidance	24	3.1	129	2.3	5.77E-01	5.77E-01	1.89E-01	1.89E-01
Colorectal cancer	25	3.1	84	3.6	3.12E-01	3.12E-01	1.91E-01	1.91E-01
Prostate cancer	26	3.0	90	2.2	6.18E-01	6.18E-01	1.96E-01	1.96E-01
Pancreatic cancer	27	3.0	72	4.2	2.36E-01	2.36E-01	2.01E-01	2.01E-01
Natural killer cell mediated cytotoxicity	28	3.0	135	1.5	7.99E-01	7.99E-01	2.01E-01	2.01E-01
Homologous recombination	29	3.0	28	7.1	1.30E-01	1.30E-01	2.03E-01	2.03E-01
B cell receptor signaling pathway	30	3.0	65	3.1	4.50E-01	4.50E-01	2.05E-01	2.05E-01
Insulin signaling pathway	31	2.9	138	3.6	2.12E-01	2.12E-01	2.19E-01	2.19E-01
VEGF signaling pathway	32	2.9	74	2.7	5.03E-01	5.03E-01	2.23E-01	2.23E-01
Basal transcription factors	33	2.8	37	5.4	1.79E-01	1.79E-01	2.33E-01	2.33E-01
T cell receptor signaling pathway	34	2.7	108	1.9	7.16E-01	7.16E-01	2.49E-01	2.49E-01
Chronic myeloid leukemia	35	2.7	75	2.7	5.25E-01	5.25E-01	2.51E-01	2.51E-01
Amyotrophic lateral sclerosis (ALS)	36	2.7	56	3.6	3.68E-01	3.68E-01	2.54E-01	2.54E-01
Regulation of autophagy	37	2.6	35	5.7	1.71E-01	1.71E-01	2.59E-01	2.59E-01
Melanoma	38	2.6	71	1.4	8.13E-01	8.13E-01	2.60E-01	2.60E-01
Base excision repair	39	2.6	36	5.6	1.71E-01	1.71E-01	2.60E-01	2.60E-01
Acute myeloid leukemia	40	2.6	59	1.7	7.40E-01	7.40E-01	2.65E-01	2.65E-01
Taste transduction	41	2.4	53	1.9	6.54E-01	6.54E-01	2.99E-01	2.99E-01
Endometrial cancer	42	2.4	52	3.8	3.43E-01	3.43E-01	3.01E-01	3.01E-01
Melanogenesis	43	2.4	102	2.9	4.20E-01	4.20E-01	3.10E-01	3.10E-01
Jak-STAT signaling pathway	44	2.4	155	2.6	4.75E-01	4.75E-01	3.10E-01	3.10E-01
ABC transporters	45	2.3	44	4.5	2.74E-01	2.74E-01	3.22E-01	3.22E-01
Fc epsilon RI signaling pathway	46	2.3	78	2.6	5.32E-01	5.32E-01	3.34E-01	3.34E-01
Cardiac muscle contraction	47	2.2	87	2.3	5.18E-01	5.18E-01	3.49E-01	3.49E-01
Non-small cell lung cancer	48	2.2	54	1.9	7.21E-01	7.21E-01	3.66E-01	3.66E-01
ECM-receptor interaction	49	2.1	84	2.4	5.80E-01	5.80E-01	3.78E-01	3.78E-01
Epithelial cell signaling in Helicobacter pylori infection	50	2.1	68	1.5	7.99E-01	7.99E-01	3.82E-01	3.82E-01
Tight junction	51	2.1	135	2.2	5.92E-01	5.92E-01	3.87E-01	3.87E-01

Glioma	52	2.1	65	1.5	7.85E-01	7.85E-01	3.88E-01	3.88E-01
Ubiquitin mediated proteolysis	53	2.0	138	2.9	3.60E-01	3.60E-01	4.01E-01	4.01E-01
Autoimmune thyroid disease	54	2.0	53	3.8	3.17E-01	3.17E-01	4.18E-01	4.18E-01
TGF-beta signaling pathway	55	1.9	87	2.3	5.73E-01	5.73E-01	4.24E-01	4.24E-01
Toll-like receptor signaling pathway	56	1.9	102	2.9	4.13E-01	4.13E-01	4.32E-01	4.32E-01
ErbB signaling pathway	57	1.9	87	2.3	6.05E-01	6.05E-01	4.34E-01	4.34E-01
Cell adhesion molecules (CAMs)	58	1.9	134	1.5	7.99E-01	7.99E-01	4.47E-01	4.47E-01
Alzheimer''s disease	59	1.8	178	1.7	7.24E-01	7.24E-01	4.50E-01	4.50E-01
Mismatch repair	60	1.8	23	4.3	4.05E-01	4.05E-01	4.59E-01	4.59E-01
Renal cell carcinoma	61	1.8	69	2.9	4.80E-01	4.80E-01	4.61E-01	4.61E-01
Vibrio cholerae infection	62	1.8	62	1.6	7.58E-01	7.58E-01	4.66E-01	4.66E-01
Cell cycle	63	1.7	118	2.5	4.87E-01	4.87E-01	5.02E-01	5.02E-01
Olfactory transduction	64	1.6	382	0.3	9.26E-01	9.26E-01	5.28E-01	5.28E-01
Notch signaling pathway	65	1.6	47	2.1	6.70E-01	6.70E-01	5.36E-01	5.36E-01
Asthma	66	1.6	30	3.3	4.71E-01	4.71E-01	5.38E-01	5.38E-01
DNA replication	67	1.5	36	2.8	5.62E-01	5.62E-01	5.63E-01	5.63E-01
Huntington''s disease	68	1.5	189	2.1	5.67E-01	5.67E-01	5.63E-01	5.63E-01
Adipocytokine signaling pathway	69	1.5	67	1.5	7.90E-01	7.90E-01	5.74E-01	5.74E-01
Proteasome	70	1.5	48	2.1	6.29E-01	6.29E-01	5.74E-01	5.74E-01
Allograft rejection	71	1.4	38	2.6	5.41E-01	5.41E-01	5.85E-01	5.85E-01
Type II diabetes mellitus	72	1.4	45	2.2	6.20E-01	6.20E-01	5.88E-01	5.88E-01
Graft-versus-host disease	73	1.4	42	2.4	5.52E-01	5.52E-01	5.91E-01	5.91E-01
SNARE interactions in vesicular transport	74	1.4	38	2.6	5.83E-01	5.83E-01	6.00E-01	6.00E-01
Nucleotide excision repair	75	1.4	44	2.3	6.38E-01	6.38E-01	6.06E-01	6.06E-01
Type I diabetes mellitus	76	1.3	44	2.3	5.92E-01	5.92E-01	6.16E-01	6.16E-01
Cytokine-cytokine receptor interaction	77	1.3	263	1.5	8.44E-01	8.44E-01	6.24E-01	6.24E-01
Parkinson''s disease	78	1.3	137	1.5	7.48E-01	7.48E-01	6.36E-01	6.36E-01
PPAR signaling pathway	79	1.3	70	1.4	7.95E-01	7.95E-01	6.44E-01	6.44E-01

p53 signaling pathway	80	1.2	69	1.4	7.99E-01	7.99E-01	6.68E-01	6.68E-01
Hematopoietic cell lineage	81	1.1	87	1.1	8.59E-01	8.59E-01	6.92E-01	6.92E-01
Adherens junction	82	1.1	78	1.3	8.34E-01	8.34E-01	7.05E-01	7.05E-01
Neuroactive ligand-receptor interaction	83	1.0	256	0.8	9.82E-01	9.82E-01	7.48E-01	7.48E-01

Table 23 Genes with ChIP-on-CHIP bindings sites (region p-value < 0.05) and siRNA expression values (Note *significant differentially expressed genes in bold) of the KEGG MAPK signaling pathway

		ChIP-on-CHIP enriched region					Expression	
Gene symbol	**Gene Name**	**Chromosome region**	**Length(bps)**	**Probes in region**	**p-value**	**MAT-score**	**Fold change**	**p-value**
MAPK11	mitogen-activated protein kinase 11	chr22:49035213-49036046	834	24	1.85E-03	18.40	-1.27	5.42E-02
MAPK12	mitogen-activated protein kinase 12	chr22:49035213-49036046	834	24	1.85E-03	18.40	-1.04	6.87E-01
FLNA	filamin A, alpha (actin binding protein 280)	chrX:153235798-153237011	1214	33	2.29E-03	17.64	-1.33	5.78E-02
FGF22	fibroblast growth factor 22	chr19:591265-592254	990	23	2.72E-03	17.14	-1.07	5.33E-01
MAP3K6	mitogen-activated protein kinase kinase kinase 6	chr1:27576823-27577534	712	16	5.71E-03	14.79	-1.25	1.50E-01
CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	chr19:13477805-13478560	756	18	9.86E-03	13.13	-1.17	1.44E-01
MAP3K12	mitogen-activated protein kinase kinase kinase 12	chr12:52196249-52197268	1020	29	1.05E-02	12.94	-1.20	1.23E-01
CACNG2	calcium channel, voltage-dependent, gamma subunit 2	chr22:35435808-35436315	508	14	1.17E-02	12.60	-1.02	8.57E-01
MAP2K3	mitogen-activated protein kinase kinase 3	chr17:21125336-21126121	786	22	1.29E-02	12.35	-1.43	1.41E-02
HSPA1L	heat shock 70kDa protein 1-like	chr6:31873223-31873813	591	15	1.39E-02	12.13	1.17	1.74E-01
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	chrX:153537304-153537888	585	13	1.65E-02	11.67	-1.15	1.59E-01
RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	chr11:64235895-64236992	1098	31	1.73E-02	11.55	1.23	2.02E-01
NTRK1	neurotrophic tyrosine kinase, receptor, type 1	chr1:155096881-155097821	941	24	1.75E-02	11.51	-1.01	9.34E-01
MKNK2	MAP kinase interacting serine/threonine kinase 2	chr19:2008501-2009234	734	20	1.78E-02	11.47	-1.21	1.82E-01

MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	chr16:1766988-1768014	1027	28	1.84E-02	11.40	-1.10	4.64E-01
PTPN7	protein tyrosine phosphatase, non-receptor type 7	chr1:200391831-200392552	722	18	1.90E-02	11.28	1.03	4.91E-01
PDGFB	platelet-derived growth factor beta polypeptide	chr22:37978948-37979686	739	20	1.99E-02	11.15	-1.13	3.52E-01
PLA2G2F	phospholipase A2, group IIF	chr1:20337136-20337759	624	15	2.09E-02	11.00	-1.04	5.74E-01
DDIT3	DNA-damage-inducible transcript 3	chr12:56205980-56206818	839	24	2.23E-02	10.79	1.07	7.96E-01
SMAD4	SMAD family member 4	chr18:46825439-46825879	441	13	2.25E-02	10.77	-1.23	4.19E-02
CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	chr3:50349280-50350005	726	20	2.37E-02	10.62	-1.30	3.65E-02
JUN	jun oncogene	chr1:59020523-59021495	973	27	2.54E-02	10.44	1.44	1.81E-01
MAX	MYC associated factor X	chr14:64638099-64638744	646	17	2.66E-02	10.29	-1.22	4.23E-02
MAPK13	mitogen-activated protein kinase 13	chr6:36198896-36199646	751	21	2.72E-02	10.25	-1.08	3.87E-01
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	chr5:149480346-149480990	645	18	2.72E-02	10.24	1.06	5.67E-01
CACNG4	calcium channel, voltage-dependent, gamma subunit 4	chr17:62389856-62390809	954	27	2.77E-02	10.19	1.05	5.84E-01
PRKX	protein kinase, X-linked	chrX:3643072-3643939	868	25	2.88E-02	10.09	-1.37	3.83E-02
MKNK1	MAP kinase interacting serine/threonine kinase 1	chr1:46790394-46791066	673	19	2.91E-02	10.05	-1.07	3.16E-01
FGF1	fibroblast growth factor 1 (acidic)	chr5:141986937-141987647	711	20	2.93E-02	10.04	-1.09	1.56E-01
FGF8	fibroblast growth factor 8 (androgen-induced)	chr10:103527007-103527730	724	20	3.01E-02	9.96	-1.01	9.39E-01
STMN1	stathmin 1/oncoprotein 18	chr1:26105057-26105706	650	18	3.38E-02	9.65	-1.22	1.22E-01
GNA12	guanine nucleotide binding protein (G protein) alpha 12	chr7:2740139-2740820	682	19	3.39E-02	9.63	1.16	2.73E-01
JUND	jun D proto-oncogene	chr19:18256743-18257344	602	15	3.42E-02	9.61	1.17	2.68E-01
TGFB3	transforming growth factor, beta 3	chr14:75517201-75517968	768	21	3.47E-02	9.56	1.04	3.71E-01
AKT2	v-akt murine thymoma viral oncogene homolog 2	chr19:45477316-45477991	676	17	3.55E-02	9.50	-1.66	6.57E-03
CACNB4	calcium channel, voltage-dependent, beta 4 subunit	chr2:152664408-152665082	675	19	3.57E-02	9.49	-1.02	7.96E-01
PTPN5	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	chr11:18706089-18706805	717	20	3.66E-02	9.43	1.09	4.36E-01
FGF14	fibroblast growth factor 14	chr13:101850962-101851659	698	19	3.76E-02	9.36	1.01	7.32E-01
CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	chr22:38294186-38294777	592	17	3.90E-02	9.26	-1.13	1.81E-01

PTPRR	protein tyrosine phosphatase, receptor type, R	chr12:69604288-69605016	729	21	3.92E-02	9.25	-1.05	7.42E-01
FGFR4	fibroblast growth factor receptor 4	chr5:176448835-176449531	697	16	3.94E-02	9.24	1.01	7.60E-01
MRAS	muscle RAS oncogene homolog	chr3:139568666-139569273	608	12	3.98E-02	9.22	-1.13	4.60E-02
CACNA1B	calcium channel, voltage-dependent, N type, alpha 1B subunit	chr9:139888580-139889214	635	18	4.00E-02	9.20	-1.11	1.48E-01
MAP2K2	mitogen-activated protein kinase kinase 2	chr7:128551685-128552287	603	17	4.13E-02	9.12	-1.19	1.04E-01
DUSP2	dual specificity phosphatase 2	chr2:96178127-96178804	678	16	4.14E-02	9.11	1.48	1.64E-01
FGF11	fibroblast growth factor 11	chr17:7260904-7261636	733	22	4.21E-02	9.06	-1.17	1.08E-01
TAOK2	TAO kinase 2	chr16:29909731-29910337	607	17	4.46E-02	8.91	-1.11	5.15E-01
NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	chr14:23906236-23906838	603	16	4.52E-02	8.86	-1.09	4.20E-01
HSPA1B	heat shock 70kDa protein 1B	chr6:31904789-31905394	606	17	4.72E-02	8.75	1.13	2.54E-01
ELK1	ELK1, member of ETS oncogene family	chrX:47379659-47380243	585	14	4.84E-02	8.68	-1.23	3.72E-02
HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	chr11:530259-530861	603	17	4.86E-02	8.67	-1.14	4.43E-01
SRF	serum response factor (c-fos serum response element-binding transcription factor)	chr6:43254307-43254904	598	17	4.91E-02	8.65	-1.35	1.22E-02
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	chr10:74861293-74861781	489	14	4.98E-02	8.61	-1.15	1.05E-03

Table 24 Quantitative real-time PCR validation of genes with ChIP-on-CHIP bindings sites (region p-value < 0.05) and signififcant HEK & HeLA siRNA expression values and additional expression of patient versus 4 control lymphoblastoid cell lines values (note significant differential fold changes in bold) of the KEGG MAPK signaling pathway. (NTRK1 and DUSP2 were included as negative controls)

	Whole genome expression array HEK & HeLa siRNA expression		**Quantitative real-time PCR validation HEK & HeLa siRNA expression**		**Whole genome expression array patient *vs.* controls expression**	
Gene symbol	**Fold change**	**p-value**	**Fold change**	**p-value**	**Fold change**	**p-value**
MAP2K3	**-1.43**	1.41E-02	**-1.81**	1.23E-14	**-1.26**	2.41E-02
NTRK1	-1.01	9.34E-01	-0.68	1.03E-01	1.05	4.29E-01
SMAD4	**-1.23**	4.19E-02	**-1.49**	1.02E-03	**-1.19**	3.21E-04
MAX	**-1.22**	4.23E-02	**-1.51**	1.93E-04	**-1.45**	6.65E-03
PRKX	**-1.37**	3.83E-02	**-1.49**	1.77E-04	**-1.7**	1.33E-02
AKT2	**-1.66**	6.57E-03	**-1.34**	6.64E-05	**-1.48**	2.18E-02
MRAS	**-1.13**	4.60E-02	**-1.42**	4.86E-05	**-1.15**	7.88E-06
DUSP2	1.48	1.64E-01	-1.01	9.58E-01	-1.7	4.42E-01
ELK1	**-1.23**	3.72E-02	**-1.47**	2.79E-04	**-1.11**	3.23E-02
SRF	**-1.35**	1.22E-02	**-1.60**	7.35E-06	**-1.14**	2.50E-04
PPP3CB	**-1.15**	1.05E-03	-1.30	2.07E-01	**-1.15**	1.05E-03

Table 25 Tissue expression pattern of significantly enriched genes (p-value < 0.05) with ChIP-on-CHIP binding sites (MAT score p-value < =.05)

Uniprot-Term	Observed genes	%	p-value*	Benjamini*
Brain	30	45.5	7.00E-04	4.09E-01
Muscle	7	10.6	1.02E-02	9.79E-01
Lymphocyte	3	4.5	1.83E-02	9.90E-01
Spleen	7	10.6	2.09E-02	9.81E-01
Fetal brain	6	9.1	2.63E-02	9.82E-01
Epithelium	11	16.7	2.98E-02	9.77E-01

*p-values and Benjamini-Hochberg p-values were caclulated using the DAVID funtional annotation of Uniprot tissue expression