Supplemental Data:

Table 1. Differentially-expressed genes at 72hrs after light onset, rank ordered by log2 difference in average fluorescence intensity between control and experimental chips (see column M).

Supplemental Figure 1. Housing pigmented zebrafish to intense bright fluorescent light induces photoreceptor loss followed by regeneration. Panels a-e illustrate Nissl-stained sections from control retina (a) and retinas exposed to bright, constant light for 24hrs (b), 72hrs (c), 10 days or (d) 10 days following by 18 days of recovery. Panels f-g illustrate quantitative measurements of the photoreceptor, outer nuclear and rod nuclear layers, respectively (see panel a), normalized to the thickness of the inner nuclear layer. Note that there is a significant decrease in the thickness of the various layers starting at 72h of light exposure. Panels i-k illustrate analysis of *rhodopsin*, *red opsin* and *PCNA* expression by quantitative real-time PCR. ROS, rod outer segments; OLM, outer limiting membrane; OPL, outer plexiform layer; IPL, inner plexiform layer; ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer; PL, photoreceptor layer; rod ONL, rod outer nuclear layer. Scale bar equals 50μm, $^*p<0.05$, $^{**}p<0.01$.

Supplemental Figure 2. Sense probes do not produce specific cellular labeling. Panels a-d illustrate *in situ* hybridizations comparing *mdka* antisense (a, c) and sense (b, d) probes. Panels a and b are from a 96hpf larva and panels c and d are from an adult retina. Panels e-f illustrate *in situ* hybridizations comparing *mdkb* antisense (e, g) and sense (f, h) probes. Panels e and f are from a 96hpf larva, whereas panels g and h are from an adult. Arrows and arrowheads illustrate specific cellular expression when using antisense probes. GCL – ganglion cell layer; INL – inner nuclear layer; ONL – outer nuclear layer.

Supplemental Figure 3. In the adult retina *mdka* or *mdkb* is not expressed in dividing cells. Panels a and d illustrate *in situ* hybridizations that show the cellular expression of *mdka* and *mdkb*, respectively, in the adult retina. Panels b and e are the same sections as in a and d, following immunostaining with antibodies against PCNA, and illustrate PCNA-positive cells (rod progenitors) (arrowheads) within the outer nuclear layer. Panels c and f are digital overlays. Note that the PCNA immunostaining does not co-localize with the expression of midkines. ONL – outer nuclear layer; INL – inner nuclear layer; GCL – ganglion cell layer.

Supplemental Figure 4. Time course of *mdka* and *mdkb* expression during and after the light lesion. Panels a-h illustrate the time course of the injury-induced expression of *mdka,* whereas panels i-p illustrate the time course of the injury-induced expression of *mdkb*. Note that the expansion of *mdkb* expression into the vitreal inner nuclear layer begins by 24hrs after light onset (cf. panel I with Fig. 5a) and returns to normal only at 14 days after the onset of the light exposure. In contrast, the expression of *mdka* varies relatively little over the same time course. onl, outer nuclear layer; inl inner nuclear layer; gcl, ganglion cell layer. Scale bar equals 50µm.

Probe Set ID	Affy_Gene Symbol	Gene Symbol	Affy_Gene Title	Gene Title	Affy_GO biological pro	GO Biological Process	Affy_GO cellular comp	GO Cellular Componen	Affy_GO molecular fun	GO Molecular Function Descriptio	FDR#	pvalue	FoldChange LL vs. cntl
Dr.3374.1.S1_at	zgc:55862	zgc:55862	zgc:55862	similar to cathepsin B	proteolysis /// regulation	proteolysis and peptidoly	---	---	cysteine-type endopeptid	cysteine-type endopeptidase activity		0.0007	4.19
Dr.967.1.S1_at	mmp9	---	matrix metalloproteinase	CDNA clone MGC:64165	proteolysis /// calcium ion	---	proteinaceous extracellul	---	---	---		0.0001	3.74
Dr.8723.1.S1_at	zgc:92903	Vtn	zgc:92903	similar to vitronectin	cell redox homeostasis	---	---	---	---	---		0.0001	3.37
Dr.5112.1.S2_at	sox11b	sox11b	SRY-box containing gene	SRY-box containing gene	regulation of transcriptio	regulation of transcriptio	---	---	DNA binding	DNA binding		0.0000	3.31
Dr.22517.1.S1_at	LOC566223	---	hypothetical LOC566223	Transcribed sequences	---	---	---	---	---	---		0.0000	3.31
Dr.8594.1.S1_at	LOC794531 /// LOC7974	---	zgc:100919 /// hypothetic	CDNA clone IMAGE:6959	transport	---	membrane attack comple	---	transporter activity /// lipi	---		0.0001	3.25
Dr.14307.1.S1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---		0.0002	3.14
Dr.21244.1.S1_at	LOC798012 /// ucp2	ucp2	uncoupling protein 2 /// si	uncoupling protein 2	transport /// mitochondria	transport /// mitochondria	membrane attack comple	mitochondrion /// membra	transporter activity /// bin	binding		0.0003	3.10
Dr.24763.1.S1_at	LOC795027	yy1	hypothetical protein LOC	YY1 transcription factor	---	---	---	nucleus	---	nucleic acid binding /// zinc ion bindi		0.0001	3.08
Dr.5112.1.S1_at	sox11b	sox11b	SRY-box containing gene	SRY-box containing gene	regulation of transcriptio	regulation of transcriptio	---	---	DNA binding	DNA binding		0.0003	3.08
Dr.839.2.S1_a_at	LOC571955	---	Similar to hCG1987869	Transcribed sequences	---	---	---	---	---	---		0.0006	3.01
Dr.17659.1.S1_at	LOC558956	wu:fc85f03	similar to ubquitin-like pr	wu:fc85f03	---	---	---	---	---	---		0.0021	2.96
Dr.19380.1.S1_at	LOC100002634 /// tmsb	LOC402820	thymosin, beta /// similar	beta-thymosin	cytoskeleton organizatio	---	cytoplasm /// cytoskeleto	---	actin binding	---		0.0001	2.95
Dr.1691.1.S1_at	rrm2	rrm2	ribonucleotide reductase	ribonucleotide reductase	DNA replication /// iron io	DNA replication /// deoxy	cytoplasm	---	ribonucleoside-diphospha	ribonucleoside-diphosphate reductas		0.0009	2.95
Dr.14307.1.S1_s_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---		0.0002	2.94
Dr.4748.1.S1_at	grn2	wu:fb14a12	granulin 2	wu:fb14a12	---	---	---	---	protease inhibitor activity	---		0.0266	2.94
Dr.14282.1.S1_at	atf3	zgc:55526	activating transcription fa	similar to activating transc	regulation of transcriptio	regulation of transcriptio	nucleus	nucleus	DNA binding /// transcript	DNA binding		0.0058	2.92
Dr.17784.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---		0.0008	2.86
Dr.1192.1.S1_at	ptgds	---	prostaglandin D2 syntha	MRNA for lipocalin-type p	lipid metabolic process //	---	---	---	retinoic acid binding /// pr	---		0.0011	2.79
Dr.16296.1.S1_a_at	LOC565189 /// LOC7950	---	hypothetical LOC565189	Transcribed sequences	---	---	---	---	---	---		0.0011	2.75
Dr.5820.1.S1_at	ctsll	---	cathepsin L, like	Transcribed sequence with	proteolysis	---	---	---	cysteine-type endopeptid	---		0.0554	2.61
Dr.13015.1.S1_at	lgals1l2	LOC405830	lectin, galactoside-bindin	proto galectin Gal1-L2	vasculature development	---	---	---	sugar binding /// galactos	---		0.0001	2.59
Dr.5677.1.S1_at	c6orf115	---	chromosome 6 open rea	CDNA clone IMAGE:6796	---	---	---	---	---	---		0.0001	2.55
Dr.25862.1.A1_at	LOC791953	zgc:73232	hypothetical protein LOC	wu:fj85f11	---	---	---	---	sugar binding	---		0.0012	2.53
Dr.1691.4.A1_at	kpna2 /// LOC793989 ///	---	karyopherin alpha 2 (RA	Transcribed sequence with	protein import into nucle	---	nucleus /// nuclear pore /	---	binding /// protein transp	---		0.0019	2.53
Dr.4416.1.A1_at	tubb5	tubb5	tubulin, beta 5	tubulin, beta 5	microtubule-based proce	microtubule-based move	cytoplasm /// cytoskeleto	microtubule	nucleotide binding /// GT	structural molecule activity		0.0002	2.51
Dr.4219.1.S1_at	zgc:154095	---	zgc:154095	Transcribed sequence with	---	---	---	---	catalytic activity /// kinase	---		0.0037	2.51
Dr.7608.2.S1_at	jun	zgc:65863	v-jun sarcoma virus 17 o	wu:fj36h07	regulation of transcriptio	---	nucleus	---	DNA binding /// transcript	---		0.0001	2.50
Dr.20010.2.A1_at	tuba8l	wu:fb03a02	tubulin, alpha 8 like	wu:fb03a02	microtubule-based proce	---	microtubule /// protein co	---	nucleotide binding /// GT	---		0.0008	2.49
Dr.3153.1.A1_at	zgc:109978	zgc:56113	zgc:109978	wu:fc31g07	---	---	---	---	calmodulin binding	---		0.0026	2.47
Dr.8283.1.S1_at	mibp	mibp	muscle-specific beta 1 in	muscle-specific beta 1 inte	integrin-mediated signali	integrin-mediated signali	---	---	kinase activity	uridine kinase activity /// ATP binding		0.0016	2.42
Dr.24753.1.S1_at	ccnd1 /// LOC562165	ccnd1	cyclin D1 /// similar to Cy	cyclin D1	cell cycle /// camera-type	regulation of cell cycle ///	nucleus	nucleus	---	---		0.0013	2.42
Dr.4268.1.S1_at	LOC100000085	---	similar to Lysosome-ass	Transcribed sequence with	---	---	---	---	---	---		0.0057	2.39
Dr.6431.1.S1_at	socs3	zgc:56537	suppressor of cytokine s	wu:fj09e12	ubiquitin cycle /// intracel	intracellular signaling cas	---	---	protein binding	---		0.0022	2.38
DrAffx.2.25.A1_at	LOC553977 /// zgc:1363	---	granulin 1 /// zgc:136318	Progranulin-1/progranulin-	---	---	---	---	protease inhibitor activity	---		0.0353	2.37
Dr.7787.1.S1_at	zgc:136826	---	zgc:136826	Transcribed sequence with	translation /// zinc ion tra	---	intracellular /// ribosome /	---	structural constituent of ri	---		0.0002	2.36
Dr.24753.1.S2_at	LOC562165	zgc:65820	similar to Cyclin D1	wu:fd21g02	cell cycle /// camera-type	---	nucleus	---	---	---		0.0002	2.35
Dr.16296.1.S1_x_at	LOC565189	---	hypothetical LOC565189	Transcribed sequences	---	---	---	---	---	---		0.0114	2.34
Dr.11147.2.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---		0.0076	2.34
Dr.7608.1.A1_at	jun	zgc:65863	v-jun sarcoma virus 17 o	wu:fj36h07	regulation of transcriptio	---	nucleus	---	DNA binding /// transcript	---		0.0004	2.34
Dr.4975.1.A1_at	wu:fb99e11	---	wu:fb99e11	Transcribed sequences	---	---	---	---	---	---		0.0003	2.30
Dr.1260.1.S1_at	anxa2a	anxa2a	annexin A2a	annexin A2a	calcium ion transport	---	---	---	phospholipase inhibitor a	phospholipase inhibitor activity /// cal		0.0076	2.27
Dr.26458.1.S1_at	zgc:64022	zgc:64022	zgc:64022	hypothetical protein MGC6	small GTPase mediated	small GTPase mediated	---	---	nucleotide binding /// GT	GTP binding		0.0138	2.24
Dr.20850.1.S1_at	fabp7a	fabp7	fatty acid binding protein	fatty acid binding protein 7	transport	transport	---	---	transporter activity /// bin	transporter activity /// binding /// lipid		0.0002	2.23
Dr.25257.1.A1_at	bhlhb3l	---	Basic helix-loop-helix do	Transcribed sequences	regulation of transcriptio	---	nucleus	---	DNA binding /// transcript	---		0.0092	2.21
Dr.4833.2.S1_at	zgc:112133	ccna2	zgc:112133	cyclin A2	mitosis	regulation of cell cycle ///	---	nucleus	---	---		0.0001	2.21
Dr.11010.1.S1_at	zgc:64003	zgc:64003	zgc:64003	hypothetical protein MGC6	immune response /// anti	immune response	membrane /// MHC class	membrane	---	---		0.0013	2.21
Dr.5809.1.A1_at	grna /// LOC791524	---	granulin a /// hypothetical	Granulin-A precursor, mR	---	---	---	---	protease inhibitor activity	---		0.0024	2.20
Dr.26422.1.A1_at	zgc:65794	---	zgc:65794	CDNA clone MGC:65794	actomyosin structure org	---	---	---	actin binding	---		0.0023	2.20
Dr.13699.1.S1_at	foxn4	foxn4	forkhead box N4	forkhead box N4	regulation of transcriptio	regulation of transcriptio	nucleus	nucleus	DNA binding /// transcript	transcription factor activity		0.0021	2.19
Dr.11274.1.A1_at	silvb	---	silver homolog (mouse)	Transcribed sequence with	---	---	---	---	---	---		0.0036	2.18
Dr.18396.1.S1_at	txnip	txnip	thioredoxin interacting p	thioredoxin interacting prot	---	---	---	---	---	---		0.0001	2.18
Dr.11310.2.S1_at	tuba1	tuba1	tubulin, alpha 1	tubulin, alpha 1	microtubule-based proce	microtubule-based move	microtubule /// protein co	microtubule	nucleotide binding /// GT	structural molecule activity		0.0004	2.18
Dr.964.1.A1_at	tnfrsf21	---	tumor necrosis factor rec	Transcribed sequences	signal transduction	---	---	---	receptor activity /// protei	---		0.0026	2.16
Dr.24055.1.S1_at	LOC563952	---	similar to CC chemokine-	Transcribed sequences	---	---	---	---	---	---		0.0001	2.15
Dr.3182.1.A1_at	wu:fc05b06	---	wu:fc05b06	Transcribed sequences	---	---	---	---	---	---		0.0061	2.14
Dr.26404.3.S1_at	LOC564072	tctp	hypothetical LOC564072	translationally controlled tu	---	---	---	cytoplasm	---	---		0.0020	2.13
Dr.23446.1.A1_at	LOC100004225	---	hypothetical protein LOC	CDNA clone IMAGE:6966	---	---	---	---	---	---		0.0026	2.13
Dr.8135.1.S1_at	psme1	psme1	proteasome activator su	proteasome activator subu	---	---	cytosol /// proteasome ac	proteasome activator co	proteasome activator acti	proteasome activator activity		0.0036	2.12
Dr.6924.1.S1_at	ahcy	ahcy	S-adenosylhomocysteine	S-adenosylhomocysteine	one-carbon compound m	one-carbon compound m	membrane /// integral to	---	catalytic activity /// adeno	adenosylhomocysteinase activity		0.0000	2.11
Dr.12817.1.A1_at	si:rp71-39b20.7	---	si:rp71-39b20.7	Transcribed sequence with	signal transduction /// res	---	---	---	receptor binding	---		0.0006	2.11
Dr.4049.1.S1_at	nutf2	---	nuclear transport factor 2	Transcribed sequence with	transport	---	intracellular	---	---	---		0.0011	2.10
Dr.1050.1.S1_at	LOC792382 /// zgc:1101	---	zgc:110113 /// hypothetic	Transcribed sequence with	---	---	---	---	---	---		0.0109	2.08
Dr.12145.1.A1_at	LOC794585	---	hypothetical protein LOC	Clone IMAGE:5601466, m	---	---	---	---	---	---		0.0030	2.07
Dr.16949.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---		0.0175	2.07
Dr.13301.1.S1_at	zgc:110339	---	zgc:110339	Transcribed sequence with	metabolic process	---	---	---	catalytic activity /// bindin	---		0.0004	2.05
Dr.4782.1.S1_at	ctsc	ctsc	cathepsin C	cathepsin C	proteolysis	---	---	---	cysteine-type endopeptid	---		0.0069	2.04
Dr.4932.1.S1_at	anxa4 /// LOC792474	anxa4	annexin A4 /// similar to a	annexin A4	calcium ion transport	---	---	---	calcium channel activity /	calcium ion binding /// calcium-depe		0.0010	2.04
Dr.25140.2.S1_x_at	icn	icn	ictacalcin	ictacalcin	---	---	---	---	calcium ion binding /// cal	calcium ion binding		0.0005	2.03
Dr.10228.1.A1_at	LOC560341	---	similar to c-Myc	Transcribed sequences	---	---	---	---	---	---		0.0067	2.03
Dr.5690.1.S1_at	wu:fc59b06	---	wu:fc59b06	Transcribed sequences	---	---	---	---	---	---		0.0088	2.03
Dr.25140.2.S1_at	icn	icn	ictacalcin	ictacalcin	---	---	---	---	calcium ion binding /// cal	calcium ion binding		0.0011	2.03
Dr.14011.1.S1_at	LOC572231	---	hypothetical LOC572231	Transcribed sequence with	protein folding	---	prefoldin complex	---	unfolded protein binding	---		0.0003	1.99
Dr.16385.1.A1_at	si:ch211-284a13.1	---	si:ch211-284a13.1	Transcribed sequences	---	---	---	---	---	---		0.0634	1.99
Dr.22797.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---		0.0051	1.97
Dr.21781.1.A1_at	wu:fc55f06	---	wu:fc55f06	Transcribed sequence	---	---	---	---	---	---		0.0075	1.96
Dr.301.1.S1_at	LOC799355	---	similar to Pfn2l protein	Transcribed sequence with	---	---	---	---	---	---		0.0014	1.96
Dr.5674.2.S1_at	LOC570638	zgc:73183	hypothetical LOC570638	wu:fa95b03	---	---	---	---	---	---		0.0005	1.95
Dr.16029.1.S1_at	hsd11b3 /// LOC1000067	zgc:56373	hydroxysteroid (11-beta)	hypothetical protein MGC5	metabolic process	metabolism	---	---	catalytic activity /// bindin	oxidoreductase activity		0.0282	1.94
Dr.11828.1.A1_at	zgc:77806	zgc:77806	zgc:77806	hypothetical protein zgc:77	---	---	---	---	---	---		0.0056	1.93
Dr.11335.1.S1_at	LOC561086	---	similar to putative adeny	Transcribed sequence with	---	---	---	---	---	---		0.0058	1.91
Dr.24922.2.S1_at	zgc:103420	---	zgc:103420	Transcribed sequence with	proteolysis	---	---	---	cysteine-type endopeptid	---		0.0023	1.91
Dr.7306.1.S1_at	scpep1	zgc:56081	serine carboxypeptidase	similar to retinoid-inducible	proteolysis	proteolysis and peptidoly	---	---	carboxypeptidase activity	catalytic activity /// serine carboxype		0.0061	1.90
Dr.7155.2.S1_a_at	LOC567446	---	similar to nucleolar and s	YF-9 mRNA for hypothetic	cell cycle /// mitosis /// ce	---	nucleus /// cytoplasm ///	---	DNA binding	---		0.0075	1.90
Dr.3432.1.S1_at	capg	wu:fb14e07	capping protein (actin fila	wu:fb14e07	---	---	---	---	actin binding	actin binding		0.0079	1.88
Dr.25378.1.A1_at	LOC100003788 /// LOC1	---	zgc:110540 /// similar to	Transcribed sequence with	nucleobase, nucleoside,	---	---	---	deoxycytidine kinase acti	---		0.0185	1.87
Dr.59.1.S1_at	anxa1a	anxa1a	annexin A1a	annexin A1a	calcium ion transport	---	---	---	phospholipase inhibitor a	phospholipase inhibitor activity /// cal		0.0681	1.87
Dr.3459.1.S1_at	cd63	cd163	Cd63 antigen	Cd63 antigen	---	---	membrane attack comple	---	---	---		0.0012	1.85
Dr.24379.1.S1_at	cdc2	cdc2	cell division cycle 2	cell division cycle 2	protein amino acid phosp	cytokinesis /// protein am	---	---	nucleotide binding /// prot	protein kinase activity /// protein seri		0.0149	1.85
Dr.314.1.S1_at	ascl1a	asha	achaete-scute complex-li	achaete scute homolog A	---	neurogenesis	nucleus /// nucleus	nucleus	DNA binding /// transcript	transcription factor activity		0.0158	1.83
Dr.12986.1.A1_a_at	fos	fos	v-fos FBJ murine osteos	v-fos FBJ murine osteosa	regulation of transcriptio	---	nucleus	---	DNA binding /// double-st	---		0.0314	1.83
Dr.6437.1.S1_at	ptpn6	ptpn6	protein tyrosine phospha	protein tyrosine phosphata	protein amino acid deph	protein amino acid deph	---	---	protein tyrosine phospha	phosphoprotein phosphatase activity		0.0077	1.83
Dr.5112.1.S3_at	sox11b	sox11b	SRY-box containing gene	SRY-box containing gene	regulation of transcriptio	regulation of transcriptio	---	---	DNA binding	DNA binding		0.0041	1.83
Dr.9743.2.S1_a_at	hmgb2	---	high-mobility group box 2	Transcribed sequence with	regulation of transcriptio	---	chromatin /// nucleus	---	DNA binding	---		0.0317	1.82
Dr.4788.1.S1_at	tax1bp3	---	Tax1 (human T-cell leuk	MRNA similar to Tax inter	convergent extension inv	---	---	---	protein binding	---		0.0004	1.82
Dr.20131.1.S1_at	crabp2a	crabp2	cellular retinoic acid bind	cellular retinoic acid bindin	transport	transport	---	---	transporter activity /// bin	transporter activity /// binding /// lipid		0.0305	1.81
Dr.25759.2.A1_a_at	ak2	ak2	adenylate kinase 2	adenylate kinase 2	nucleobase, nucleoside,	---	---	---	---	adenylate kinase activity /// ATP bin		0.0001	1.81
Dr.16296.1.S1_at	LOC565189	---	hypothetical LOC565189	Transcribed sequences	---	---	---	---	---	---		0.0365	1.81
Dr.25140.2.S1_a_at	icn /// zgc:171263	icn	ictacalcin /// zgc:171263	ictacalcin	---	---	---	---	calcium ion binding /// cal	calcium ion binding		0.0007	1.81
Dr.18825.1.S1_at	LOC796252	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---		0.4150	1.81
Dr.1047.1.S1_at	tyms	tyms	thymidylate synthase	thymidylate synthase	dTMP biosynthetic proce	dTMP biosynthesis /// nu	---	---	thymidylate synthase acti	thymidylate synthase activity /// met		0.0039	1.81
Dr.9809.2.S1_at	uhrf1	---	ubiquitin-like, containing	CDNA clone MGC:63539	protein modification proc	---	---	---	protein binding /// zinc io	---		0.0009	1.81
Dr.15991.1.S1_at	LOC100000332 /// LOC5	---	hypothetical LOC569520	Transcribed sequence with	---	---	---	---	---	---		0.0282	1.79
Dr.2490.1.A1_at	wu:fj66a01	zgc:66340	wu:fj66a01	wu:fb73e11	---	---	---	---	---	---		0.0168	1.78
Dr.13635.1.S1_at	nhp2l1	zgc:56265	NHP2 non-histone chrom	sb:cb127	ribosome biogenesis and	protein biosynthesis	ribonucleoprotein comple	intracellular /// ribosome	---	structural constituent of ribosome		0.0013	1.78
Dr.11310.2.S1_x_at	tuba1	tuba1	tubulin, alpha 1	tubulin, alpha 1	microtubule-based proce	microtubule-based move	microtubule /// protein co	microtubule	nucleotide binding /// GT	structural molecule activity		0.0089	1.78
Dr.6210.1.S1_at	zgc:165343	---	zgc:165343	Transcribed sequence with	---	---	---	---	---	---		0.0079	1.78
Dr.18287.1.S1_at	cx43.4	cx43.4	connexin 43.4	connexin 43.4	cell communication	cell communication	membrane attack comple	gap junction /// connexon	---	connexon channel activity		0.0005	1.78
Dr.2438.1.S1_at	LOC792272 /// zgc:9253	---	zgc:92530 /// hypothetica	Transcribed sequence with	proteolysis	---	---	---	carboxypeptidase activity	---		0.1251	1.78
Dr.5351.1.A1_at	MGC162200	---	hypothetical LOC558638	Transcribed sequences	---	---	---	---	---	---		0.0459	1.76
Dr.24758.2.S1_at	marcks	---	myristoylated alanine ric	CDNA clone IMAGE:26017	---	---	---	---	calmodulin binding /// kin	---		0.0002	1.74
Dr.19224.1.S1_at	aldob	aldob	aldolase b, fructose-bisp	aldolase b, fructose-bisph	glycolysis /// metabolic p	glycolysis	---	---	catalytic activity /// fructo	fructose-bisphosphate aldolase activ		0.0090	1.73
Dr.4376.1.S1_at	npc2	npc2	Niemann-Pick disease, t	Niemann-Pick disease, typ	negative regulation of sig	---	extracellular region /// sig	---	---	---		0.0183	1.73
Dr.17438.1.S1_at	LOC100006206	---	similar to TRAF2 binding	Transcribed sequences	---	---	---	---	---	---		0.0065	1.73
Dr.20778.1.S1_at	zgc:103456	---	zgc:103456	Transcribed sequence with	---	---	integral to membrane	---	---	---		0.0008	1.73
Dr.7590.1.A1_at	wu:fj68b05	---	wu:fj68b05	Transcribed sequences	---	---	---	---	---	---		0.0225	1.73
Dr.4878.1.S1_at	LOC558130	---	hypothetical LOC558130	Transcribed sequence with	---	---	---	---	---	---		0.1276	1.73
Dr.12551.1.S1_at	LOC569378	---	hypothetical LOC569378	Transcribed sequence with	---	---	---	---	---	---		0.0270	1.72
Dr.3502.1.S1_at	cdkn1c	---	cyclin-dependent kinase	Transcribed sequence with	cell fate specification /// c	---	nucleus	---	cyclin-dependent protein	---		0.0128	1.71
Dr.16014.1.S1_at	zgc:101897	---	zgc:101897	Transcribed sequence with	metabolic process	---	cytoplasm	---	glutathione transferase a	---		0.0122	1.70
Dr.11147.1.S1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---		0.0719	1.70
Dr.24852.1.S1_at	Slbp	---	similar to stem-loop bindi	CDNA clone IMAGE:5412	---	---	---	---	---	---		0.0027	1.70
Dr.14671.1.S1_at	birc5a	birc5a	baculoviral IAP repeat-c	baculoviral IAP repeat-con	angiogenesis /// anti-apo	anti-apoptosis	intracellular	intracellular	---	---		0.0047	1.70
Dr.3337.1.S1_at	zgc:111795	---	zgc:111795	Transcribed sequence with	DNA repair /// zinc ion tra	---	nucleus	---	zinc ion binding /// acyltra	---		0.0123	1.70
Dr.1320.1.S1_at	nme2	nme2	non-metastatic cells 2, p	non-metastatic cells 2, pro	GTP biosynthetic proces	GTP biosynthesis /// UT	---	---	nucleotide binding /// ma	nucleoside-diphosphate kinase activ		0.0013	1.69
Dr.9210.2.S1_a_at	LOC554736 /// zgc:7320	zgc:73201	zgc:73201 /// hypothetica	wu:fc18b03	amino acid biosynthetic	---	nucleus /// cytoplasm ///	---	protein binding /// nickel	---		0.0011	1.69
Dr.22685.1.A1_at	zgc:91929	---	zgc:91929	Transcribed sequence	protein amino acid deph	---	---	---	protein tyrosine phospha	---		0.0073	1.68
Dr.18310.2.A1_at	cry-dash	zcry-dash	cryptochrome DASH	cryptochrome dash	photoreactive repair /// D	---	---	---	damaged DNA binding //	---		0.1063	1.67
Dr.15881.1.S1_at	rbp1b	rbp1b	retinol binding protein 1b,	cellular retinol-binding prot	transport	---	---	---	transporter activity /// bin	---		0.0269	1.67
Dr.5123.1.A1_at	tjp2b	---	tight junction protein 2b (	Transcribed sequence with	---	---	---	---	protein binding	---		0.0057	1.67
Dr.4556.1.S1_at	rpa2	rpa2	replication protein A2	replication protein A2	nucleotide-excision repai	nucleotide-excision repai	---	---	nucleic acid binding /// si	nucleic acid binding /// single-strand		0.0063	1.66
Dr.17331.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---		0.0784	1.66
Dr.25214.1.A1_at	cyp24a1l	---	cytochrome P450, family	Transcribed sequence with	electron transport /// hem	---	mitochondrion	---	monooxygenase activity /	---		0.0922	1.65
Dr.11310.3.S1_at	LOC573216 /// zgc:1232	tuba1	similar to tubulin alpha ///	tubulin, alpha 1	microtubule-based proce	microtubule-based move	microtubule /// protein co	microtubule	nucleotide binding /// GT	structural molecule activity		0.0357	1.65
Dr.737.1.A1_at	junbl	wu:fj44e11	jun B proto-oncogene, lik	wu:fj44e11	regulation of transcriptio	---	nucleus	---	DNA binding /// transcript	---		0.0460	1.65
Dr.24858.1.S1_at	LOC100003788 /// zgc:1	---	zgc:110540 /// similar to	Transcribed sequence with	nucleobase, nucleoside,	---	---	---	deoxycytidine kinase acti	---		0.0075	1.65
Dr.9659.1.S1_at	gng5	---	guanine nucleotide bindi	Clone RK133A4G08 guan	nucleosome assembly ///	---	nucleosome /// nucleus //	---	DNA binding /// signal tra	---		0.0003	1.63
Dr.25190.1.S1_at	ccna2	ccna2	cyclin A2	cyclin A2	cell cycle /// cell division	regulation of cell cycle ///	nucleus	nucleus	---	---		0.0349	1.63
Dr.26405.1.S1_at	sdc4l	---	syndecan 4 like	Transcribed sequence with	cell adhesion /// negative	---	signal recognition particle	---	cytoskeletal protein bindi	---		0.0118	1.62
Dr.683.1.A1_at	wu:fa17f05	---	wu:fa17f05	Transcribed sequences	---	---	---	---	---	---		0.0869	1.62
Dr.17450.1.A1_at	zgc:63663	zgc:63663	zgc:63663	hypothetical protein MGC6	---	---	---	---	nucleotide binding /// AT	---		0.0362	1.62
Dr.25714.1.A1_at	ctssb.2	zgc:66318	cathepsin S, b.2	hypothetical protein MGC6	proteolysis	purine nucleotide biosynt	---	---	cysteine-type endopeptid	adenylosuccinate synthase activity //		0.0297	1.62
Dr.955.1.A1_at	LOC562529	---	hypothetical LOC562529	Transcribed sequence with	---	---	---	---	---	---		0.0255	1.61
Dr.7105.1.S1_at	arpc1b	---	actin related protein 2/3 c	CDNA clone MGC:64056	---	---	---	---	---	---		0.0154	1.61
Dr.1077.1.S1_at	zgc:153129	---	zgc:153129	Transcribed sequence with	---	---	intracellular	---	endopeptidase inhibitor a	---		0.0153	1.60
Dr.14161.1.S1_at	LOC562246	---	similar to chemokine CX	Transcribed sequence with	---	---	---	---	---	---		0.0989	1.60
Dr.17141.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---		0.0023	1.59
Dr.12552.1.S1_at	crabp1a	crabp1	cellular retinoic acid bind	cellular retinoic acid bindin	transport	transport	---	---	transporter activity /// bin	transporter activity /// binding /// lipid		0.0078	1.58
Dr.982.1.S1_at	tmem49	wu:fb05d08	transmembrane protein 4	wu:fb05d08	---	---	membrane attack comple	---	---	---		0.0338	1.58
Dr.1691.6.A1_at	LOC554742	rrm2	similar to Family with seq	ribonucleotide reductase	---	DNA replication /// deoxy	---	---	---	ribonucleoside-diphosphate reductas		0.0071	1.58
Dr.9617.1.A1_at	zgc:77038	---	zgc:77038	CDNA clone MGC:77038	ubiquitin cycle /// intracel	---	---	---	protein binding	---		0.0982	1.57
Dr.17357.1.A1_at	h2afx	zgc:56329	H2A histone family, mem	similar to H2A histone fam	DNA repair /// DNA reco	nucleosome assembly ///	nucleosome /// nucleus //	nucleosome /// nucleus	DNA binding	DNA binding		0.0079	1.56
Dr.6401.1.S1_at	LOC794601	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---		0.0695	1.56
Dr.804.1.S1_at	sae1	---	SUMO1 activating enzym	###################	protein modification proc	---	nucleus	---	catalytic activity /// bindin	---		0.0437	1.56
Dr.4759.1.S1_at	ifi30	---	interferon gamma induci	Transcribed sequence with	---	---	---	---	---	---		0.0307	1.56
Dr.25291.1.S1_at	LOC792781	---	hypothetical protein LOC	D93 mRNA, 3'UTR, partial	---	---	---	---	---	---		0.0028	1.55
Dr.20115.1.S1_at	cfl1	---	cofilin 1 (non-muscle)	MRNA similar to cofilin 1 (	---	---	intracellular	---	actin binding	---		0.1030	1.54
Dr.21051.1.S1_at	zgc:56310	zgc:56310	zgc:56310	similar to replication protei	---	---	---	---	---	nucleic acid binding		0.0085	1.54

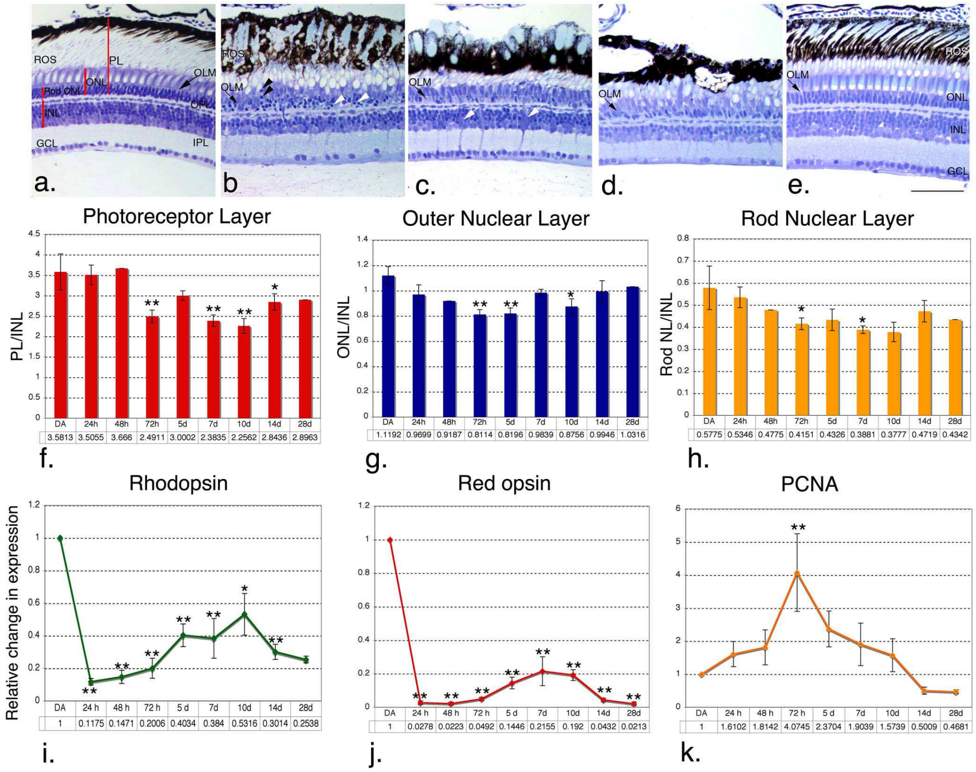
Dr.11384.1.A1_at	LOC795119	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.0065	1.54
Dr.26511.1.S1_at	LOC556820 /// zgc:1365	zgc:56640	hypothetical LOC556820	wu:fa93d05	translation	protein biosynthesis	intracellular /// ribosome	intracellular /// ribosome	structural constituent of ri	structural constituent of ribosome	0.0041	1.53
Dr.12080.1.A1_at	LOC100001628	---	similar to LOC443705 pro	Transcribed sequence with	---	---	---	---	---	---	0.0026	1.53
Dr.25182.2.S1_at	zgc:101026	be1	zgc:101026	embryonic 1 beta-globin (b	cell cycle	---	---	---	cyclin-dependent protein	---	0.0602	1.53
Dr.23788.2.A1_at	rplp2l	gstp1	ribosomal protein, large F	glutathione S-transferase p	translational elongation	metabolism	intracellular /// ribosome	---	structural constituent of ri	glutathione transferase activity /// tra	0.0021	1.52
Dr.20029.1.A1_at	LOC796294 /// tfpia	tfpia	tissue factor pathway inh	tissue factor pathway inhib	blood coagulation	blood coagulation	extracellular region	extracellular	serine-type endopeptidas	serine-type endopeptidase inhibitor a	0.0693	1.51
Dr.820.1.A1_at	tnfrsf21	---	tumor necrosis factor rec	Transcribed sequences	signal transduction	---	---	---	receptor activity /// protei	---	0.1804	1.51
Dr.7103.1.S1_at	id3	id3	inhibitor of DNA binding 3	inhibitor of DNA binding 3	regulation of transcription	---	nucleus	---	transcription regulator ac	---	0.0282	1.51
Dr.14041.1.S1_at	c1qc	---	complement component	Transcribed sequence with	phosphate transport /// co	---	cytoplasm	---	---	---	0.0626	1.51
Dr.4867.1.A1_at	LOC793231	---	similar to beta-microsemi	Transcribed sequences	---	---	---	---	---	---	0.1726	1.51
Dr.297.1.S1_at	ssr3	zgc:56300	signal sequence receptor	wu:fb01d07	cotranslational protein ta	---	translocon complex /// int	---	receptor activity	receptor activity	0.0010	1.50
Dr.5578.2.S1_a_at	odc1	odc1	ornithine decarboxylase	ornithine decarboxylase 1	polyamine biosynthetic p	---	---	---	catalytic activity	catalytic activity	0.0068	1.50
Dr.808.1.S1_at	h2afza	H2AV	histone 2A family membe	similar to H2A histone fami	nucleosome assembly	---	nucleosome /// nucleus //	---	DNA binding	---	0.0028	1.49
Dr.5476.1.A1_at	si:ch211-51e12.5	---	si:ch211-51e12.5	Transcribed sequences	intracellular signaling cas	---	---	---	---	---	0.1932	1.49
Dr.18661.1.A1_at	LOC564023	---	similar to CG6282-PA, is	Transcribed sequence with	lipid metabolic process	---	cytoplasm /// integral to m	---	oxidoreductase activity, a	---	0.0097	1.49
Dr.22408.1.A1_at	zgc:153950	---	zgc:153950	Transcribed sequences	---	---	membrane attack comple	---	---	---	0.0112	1.49
Dr.8587.1.A2_at	igfbp1	igfbp1	insulin-like growth factor	insulin-like growth factor bi	regulation of cell growth /	regulation of cell growth /	extracellular region	extracellular	insulin-like growth factor	insulin-like growth factor binding	0.0165	1.48
Dr.11425.1.S1_at	psat1	zgc:55738	phosphoserine aminotran	wu:fi15b02	L-serine biosynthetic pro	L-serine biosynthesis /// r	---	---	catalytic activity /// transa	transaminase activity /// transferase a	0.0291	1.48
Dr.5399.1.S1_at	zgc:91854	---	zgc:91854	Transcribed sequence with	metabolic process	---	---	---	catalytic activity /// bindin	---	0.0059	1.48
Dr.3374.2.S1_at	ctsba	---	cathepsin B, a	CDNA clone MGC:65809 I	proteolysis /// regulation	---	---	---	cysteine-type endopeptid	---	0.0042	1.48
Dr.5040.1.S1_at	cyb5a	---	cytochrome b5 type A (m	CDNA clone MGC:64123 I	heme biosynthetic proces	---	---	---	iron ion binding /// heme l	---	0.0143	1.48
Dr.12775.1.A1_at	zgc:73226	nip2	zgc:73226	BCL2/adenovirus E1b 19 k	positive regulation of apo	---	mitochondrial envelope //	---	---	---	0.0217	1.47
Dr.21056.1.S1_at	zgc:77734	zgc:56108	zgc:77734	wu:fb63e10	---	---	---	---	acyl-CoA binding /// bindi	acyl-CoA binding	0.0027	1.47
Dr.9654.1.A1_at	ppia	wu:fb15a05	peptidylprolyl isomerase	wu:fb15a05	protein folding	protein folding	---	---	peptidyl-prolyl cis-trans is	isomerase activity	0.0434	1.47
Dr.9329.1.S1_at	LOC561168 /// zgc:1533	---	hypothetical LOC561168	Transcribed sequence with	---	---	---	---	---	---	0.0026	1.46
Dr.2291.1.S1_at	mcm2	mcm2	MCM2 minichromosome	MCM2 minichromosome m	DNA replication initiation	DNA replication initiation	nucleus	nucleus	nucleotide binding /// DN	DNA binding /// ATP binding /// DNA-	0.0498	1.46
Dr.23441.1.S1_at	LOC791831 /// zgc:8564	---	zgc:85644 /// hypothetica	CDNA clone MGC:85644 I	---	---	---	---	---	---	0.0524	1.45
Dr.18349.1.A1_at	LOC558047 /// zgc:6602	zgc:66026	zgc:66026 /// hypothetica	N-acylsphingosine amidoh	---	---	---	---	---	---	0.1826	1.45
Dr.25673.1.S1_at	cdc25	mdkb	cdc25	midkine-related growth fac	M phase of mitotic cell cy	brain development /// sec	intracellular	extracellular	protein tyrosine phosphat	growth factor activity	0.0495	1.45
Dr.23911.1.A1_at	LOC100000090 /// slc20a	---	solute carrier family 20, n	CDNA clone MGC:85672 I	transport /// phosphate tr	---	membrane attack comple	---	inorganic phosphate tran	---	0.1636	1.45
Dr.9743.1.S1_at	hmgb2	---	high-mobility group box 2	Transcribed sequence with	regulation of transcription	---	chromatin /// nucleus	---	DNA binding	---	0.0122	1.44
Dr.973.1.S1_at	LOC559276	---	similar to AHNAK nucleo	Transcribed sequence with	---	---	---	---	protein binding	---	0.0595	1.44
Dr.8109.1.S1_at	lcp1	lcp1	lymphocyte cytosolic plas	lymphocyte cytosolic plasti	calcium ion transport	---	cytoplasm	---	actin binding /// calcium c	actin binding	0.1213	1.44
Dr.19532.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.0091	1.43
Dr.4042.1.A1_at	LOC799242 /// zgc:1583	---	zgc:158367 /// hypothetic	Transcribed sequence with	---	---	intracellular	---	nucleic acid binding /// zi	---	0.0501	1.43
Dr.20555.1.S2_s_at	anx /// anxa5	anxa5	annexin /// annexin A5	annexin A5	calcium ion transport /// n	---	cytoplasm	cytoplasm	calcium channel activity /	calcium ion binding /// calcium-deper	0.0429	1.42
Dr.1400.1.S1_at	zgc:77702	zgc:77702	zgc:77702	hypothetical protein MGC7	translation	---	intracellular /// ribosome	---	structural constituent of ri	---	0.0017	1.42
Dr.23829.1.A1_at	---	---	---	---	carbohydrate transport	---	membrane /// integral to	---	transporter activity /// sug	---	0.0174	1.41
Dr.3407.1.A1_at	LOC567110	---	similar to Col9a3-prov pr	CDNA clone IMAGE:6970	---	---	---	---	---	---	0.1307	1.41
Dr.4416.3.A1_at	tubb5	tubb5	Tubulin, beta 5	tubulin, beta 5	microtubule-based proce	microtubule-based mover	cytoplasm /// cytoskeleto	microtubule	nucleotide binding /// GT	structural molecule activity	0.0164	1.40
Dr.5410.1.A1_at	ugt1aa	---	UDP glucuronosyltransfe	Transcribed sequences	metabolic process	---	---	---	transferase activity /// tra	---	0.0912	1.40
Dr.20052.1.S1_at	LOC100001907 /// LOC7	---	peptidylprolyl isomerase	CDNA clone MGC:73214 I	protein folding	---	---	---	peptidyl-prolyl cis-trans is	---	0.0040	1.40
Dr.15059.1.S1_at	zgc:56567	---	zgc:56567	MRNA similar to elongation	---	---	integral to membrane	---	---	---	0.1818	1.40
Dr.781.1.S1_at	mibp2	mibp2	muscle-specific beta 1 in	muscle-specific beta 1 inte	integrin-mediated signali	integrin-mediated signali	---	---	uridine kinase activity ///	uridine kinase activity /// ATP binding	0.0022	1.40
Dr.3211.1.A1_at	LOC571720	---	similar to kainate recepto	Transcribed sequence with	---	---	---	---	---	---	0.0074	1.40
Dr.15783.1.S1_at	zgc:92630	---	zgc:92630	Transcribed sequence with	metabolic process	---	---	---	catalytic activity /// bindin	---	0.0136	1.40
Dr.16564.1.S1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.0120	1.39
Dr.784.1.S1_at	mcm3	mcm3	MCM3 minichromosome	MCM3 minichromosome m	DNA replication initiation	DNA replication initiation	nucleus	nucleus	nucleotide binding /// DN	DNA binding /// ATP binding /// DNA-	0.0140	1.39
Dr.5589.1.S1_at	zgc:86726	---	zgc:86726	Transcribed sequence with	vesicle-mediated transpo	---	membrane attack comple	---	---	---	0.0059	1.39
Dr.11718.1.S1_at	zgc:123333	---	zgc:123333	Transcribed sequence with	carbohydrate metabolic p	---	---	---	catalytic activity /// hydrol	---	0.0594	1.39
Dr.358.1.A1_at	tspan7	---	tetraspanin 7	CDNA clone MGC:63823 I	---	---	membrane attack comple	---	---	---	0.0138	1.39
Dr.1372.1.S1_at	krt18	krt18	keratin 18	keratin 18	---	---	intermediate filament	intermediate filament	structural molecule activi	structural molecule activity	0.3374	1.39
Dr.14213.1.A1_at	---	---	Transcribed locus, strong	Transcribed sequences	---	---	---	---	---	---	0.0590	1.38
Dr.16685.1.S1_at	LOC100004443 /// LOC1	---	zgc:92656 /// hypothetica	Transcribed sequence with	---	---	---	---	---	---	0.0009	1.38
Dr.6804.1.A1_at	LOC565636 /// LOC7934	---	similar to g-RICH	MRNA for hypothetical pro	---	---	---	---	---	---	0.0692	1.37
Dr.21921.1.A1_at	zgc:103654	---	zgc:103654	Transcribed sequence with	metabolic process	---	---	---	catalytic activity /// bindin	---	0.0225	1.37
Dr.1280.1.A1_at	cebpd	cebpd	CCAAT/enhancer binding	CCAAT/enhancer binding p	regulation of transcription	regulation of transcription	nucleus	nucleus	DNA binding /// transcript	DNA binding	0.1597	1.37
Dr.1116.1.S1_at	LOC100007066 /// si:dke	---	si:dkey-78d16.1 /// hypot	Transcribed sequence with	---	---	---	---	calcium ion binding	---	0.2110	1.37
Dr.24562.1.S1_a_at	LOC799075 /// mvp	mvp	major vault protein /// sim	major vault protein	---	---	cytoplasm /// ribonucleop	---	---	---	0.1415	1.36
Dr.17325.1.S1_at	zgc:56530	zgc:56530	zgc:56530	similar to cystatin B (stefin	---	---	intracellular	intracellular	endopeptidase inhibitor a	endopeptidase inhibitor activity /// cy	0.1712	1.36
Dr.1348.1.S1_at	pcna	pcna	proliferating cell nuclear a	proliferating cell nuclear an	DNA replication /// regula	DNA replication /// regula	nucleus /// nucleus /// PC	nucleus /// delta-DNA pol	DNA binding /// DNA poly	DNA binding /// DNA polymerase pro	0.0010	1.36
Dr.20805.1.S1_at	bzw1l	---	basic leucine zipper and	MRNA similar to basic leuc	transcription /// transcripti	---	---	---	translation initiation facto	---	0.1990	1.36
Dr.26392.1.A1_at	sdc4l	---	syndecan 4 like	Transcribed sequence with	cell adhesion /// negative	---	signal recognition particle	---	cytoskeletal protein bindi	---	0.0970	1.35
Dr.8198.1.A1_at	LOC791823	krml2	hypothetical protein LOC	Kreisler (mouse) maf-relate	regulation of transcription	regulation of transcription	nucleus	nucleus	DNA binding /// transcript	DNA binding	0.3529	1.35
Dr.9515.1.A1_at	coro1a	coro1a	coronin, actin binding pro	coronin, actin binding prote	---	---	---	---	---	---	0.1418	1.35
Dr.20170.1.S1_at	dad1	---	defender against cell dea	CDNA clone MGC:66204 I	---	---	---	---	---	---	0.0679	1.34
Dr.3342.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0900	1.34
Dr.5005.2.S1_at	wu:fb95e12	---	wu:fb95e12	Transcribed sequence with	---	---	---	---	---	---	0.0288	1.33
Dr.9110.1.A1_at	LOC100003688 /// LOC5	---	hypothetical LOC567253	Transcribed sequence with	---	---	---	---	---	---	0.0405	1.33
Dr.4828.2.A1_at	arf1	arf1	ADP-ribosylation factor 1	ADP-ribosylation factor 1	small GTPase mediated	small GTPase mediated	intracellular	---	nucleotide binding /// GT	GTP binding	0.0664	1.32
Dr.7311.1.S1_at	gnl3	---	guanine nucleotide bindir	Transcribed sequence with	regulation of cell prolifera	---	intracellular /// nucleus ///	---	nucleotide binding /// prot	---	0.2587	1.32
Dr.12699.1.S1_at	wu:fc44b02	---	wu:fc44b02	Transcribed sequences	---	---	---	---	---	---	0.0606	1.32
Dr.828.1.A1_at	zgc:77115	---	zgc:77115	CDNA clone MGC:77115 I	cell cycle /// mitosis /// ce	---	nucleus	---	---	---	0.0080	1.32
Dr.880.1.A1_at	ltb4dh	---	leukotriene B4 12-hydrox	Transcribed sequence with	metabolic process	---	---	---	catalytic activity /// bindin	---	0.1477	1.32
Dr.4796.1.A1_at	casp3a	---	caspase 3, apoptosis-rela	Transcribed sequences	proteolysis /// apoptosis /	---	---	---	endopeptidase inhibitor a	---	0.1458	1.32
Dr.20010.4.S1_at	cdca8l	---	cell division cycle associa	Transcribed sequence with	cell cycle /// mitosis /// ce	---	chromosome, pericentric	---	---	---	0.1183	1.32
Dr.8587.1.A1_at	igfbp1	igfbp1	insulin-like growth factor	insulin-like growth factor bi	regulation of cell growth /	regulation of cell growth /	extracellular region	extracellular	insulin-like growth factor	insulin-like growth factor binding	0.3094	1.32
Dr.9616.1.A1_at	wu:fj94h02	---	wu:fj94h02	Transcribed sequences	---	---	---	---	---	---	0.1142	1.31
Dr.3123.1.A1_at	zfand5a	---	zinc finger, AN1-type dor	CDNA clone MGC:73363 I	zinc ion transport	---	---	---	DNA binding /// zinc ion b	---	0.0455	1.31
Dr.7171.1.S1_at	gpt2	GPT2	glutamic pyruvate transa	similar to glutamic pyruvate	biosynthetic process	---	---	---	catalytic activity /// alanin	---	0.3964	1.30
Dr.5372.9.S1_s_at	her4.2	---	hairy-related 4.2	MRNA similar to hairy and	somite specification /// re	---	nucleus	---	DNA binding /// double-st	---	0.1117	1.30
Dr.2813.1.S1_at	zgc:55461	---	zgc:55461	CDNA clone MGC:55461 I	microtubule-based proce	---	cytoplasm /// microtubule	---	nucleotide binding /// GT	---	0.2003	1.30
Dr.7590.2.S1_at	wu:fj68b05	---	Wu:fj68b05	Transcribed sequences	---	---	---	---	---	---	0.5774	1.30
Dr.144.1.A1_at	wu:fb79b02	---	wu:fb79b02	Transcribed sequences	---	---	---	---	---	---	0.1720	1.29
Dr.7340.1.A1_at	slc16a9a	zgc:64089	solute carrier family 16 (r	hypothetical protein MGC6	transport	transport	integral to membrane	integral to membrane	transporter activity	transporter activity	0.0368	1.29
Dr.10639.1.S1_at	LOC100002041 /// scinla	gsn	scinderin like a /// similar	gelsolin (amyloidosis, Finni	eye development /// brair	---	---	---	actin binding	actin binding	0.5393	1.29
Dr.5186.1.A1_at	si:dkey-222f8.3	---	si:dkey-222f8.3	Transcribed sequence with	---	---	---	---	---	---	0.3008	1.29
Dr.10201.1.S1_at	sepw1	sepw1	selenoprotein W, 1	selenoprotein W, 1	cell redox homeostasis	---	---	---	selenium binding	---	0.0185	1.28
Dr.20538.1.A1_at	LOC554736 /// zgc:7320	zgc:73201	zgc:73201 /// hypothetica	wu:fc18b03	amino acid biosynthetic p	---	nucleus /// cytoplasm /// p	---	protein binding /// nickel i	---	0.2230	1.28
Dr.17446.1.S1_at	phf5a	phf5a	PHD finger protein 5A	PHD finger protein 5A	---	---	---	---	---	---	0.3919	1.28
Dr.14988.1.S1_at	snrpd3l	---	small nuclear ribonucleop	Transcribed sequence with	mRNA metabolic process	---	ribonucleoprotein comple	---	nucleic acid binding	---	0.0173	1.28
Dr.3763.1.S1_at	lima1	eplin	LIM domain and actin bin	epithelial protein lost in nec	zinc ion transport	---	---	---	zinc ion binding /// metal	---	0.0428	1.28
Dr.2536.1.S1_at	itm2bl	---	integral membrane protei	CDNA clone MGC:64142 I	---	---	---	---	---	---	0.2388	1.28
Dr.24146.1.S1_at	slc16a9b	---	solute carrier family 16 (r	Transcribed sequences	transport	---	integral to membrane	---	transporter activity	---	0.0542	1.28
Dr.6332.1.S1_at	eif3h	---	eukaryotic translation init	Transcribed sequence with	---	---	---	---	translation initiation facto	---	0.0580	1.27
Dr.14477.1.S1_at	ssr4	---	signal sequence receptor	Transcribed sequence with	---	---	endoplasmic reticulum ///	---	receptor activity	---	0.0159	1.27
Dr.5802.1.S1_at	LOC563410	---	hypothetical LOC563410	Transcribed sequence with	---	---	---	---	---	---	0.1723	1.27
Dr.16174.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.6519	1.27
Dr.6581.1.A1_at	zgc:63587	zgc:63587	zgc:63587	hypothetical protein MGC6	cell cycle	cell cycle	---	---	nucleotide binding /// GT	GTP binding	0.0586	1.27
Dr.1081.1.S1_at	eef1b2	zgc:56277	eukaryotic translation elo	wu:fj06d02	translation /// translationa	translational elongation	eukaryotic translation elo	eukaryotic translation elo	translation elongation fac	translation elongation factor activity	0.0288	1.27
Dr.3422.1.S1_at	LOC564334	---	similar to LOC496019 pro	Transcribed sequence with	---	---	---	---	---	---	0.1192	1.27
Dr.20822.1.S1_at	rab13	rab13	RAB13, member RAS on	RAB13, member RAS onc	regulation of transcription	two-component signal tra	intracellular	---	nucleotide binding /// ATP	DNA binding /// GTP binding	0.2108	1.26
Dr.914.1.A1_a_at	irf11 /// LOC792160	IRF1	interferon regulatory fact	interferon regulatory factor	regulation of transcription	---	nucleus	---	transcription factor activit	---	0.1709	1.26
Dr.541.1.S1_at	id1	id6	inhibitor of DNA binding 1	inhibitor of DNA binding 6	regulation of transcription	---	nucleus	---	DNA binding /// transcript	---	0.0594	1.26
Dr.1202.2.S1_at	rps12	zgc:73055	ribosomal protein S12	wu:fa95a02	translation	---	intracellular /// ribosome /	---	structural constituent of ri	---	0.0049	1.26
Dr.11651.1.S1_at	mcm5	mcm5	MCM5 minichromosome	MCM5 minichromosome m	mitotic cell cycle /// DNA	DNA replication initiation	nucleus	nucleus	nucleotide binding /// DN	DNA binding /// ATP binding /// DNA-	0.0810	1.25
Dr.126.1.A1_at	wu:fb12h08	---	wu:fb12h08	Transcribed sequences	---	---	---	---	---	---	0.2234	1.25
Dr.473.1.S1_at	inhbb	inhbb	inhibin, beta B	inhibin, beta B	oocyte differentiation /// g	electron transport /// cell	extracellular region	extracellular	hormone activity /// growt	hormone activity /// electron transpor	0.4130	1.25
Dr.25051.1.S2_at	lmnb1	lmnb1	lamin B1	lamin B1	---	---	intermediate filament	intermediate filament	structural molecule activi	structural molecule activity	0.1292	1.25
Dr.7564.1.S1_at	LOC798137 /// scamp2	---	secretory carrier membra	MRNA similar to secretory	protein transport	---	integral to membrane	---	---	---	0.1293	1.25
Dr.400.1.A1_at	sp2	---	Sp2 protein	Transcribed sequence with	---	---	intracellular	---	nucleic acid binding /// zi	---	0.1569	1.25
Dr.10453.1.S1_at	atoh7	atoh7	atonal homolog 7	atonal homolog 7	---	regulation of cell cycle ///	nucleus	---	DNA binding /// transcript	---	0.0768	1.24
Dr.2677.1.S1_at	LOC793857	---	similar to Wu:fc25c04 pro	Transcribed sequences	---	---	---	---	---	---	0.1388	1.24
Dr.20340.1.A1_at	zgc:77235	zgc:77235	zgc:77235	wu:fa93g12	translation	---	intracellular /// ribosome /	---	structural constituent of ri	---	0.0297	1.24
Dr.1131.2.S1_at	zgc:110340	---	zgc:110340	Transcribed sequence with	---	---	---	---	---	---	0.3314	1.24
Dr.17599.1.A1_at	LOC558540	---	similar to transcriptional r	Transcribed sequences	regulation of transcription	---	---	---	DNA binding	---	0.1469	1.24
Dr.13132.1.A1_at	akr1a1b	---	aldo-keto reductase famil	Transcribed sequence with	---	---	---	---	oxidoreductase activity	---	0.0445	1.24
Dr.10330.1.S1_at	cry2b	cry2b	cryptochrome 2b	cryptochrome 2b	DNA repair /// transport	DNA repair /// transport	membrane	membrane	DNA photolyase activity /	DNA photolyase activity /// transporte	0.0960	1.24
Dr.25576.1.A1_at	LOC100003388 /// LOC1	crabp2	hypothetical protein LOC	cellular retinoic acid bindin	---	transport	---	---	---	transporter activity /// binding /// lipid	0.2185	1.24
Dr.4829.1.A1_at	alas1	alas1	aminolevulinate, delta-, s	aminolevulinate, delta-, syn	metabolic process /// bios	heme biosynthesis /// me	---	---	catalytic activity /// 5-ami	5-aminolevulinate synthase activity /	0.0706	1.23
Dr.1108.1.S1_at	ddx39b	---	DEAD (Asp-Glu-Ala-Asp)	CDNA clone MGC:55433 I	---	---	---	---	nucleic acid binding /// he	---	0.0270	1.23
Dr.23975.1.A1_at	zgc:63471	zgc:63471	zgc:63471	wu:fi06a10	small GTPase mediated	small GTPase mediated	---	---	nucleotide binding /// GT	GTP binding	0.0916	1.23
Dr.12986.1.A1_at	fos	fos	v-fos FBJ murine osteosa	v-fos FBJ murine osteosar	regulation of transcription	---	nucleus	---	DNA binding /// double-st	---	0.0412	1.23
Dr.19902.1.S1_at	ctsl1a	ctsla	cathepsin L1, a	cathepsin L, a	proteolysis	proteolysis and peptidoly	---	---	cysteine-type endopeptid	cysteine-type endopeptidase activity	0.0773	1.23
Dr.16938.1.A1_at	---	---	Transcribed locus	---	---	---	---	---	---	---	0.3200	1.23
Dr.24885.1.S1_a_at	snrpfl	---	small nuclear ribonucleop	Transcribed sequence with	mRNA metabolic process	---	ribonucleoprotein comple	---	nucleic acid binding	---	0.0217	1.22
Dr.908.1.S1_at	eef2l	eef2l	eukaryotic translation elo	eukaryotic translation elon	embryonic development	protein biosynthesis /// tra	---	---	nucleotide binding /// tran	translation elongation factor activity /	0.0076	1.22
Dr.4573.1.A1_at	zgc:92326	---	zgc:92326	Clone RK009A2G07 galac	---	---	---	---	sugar binding	---	0.5340	1.22
Dr.1259.1.A1_at	wu:fa98e11	---	wu:fa98e11	Transcribed sequences	---	---	---	---	---	---	0.0663	1.22
Dr.6609.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---	0.0168	1.22
Dr.1398.1.S1_at	LOC792219 /// zgc:5609	---	zgc:56095 /// hypothetica	CDNA clone MGC:56095 I	iron ion transport /// cellul	---	---	---	binding /// ferric iron bindi	---	0.0334	1.21
Dr.1438.1.S1_at	dut	---	dUTP pyrophosphatase	Transcribed sequence with	nucleotide metabolic pro	---	---	---	hydrolase activity	---	0.0558	1.21
Dr.6798.1.S1_at	cxcr4b	cxcr4b	chemokine (C-X-C motif)	chemokine (C-X-C motif), r	---	G-protein coupled recept	membrane /// integral to	integral to membrane	rhodopsin-like receptor a	rhodopsin-like receptor activity /// G-	0.3466	1.21
Dr.7790.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0120	1.21
Dr.1506.1.S1_at	LOC100003787 /// nola2	wu:fb36b10	nucleolar protein family A	wu:fb36b10	rRNA processing /// rRNA	---	nucleus /// small nucleola	---	RNA binding /// snoRNA	---	0.4910	1.21
Dr.92.1.A1_at	gap43	gap43	growth associated protein	growth associated protein	regulation of growth /// tis	regulation of growth	---	---	---	---	0.3856	1.21
Dr.17557.1.S1_at	LOC556178	---	similar to neurocalcin	Transcribed sequence with	---	---	---	---	---	---	0.1012	1.20
Dr.10689.1.S1_at	zic2b	---	zic family member 2 (odd	Zinc finger protein Zic2 (zic	---	---	intracellular	---	nucleic acid binding /// zi	---	0.0064	1.20
Dr.1658.1.A1_at	slc4a2	---	solute carrier family 4, an	Transcribed sequence with	kidney development /// tr	---	membrane /// integral to	---	transporter activity /// ino	---	0.2474	1.19
Dr.19463.1.S1_at	LOC794799	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.4343	1.19
Dr.5372.7.A1_at	her4.2	---	hairy-related 4.2	MRNA similar to hairy and	somite specification /// re	---	nucleus	---	DNA binding /// double-st	---	0.1197	1.19
Dr.25520.1.A1_at	zgc:100907	FBXO25	zgc:100907	F-box only protein 25	---	---	---	---	---	---	0.1965	1.19
Dr.4714.1.A1_at	LOC565013	---	similar to groucho-relatec	Transcribed sequence with	---	---	---	---	---	---	0.1157	1.18
Dr.12990.1.A1_at	zgc:85645	---	zgc:85645	CDNA clone MGC:85645 I	G-protein coupled recept	---	heterotrimeric G-protein	---	signal transducer activity	---	0.0329	1.18
Dr.5623.1.S1_at	zgc:55345	zgc:55345	zgc:55345	similar to lipase, endotheli	lipid metabolic process	lipid metabolism	---	---	catalytic activity /// lipopro	catalytic activity	0.6480	1.18
Dr.10113.1.S1_at	cox17	---	COX17 cytochrome c oxi	Transcribed sequence with	copper ion transport	---	mitochondrial intermemb	---	copper ion binding /// cop	---	0.1485	1.18
Dr.5845.1.A1_at	wu:fj01a06	---	wu:fj01a06	Transcribed sequence	---	---	---	---	---	---	0.5025	1.18
Dr.96.1.A1_at	LOC100003460 /// LOC5	---	similar to complement pr	Transcribed sequence with	---	---	---	---	---	---	0.6465	1.18
Dr.25187.3.S1_at	LOC792171	her8a	hypothetical protein LOC	hairy-related 8a	---	regulation of transcription	---	---	---	DNA binding	0.2353	1.18
Dr.7107.1.A1_at	zgc:65782	zgc:65782	zgc:65782	hypothetical protein MGC6	---	---	nucleus /// nucleolus	---	RNA binding	---	0.0558	1.18
Dr.14705.1.S1_at	zgc:56183	zgc:56183	zgc:56183	similar to cyclic AMP phos	---	---	---	---	---	---	0.3243	1.18
Dr.9746.1.S1_a_at	rrm1	rrm1	ribonucleotide reductase	ribonucleotide reductase M	DNA replication	DNA replication	cytoplasm /// ribonucleos	ribonucleoside-diphospha	nucleotide binding /// cata	ribonucleoside-diphosphate reductas	0.3822	1.18
Dr.23583.1.A1_at	wu:fb13g09	---	wu:fb13g09	Transcribed sequence	---	---	---	---	---	---	0.7005	1.18
Dr.2634.1.A1_at	si:ch211-142e24.2	---	si:ch211-142e24.2	Transcribed sequences	metabolic process /// nuc	---	---	---	nucleic acid binding /// er	---	0.2085	1.17
Dr.1131.1.A1_at	zgc:110340	---	zgc:110340	Transcribed sequence with	---	---	---	---	---	---	0.4314	1.17
Dr.20947.2.A1_a_at	nasp	zgc:56007	nuclear autoantigenic spe	wu:fd20g12	---	---	---	---	binding	---	0.1023	1.17
Dr.25714.2.S1_at	ctssb.2	zgc:66318	cathepsin S, b.2	hypothetical protein MGC6	proteolysis	purine nucleotide biosynt	---	---	cysteine-type endopeptid	adenylosuccinate synthase activity //	0.6070	1.16
Dr.17186.1.S1_at	zgc:56126	zgc:56126	zgc:56126	similar to epoxide hydrolas	response to toxin	---	microsome /// membrane	---	catalytic activity /// epoxic	catalytic activity /// hydrolase activity	0.4183	1.16
Dr.16025.1.S1_at	zgc:56682	zgc:56682	zgc:56682	similar to small nuclear ribo	mRNA processing /// RN	---	nucleus /// ribonucleopro	nucleus /// small nucleola	RNA binding	pre-mRNA splicing factor activity	0.0589	1.16

Dr.5342.1.A1_at	DKEY-1K23.2	zgc:64202	novel protein similar to ve	wu:fc09c11	---	---	---	---	---	---	0.2770	1.16
Dr.377.1.S1_at	prim1	prim1	primase polypeptide 1	primase polypeptide 1	DNA replication /// DNA r	DNA replication, synthesi	alpha DNA polymerase:p	---	DNA primase activity /// D	DNA primase activity	0.2454	1.16
Dr.17883.1.S1_at	cdk2	---	cyclin-dependent kinase	CDNA clone MGC:56598 I	protein amino acid phosp	---	---	---	nucleotide binding /// prot	---	0.4879	1.16
Dr.20170.2.A1_at	apex1	---	APEX nuclease (multifun	CDNA clone MGC:66204 I	heart looping /// DNA rep	---	intracellular	---	DNA binding /// nuclease	---	0.2263	1.16
Dr.18605.1.A1_at	zgc:136987	---	zgc:136987	Transcribed sequence with	---	---	intracellular	---	actin binding /// growth fa	---	0.3652	1.15
Dr.7936.1.A1_at	snrpb	Snrpn	small nuclear ribonucleop	snRNP-associated protein	mRNA metabolic process	---	ribonucleoprotein comple	---	nucleic acid binding	---	0.3504	1.14
Dr.5513.1.S1_at	slc3a2	slc3a2	solute carrier family 3, me	solute carrier family 3, mer	carbohydrate metabolic p	carbohydrate metabolism	---	---	catalytic activity /// cation	alpha-amylase activity	0.2028	1.14
Dr.18724.1.A1_at	LOC557911	---	hypothetical LOC557911	Transcribed sequences	---	---	---	---	---	---	0.2661	1.14
Dr.25185.1.S1_s_at	im:6791170	---	im:6791170	Transcribed sequence with	---	---	---	---	---	---	0.7154	1.14
Dr.7155.2.S1_at	LOC567446	---	similar to nucleolar and s	YF-9 mRNA for hypothetic	cell cycle /// mitosis /// ce	---	nucleus /// cytoplasm /// r	---	DNA binding	---	0.3159	1.13
Dr.2620.1.A1_at	LOC553336	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---	0.4020	1.13
Dr.20156.1.S1_at	psma5	PSMA5	proteasome (prosome, m	proteasome subunit, alpha	ubiquitin-dependent prote	---	cytoplasm /// cytosol /// pr	---	endopeptidase activity ///	---	0.4012	1.13
Dr.18112.2.A1_at	LOC794796	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---	0.6556	1.13
Dr.988.1.S1_at	dci	wu:fi31d10	dodecenoyl-Coenzyme A	wu:fi31d10	metabolic process	metabolism	---	---	catalytic activity	catalytic activity	0.1183	1.13
Dr.3936.1.A1_at	LOC564559	---	similar to CCCH zinc fing	Transcribed sequence with	---	---	---	---	nucleic acid binding /// zir	---	0.5083	1.12
Dr.5620.1.S1_at	pfdn5	---	prefoldin 5	Transcribed sequence with	protein folding	---	prefoldin complex	---	unfolded protein binding	---	0.2184	1.12
Dr.1241.1.S1_at	rtcd1	rtcd1	RNA terminal phosphate	RNA terminal phosphate c	RNA processing	---	---	---	catalytic activity /// RNA-3	RNA-3'-phosphate cyclase activity	0.5484	1.12
Dr.14542.1.S1_at	rab5al	rab5al	RAB5A, member RAS or	RAB5A, member RAS onc	small GTPase mediated s	small GTPase mediated s	---	---	nucleotide binding /// GTI	GTP binding	0.7590	1.12
Dr.20010.1.S2_at	zgc:85677	---	zgc:85677	Clone IMAGE:3819333, m	regulation of transcription	---	chromatin /// nucleus	---	DNA binding	---	0.2540	1.12
Dr.3582.1.A1_at	LOC571548	---	similar to caspase 8	Transcribed sequences	---	---	---	---	---	---	0.4183	1.12
Dr.25607.1.S1_at	LOC799650	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.2631	1.12
Dr.14228.1.S1_at	zgc:103688	---	zgc:103688	Transcribed sequence with	mRNA metabolic process	---	ribonucleoprotein comple	---	---	---	0.3125	1.11
Dr.15653.1.S1_at	im:7151414 /// LOC7954	---	im:7151414 /// similar to	Transcribed sequences	---	---	---	---	---	---	0.4354	1.11
Dr.4096.1.S1_at	zgc:65861	zgc:65861	zgc:65861	wu:fb23b02	nucleosome assembly	---	nucleosome /// nucleus //	---	DNA binding	---	0.1458	1.11
Dr.5091.1.S1_at	mcm4	mcm4	MCM4 minichromosome	MCM4 minichromosome m	DNA replication initiation	---	nucleus	---	nucleotide binding /// DNA	---	0.4763	1.11
Dr.18007.1.S1_at	LOC100004286 /// zgc:16	---	zgc:162244 /// hypothetic	Transcribed sequences	---	---	---	---	---	---	0.4340	1.11
Dr.776.1.S1_at	si:dkey-235d18.4	---	si:dkey-235d18.4	Transcribed sequence with	translation /// translationa	---	eukaryotic translation elo	---	translation elongation fac	---	0.2027	1.11
Dr.5621.1.A1_at	arpc5a	---	actin related protein 2/3 c	Transcribed sequences	regulation of actin filamen	---	cytoskeleton	---	---	---	0.4116	1.10
Dr.15777.1.A1_at	zgc:92791	---	zgc:92791	Transcribed sequence with	ubiquitin-dependent prote	---	nucleus /// cytoplasm /// c	---	endopeptidase activity ///	---	0.4433	1.10
Dr.17499.1.A1_at	---	zgc:63645	Transcribed locus	hypothetical protein MGC6	---	---	---	---	---	---	0.8360	1.10
Dr.25528.1.A1_at	zgc:152751	---	zgc:152751	Transcribed sequence with	---	---	---	---	protein binding	---	0.8833	1.10
Dr.3785.1.S1_at	wu:fc39c04	---	Wu:fc39c04	Transcribed sequence with	---	---	---	---	---	---	0.5227	1.09
Dr.17596.1.A1_at	LOC100000591	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.6162	1.09
Dr.4249.1.S1_at	lipf	---	lipase, gastric	MRNA similar to lipase A (	response to hypoxia /// lip	---	---	---	catalytic activity	---	0.8229	1.09
Dr.14639.1.S1_at	pcbd1	zgc:73389	6-pyruvoyl-tetrahydropter	hypothetical protein MGC7	---	---	---	---	lyase activity	---	0.7387	1.09
Dr.1149.1.A1_a_at	hnrnpa0	zgc:77280	heterogeneous nuclear ri	wu:fi36h08	---	---	ribonucleoprotein comple	---	nucleotide binding /// nuc	---	0.3500	1.08
Dr.15038.1.S1_at	psmb1	---	proteasome (prosome, m	Transcribed sequence with	ubiquitin-dependent prote	---	nucleus /// cytoplasm /// c	---	endopeptidase activity ///	---	0.3490	1.08
Dr.25226.1.S1_s_at	ccnb1	ccnb1	cyclin B1	cyclin B1	cell cycle /// cell division	regulation of cell cycle ///	nucleus	nucleus	---	---	0.5116	1.08
Dr.23163.1.A1_at	---	sult1st1	Transcribed locus	sulfotransferase family, cyt	---	xenobiotic metabolism	---	---	---	sulfotransferase activity /// transferas	0.6324	1.08
Dr.15949.3.S1_a_at	rhoad	---	ras homolog gene family,	Transcribed sequence with	small GTPase mediated s	---	intracellular	---	nucleotide binding /// GTI	---	0.5594	1.08
Dr.11189.1.S1_at	fryl	---	furry homolog-like (Drosc	Transcribed sequences	---	---	---	---	---	---	0.5723	1.08
Dr.24241.1.S1_at	mdkb	mdkb	midkine-related growth fa	midkine-related growth fac	brain development /// sec	brain development /// sec	extracellular region	extracellular	growth factor activity	growth factor activity	0.6030	1.08
Dr.19935.1.S1_at	rpl36a	rpl36a	ribosomal protein L36A	ribosomal protein L36A	translation	protein biosynthesis	intracellular /// cytoplasm	intracellular /// ribosome /	structural constituent of ri	structural constituent of ribosome	0.3188	1.08
Dr.1162.1.S1_at	zgc:73237	HN1	zgc:73237	hematological and neurolo	---	---	---	---	---	---	0.4683	1.08
Dr.25174.2.A1_at	tcf12	---	transcription factor 12	Transcribed sequence with	regulation of transcription	---	nucleus	---	DNA binding /// transcript	---	0.3979	1.08
Dr.1055.1.S1_at	mcm7	mcm7	MCM7 minichromosome	MCM7 minichromosome m	DNA replication initiation	DNA replication initiation	nucleus	nucleus	nucleotide binding /// DNA	nucleotide binding /// DNA binding ///	0.5758	1.08
Dr.3485.1.S1_at	LOC791632 /// zgc:65802	zgc:65802	zgc:65802 /// hypothetica	wu:fb36c08	proteolysis	---	---	---	serine carboxypeptidase	---	0.3903	1.07
Dr.10840.1.S1_at	mapre1l	zgc:77807	microtubule-associated p	wu:fi33c06	---	---	---	---	microtubule binding	microtubule binding	0.5797	1.07
Dr.25645.1.S1_at	LOC556178	ctsf	similar to neurocalcin	cathepsin F	---	---	---	---	---	---	0.2670	1.07
Dr.20875.1.S1_s_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.8950	1.07
Dr.19.1.A1_at	si:xx-bac7cse.2	---	si:xx-bac7cse.2	Transcribed sequences	---	---	---	---	---	---	0.7238	1.07
Dr.199.1.A1_at	eaf2	---	ELL associated factor 2	Transcribed sequence with	---	---	---	---	---	---	0.6806	1.06
Dr.15378.2.A1_at	zgc:110314	---	Zgc:110314	Transcribed sequence with	---	---	---	---	---	---	0.6322	1.06
Dr.13680.1.S1_at	fdx1 /// LOC565069	---	hypothetical LOC565069	Transcribed sequence with	---	---	---	---	---	---	0.5578	1.06
Dr.3920.1.S1_at	olig2	olig2	oligodendrocyte lineage t	oligodendrocyte lineage tra	neuroblast fate determina	neuroblast cell fate detern	nucleus	---	transcription regulator ac	---	0.6133	1.06
Dr.20785.1.S1_a_at	zgc:152751	---	zgc:152751	Transcribed sequence with	---	---	---	---	protein binding	---	0.9834	1.06
Dr.3139.1.S1_at	zfp36l2	---	zinc finger protein 36, C3	Transcribed sequence with	---	---	---	---	nucleic acid binding /// zir	---	0.6926	1.06
Dr.19577.2.S1_at	fabp1a /// LOC791610	---	fatty acid binding protein	Transcribed sequence with	transport	---	---	---	transporter activity /// bin	---	0.7582	1.05
Dr.696.1.S1_at	LOC568707	---	type IV antifreeze protein	Transcribed sequences	---	---	---	---	---	---	0.7594	1.05
Dr.16606.1.S1_at	zgc:56218	zgc:56218	zgc:56218	wu:fc49b02	translation /// negative re	electron transport /// prot	membrane attack comple	intracellular /// ribosome	RNA binding /// structural	RNA binding /// structural constituent	0.3829	1.05
Dr.18762.1.S1_at	rhoae	zgc:64015	ras homolog gene family,	similar to ras homolog gen	small GTPase mediated s	small GTPase mediated s	intracellular	---	nucleotide binding /// GTI	GTP binding	0.9360	1.05
Dr.3747.1.S1_at	LOC573055 /// zgc:6413	zgc:64137	hypothetical LOC573055	wu:fc04h09	negative regulation of tra	---	---	---	eukaryotic initiation facto	---	0.9310	1.04
Dr.1557.1.S1_at	kif11	kif11	kinesin family member 11	kinesin family member 11	microtubule-based move	---	microtubule /// microtubul	microtubule associated c	nucleotide binding /// mot	motor activity /// ATP binding	0.7830	1.04
Dr.6430.1.A1_at	wu:fj20f10	---	wu:fj20f10	Transcribed sequences	---	---	---	---	---	---	0.7898	1.04
Dr.771.1.S1_at	ckmt1	ckmt1	creatine kinase, mitochor	creatine kinase, mitochond	---	---	---	---	catalytic activity /// kinase	kinase activity /// transferase activity,	0.4847	1.04
Dr.184.1.S1_at	b2m /// LOC796027 /// LO	b2m	beta-2-microglobulin /// si	beta-2-microglobulin	antigen processing and p	antigen presentation, enc	extracellular region /// sig	---	---	MHC class I receptor activity	0.7840	1.04
Dr.361.1.S1_at	seph	seph	Selenoprotein H	selenoprotein H	nucleosome assembly ///	nucleosome assembly ///	chromosome, pericentric	nucleosome /// nucleus	DNA binding /// selenium	DNA binding	0.3879	1.04
Dr.4408.1.S1_at	adka	adka	adenosine kinase a	adenosine kinase a	purine ribonucleoside sal	purine ribonucleoside sal	---	---	adenosine kinase activity	adenosine kinase activity /// kinase a	0.6996	1.04
Dr.1149.2.A1_at	hnrnpa0	zgc:77280	heterogeneous nuclear ri	wu:fi36h08	---	---	ribonucleoprotein comple	---	nucleotide binding /// nuc	---	0.5522	1.04
Dr.18521.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---	0.7283	1.04
Dr.14292.1.S1_at	zgc:73351	zgc:73351	zgc:73351	hypothetical protein MGC7	---	---	intracellular	---	DNA binding /// sequence	---	0.8975	1.04
Dr.198.1.S2_at	fst	fst	follistatin	follistatin	dorsal/ventral pattern for	dorsal/ventral pattern for	extracellular region /// sig	extracellular	---	---	0.6260	1.04
Dr.25291.5.A1_at	rpl26	---	ribosomal protein L26	CDNA clone MGC:66190 I	translation	---	intracellular /// ribosome /	---	structural constituent of ri	---	0.5822	1.03
Dr.14998.2.S1_at	LOC100000879 /// LOC1	---	zgc:101710 /// hypothetic	Transcribed sequence with	metabolic process	---	---	---	catalytic activity	---	0.5543	1.03
Dr.10390.1.S1_at	arpc5b	arpc5b	actin related protein 2/3 c	actin related protein 2/3 co	regulation of actin filamen	regulation of actin filamen	cytoskeleton	cytoskeleton	---	---	0.8387	1.03
Dr.19937.1.S1_at	npm1	npm1	nucleophosmin 1	nucleophosmin 1	---	---	nucleus	nucleus	nucleic acid binding	nucleic acid binding	0.9964	1.03
Dr.8332.1.A1_at	stka	stka	serine/threonine kinase a	serine/threonine kinase a	protein amino acid phosp	DNA methylation /// prote	nucleus	---	---	DNA binding /// protein kinase activit	0.8878	1.03
Dr.25133.8.S1_at	gamt /// LOC796865 /// LO	Gamt	guanidinoacetate N-meth	guanidinoacetate N-methyl	---	---	---	---	methyltransferase activity	---	0.6385	1.03
Dr.14685.1.S1_at	zgc:92379	---	zgc:92379	Transcribed sequence with	mRNA metabolic process	---	ribonucleoprotein comple	---	---	---	0.7730	1.03
Dr.26507.1.A1_at	LOC571517	---	hypothetical LOC571517	Transcribed sequence with	---	---	---	---	---	---	0.7898	1.03
Dr.12425.2.S1_a_at	zgc:92066	---	zgc:92066	Transcribed sequence with	iron ion transport /// cellu	---	---	---	binding /// iron ion binding	---	0.7670	1.03
Dr.10336.1.S1_at	dct	dct	dopachrome tautomerase	dopachrome tautomerase	metabolic process	metabolism	---	---	oxidoreductase activity ///	structural molecule activity /// oxidore	0.8780	1.03
Dr.18559.1.S1_at	tpm3	tpm3	tropomyosin 3	tropomyosin 3	---	---	---	---	---	---	0.9240	1.03
Dr.13967.1.A1_at	MGC173792 /// zgc:9282	---	zgc:92822 /// zgc:92822	Transcribed sequence with	---	---	---	---	peptide-methionine-(S)-S	---	0.9078	1.02
Dr.5605.4.S1_at	zgc:123210	tubb2	zgc:123210	tubulin, beta, 2	---	---	chromatin /// nucleus	---	DNA binding	---	0.8988	1.02
Dr.18431.1.S1_at	gnpda1	---	glucosamine-6-phosphate	Transcribed sequence with	carbohydrate metabolic p	---	---	---	glucosamine-6-phosphate	---	0.9598	1.02
Dr.9073.1.A1_at	LOC100006020	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---	0.6650	1.02
Dr.10279.1.S1_at	h3f3a	---	H3 histone, family 3A	CDNA clone MGC:56193 I	nucleosome assembly	---	nucleosome /// nucleus //	---	DNA binding	---	0.9293	1.01
Dr.4661.1.A1_at	LOC559003	---	hypothetical LOC559003	Transcribed sequence with	---	---	---	---	---	---	0.6940	1.01
Dr.8134.1.S1_at	psme2	psme2	proteasome activator sub	proteasome activator subu	---	---	cytosol /// proteasome ac	proteasome activator cor	proteasome activator acti	proteasome activator activity	0.9734	1.01
Dr.14922.1.A1_at	abhd4	---	abhydrolase domain cont	Transcribed sequence with	proteolysis /// aromatic c	---	---	---	aminopeptidase activity /	---	0.9052	1.01
Dr.20131.4.S1_at	LOC573469 /// plk1	crabp2	polo-like kinase 1 (Droso	cellular retinoic acid binding	protein amino acid phosp	transport	---	---	nucleotide binding /// prot	transporter activity /// binding /// lipid	0.9263	1.01
Dr.1899.3.A1_at	hes5	hes5	hairy and enhancer of sp	hairy and enhancer of split	eye development /// somi	---	nucleus	---	DNA binding /// transcript	---	0.8573	1.01
Dr.8069.1.S1_at	cryab	cryab	crystallin, alpha B	crystallin, alpha B	---	---	---	---	structural constituent of e	---	0.8690	1.01
Dr.13632.1.S1_at	MGC162944	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.9829	1.01
Dr.956.1.S1_at	zgc:92631	---	zgc:92631	Transcribed sequence with	electron transport	---	mitochondrion	---	cytochrome-c oxidase ac	---	0.8798	1.01
Dr.5515.1.A1_at	zgc:85963	---	zgc:85963	Transcribed sequence with	---	---	cytoplasm /// cytoskeleton	---	actin binding /// structural	---	0.7561	1.01
Dr.24740.1.A1_at	si:dkey-171o17.2	---	Si:dkey-171o17.2	Transcribed sequence	protein complex assembl	---	mitochondrion	---	---	---	0.9918	-1.00
Dr.7609.1.A1_at	wu:fj65c07	---	wu:fj65c07	Transcribed sequences	---	---	---	---	---	---	0.9258	-1.01
Dr.10199.1.S1_at	tob1b	---	transducer of ERBB2, 1b	CDNA clone MGC:65837 I	---	---	---	---	---	---	0.8854	-1.01
Dr.7928.1.A1_at	zgc:112335	---	zgc:112335	Transcribed sequence with	microtubule-based proce	---	cytoplasm /// microtubule	---	nucleotide binding /// GTI	---	0.9260	-1.01
Dr.26398.2.S1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.8060	-1.02
Dr.24954.1.A1_at	hnrnpa0	---	heterogeneous nuclear ri	Transcribed sequences	---	---	ribonucleoprotein comple	---	nucleotide binding /// nuc	---	0.9524	-1.02
Dr.12213.1.A1_at	---	---	Transcribed locus	Transcribed sequence	---	---	---	---	---	---	0.5410	-1.02
Dr.7462.1.A1_at	mbp	---	myelin basic protein	Transcribed sequence with	---	---	---	---	structural constituent of n	---	0.8812	-1.02
Dr.25756.1.S1_at	hdac9b	hdac9	histone deacetylase 9b	histone deacetylase 9	transcription /// transcripti	---	nucleus	---	---	---	0.7946	-1.02
Dr.9125.1.S1_at	syt11	---	synaptotagmin XI	MRNA similar to synaptota	transport	---	synaptic vesicle /// memb	---	transporter activity	---	0.9240	-1.03
Dr.5994.1.A1_at	zgc:100804	---	zgc:100804	Transcribed sequence with	pentose-phosphate shun	---	---	---	catalytic activity /// phosp	---	0.9602	-1.03
Dr.20545.1.S1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.7406	-1.03
Dr.25767.1.S1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.9414	-1.03
Dr.4549.1.S1_at	zgc:63904	zgc:63904	zgc:63904	wu:fc69b04	---	---	---	---	calcium ion binding	calcium ion binding	0.8020	-1.04
Dr.12380.1.S1_at	sall1	---	sal-like 1 (Drosophila)	Transcribed sequences	---	---	---	---	---	---	0.6024	-1.04
Dr.16666.1.A1_at	LOC791902 /// zgc:1108	---	zgc:110843 /// hypothetic	Transcribed sequence with	---	---	---	---	---	---	0.7409	-1.04
Dr.4316.1.S1_at	wu:fb95f11	---	wu:fb95f11	Transcribed sequences	---	---	---	---	---	---	0.8388	-1.04
Dr.12878.3.A1_at	ogt	---	O-linked N-acetylglucosa	Transcribed sequence with	protein amino acid O-link	---	---	---	binding /// protein binding	---	0.9129	-1.04
Dr.15690.2.S1_a_at	sltm	---	SAFB-like, transcription r	CDNA clone MGC:65985 I	---	---	---	---	nucleotide binding /// nuc	---	0.8109	-1.04
Dr.24191.1.S1_at	LOC100000252 /// LOC5	zgc:55564	phosphoinositide-3-kinas	similar to phosphoinositide	intracellular signaling cas	intracellular signaling cas	phosphoinositide 3-kinas	phosphoinositide 3-kinas	protein binding /// kinase	kinase activity /// phosphatidylinosito	0.7505	-1.04
Dr.20660.1.A1_at	pdc1	pdc1	phosducin 1	phosducin 1	---	---	---	---	---	---	0.8600	-1.04
Dr.21469.1.A1_at	LOC553318	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	binding	---	0.9560	-1.04
Dr.11168.1.A1_at	LOC557688	---	similar to proteasome (pr	Transcribed sequences	---	---	---	---	binding	---	0.9550	-1.05
Dr.11127.2.A1_at	syt1	---	Synaptotagmin I	Transcribed sequences	transport	---	synaptic vesicle /// memb	---	transporter activity	---	0.6934	-1.05
Dr.2360.1.S1_at	rhpn2	rhpn2	rhophilin, Rho GTPase bi	rhophilin, Rho GTPase bin	signal transduction	signal transduction	intracellular /// cytoplasm	intracellular	protein binding	protein binding	0.9770	-1.05
Dr.9874.1.A1_at	camk1g	zgc:73127	calcium/calmodulin-depe	wu:fk53c02	protein amino acid phosp	---	---	---	nucleotide binding /// prot	---	0.7490	-1.05
Dr.9268.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---	0.8959	-1.05
Dr.11473.2.S1_at	zgc:92578	---	zgc:92578	Transcribed sequence with	---	---	mitochondrion	---	nucleotide binding /// ATF	---	0.8285	-1.06
Dr.26401.1.S1_at	wu:fb95f11	---	Wu:fb95f11	Transcribed sequences	---	---	---	---	---	---	0.6103	-1.06
Dr.12571.1.S1_at	gria2b /// LOC795873	gria2.2	glutamate receptor, ionot	glutamate receptor, ionotro	transport /// ion transport	transport /// ion transport	membrane attack comple	membrane	receptor activity /// ionotr	receptor activity /// inotropic glutamat	0.6147	-1.06
Dr.8056.1.S1_at	dkk1	dkk1	dickkopf 1	dickkopf 1	---	development /// ectoderm	extracellular region /// ext	extracellular	protein binding /// Wnt-pr	Wnt-protein binding	0.6470	-1.06
Dr.16091.1.A1_at	---	---	---	Transcribed sequences	cell adhesion /// homophi	---	membrane /// integral to r	---	calcium ion binding /// pro	---	0.7003	-1.06
Dr.24209.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.5010	-1.06
Dr.26436.1.A1_at	rds4	rds4	retinal degradation slow 4	retinal degradation slow 4	visual perception	---	integral to membrane	integral to membrane	---	---	0.5152	-1.07
Dr.12878.3.A1_a_at	LOC100006286 /// LOC5	---	O-linked N-acetylglucosa	Transcribed sequence with	protein amino acid O-link	---	---	---	binding /// protein binding	---	0.7777	-1.07
Dr.382.2.S1_at	LOC797626 /// LOC7984	kpna4	beta thymosin-like protein	karyopherin alpha 4 (impor	cytoskeleton organization	protein-nucleus import ///	cytoplasm	---	actin binding	protein transporter activity	0.6385	-1.07
Dr.13616.1.A1_at	---	---	Transcribed locus, strong	Transcribed sequences	---	---	---	---	---	---	0.7799	-1.07
Dr.1216.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.8798	-1.07
Dr.22947.1.A1_at	zgc:110290	---	zgc:110290	Transcribed sequence	phosphate transport	---	integral to membrane	---	phosphate transmembran	---	0.7760	-1.07
Dr.16700.1.A1_at	bsg	---	basigin	Transcribed sequence with	---	---	membrane	---	---	---	0.4970	-1.08
Dr.9366.1.A1_at	rassf1	---	Ras association (RalGDS	Transcribed sequence with	zinc ion transport /// signa	---	---	---	receptor activity /// protei	---	0.4617	-1.08
Dr.9243.1.A1_at	zgc:92434	---	zgc:92434	Transcribed sequences	transcription /// transcripti	---	nucleus	---	DNA binding /// transcript	---	0.8625	-1.08
Dr.12138.1.S1_at	ext1a	---	exostoses (multiple) 1a	Transcribed sequences	heparan sulfate proteogly	---	membrane attack comple	---	---	---	0.3208	-1.08
Dr.24232.1.A1_at	ihpk2	ihpk2	inositol hexaphosphate k	inositol hexaphosphate kin	---	---	---	---	inositol trisphosphate 3-k	---	0.4300	-1.08
Dr.17628.1.A1_at	zgc:63812	zgc:63812	zgc:63812	ribonucleoprotein	---	---	---	viral nucleocapsid /// ribo	nucleotide binding /// nuc	---	0.6720	-1.09
Dr.21559.1.A1_at	LOC553493	---	hypothetical protein LOC	Transcribed sequence with	regulation of Rho protein	---	intracellular	---	Rho guanyl-nucleotide ex	---	0.6900	-1.09
Dr.6033.1.A1_at	wu:fe14d02	---	wu:fe14d02	Transcribed sequence with	---	---	---	---	---	---	0.9585	-1.09
Dr.1461.1.S1_at	es1	es1	es1 protein	es1 protein	---	---	mitochondrion	mitochondrion	---	---	0.1056	-1.09
Dr.9850.1.A1_at	opn1mw2	opn1mw2	opsin 1 (cone pigments),	opsin 1 (cone pigments), m	signal transduction /// G-p	G-protein coupled recept	membrane attack comple	integral to membrane	rhodopsin-like receptor a	rhodopsin-like receptor activity	0.1347	-1.09
Dr.25167.1.S2_at	elavl3	elavl3	ELAV (embryonic lethal,	ELAV (embryonic lethal, at	---	---	ribonucleoprotein comple	viral nucleocapsid	nucleotide binding /// nuc	RNA binding	0.4424	-1.09
Dr.25218.1.A1_at	wu:fb78d08	---	wu:fb78d08	Transcribed sequences	---	---	---	---	---	---	0.6315	-1.09
Dr.12384.1.S1_at	glra3	glra3	glycine receptor, alpha 3	glycine receptor, alpha 3	transport /// ion transport	transport /// ion transport	membrane attack comple	membrane /// integral to r	receptor activity /// GABA	receptor activity /// ion channel activi	0.5300	-1.09
Dr.4590.1.A1_at	tob1a	tob1	transducer of ERBB2, 1a	transducer of ERBB2, 1	dorsal/ventral pattern for	---	nucleus /// cytoplasm	---	protein binding	---	0.6294	-1.10
Dr.8182.1.S1_at	pax6b	pax6b	paired box gene 6b	paired box gene 6b	---	transcription /// regulation	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.8760	-1.10
Dr.15720.1.S1_at	cx55.5	---	connexin 55.5	---	cell communication	---	membrane attack comple	---	gap junction hemi-channe	---	0.3666	-1.10
Dr.7607.1.A1_at	LOC100004503 /// zgc:1	---	zgc:110335 /// hypothetic	Transcribed sequence with	translation /// translationa	---	cytoplasm	---	nucleotide binding /// tran	---	0.4639	-1.11
Dr.25522.1.A1_at	---	gria2.2	Transcribed locus	glutamate receptor, ionotro	---	transport /// ion transport	---	membrane	---	receptor activity /// inotropic glutamat	0.5050	-1.11
Dr.17685.1.A1_at	mdm1	---	Mdm4, transformed 3T3 c	Transcribed sequence with	---	---	nucleus	---	---	---	0.4614	-1.11
Dr.5742.1.S1_at	efnb2a	efnb2a	ephrin B2a	ephrin B2a	---	development /// neuroger	membrane attack comple	membrane /// integral to r	---	---	0.6122	-1.11
Dr.12903.1.A1_at	zgc:92338	---	zgc:92338	Transcribed sequence with	---	---	membrane attack comple	---	protein binding	---	0.7423	-1.11
Dr.12481.1.S1_at	LOC796921	---	similar to polyprotein	Transcribed sequence with	---	---	---	---	---	---	0.6504	-1.11
Dr.12674.1.S1_at	zgc:112307	zgc:63634	zgc:112307	hypothetical protein MGC6	protein amino acid phosp	---	---	---	protein kinase activity ///	---	0.2611	-1.12

Dr.4551.2.A1_at	LOC561437	---	hypothetical LOC561437	---	---	---	---	---	---	---	0.1471	-1.12
Dr.8577.1.A1_at	wu:fb93g02	---	wu:fb93g02	Transcribed sequences	---	---	---	---	---	---	0.7817	-1.12
Dr.15262.1.S1_at	stk38l	zgc:55777	serine/threonine kinase 3	similar to serine/threonine	protein amino acid phosp	protein amino acid phosp	---	---	nucleotide binding /// prot	protein kinase activity /// protein seri	0.5296	-1.12
Dr.25285.1.S1_at	zgc:73223	zgc:73223	zgc:73223	hypothetical protein MGC7	---	---	---	---	---	---	0.0720	-1.12
Dr.11206.1.S1_at	tpi1a	tpi1a	triosephosphate isomera	triosephosphate isomerase	metabolic process	gluconeogenesis /// glyco	---	---	catalytic activity /// triose-	triose-phosphate isomerase activity /	0.2250	-1.13
Dr.15574.1.A1_at	hprt1l	---	hypoxanthine phosphorib	Transcribed sequences	purine ribonucleoside sal	---	cytoplasm	---	hypoxanthine phosphorib	---	0.4472	-1.13
Dr.24454.1.S1_at	LOC100007687	rbm5	similar to putative tumor	RNA binding motif protein	---	---	---	---	---	---	0.4487	-1.13
Dr.25238.1.A1_at	tom1	---	target of myb1 (chicken)	Transcribed sequences	intracellular protein trans	---	intracellular	---	---	---	0.7546	-1.13
Dr.19215.1.S1_at	zgc:136828	---	zgc:136828	Transcribed sequence with	---	---	---	---	sulfotransferase activity /	---	0.4655	-1.13
Dr.9878.1.S1_at	atp1a3b	atp1a3b	ATPase, Na+/K+ transpo	ATPase, Na+/K+ transport	transport /// cation transp	cation transport /// potass	membrane attack comple	integral to plasma memb	---	---	0.3558	-1.14
Dr.25318.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.8224	-1.14
Dr.16181.1.A1_at	zgc:77260	---	zgc:77260	CDNA clone MGC:77260	transcription /// transcript	---	nucleus	---	DNA binding /// transcript	---	0.2414	-1.14
Dr.11236.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.6985	-1.14
Dr.11266.1.S1_at	ywhag1	---	3-monooxygenase/trypto	CDNA clone MGC:73131	---	---	cytoplasm	---	protein domain specific b	---	0.6212	-1.14
Dr.11062.1.A1_at	LOC100006450 /// zgc:9	---	zgc:92294 /// hypothetica	Transcribed sequence with	---	---	cytoplasm	---	guanyl-nucleotide exchar	---	0.5295	-1.14
DrAffx.1.4.S1_at	tnr	tnr	tenascin R (restrictin, jan	tenascin R (restrictin, janus	signal transduction /// ax	---	---	---	receptor binding	---	0.6600	-1.14
Dr.12783.1.S1_at	LOC559207	---	hypothetical LOC559207	Transcribed sequences	---	---	---	---	---	---	0.5445	-1.14
Dr.25552.2.S1_at	LOC565483	---	hypothetical LOC565483	CDNA clone MGC:55996	---	---	---	---	---	---	0.5777	-1.15
Dr.11441.1.A1_at	LOC569678	---	hypothetical LOC569678	Transcribed sequence with	---	---	---	---	---	---	0.4358	-1.15
Dr.7274.1.S1_at	pfkfb1	zgc:55328	6-phosphofructo-2-kinase	wu:fi11h10	fructose 2,6-bisphosphat	fructose 2,6-bisphosphat	---	---	catalytic activity /// ATP b	catalytic activity /// ATP binding /// ki	0.6040	-1.15
Dr.16580.1.A1_at	epas1	---	endothelial PAS domain	Transcribed sequence with	transcription /// transcript	---	nucleus	---	DNA binding /// signal tra	---	0.6371	-1.15
Dr.25060.1.S1_at	zgc:55492	zgc:55492	zgc:55492	wu:fd19c10	protein folding	protein folding	---	---	heat shock protein bindin	chaperone activity	0.6290	-1.15
Dr.3661.1.S1_at	LOC798605 /// nktr	---	natural killer-tumor recog	Transcribed sequence with	protein folding	---	---	---	peptidyl-prolyl cis-trans is	---	0.4064	-1.16
Dr.9425.1.A1_at	ak5	---	adenylate kinase 5	Transcribed sequences	---	---	---	---	---	---	0.1880	-1.16
Dr.8000.1.S1_at	gpx1b	---	glutathione peroxidase 1	Transcribed sequence with	response to oxidative str	---	---	---	peroxidase activity /// glu	---	0.3556	-1.16
Dr.11473.1.A1_at	zgc:92578	---	zgc:92578	Transcribed sequence with	---	---	mitochondrion	---	nucleotide binding /// AT	---	0.5448	-1.16
Dr.12931.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.1216	-1.16
Dr.2506.1.S1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.2236	-1.17

Dr.58.1.A1_at	zgc:73230	---	zgc:73230	CDNA clone MGC:73230 I	intracellular signaling cas	---	phosphoinositide 3-kinas	---	protein binding /// phosph	---	0.5075	-1.18
Dr.3418.1.A1_at	si:dkey-18o7.1	---	si:dkey-18o7.1	Transcribed sequence with	transport /// cation transp	---	membrane attack comple	---	---	---	0.6362	-1.18
Dr.20996.1.S1_at	gc3	gc3	guanylyl cyclase 3	guanylyl cyclase 3	cGMP biosynthetic proce	protein amino acid phosp	---	---	guanylate cyclase activity	guanylate cyclase activity /// protein I	0.1632	-1.18
Dr.19931.1.S1_at	tph1	tph	tryptophan hydroxylase 1	tryptophan hydroxylase (tr	proteolysis /// metabolic p	metabolism /// aromatic a	---	---	cysteine-type endopeptid	monooxygenase activity /// tryptopha	0.2074	-1.18
Dr.20055.1.A1_at	LOC100006061	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---	0.2396	-1.19
Dr.11184.1.A1_at	zgc:73126	zgc:73126	zgc:73126	hypothetical protein MGC7	calcium ion transport	---	---	---	calcium channel activity /	---	0.0324	-1.19
Dr.18845.1.S2_at	dmbx1a	otx3	diencephalon/mesencepl	orthodenticle homolog 3 (D	eye development /// trans	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.5880	-1.19
Dr.11343.1.A1_at	---	---	---	Transcribed sequence	---	---	---	---	---	---	0.3675	-1.19
Dr.24934.1.S1_at	mak	zgc:56603	male germ cell-associate	wu:fj04c02	protein amino acid phosp	protein amino acid phosp	---	---	nucleotide binding /// prot	protein kinase activity /// protein seri	0.2633	-1.20
Dr.17310.1.S1_at	zgc:56235	zgc:56235	zgc:56235	hypothetical protein MGC5	anion transport	anion transport	mitochondrial outer mem	mitochondrial outer mem	voltage-gated anion char	voltage-dependent ion-selective char	0.3268	-1.20
Dr.12807.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.5610	-1.20
Dr.11176.1.A1_s_at	aanat1	aanat1	arylalkylamine N-acetyltr	arylalkylamine N-acetyltrar	metabolic process	---	---	---	aralkylamine N-acetyltrar	---	0.2760	-1.20
Dr.5054.2.S1_at	---	pax6b	Transcribed locus	paired box gene 6b	---	transcription /// regulatior	---	nucleus	---	DNA binding /// transcription factor a	0.5602	-1.20
Dr.25650.1.A1_at	si:dkeyp-1h4.2	dbx1a	si:dkeyp-1h4.2	developing brain homeobo	transport /// intracellular p	regulation of transcriptior	nucleus	nucleus	nucleotide binding /// GTI	DNA binding /// transcription factor a	0.2673	-1.21
Dr.4262.1.S1_at	wu:fb81e12	---	wu:fb81e12	Transcribed sequences	---	---	---	---	---	---	0.0716	-1.21
Dr.24337.1.A1_at	zgc:66337	---	zgc:66337	Transcribed sequences	---	---	---	---	---	---	0.0249	-1.22
Dr.9860.1.S1_at	mdh1b	mdh1b	malate dehydrogenase 1	malate dehydrogenase 1b,	carbohydrate metabolic p	tricarboxylic acid cycle	---	cytoplasm	catalytic activity /// bindin	oxidoreductase activity /// malate del	0.2877	-1.22
Dr.12129.1.A1_at	wu:fc46a10	---	wu:fc46a10	Transcribed sequences	---	---	---	---	---	---	0.0718	-1.22
Dr.16287.1.A1_at	zgc:162186	---	zgc:162186	Transcribed sequence with	---	---	---	---	---	---	0.3748	-1.23
Dr.17264.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.4174	-1.23
Dr.17476.1.A1_at	LOC792610	---	Small heat shock protein	Transcribed sequence with	response to stress	---	---	---	---	---	0.1928	-1.23
Dr.15260.2.A1_at	reverbb2	reverbb	rev erb beta 2	rev-erb-beta	transcription /// transcripti	transcription /// regulatior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.1949	-1.23
Dr.7691.1.A1_at	zgc:101761	---	zgc:101761	Transcribed sequence with	protein amino acid ADP-r	---	---	---	nucleotide binding /// sigr	---	0.5542	-1.24
Dr.15883.1.S1_at	ppp2r5e1	ppp2r5e1	protein phosphatase 2, re	protein phosphatase 2, reg	signal transduction	signal transduction	protein phosphatase type	protein phosphatase type	protein phosphatase type	protein phosphatase type 2A regulat	0.0393	-1.24
Dr.16054.1.S1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.1484	-1.24
Dr.15221.1.S1_at	ankrd10a	zgc:55353	ankyrin repeat domain 10	similar to ankyrin repeat do	translation /// tRNA amino	tRNA aminoacylation for	cytoplasm	---	nucleotide binding /// ami	tRNA ligase activity /// ATP binding	0.1014	-1.24
Dr.25500.1.S1_at	vamp1	---	vesicle-associated memb	CDNA clone MGC:73378 I	vesicle-mediated transpo	---	membrane attack comple	---	---	---	0.0564	-1.24
Dr.264.1.S1_at	gefiltin	gefiltin	gefiltin	gefiltin	---	---	intermediate filament	intermediate filament	structural molecule activi	structural molecule activity	0.0940	-1.24
DrAffx.2.8.S1_at	aanat1	aanat1	arylalkylamine N-acetyltr	arylalkylamine N-acetyltrar	metabolic process	---	---	---	aralkylamine N-acetyltrar	---	0.1013	-1.25
Dr.17491.2.S1_at	pygmb	---	phosphorylase, glycogen	---	carbohydrate metabolic p	---	---	---	phosphorylase activity	---	0.0667	-1.25
Dr.11303.1.S1_at	wu:fk57h01	---	wu:fk57h01	Transcribed sequences	---	---	---	---	---	---	0.2602	-1.25
Dr.7233.1.A1_at	wu:fj67h05	---	wu:fj67h05	CDNA clone IMAGE:56043	---	---	---	---	---	---	0.0375	-1.25
Dr.19528.1.A1_at	LOC562053	---	hypothetical LOC562053	Transcribed sequences	---	---	---	---	---	---	0.0501	-1.25
Dr.14159.1.A1_at	id:ibd5024	---	Id:ibd5024	Transcribed sequences	---	---	---	---	---	---	0.0970	-1.25
Dr.7840.1.S1_at	atp1a1b	atp1a1b	ATPase, Na+/K+ transpo	ATPase, Na+/K+ transport	transport /// cation transp	cation transport /// potass	membrane attack comple	integral to plasma memb	###################	############################	0.0490	-1.28
Dr.811.1.S1_at	rps6kal	zgc:66139	ribosomal protein S6 kina	wu:fj94b02	protein amino acid phosp	---	---	---	nucleotide binding /// mag	---	0.1657	-1.28
Dr.3986.1.S1_at	nr2f2	nr2f2	nuclear receptor subfami	nuclear receptor subfamily	transcription /// transcripti	transcription /// regulatior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.2910	-1.29
Dr.24957.1.S1_at	opn4l	opn4	opsin 4, like	opsin 4 (melanopsin)	signal transduction /// G-p	G-protein coupled recept	membrane attack comple	integral to membrane	rhodopsin-like receptor a	rhodopsin-like receptor activity	0.2940	-1.29
Dr.12531.1.S1_at	zgc:112103	---	zgc:112103	Transcribed sequence with	---	---	mitochondrion	---	---	---	0.2776	-1.29
Dr.13244.1.A1_at	zgc:152987	---	zgc:152987	Transcribed sequence with	---	---	---	---	---	---	0.2685	-1.30
Dr.10511.1.A1_at	ogt	---	O-linked N-acetylglucosa	Transcribed sequence with	protein amino acid O-link	---	---	---	binding /// protein binding	---	0.5996	-1.31
Dr.25212.1.A1_at	zgc:153744	zgc:56528	zgc:153744	similar to calsyntenin 1	proteolysis /// homophilic	homophilic cell adhesion	membrane	membrane	cysteine-type endopeptid	calcium ion binding	0.2719	-1.31
Dr.3661.2.S1_x_at	LOC798605 /// nktr	---	natural killer-tumor recog	Transcribed sequence with	protein folding	---	---	---	peptidyl-prolyl cis-trans is	---	0.4007	-1.31
Dr.8209.1.S2_at	foxo5	foxo5	forkhead box O5	forkhead box O5	regulation of transcriptior	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	transcription factor activity	0.0280	-1.32
Dr.26292.1.A1_at	wu:fj68b04	---	wu:fj68b04	Transcribed sequences	---	---	---	---	---	---	0.0309	-1.32
Dr.22015.1.A1_at	LOC794288 /// zgc:1581	---	zgc:158135 /// hypothetic	Transcribed sequence	phospholipid biosynthetic	---	---	---	phosphatidylserine decar	---	0.0076	-1.32
Dr.12058.1.A1_at	LOC557926	---	similar to MGC81043 pro	Transcribed sequence with	---	---	---	---	phosphoprotein phospha	---	0.0340	-1.34
Dr.6935.1.S1_at	sema6d	---	sema domain, transmem	CDNA clone MGC:56170 I	---	---	integral to membrane	---	---	---	0.0033	-1.34
Dr.10592.1.A1_at	wu:fk54d01	---	wu:fk54d01	Transcribed sequences	---	---	---	---	---	---	0.2471	-1.34
Dr.15260.1.S1_at	reverbb2	reverbb	rev erb beta 2	rev-erb-beta	transcription /// transcripti	transcription /// regulatior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0134	-1.34
Dr.13682.1.S1_at	LOC100002031 /// LOC1	---	hypothetical LOC565631	Transcribed sequence with	---	---	---	---	---	---	0.0952	-1.35
Dr.18282.7.S1_at	khdrbs1	khdrbs1	KH domain containing, R	KH domain containing, RN	nucleosome assembly	---	nucleosome /// nucleus //	---	DNA binding /// RNA binc	nucleic acid binding	0.2163	-1.35
Dr.16503.1.A1_at	---	---	Transcribed locus	Transcribed sequence	---	---	---	---	---	---	0.0933	-1.35
Dr.13030.1.A1_at	zgc:64006	zgc:64006	Zgc:64006	wu:fj30h05	---	---	---	---	signal transducer activity	signal transducer activity	0.2036	-1.36
Dr.16658.1.S1_at	LOC792055	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.2146	-1.37
Dr.610.2.S1_at	DKEY-241L7.8	hsp90a	similar to Heat shock pro	heat shock protein 90-alph	protein folding /// respons	protein folding /// positive	---	---	nucleotide binding /// prot	chaperone activity /// heat shock prot	0.5332	-1.37
Dr.18285.1.A1_at	ell2	---	Elongation factor, RNA p	Transcribed sequences	---	---	---	---	---	---	0.0089	-1.37
Dr.26436.1.S1_at	rds4	rds4	retinal degradation slow 4	retinal degradation slow 4	visual perception	---	integral to membrane	integral to membrane	---	---	0.0507	-1.37
Dr.3661.1.S1_a_at	LOC798605 /// nktr	---	natural killer-tumor recog	Transcribed sequence with	protein folding	---	---	---	peptidyl-prolyl cis-trans is	---	0.3766	-1.38
Dr.17111.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.0160	-1.38
Dr.11178.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.2889	-1.39
Dr.19223.1.S1_at	aldoc	aldoc	aldolase c, fructose-bisph	aldolase c, fructose-bispho	glycolysis /// metabolic pr	glycolysis	---	---	catalytic activity /// fructos	fructose-bisphosphate aldolase activ	0.0017	-1.41
Dr.13670.1.S1_at	zgc:77529	---	zgc:77529	CDNA clone MGC:73160 I	signal transduction	---	protein phosphatase type	---	protein phosphatase type	---	0.1174	-1.41
Dr.2619.1.S2_at	LOC100008131 /// rbmx	rbmx	RNA binding motif protein	RNA binding motif protein,	---	---	---	---	nucleotide binding /// nuc	---	0.0111	-1.41
Dr.26033.1.A1_at	---	---	---	Transcribed sequence	---	---	---	---	---	---	0.1202	-1.41
Dr.24938.1.S1_x_at	---	zgc:66318	---	hypothetical protein MGC6	---	purine nucleotide biosynt	---	---	---	adenylosuccinate synthase activity //	0.1554	-1.42
Dr.2204.1.A1_at	wu:fc15g08	zgc:55468	wu:fc15g08	hypothetical protein MGC5	---	---	---	---	---	catalytic activity	0.3374	-1.43
Dr.6534.1.A1_at	wu:fe11a06	---	wu:fe11a06	Transcribed sequences	---	---	---	---	---	---	0.0337	-1.43
Dr.26493.1.A1_a_at	gnb1	gnb1	guanine nucleotide bindir	guanine nucleotide binding	signal transduction	---	---	---	signal transducer activity	---	0.0398	-1.43
Dr.9899.1.S2_at	gnat1	gnat1	guanine nucleotide bindir	guanine nucleotide binding	signal transduction /// G-p	G-protein coupled recept	---	---	nucleotide binding /// sigr	signal transducer activity /// GTP bin	0.0208	-1.44
Dr.18344.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.0253	-1.44
Dr.11661.1.S1_at	LOC791521 /// ypel3	ypel3	yippee-like 3 /// hypotheti	yippee-like 3	---	---	---	---	---	---	0.2879	-1.44
Dr.9870.1.A1_at	zgc:110777	---	zgc:110777	Transcribed sequence with	zinc ion transport	---	---	---	zinc ion binding /// transfe	---	0.0028	-1.45
Dr.12206.2.S1_at	tceb2	---	transcription elongation f	CDNA clone IMAGE:59150	protein modification proc	---	---	---	---	---	0.0574	-1.45
Dr.6208.1.A1_at	wu:fj58c09	---	wu:fj58c09	Transcribed sequences	---	---	---	---	---	---	0.4673	-1.45
Dr.20997.1.S1_at	gc2	gc2	guanylyl cyclase 2	guanylyl cyclase 2	protein amino acid phosp	protein amino acid phosp	---	---	protein kinase activity /// p	guanylate cyclase activity /// protein I	0.0019	-1.46
Dr.3889.1.A1_at	ptena	zgc:73086	phosphatase and tensin l	wu:fc52g04	blood vessel developmer	---	---	---	protein tyrosine phosphat	---	0.0456	-1.46
Dr.12486.1.S1_at	zgc:92247	---	zgc:92247	Transcribed sequence with	---	---	membrane attack comple	---	structural molecule activi	---	0.0093	-1.47
Dr.23065.1.S1_at	si:busm1-57f23.1	---	si:busm1-57f23.1	Transcribed sequence with	protein amino acid phosp	---	membrane /// integral to r	---	nucleotide binding /// prot	---	0.0274	-1.47
Dr.12138.2.A1_at	ext1a	---	exostoses (multiple) 1a	Transcribed sequences	heparan sulfate proteogly	---	membrane attack comple	---	---	---	0.0282	-1.47
Dr.12204.1.S1_at	rds4	rds4	retinal degradation slow 4	retinal degradation slow 4	visual perception	---	integral to membrane	integral to membrane	---	---	0.0320	-1.47
Dr.10226.1.S1_at	LOC557176	---	similar to phosphoinositid	Transcribed sequences	signal transduction	---	intracellular /// phosphoin	---	protein binding /// phosph	---	0.0068	-1.48
Dr.13441.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0009	-1.48
Dr.19751.1.A1_at	LOC555980	---	Hypothetical LOC555980	Transcribed sequence	---	---	---	---	---	---	0.0152	-1.51
Dr.6708.1.A1_at	---	---	Transcribed locus	MRNA similar to guanine n	---	---	---	---	---	---	0.0053	-1.51
Dr.6604.2.A1_a_at	zgc:77112	---	zgc:77112	CDNA clone MGC:77112 I	---	---	---	---	---	---	0.1717	-1.51
Dr.12802.1.A1_at	---	---	Transcribed locus	Transcribed sequence	---	---	---	---	---	---	0.0083	-1.52
Dr.17415.1.S1_at	zgc:56306	zgc:56306	zgc:56306	hypothetical protein MGC5	---	---	---	---	insulin receptor binding	insulin receptor binding	0.0025	-1.52
Dr.20391.1.A1_at	LOC563577	---	similar to novel apoptosis	Transcribed sequence with	---	---	---	---	---	---	0.0357	-1.53
Dr.9155.1.S1_at	nsf	nsf	N-ethylmaleimide-sensiti	N-ethylmaleimide-sensitive	---	---	---	---	nucleotide binding /// binc	nucleotide binding /// ATP binding	0.0207	-1.53
Dr.11235.1.A1_at	---	PrPL-P1-like	Transcribed locus	prion-like protein 1	---	---	---	---	---	---	0.0028	-1.53
Dr.610.2.S1_a_at	DKEY-241L7.8 /// hsp90a	hsp90a	heat shock protein 90-alp	heat shock protein 90-alph	protein folding /// respons	protein folding /// positive	cytoplasm	---	nucleotide binding /// prot	chaperone activity /// heat shock prot	0.2605	-1.54
Dr.12870.1.A1_at	LOC570928	---	hypothetical LOC570928	Transcribed sequence with	---	---	---	---	---	---	0.0362	-1.54
Dr.539.1.S1_at	rx2	rx2	retinal homeobox gene 2	retinal homeobox gene 2	transcription /// transcripti	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0813	-1.54
Dr.11351.1.A1_at	zgc:73324	zgc:73324	zgc:73324	hypothetical protein MGC7	---	---	mitochondrion	---	---	---	0.0328	-1.54
Dr.20080.1.S1_at	ca2 /// LOC792230 /// LO	ca2	carbonic anhydrase II /// l	carbonic anhydrase II	one-carbon compound m	---	---	---	carbonate dehydratase a	---	0.1285	-1.55
Dr.23461.1.A1_at	stc2 /// zgc:136650	---	stanniocalcin 2 /// zgc:136	Transcribed sequence with	---	---	extracellular region	---	hormone activity	---	0.0830	-1.57
Dr.25848.1.A1_at	wu:fj12d05	env	wu:fj12d05	envelope protein	---	---	---	---	---	---	0.0031	-1.58
Dr.14001.1.A1_at	pttg1ip	---	pituitary tumor-transformi	Transcribed sequence with	multicellular organismal c	---	---	---	---	---	0.0492	-1.59
Dr.11194.1.A1_at	---	---	Transcribed locus	Transcribed sequence	---	---	---	---	---	---	0.0163	-1.59
Dr.14001.2.S1_at	pttg1ip	---	pituitary tumor-transformi	Transcribed sequence with	multicellular organismal c	---	---	---	---	---	0.0244	-1.59
Dr.19459.1.A1_at	zgc:162324	---	zgc:162324	Transcribed sequences	---	---	---	---	---	---	0.0073	-1.60
Dr.7806.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0186	-1.60
Dr.25688.1.A1_at	zgc:136936	---	zgc:136936	Transcribed sequences	---	---	---	---	zinc ion binding	---	0.0013	-1.61
Dr.14771.1.S1_at	foxo3a	---	forkhead box O3A	Clone RK137A2F09 prima	regulation of transcriptior	---	nucleus	---	DNA binding /// transcript	---	0.0039	-1.62
Dr.17180.1.A1_at	LOC795838	---	hypothetical protein LOC	Transcribed sequence with	---	---	---	---	---	---	0.0073	-1.63
Dr.9072.1.S1_at	cab39	---	calcium binding protein 3	MRNA similar to MO25 prc	---	---	---	---	binding	---	0.0004	-1.63
Dr.12838.1.A1_at	zgc:73336	zgc:73336	zgc:73336	hypothetical protein MGC7	visual perception	---	integral to membrane	---	---	---	0.0011	-1.63
Dr.25148.1.S1_at	amd1	zgc:55614	adenosylmethionine deca	similar to S-adenosylmethi	spermine biosynthetic pr	spermine biosynthesis ///	---	---	adenosylmethionine deca	adenosylmethionine decarboxylase a	0.0063	-1.63
Dr.26437.1.S1_at	atp1b2a	atp1b2a	ATPase, Na+/K+ transpo	ATPase, Na+/K+ transport	transport /// ion transport	potassium ion transport /	membrane attack comple	membrane	sodium:potassium-excha	sodium/potassium-exchanging ATPa	0.0520	-1.63
Dr.9906.1.S1_at	zgc:56548	zgc:56548	zgc:56548	similar to retinal degenerat	visual perception	---	integral to membrane	integral to membrane	---	---	0.0019	-1.64
Dr.5428.2.A1_at	LOC100000252 /// LOC5	id2	phosphoinositide-3-kinas	inhibitor of DNA binding 2,	intracellular signaling cas	---	phosphoinositide 3-kinas	---	protein binding /// kinase	---	0.0013	-1.64
Dr.24938.1.S1_a_at	---	zgc:66318	---	hypothetical protein MGC6	---	purine nucleotide biosynt	---	---	---	adenylosuccinate synthase activity //	0.0414	-1.64
Dr.14576.2.S1_at	zgc:112131	---	zgc:112131	Transcribed sequence with	---	---	cytoplasm	---	---	---	0.0064	-1.65
Dr.17137.1.S1_at	rorab	zgc:55954	RAR-related orphan rece	similar to RAR-related orpl	transcription /// transcripti	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0195	-1.67
Dr.11372.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0037	-1.67
Dr.5434.4.S1_at	LOC100000919 /// LOC1	---	parvalbumin 9 /// similar t	---	calcium ion transport	---	---	---	calcium channel activity /	---	0.0037	-1.68
Dr.12591.1.S1_at	gucy2f	---	guanylate cyclase 2F, ret	---	protein amino acid phosp	---	---	---	protein kinase activity /// p	---	0.0005	-1.68
Dr.14327.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0015	-1.70
Dr.7788.1.A1_at	LOC564852	---	similar to 6-phosphofruct	Transcribed sequence with	---	---	---	---	---	---	0.0005	-1.70
Dr.15036.1.S1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0178	-1.71
Dr.8103.1.S1_at	opn1mw4	opn1mw4	opsin 1 (cone pigments),	opsin 1 (cone pigments), n	signal transduction /// G-p	G-protein coupled recept	membrane attack comple	integral to membrane	rhodopsin-like receptor a	rhodopsin-like receptor activity /// G-p	0.0147	-1.71
Dr.26433.1.S1_at	clk4	wu:fb37c01	CDC-like kinase 4	wu:fb37c01	---	---	---	---	---	---	0.1034	-1.71
Dr.11161.1.A1_at	LOC569122	---	hypothetical LOC569122	Transcribed sequence with	---	---	---	---	---	---	0.0015	-1.72
Dr.6680.1.S1_at	zgc:55587	wu:fi34c11	zgc:55587	wu:fi34c11	protein amino acid phosp	protein amino acid phosp	---	---	nucleotide binding /// prot	protein kinase activity /// protein seri	0.0052	-1.73
Dr.26000.1.A1_at	grb10	---	growth factor receptor-bo	Transcribed sequence with	signal transduction /// intr	---	---	---	receptor activity /// protei	---	0.1093	-1.73
Dr.21065.1.S1_at	zgc:55965	zgc:55965	zgc:55965	wu:fj33d07	transport /// protein trans	---	cytoplasm	---	---	---	0.0005	-1.75
Dr.13864.1.S1_at	spata18	---	spermatogenesis associa	Transcribed sequences	multicellular organismal c	---	cytoplasm	---	---	---	0.0012	-1.76
Dr.9847.1.A1_at	pdc1	pdc1	phosducin 1	phosducin 1	---	---	---	---	---	---	0.0016	-1.77
Dr.12400.1.S1_at	atp1b2b	atp1b2b	ATPase, Na+/K+ transpo	ATPase, Na+/K+ transport	potassium ion transport /	potassium ion transport /	membrane	membrane	sodium:potassium-excha	sodium/potassium-exchanging ATPa	0.0061	-1.77
Dr.12730.1.A1_at	gpsm2	zgc:63574	G-protein signalling modu	hypothetical protein MGC6	signal transduction	signal transduction	---	---	GTPase activator activity	GTPase activator activity	0.0010	-1.78
Dr.14343.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0025	-1.80
Dr.9899.1.S1_at	gnat1	gnat1	guanine nucleotide bindir	guanine nucleotide binding	signal transduction /// G-p	G-protein coupled recept	---	---	nucleotide binding /// sigr	signal transducer activity /// GTP bin	0.0041	-1.82
Dr.539.1.S1_s_at	rx2	rx2	retinal homeobox gene 2	retinal homeobox gene 2	transcription /// transcripti	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0190	-1.83
Dr.6759.1.A1_at	wu:fb81c07	---	wu:fb81c07	Transcribed sequences	---	---	---	---	---	---	0.0234	-1.83
Dr.12454.1.S1_at	gchfr	zgc:73253	GTP cyclohydrolase I fee	hypothetical protein MGC7	negative regulation of bic	---	---	---	protein binding	---	0.0037	-1.83
Dr.4198.1.S1_at	mhc1ufa	mhc1ubal	major histocompatibility c	major histocompatibility co	immune response /// anti	immune response	membrane /// MHC class	membrane /// integral to r	---	---	0.0955	-1.83
Dr.11188.1.A1_at	---	---	Transcribed locus	Transcribed sequence with	---	---	---	---	---	---	0.0015	-1.86
Dr.11069.1.A1_at	zgc:77752	zgc:77752	zgc:77752	hypothetical protein MGC7	protein amino acid dephc	---	---	---	protein tyrosine phosphat	---	0.0008	-1.89
Dr.12863.1.A1_at	rnf144a	---	ring finger protein 144a	Transcribed sequence with	electron transport /// ubiq	---	membrane /// integral to r	---	protein binding /// zinc ior	---	0.0030	-1.91
Dr.11069.2.S1_at	zgc:77752	zgc:77752	zgc:77752	hypothetical protein MGC7	protein amino acid dephc	---	---	---	protein tyrosine phosphat	---	0.0029	-1.95
Dr.9972.1.S1_at	wu:fb71e04	env	wu:fb71e04	envelope protein	---	---	---	---	---	---	0.0014	-2.00
Dr.9908.1.A1_at	LOC557454	---	similar to ENSANGP000	Transcribed sequence with	---	---	---	---	---	---	0.0002	-2.14
Dr.9847.2.A1_at	pdc1	pdc1	Phosducin 1	phosducin 1	---	---	---	---	---	---	0.0021	-2.19
Dr.23271.1.A1_at	LOC100004884 /// LOC1	---	hypothetical protein LOC	Transcribed sequence	---	---	---	---	---	---	0.0017	-2.20
Dr.11234.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.0001	-2.21
Dr.26330.1.S1_at	gnb1l	---	guanine nucleotide bindir	MRNA similar to guanine n	signal transduction	---	---	---	signal transducer activity	---	0.0013	-2.22
Dr.9824.1.A1_at	LOC555324	---	hypothetical LOC555324	Transcribed sequences	---	---	---	---	---	---	0.0006	-2.26
Dr.17113.1.A1_a_at	ptena	zgc:73086	phosphatase and tensin l	wu:fc52g04	blood vessel developmer	---	---	---	protein tyrosine phosphat	---	0.0261	-2.27
Dr.25814.1.S1_at	LOC566570	---	similar to renal organic ar	Transcribed sequence with	---	---	---	---	---	---	0.0020	-2.30
Dr.24315.1.S1_at	ca7	zgc:73385	carbonic anhydrase VII	hypothetical protein MGC7	one-carbon compound m	one-carbon compound m	---	---	carbonate dehydratase a	carbonate dehydratase activity /// zin	0.0081	-2.35
Dr.12789.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---	0.0001	-2.36
Dr.538.1.S1_at	LOC567374 /// rx1	rx1	retinal homeobox gene 1	retinal homeobox gene 1	transcription /// transcripti	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0003	-2.41
Dr.14334.1.A1_at	---	---	---	---	---	---	---	---	---	---	0.0036	-2.41
Dr.12479.1.A1_at	LOC798660	---	hypothetical protein LOC	Transcribed sequences	---	---	---	---	---	---	0.0005	-2.43
Dr.9894.1.A1_at	wu:fk56b02	---	wu:fk56b02	Transcribed sequences	---	---	---	---	---	---	0.0003	-2.50
Dr.2863.1.A1_at	slc25a25	---	solute carrier family 25 (r	CDNA clone MGC:77454 I	transport	---	membrane attack comple	---	transporter activity /// bin	---	0.0001	-2.51
Dr.7714.1.S1_at	erm	erm	ets related protein erm	ets related protein erm	regulation of transcriptior	regulation of transcriptior	nucleus	nucleus	DNA binding /// transcript	DNA binding /// transcription factor a	0.0000	-2.56
Dr.23223.1.A1_at	---	---	---	Transcribed sequence with	---	---	---	---	---	---	0.0000	-2.63

Dr.9851.1.A1_at	---	---	Transcribed locus	Transcribed sequences	---	---	---	---	---	---	0.0005	-2.74
Dr.4119.1.S1_at	guca1b	guca1b	guanylate cyclase activat	guanylate cyclase activato	calcium ion transport	---	---	---	calcium channel activity /	calcium ion binding	0.0001	-2.76
Dr.20008.3.A1_at	gnb1	gnb1	guanine nucleotide bindi	guanine nucleotide binding	signal transduction	---	---	---	signal transducer activity	---	0.0107	-3.00
Dr.12836.1.S1_at	id2b	zgc:73382	inhibitor of DNA binding 2	hm:zeh0152	regulation of transcriptio	carbohydrate metabolis	nucleus	---	DNA binding /// transcript	DNA binding /// hydrolase activity, hy	0.0000	-3.00
Dr.12836.2.A1_at	id2b	zgc:73382	inhibitor of DNA binding 2	hm:zeh0152	regulation of transcriptio	carbohydrate metabolis	nucleus	---	DNA binding /// transcript	DNA binding /// hydrolase activity, hy	0.0000	-3.10
Dr.9853.1.A1_at	pde6a	---	phosphodiesterase 6A, c	Transcribed sequence with	signal transduction	---	---	---	catalytic activity /// 3',5'-c	---	0.0013	-3.24
Dr.11183.1.A1_at	---	---	---	Transcribed sequences	---	---	---	---	---	---	0.0001	-3.26
Dr.9912.1.A1_at	wu:fk57g06	---	wu:fk57g06	Transcribed sequences	---	---	---	---	---	---	0.0000	-4.06



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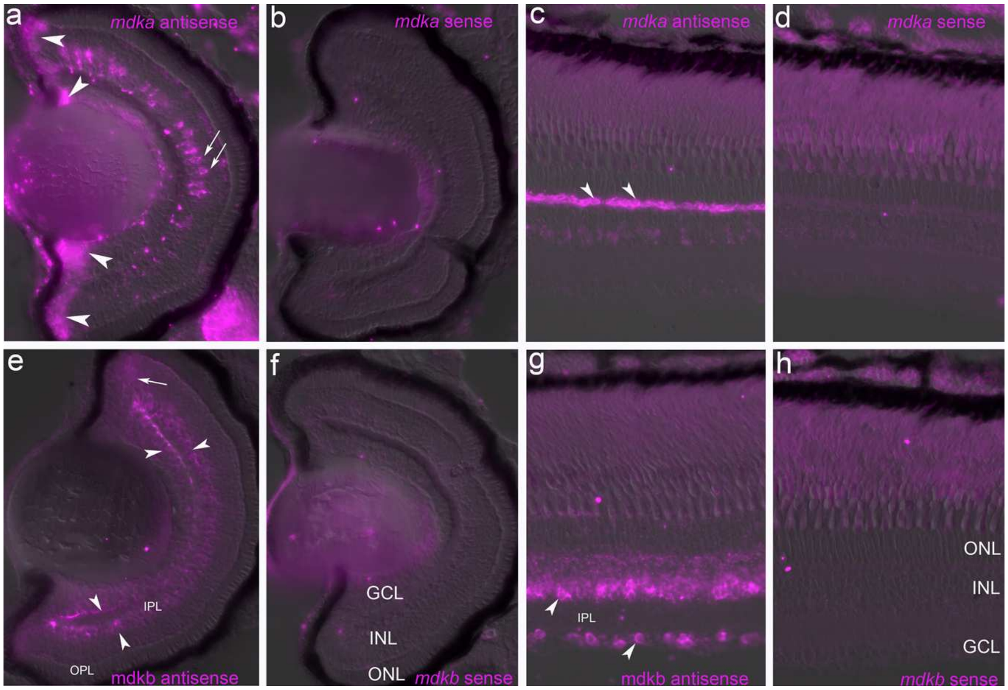

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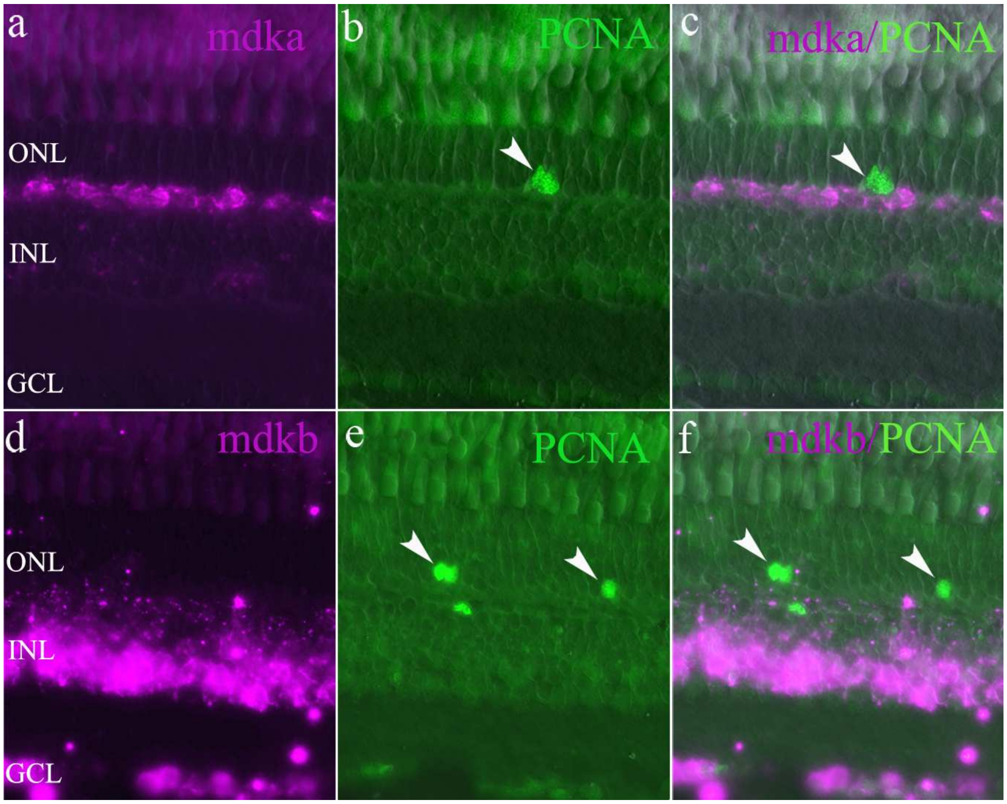

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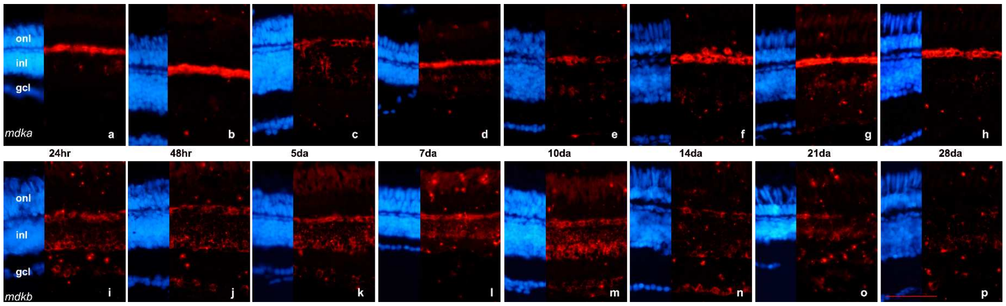

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